Library Number	RMK006
Library Name	Inborn Errors of Metabolism Library - IEM (All)
Old Document Name	IEM (All) Library (Andrew)
Library Purpose	CRISPR/Cas9 Knockout of genes associated with Inborn Errors of Metabolism in mouse T cells. Genes were identified from IEMBase.org as it stood in early 2019.
Location	Main Lab, '-20 Freezer, IEM (All) box
Designer Name	Andrew Patterson
Designing Date	January 2019
Design Reference	Ferreira 2018, Genetics in Medicine; IEMBase
Usage Reference	n/a
Species	Mouse (Mus musculus)
Total Gene #	1038
Total Target #	4194
Gene Group	
1. Negative Controls	(Nontargeting controls from BRIE library)42
2. Positive Controls	n/a
3. IEM Genes	1038
Target Number	
1. Negative Controls	42*1=42
2. Positive Controls	n/a
3. IEM Genes	1038*4=4152

Note: The Inborn Errors of Metabolism Genes Library was designed from genes that cause IEM when mutated as identified in IEMBase.org in 2019 (DOI: 10.1038/s41436-018-0022-8). Genes without mouse orthologs, mitochondrial DNA-encoded genes, genes encoding noncoding RNAs, and genes without guides in either the BRIE or Gecko libraries were excluded. 42 NTCs (~1%) were added from the BRIE library controls. This brings total # of guides to 4194 guides. Available in GFP and BFP vectors.

Number	**Genes**	**Guide sequence**
1	Abca1	ACATGTCATCAACATAACAG
2	Abca1	GTGGACCCGTACTCTCGCAG
3	Abca1	CAAGCTGTCAAGCAACACTG
4	Abca1	GGTATACACAGAGCCATTTG
5	Abcb7	GATTAAATACTAACGCACTG
6	Abcb7	CGCTGGGACGAACTCCATCG
7	Abcb7	ACAGTTACTAGATGCTACAA
8	Abcb7	TCACAGTTGCAGTTACACGG
9	Acadl	AGGCGATCGAGCTTCACGGT
10	Acadl	AGAGCGTACTCCAATTGCAC
11	Acadl	AACATCGCAGAGAAACATGG
12	Acadl	CCGGAAAATGTCATGCTCCG
13	Acadm	AAGATGTGGATAACCAACGG
14	Acadm	CCCGGAATATGACAAAAGCG
15	Acadm	TCGAACACAACACTCGAAAG
16	Acadm	AGCAGGTTTCAAGATCGCAA
17	Acadvl	CAAAGCATCTAACACGTCAG
18	Acadvl	CAACAACGGAAGATTCGGGA
19	Acadvl	GCTACATCGGATCCACTCGA
20	Acadvl	CCAGCGACTTTATGCCAGGG
21	Acads	GGTGACTCATGGGTCCTCAA
22	Acads	GCTCATGATAACTCCCGTGG
23	Acads	GATGGGCTTCAAAATAGCCA
24	Acads	GCTCACCCATCTTCTTAACC
25	Slc33a1	GTGACTTACCTAAAGCCCCG
26	Slc33a1	ATGTTATCCCGGGAAAACGT
27	Slc33a1	GAAAGGGTAACGATTCCCCT
28	Slc33a1	AAATATTGATGGCAGAACAC
29	Aco2	AGATCCGTGCCACTATTGAG
30	Aco2	GCGTTTACGGCCCGACCGGG
31	Aco2	TGGGTGAGGTCCAACCAGAG
32	Aco2	GATTGAAATTAACCTCAATG
33	Acox1	CGATCCAGACTTCCAACATG
34	Acox1	AATGTCGGATGGCTTGCGGT
35	Acox1	CCTCACAGCACTGTATCGAA
36	Acox1	TCTCTTCATAACCAAACTTG
37	Aspa	ATTCATTACCAATCCAAGGG
38	Aspa	AGTGCAACCCATGTTAGAAG
39	Aspa	ACCAACAGGATACTTGGCAA
40	Aspa	CTTGCCATATGAAGTGAGAA
41	Ada	GTTGTGGATCTTGTGAACCA
42	Ada	ATTCATCGGACCGTCCACGC
43	Ada	CTTCATCTCCACAAACTCGT
44	Ada	GCTGCGCAACATTATCGGCA

Number	Genes	Guide sequence
45	Adk	TGTGCTGCGTGTATCACTGG
46	Adk	CACTTTCAATACCGACTCTG
47	Adk	ATAAGGCATGACGTCCATCA
48	Adk	CATTGGGATAGATAAGTTTG
49	Adsl	AAAGTGTGTGAAACCTAACG
50	Adsl	CCAGTGCGATGCCGTACAAG
51	Adsl	GCTGCGGGCATTATTCATCT
52	Adsl	TCACAGGACAGACGTACACA
53	Aga	CCAGATCCCTCAAAATACTG
54	Aga	AGGCCAAGTGTTGACGACCA
55	Aga	TGGTGGACATTGCTATCTGG
56	Aga	ATGGATTACAACCATGCCTA
57	Gla	CTAAACTCACGTAATTTGCG
58	Gla	CATAGGATCCAAAACTCCCG
59	Gla	TCATACAGGTTATAAGTACA
60	Gla	CATTGGACAATGGCTTGGCG
61	Agxt	AGCCCCTGTCAGTTCCTACG
62	Agxt	AGAACATTATACACTGCAGG
63	Agxt	ACATACTTGGCCAAATTGTG
64	Agxt	GTAGATAGGAACCCCGCCCA
65	Aicda	GTAGGAACAACAATTCCACG
66	Aicda	TTCACAGAAGTAGAGGCGCG
67	Aicda	ACCAGGTGACGCGGTAACAC
68	Aicda	TGAGACCTACCTCTGCTACG
69	Ak1	CTACACCCACCTGTCTACTG
70	Ak1	GATCGACGGCTACCCGAGGG
71	Ak1	GTCAGCTCTGGATCGGAGAG
72	Ak1	CTTTGGCTAACATAGCATCT
73	Ak2	TGAAGGCGACAATGGATGCA
74	Ak2	GGTAGGACCGGCCACTCTTG
75	Ak2	TCCGAACCGGAGATTCCGAA
76	Ak2	TCAGCCAGTTTGGGTGCCTG
77	Alpl	GGATAACGAGATGCCACCAG
78	Alpl	CTAGGAGGCAGGATTGACCA
79	Alpl	ACCTAAGAGGTAGTCCACCC
80	Alpl	GTTGCATCGCGTGCGCTCTG
81	Akt2	CATACTCCATCACAAAGCAT
82	Akt2	TACAGAGAAATTGTTCAGGG
83	Akt2	TGTGGTGTACCGTGACATCA
84	Akt2	AGTGGACCACAGTCATCGAG
85	Alas2	ATCCAAGGCATTCGCAACAG
86	Alas2	ACATCACACAATTCCTCCAG
87	Alas2	AATACTAAATAGGAACTGGT
88	Alas2	AGGTACCAGCAAGTTTCATG

Number	**Genes**	**Guide sequence**
89	Aldh3a2	CTGTATGCGATTGTTAATGG
90	Aldh3a2	GGAAATCTTAGCAGCCATCG
91	Aldh3a2	AGTCTCTGTCAATGTAACAA
92	Aldh3a2	TCTGGAGGGAGGCTTCGCAC
93	Aldoa	AATGGCGAGACAACTACCCA
94	Aldoa	CCTTGCCCGGAGCCACAATG
95	Aldoa	CCACGAGACACTGTACCAGA
96	Aldoa	GCCAGCATCTGCCAGCAGGT
97	Gfer	AGAATTGGGTCGCCACACCT
98	Gfer	ACGACCTGGTGACTGACGCG
99	Gfer	CCTGCGTGGACTTCAAGTCG
100	Gfer	TTCCCGTGCTCCAAACCTTG
101	Ampd3	TACCTGGTTCGCATGCACGG
102	Ampd3	GTCCTCGGGGACAGTAAACA
103	Ampd3	TGATCCGGGAGAAGTATGCA
104	Ampd3	AGTAGCTCCGGGAACCAGAG
105	Mat1a	ACAGGTATGGTGCTACTGTG
106	Mat1a	CTATGCTACTGATGAGACCG
107	Mat1a	GTGTTGCACAGAGATGACGA
108	Mat1a	GACACATTGGGCAATATCTG
109	Slc25a4	CAGTTTGACCCTCTCGATCG
110	Slc25a4	GGAAGATCCCTTGCCCACGT
111	Slc25a4	TTGTGTCGTGAGAATCCCCA
112	Slc25a4	GGGGAAGTACCGGATCACGT
113	Ap1s1	CCAAGAGCTCTACGTATCGG
114	Ap1s1	GAGCTCTTGGACAAGTACTT
115	Ap1s1	TCAGCCGGCAGGGAAAACTT
116	Ap1s1	TGGCCACCTCAGACAAGGAG
117	Atg5	AAGAGTCAGCTATTTGACGT
118	Atg5	AAATGTACTGTGATGTTCCA
119	Atg5	CCTTCTACACTGTCCATCCA
120	Atg5	AAGAAAAACTCACCATTTCA
121	Apoa1	GGAGCTCTACCGCCAGAAGG
122	Apoa1	CAAGGAGGAGGATTCAAACT
123	Apoa1	GTCCCAATGGGACAAAGTGA
124	Apoa1	CTGGAAAACTGGGACACTCT
125	Apoc2	AAGTTACTGGACCTCTGCCA
126	Apoc2	AGAGGTCCAGTAACTTAAGA
127	Apoc2	GGGAACCAGGAAGATGACTC
128	Apoc2	GAAGACATACCCGATCAGCA
129	Apoc3	GCAGGAGTCCGATATAGCTG
130	Apoc3	CATGGAACAAGCCTCCAAGA
131	Apoc3	GGATGCGCTAAGTAGCGTGC
132	Apoc3	GCCCCGGACGCTCCTCACTG

Number	Genes	Guide sequence
133	Aprt	GAGTCCGGGTCTTTCAAGAG
134	Aprt	CTAACAGGTCTAGACTCCAG
135	Aprt	TGTGTGCTCATCCGGAAACA
136	Aprt	CGCACCTGAACAGCACGCCC
137	Aqp7	GCCACTCACCATCATGACAT
138	Aqp7	AGTCACTGCGGCATTCATGT
139	Aqp7	ACACCCCAAGGACGGTAACA
140	Aqp7	TTCCTGAATACATGACACTG
141	Ar	GGTGGAAAGTAATAGTCGAT
142	Ar	ACCAGGATACCACACTTCGG
143	Ar	GACTTGGGTAGTCTACATGG
144	Ar	GCTCCTGGGAGGTCCACCCG
145	Arg1	AATAAACTTACTGTTCCCCA
146	Arg1	AGTATGACGTGAGAGACCAC
147	Arg1	AAATGACACATAGGTCAGGG
148	Arg1	AGATGTACCAGGATTCTCCT
149	Arsb	GGTGGGCAGACTAGGTCTGG
150	Arsb	GAATGTCTGCCGACACGCCG
151	Arsb	AGCACAGACGTATTTATGCA
152	Arsb	GCCAGCACGAAGACCACATG
153	Arsa	AAGCACGTTAGGTTCTGACA
154	Arsa	AGGAGTCCCCAAATGGCCCA
155	Arsa	GTGACCTGGCCAGTAGACCA
156	Arsa	TCGGGAGAAAGACACATACC
157	Asah1	GCAAGGTGTACGTTACCTAG
158	Asah1	TAACATTTATAACATACCGC
159	Asah1	AGTGATAAACCCTACCCACT
160	Asah1	GAATATAAATAATAACACTT
161	Ass1	TAACATCTTACCTTAATCTG
162	Ass1	TGGGATCCTGGAAAACCCCA
163	Ass1	AAGGCACTTCCTCACCAGGT
164	Ass1	TGCCTTCACCTGTAGCAACA
165	Fxyd2	ACCGGCTTACCGTACTCGAA
166	Fxyd2	TATGAAACCGTCCGCAAAGG
167	Fxyd2	GATGAGGAGGCCCACGACGA
168	Fxyd2	CCCACTTACTGAGAATGATG
169	Atp6v1a	TGACTGCTGATATCCGACAG
170	Atp6v1a	AGTCGGCCATCATACTGACG
171	Atp6v1a	ATGTTGCCCCCACGTAACAG
172	Atp6v1a	CTTACGGGAAAAGGGCATCG
173	Atp6v1e1	CCAACTTGATGAATCAAGCA
174	Atp6v1e1	TTTGTAGGATCTGCTAAATG
175	Atp6v1e1	TCAGTCTTTGCGTTTGCACA
176	Atp6v1e1	AGGCATCCAAGCATACCTGA

Number	**Genes**	**Guide sequence**
177	Atp7a	TCTATAGGGCAAAACCTCCG
178	Atp7a	ACACGGTATTGGTTAAGACA
179	Atp7a	CAATTATAATCCACACCAAG
180	Atp7a	AGGGATCTTCTACTGCTCTG
181	Atp7b	AAATATAGGCCAACTCCCGG
182	Atp7b	AAAATGGCTCCCGACACTAG
183	Atp7b	AGTTGTGTCATTACCCACAT
184	Atp7b	AGACCATCAATCCCATGACG
185	Slc7a2	AGGACGTCACTATTCCGATG
186	Slc7a2	GAACGGAACAAGCATCTACG
187	Slc7a2	GTATCTATACACTTACGTCA
188	Slc7a2	CCGAGACAACATATTTGGCG
189	Auh	CAATGTCATTGATCACCGAT
190	Auh	GGTTTAGTTATCAAAAGCGG
191	Auh	GAGGAGGGGCTACAGCTCGG
192	Auh	CCCTCCCTAACCAGGCATTG
193	Baat	AGGACCAGAAAAGGCCCATG
194	Baat	AGGCCCATTGATAAGTACAG
195	Baat	GTAAAGGAAAGCCGCATCCG
196	Baat	AAGGCACACCACCTGAAAGG
197	Bcat2	ACGGAACGAGCCTCTACGTG
198	Bcat2	CAGGAACTATGGACCCACTG
199	Bcat2	GTGGAGTGGAATAACAAGGC
200	Bcat2	GCACAGAATGACGTACAGGA
201	Bckdha	CATGACCAACTATGGCGAGG
202	Bckdha	CAGCGAAATTGAAACCGGCG
203	Bckdha	CTTGTCTACAAACTCTGCAG
204	Bckdha	CTGGCCACGCAGATCCCTCA
205	Bckdk	ACAGCACGAGCTATACATCC
206	Bckdk	AGTCCGCATCAACGGACATG
207	Bckdk	GCGACCGGAATAGAGCATCA
208	Bckdk	TGTCTTCATGTAGCGCCAAG
209	Glb1	GCGTAGGTAGTCGTAATCGC
210	Glb1	CTTCCCGAGATGTATCGGAA
211	Glb1	GGGTACTCACAAGTTCACGT
212	Glb1	GCAGGACCTGTACGCCACAG
213	Blk	TTATTACAAAAATAACATGA
214	Blk	ACTTGAATAGTGCTGCACCA
215	Blk	CGTGAAAGATATCACCACCC
216	Blk	AAGGTCCCTGTCATTCACAG
217	C1qbp	ATCAGTCAAGAATTCAACGA
218	C1qbp	CGTACGCTGAGCAAACCGAA
219	C1qbp	GTTGAAGTTACCAAGACTGA
220	C1qbp	TCCTCCTCACCATCAAATGT

Number	Genes	Guide sequence
221	Cat	AACTTAATATCATGACCGCG
222	Cat	TGGCATTGAAAAGATCTCGG
223	Cat	GGAGTATCTGGTGATATCGT
224	Cat	AGTGACCGAGGGATTCCCGA
225	Cbs	ACACTACGATGACACCGCCG
226	Cbs	TCGCCATGCCACTCCCACGT
227	Cbs	GTGAGTTCTTCAATGCGGGT
228	Cbs	ATAATGTGGGGAGTCCGCCA
229	Scarb2	ATAGAACAGGCCGAAATTCG
230	Scarb2	AAATAAAACTGGATGTACAC
231	Scarb2	AATATGATTAACGGGACAGA
232	Scarb2	ATAATGACACGTACCAACAG
233	Chkb	ATGGTCCCAAACAACCATCG
234	Chkb	GGTGCTGCTACGACTCTACG
235	Chkb	CGTGGTTCGGTAGTGAGCAT
236	Chkb	CAGAGCCAATCCCCAATCGG
237	Tpp1	TGAGTTTCATCGCTATGTAG
238	Tpp1	TTATGGTAGAAGGTTACCTG
239	Tpp1	AACCTGACAGCCAAAGATGT
240	Tpp1	GATCGAGGCCAGTCTAGATG
241	Cln3	ACACTCCGACTATCCAACCG
242	Cln3	AATCGAGATGAGCTGTTGTG
243	Cln3	GGACCCTGGAGGGGAAAACG
244	Cln3	CAGGAGTTTGATGACAAGGG
245	Abcc2	AAGACCCTGACTCATATCCG
246	Abcc2	GCATTCGGAAGAAAGAACTC
247	Abcc2	ACTCGGATCTTGGTTACACA
248	Abcc2	GTTTAAGACGATCATGACAA
249	Cox6a1	TGAGGGTAGGCAACGAACGG
250	Cox6a1	CCGTGGGCGCCACTCGACAT
251	Cox6a1	CGCCGCAGCTCGGATGTGGA
252	Cox6a1	TCAACGTGTTCCTCAAGTCG
253	Cox8a	GCCTGACCGGCTCGGCCCGG
254	Cox8a	TTCGAGTGGACCTGAGCCCG
255	Cox8a	TCTGTGTAGGATATCACCAT
256	Cox8a	GCTCCCGCGCCGGCTTCGAG
257	Cp	CATATAAGCATCAATTAGGG
258	Cp	GCTGTGAGGAGCGACCTGGT
259	Cp	ATGAAAAGTGTAGATCCTAG
260	Cp	GCTGAACAAATACCACACGA
261	Cpox	TGGGCGCATAAGGATTCTTG
262	Cpox	GAAGCAGCGAACCAAATGAG
263	Cpox	ACCGACATACTTGAACCAAG
264	Cpox	CGGACCCGCCTCTAGCCCAG

Number	**Genes**	**Guide sequence**
265	Cpt1a	CACATTGTCGTGTACCACAG
266	Cpt1a	CATACTGCTGTATCGTCGCA
267	Cpt1a	ACCTTGGACCCAAATTGCAG
268	Cpt1a	ACGTTGGACGAATCGGAACA
269	Cpt2	TCACTGGTCAAATAAGCCAG
270	Cpt2	TCGGGAAGTCATCTAAGCAG
271	Cpt2	AAATATTGGGACATATCCAG
272	Cpt2	TTAAATACATATCAAACCAG
273	Crat	ACCACCCACGCATATAACCG
274	Crat	GCAGGCCAGATGCTACATGG
275	Crat	TCCACAAGTGCAACTATGGG
276	Crat	TTTGCTGCCAAACTCATCGA
277	Pcyt1a	AATACGTATCTAATTGTGGG
278	Pcyt1a	ATGCAAGACGGAACCTACAG
279	Pcyt1a	GCACCACCTCGTCCACGTAG
280	Pcyt1a	CTTTAGTAAGCCCTATGTCA
281	Ctsc	CTGCAAGATACAACCTCCTG
282	Ctsc	GGCAGTAACTGATAGCTGTG
283	Ctsc	TCACAACCACAACTTTGTGA
284	Ctsc	CTGTATTTCATCAGTCATCG
285	Ctsd	TATCCGTCGGACTATGACGG
286	Ctsd	TGACTCCAAGTACTACCACG
287	Ctsd	GACTGTGAAACACTGCGGCG
288	Ctsd	ACGTCCTTTGACATCCACTA
289	Ctsk	AAGTTGTATGTATAACGCCA
290	Ctsk	CACTCTCTATACCCCAGAGT
291	Ctsk	CAATACGTGCAGCAGAACGG
292	Ctsk	AAGCCCAACAGGAACCACAC
293	Cyb561	ATGCCTATGACCATGCAGAG
294	Cyb561	GCACGACCAAGATCTTGCAT
295	Cyb561	TGCTGCACTGCCGTACTATG
296	Cyb561	GTTCAGGAACTCACCCACCA
297	Cycs	TCTTCCGCCCGAACAGACCG
298	Cycs	TTCTGTTTAGGCATCACCTG
299	Cycs	GTTCGGGCGGAAGACAGGCC
300	Cycs	CTGGGGAGAGGATACCCTGA
301	Cyp11a1	AGAGTATCGACGCATCCTTG
302	Cyp11a1	GTATTATCAGAGGCCCATTG
303	Cyp11a1	GGACCTAGGACTGCTAGTAG
304	Cyp11a1	CCTTACACTCAAAGGAAAAG
305	Cyp11b2	TGGAGAGTATGCTCCCCCGT
306	Cyp11b2	GACCGTGTCAACGCTCCCAG
307	Cyp11b2	AGGTGCTTCAAAATGCTCGT
308	Cyp11b2	TTCCGCCACAATGCCACTGT

Number	Genes	Guide sequence
309	Cyp17a1	GGAGCTACTACTATCCGCAA
310	Cyp17a1	AAACGGTAGACTACCCACCA
311	Cyp17a1	TAAAATTCGAGAAAAAACAC
312	Cyp17a1	TACCATACAGACCTTTACAG
313	Cyp19a1	AGTGACCGACATGGTGTCAG
314	Cyp19a1	AAGGGCGAATTGTTCTCCAA
315	Cyp19a1	GAGAGCTCGTCTTCAATACC
316	Cyp19a1	CCATCAAGCAGCATTTGGAC
317	Cyp24a1	TTCGTTGCGATGGTCCCGAT
318	Cyp24a1	CTTGCTGATAAATATCACAA
319	Cyp24a1	AGCGCCTCAACACCAAAGTG
320	Cyp24a1	GCTGGACAAGAAAATCAATG
321	Cyp27b1	GAGAGCGTATTGGATACCTG
322	Cyp27b1	TGCGACGACTAAGGCGCCAG
323	Cyp27b1	CTCAGGTGCATGGCGCTGCG
324	Cyp27b1	TTAGCAATCCGCAAGCACGC
325	Cyp7a1	GGTGAACCTCCTTTGGACAA
326	Cyp7a1	TTTGATTTAGGAAGGCCCGG
327	Cyp7a1	AGTATTTCCGGCACTAGTGG
328	Cyp7a1	AGCACAAGAACCTGTACATG
329	Cyp7b1	GTATGTCAGATACTAAGTAT
330	Cyp7b1	ACTGTCAATTTCGTCACGCA
331	Cyp7b1	TTTATCAAGGGTGGTTCACG
332	Cyp7b1	AGCAGAGCTTCTTACCCACA
333	Slc6a3	TAGATGATGAAGATCAACCC
334	Slc6a3	GCTCGTCAGGGAGTTAATGG
335	Slc6a3	CAGGGAGGGTGACTCCACGC
336	Slc6a3	TTACTCAAAATACTCAGCAG
337	Dbh	AGTGATATAGCACCAGTACG
338	Dbh	AACTTCCAGTCGGAGAAACG
339	Dbh	AGAGCTCTAAAATCCCTTCG
340	Dbh	CGTGCCGGCAGTAGTTGAGT
341	Dbt	TAGATGATATCGCTTATGTG
342	Dbt	TCATCACAATACCCGAAGTG
343	Dbt	CTGTGAAGTTCAAAGTGACA
344	Dbt	TGGAGGCTTTGCTATCGGCG
345	Pcbd1	AGCTGGACCACCATCCCGAG
346	Pcbd1	ACTGCTTGAAGATAGCATCT
347	Pcbd1	GGCACACAGGCTGAGCGCCG
348	Pcbd1	TGCCAAACCTGAGGGCTGTG
349	Ddc	CCTAGGTGGTCGCTACACTG
350	Ddc	TAACCCAGCTCTTTCTACAG
351	Ddc	CCGGTATCTTCTGAATGGTG
352	Ddc	AGCCAGTAGGGCCACCAAGG

Number	Genes	Guide sequence
353	Ddost	GAACTCCCCGTACTTAATGA
354	Ddost	CCCAGATAAACCAATCACCC
355	Ddost	AGGCAACTATGAACTAGCTG
356	Ddost	GGTCAGAAACATCATAGTTG
357	Dgat1	AGTGGTTTCAGCAATTATCG
358	Dgat1	AAAGCGCTTTCGTATTCGGG
359	Dgat1	ATACCCGGGACAAAGACGGG
360	Dgat1	GCTCACCAATAATCACGCAT
361	Slc25a1	ATGAACGAGCGAACCCACCG
362	Slc25a1	GAATAATCTCTCTAACCCCG
363	Slc25a1	ACTGCGACTGTACTGAAGCA
364	Slc25a1	CTTCACGTATTCGGTCGGGA
365	Dhcr7	CTGTAGCTATATCCAATGCG
366	Dhcr7	TGTTCTTCAATGGACGACCA
367	Dhcr7	GCCCTTGATCATTGCGAACG
368	Dhcr7	AGCCTAGGTACCACCCAAAG
369	Dhfr	GACATGGTTTGGATAGTCGG
370	Dhfr	AACCTCAGAGAACCACCACG
371	Dhfr	TCGCCGTGTCCCAAAATATG
372	Dhfr	CAGCCCGGCCAATACCTGAG
373	Dld	GGTGGAACATGCTTGAACGT
374	Dld	GCAGTAAAAGCATTAACAGG
375	Dld	AGAGAAGCTGGTTGTTATTG
376	Dld	CAAAAACATCCTTGTAGCTA
377	Dpagt1	CTTTGGCAATACAACCATCG
378	Dpagt1	TCCTGTACTACGTCTACATG
379	Dpagt1	CATGCCCGCAAAGTAACAGA
380	Dpagt1	AGCACCGCTGATCACTCCCT
381	Dpm1	ATGGAATCAAACACGCCACG
382	Dpm1	TCTCTGGAACTCGATACAAG
383	Dpm1	TGATTAATTTGGCAGCCGTG
384	Dpm1	GAGAAGCCCCTTCTACCTCT
385	Dpm2	TGATCAAGCTAACGGCGACA
386	Dpm2	CTTCACCTACTACACCACTT
387	Dpm2	ACCGGGACAGACCAAGCAGT
388	Dpm2	ACATGCTGGCTGTCAATGAA
389	Slc26a2	GAGCCGACACCATGACTCCG
390	Slc26a2	ATGGCCGGAGAGCTTTCCGT
391	Slc26a2	ACTGTGCCTTATGATTGGTG
392	Slc26a2	TCCAAAATGAGAAGCCAATG
393	Ebp	GAAAGGCAATCACTACCCAT
394	Ebp	GGGGCCTAATTGTGATCACG
395	Ebp	CCAGGATATGCGAAGTCGGG
396	Ebp	AAGCTGTAGGACAAAGCGGA

Number	Genes	Guide sequence
397	Egf	TCACCGTAACAGATATGACA
398	Egf	AGACTGTTCTGGACGGACGT
399	Egf	TGTTCATCGCCTGACAATGG
400	Egf	GTGTCACAAAGGATGGATGG
401	Eno3	AGCCGGTTACCCGGACAAGG
402	Eno3	GAGACAAAGCACGATACCTG
403	Eno3	CTTCCAGAAACTAAGTGTTG
404	Eno3	CTGCAAGATCTGCGATGTGT
405	Ephx1	CAGAAGTTCTACATTCAAGG
406	Ephx1	TGGAAGCGACTGCCCTCCAA
407	Ephx1	CCCCACCACCCATCTTCAAG
408	Ephx1	GGAGGAATGAGTTTGACTGG
409	Epm2a	TGTACCAGAACGTGTCAACG
410	Epm2a	CCGTTGCTGCACATATAATG
411	Epm2a	GCCCGGCCTGTGGCTCGCCG
412	Epm2a	GTCACATGTTCCAGTTGGCG
413	Esr1	GGCATACGGAAAGACCGCCG
414	Esr1	CACTGTGTTCAACTACCCCG
415	Esr1	TATTCAGAATAGATCATGGG
416	Esr1	AGAGGCATAGTCATTGCACA
417	Esr2	TGGCGCTTGGACTAGTAACA
418	Esr2	TTCGTGACGGCTCTCTACAT
419	Esr2	GAAGTAGGAATGGTCAAGTG
420	Esr2	CGGCTCACTAGCACATTGGG
421	Ext1	CTTATATCACGTCCATAACG
422	Ext1	GATTGTATTAACTACACTAG
423	Ext1	CTGACTACACTGAGGACGTG
424	Ext1	CAAAGGCAAGAAGTGCCGCA
425	Ext2	TGTTTCGATGTCTACCGCTG
426	Ext2	CTGGAGGACTCAATGGAGTG
427	Ext2	TCCTGCAGAACATCCCACAG
428	Ext2	AGGGCAGTGTTGTAATCTGG
429	Fah	CCCCGATTCGAAGACCCATG
430	Fah	CCGATGGCTACACCAATCCG
431	Fah	ACATCAACATGTCTTCGATG
432	Fah	AATGGGAGTACGTCCCACTT
433	Fbp1	CATGGCAAGGACCAACATGG
434	Fbp1	CACAAGAACACAGGTAGCGT
435	Fbp1	TGGCTCAACCAATGTGACTG
436	Fbp1	AACATCTACAGCCTTAATGA
437	Fdxr	CCAGAAAACAGACATCACAG
438	Fdxr	TCCATTGTACCAGCCCACAA
439	Fdxr	GCTTCTCGTAGATGTCTACG
440	Fdxr	CAGATGTCCCCCGTCCAAGG

Number	Genes	Guide sequence
441	Fech	CATTTACAGATACTATAACG
442	Fech	CGTACTTACAGACATCGGCA
443	Fech	GGCATGATGTACCTTCTCCG
444	Fech	GGCATATTGATGTTAAACAT
445	Lpin1	GGGGGTACGTTGAAATCGAG
446	Lpin1	CAGTCGCCAACAATGGCCCG
447	Lpin1	GACCACAGAGAGATCACCAA
448	Lpin1	CCATTTAAAACAGGCCACTG
449	Folr1	GACAATTTACACGACCAGGT
450	Folr1	AGTTCGGGGAACACTCATAG
451	Folr1	CCAGTTGAACCGGTACAGGT
452	Folr1	CTCCACCTACTCCTTACCCG
453	Fxn	AGGGAACCGATCGTAACCTG
454	Fxn	CGAAGCGCGTACTCACGGCG
455	Fxn	GCGCGGGTTCCCGACCCAGG
456	Fxn	TGGGGACATTGGACAACCCA
457	Ftcd	CAGGTTAAGAGCAATACGGT
458	Ftcd	CCGAACAAAACCGCGCAGTG
459	Ftcd	GCACTGTCTACACTTTCGTG
460	Ftcd	CACAGCTCAAACAGGCCGAG
461	Fth1	CACCATAGACAGATAGACGT
462	Fth1	AGTGCGCCAGAACTACCACC
463	Fth1	GGAGAGCGGGCTGAATGCAA
464	Fth1	TCTTCAGAGCCACATCATCT
465	Ganab	GATAAAGTTAGTCTCGCGCT
466	Ganab	CAGACCCATATAGAGCCATG
467	Ganab	AAGTCCAAACCTACAGACGT
468	Ganab	ACTCGGTATCGAGGCCGCCG
469	G6pc	GGTGTTTGAACGTCATCTTG
470	G6pc	GTTGTCCAAACAGAATCCTG
471	G6pc	GGTCAGCAATCACAGACACA
472	G6pc	ACAAGACTCCAGCCACGACC
473	Slc37a4	CTACGTTGACCAGACCAACC
474	Slc37a4	TCTTTACTCCGAAGACCACG
475	Slc37a4	CACAAACTTGCTGATGGCGT
476	Slc37a4	CAGAGCGATCTCATCCACCA
477	Gaa	ACCATCCCCACTTTACAGCG
478	Gaa	GAGTTACAGGCCCTACGACG
479	Gaa	CTAACCTGGAGGTCAACGGG
480	Gaa	ACCTGAGCTCTACAGAGTCG
481	Gabra1	CAGAGAGCCAGCCCGTTCAG
482	Gabra1	CAGTGTCACTTACCATATCG
483	Gabra1	AGAATAACTGTCATTATGCA
484	Gabra1	ACGCAGGAGCTTATTAGGCA

Number	Genes	Guide sequence
485	Gabra6	GGAAGTTAACCAATCTCATG
486	Gabra6	GGGACTTCTACTGAGTAAAG
487	Gabra6	TCTACTCTGAAAATGTCAGT
488	Gabra6	TTAAGCTCAGAATCTCAGCA
489	Gabrb1	TCTGTCCACAGGAATCACTA
490	Gabrb1	CACTTCAGATGGCTATACCA
491	Gabrb1	ATAGTCGTGGATATGCCCCT
492	Gabrb1	CAAGAAATCATTTGTGCATG
493	Gabrb2	ATGATTCGATTGCATCCCGA
494	Gabrb2	TAACCAGCGACATATTACTA
495	Gabrb2	CTTGACTTTGGACAACCGAG
496	Gabrb2	GATGAGTTTATAATCTACGA
497	Gabrb3	CCTCACGCTTGACAATCGAG
498	Gabrb3	CCTGGTAGATGGCTACACTA
499	Gabrb3	CGCCTGAGACCCGACTTCGG
500	Gabrb3	CGAAAACTCAATGAAAGTCG
501	Gabrd	TGTGGCGCTTGCCCTAGAGG
502	Gabrd	GTAACTGGTGATAGTGAACT
503	Gabrd	AACCATACCAACGAGACCTT
504	Gabrd	TATCCGCCTACAGCCTGATG
505	Gabrg2	AACAAACTTCGACCTGACAT
506	Gabrg2	GGTTGAATAGCAATATGGTG
507	Gabrg2	TCCTGCTATCGCTCTACCCA
508	Gabrg2	TACAACTGGAGAACTCCAGG
509	Gad1	CTATTCCATAAAGAAAGCCG
510	Gad1	GACATTTGATCGCTCCACCA
511	Gad1	GCGGTTGCATTGACATAAAG
512	Gad1	AGATGAGAGAGATCGTTGGA
513	Galc	AGTTGCCTTATGGACGAAGT
514	Galc	CTAGATGAGAATTATTTCCG
515	Galc	GTCGGAGTCGTCTAGCACGT
516	Galc	CATAGCGAGCGATAATCTCT
517	B4galnt1	TCTAGCAGATCGAGTCTCGG
518	B4galnt1	TGACCGTAGGGTAAAAGCGT
519	B4galnt1	GTTCGCAGGTCGGAACCTGG
520	B4galnt1	TGCAGTTGTGAATCCAAGGG
521	Galnt3	TACGGAAGCAACCATAACCG
522	Galnt3	AGCTGCCCCTAGCAACCGCG
523	Galnt3	AAAAACCGGCTTCAACTCCG
524	Galnt3	GTGGACGGTCCTAAGCAGCG
525	Galt	AGAAAGGTACCATCATAGTG
526	Galt	GCAGCGTCACATCCGACCAG
527	Galt	GGGTTGAGTGGGTCGTGGCG
528	Galt	GGACGAGTGGGTGTTAGTGT

Number	Genes	Guide sequence
529	Gamt	AGACGCGTCATAGGCCGCGG
530	Gamt	CTATATGCATGCGCTAGCGG
531	Gamt	GATTATTGAGTGCAATGATG
532	Gamt	ATCAAAGTGACCGTCAGGCA
533	Gata1	GTCACCGGCAGTGCTTACGG
534	Gata1	AGTATGGAGGGAATTCCTGG
535	Gata1	GAGCAACGGCTACTCCACTG
536	Gata1	GGCCTCAGCTTCTCTGTAGT
537	Gba	CGTTACGAGAGCACTCGACG
538	Gba	GGATAACTGGAAGTCGTTAG
539	Gba	GACTGGCAAAGAGTGAAATG
540	Gba	CGGAGAATGAACCTACAGCA
541	Gch1	GCACCAATGGGTTCTCCGAG
542	Gch1	CCCTTCCTACAAATGGAACA
543	Gch1	GGTGAACCTCCCCAAACTGG
544	Gch1	GTACTTCACCAAGGGATACC
545	Gdap1	TCCTTGTGGTTGCATAAGCG
546	Gdap1	AAGATAATCAATGATCTGAG
547	Gdap1	TGTGTAAGCATCCATTGGCA
548	Gdap1	AGAAAACCCTGACTTACAAG
549	Gpd1	GATGGGGTACCACAAAAACC
550	Gpd1	ACCCAACTTTCGCATCACTG
551	Gpd1	GTCTTCCTCAAACACCCACA
552	Gpd1	GTTGGAGCTCACCACATTGG
553	Gfpt1	TGTGGCACAAGTTACCACGC
554	Gfpt1	AAGCTGCGGTCTTTCCCGTG
555	Gfpt1	GGAGAGAGGAGCCTTAACTG
556	Gfpt1	TCTGTTGTGAACACAATGAG
557	Ggps1	GAGCCACTGGGAAACCACGT
558	Ggps1	AGCCCAAGTGTGTCAAGCAG
559	Ggps1	GGTGAGAAGCAAACTTTCAC
560	Ggps1	TGTCCCTCCAGTAAATATCG
561	B4galt1	GGCCAGAGAGGTAATAGACG
562	B4galt1	CAGGGCTGGAGTCGAGACCC
563	B4galt1	GCTCAATATTGGCTTTCAAG
564	B4galt1	TGATGTGGACCTCATTCCGA
565	Ggt1	ACTGACGTATCACCGTATCG
566	Ggt1	CGTACAGGGTCGCATCACCG
567	Ggt1	GAATTCAGGCTCATAGTAGG
568	Ggt1	CGACCACGTGTACTCCAGGG
569	Gif	ACGTGAGAGCCATAACGGTG
570	Gif	CCTGGCCGGCGCCTACAACG
571	Gif	TACTCAACGAGATTAAGCAA
572	Gif	TATGTACAACAAGATTCCTG

Number	Genes	Guide sequence
573	Gclc	TGTGCCGGTCCTTGACTGCG
574	Gclc	CAATATGAGGAAACGCCGGA
575	Gclc	AGAAACATCCGGCATCGGAG
576	Gclc	TGTAGATGATAGAACACGGG
577	Galk1	CTGGAAAGCCCACCCCCCAG
578	Galk1	GGGCCGCGTCAACCTCATCG
579	Galk1	AGTTGGTCCATGATGCCACA
580	Galk1	ACAGTGGGCCAATTATGTCA
581	Glul	GATTACGGGGACAAATGCGG
582	Glul	TGGAAGGCCAACCAAATGGG
583	Glul	CTTGCCCAGAGTTACCTGAG
584	Glul	TATTTCTAGAGACCAACTTG
585	Glra1	CCACTTCCACGAAATCACCA
586	Glra1	TTCCATCGCTGAGACAACCA
587	Glra1	ATGCTGCACCAGCTCGTGTG
588	Glra1	TCCTGGATAAGCTCATGGGG
589	Glrb	AGGTTACTACACTTGTGTGG
590	Glrb	GGAAACAGAGTTAAGTCTAG
591	Glrb	CACAGCGTACTCCACGAGGG
592	Glrb	CCACCATGTATAAGTGCTTG
593	Slc6a9	ATACCTCTGCTATCGCAACG
594	Slc6a9	GTAGTACATGATACCCGTGA
595	Slc6a9	ATGGTGGTGTCCACATACAT
596	Slc6a9	TGTGCTACCAGCGTCTACGC
597	Gm2a	GATCCAACCTGACCCCATTG
598	Gm2a	ATTCCTTGTGTAGAACAGCT
599	Gm2a	CCACCAAGTTGGGAAAGCTA
600	Gm2a	GTGACAGGTGGAGCTCACCG
601	Bscl2	GTTTCATGTTATACCAGAGG
602	Bscl2	CCTGGGCCCACAGTAAGGCG
603	Bscl2	CAAAGGATCAGACAAAGACG
604	Bscl2	AATGTCTCACTGGCTAAGAG
605	Gnmt	TGTGTGGCAGCTGTACATCG
606	Gnmt	AGAACATTGCAAGCATGGTG
607	Gnmt	GAGCCATCCTTTGACAATTG
608	Gnmt	GGGCTTCAGCGTGATGAGCG
609	Gnpat	CCTTCGGCTTAGGAACTCCG
610	Gnpat	TACACCCCGCCCTTGTATAG
611	Gnpat	CTCACCAAACTTAGGAGTCA
612	Gnpat	ATGAGCCACAAACTGCGCAT
613	Got2	TGGAGGTCCCATTTCAACAT
614	Got2	TTTCTGCCCAAACCATCCTG
615	Got2	CATCCTCCTCACCTTCACCA
616	Got2	AGCTCACCTTCCGGACACTG

Number	Genes	Guide sequence
617	Gpaa1	GTGGAGGCACTAACCCTACG
618	Gpaa1	CCGCAGGATGCCATACACGT
619	Gpaa1	GTCCCTCCACTGTCACATCG
620	Gpaa1	AGAGTCCGATGGAGACAAAG
621	Pigq	CAGGATATGCTCAATAAAGG
622	Pigq	TGACACAGTGGCACGCAGCG
623	Pigq	GAAGGCCAGTCAAGTACCAG
624	Pigq	CAATAACCGAATTGGACAGC
625	Gsr	GGCTATGCAACATTCGCAGA
626	Gsr	CGGCCCCCACGATGACGCTG
627	Gsr	GCTGTGAGGGTAAATTCAGT
628	Gsr	AACATCTGGAATCATGGTCG
629	Gria4	TGCATACATTGGTGTCAGCG
630	Gria4	GCATGTCAGTGCGATATGTG
631	Gria4	ACGTAGAGTTAATTACACAA
632	Gria4	TGCACCTCTGACAATCACGT
633	Grin1	AACATCACTGATCCACCGCG
634	Grin1	GTGGACATCTGGTATCCTCG
635	Grin1	CTGTCCTATGACAACAAGCG
636	Grin1	AACCAGGCCAATAAGCGACA
637	Grin2a	ATGGTAAAAGAAGGCCCATG
638	Grin2a	AGAAGAAATCGTAGCCGGTG
639	Grin2a	ATCTTGACAAACTTCCGACA
640	Grin2a	TGTGTGCGACCTCATGTCCG
641	Grin2b	TATCCTACGCTTGCTCCGAA
642	Grin2b	GGCACCGGTTGTAACCCACA
643	Grin2b	ACATCATGGAAGAATACGAC
644	Grin2b	TGACTGGCTACGGCTACACA
645	Nr3c1	CATTATGGGGTGCTGACGTG
646	Nr3c1	AGCTTGCCTGGCAATAAACC
647	Nr3c1	AAAGCCGTTTCACTGTCCAT
648	Nr3c1	AAAACTGGAATAGGTGCCAA
649	Grm1	GGGTGACAAATAGCGTCACG
650	Grm1	TAGTGTACAGCTGACACTAG
651	Grm1	ACTCTCCCACGACGCCAAGG
652	Grm1	AGATAAGATTAATGCGGACC
653	Grn	CCTATCCAAGAACTACACCA
654	Grn	CCCTGCACAAAAGACCAACA
655	Grn	GACACTGGACAGCACCCAAG
656	Grn	CACCTAGTGAAGTCATCACA
657	Gss	GTTCTCTGGACCAAAACCGA
658	Gss	AGTCAGTATAATTCACAGGT
659	Gss	ACAGCTGGCTGGGACTAAGA
660	Gss	TCAGATTACATGTTCCAGTG

Number	Genes	Guide sequence
661	Gstz1	GTCAGAAATCATGCGCACGA
662	Gstz1	AAGAGACTCGGCCTATCCCA
663	Gstz1	ATTTCTGACCTCATCGCTAG
664	Gstz1	TAATGACTCACCGTTAAAGC
665	Gys1	TTGGGACACCTGCAACATCG
666	Gys1	CAACGCCCAAAATACACCTG
667	Gys1	TGTTGTGGGTGCACACTGGT
668	Gys1	ATCCCAGATCACCGCAATCG
669	Hadh	CCTTTCAACCAGCACCGATG
670	Hadh	AGCAAATCGGTCTTGTCTGG
671	Hadh	AAGCATGTGACCGTCATCGG
672	Hadh	TGGCCATACAGTAGTATTGG
673	Hsd17b10	TGTTAATGATAACTCCACGT
674	Hsd17b10	GCTACGGCCAAAAGACTGGT
675	Hsd17b10	TTGGTCGCGGTAGTAACTGG
676	Hsd17b10	GTCACGACTCACATTTGCTG
677	Hal	ATGCTGTCCGACCTCACCGT
678	Hal	AAAAGATACAGGATTGTCTG
679	Hal	GGACAATGGTGGCTTCACTT
680	Hal	TCTTAGCCAAAGGTTACAGT
681	Hao1	CAGCATGCCAATATGTGTTG
682	Hao1	ACTGTGGACACCCCTTACCT
683	Hao1	GCAACGTTGCGAAGCATCCG
684	Hao1	GTATGACTATTACAGGTCTG
685	Hccs	CAAAGTAAATGGCTGATCTG
686	Hccs	TAGCTCTAGCACCAGTAACA
687	Hccs	TCCAGAACATCTGTTCAGAA
688	Hccs	ATCAGAATAATGAGCAAGCG
689	Hcfc1	GGTACCCTTCACAACCAATG
690	Hcfc1	ACAGCAGTATGTGACTCCCG
691	Hcfc1	TGGAAGGGCTAGTTGCACAA
692	Hcfc1	CCCAAGGTTAGCCACAACAG
693	Hexa	ACGCCCCGGTGAGGGAATCG
694	Hexa	AGGAGGTCATTGAATACGCA
695	Hexa	AGTGAAGCTCTCATATGGGA
696	Hexa	AGCAAGGTGTTAATAACCCA
697	Hexb	GCTCAGCTCGAAATCTAGCA
698	Hexb	TACACCAAACGATGTCCGGA
699	Hexb	GCGGAGATGTACAACAGCCG
700	Hexb	TAACGCTCCCCAAACGCTGT
701	Hfe	TGCTCCACGTACCCTTACTG
702	Hfe	TTCCTCCCGCACTCACGCGG
703	Hfe	GATCCGTGCCAAACAGAACA
704	Hfe	CATGAAGACAACAGTACCAG

Number	Genes	Guide sequence
705	Hgd	GAAGATCGTCGAGTGCCAGG
706	Hgd	CCCTTTGAGTCCATCGACCA
707	Hgd	GGAGACATCAAGTCTAACAA
708	Hgd	GATGTCTTTGAGGAGACCAG
709	Hk1	CCGACAATCCAAAATAGACG
710	Hk1	CGTAGCCGCCATTGAAACGT
711	Hk1	GGATCTTTACCAGTAGGACT
712	Hk1	CTCCCGGGATTATAACCCAA
713	Hmbs	AAGATGAGGGTGATTCGAGT
714	Hmbs	CCTGGTCGTTCACTCCCTGA
715	Hmbs	AGAGAAGAGCCTGTTTACCA
716	Hmbs	CTCAGTTGCTATGTCCACCA
717	Hmgcl	CACCTCAGCAACTTTAGCCG
718	Hmgcl	CTTGGGAGAAACAAAGCTGG
719	Hmgcl	CTTGGGGACACCATCGGCGT
720	Hmgcl	GGGGTGGGTACAATACTCTG
721	Hmgcs2	GACATTGCAGTCTACCCGAG
722	Hmgcs2	TTTATTACGAACCTTGCTCG
723	Hmgcs2	GAGGGATTGTAGAAAACCTG
724	Hmgcs2	TCATATACTGCACATCATCG
725	Hmox1	TCGTGCTCGAATGAACACTC
726	Hmox1	TCAGGACCTGACCCCCTGAG
727	Hmox1	ACGCTTTACATAGTGCTGTG
728	Hmox1	TTCCTTGTACCATATCTACA
729	Hnf4a	GCAATGACTACATCGTCCCT
730	Hnf4a	AATGTGCAGGTGTTGACCAT
731	Hnf4a	AGCGGGACCGGATCAGCACG
732	Hnf4a	GGCTCCGTAGTGTTTGCCGG
733	Hpd	GAAAGACATCGCATTCGAGG
734	Hpd	CATTGTGGTGACCAACTACG
735	Hpd	AGATACCACACACACCCTGG
736	Hpd	ATGATCTCAAGGTTACATCT
737	Hpgd	GCTGCTAACCTCATGAAAAG
738	Hpgd	TACATGAGTAAGCAAAACGG
739	Hpgd	CATAGGCAAAGCCTTCGCTG
740	Hpgd	GCTGACCAGAAACAACTGAG
741	Lipc	TTATCATGATCATCCACGGG
742	Lipc	AGGAGAAAGGCGCTCGTTGG
743	Lipc	CATAACCCAGAGTGTTGCAA
744	Lipc	GGTGTAGTGCTGGTATGCCA
745	Hsd11b1	CCTGGCAGTCAATACCACAT
746	Hsd11b1	ACAGCGAGGTCTGAGTGATG
747	Hsd11b1	AAAGAAAGTGATTGTCACTG
748	Hsd11b1	GTAGGGAGCAATCATAGGCT

Number	**Genes**	**Guide sequence**
749	Hsd11b2	CCACTCTTGCGTCACTCGAG
750	Hsd11b2	GGTGATGAGCACCGCGCGAG
751	Hsd11b2	GCTAAGAAACTGGATGCCAT
752	Hsd11b2	CGCTGGCCTCAATATCGTAG
753	Hsd17b3	CAACATTACCTCCGTAGTCA
754	Hsd17b3	AAGCCTATTCATTTGAGGTG
755	Hsd17b3	GCTGAGTACAGGCTGTAAAG
756	Hsd17b3	TTTCTGCCAGTCAACAACGT
757	Hsd17b4	TCTAACATAGGCTCTTCACG
758	Hsd17b4	ACCAAACCGTACCAGTCACG
759	Hsd17b4	TGGGCGCCATCGTCAGAAAG
760	Hsd17b4	TGCAGTGAACGACTTAGGAG
761	Hsd3b2	CTTCAGACCAGAAACAAGGA
762	Hsd3b2	GATTGTCTTGAATGGCCATG
763	Hsd3b2	ATATGTGGGCAATGTAGCCT
764	Hsd3b2	ATTATTATGTTAGAAATGAG
765	Hspd1	CGGAGAAGCTCTAAGCACGC
766	Hspd1	TCTTGAACTAGGTGTGATGT
767	Hspd1	AGGGACAATGGACTGAACAC
768	Hspd1	TGACTTAGGAAAAGTTGGGG
769	Hspa9	CAACTTGCCATACCTTACCA
770	Hspa9	CTCAACCCAAGCATCACCAT
771	Hspa9	GCCCTCCATAACAGCCACAC
772	Hspa9	GTGAATCATTGAAATAAGCA
773	Ndst1	CATCCAGGTTGACATACTTG
774	Ndst1	CTATGTGACACGGCCCAGTG
775	Ndst1	TTCTACAACGAGTACCCTGG
776	Ndst1	CCCCACAGATATGGGCTATG
777	Hyal1	TTGGCCAGAAACTTTAGTGG
778	Hyal1	CCCCTACTATACACCCACAG
779	Hyal1	CTGCAGGCAAATAAATACTG
780	Hyal1	TGAGAAGTCAGGTTCAGGCA
781	Ids	GTCTCCATAACAGCCCAGGG
782	Ids	CATTCTCCTTGAAGTATTGG
783	Ids	TCCCTTGGAAAACATAACCC
784	Ids	TCCCTATGGACCAATTCCTG
785	Idua	TACCCCTATTTACAATGACG
786	Idua	GTTGGACAGCAATCATACAG
787	Idua	GGTCCAAGAATGCATCCAAG
788	Idua	ACTATGATGCCTGCTCTGAG
789	Inppl1	AGAATCCGGTCACACCACGA
790	Inppl1	CCTGGATATCCATGTCTAAG
791	Inppl1	TCACACTGGACGTACTGACG
792	Inppl1	GCAGGGCACAAACAAGACCC

Number	Genes	Guide sequence
793	Insr	CGAGGATTACCTGCACAACG
794	Insr	GTGATACCAGAGCATAGGAG
795	Insr	CACACTGCACCTCTCATCTG
796	Insr	TATAGCCAGACGGGCACTCG
797	Stt3a	AAGGTGGTACGTAACGATGG
798	Stt3a	TACCATGTAGAAATAAGCGA
799	Stt3a	GTTTACCTGGAAACCAACAA
800	Stt3a	ACTTTAATTATCGGACTACC
801	Itpa	ATAGCAGTACTCACATGTAG
802	Itpa	TGATAAGTGCCTGAGTACCA
803	Itpa	AAACGCCAAGAAGCTGGAGG
804	Itpa	TGGCCTCTGAAGAGAAGCAC
805	Itpr1	CTGTGAAATATGCCCGACTG
806	Itpr1	ACACGAACGATGTCATCGAG
807	Itpr1	AAACGTGTCAATCTCTGCCG
808	Itpr1	GGAAGCTGAGAACTCCACAG
809	Itpr2	TCTGATACAGGATTCTACGG
810	Itpr2	CAAGTGCCTTAACCGCACGT
811	Itpr2	AATGCCGTAATCAACACCAG
812	Itpr2	TGTTGTGAGACTCTTTCATG
813	Kcna1	CGACACAATGGCAATAACCC
814	Kcna1	TTCTGAACACCCTTACCAAG
815	Kcna1	GGACTGGTAGTAATAAAGGA
816	Kcna1	CGCAGCATTCGTGGTCGTCG
817	Kcnj10	AGGTCGTCCATAGATCCTTG
818	Kcnj10	TGGCCCCAGGAATACGCCGG
819	Kcnj10	GCAACCCGGATCATAAGGCA
820	Kcnj10	CTGCGCAATAAGAAGCACGA
821	Kcnj11	CCAGGTACCGTACTCGAGAG
822	Kcnj11	GAGTGGATGCTTGTGACGCA
823	Kcnj11	CGGCGGGCGCATGGTGACAG
824	Kcnj11	GAGGCACAACTTCGCCCTCG
825	Khk	TCCGATGCATTCCGGCCCTG
826	Khk	AACTGGAAGAGCTCCTCACG
827	Khk	TGTGGTGGACAAATACCCAG
828	Khk	AAGAGCCCATGAAGGCACAG
829	Lamp2	GAGTGTAGTTGTAGTCGACG
830	Lamp2	CCTGACAAGGCGACACACGA
831	Lamp2	CACTTAAAGATGACATCCAA
832	Lamp2	GCTGCAGCTGAACATCACTG
833	Lcat	GATGTGCTACCGTAAGACAG
834	Lcat	CCTGTCCTAGGTGACAACCA
835	Lcat	GTGCAGAATCTGGTTAACAA
836	Lcat	GCGGGGGGAAGAGCACATTG

Number	Genes	Guide sequence
837	Ldha	CAAGCTGGTCATTATCACCG
838	Ldha	GTTGCAATCTGGATTCAGCG
839	Ldha	GGAGAACATGGCGACTCCAG
840	Ldha	GTCATGGAAGACAAACTCAA
841	Ldhb	AAATTGTGGCCGATAAAGGT
842	Ldhb	GTCTTCCAACACATCCACCA
843	Ldhb	GCTCGCCCAGGATCCATCCG
844	Ldhb	GGGCTGTACTTGACGATCTG
845	Cog1	GGGCTGGAACTCGATAATGG
846	Cog1	TGAGGATTGGAAATCTCGAG
847	Cog1	GTGGACATGCTTGTTCGATG
848	Cog1	CAGCAGCAGCTTAATCTGGG
849	Ldlr	AAAATGCATCGCTAGCAAGT
850	Ldlr	GGTGTCGTAGGACAAGTTAG
851	Ldlr	GCAGACTGGTGTACTCGCTG
852	Ldlr	TGACCGTGAACATGACTGCA
853	Lfng	GGCGATGAAGACGTCGCGAG
854	Lfng	AGACGCGGATCCACCGCCCG
855	Lfng	CACACCCAAGACGTGTACAT
856	Lfng	GGAGAGGCTATGCACCTCGC
857	Lipa	ACCGAGATAATCATGCGCTG
858	Lipa	GTATTCACCGAATCCCTCGT
859	Lipa	ACTTCAGCATCGCACTCTGA
860	Lipa	TGTAGTTAATTGAAGCAGGT
861	Lipe	GAGTATGTCACGCTACACAA
862	Lipe	CACTTAGAGAGTACGCTCAG
863	Lipe	TGCGGTTAGAAGCCACATAG
864	Lipe	AGAGCGGATATGCCTTGCAG
865	Phyh	CTCATTATAACGATCCCTGG
866	Phyh	CCCAAAGGATACAATCGTTG
867	Phyh	AAACAATTAGGTTGCTAGGT
868	Phyh	GAGCACATTGACAGAAACAA
869	Lpl	GAAAAACGTACCGTCTGCTG
870	Lpl	CCATCCATGGATCACCACGA
871	Lpl	TGGATTCCAATACTTCGACC
872	Lpl	TGACACTGGATAATGTTGCT
873	Ltc4s	CTTGCAACAGAACTCCCACG
874	Ltc4s	AGACGCGCTCGAACTCGGGA
875	Ltc4s	CGTATCCCTGGAAATAGCGG
876	Ltc4s	TACAGGTGATCTCTGCACGA
877	Alad	AAATGGAGCATTCCTAGCAG
878	Alad	ACGGACAGCCTCAATAGTTG
879	Alad	GCTCCGTCAGACATGATGGA
880	Alad	AAAACATGGACTTGGCAACA

Number	Genes	Guide sequence
881	Amacr	GCAGGTCATCGATTCAAGCA
882	Amacr	GGACAAAACATCTTAGATGG
883	Amacr	GCGGCGCATGTGCGCACGCG
884	Amacr	AAGCCAAATAGTTGATGTCA
885	Man2b1	ATGTTGTAAATGACTACGCG
886	Man2b1	TGAGTTCAATGCAAAAACGT
887	Man2b1	CTTGATAGTCAATGCGCCCA
888	Man2b1	AGCTCCCAGAGGTAACACGT
889	Man2b2	CAATGTCTACACTACCGTGG
890	Man2b2	TGGTGGCCAACGTTAAACAG
891	Man2b2	CAGGCCTTGTGTCTACCGAG
892	Man2b2	TCAAGTCATGCACGCCCGCG
893	Maoa	TCTTGGCAGTCAAAACCGGT
894	Maoa	TAGGAACGGAAATTTGTAGG
895	Maoa	GTTGTAATCCAAATATGCCA
896	Maoa	ATGGCAAGCAAGACATGCTG
897	Mc2r	ATGGGTTATCTTAAGCCTCG
898	Mc2r	ACAATCGGAGTTATTTCTTG
899	Mc2r	GGCGCATGGTCACAATGCTA
900	Mc2r	AGATAGAGCCCAGCAAAGAG
901	Rdh11	CCGGCAAGCTAAATACACAC
902	Rdh11	GCACCTTCTCATCAACAATG
903	Rdh11	GGAACAGTCAGGTCTTCGTA
904	Rdh11	TCCACTTCCATAACCTGCAG
905	Mocs2	ATCATCCCGCCAATCAGTGG
906	Mocs2	GAGACACTGCACCACACAGA
907	Mocs2	GAATACTGCTATGTGTCTCA
908	Mocs2	ATATGAAGCGTATGTACCGA
909	Mdh2	TCACGCACCTGAGAGATCAG
910	Mdh2	CGATATCGTAGAGGGTCAGG
911	Mdh2	GTTCGCTCTGACGATGTCAA
912	Mdh2	GTTGGCAATGATGCAAACCA
913	Mpv17	CATTGAGTATCCCGACCAGT
914	Mpv17	TGTACCAGCCTCCGACGACA
915	Mpv17	ACAGGATCACTGATGGGCGT
916	Mpv17	GGGATACCATGGTCAGAGTG
917	Mthfr	AGACCCTGTAGGTGACCACT
918	Mthfr	GACTGGGATGAGTTTCCTAA
919	Mthfr	AGGTAACATCTACGAAGAGG
920	Mthfr	CGAAGCTCTCTGCATCGGGG
921	Mtm1	AGGGAACCACCAAAAGAGCA
922	Mtm1	TTACCACTCATACCGACAAG
923	Mtm1	ATGGGAGGCGCGACAAGTAG
924	Mtm1	TCTGACCGGTGCCATTCAAG

Number	**Genes**	**Guide sequence**
925	Mttp	TGAGCGGTCTGGATTTACAA
926	Mttp	TGATCAAGTGATCCAAGTCA
927	Mttp	GATATACCACCAGAATCGTA
928	Mttp	ATCCTTTGCAGACACGCTCG
929	Mut	TTTGACTTGGCAACACATCG
930	Mut	TTATATGGCACACCCCAGAA
931	Mut	AGAGTTCGTATGCAAAGACT
932	Mut	ATCATGTACGACCCTCCCCA
933	Mvk	AGCGTCAATTTACCCAACAT
934	Mvk	GTGGTCGGAACTTCCCCCCG
935	Mvk	CAAGGTCCCGCGGAGTACCA
936	Mvk	TCTGAAGTCAATCAACAAGT
937	Naga	GCTAGGAAGGCAATCCCGTG
938	Naga	TGTTGAGGTATACATAGCCC
939	Naga	TCTCACAAACCAGTCCAGGA
940	Naga	TGTTCAGGTGAACTACACCG
941	Ndufa2	GCAGGGATTTCATCGTGCAA
942	Ndufa2	TCTGATCCGCGAATGCTCGG
943	Ndufa2	ATTCGCGGATCAGAATGGGC
944	Ndufa2	GGCTGCCGCTGCTAGCCGAG
945	Ndufa4	AAAGACCGTGAACTTACGCT
946	Ndufa4	AGCACTGTATGTGATGCGCT
947	Ndufa4	CACTGTTTAATCCAGATGTC
948	Ndufa4	TCTTCGTATTTATTGGAGCA
949	Ndufs4	CCTGGATGGAACTCTACAGA
950	Ndufs4	AGAGCACATCAAAACCAGAA
951	Ndufs4	GTTGATGCCCAACCCATCAA
952	Ndufs4	GTTGTCTGCCAGCTTCCAAG
953	Neu1	ACAGCCTTCATCGTAGACGA
954	Neu1	TTGGTTTGGAGTAAGGACGA
955	Neu1	TGTGTGTGGACACGGGACGC
956	Neu1	GAAAAAATCTGCATCCGATG
957	Neurod1	GAGCTGTCCATGGTGCCGTA
958	Neurod1	CCGGCGACCAAATTGGTAGT
959	Neurod1	AGCAAGGTACCACCTTGCGC
960	Neurod1	GTGTCTCAGTTCTCAGGACG
961	Nfs1	CTAGTGAAAATGATCTCCCG
962	Nfs1	TCACAGTCATAACGGAGACC
963	Nfs1	AGGGCCTCCACACGTACCCG
964	Nfs1	CCTCTGTTAGTCCTTACCAG
965	Npc1	GGGGAAGGTGATCACAAGCG
966	Npc1	CATCATGTGGGTCACCTACG
967	Npc1	CGGTTCGTAGATATGAACAC
968	Npc1	CCATCCCTACCTGAAAACAC

Number	Genes	Guide sequence
969	Slc11a2	ATGTCACCGTCAGTATCCCA
970	Slc11a2	AAACACAAAAGTGTCTGCGA
971	Slc11a2	TGAGAAAATCCCCATTCCTG
972	Slc11a2	CCTTGACTAAGGCAGAATGC
973	Nsdhl	TAGGCTTCATGGCGTAAGGG
974	Nsdhl	CTATAAAGAACTGCACCCGG
975	Nsdhl	CTTGGGCCGAAAATGCCATG
976	Nsdhl	CCTGTGTACCCACAGAAATG
977	Oat	CCGTTCAAAAATGTACTCGG
978	Oat	TGTACTCCTCGTATTCACCA
979	Oat	ATCATAACTGGTCGGATCTG
980	Oat	ACCCTGATGTACCTCCAGTG
981	Ogdh	TTGGCCCACTCATAGATACG
982	Ogdh	GACTAGTTCGAACTATGTGG
983	Ogdh	GTAAGTGGAAGACCTTGTCA
984	Ogdh	AAAGCTGAACAGTTCTACTG
985	Slc25a15	ACCTTTCCAGACCTCTACCG
986	Slc25a15	GCCCATGGTAGAAGCCCAAG
987	Slc25a15	GCACAGCATGCGTACTGACT
988	Slc25a15	GGACAGCACTTACTTCTGAC
989	Otc	CAGTCCATTGACAATTGGGA
990	Otc	CCTTCAAGCAGCTACTCCAA
991	Otc	TAGAAAGGGTCACACTTCTG
992	Otc	AAATTCAGGATCAAGCAGAA
993	Pah	CCTCTTCTGGAAAAGTACTG
994	Pah	CACTTACCTCAAATAAGCGC
995	Pah	GCAGCATCATCAAGAGCCTG
996	Pah	TCCTCGGGTGGAATACACAG
997	Pax4	TTGGAACCCAAGTGTATTGG
998	Pax4	AGGGTACTCATCCTTTAGCT
999	Pax4	ACTCAACTCAGATCACCAGG
1000	Pax4	GTCTCTACAGAGTTTCAGCG
1001	Pck1	ACTGACAGACTCGCCCTATG
1002	Pck1	GTGGCCGAGACTAGCGATGG
1003	Pck1	CCTTTGGAAGCGGATATGGT
1004	Pck1	TCGCAGATGTGGATATACTC
1005	Pdha1	AGAACAACCGCTATGGCATG
1006	Pdha1	ATCACTGCCTATCGAGCACA
1007	Pdha1	GCGCCGGATGGAGCTAAAGG
1008	Pdha1	TGTTTGACATTATACGGCGA
1009	Enpp1	TACAACGCAAGTTGCCACTG
1010	Enpp1	GGTGACCGCTAATCATCAGG
1011	Enpp1	ATGTGAAAGCATCGATACCC
1012	Enpp1	AACGTCTTGGTAGGGTACAT

Number	Genes	Guide sequence
1013	Pdx1	GACCCGTACTGCCTACACCC
1014	Pdx1	ACTGCCAGCTCCACCCGGCG
1015	Pdx1	AATCCACCAAAGCTCACGCG
1016	Pdx1	CCATTCGGGAAAGGTCCGGG
1017	Pepd	CACAAATCGGATCTCCAGCG
1018	Pepd	CTGCTATGGTGTCATCGATG
1019	Pepd	GCCCTGCAACACGACAGCTG
1020	Pepd	CTTGCTAATGCCCTCGAAGG
1021	Pex11b	CTCTACAAGTGCTACGCCTG
1022	Pex11b	CAAAGTACAAGGCTCGGTTG
1023	Pex11b	GGCGAATCTCATAAGCATCA
1024	Pex11b	ATCTCAGAACGACATCTGAC
1025	Pex16	GCTTCGAAAAAAGTTGCCTG
1026	Pex16	TGAATCGGAGAAGCGACCTA
1027	Pex16	TGAGAGCAATGACGAGCCAA
1028	Pex16	GCCAGGAGCCATCATATGTG
1029	Pex7	GATGCCGTAGTGCTGCGCCG
1030	Pex7	ATGGGATCAAACTGTCAAAG
1031	Pex7	CATCACCACTACAGGTGACA
1032	Pex7	CTATAAAGAGCACACGCAGG
1033	Pfkm	CCTCACGGTAGAGCGAACAG
1034	Pfkm	GCGCCTTGGATATGACACCC
1035	Pfkm	TTAGACCAAAGACGTGACCA
1036	Pfkm	CATAGACACGCTCTCCCACG
1037	Pgk1	TAAGGTGCTCAACAACATGG
1038	Pgk1	TCAAGAACAGAACATCCCTG
1039	Pgk1	GGACTGCACACCGAGCCCAT
1040	Pgk1	CTTCCTCTACATGAAAGCGG
1041	Pgr	CTCTGGCCGACTCATGAGCG
1042	Pgr	AGGAGGAGTCGCAGCCAACG
1043	Pgr	GGCGCGAACGAACCCTGCGT
1044	Pgr	CAGTCTGGGAAGTCACCGCA
1045	Abcb4	GATGACATCTGCGTTCCGGA
1046	Abcb4	AGGACCGTGATAGCTTTCGG
1047	Abcb4	TAGCGAAAGCATCAATACAG
1048	Abcb4	TACTACTATTCGGGACTAGG
1049	Phka1	GTAGAAAACCTACGATTCAG
1050	Phka1	AGTGTAGTGAAGTTAATGAG
1051	Phka1	GAGATAGGGAAAGTGATCGT
1052	Phka1	CTAAACTAGCTCCTACCTCA
1053	Piga	TCTTCCACGCCAAGACAATG
1054	Piga	ATGGGTGCAGGTCCTATCGT
1055	Piga	CAGACTGTGAAAGAGAGTCG
1056	Piga	CCATGCTTATGGAAATCGAA

Number	Genes	Guide sequence
1057	Pik3r1	GAGCTTTATAAGGAGAGGCG
1058	Pik3r1	TCCATTAACCTTCAACTCTG
1059	Pik3r1	TGGCTACAATGAAACCACTG
1060	Pik3r1	CTGGAAATCTGAAAAGCACG
1061	Pip5k1c	TGGTGGCAAGAACATCCGCG
1062	Pip5k1c	CCGACGCATCCACGCCTCGG
1063	Pip5k1c	TTACCAAATAGTCATCTGGA
1064	Pip5k1c	GCCATGGAGTCTATCCAGGG
1065	Pklr	TGTACGAAAAGCCAGTGATG
1066	Pklr	GGGTTCACTCCAGACCTGTG
1067	Pklr	GGGCGATGCAAAGACAGTGT
1068	Pklr	CTGGTGACCGAAGTGGAACA
1069	Plcb1	CAAATACTTACGAATCCACG
1070	Plcb1	CCTGCACAGGCAATATCCGG
1071	Plcb1	GGAACAGCGCATGATAACTG
1072	Plcb1	TCCCAACTTTCTTATCAGAG
1073	Plcb3	GAAGGTGGGCATCTACGTCG
1074	Plcb3	CATACCGGGTATTTGTCGAG
1075	Plcb3	TTGATAAAATATGCGCTCAG
1076	Plcb3	CAGTGAGGTCAATGCCACGG
1077	Plcb4	TGAAGTAATGAGCCAGCGGG
1078	Plcb4	TAAGAAGATCGGGACATACG
1079	Plcb4	CAAGTACGGATGGATGTTCG
1080	Plcb4	CTTGGCGAATACTGTTGATG
1081	Plcd1	ATTTGCCAGAGACATACCCG
1082	Plcd1	GGGAAGAAGACACTAAGTAG
1083	Plcd1	AGGTGGATGACAGCTACGCC
1084	Plcd1	GTAGCGCTCAATGAGAGAGA
1085	Pnp	AGATGCTGTGTGATGATGCA
1086	Pnp	TCAGTGCCTGGAAACAAATG
1087	Pnp	TGTGGCCAGAACCCTCTCCG
1088	Pnp	CCTCAAGTGGCAGTGATCTG
1089	Polg	TGCTCATAAACGTATCAGGT
1090	Polg	CGGCGGGGAAATGCCCGACG
1091	Polg	CCGTTGCCATGGTGATACGT
1092	Polg	AGATCCTGGCCCGCCCAGCG
1093	Por	TGGCTCCCAGACGGGAACCG
1094	Por	ATGTCTCTAAACAATCTCGA
1095	Por	AAGAGGATTTCATCACATGG
1096	Por	TCCAAGACTACCCGTCCCTG
1097	Ctsa	GTGGTGCTTTGGCTTAACGG
1098	Ctsa	GGACTCGATATACAGCACGT
1099	Ctsa	CTCCGGCTACCTCAGAGCAT
1100	Ctsa	CATGACCAGTACAGCCAAGG

Number	Genes	Guide sequence
1101	Ppox	CCAGCCGGCCTAATCCCTCG
1102	Ppox	CCGGGCCTGACGAATTAGTG
1103	Ppox	GTACTCAGGATTCGAGCTAG
1104	Ppox	TAATAGTGAGGTGTTACCTG
1105	Inpp5k	TTGTGCAGGAGAGTATAACG
1106	Inpp5k	ACAGCGTACATGTTGTGACG
1107	Inpp5k	AGGATGCGGTCAGTCCACGC
1108	Inpp5k	TACCTTGACAAAGTTCAGTG
1109	Ppt1	GGTACACACTCTCCTTGATA
1110	Ppt1	TGTTAATGTCCAAGTCAACA
1111	Ppt1	AGAGACAGGACGTAAATCCC
1112	Ppt1	CCATGCCAGATCACCAGCGG
1113	Prkcsh	AAGACCAGGTAGAAACACTG
1114	Prkcsh	CAGGGACAAGTACCGCTCTG
1115	Prkcsh	GGCACAGACGAGTACAACAG
1116	Prkcsh	AACTTGACGACAACATGGAT
1117	Prodh	AGGAGGCGTATCGCAGCCGG
1118	Prodh	CCTGCTGTCACGGTTCACTG
1119	Prodh	CAGGATAAAGCCAACACCAA
1120	Prodh	TCTCCCAGGAGCAAATAAGA
1121	Prps1	GATGACTGCAGTAACCCGGC
1122	Prps1	TGCAGATCATATTATCACCA
1123	Prps1	CATCTCCCACAAGTACCATG
1124	Prps1	ATGTCTACATTGTTCAAAGT
1125	Psap	CTACGTGGACCAGTATTCCG
1126	Psap	GTCAACCACCTCCTTGCACG
1127	Psap	CCTCAGCTAACCTTAGGTTG
1128	Psap	TCTGGCATAAAATCACATTG
1129	Pten	CCTCCAATTCAGGACCCACG
1130	Pten	TGTGCATATTTATTGCATCG
1131	Pten	ACTATTCCAATGTTCAGTGG
1132	Pten	GGTTTGATAAGTTCTAGCTG
1133	Pts	GGGAAATGCAACAATCCGAA
1134	Pts	CGAGGCGCGACAGTCGCGCG
1135	Pts	CGGGCACAACTATAAAGGTG
1136	Pts	GTGATCAAGAGGCTTCATGA
1137	Pex19	ACAGCACATCCTTAGACAGG
1138	Pex19	GCTGGCTTCCCAAGCTACTG
1139	Pex19	GATGGTCGGAGCATGTTCTG
1140	Pex19	TGGAACTGCTCCACCAGATG
1141	Abcd3	GCTCACACGGTACCTCTACG
1142	Abcd3	AACCAGGTACCCGACGACAG
1143	Abcd3	GTGAAATGACTAGATTGGCT
1144	Abcd3	AGAATGGGACGCTCATTGAG

Number	**Genes**	**Guide sequence**
1145	Abcd4	AGACTCCATAATACTGACTG
1146	Abcd4	GGACGACATTGATAATCCGT
1147	Abcd4	ATGTTGCCGGTTACACACAC
1148	Abcd4	CATCTTTGGATATTTCATCG
1149	Pex2	GTATGCTGTGTGCACCATTG
1150	Pex2	TCCCAAAAGACGCTAAATGA
1151	Pex2	GTTCTGGGGCTTGCAAAATA
1152	Pex2	ATGAAAGCACTGAGTAAACT
1153	Pex5	CTGGACTCACCATCGATCAG
1154	Pex5	TCTTGTAAACTGATCAACCC
1155	Pex5	TCGTGCGGCAGATTGGCGAG
1156	Pex5	AGAAGGGCTGCATCGACTGG
1157	Pygm	GTAGCCGCCAACATTGACTG
1158	Pygm	ACTTGGAGGACTTGAAACGT
1159	Pygm	GGATCCAGCGTCCCACGAGG
1160	Pygm	GCAGCCTATCTACGTCCCCA
1161	Rbp3	TAAGCAGGTACACTCCACGC
1162	Rbp3	TTACGAGCCCAGTACCCTCG
1163	Rbp3	CAGCACTGTATCTCTCCCCG
1164	Rbp3	CTGCAATCTAAGTTGGCCCA
1165	Rbp4	AACTTCGACAAGGCTCGTGT
1166	Rbp4	CTTGCAAAAAGAGACCCTCG
1167	Rbp4	AGGGACGAGTCCGTCTTCTG
1168	Rbp4	CCCACTACTCACTTCCTCGC
1169	Rdh5	TGATATCCAGTAGTGTTGTG
1170	Rdh5	ATGGAGACTTGTACTCCGAA
1171	Rdh5	AAATCATCCTGTGTTAGCCA
1172	Rdh5	AAGTGGGTGAAGACACGTGT
1173	Rlbp1	TCGGGACAAGTATGGTCGAG
1174	Rlbp1	ATCCGGCCTCGATAGTGCAG
1175	Rlbp1	CCGTGCCCGCAAGTTCGATG
1176	Rlbp1	ACCTCACCTTCTGCAAAGTG
1177	Rnaseh1	TGGGCGACAGACAAACCAGA
1178	Rnaseh1	AGAGTCAGTCGTTGTCTACA
1179	Rnaseh1	AGCAGGAAACCGGTCCACCT
1180	Rnaseh1	AGGAGCTCTTCAAGCCCGGA
1181	Rpe65	CAAAGAGCCCTGGCCCACAT
1182	Rpe65	TCGAGTCCAATGAAAGCATG
1183	Rpe65	CCTTGTAAATATCTACCCAG
1184	Rpe65	TCAAGCCATCTTATGTACAC
1185	Rpia	ACTGCACGTGGGAACCCGAG
1186	Rpia	CGTGGTTCTCCACCGCCGTG
1187	Rpia	ATGATGTACCTGGAAAGATG
1188	Rpia	TGACCTGGATCAACACCCAG

Number	Genes	Guide sequence
1189	Nr1h4	AAACGGGACATTGTTGTATG
1190	Nr1h4	TGATGGACATGTACATGCGC
1191	Nr1h4	TGTGACAAAGAAGCCGCGAA
1192	Nr1h4	AGTGTAAATCTAAACGGCTA
1193	Scp2	ACAGATCCCTTACTCCGCAG
1194	Scp2	AAGTGGGTCATCAACCCTAG
1195	Scp2	CTCCTCGCTGGACAGAATCG
1196	Scp2	GCTGTATTCATCTTGGAACT
1197	Sord	CAGTACTCATCTACTTCTCG
1198	Sord	GTTACTAAAGATGCACTCGG
1199	Sord	TGTGCTTGTAGAATCGGCAG
1200	Sord	TCTTACCAGCGCCACACACA
1201	Selenbp1	AGTCATGGTCAGCACCTTGG
1202	Selenbp1	CATCTCCTCCCGCATCTACG
1203	Selenbp1	TGCAGGAAGCGGATCTCCAG
1204	Selenbp1	CCAGCCTCGACACAATGTCA
1205	Sgpl1	ATATAAAATCCCACTCCATG
1206	Sgpl1	AGGCTTATGGAGAATTCACG
1207	Sgpl1	ATTGCACCAAATATGAGCCC
1208	Sgpl1	GGGAACGGAAAGCATCCTGA
1209	St3gal3	GCTGGACAAACCCTAGGCAC
1210	St3gal3	CCTACGCATCACCTACCCTG
1211	St3gal3	ACGACTATGACATTGTGATC
1212	St3gal3	GATCCTAGCCCACTTGCGAA
1213	St3gal5	GTTCGGGCAGCATATCCAAG
1214	St3gal5	TAGTATTCAACGTCCGACAG
1215	St3gal5	CGCCCTCAACCAGTTCGATG
1216	St3gal5	AGCTGAGAAGTGATTGCTCA
1217	Clpb	AGGACCGCGTTCCGACGAGG
1218	Clpb	GGAGAACGGCTGGTACGATG
1219	Clpb	CGTTGTCACCGGAGACCGCG
1220	Clpb	CTCTCGAGTGACTAGGACTG
1221	Slc10a1	TACAGCAAAGGAATCTACGA
1222	Slc10a1	TTAACCCTCGGTCCTACCTG
1223	Slc10a1	AGGACGTAGGGTACATAGTG
1224	Slc10a1	GAGGGGCATGATACCGTACT
1225	Slc10a2	CTATTGGATAGATGGCGACA
1226	Slc10a2	GTTGCTCTCAGGTACTACGC
1227	Slc10a2	TAGGACATATAAAGAGACCA
1228	Slc10a2	GCTCACCATCCTCTTAGCCA
1229	Slc12a3	AACCTGGTACCCGACTGGAG
1230	Slc12a3	CGGTTACAACACCATAGACG
1231	Slc12a3	TGTGGTCTTCCACCTCGTTG
1232	Slc12a3	CACAGGCTAGCCCTTCGCAG

Number	Genes	Guide sequence
1233	Slc16a1	ACTACTAAGAAAGACCAAAG
1234	Slc16a1	CACCAGCGATCATTACTGGA
1235	Slc16a1	GACTTGCAGCCAACACCAAG
1236	Slc16a1	AGGCCCTATTGGTCTCATCA
1237	Slc1a1	CGACTCACCTAGTACCACGG
1238	Slc1a1	TAGGATTACAGCAATGACGG
1239	Slc1a1	ATCATGCTGGATACGATCAG
1240	Slc1a1	TCACCTGATCAGGTCCAACA
1241	Slc1a2	CATGTTGATAGCCTTCCCGG
1242	Slc1a2	CCATAGCTCTCGTGCCTAGG
1243	Slc1a2	TAATTGCCCATAGGTCTGAT
1244	Slc1a2	GTTCATGGTTTCATTCAACA
1245	Slc1a3	GTATAAAATGAGCTACCGGG
1246	Slc1a3	GACTCTGACCCGGATCCGGG
1247	Slc1a3	GAGGCCGACAATGACTGTCA
1248	Slc1a3	AGGCTTCTACCAGATTGGGA
1249	Slc22a5	TTTATGATCTGATCCGAACA
1250	Slc22a5	GGGTCAGATCTCCAACTACG
1251	Slc22a5	CACAAGGCAACGGTGCTCCG
1252	Slc22a5	CACACCCACGAAAAACAAGG
1253	Slc22a12	GGGCCTGGGAGTTACATACC
1254	Slc22a12	ACGGTAGGCAAGCTGGACCA
1255	Slc22a12	GAGGTGCTATTGTCCAGGAG
1256	Slc22a12	CATCACCAAAGGGCTACCCT
1257	Slc2a1	CCTGCTCATCAATCGTAACG
1258	Slc2a1	TCAGCATGGAGTTCCGCCTG
1259	Slc2a1	GTGTCACCTACAGCTCTACG
1260	Slc2a1	CAAACATGGAACCACCGCTA
1261	Slc2a2	AGAGGGCTCCAGTCAATGAG
1262	Slc2a2	TTACCGACAGCCCATCCTCG
1263	Slc2a2	GGACTGGTTCCAATGTACAT
1264	Slc2a2	TGTGATCAATGCACCTCAAG
1265	Slc3a1	CCATATACCAGATCTACCCG
1266	Slc3a1	ATCCTTGGTTCCAATCGAGT
1267	Slc3a1	AGAGGAGCCTCACCTAAAGG
1268	Slc3a1	TGGCAAGCCATAGTACATCA
1269	Slc5a1	AGGAAGAATGCTACACACCG
1270	Slc5a1	GAGACATGTTCTTGGCCGAG
1271	Slc5a1	CATCGCCTACCCCACGCTCG
1272	Slc5a1	CCGGCCACCACACCATACTT
1273	Slc7a5	GCCCTCCTCGCAGTACATCG
1274	Slc7a5	ACCCCTACTTACGCACGCAG
1275	Slc7a5	AGCGGCCTCTTCGCCTACGG
1276	Slc7a5	GTAGCAGAGTGCGCCCACGA

Number	Genes	Guide sequence
1277	Slc7a7	AAGAGATCAGGAACCCCGAG
1278	Slc7a7	CAGCGCCAACACCTTAGCAT
1279	Slc7a7	GGCCCCGGATTTCTTAATGG
1280	Slc7a7	GAGACACACGCCATTAAGCA
1281	Smpd1	AGGCTTTCTAGCGTTCGCAA
1282	Smpd1	GAAGAGGACACGGCTGACAG
1283	Smpd1	AGTCTCGCCAAGATCAGCTG
1284	Smpd1	GCTGACTGGCACACATCTAG
1285	Sms	ACTTACTAACATCCCCGCTG
1286	Sms	TTACCACCCATAGTTCGCGG
1287	Sms	CTTACACGAACAAGAATGGC
1288	Sms	AAACAAGAAACTGACAGCGT
1289	Spr	GCGTGCGCTTACGAGCATCA
1290	Spr	GCGCAGTACGCGAGCTCCCG
1291	Spr	AGCCTCGGTGCCCAGATCGG
1292	Spr	TACAGACCCCAGCCTTTGTA
1293	Sptlc2	GTTGTGTTTGAAGATTCGAA
1294	Sptlc2	TGAGAGCAATCACTTCAGGA
1295	Sptlc2	AATCTCGAAGATATCCAAAG
1296	Sptlc2	ACAACTATCTTGGATTTGCG
1297	Scarb1	GGGGCCGTGAAGCGATACGT
1298	Scarb1	TGCGGTTCATAAAAGCACGC
1299	Scarb1	GATGAACAACTCGAATTCTG
1300	Scarb1	GAGGATTCGGGTGTCATGAA
1301	Ssr4	TAGTAAGAAGGGGTGATCTG
1302	Ssr4	AAACAATTTCCTGTAACCCG
1303	Ssr4	TACAGAGACTGTATTCATCG
1304	Ssr4	CACCTTCCTTAGGAGGCTAT
1305	Star	AGAACTTGTGGACCGCATGG
1306	Star	CGAACTTGACCCATCCACCC
1307	Star	GAAGCTCCTATAGACATATG
1308	Star	CGCACGCTCACGAAGTCTCG
1309	Stra6	TCTTCAAGCACTACACCGAG
1310	Stra6	CAAGTTGTACTGGATACCAA
1311	Stra6	CCAGACCTGAACACCAAAGT
1312	Stra6	GAAGCATCACCTATGGACTG
1313	Sucla2	CAGAGCGTAACATACTGTCA
1314	Sucla2	TGTGCACTTCCTATCAGTAC
1315	Sucla2	GTAGAAGATTCTGACGGAAA
1316	Sucla2	TCAAGTATTCATGCAGCGAA
1317	Abcc8	ATGGCTGCTAAATGCCACGG
1318	Abcc8	CAGACCAACGAGATGCTCCG
1319	Abcc8	TGGACAATGAAGATCATCGG
1320	Abcc8	GAAACTGGGATTAACCTGAG

Number	**Genes**	**Guide sequence**
1321	Surf1	TGTTTCTATAGGTCCAACGT
1322	Surf1	ATGGAAAGGAGTAACTACAT
1323	Surf1	GTGGTCGCAATGGGCCTACG
1324	Surf1	TTATGTACAACTCTTTAGAG
1325	Taldo1	GCGCATCCTTGATTGGCATG
1326	Taldo1	CTTCTTTGTAAAGCTCGATG
1327	Taldo1	TTCTGAATTCAGGCCTCAAG
1328	Taldo1	GCTTGTATTCATCGATGGCT
1329	Tbxas1	TCACAGGCTTGGCTGATGAG
1330	Tbxas1	CCACACTTACCATTTCAGGA
1331	Tbxas1	ACAGAGGCCCGTATCGCTCT
1332	Tbxas1	CTGCTGTTACACCATAGATG
1333	Hnf1a	CCTATAACGGACCTCCACCG
1334	Hnf1a	GACGTACCAGGTGTACAGAG
1335	Hnf1a	TGCCAACTAAGAAGGGGCGT
1336	Hnf1a	CGGACAGTCTGCAACCAGTG
1337	Hnf1b	CAGCTTCACCCCGAAATTCG
1338	Hnf1b	CTGGTTCGCAAACCGCCGGA
1339	Hnf1b	GCCGCAACCGGTTTAAATGG
1340	Hnf1b	CTTGGTACGTCAGAAAGCAA
1341	Tcn2	GAAGCGGCTCCATGACAGCG
1342	Tcn2	TCTGAGACCACGAATCACCA
1343	Tcn2	GAGACTAGCAATACCGCAGG
1344	Tcn2	GAATATCTATAGCACCCCAC
1345	Tfam	TAAATGTTATATGCTGAACG
1346	Tfam	GGAGCGTGCTAAAAGCACTG
1347	Tfam	CTAACTCCAAGTCAGCTGAT
1348	Tfam	GCTGTTCTGTGGAAAATCGA
1349	Th	GGGTGAGCCAATTCCCCACG
1350	Th	ACTGTGTGCACTGAAACACA
1351	Th	CCCCAAGGTTCATTGGACGG
1352	Th	GTGCGCTTCGAGGTGCCCAG
1353	Tkt	CGTGGACGGACACAGCGTGG
1354	Tkt	CAGCGCTGCAGCATGATGTG
1355	Tkt	CCCACAGATAGCCACCCGGA
1356	Tkt	CTCCGAGGGCTCCGTCTGGG
1357	Tmem165	GGCATTAGAATGCTTCGGGA
1358	Tmem165	ACATAGTATGTATACACCCT
1359	Tmem165	GCAGCTGCCCAGACGAATCT
1360	Tmem165	GTCATCATAGTGTCCGAACT
1361	Tpi1	TGAAGGTCAGTACAAACGCA
1362	Tpi1	AAGTCGATGTAAGCGGTGGG
1363	Tpi1	AGTGAGCCACGCCCTAGCAG
1364	Tpi1	CCAACGAAGAACTTCCTGGT

Number	**Genes**	**Guide sequence**
1365	Tpmt	AAAGAACCAAGTACTAACCC
1366	Tpmt	TTCTGCAGGTTCGCAGATCG
1367	Tpmt	GCATTAGTGGCTATCAATCC
1368	Tpmt	AAAACACTCGCAGTCCACTC
1369	Trex1	TTTCCTCGAACCATTCCCTG
1370	Trex1	ACACAGAAGGTACCATCTAG
1371	Trex1	AGCTTGTCCACCACACGGGG
1372	Trex1	GGAGCAGAGGAAAGTCATAG
1373	Tfrc	CTACACGCTTACAATAGCCC
1374	Tfrc	GAATACATACACTCCTCGTG
1375	Tfrc	GGGCTCCTACTACAACATAA
1376	Tfrc	AACCCTCGGGAGACTCCACT
1377	Cmpk2	TCGGCCGCGGCGCTTCACTG
1378	Cmpk2	GGTGTTCCAAGACCGGGACG
1379	Cmpk2	AGTCGCGCCGAGTGTCCGGG
1380	Cmpk2	AGTTGACCAGTGCCCAAAGG
1381	Tyr	AGAAATTCGAGAACTAACTG
1382	Tyr	TTTATGCGATGGAACACCTG
1383	Tyr	ATGTTGATATCATTAAACAT
1384	Tyr	ACCCCTTTGAAGGGGAACTG
1385	Ucp2	TCTGGGTACCATCCTAACCA
1386	Ucp2	GTCAAACAGTTCTACACCAA
1387	Ucp2	AGACCATTGCACGAGAGGAA
1388	Ucp2	CGGACCTTGGCGGTATCCAG
1389	Slc35a2	TCACCCGCTGTAGTGGACCC
1390	Slc35a2	CTGCTCTTCGCACAAAAGAG
1391	Slc35a2	CTGCAAGGTATAGATGAGAG
1392	Slc35a2	GGCCACTGGATCAGAACCCG
1393	Ugcg	CGGCTACATACGGCAGCCCG
1394	Ugcg	TGGCCAAAGCAATAGCCGAC
1395	Ugcg	AAGGATGTGCTAGATCAGGC
1396	Ugcg	CAGCCGTATAGCAAGCTCCC
1397	Umps	GAGCAGATAACTGTCGCCAG
1398	Umps	CCGCAGGTCGATGTAGACTG
1399	Umps	AGAGCGTGCACACGGCGTGG
1400	Umps	TCTGTCTGCCGATGTGTCGG
1401	Ung	ACGGACCTAATCAAGCTCAC
1402	Ung	TTGTCAGGGTGGGCCCGACA
1403	Ung	CCAACCCCGACTCTGACTCC
1404	Ung	CCACAAGGTCTATCCGCCCC
1405	Uqcrq	GATCCCTACAGCGTTTGTAG
1406	Uqcrq	CTCAAAGGGCGACAAGCTGT
1407	Uqcrq	GCAGGATGCGCTCGCGAGTG
1408	Uqcrq	TTTGCTGAAATAGCTTGGGA

Number	Genes	Guide sequence
1409	Urod	CCATCACCCTTACTCGACAA
1410	Urod	GTGGACCCTAATGACATACA
1411	Urod	ACTGCCCTACATTCGTGATG
1412	Urod	CAGCACCTGCCGATCTCCCG
1413	Uros	TCTCCTTTGATAGTTCCACA
1414	Uros	TGACAGCACAGGAATCAGTG
1415	Uros	GCCAAGTCTGTGTACGTGGT
1416	Uros	AGACATGCATGCTTTCCATG
1417	Usp9x	GCAGATATGGAAACTCGAAG
1418	Usp9x	ATGGGTATAGTATGACACAC
1419	Usp9x	GAAGTTGATTGATTAAGTCA
1420	Usp9x	TATCCAAACACATCATCCCT
1421	Vdr	TGGAGATTGCCGCATCACCA
1422	Vdr	AGCGTTGAAGTGGAAGCCCG
1423	Vdr	TTCTTCATTCAGATCCATCG
1424	Vdr	TTCGTGCAGACGTAAGTACA
1425	Xdh	CCAGCATGCAACGTACAGGG
1426	Xdh	CATACTCATGACAATACCAG
1427	Xdh	TCAAAACGCAACGTCTTCCG
1428	Xdh	GGAATTCCACCATCCCACCA
1429	Nt5e	TCATGAATTTGATAACGGTG
1430	Nt5e	TGAATAAGATCATCGCCCTG
1431	Nt5e	TATGCCTTTGGCAAATACCT
1432	Nt5e	CCTGAAGCGGCACGTCTGAG
1433	Papss2	GAATATCCGCCGGATCGCGG
1434	Papss2	AGTCGATCAAATCCGAGCTG
1435	Papss2	CTTGATGTACGAAGGTCGGA
1436	Papss2	GGTGCTAGAGAGAATAAGGT
1437	Slco2a1	CCCACGGATGATCGGCATAG
1438	Slco2a1	ACTCGGGGGATGGTTTGCAG
1439	Slco2a1	CTTCGTGGACTACGGCAGAG
1440	Slco2a1	CTCTGCAAAGTCGTCCACAT
1441	Slc35a1	GAACACTCAGCAAATTACAG
1442	Slc35a1	ATAGCACCAAAGCCTAACAA
1443	Slc35a1	TGCACAGCATACACTAGTGA
1444	Slc35a1	TCTTAAAGCTACGGTGTAAG
1445	Mpdu1	TTCCTGGTCATGCACTACAG
1446	Mpdu1	CTAGCTCCAGCATTACTGAC
1447	Mpdu1	ACTACAGCCAGAGGCGTGAG
1448	Mpdu1	ACGACCAGCTCTTCGTGCAA
1449	Rbck1	TGCTTCATACCAGCCTGACG
1450	Rbck1	AGTACGCCCGGATATGACAG
1451	Rbck1	TGCATTCACACGGCATTCGG
1452	Rbck1	ACCCGAGGTCTCCCCAACAC

Number	Genes	Guide sequence
1453	Btd	CTTGCTGTTCATAGACGTCG
1454	Btd	GTACCAAAAGGACTTGAGAG
1455	Btd	ATACCAGTTTAACACAAATG
1456	Btd	CCGCGAGGCTGAGTACTACG
1457	Slc27a5	GTGGGCTTAATGAACTATGT
1458	Slc27a5	TACCTCTGTACCATACGATA
1459	Slc27a5	GTAACAGTGATCTTGTATGT
1460	Slc27a5	CCTTTGTGGATGCTTTAGAG
1461	Txnrd2	TATCCAGTCCAATTCCAGTG
1462	Txnrd2	TGAGCACACAGTTCGCGGTG
1463	Txnrd2	GGTGGCACCTGTGTCAACGT
1464	Txnrd2	CGGTGGCCTAGCTTGTGCCA
1465	Slc27a4	CAAACGGATAGGGTACACAA
1466	Slc27a4	TCTACACATCGGGCACCACG
1467	Slc27a4	TGACTTCAGGAAACATCGTG
1468	Slc27a4	ACAGACCCACAAACTCATTG
1469	Cln8	GCTCATCTCTAGGAGCAACG
1470	Cln8	GTGTTGGTTTCACATCACCA
1471	Cln8	AAAGGTGCGGAAGAACAGGT
1472	Cln8	CTTTGTCGGCATAGAGCACG
1473	Mecr	CGTGGCGGTACCAAGCCTCG
1474	Mecr	AAGGATCTGACGTCCACGTG
1475	Mecr	ATCCAGAATGCATCCAACAG
1476	Mecr	AGCACTGATTGGAATCCCTA
1477	Aifm1	CTGCCTAATATTGAGAACGG
1478	Aifm1	ACCATGGAAAAAGTCAAACG
1479	Aifm1	GTCAATTACAGTTATCGGCG
1480	Aifm1	AAGTCTGTCTGCCATCGATA
1481	Sgsh	CTGACCTAGAAGGCTCACGT
1482	Sgsh	CGTTACGGAAGATAAGGCTG
1483	Sgsh	TGTACCGGGCCAGTACAGGT
1484	Sgsh	TCCTGAGGGTCGTAGATCTG
1485	Asns	GCATGCCATCTATGACAGCG
1486	Asns	GAATGCAGCCGATAAGAGTG
1487	Asns	GCTGTGTGTTCAGAAGCTAA
1488	Asns	ATTTGAATATCAGACCAATG
1489	Sec23b	GCAACACCAGTGGACCGCAG
1490	Sec23b	AATGGCGTTTGGTGCTACGT
1491	Sec23b	AAAAGTGATGAGACCAACCA
1492	Sec23b	GTGTTGGTGGCACAAGTCAG
1493	Dguok	AGAAAGGGTCTGGAATGTGT
1494	Dguok	TTTCATGAGTAACTTCACAA
1495	Dguok	CGTGGACGCGCCACACGCCA
1496	Dguok	TCCTGCAGGAGTTCGCAAAC

Number	Genes	Guide sequence
1497	Slc25a10	CATGCGGGACTACATGACCA
1498	Slc25a10	TACACGGTACAGACCATCCA
1499	Slc25a10	GTCAGAGAGTAGGTCATCTG
1500	Slc25a10	GACATTGACCAAATCTGCTG
1501	Yme1l1	CAGGACGTATTAAGGCACTA
1502	Yme1l1	TTAACTATTACCTCACTACT
1503	Yme1l1	TCATCGATGAATATAACACA
1504	Yme1l1	CTTGGAGGTAAACTTCCCAA
1505	Pign	CCAGCTCCCCAAGTAACGAA
1506	Pign	GTGTTGTTAAGATAACCCAC
1507	Pign	TGCCACAAAACTGGATACGT
1508	Pign	AAGTCAATAGTGATTCAACC
1509	Pdhx	CTTTAGTGAAGATCCCGCGA
1510	Pdhx	GTTAGACGAGATCTGGTCAA
1511	Pdhx	TGTCTCCTACGATGGAGCAA
1512	Pdhx	TCCTGGGCAACCGAATGCAG
1513	Abcg5	GCTGATAGAGCAGCCCCACG
1514	Abcg5	AGCTTGCCGAACATCCCAGG
1515	Abcg5	CAATCATTTGGTCCGCCACG
1516	Abcg5	GGATTGGAATGTTCAGGACA
1517	Abcb11	TACGCACCATGCCTTCGCAG
1518	Abcb11	ATGAAGGCGAGTACACACCA
1519	Abcb11	CCACTGTTCGAATAGATGAG
1520	Abcb11	AAGGTTGTGGGTAATCACTG
1521	Naglu	TGCACACATTCTGGTAATAG
1522	Naglu	GAGATCGATACGTACTTCAC
1523	Naglu	AGGAAGAGGTTCCCGATGAG
1524	Naglu	GCCCTCGAGGATGTGAACCG
1525	Abcc6	GTGACCGCAACTCCTCGGCG
1526	Abcc6	CCTCTGTGGAGGATCCACCA
1527	Abcc6	AACAGGGTGTAGGTACAGAG
1528	Abcc6	TGCACTGCATCGTTCAGGTG
1529	Tango2	GTTTGCTACTATGGAAACCG
1530	Tango2	GGCTGGGCATCAGCACACGT
1531	Tango2	CCTGAAGAAGGTCTCTACAG
1532	Tango2	TAGATGCCTTACCTCTACCA
1533	Vkorc1	GTACGCACTGCACGTGAAGG
1534	Vkorc1	GTGAGAGGGCTAAGCCAGCG
1535	Vkorc1	GGTGGAGCACATGCTAGGAG
1536	Vkorc1	CCATGTCTGCACGCACCGAG
1537	Gfm1	GAACGGGTGCTATACTACAC
1538	Gfm1	GAAGCACCATCTACAACACG
1539	Gfm1	AGCAATGAGGCCTTCTAACA
1540	Gfm1	TTACTCTGTAGCGAGCAATC

Number	Genes	Guide sequence
1541	Tpk1	CTTGCCTGAATTCGTCAGTG
1542	Tpk1	GAACTTGAAATACTGCCTTG
1543	Tpk1	GACACTTGGTAAAGTCAGTG
1544	Tpk1	CACTTATATGATCTCACTGA
1545	Dnajc12	GAGCCCGCTATGACCATTGG
1546	Dnajc12	GAGCTCATCGCATCCCAGCA
1547	Dnajc12	TGTCAATGCCGTTCGAGCAG
1548	Dnajc12	AATTTCTGAAAAGTCTCCAC
1549	Angptl3	TGCTCTGCCGTTTATAACAG
1550	Angptl3	TACACTACAAGTTAAAAACG
1551	Angptl3	CATGGACATTAATTCAACAC
1552	Angptl3	GAAGACAGCCCTTCAACACA
1553	Aass	GAAACTTCTCTTAATTCGTG
1554	Aass	GCAAATTATTCACGACAGGT
1555	Aass	TAGGCAGTGATTACGTCCAA
1556	Aass	GGATAGTGGCTTTCGGACAG
1557	Slc7a9	GAGCACTTACCAACCATCGT
1558	Slc7a9	CAAAGGCCTCCATCAGATAG
1559	Slc7a9	GGACTGCAAGAGCTCCGTTG
1560	Slc7a9	GCTGGCCAACACAGAATCCG
1561	Hacd1	GCAACTCACCGATCAGACAA
1562	Hacd1	CTGGCCCATTTAATGAAGTG
1563	Hacd1	GATCCAGAATGAAGAGAGCG
1564	Hacd1	CTTCTACAATATCGCCATGA
1565	Ttpa	GAGGTGGAAACTCAACGCAA
1566	Ttpa	CAGATCCAGATCGAAATCCC
1567	Ttpa	GAAGTCCAAGGATACTTCTA
1568	Ttpa	TTTATTTGTTGTAGCATACT
1569	Mrps7	GGAATATTACCGCAAGCCGG
1570	Mrps7	GGCCGCGACTGAAACCAGCT
1571	Mrps7	CCCCTACAGGATCTTCCACG
1572	Mrps7	GAGGCAACAAAGTTCTGGCC
1573	Tfr2	GAGGTCGCTCCAGTACAACG
1574	Tfr2	AGTGCGTGTCAGTCCACACG
1575	Tfr2	TGGTGTACGCCCACTACGGG
1576	Tfr2	ACCCCCAGTGAAGATTAGCA
1577	Pnpla6	CTCCGTAGTGTCATCCAACG
1578	Pnpla6	GCCATGTCAAAATCAGAACG
1579	Pnpla6	AGGAGACTCCGACCCTACAA
1580	Pnpla6	GGCCTGGCGCAGACAACGGA
1581	Atp8a2	GCAAGCCCTCTTCATAAACT
1582	Atp8a2	GGCCCTTATCCTATTGAAGG
1583	Atp8a2	ACAACTTCGACTCTACTGCA
1584	Atp8a2	CAGTGTTAAGAAATGGCATG

Number	Genes	Guide sequence
1585	Polg2	GAAAGAACCTAGCCTCACAG
1586	Polg2	TGTGGGAGTAAACCATACCA
1587	Polg2	TGACGCCCCCGAGCATGCGG
1588	Polg2	GCAATTAACATAGTGCTCCA
1589	Hs6st1	GGCGCACGTTCTGCACTAGG
1590	Hs6st1	ATGGCGACATGTACAGCGTG
1591	Hs6st1	CTCATCCTTTACCAGTACGC
1592	Hs6st1	CCTATAACCTGGCTAACAAC
1593	Acsl4	GTCCAGGGATACGTTCACAC
1594	Acsl4	GCCCATATCCCTGACCAATG
1595	Acsl4	CAATAGAGCAGAGTACCCTG
1596	Acsl4	GGAACAGCGGCCATAAGTGT
1597	Gne	ACGTCCAACTCAAAGAACGC
1598	Gne	TTGCAGCTCAAAGATATATG
1599	Gne	GCTCCACACGATTGTTAGAG
1600	Gne	CCTCTTGTTAAACGAGATCA
1601	Slc25a13	GGGGCGACTCCCAGTAACTG
1602	Slc25a13	CAGATTTATATGAGCCGAGG
1603	Slc25a13	ACAAGGCATCCGGAGCACAC
1604	Slc25a13	TACAAGATCGATAGGATACA
1605	Galns	AGCAGTAGCACGATGTTGGG
1606	Galns	CCCAATTAACCGGAAGACTG
1607	Galns	GGCGTAAACTGGTGCATGAG
1608	Galns	GAGAGACCCCAAATTTAGAC
1609	Nus1	GTGGTCGTAGACGCTAATGT
1610	Nus1	TCCAGGTGCCGAAGCGAACG
1611	Nus1	ACAGCACCTTCACTGCCGAA
1612	Nus1	CCAGCGCAGCCGAGGATGGG
1613	Coq5	CTTCGGGTTTGAGACCGTGT
1614	Coq5	GTTGTGCCTGAACGTAACTA
1615	Coq5	ATGAATGACATGATGAGTCT
1616	Coq5	GCCAGGATCTATGACACCCG
1617	Hgsnat	CCTGCAGGTTAACTCCACCT
1618	Hgsnat	ATGACTTCTATCCTGCAACG
1619	Hgsnat	GATGTGTGGACACATTTAGG
1620	Hgsnat	GTTGGGAGTGACATACTTCG
1621	Slc46a1	AGAGCTAACATCTGCCACAG
1622	Slc46a1	GGGCAATGGATCGATGATGG
1623	Slc46a1	TGGACCAGAAGAGTCCCACC
1624	Slc46a1	GAACTGTGGGAACCAAAGCG
1625	Coa3	GATACAAATAGCTAACACCA
1626	Coa3	CTCAGCGCATCGACCCGTCG
1627	Coa3	GGGTCGATGCGCTGAGCGAA
1628	Coa3	CATAAACTGCAACTGCGCTG

Number	Genes	Guide sequence
1629	Trmt10c	CTTACGGTATCTGTATGGGA
1630	Trmt10c	TTATTATGACAAGACAAAGA
1631	Trmt10c	TTAGTTCTCTGGTTGAGGCG
1632	Trmt10c	TAGGCCATGTCAAAAACCAA
1633	Slc52a2	TGTTGTGGGTTCAGATGTCG
1634	Slc52a2	ATGGGAGACACCTCGATCGG
1635	Slc52a2	GGCCTCTCTGTGGAACCACG
1636	Slc52a2	AAGACCGTAAAAAGGGGGGT
1637	Sco1	AAATCAATACCCATTGACCC
1638	Sco1	AAAAATGATTGAAGTCGTGG
1639	Sco1	TTGGGAAGCCTTTACTAGGG
1640	Sco1	CACTCACCCCAGGCTTCGGG
1641	Pla2g6	AAATCCATGGCCTATATGCG
1642	Pla2g6	GGCACCTGCATTAGCCCCGT
1643	Pla2g6	AGTCTCCCCAAAGTCGTTTG
1644	Pla2g6	CCATTGGGCCAAGAACGCCG
1645	Chst3	CCACGAACGAGGAACCCGTG
1646	Chst3	AACCTCGGGTCCTCAACTAG
1647	Chst3	ACTCAGTTCCTGTTCCGCCG
1648	Chst3	AAACTATGACCACAAATGCC
1649	Fut8	TGAAACAGTAGACCACGTGA
1650	Fut8	AAATGACAAAAACATTCAAG
1651	Fut8	CCAGAAGGCCCCATTGACCA
1652	Fut8	AATCAAGTATTTGACAAACT
1653	Gria3	TGTGACGAAAGATGTATGCA
1654	Gria3	GTACAATGTCAGTAAAACCC
1655	Gria3	TACCTCTATGACACAGAACG
1656	Gria3	AGGAATCCAAGTGGTCTACG
1657	Porcn	ACAACTTCCACCATGGACCG
1658	Porcn	GTGACATGGCACAAGATGCG
1659	Porcn	CCACCTTCTTCAGCCATCGG
1660	Porcn	GAAGGAGACAGCACTCTCGT
1661	Clpp	GCGCTTATGACATATACTCG
1662	Clpp	CCTGCAGATTGACGACAGTG
1663	Clpp	CATATGTATATCAACAGCCC
1664	Clpp	CAACACACCACGTGCAGATG
1665	Slc40a1	CAGGGTACGCCTACACTCAG
1666	Slc40a1	CCTTTGGATTGTGATCGCAG
1667	Slc40a1	TCATCAGGATGATTCCGCAG
1668	Slc40a1	CCCATCCATCTCGGAAAGTG
1669	Pmm2	ATTCAATGAAAGTTCCCCTG
1670	Pmm2	AAGACCAAAATTGGAGTGGT
1671	Pmm2	GCTTGGTAGCGTACAAAGAT
1672	Pmm2	AAAAGTTCGTAGCAGACCTG

Number	Genes	Guide sequence
1673	Sult2b1	GGGAGACCACGACATCGCGG
1674	Sult2b1	GGGCTCCGATCGGATCCACG
1675	Sult2b1	AATGTTTCCGAAATGAGGTG
1676	Sult2b1	AGGTGAGAGCTCATAATGCG
1677	Cd320	TGGTCTCAGAACAGGCCTAG
1678	Cd320	GCAACCACTGATGTTGTCAC
1679	Cd320	CCATCACAGCGCCACGTGTG
1680	Cd320	ACCTTCCAGTGTCTTACCAG
1681	Elovl1	GGCTATTGGAAAAGTCTATG
1682	Elovl1	GGGCAGACAATCCATAGTAG
1683	Elovl1	TCCAAAGCTACCCTCTGATG
1684	Elovl1	CGATAGGATGAAGTACACAT
1685	Ndufa1	CATCCACAAATTCACCAACG
1686	Ndufa1	TGTACGCAGTGGACACCCCG
1687	Ndufa1	GAATTTGTGGATGTACGCAG
1688	Ndufa1	CGCGTTCCATCAGATACCAC
1689	Atp6ap1	GAGGATTTCACAGCATACGG
1690	Atp6ap1	GATATGACCCTCATGTGTGT
1691	Atp6ap1	TAGCTAGATCCACATGCAAG
1692	Atp6ap1	GTGTCATTGTAACTCACAGG
1693	Extl3	GCCCAAGCCTCGCGTCACAG
1694	Extl3	TCAGACATAGCATGGACAAG
1695	Extl3	CCACACAGTGCCCACTCAGT
1696	Extl3	ATTGCGGAGGTATTTAGGTG
1697	Wdr45	GACACTCGGGACAACCCCAA
1698	Wdr45	AGGCGTCCGGATCTACAATG
1699	Wdr45	AAGCTGGTAGAGCTTCGAAG
1700	Wdr45	GTGTGGAAGTCTGCAACTTG
1701	Atp8b1	AATGCCACACCGTCCTACCG
1702	Atp8b1	AGCGTTGGATAAAGTGTACG
1703	Atp8b1	GCTGATAAAATCCTGTTACG
1704	Atp8b1	GATTTGCCATACGGTCATGG
1705	Mpc1	ACTTCCGGGACTATCTCATG
1706	Mpc1	GGCGGACTATGTCCGGAGCA
1707	Mpc1	AAATCTCCAGAGATTATCAG
1708	Mpc1	TGGGGCCCAGTTGCCAACTG
1709	Slc1a4	GTCTGCAACCGATTACACAG
1710	Slc1a4	TAGAGCCACTCCTAACACCA
1711	Slc1a4	GATGCCACCCAGACGCCCGA
1712	Slc1a4	ACCCACCAACACTCCCGACA
1713	Pgam2	GGATGTTACGGACCAAATGT
1714	Pgam2	AACCAAGAGAACCGTTTCTG
1715	Pgam2	GCTTCAAGCCTGCATAGCGG
1716	Pgam2	GTTTGACATCTGCTACACGT

Number	Genes	Guide sequence
1717	Samhd1	ATCCTTACATTATGTCGATG
1718	Samhd1	GCTTGATATAGCGAAGTCGC
1719	Samhd1	CTTGGGCTGCCATCGCAGCG
1720	Samhd1	TTAGGATCTTACCTAGGTCG
1721	Pdss1	AGCCTTTAGACCGATTATTG
1722	Pdss1	GAGGCGGCACGTGTTCCGAG
1723	Pdss1	TATACTATGCATAGTTGGGG
1724	Pdss1	GTTATTGAAGATTTGGTGCG
1725	Dgke	TCTCGTAGTGGAACTAACAT
1726	Dgke	GATCATGCTCAAGAACGACA
1727	Dgke	GTCCACGACGAGTGCATGCG
1728	Dgke	ACAAGAAAAATACATTCCAG
1729	Pigp	TCTCTTGTGCAGATACTGGG
1730	Pigp	TGCAGTACTTTATCTTGTGT
1731	Pigp	AAGGAGTTTAACCAAGATTC
1732	Pigp	ATGAATGGAGTCAAGTGGAG
1733	Prodh2	TAGTCCATGAGTGACCAAAG
1734	Prodh2	CCTGTGCCACTCGGTGCAAG
1735	Prodh2	GGACTTATCCCGAGCCCTCG
1736	Prodh2	GTTGGCAGTACCCACCGAGG
1737	Pex14	CTTCACTGGGATCTGCCAGG
1738	Pex14	ATGCTCTCCTGGTCGCAAGT
1739	Pex14	GGAACAGGTGACTTACTGTA
1740	Pex14	ATACTTACCAGTGGCTCTCG
1741	Mrpl12	TCTTTGGGAGCATTATCCAG
1742	Mrpl12	ATACCTTCAGGAGTTCGTTG
1743	Mrpl12	TGCCCAGCGTCTGTGCAGCG
1744	Mrpl12	GCCCCCCGGAGTCCAAGCCG
1745	Ggcx	TGTGTGTATAAGAGGTCCCG
1746	Ggcx	GCCTGCACGATGTCCACACG
1747	Ggcx	AGAACTGTGTAGTTCCAAAG
1748	Ggcx	GCTCGCCCGTGAGGCCGTCG
1749	Timm22	GCTGGCATTGATACCAACGT
1750	Timm22	AGAAGAAGGCTGTACTGCAA
1751	Timm22	TGGGCGACAAGCGTCAGCCC
1752	Timm22	CCTCTAGGGTTTGTCTTGGG
1753	Ivd	AATATCGAGTGGGCCCGCCG
1754	Ivd	CTCCTGGCTCAGGACGTTAG
1755	Ivd	GGTAATGGAAGAGATATCCC
1756	Ivd	TTCTTGGAGGTACTAAAACC
1757	Pus1	CCTGCAAAGAGGGTCAAGGG
1758	Pus1	CTTACCCAGAATCCGAATGT
1759	Pus1	TACTCGGGCAAGGGCTACCA
1760	Pus1	TCCAGGCCCTCACGTACGAA

Number	**Genes**	**Guide sequence**
1761	Adar	ACTCCAACAAGCCGCCTACG
1762	Adar	AGAGGTAACCCCAGTAACAG
1763	Adar	TTCTTGTAGGGTGAACACCG
1764	Adar	TGTATCCAGGAATTCCCTAG
1765	Suclg1	GAGTACGGCACCAAACTCGT
1766	Suclg1	AACAGAATGGGATACGACAC
1767	Suclg1	TGACACGCCAGGGAACGACG
1768	Suclg1	CATTAATGAAGCAATCGACG
1769	Aldh18a1	CAAGTCTAGAGTGGGCCTAG
1770	Aldh18a1	CGATGGGGACGATGTTCATG
1771	Aldh18a1	CGTCCGAGAGGACAATCAAG
1772	Aldh18a1	TGAGGGGTACCGTGATAAAG
1773	Ctsf	ACAATTACGGCCGTGCTGCG
1774	Ctsf	AAAGACAGTCAATCGCCACT
1775	Ctsf	ACCAGGGGATCATTGCAAGG
1776	Ctsf	CCTGAATCCCCTCTTACAGA
1777	Tbk1	TGCCGTTTAGACCCTTCGAG
1778	Tbk1	CTTCTCGCTACAACACATGA
1779	Tbk1	CAACATCATGCGCGTCATAG
1780	Tbk1	CGGGAACAACTCAATACCGT
1781	Pex3	AAACAAGCTGGAAATATGGG
1782	Pex3	TCATTAAACAAGCTGTACAA
1783	Pex3	CATGCTGCCGACACTGAGAG
1784	Pex3	TACTGCTGCTGTACATCCGG
1785	Txn2	AGACCACCAGCATTGTACTG
1786	Txn2	AGGGAAGCCCACACACCCTG
1787	Txn2	GCGGTCCTAGGATCTTGCAG
1788	Txn2	AAAGGTCGTCAAACAGACTC
1789	Mlycd	GACTTCGTGAGCTTCTACGG
1790	Mlycd	TGGAAGAGGCCGCGATACCG
1791	Mlycd	CTCCGACTGAAACCGAGGAG
1792	Mlycd	CCGCACAGCCGACGTCCCCG
1793	Tdo2	GATAGCTCGGATGCATCGTG
1794	Tdo2	TGATGAATAGGTGCTCGTCA
1795	Tdo2	AATCCATTTGGCTCTAAACC
1796	Tdo2	CACTATCGTGATAACTTTGG
1797	Alg2	CAGAAAGACCATGCGCACGT
1798	Alg2	GCTCTCGGTGCAATGCGCAG
1799	Alg2	TCTCTATCAACCGATACGAA
1800	Alg2	ACTGGCCAGACGGCGTAAGA
1801	Mocs1	CACTTGGATTCCGAACACGG
1802	Mocs1	TAGGTCTCGAGGGCTCCCCG
1803	Mocs1	CGATGTCCACCACATCCGGT
1804	Mocs1	AGGCCAGTATTGCATGCCCG

Number	Genes	Guide sequence
1805	Nfu1	ACTGTACCTGTGTTACACAA
1806	Nfu1	GAAACAGTACCTGGCCAGAG
1807	Nfu1	GTGTAGTCCGGCTGTGCAGG
1808	Nfu1	GCGCTACCTGCTTCTCCCGG
1809	Dhodh	TTGATCCAGAGTCGGCGCAC
1810	Dhodh	GTAGAAATGGTCGTCCCCCG
1811	Dhodh	ATAAATTCCGAAATCCAGTA
1812	Dhodh	GGTATGGATTCAACAGCCAC
1813	Stap1	GTTGGCCAGTAAGGCACACG
1814	Stap1	GGAGCCAGTACAAGACTATG
1815	Stap1	CTTCATTCTTACAGTAACAG
1816	Stap1	GGAGTACAAACACTATTGGA
1817	Aldh1a3	CACCAGGCATGAGCCCATCG
1818	Aldh1a3	TGCATCCAGCCGGCGCCACG
1819	Aldh1a3	CCACCCGGCAAAATATCTGA
1820	Aldh1a3	AACACTAGAGAAAATATGTG
1821	Slc25a20	ATAGGGGTGACTCCAATGAT
1822	Slc25a20	TCCAAGGTCCCAGAGTACAT
1823	Slc25a20	TCAGGGGAGAACAAGTACAG
1824	Slc25a20	TCCCAGCTGTAAACAGCTGT
1825	Srd5a3	ACTGCTTGGTCTTCCCGTAG
1826	Srd5a3	AGCACTCAAAGAGTCTCCGA
1827	Srd5a3	ATCTACTGATACAAGCCCGG
1828	Srd5a3	TCTACGTCATCTCAGTTGTG
1829	Mogs	TCTAGGTCATTCTTCCCACG
1830	Mogs	TCGGCAGCATATCCACGATG
1831	Mogs	TGCCGAAATAGACGTGTGGG
1832	Mogs	GAGGTCCTACTACCAGAGAT
1833	Tk2	CTCCAATACAACAGACGTCG
1834	Tk2	TTGAGGGCAATATTGCAAGT
1835	Tk2	AGAATCGCGTAGTCAACCTC
1836	Tk2	TACCATGATGCCAGCCGATG
1837	Cldn10	GCCCGAGATGGAGACTACGA
1838	Cldn10	CAGACCATCCAACGCCAGCA
1839	Cldn10	TAGAGGACTAATGATCGCTG
1840	Cldn10	ATCTGCGTTACCGATTCCAC
1841	Chst11	AGCCAACGAAGCCCACGTGT
1842	Chst11	GCAGACACCAGCCTCTCGAA
1843	Chst11	AGCAGATGTCCACACCGAAG
1844	Chst11	ACCTCCTTCCACAAGCGCTA
1845	Treh	AGATTAGGGAGGACCTCTCG
1846	Treh	AGCTACGGACATATCCCCAA
1847	Treh	AGGGGACCGAGAGACTCTGT
1848	Treh	AGGAACGCGTTCAGATCAGC

Number	Genes	Guide sequence
1849	Hibadh	AGCTCCACAGTATACCACGT
1850	Hibadh	GCTGCCCTCCAGTATGAATG
1851	Hibadh	CGTGTTCCCTGATGTATGCA
1852	Hibadh	GGAAACCTTACATTTATGGT
1853	Sumf1	GCAGCCGCACGAGCCCGCAA
1854	Sumf1	CTCGACTGGCTATTTGACAG
1855	Sumf1	AGTGAAAACGCATATCCACC
1856	Sumf1	AGCTAATTGGAGACACCCAG
1857	Ngly1	GAGCTTCAAACCCTAATGCA
1858	Ngly1	AGAGACTAGATCTAGAGATG
1859	Ngly1	GCTACACTGTGATGCATGTG
1860	Ngly1	GCTGGGTTAATACGGCACTC
1861	Thap11	AGCCTGGTTGCTGTCTACGG
1862	Thap11	GCTGCTACAACAATTCACAC
1863	Thap11	GGGACACGTTCTTGAGCCAG
1864	Thap11	CCACGCAGCGGGAAAATGGT
1865	C1galt1c1	ATATGGACACAAATGACATG
1866	C1galt1c1	TGTGCCTTGATCACTATGCT
1867	C1galt1c1	CAAGAACTATACAGTATACC
1868	C1galt1c1	CAATAACAGCGAAAGTAGTG
1869	Bco1	GACATGATGGAAGACCACCA
1870	Bco1	GAAGAGTCCCGTGAAGCACG
1871	Bco1	TAACATGGGCACATCCGTCG
1872	Bco1	GGGCACAGCAAACCTCCTGA
1873	Slc29a1	GCTGATGCAGAAACGAGTTG
1874	Slc29a1	GCATGATTGATCAGTGTCCG
1875	Slc29a1	TACACAGCCCCCATCATGAG
1876	Slc29a1	GGCCAAAATGACAACTGCAC
1877	Inpp5e	GAGGTCCCTACGGATAAACA
1878	Inpp5e	AGTGATCGTCACCAGCCAAG
1879	Inpp5e	CACCGAGGCTGACTACACTC
1880	Inpp5e	GGAGATACCTAAGTCCCGAA
1881	Mrps22	CCGATGCTCTGCTCGCGACG
1882	Mrps22	ATTTCTTTAGGCTACTAGAC
1883	Mrps22	AATAAATGACGTATTAGCTG
1884	Mrps22	TGGTATATACTCACCCGATG
1885	Mrps23	TTATATATGTCATACCACAG
1886	Mrps23	GCTTTGCCGTATCGCAAGCG
1887	Mrps23	ACTTCAAGTCTACCTGTCAG
1888	Mrps23	AGCTTTCTGACCAGATCCAT
1889	Htra2	AAACGGATCAGGATTCGTAG
1890	Htra2	GCCTCATAAGTATCCCCGCT
1891	Htra2	GTACAATTTCATCGCAGATG
1892	Htra2	CGGAGGTCAGGAGCTAACAG

Number	Genes	Guide sequence
1893	Dpys	GTGTGCGTGTCGATGCCCCC
1894	Dpys	GTGGCGATTTGACCACAACA
1895	Dpys	CGAAGGTGGTAGCCGATGCG
1896	Dpys	GAAAGGCAGCTCCCTCATCG
1897	Lpin2	GGATACTCACGTTTCTAATG
1898	Lpin2	GGTTATATATCCGGATCACG
1899	Lpin2	TGCAGGTCACCAAAAGAGAA
1900	Lpin2	AACCTGGATCCGTGTCACTG
1901	Cubn	GTGTATCTGGAACATTCGCG
1902	Cubn	AGTTATCAACTTCACCCACG
1903	Cubn	ACAGCTCCGAATGCTACTGG
1904	Cubn	CCACCTGTGTGAACACTATG
1905	Sdhc	TACTTGTAGATAGTCAAATG
1906	Sdhc	TCTGGAATAGCCTTGAGTGG
1907	Sdhc	TTTGGGAACCACAGCTAAGG
1908	Sdhc	CAGGAAGCAGCAGTGCCGAC
1909	Ethe1	GGGCTCAAGCTGTTGTACGC
1910	Ethe1	AACTCACAAAGCGTCCAAAG
1911	Ethe1	TCCACACCCTCGGATCAGCA
1912	Ethe1	GGGTGACCGGGAGTCAAGAG
1913	Sdhaf2	CTCTATGAGAGCAGAAAGAG
1914	Sdhaf2	CGTTAATCAGGCGATCATAG
1915	Sdhaf2	AATGATGTCACACTAGGCAA
1916	Sdhaf2	GCAGATACTCTTTAGCAAAC
1917	Rmnd1	CGGGTCCGGGATGCTTTCAG
1918	Rmnd1	GAAGTGACAAGCCTGCCTAG
1919	Rmnd1	GAAAGTACAACATGCCACAA
1920	Rmnd1	GGACAATCAAAACTGCACAG
1921	Ndufa9	GGTTAACAACGTATCGACCC
1922	Ndufa9	CCAGGTCACCCATCAGACGA
1923	Ndufa9	GATGCCTGAGCTATTGCTCG
1924	Ndufa9	GTCATACCTCACGGGAAAGG
1925	Apoa5	CAAACTCACACGTAAGGCGA
1926	Apoa5	TCACCAAGCGTTCTGCGTAA
1927	Apoa5	GCAGTTGAAACCCTACACGG
1928	Apoa5	AAAAGCTGGGACCCTTGAGA
1929	Cox7b	TTATCTGCTCACCTTGGAGA
1930	Cox7b	GGGAATGCTATATTAGCAGG
1931	Cox7b	AACTAGGTGCCCTCTTCTGG
1932	Cox7b	TAGCATTCCCATATTTGTCA
1933	Acer3	ACAGAACTCAGCGACGAACA
1934	Acer3	ATACAGTTTAACAGTAACTA
1935	Acer3	TCAGGTCATGTATGGAATGT
1936	Acer3	TGAATTGCACCAAAAATTGG

Number	Genes	Guide sequence
1937	Ndufb9	TGTGGATACACCATGACTCG
1938	Ndufb9	GTAGCACTCATATCTCTCGA
1939	Ndufb9	AGAATGAGAAGGATATGATG
1940	Ndufb9	AGGATACATTGCTTTCTCAG
1941	Msmo1	TAGTATGTTCCACAAATCAG
1942	Msmo1	AAAGTTCCAGATCGCAACCT
1943	Msmo1	GATAAACCAGAAACCTTCGA
1944	Msmo1	ACAGGTACTTAACTTTGGCA
1945	Mrps16	TGCTCACAACAAGTGCCCCA
1946	Mrps16	GCCACCCAAAGCAAGGCGTA
1947	Mrps16	AAAACTAGTTGCCCTCAACC
1948	Mrps16	GGCCGATTTGTGGAGCAGTT
1949	Tmem126a	TTTGGCTATACCCGTCAATG
1950	Tmem126a	AACTAGTGCACCCCGTGTTG
1951	Tmem126a	TAAAACATACCTGTACTCAA
1952	Tmem126a	AACAACTTCCAGAATCAGAC
1953	Cox20	CGCCCCGGAGCCCCACGAGA
1954	Cox20	TAGCGAAATTATACCTACAG
1955	Cox20	AGTATAGATTCTCGAGCACA
1956	Cox20	ATTAGAAGATCATGTGATGT
1957	Cox14	CACAGTGAGGAGCATCATCG
1958	Cox14	GGTAACCCCCATACACAGTG
1959	Cox14	GCGCAGCTGGAGGTAACGGT
1960	Cox14	GCCAAGCAGCTAGCCGATAT
1961	Iscu	TATGAAAACCCTCGGAACGT
1962	Iscu	CCAGCTCCTTAGCCACAGAG
1963	Iscu	TTCATGACGTCACCACATGC
1964	Iscu	GGCCAGGCTCTACCACAAGA
1965	Sar1b	AAGAATTAGAATAGGCACGT
1966	Sar1b	ACTTACTGGGATGTAGCGTT
1967	Sar1b	TCCCGGCATTATCCAATCCA
1968	Sar1b	CAATGCCATTGATAGCAGGA
1969	Tsfm	CAGATACTCACCAATCGCTA
1970	Tsfm	CCATGGCTCACGTTTCACGC
1971	Tsfm	ACTGTCAGAACCTGACGGAT
1972	Tsfm	AGGAGCTCCTTATGAAACTG
1973	Cyc1	TAGCTCGAACGATGTAGCTG
1974	Cyc1	GGTGGGAGTGTGCTACACGG
1975	Cyc1	AGCTACCCATGGTCTCATCG
1976	Cyc1	GGTCCCGGCAGCTTCCATTG
1977	Pam16	TCACCTTCTGGACCTCCTCG
1978	Pam16	CCTGGCCCAGATCATTGTGA
1979	Pam16	AGGCAGCCGCTGACGCTCGA
1980	Pam16	CCGTGTATCCACAGCCAGCC

Number	**Genes**	**Guide sequence**
1981	Nmnat1	AAAGGCATTATCTCACCGGT
1982	Nmnat1	GAACAGCCTGAGGTGCATGT
1983	Nmnat1	GTTCTGCCATGATGATTCGG
1984	Nmnat1	GGAGGACATCACGCAAATCG
1985	Ndufb3	GCTGGACATGGACATGAACA
1986	Ndufb3	AACTTCCAGATTACAGACAG
1987	Ndufb3	GACTCATCTTACCGAGCCCA
1988	Ndufb3	CATGGACATGAACATGGACA
1989	Timm50	GACGCCACCAGATATATGGA
1990	Timm50	GGGTCCACACTATCAATGAG
1991	Timm50	ACTGGTCCTGGAGCTTACCG
1992	Timm50	ATTCCTGATGAATTCGACAG
1993	Pgm1	CATTACCGATGGACGCGCTG
1994	Pgm1	ATCATCTCTCCCCACGATCG
1995	Pgm1	TGGGGGTTATATCAGAGAAG
1996	Pgm1	AGGCCAACTGCACAAACTCG
1997	Alg14	TGTCCAATGCCTATTCACCA
1998	Alg14	CCGAATTCCGAGAAGCCGGG
1999	Alg14	AAGAGTCTGAGAGACTCTCG
2000	Alg14	GCTTTATTCGGAGAACCAGT
2001	Taz	TTTGGAGAAGCTTAACCATG
2002	Taz	GGTCATCCATGCAAGACTGG
2003	Taz	AGCAGCTCACCTCGACACAC
2004	Taz	TATGAGCTCATTGAGAACCG
2005	Etfdh	GGTACGGATTCTGATAGTCG
2006	Etfdh	GAGTAGATCACACTGTTGGT
2007	Etfdh	GGCGGGAAGAGGATAGCCTA
2008	Etfdh	GGCAATTACATCGTACGCCT
2009	Pnpla2	GGCAGGAGGCCACGCCAATG
2010	Pnpla2	TGTTCTTGCAAAGCGCTATG
2011	Pnpla2	AGCAGGTGCCAACATTATTG
2012	Pnpla2	CCTGTTTGCACATCTCTCGG
2013	Pmpca	AGAGCTCACACACATCATGG
2014	Pmpca	AGAAATTGAGATGACGAGGA
2015	Pmpca	TGAAACCAAAGTTACCACTC
2016	Pmpca	TCAGTGGCACAGTACACTGG
2017	Acadsb	GAGGATTTGAGGACACGAGG
2018	Acadsb	CATAGCGAAAGAGTCGCTAC
2019	Acadsb	AAGTTGAAGCACAATATGGA
2020	Acadsb	TTCAAATGTTAACTGACAGG
2021	Pccb	GGAAATTGAAGAATTCACGC
2022	Pccb	GGAGTCCTTGGCTGGCTACG
2023	Pccb	GCTTGTGCTGCGCGTCGATG
2024	Pccb	TGTGAAGTCTGTTACCAATG

Number	Genes	Guide sequence
2025	Sdhd	GCAGAGAGGACATACAGTGG
2026	Sdhd	AGGACCAGCCTACCCAAGGA
2027	Sdhd	TGCAGTGGCCAAGGAGCTCG
2028	Sdhd	AGGGATTCAAGTACCCAGCA
2029	Sdha	GTCAGTTACCTCAACCACAG
2030	Sdha	TTCTACTCAATACCCAGTGG
2031	Sdha	TGCACAGTGCAATGACACCA
2032	Sdha	ACTGTGCATTACAACATGGG
2033	Acad8	TGGCTCCCAATATGGCGGAG
2034	Acad8	CCAACAGGATTGGGACCGAG
2035	Acad8	TCTCCATGGTACAGAGCGGT
2036	Acad8	GTGGATGCTTATATAGGCAG
2037	Trit1	GCCACTTGTAGTGATTCTCG
2038	Trit1	TGAGCGCTTGGATAAAAGAG
2039	Trit1	CCATAAACGGCTAAGCCAGG
2040	Trit1	TGTGACCAGCTACACCGTGG
2041	Plin5	AGGGACTTAGACTCACACTG
2042	Plin5	GCAGAGCAAACACCGTACCC
2043	Plin5	GAATGTGGTGAATCGAGTGG
2044	Plin5	ATGGTGGACCTGGCCCAAAG
2045	Uqcrc2	AACAAGCCGATTCTTGACAG
2046	Uqcrc2	ACAGTACAAAGGATTAGCCA
2047	Uqcrc2	CATCTTTCAAGATAACCCGT
2048	Uqcrc2	GCAAAAGCCAAATACCGTGG
2049	Oxct1	GAAGCGTTTATCACTCCGAA
2050	Oxct1	CATTGCCAGCAAGCCACGAG
2051	Oxct1	AGCTGCAGGAACTACCGTGG
2052	Oxct1	TCTAGGGCACACTTGCCGAG
2053	Magt1	TGTGTGTGCGATCGCAGCGG
2054	Magt1	CAGCTGAGCAGATTGCCCGG
2055	Magt1	TTATGCTGGACCCCTAATGT
2056	Magt1	GTGGAGCTTTAACAAGACGA
2057	Gatm	ATCAAAGACTACTTCCATCG
2058	Gatm	ATTCGTTGTAAGAGGAGACA
2059	Gatm	ACTTGAGTGACCAGTCGATG
2060	Gatm	ACAACCATCAGGATGTCTCG
2061	Trak1	GTGGAAGTAATTCTGGACGG
2062	Trak1	TCCGCTCTTAGCTTGTAATG
2063	Trak1	TTAGGCGGCTATCCCTACGC
2064	Trak1	TTACCATGTTTAGTGCGCGG
2065	Mmachc	CAAACCAGCCCCCAAATCGG
2066	Mmachc	CCAAACACTGAGAGACCCGG
2067	Mmachc	GAAGTTTATCCCTTCCAGGT
2068	Mmachc	ACTATGAGGTACACCCCAAT

Number	Genes	Guide sequence
2069	Ndufa6	GCACCTCCCGATACCAAGCG
2070	Ndufa6	ATATCACGGTGAAACAAGGA
2071	Ndufa6	ACTGAAAATGGGCTTCACCG
2072	Ndufa6	ACCTGAACGAGGCCAAGCGG
2073	Rnaseh2b	CTCCTAGGTCAACCAAACTG
2074	Rnaseh2b	TCAGCCCTTGGACCAAGTCG
2075	Rnaseh2b	CAGCCTTTAGGAGATAGTGA
2076	Rnaseh2b	TGGCCAGCTTTACGAACAGG
2077	Lipt2	TACACGGGCGGGCTACGCGG
2078	Lipt2	ACCCGCTTTGGTCCCCGACA
2079	Lipt2	CCGAAGTTCGCACAGTCGCA
2080	Lipt2	CAGACGCCAGTGTAGGGCGG
2081	Pdzk1ip1	CGGCGAAGACGATTGCAACA
2082	Pdzk1ip1	AGAACACAGCGACAGCAATG
2083	Pdzk1ip1	GCACCTGCCAGCTGTCAACA
2084	Pdzk1ip1	CAACCACTTCTGGTGCCAGG
2085	Ndufa13	GGTTCCGCTTGTAGTCGATG
2086	Ndufa13	ACTGACCCGACAGTCCCCGG
2087	Ndufa13	GATTCTCCGGGAAAACCTGG
2088	Ndufa13	GTGGAACCAGGAGCGCAGGT
2089	Ndufb8	GGGGTCCTAGGATATGACCC
2090	Ndufb8	CAAGAAGTATAACATGCGAG
2091	Ndufb8	CATGTACATCAGGAATCGTG
2092	Ndufb8	CAACCGATCACAGCATGAGA
2093	Uqcc2	CCAGTGGACGAGACCAAACG
2094	Uqcc2	TTCAAACTACTACAAGCACA
2095	Uqcc2	GCTCTCGTACATCTGATCAC
2096	Uqcc2	CACAGAGCTTAAGGAAACGC
2097	Ndufa10	TCGATATAGATGACTGCGTG
2098	Ndufa10	CCACTAAACTCTATGTCGAG
2099	Ndufa10	TGGGAAAAACAAGCTCGCAA
2100	Ndufa10	CTGGAGGCAATGTACAACCA
2101	Slc25a19	ACGGACCATGTATAAGACCG
2102	Slc25a19	TCAGCGCACTTTGTGTGCGG
2103	Slc25a19	GACCCCAATGCCAAATACCA
2104	Slc25a19	AGAACTGCAGGCCCGCGTAG
2105	Pigc	TGTACTGACAGACTCCGTCA
2106	Pigc	GAATAAAACATACCCAACCA
2107	Pigc	TCCGGAAAAACATCTATGCC
2108	Pigc	GGCCGACCTGAAGAGTACTC
2109	Far1	CTCTCGAACAGGCCTTCAGA
2110	Far1	ACATAGACAGAATTCACCCT
2111	Far1	CGTCGATCGTCGGCGCCAGT
2112	Far1	TCTCGTTCCTGTAGATGTAG

Number	Genes	Guide sequence
2113	Dhdds	GGATGTCGGGATGAGGAGAG
2114	Dhdds	CTATGCCAAGAAGTGTCAGG
2115	Dhdds	CTTCAAACGTTCCAAGAGTG
2116	Dhdds	GCAGCAGATGCAGATCACCC
2117	Hoga1	GCGGCCACGATAGTAACAAG
2118	Hoga1	ACAGTGTCCCAGCCAATACG
2119	Hoga1	TGGGTATGGCCTGGCGCACG
2120	Hoga1	CTTCCCTCTTACCTCGAAAG
2121	Mtpap	TTTGCCAAATGTGTTCACTG
2122	Mtpap	CAGTTGTCCAGGGACTATTG
2123	Mtpap	TGTTAGCAGTCAGATCACAC
2124	Mtpap	ATGTATCAAAACAGTCCGCT
2125	Pnpla8	GAAGGCGTACAAGCCTTAGT
2126	Pnpla8	AGTAATACAGAGCTTTGGGT
2127	Pnpla8	CTTAGCACTTCTGCTCCCAA
2128	Pnpla8	CATGCCGCTGGATGAATGTG
2129	Slc25a46	GTGAATTTACACCTTTACCG
2130	Slc25a46	TGAGATGGTAATGCCGAGCA
2131	Slc25a46	GCGGAACCCTCGAGCGTCGG
2132	Slc25a46	AATTGGACGAGTGATAGGCT
2133	Abhd5	AGTTTGGATCAGGGCCCTAG
2134	Abhd5	TTGAAGATCTAAGCACCGAT
2135	Abhd5	CGGCAGCCAAGAACCCTCCC
2136	Abhd5	GAGCCTGTGCGCATATCCAA
2137	Abcg8	GCGCCGACGAGTGAGCATTG
2138	Abcg8	GGTTGCTATAGCGAGGACAA
2139	Abcg8	AGTCTGTACTTCACCTACAG
2140	Abcg8	TGTGATCACGTCGAGTAGTG
2141	Agpat2	TGATTAGAGATGATGACACA
2142	Agpat2	GGGTACACGCAACGACAATG
2143	Agpat2	AGCGTGAGCTAATGTTCACA
2144	Agpat2	GCCGCACCGTGGATAACATG
2145	Uqcrb	ATGCCTCATAGTCAGGTCCA
2146	Uqcrb	GCTGCAGGATTCAATAAACT
2147	Uqcrb	TAGTTTCAGCATCAAGCAAG
2148	Uqcrb	AGCCATAAGAAGGCTTCCTG
2149	Cog6	AGTCGTTGGGCATATCACCG
2150	Cog6	TTGTGCAGCTTACGCGACAG
2151	Cog6	CGGACTCGAAGAAATTTACG
2152	Cog6	GGTCAATCACTATACCTCAG
2153	Slc39a8	TCAGCTGCTGTAAGATCGCG
2154	Slc39a8	AGGGGGTTAAAATCAATCCC
2155	Slc39a8	CGTTAGGCTCAGTGACAGCG
2156	Slc39a8	CGGCGCCAACCGGAGCCTGT

Number	Genes	Guide sequence
2157	Pigm	GTTTGTACGACTTCCTGAGG
2158	Pigm	CCGCGCGCTTCGTCACGGAA
2159	Pigm	CGCGAAGCCATAGAACACCG
2160	Pigm	AGTACGGAGAGAAATTATGG
2161	Alg13	GATCTTGTCATTAGCCACGC
2162	Alg13	GTGAATGACTCAGTACGGAA
2163	Alg13	GGTTGTAACCCAGACTCTCG
2164	Alg13	TTTCGACGAGCTCGTCGCAC
2165	Slc25a26	GGCATTCAAGGACTGTACCG
2166	Slc25a26	AACACCCTTACCGTTAGGAA
2167	Slc25a26	CCAGCCTTGTTAAATCCCTG
2168	Slc25a26	ACTTTCAAGGATTCCCACAA
2169	Sdhb	TGCGCCATGAACATCAACGG
2170	Sdhb	ACAGTATCTGCAGTCCATCG
2171	Sdhb	ACCTCGAATGCAGACGTACG
2172	Sdhb	TAGAAGTTACTCAAATCCTG
2173	Dnajc19	AATTTCTTTCAGGCATTCGG
2174	Dnajc19	TTAGCCCTACTGCCAATAAA
2175	Dnajc19	TTTACAAGCCATGAAGCATG
2176	Dnajc19	CCAGCACAGTGGTAGCAGTC
2177	Jagn1	GCACTACCAGATGAGGTACG
2178	Jagn1	GTACCTCATCTGGTAGTGCA
2179	Jagn1	AGTGCATGGCGACGCGCTCC
2180	Jagn1	CCGTCGGTGCCGGCCGCTCG
2181	Dcxr	TATGGTTGGTCAGTGCACGT
2182	Dcxr	GGCGGTGAGTCGGACGCGAG
2183	Dcxr	GCCAAGGGCATGATAGCTCG
2184	Dcxr	CCTAAGCAATGTGGGACCCG
2185	Coa6	CAGCCCCTTCCATGAAGGAA
2186	Coa6	GCGGGACTTACCCACTGCTG
2187	Coa6	CGTCCAGGCAGCGCCAGTAC
2188	Coa6	GCGCTGCCTGGACGACAACG
2189	Coq9	CTCAGGTACACAGACCAGAG
2190	Coq9	GTGCCTTCCACACTGCCGTG
2191	Coq9	GGGGCCAGTGCTCAATGTAG
2192	Coq9	GTTGAGGCGAGCATTGCACT
2193	Npc2	GTCAACATCACCTTTACCAG
2194	Npc2	TAAGGTGGGAGTTATAAAGG
2195	Npc2	CCCCTGCACTTCAAGGACTG
2196	Npc2	GTCAGGCTCAGGAATAGGGA
2197	Atad1	TACGCACATGCATATTAAGA
2198	Atad1	TAGATGCCATTGACCCCACC
2199	Atad1	AAGGCTGTAGCTTTATGGCA
2200	Atad1	CACTTATCAGTCAGTGTCGA

Number	**Genes**	**Guide sequence**
2201	Apopt1	TGAGCGCCCTACGGATCACA
2202	Apopt1	TGTGAAAATGAACGGGACGA
2203	Apopt1	CAGTCTTGCCATGATTGGAT
2204	Apopt1	AGAATGGAATCAACAGTTCT
2205	Gcsh	GCGGCGGCGCTCGGTACACA
2206	Gcsh	AGAGGAAGGTATTGGAACGG
2207	Gcsh	AATTCACAGAGAAACATGAG
2208	Gcsh	GGGACAAAATTGAAAAAACA
2209	Rnaseh2c	CGTGAAGAAGCGATCTACCG
2210	Rnaseh2c	CGGCTGACTAGAACGTCGCA
2211	Rnaseh2c	AGGGTTTGCGGGATTCGTGA
2212	Rnaseh2c	ACCGTCTGCATCGTGGCGGA
2213	Pdhb	TCTTAATTGTAGGTTAGCAG
2214	Pdhb	GGGCACAGGCTGAAGGCCAG
2215	Pdhb	TGAAGCTATTAATCAAGGTA
2216	Pdhb	GCCATTCGTGATAATAACCC
2217	Slc25a22	GTGTCTTAGCCAGGTCGATG
2218	Slc25a22	ATACATGCCGAAGTAGCCCT
2219	Slc25a22	TGATTCAGGTTGGCAAACAG
2220	Slc25a22	GACACCAGCTCTCTAAGGAT
2221	Pomgnt1	GCCTTCGTGGGACGAAAAGG
2222	Pomgnt1	CACTCGGAGAGCAATCAGCG
2223	Pomgnt1	GCTGTGTGTTCATACCCCTA
2224	Pomgnt1	GGGCTGAACTCAATAGGCGT
2225	Mto1	TTCGACGTGGTAGTTATCGG
2226	Mto1	AGTGTAACAGATAACCCTTG
2227	Mto1	ATGGACTCTTTAGCGAGTCG
2228	Mto1	ACTTTATAAACAGAACATGC
2229	Stt3b	AGGGTACATATCTCGGTCAG
2230	Stt3b	CGACAGCATGCAGACGACCG
2231	Stt3b	GTCATCTATCTGACATACAC
2232	Stt3b	TACAGCAAGAGAGTCTACAT
2233	Sdhaf1	CGGACCCCGCGGGCGCACGA
2234	Sdhaf1	GCAGCACGTCGGTTCGCGGA
2235	Sdhaf1	GTATCGAGTATCTGTATCGC
2236	Sdhaf1	AGGTACCCATGGCCGTGGCG
2237	Ndufs3	TTGTGGGTCACATCACTCCG
2238	Ndufs3	TACGTGCTGCCACAGCACGG
2239	Ndufs3	CAGCGTTGGGATGACTCCAT
2240	Ndufs3	GGGTGTCAGCTCATCTGCAT
2241	G6pc3	TAGGCCGACTGCCAATAGGA
2242	G6pc3	TTCCCGGGCTAGAGAATATG
2243	G6pc3	GGGGCTCATTAGCCAGCCAA
2244	G6pc3	TAAAGAGAGTCCAATACATG

Number	Genes	Guide sequence
2245	Lmbrd1	TTACAAACAGCAACGCAACG
2246	Lmbrd1	AAGGCACGTCTATCCCTCGC
2247	Lmbrd1	CATCATCTGTTTCAGGCGTA
2248	Lmbrd1	AACGGTATTCTCAATCTGTA
2249	Slc39a13	ATAAAGAAAGCGAGTCCTGG
2250	Slc39a13	TACACCTGTAACATCACCCC
2251	Slc39a13	CTCACCTTCTGACTGTAACA
2252	Slc39a13	CTGGGGCTATGGGTCATCGC
2253	Gpihbp1	GCAGGTATCAGTACACCACA
2254	Gpihbp1	CACTGTGCAATATTCCACCC
2255	Gpihbp1	CTGTCAAGTGCTTCACAGCG
2256	Gpihbp1	CCTGCTTCCAGGGATCATGT
2257	Tmem126b	AAGATGGCACTTTATAAACA
2258	Tmem126b	AAAGAGCTTGTAAGAAACGA
2259	Tmem126b	GCACTAATTGGCATGGCATG
2260	Tmem126b	CCGTCTAGGTGACATAAGCA
2261	Ndufaf4	TAACGTATACATTACCGGCA
2262	Ndufaf4	AATATCACGGACATTCCCAA
2263	Ndufaf4	AAGGAATTCAGACTGCCGAT
2264	Ndufaf4	CGCCTTAAGGAACTTCAACG
2265	Dpm3	AAGTTAACACAGTGGCTTTG
2266	Dpm3	GCGATAGCCCACCGTGCCCA
2267	Dpm3	GGCCACAGGACCTCTCGGCA
2268	Dpm3	ACCAACAGGTAGGCAGGCAG
2269	Mocos	GCTTCAGCGCTATTACATCG
2270	Mocos	GCTGTAAATGCGCACCACAG
2271	Mocos	GGTGTGGAAGCTGACAGTCG
2272	Mocos	CAAACTCACCCACGACACTG
2273	Pmvk	AGCTGGTGAGTGACACACGG
2274	Pmvk	CTACAAGGAGACCTATCGGA
2275	Pmvk	GCTCTCTGGTCCACTCAAGG
2276	Pmvk	TGTCTGTATCACAGCCCCAT
2277	Elac2	TGTGCTGCGCAGGTGAACGG
2278	Elac2	GGGAAGAGTATCACTTACGA
2279	Elac2	CTCAGCGTGCCAACAGTTCG
2280	Elac2	ATGCATTGGTCAAATGTTGG
2281	Nadk2	GCCTTACGGAGGTTCTCTCG
2282	Nadk2	CCTCCGAGAGCTCCGCGTAG
2283	Nadk2	ACTTCATTGAGCGCTCTCAC
2284	Nadk2	GGTGGTAGCCCCGCCGACGG
2285	Elovl5	CTGCCAGGGAACACGCAGCG
2286	Elovl5	AGATGTTGAGCATGGTAGCG
2287	Elovl5	GACCATAGTACGAGTACATG
2288	Elovl5	ATCCTGCAGTTGTATAACCT

Number	Genes	Guide sequence
2289	Vars2	ATCCCCGGGTCTGATCACGC
2290	Vars2	TCCAGATGACCCGAGATACA
2291	Vars2	CCAACCCACGTCACCTCTCG
2292	Vars2	TGCAGATGGGCAGTACCATG
2293	Pink1	CATGGTGGCTTCATACACAG
2294	Pink1	GTCGGACTTGAGATCCCGAT
2295	Pink1	CGAGGAACAGTGTGCGACCG
2296	Pink1	CCAGCCCAGCTACCGACTGG
2297	Phkg2	AATGTGCATCTCTCGCCGTG
2298	Phkg2	CGGTAGCTCGATGGACACAG
2299	Phkg2	CATGAAGCTAGAAGACTCGT
2300	Phkg2	GTAGCATCAGGATTTGGCGC
2301	Isca1	CTTGCTCACAGCCCGCACGG
2302	Isca1	GAGGTGACTCACCAGTGTGA
2303	Isca1	AAAGTTGGCGTGCGAACCAG
2304	Isca1	CAACAGTTACTTACATGCTC
2305	Pycr2	GGTGCCCGTGGCATACACGG
2306	Pycr2	GATGTGCCTCTCCTGCACGT
2307	Pycr2	CGTGGGCAGGTCCATATCCG
2308	Pycr2	GATGCTATCACCGGGCTCAG
2309	Gmppa	GGAGCCAGATCAAGTCTGCA
2310	Gmppa	TGGAAGGTTAAACTCCTGCT
2311	Gmppa	AGGACACAATCCCTCAACTA
2312	Gmppa	ATCAGTGACATCATCAACTG
2313	Mrpl44	AAACTGGGATTACCATGCGG
2314	Mrpl44	TAGACTCTCAGTGCCTTCGG
2315	Mrpl44	TTCTTCACTCCCCGAACCGG
2316	Mrpl44	TGAGGCAGTTGTCTGTCACG
2317	Ndufaf5	GCGACACACTCTATGAACTC
2318	Ndufaf5	TCAGGTAGTCAAATTTCATG
2319	Ndufaf5	ATCGAGCGGCAGTCGCAGGG
2320	Ndufaf5	TCAGCTAAAATATTCACAGT
2321	Hfe2	GGCTCACCGGACACGCCGCG
2322	Hfe2	GTTGGCTCCCGACGAAACCG
2323	Hfe2	CTATGCCATGCACCGCAGAG
2324	Hfe2	ACAAACTCGAGCCCCCAGGT
2325	Afg3l2	AAAAGCGATAATGAGTACGG
2326	Afg3l2	GTTCGTGTGACCTTTACACC
2327	Afg3l2	GCCTGCCAGGATGACCACAT
2328	Afg3l2	GTGAAGTTTAAAGATGTGGC
2329	Mtfmt	GTGTACGAGTGGCCCGACGT
2330	Mtfmt	GTGCCTTCGCTATCCCCCAA
2331	Mtfmt	ACCGTGTGGATTATCGGAGC
2332	Mtfmt	GTCAAAACTTGGTGCCAACA

Number	Genes	Guide sequence
2333	Pitrm1	TTGGGTGATAATGAGTAGCG
2334	Pitrm1	ATATAATGGCTATACACGGG
2335	Pitrm1	AGGGAATTCCATATAACATG
2336	Pitrm1	GGTGAATTCTCTCTCCCCGG
2337	Ccdc115	AGCTGACGCCCAGACCCCCG
2338	Ccdc115	ACAGCTGCTCAGTGACCTGG
2339	Ccdc115	CTAACTCTTTGGTCTTGGTG
2340	Ccdc115	GACCTGAGGCTCCATACGCG
2341	Slc52a3	GTGACCTCCTGGATACAGGG
2342	Slc52a3	TGTCTCCGTGACATTGACAC
2343	Slc52a3	GCTGGTGACTGAGTTGCCCG
2344	Slc52a3	GGGTCGGAAGCGGTGCATCA
2345	Ndufaf1	AGACGGCCGCCCATTACAAG
2346	Ndufaf1	GAACAGGCCACACCTACCCG
2347	Ndufaf1	TCTGTATCTCCGAGTTCGTG
2348	Ndufaf1	ACTTCTGATAAGACAATTGG
2349	Cad	CGCAGGGGTACCCGACCGTG
2350	Cad	AGGATTAGAACCTTTCGTGG
2351	Cad	ATGGTGAGTGCCCACCACAA
2352	Cad	CTCAGAAACTCTGTTACGGG
2353	Rnaseh2a	TGTCACACGATACAGCTGCG
2354	Rnaseh2a	GTAACAGATGGCGTAGACCA
2355	Rnaseh2a	AGACCTTGACAGAGAACGAG
2356	Rnaseh2a	GGCTCCTTGAGACACACAGC
2357	Ndufa11	CAACCCCGCAGATTCCACCC
2358	Ndufa11	TCTTACCATGAGGTCCCCGA
2359	Ndufa11	GGCCGGTACACATTCACTGC
2360	Ndufa11	AGCGGAGCCGATTATGCCTG
2361	Coa7	GTTGAATCCTGTCACAACGT
2362	Coa7	CTACCAATGCTACCGCGAGA
2363	Coa7	AACTGTGAGAAATACGGGCA
2364	Coa7	AGGATGGCCAGCCTGACCTG
2365	Slc25a32	CGGATCTTCACGAGGTCGAG
2366	Slc25a32	GGTTCTCGTACCGGACGTGG
2367	Slc25a32	GGAGTAACCCCGAATGTGTG
2368	Slc25a32	AGGTGTGCGTGGATTATACA
2369	Agk	ATATTGCAGACGGATTATGA
2370	Agk	CTCTGAAAGATCCCCACCGG
2371	Agk	GAAATACCCTTTGCAAGCTG
2372	Agk	AGTACTGAGAAGAACAGATG
2373	Fars2	CACACACATCAGCGCATCAG
2374	Fars2	ACCTTAAACAAGTACTGACT
2375	Fars2	TGGAGGAAGCTGGTCATAGA
2376	Fars2	ACTTGGTAAATCCTACCCTC

Number	Genes	Guide sequence
2377	Trnt1	CATGAATTAAGAATAGCAGG
2378	Trnt1	ATTCGCATGATCAACAACAA
2379	Trnt1	AACCTGTTCTCACCTATGTG
2380	Trnt1	GGCAGAATTGTCGACAGACC
2381	Sdr9c7	CACCGCCGAATATAGCCACA
2382	Sdr9c7	AGGTCAGCATCATTGAGCCA
2383	Sdr9c7	CCGACTTGGTGACATCTAGG
2384	Sdr9c7	GCCAAACAACTGGTTGATAG
2385	Yars2	CCACGAGCGCGATCACGTTG
2386	Yars2	TCCCCCCAGACGGTGTACTG
2387	Yars2	CTGGGCGGATCAGATCAGTT
2388	Yars2	AGAACTCCTTGAACAAGCCG
2389	Taco1	GCGATGCCTCGGGTTCCGCG
2390	Taco1	GCTGACTCGATGGTTGACTT
2391	Taco1	ATTGAGGCGTTATCAAACAG
2392	Taco1	CCACTTATTGTGTCCCGCCG
2393	Pigw	TGTGGCTGTCAGCATAACTG
2394	Pigw	ACAGTCAGAGTGATCACTAG
2395	Pigw	TGTTGTATCAGATATACCAC
2396	Pigw	GTTCCAGTGAATGCCGTACT
2397	Gtpbp3	GTGGAGTTTCACGTACACGG
2398	Gtpbp3	CCACAACATTTGCCCCCGAG
2399	Gtpbp3	GTCAATGTAGGCCTCCACAT
2400	Gtpbp3	AGTCTCCAGCACGTCACGGG
2401	Cox10	TCTGTCCCGGAAGCCAAATG
2402	Cox10	GGGAGTGAATCCACTCACAG
2403	Cox10	TATACAGGGATTGCCACACA
2404	Cox10	AGTTGGCAGCACAGGATGCG
2405	Tmem70	CGGGATCGCTTTCTGGCGTG
2406	Tmem70	GAAGGTACGGCAAGAATGCA
2407	Tmem70	GCTGATTTATACTGGAAACC
2408	Tmem70	GTAAGAAGGTGAAGCAGCGT
2409	Mipep	TCCACGTTTGTATTCAACCT
2410	Mipep	GATTGCCACTTCACCATCCG
2411	Mipep	TGGGACCCTCCCTACTACAG
2412	Mipep	CTGGGGCTTGACGTTGAAGG
2413	Atp6ap2	TTAGCATATTAAGATCGCCA
2414	Atp6ap2	TGAACTTGGGAAGCGTTATG
2415	Atp6ap2	CCGGTGGAATAGGTTACCCA
2416	Atp6ap2	TGGACAGTGCAGCTACGTCT
2417	Wars2	GAGCTGGGTGAACTTACAGG
2418	Wars2	CACACACGTTCCTGTCGGGG
2419	Wars2	CAGAAGCATGATGGGACCGT
2420	Wars2	TGGTGTAAATGCTGCAATCG

Number	Genes	Guide sequence
2421	Kynu	GCGGATGGTAAAGCCACGAG
2422	Kynu	CAAACGCCCTTGGATTGTAG
2423	Kynu	TCTTTAAGCCTACTCCAAAG
2424	Kynu	CAACACCCCAGTCATGTAAG
2425	Slc29a3	AATGATGGCCATGCACGCGA
2426	Slc29a3	GGGAAACTGCGCAGAACCCG
2427	Slc29a3	CAAGGAAGACTGCTGCCATG
2428	Slc29a3	ACCAGAAAACACTCGAACTG
2429	Pdss2	ATGATATTGGAATCTCGACC
2430	Pdss2	TGCGTGTCAGAACTACGACA
2431	Pdss2	CGGCATAACCTACAACTGCG
2432	Pdss2	AGCTCTTCTACAGAACACCA
2433	Pex1	TTGGTCCCAAGGAAATACGT
2434	Pex1	TATTACCAAAGGAAGCATCG
2435	Pex1	GCAGCTTCATACGAACTCAG
2436	Pex1	AGTGTTGTGAAGAATAAACT
2437	Cyp2u1	GCTCCTTAAATGGACCAAAG
2438	Cyp2u1	CAGGCGCAGCAGCTTCGACG
2439	Cyp2u1	GAAATGACGAAGCGTCGAGT
2440	Cyp2u1	AAGTGTTCAGTGACCGCCCG
2441	Fuca1	ACTGCCGAGCTGGTTCGATG
2442	Fuca1	GTTCGGCCCACTGATCCGGG
2443	Fuca1	CCAACTCACCGACCAAATCA
2444	Fuca1	GTGATAGTGAATGACCGGTG
2445	Pnpt1	AATGTGTCGTTAACCCAACA
2446	Pnpt1	ACCAACGGCATGAATTGGGA
2447	Pnpt1	GAAGAGATCTGACTTCACTT
2448	Pnpt1	TTGCCATGCTATCAAAGTTG
2449	Ubiad1	GGCTTCCCGAACGATCCTGG
2450	Ubiad1	CCAAATCGAACAACATCCTG
2451	Ubiad1	CCAGCGGGCCGAAAGTGATG
2452	Ubiad1	TCAGAGCGGACAGGTAGTAG
2453	Tmprss6	GGTTCGATGCCTACGCACTG
2454	Tmprss6	GGAAAGCAATAGACTCCCGT
2455	Tmprss6	AAGACCTCATGATCAAAGTG
2456	Tmprss6	CCTTGATCCCGTCACACGCA
2457	Tars2	CTTTAAGCTTCATCTGATCG
2458	Tars2	AAGAGTCTATAATGCCCTGG
2459	Tars2	CTACTGCTACAGTGTAACAC
2460	Tars2	TCCCCAAAGTAGAGTTACTG
2461	Coq2	ACCAGTCTGGAAAACAACCT
2462	Coq2	ATGCGCCTGGACAAGCCCAT
2463	Coq2	AGGGCCAATGGGAGCCCGCG
2464	Coq2	CTGTCCCCCAAGGAAGACGA

Number	Genes	Guide sequence
2465	Cars2	TTAGATTTGACATTATCCGG
2466	Cars2	TCAGATCATTGCTTTCATCG
2467	Cars2	GCACATCGAGTGCTCTACCA
2468	Cars2	ACAGCAGCGACTTCGCCCTG
2469	Sars2	CCGGTCCTATTACCTGCGTG
2470	Sars2	CTGTACGAACACGCACGAGA
2471	Sars2	TCGCTTCGAAGACCTTAACC
2472	Sars2	ACGGTCCCAGACCTTCTGAG
2473	Trmu	AGGGGTATTTATGAAGAACT
2474	Trmu	GTGATGGAGGCTATTCTCCG
2475	Trmu	GCTTATTGCAGTTGATGTCG
2476	Trmu	ATTCCAATACTCCTTCACAT
2477	Slc39a4	GGTCCTGAATACGGATAGTG
2478	Slc39a4	CAGTTGGGGAAGATCTACAC
2479	Slc39a4	CATGCAGCGTGATATTGGGA
2480	Slc39a4	TGGAGAGGGTCACACCCATG
2481	Mccc1	GTTATGATCAAAGCAGTCCG
2482	Mccc1	AACAGGAGGAAGTATTACCA
2483	Mccc1	CAGGAAGAAATCCCTCTGCA
2484	Mccc1	GCAGTACCTCAGCTTCGACA
2485	Ddhd2	AGAAAATGAGCAGATCGGAA
2486	Ddhd2	TATTGTATTACACAACCCAA
2487	Ddhd2	GTCCACAATAGTCTGACAGT
2488	Ddhd2	TACCACAGTGAATATCAACA
2489	Pex13	AGATGAGATAAGGACCGCCA
2490	Pex13	TGGGAGGAAGATCATCTACA
2491	Pex13	GGCCTGGGAAGAATAGGCGG
2492	Pex13	AGCCCTGAAACTGTTATAGA
2493	Chst14	GAAACACCAAGTCACTGCGG
2494	Chst14	CGGACCTTGAGGGCCGTGTG
2495	Chst14	GCTGATGTTCGCTGTAATCG
2496	Chst14	TGTTACGGTAAGCAGACAGG
2497	Cep89	AACTGTCTGCCCAGTCAACG
2498	Cep89	TGAGATGTTAGGCTACGGGG
2499	Cep89	ACACTCTGTTCTGAATCTAG
2500	Cep89	GTTTCACTTACCAACCAGGG
2501	Mfsd8	AGCAATGTATGATCGGACAA
2502	Mfsd8	TGGACCGAGAATAAAGCCCA
2503	Mfsd8	GGATATGTACGCCTGGACCC
2504	Mfsd8	GAGCATCGTGTGGATGACTT
2505	Lrpprc	AGCTGATAGACTACTGTCGG
2506	Lrpprc	GAATAGCCGAAGCATCTAAG
2507	Lrpprc	CCGAACTGAGTCTCGCCGAG
2508	Lrpprc	GAAAGACCTTCCGATCACAG

Number	Genes	Guide sequence
2509	B3gat3	GGACTCGCGGTGTCTCAGTG
2510	B3gat3	TCTACACTGGCTGCTAGTGG
2511	B3gat3	AATGACATAGATAGTAGGCA
2512	B3gat3	ACGGAGATCAGCTTGCAACT
2513	Ttc19	CAGGTCATAAGTGTACGTGA
2514	Ttc19	TCTGCATTTCAACTCTAGAG
2515	Ttc19	AAGAGTCTAAGCACATACCA
2516	Ttc19	GCAACGATGAGTTATCTGCT
2517	Ndufv2	ATTCAATACCTTGTTCATAG
2518	Ndufv2	AAGGTGTAGTAGTGCAGACC
2519	Ndufv2	TAGTAAAAAACTACCCAGAA
2520	Ndufv2	CTCTTACCCACTGAGCAGCG
2521	Phykpl	AGACTAGCTCGACAGTACAC
2522	Phykpl	CCAGAAGGAATGGGTCCATG
2523	Phykpl	AGTACCTGTACGATGAGCAA
2524	Phykpl	CGTGTTGAAGTATTCTACAC
2525	Appl1	CCGACTGTACCTATTAATTG
2526	Appl1	AACTTAATGAGTCAAGCCCG
2527	Appl1	GCCTGCATGTATCCCAGTAG
2528	Appl1	AATTGTATCAAGCTATGCAT
2529	Glrx5	GCACGGTGTTCGCGACTATG
2530	Glrx5	GCGTTGCTGAAGCCGCACTG
2531	Glrx5	AGGTGGTGGTGTTCCTCAAG
2532	Glrx5	GGAGTAGTCTTTAATACCTG
2533	Pmpcb	GAAATATAACTAACCTCCGG
2534	Pmpcb	GGACCGACTAAGAAGCACAC
2535	Pmpcb	GAGACAGATCGTGTCTGGAT
2536	Pmpcb	CTTCCAGTGAACTTGCAGGG
2537	Slc25a42	GCTGGGTGTCATTCCCTATG
2538	Slc25a42	AGGAATCACTCGCACCATGG
2539	Slc25a42	GTACGTGAGGGAAGCCGCAG
2540	Slc25a42	CTTCATCCGAATCTCGAGAG
2541	Mcee	TGGAACTGCTTCATCCACTG
2542	Mcee	TTCAAGAATCCAGTCCTGTG
2543	Mcee	AACATCCCTGTAAAATGACG
2544	Mcee	TGCAACTGAAGTTTGGACTC
2545	Dnm1l	AATCGTGTTACAATACTCTG
2546	Dnm1l	GCACAAATAAAGCAGGACGG
2547	Dnm1l	GATGCCATGGATGTATTGAT
2548	Dnm1l	GTGACCACACCAGTTCCTCT
2549	Plce1	CAGGTATTCATCGCGCAGCG
2550	Plce1	GTGACTCCTCGGATCCATGG
2551	Plce1	CACCGGCCATCAGCTCAAGG
2552	Plce1	GTGCAGTAATCTATTGTCCG

Number	Genes	Guide sequence
2553	Abcb6	CTCCAGAGGTCACATAACGC
2554	Abcb6	TGAAGTAGACCGCTATCGAG
2555	Abcb6	GTGCAGCAGTTTACGTCCCG
2556	Abcb6	TAGGTGCCAAACCAGTTGAG
2557	Dmgdh	TTAGCCGGACTGTATAACCC
2558	Dmgdh	AGGATCCTTCCAGGTCGCGG
2559	Dmgdh	TGGGATGTGGAGACTCCACA
2560	Dmgdh	ACAGCATCAAACTTTACGAG
2561	Lonp1	TCATTCGCAACTTGTCTCCG
2562	Lonp1	GGCAGCGACGAGACCTCCGA
2563	Lonp1	GCGCTTTATCAAGATCGTGG
2564	Lonp1	CAAGGCGATGATATCCCGAA
2565	Opa1	GCGCCTGCGAGAGCTCGACA
2566	Opa1	AGGTTGTACTGTTAGCCCCG
2567	Opa1	AGAGCGTGTCATCATCTCGC
2568	Opa1	AAGTGACAAGCATTACAGGA
2569	Ehhadh	TTCATATGGATGCTTCACGG
2570	Ehhadh	CCACATCATGAGGTTACTAG
2571	Ehhadh	GTAAACCCATAGAACCCCGC
2572	Ehhadh	TCACTATGGCTCTAACCGTA
2573	Acbd5	AGTGTATGAAACCAGATTTG
2574	Acbd5	CCAGGCCGTGAAAGTTTACA
2575	Acbd5	GGAGCAATTTGGACAAGAAG
2576	Acbd5	AAAGCTACCTTTATAGCCAT
2577	Gbe1	GGCTATGAACCACATCTAGG
2578	Gbe1	AATCCCCCCTGATACCTCAT
2579	Gbe1	AGACTCGATAACAATAGCAG
2580	Gbe1	GAACTATGATTGGATACACT
2581	Gale	ATCTTCACCGATGCGCCCAG
2582	Gale	AGAACTTGGACTTGCCGTAG
2583	Gale	TTAACTCTATAGTAGTCCAG
2584	Gale	CTGGGGGTTCCCGTACACGG
2585	Isca2	CTTGTCCCTAACTGCCGAGG
2586	Isca2	TCATTCCTAGGCGCTCGGGA
2587	Isca2	GTCCTCCTTGCCTGTCGTCG
2588	Isca2	CTCAGGCTGCAAGTAGAGGG
2589	Slc6a19	ATCGGTCAGAGGCTACGCAA
2590	Slc6a19	ACAGTCATCAAAGCGCTCAG
2591	Slc6a19	AGCTGAGCAACCCCAACACG
2592	Slc6a19	TCCGTGGCATCGAGACCACT
2593	Pank2	GTCCGCAGACTCGCCGACCG
2594	Pank2	GGATCCGTAAGCCACATTGG
2595	Pank2	AAAGCAGGCATGTCATGGGT
2596	Pank2	CGAGTAGCGCGGCGCCGTCG

Number	Genes	Guide sequence
2597	Mgme1	AAAGTGGAGAAACTCACAGG
2598	Mgme1	GGAGAAGAGCACCCCCAGTG
2599	Mgme1	CTAAACGAGAGTACTTCGCT
2600	Mgme1	CAAACAGTTCCATAAAGCCT
2601	Pck2	TGCGTATTATGACCCGCCTG
2602	Pck2	TGATTGTAACTCCTTCGCAG
2603	Pck2	AGGGTTTGGATGCTACGGCA
2604	Pck2	ATGGAAGCACATACATAATG
2605	Shpk	CATGGTTTGAAATCCCAAAG
2606	Shpk	GACCAGAATGCCGCTAGCTG
2607	Shpk	GCAGGCTGTGAATGGATGGA
2608	Shpk	GTAAGGGAAGAAGGCAACTG
2609	Pomk	CCCATTCTGAAGTAGCCCGG
2610	Pomk	GAGTGAGCACGTGGTCACGC
2611	Pomk	CACATGACCCTCGTGCCCAG
2612	Pomk	CGCCACGTTCATAAGGGCCA
2613	Dhcr24	ACCTGACCCATAGACACCAA
2614	Dhcr24	GTAAGACCTTCATGTGCACG
2615	Dhcr24	AGATGCTGCGCGTGTGTCGG
2616	Dhcr24	GTCTGCCAGGATCAGCTCGT
2617	Atp13a2	CGTCATCACAGGTACGACCG
2618	Atp13a2	CCAGCTACATGACACCCCGG
2619	Atp13a2	GGGACCCCGTGTGCTAGCAG
2620	Atp13a2	TGTGGTAGTGACATGGCCAG
2621	Ppa2	TGGTTGTGGAAATACCTCGG
2622	Ppa2	CCGAACATCTTCCCTCACAA
2623	Ppa2	TACAGGGACATGACGCGGCG
2624	Ppa2	TAAGAGCACCGACTGCTGTG
2625	Ndufs7	AAGCGGTCCATGTCATAGCG
2626	Ndufs7	CATCAGAGTGTAGCCACTGA
2627	Ndufs7	TGGCACGCTTACCAACAAGA
2628	Ndufs7	CCCGGCGTGCCCAGTTGATG
2629	Secisbp2	AGTACGACTACAGCCAAGCA
2630	Secisbp2	CTGTACAAATGGATAGTAGG
2631	Secisbp2	ACCGTCAGGACTTCATAACT
2632	Secisbp2	TGCCGAACAATATAACCCAT
2633	Oplah	TGGTGCGGATTGTTCCTCGG
2634	Oplah	TGACTGTCATCACACCGGTG
2635	Oplah	CTGTGCTTCGTGAACCACAT
2636	Oplah	GCTCCAAAGTCACCAGCACG
2637	Lyrm7	TCTTAACAGATGATGAAACT
2638	Lyrm7	AATGATAAGAGAGCATTGGA
2639	Lyrm7	AGCTCTTTAAAACACTGCAC
2640	Lyrm7	GATGAAACTAGGTTCTGATG

Number	Genes	Guide sequence
2641	Ndufaf2	CAGGAGACATCCCAACCGAG
2642	Ndufaf2	ATTCTTACCTCCATAGTGGG
2643	Ndufaf2	ACGTGGGCACGGACCATCTG
2644	Ndufaf2	TTGGAGCGCCTTGTCCAGGG
2645	Gns	CCAAAGTGTTGTTAACGACG
2646	Gns	TGCTGGGAAGTATTTAAACG
2647	Gns	TCAGACAACGGCTACCACAC
2648	Gns	CAGAGGAACCTACCGTCCCG
2649	Fastkd2	ATGTGAATGCGCTTCGAGCA
2650	Fastkd2	TGAAAGAGGTATCTAACAGA
2651	Fastkd2	TAGCATTAAGGCTGAACAAG
2652	Fastkd2	ATAAGCTTGTCCATCAAACC
2653	Mff	GGATAAGCGACAAAATGCCA
2654	Mff	GCAAGTCCCAGAGAGGATCG
2655	Mff	AGGTATTAGTCAGCGAATGA
2656	Mff	TGTTCGCCAAAATGGACAGT
2657	Ispd	CGGCGGCCACGGTTCCAGGG
2658	Ispd	TAAGCGCATCTCACTAGCTG
2659	Ispd	TGGTCACTTAGACCACTCAC
2660	Ispd	TCTTAGCAGCTAAGGAACAT
2661	Cant1	GGAGTGGGATAAAGACCACG
2662	Cant1	CAGCACCCACAAAGGACGTG
2663	Cant1	CCATCAGAAAGGATCACCCA
2664	Cant1	GGAGTGGACCACCACGACAG
2665	Coa5	CCGGTATTATGAGGACAAGC
2666	Coa5	ATCCGCTACCTGGAGCACAC
2667	Coa5	GCGGGCGTGAAGGAGGATCT
2668	Coa5	GCCGGAGGGCGGCGCGTGTG
2669	Abhd12	TGACTCAGTAGGAACACCAT
2670	Abhd12	GATAATCCTGTGTATATTTG
2671	Abhd12	GCCGCACAGCGCATCCGACG
2672	Abhd12	GCAGGTATAGTATGATGGCA
2673	Grhpr	TGGAGCCCATTATGGATGTG
2674	Grhpr	TCCAGAGATTTCTTTACACG
2675	Grhpr	CTTTGGATGAAATCAAGAAG
2676	Grhpr	AAGAAACTTCTGGATGCCGC
2677	Cog2	GACGGTGTGCCAACAAAGGT
2678	Cog2	TGCCACCATTGATAAGACAC
2679	Cog2	TCTTCTCGTAACTGTCCCAA
2680	Cog2	GTGATGCCAGCTATACGCTG
2681	Trmt5	AGAGGAAAATATGCTGACCA
2682	Trmt5	CAGCAGTAAGCATCCTGTAG
2683	Trmt5	ATTCCTCGAACGTCAGAGGG
2684	Trmt5	TTTCCTAAGTCTCGGCACCA

Number	Genes	Guide sequence
2685	Lmf1	GATCTGCCCTACGTTGACCA
2686	Lmf1	CTTCAGAATCATGCTTGGAG
2687	Lmf1	GGTGGCATTCAATCAGAACA
2688	Lmf1	CCTATGCACCAACCATTATG
2689	Cln6	CCTGCACGAACGCGACACCG
2690	Cln6	CTGACATAGACTATAGACCG
2691	Cln6	TGGATCGGGAATACCAGCTG
2692	Cln6	ATAGTAGTACAACAGCTCAA
2693	Qrsl1	ACGTCCATTGAATTCACCAG
2694	Qrsl1	ATCAGGGTGCCCTACTCATG
2695	Qrsl1	TTACGCAAAGCAGGTGAACG
2696	Qrsl1	GCTGTGTATAGGAATCCCAA
2697	Mfsd2a	TCAGGGACGGAAAGTTCACA
2698	Mfsd2a	GCAGCCGGTCAACTGGTACG
2699	Mfsd2a	GAGGGACTTACTGTATGCCG
2700	Mfsd2a	TCTCTACTTACCAGGGCATG
2701	Alpi	AAACTAAGGTATTACCCATG
2702	Alpi	AAGGCCAACTACAAGACCAT
2703	Alpi	AGCCGGCACCTACGCACACA
2704	Alpi	ACAGTAACCAGTCTGGAACC
2705	Slc10a7	CCGTCGGTCGGAGTGAACGG
2706	Slc10a7	GTTGAAGAATATCGTTGCGA
2707	Slc10a7	GAAGAAGCCACCATTTGGTG
2708	Slc10a7	AACTGCCTTGGTTAAAATCA
2709	Nubpl	CCCAAAGCTCGGCACCCCCG
2710	Nubpl	GTGGAGACAATCACAGCACC
2711	Nubpl	TCAGCTGGACTATTTAGTTG
2712	Nubpl	ACACCTTACAATACCTGCGG
2713	Timmdc1	ATCCGGATTCCAGGGAACCG
2714	Timmdc1	GGAAATTGACTATATCTACA
2715	Timmdc1	ATACCGGATGAAGCCCCTTG
2716	Timmdc1	CACCGGCAGCAAAGACTCGG
2717	Ndufaf6	AATTATGCTGAGAATACGCA
2718	Ndufaf6	ACACGTTCCCACGCATCCCG
2719	Ndufaf6	AACATAACCTAACTAAAAGG
2720	Ndufaf6	GCAGTTCTGGAAAAAAGCTG
2721	Mrap	GAGAAAGAGGAGCACCACGA
2722	Mrap	GTCCATGAACATATTGGCTG
2723	Mrap	CAACCACAGGGCGATGACAA
2724	Mrap	GGTGAGCGGGACAGAGGCGT
2725	Mtmr2	TGCTCGGCCAAGTGTCAATG
2726	Mtmr2	GCCTTCTGTACTCTAGAAGG
2727	Mtmr2	GTGGCATCCTTTAGGTCACG
2728	Mtmr2	GTAATGATTCTCTCATAACA

Number	Genes	Guide sequence
2729	Agl	ACTGGTCTACCGGTACGGAG
2730	Agl	AGAAATGGCCTTATCCGCAG
2731	Agl	TGGTCATCACTTAAGTACGC
2732	Agl	AACAGACTGGTGGATGCTCG
2733	Vps33a	GCAAGAGGTTATCAAACACG
2734	Vps33a	TAATTGCTGAGAATGTACTC
2735	Vps33a	ACACAACGCTAAGACAGTCG
2736	Vps33a	GCCTGTACCACGCAGCCAAG
2737	Mboat7	TGATCAGAGAATGCAAACTG
2738	Mboat7	ATAGCAGTCGATGTTACGGA
2739	Mboat7	AGCTATAGCTACTGTTACGT
2740	Mboat7	GCCTGGATTGCGGCCGAGTG
2741	Mmab	CAGTGCATGCTACAGGACGT
2742	Mmab	ATCAAGTATTTGAAGCCGTG
2743	Mmab	GAAGCTCTTCGGCAAACATG
2744	Mmab	TGTCCCCGTTTCCAGAGCCG
2745	Rdh12	GGAAAGGTTGACCACCCGTG
2746	Rdh12	CAATTTCCGCACTAGCACCT
2747	Rdh12	TGCTAGGAAGCGTTCAGCAA
2748	Rdh12	CCCAAAGATACTTACCCAGG
2749	Sbf1	ATTGTGCCCTCATCTAGCCG
2750	Sbf1	AGAGCAGGGCTACACTACAG
2751	Sbf1	ATTGTTGCTGATCTTGACGG
2752	Sbf1	TGTGTCGTGACAGGAGACTG
2753	Mccc2	TTACCAGTTATATGGCGACG
2754	Mccc2	GAGGAGCTTTGATGTCCGAG
2755	Mccc2	TGACTGTGAAAAAGCACGTG
2756	Mccc2	GGTGGTCGTCCAAAGCATAG
2757	Cpt1c	CCACTCGGACAGGAGTATGT
2758	Cpt1c	TCATACTGGGCGGAACACAA
2759	Cpt1c	CATTTGCCAGCGCTGTAGCG
2760	Cpt1c	TGGGAGAGTGAGTCCCTACA
2761	Bola3	GCGAATGTTTGCCTCTCAGA
2762	Bola3	GCTGCGCACAGTGCCACAGA
2763	Bola3	CCCGCGCAGCAGAGGCGCAG
2764	Bola3	GTATGAAATTAAAATCGAAT
2765	Ak7	TCTCCCTTAGGACGACAACG
2766	Ak7	GGAGGCGATTGTCGCACCCA
2767	Ak7	CTCCAAACACGGGTAGTGCG
2768	Ak7	GGAGAACTTTAACATCCGCT
2769	Slc25a12	ACCCGGATGCAAAACCAGCG
2770	Slc25a12	ATAGCACTTTAGCAGGCACG
2771	Slc25a12	CTCTTGATAGGAGATCAACC
2772	Slc25a12	TCACTGGAAGTCTTACCCTG

Number	**Genes**	**Guide sequence**
2773	Pigt	GATCCGAATCCCAACGCGTG
2774	Pigt	AAACAAGTCATAGACGGCAT
2775	Pigt	GGTAACTGGTGTGGAACAAG
2776	Pigt	TGAGAGTCCGGGAGAACATG
2777	Mrps34	TGGGTACCAAACGCCAATCG
2778	Mrps34	AGTCGGGCCTCACACGCGTG
2779	Mrps34	GCGGCTCTCGCGACGCACGT
2780	Mrps34	ACGCTGACCCGGCCGCACTC
2781	Lrat	GAAATCAGCTCTTTCGTCCG
2782	Lrat	TCCTAGTCAATCACCTAGAC
2783	Lrat	CAAGGTGGCTAGCATCCGTG
2784	Lrat	TCTAATGCCTGACATCCTGT
2785	Lias	AGGTTGCCTTACCATGATCG
2786	Lias	GCAGTCACCTCTGTAACTCG
2787	Lias	ATAAACTGAAAAATACATTG
2788	Lias	GGATTATGTTGTCCTGACGT
2789	Slc19a3	CTGTCGGAGTATCACACTGG
2790	Slc19a3	TGCCAATTCAAAGAATCTAG
2791	Slc19a3	ACCAGAGGGACCAGTAAACA
2792	Slc19a3	ACAACGTGTAGCATGATGAC
2793	Ctns	AGGCATCATTACTGTCGACG
2794	Ctns	TGGAGGGCCATGACACACGC
2795	Ctns	TAACAGGTTATAGTGCCTCG
2796	Ctns	CCCAAGGGTGATGTCGACGT
2797	Elovl4	TTCATGGGATCATACAACGC
2798	Elovl4	ACACCGTGGAGTTCTATCGC
2799	Elovl4	TGCAGTGGTGGTACACGTGA
2800	Elovl4	CGATACAAAATACCACCACA
2801	Hamp	CACCTGTTGATGGAGATAGG
2802	Hamp	AGATACCAATGCAGAAGAGA
2803	Hamp	AGAGCTGCAGCCTTTGCACG
2804	Hamp	AGAAAGCAGGGCAGACATTG
2805	Cox4i2	GGGCGTAGCAGTCAACGTAG
2806	Cox4i2	CCAGCGCTCCTATCCCATGC
2807	Cox4i2	GGACAGGACTCAGAACTAGA
2808	Cox4i2	CTTCTGCACAGAGCTCAGCG
2809	Kars	CTCATCTTCTATGACCTGCG
2810	Kars	GGAGCGTTGTGAAAGGAGCA
2811	Kars	TGTATGTGATGATCTTAGAG
2812	Kars	TGTGGCTATTGACTACCTTG
2813	Acox2	TAGGCCGAAGACGAGACTGG
2814	Acox2	GATGAGCAGATTGCTAAATG
2815	Acox2	CTTGAGTGACCAGTGTCGGT
2816	Acox2	ATGCCAAGATAATTGCTCTG

Number	Genes	Guide sequence
2817	Echs1	AGTCGGCAAATCGCTAGCAA
2818	Echs1	GACAGCCAGAAATCCTCCTG
2819	Echs1	GATGACCGGTTTCTTGACCC
2820	Echs1	GTGCATTGAGTGCTTTGGGG
2821	Amn	GCAGACGTTCTCGCGCGACG
2822	Amn	ACAGACGCAGCCCGACGCGT
2823	Amn	CCAGAACCGGACCCCGTGCG
2824	Amn	GCGCGATGGATCTTTCCGCG
2825	Mrpl3	GGAGACCAGTTGCTTAACAA
2826	Mrpl3	TGTGTTAAAATACACTCCCA
2827	Mrpl3	CCCACCTTCTCTCTAAGCCG
2828	Mrpl3	GAAAACCTTTACCAATACTG
2829	Mcoln1	GACATAGGCATACCGGCCCA
2830	Mcoln1	TTTGACAATAAAGCGCACAG
2831	Mcoln1	ATACCTTTGACATTGATCCA
2832	Mcoln1	TGGCCCGGAACTTGTCACAT
2833	Nans	TATGTGACGTTCCAACACCT
2834	Nans	TATACTTCGAAGCATTCATG
2835	Nans	TCGTGCCCGGAATACCCGAT
2836	Nans	GAGATCACCATAGGACGACC
2837	Cnnm2	ACCGTCGTGGTAAATCCAGG
2838	Cnnm2	CGGCGATTGAGAATGATGTG
2839	Cnnm2	TGCTAACCGGATAAGAAGCG
2840	Cnnm2	CTGCTTCATGATAACCGGCG
2841	Srd5a2	CCCAGCAGCACATTCCCCGG
2842	Srd5a2	ACAGACATGCGGTTTAGCGT
2843	Srd5a2	CATCCCTACCGACACCACAA
2844	Srd5a2	GGTATTCCGCGCAATAAACC
2845	Sfxn4	TTAAGCCAAAAGTTATTCGG
2846	Sfxn4	AGCACATGAGACATACCACT
2847	Sfxn4	TGCAGTCAGGAACTCACCAT
2848	Sfxn4	CCATCGAGGAATTGAGGTGA
2849	Hadha	ACACTTTGTGCTTTACACCG
2850	Hadha	TATTAATTATGGCGTCAAAG
2851	Hadha	TTAAAGACACCACAGTGACG
2852	Hadha	AAGGACAATTGAATACCTAG
2853	Cog8	CTACAAGACGTTCATTCGCG
2854	Cog8	ACACACGTGTCCATAAGCTG
2855	Cog8	TGGCGTGAGAAGCCCGACGT
2856	Cog8	AGGTGGCTACCTGGATAACG
2857	B3galnt2	TAGTGGCTAAATTTCCAGTG
2858	B3galnt2	ACACCTTCCATGAATTCATG
2859	B3galnt2	ACCCACCGTTGACTTAATGT
2860	B3galnt2	GGAACAGTTCATCTTACCAG

Number	Genes	Guide sequence
2861	Kmo	GCTGTCGAAATGCATTCCGG
2862	Kmo	GATGTGTACGAAGCTAGGGA
2863	Kmo	GACAATTCCACCTAAGAATG
2864	Kmo	TTGCCCAAAAAATGGGACAA
2865	D2hgdh	GGCTCACAGAGCATACTCCG
2866	D2hgdh	AGGCCTGGGTGGGCACACAA
2867	D2hgdh	GGATACTGAATGCATGCAGT
2868	D2hgdh	GACTGGCTGAAGACCGTCCG
2869	Lbr	TTCAAGTGACCACTCCACAG
2870	Lbr	GCGCCCTGGATTGATTGGAT
2871	Lbr	GAAGTAAGTACCAACACAAG
2872	Lbr	GAGCTTGAACGAAAAACCAG
2873	Pomt1	TGTGAACAGAGAGTCCAACC
2874	Pomt1	ATAGTCGGGTAAGTAGTCCC
2875	Pomt1	GGGGCACTCACGTGTTAAGG
2876	Pomt1	GTCCACGCGTGGAATCTGAT
2877	Dpyd	CTATAACCTTCCGTGGCGAG
2878	Dpyd	GAGGCACAGCTTATACTCGC
2879	Dpyd	TTTGTCCAGGGCCATACAAG
2880	Dpyd	AGAGCTAAGAGTCATTTCAT
2881	Ldlrap1	GCTCCACCAGCGTCATACCA
2882	Ldlrap1	TCGGTCAGGATGATCCCCCG
2883	Ldlrap1	TGCAGACAAGATGCACGACA
2884	Ldlrap1	CAGAGAACTGGACGGACACG
2885	Pcsk9	GCTGCCAGGAACCTACATTG
2886	Pcsk9	TGGAGCGAATTATCCCAGCA
2887	Pcsk9	AGGACCAGCCAGTTACCTTG
2888	Pcsk9	CATGCTTCATGTCACAGAGT
2889	H6pd	TAGGCGTAGTAATCAGACAG
2890	H6pd	CTTGAAGGAGACCATAGATG
2891	H6pd	AGTTCCACGCCCATACCCAG
2892	H6pd	ATGTCTGCGTAGGCAAAGGG
2893	Psph	TTCGTACATTTCAGACACTG
2894	Psph	CTTATGCCAGGAGTCAGATG
2895	Psph	CCTGGACATTACGCTCCTGG
2896	Psph	CAGCCTATTGGCAAACACAT
2897	Acacb	AGAACAACGATATCGACACG
2898	Acacb	CCAGTGTGCCGACCACATGG
2899	Acacb	GTGGCCGTACATGTCGATGG
2900	Acacb	TTCATTACGGAACATCTCGT
2901	Eogt	GTCGACATAGCTGCAAACGG
2902	Eogt	GAGGCTGGAGTAGTCATACA
2903	Eogt	ACATCAAGAGAAACCACGAC
2904	Eogt	AACAGCCCGTACCGCATGCG

Number	Genes	Guide sequence
2905	Hsd3b7	CCTTCACCATAAATGCCCGT
2906	Hsd3b7	TGCTTGGATGCACATACTGG
2907	Hsd3b7	ATCCACAAAGTCAACGTGCA
2908	Hsd3b7	ATGTGGTCATCCATACAGCT
2909	Phkb	TCGGCCATAAAGTGTATGAG
2910	Phkb	AAGCGGTTTCCAAGTAACTG
2911	Phkb	CCGTGTTATAGATTATCTGG
2912	Phkb	AACGCAGGGTAACTGATGCA
2913	Cog4	GGAAACTCACCAACCCATCG
2914	Cog4	GCTGTGTACGAACGACTCTG
2915	Cog4	GCACAAGTAACGATGAATGT
2916	Cog4	CAACAGAAAAAATTGAACCA
2917	Lars2	GGTTAGCCATGATAACGATG
2918	Lars2	TCTTAATGAACCACTGTCGG
2919	Lars2	CAAATGCATCCCACCCCATG
2920	Lars2	CATCTATGGCATCTCCCACG
2921	Alg9	ATGAGCGGATGGCATACACG
2922	Alg9	ATACAAAACAATGTTGAGAG
2923	Alg9	TCCCGTCATGGCGATCAGCG
2924	Alg9	TCAAGTGTCTGCTCTCAGCG
2925	Slc6a8	GGAAGCGCCACACGTTACCG
2926	Slc6a8	GCATCAGTGTGACAGCCCGT
2927	Slc6a8	GCACAACGAGGACCACGTAG
2928	Slc6a8	ACTCGATGACAGGGGACCGG
2929	Upb1	TCTCGTGTACAAAAAGCGAA
2930	Upb1	CTGTACATGAGCCAGTTGAG
2931	Upb1	GTAGAGAATTCGCTTCACCT
2932	Upb1	ACTGAAGGGATATGCCTTCG
2933	Fig4	CTTGGTGGTAATCGACGACA
2934	Fig4	AAATCCGAACAGAGTCATTG
2935	Fig4	GAAGGATTAATTACACAGGG
2936	Fig4	CACAGGTGGAATGAACTAGG
2937	Pnpo	AATGCGCAAGAGTTACCGCG
2938	Pnpo	ACTAACTACGAGAGCCGGAA
2939	Pnpo	GGTAGCCACACACATAGCAT
2940	Pnpo	CTGAACAGCCTCGTCAAACC
2941	Pex12	TTTCATCAAACCACCGCCAG
2942	Pex12	TTATGGCTTAAAGCGGATTG
2943	Pex12	GGAACATGGCAGATTTCCAG
2944	Pex12	GGCCATGTTAACAAAAGGGT
2945	Plin1	ACAGCCCTGCCCAACCCGAG
2946	Plin1	GTCATGGCTCTCATCCTGAG
2947	Plin1	ATACCTGACTCCTTGTCTGG
2948	Plin1	GGTGTGTCGAGAAAGAGTGT

Number	Genes	Guide sequence
2949	Gck	TTCTGGGGTGGAACGCACGT
2950	Gck	AAGGCACGAAGACATAGACA
2951	Gck	CCATCCGGTCGTACTCCAGG
2952	Gck	CCAGATGTATTCCATCCCCG
2953	Synj1	TATGTCAATCAAGGCAACGA
2954	Synj1	GGGACAAGGTTCAATGTCCG
2955	Synj1	TAAAATATATGCAGGCACCG
2956	Synj1	GAAGAGCATCCGAATTGCAA
2957	Cyp27a1	CTACACGGATGCCTTAAACG
2958	Cyp27a1	AGACCAAGTATGGTCCAATG
2959	Cyp27a1	GAGGACGCGTCCATTTGGGA
2960	Cyp27a1	GGTCCTTCCACTGATCCATG
2961	Ndufb11	TGTAATCGCCCCATCCGGTG
2962	Ndufb11	GGACGAAAACGTCTACGCGA
2963	Ndufb11	TATTCCAGACGTCCACCACA
2964	Ndufb11	GTCGCTGCCTGTCAGCAGCG
2965	Gldc	CCACTGAAATCCATTTCGTG
2966	Gldc	TTTACTCAACTACCAGACCA
2967	Gldc	CTTGATCCAGGGATGCCACA
2968	Gldc	AGGCCACAAACAGCTACCAG
2969	Slc6a5	GGGATGGTCACCGATAACAC
2970	Slc6a5	GTGTACGCATCACTGGCGAA
2971	Slc6a5	GCTTACCGGTATGGTAGTGG
2972	Slc6a5	GAGGACGCGAACGTGAGTGT
2973	Aldh6a1	TAGATGTGTCTGCCCACGCA
2974	Aldh6a1	TAAGTTACTTACCACTGATG
2975	Aldh6a1	TTCAACAGCCATCCTCGTAG
2976	Aldh6a1	AATGTTCAGTGTTCCGTCAG
2977	Tecpr2	AGCAGACATCCTGACCCATG
2978	Tecpr2	GTGGCAAAGTCACCATCAAG
2979	Tecpr2	TCTCGCCTGAGAAACACCTG
2980	Tecpr2	AGCAGATTGGATCCCAACCA
2981	Nhlrc1	GCACGACGTGAAGTACCCAC
2982	Nhlrc1	ACTGTGCCCCAAGACCGGAC
2983	Nhlrc1	GGAGATCACCCCTCACAATG
2984	Nhlrc1	TCCCTGAAGGGGTCCTTCGG
2985	Tecr	TACGTCCAGTCGGCATACGG
2986	Tecr	ACTCTACTTCCGGGACCTCG
2987	Tecr	TGTCTGGACCCACTTACTAG
2988	Tecr	ACTTTGAAGATGTTTCGCAA
2989	Ppcs	ATAGAAATCTGACACTGCCG
2990	Ppcs	ATGCAGATAATCCGCCAAAG
2991	Ppcs	AACTTCAGTAGCGGGCGACG
2992	Ppcs	GTTCTTGTACCGAGCGCGCT

Number	Genes	Guide sequence
2993	Uqcc3	AGATGCCGGAAAGGGACTCG
2994	Uqcc3	GGACGAAGCAGTCAGGACCA
2995	Uqcc3	GGTGGCTCGTAAAGCACTTG
2996	Uqcc3	GCAGTTGCAGTGCTAGGCGG
2997	Psat1	TGGAAGGAGTGCTGACTACG
2998	Psat1	TGCAAACGAGACTGTGCACG
2999	Psat1	CAATACAGAGAATCTTGTGA
3000	Psat1	CTTTGTAGTCAAGGACTGAT
3001	Acaca	GCCATTCATTATCACTACGT
3002	Acaca	AATGCATGCGATCTATCCGT
3003	Acaca	TTGATTCATAGGTACCGAAG
3004	Acaca	AAGCCCTTCGAACATACACC
3005	Haao	TGGGTGCTAACTGCGTGCCA
3006	Haao	AGAGGTTTGCCAACACCATG
3007	Haao	GCAAACCGGAGGCTGAAAGG
3008	Haao	CGGGACGTGCCTATACGGCA
3009	Cth	TGCATGGATGAAGTGTATGG
3010	Cth	GCAATGGAATTCTCGTGCCG
3011	Cth	TTCCAAAACCAAATTGCTAG
3012	Cth	TTTGTGGACAATTTGTGCGC
3013	Mthfs	TTGCTCTGGAATTGGTACCG
3014	Mthfs	CTTCTCGCACCTTCTGCGTG
3015	Mthfs	GATGAGGTCAAGTCCACCTG
3016	Mthfs	ATCTTGCATGCTTAGAAAGA
3017	Grm6	ATTCTCATTGAACATCACTG
3018	Grm6	GGAGTCAGGAGGCACCACTC
3019	Grm6	CCGGTGTGCGACTAGGCGCG
3020	Grm6	GTGGTCAGGCGACCCCCATG
3021	Prkag2	GGGACGAGGAAGCATAGATG
3022	Prkag2	AAGAACATAAGATTGAAACG
3023	Prkag2	CCACTGAAGCTCATCCGGCG
3024	Prkag2	GCGTTTATATGCGATTCATG
3025	Atic	AGACGACTGTCACTCGAGCG
3026	Atic	GAGATGTGTCTGAGCTAACA
3027	Atic	AATTGCTTCATCGTATTGAG
3028	Atic	TTCTTTCAAGCACGTCAGCC
3029	Ogt	TTTGAGCCCAAATCATGCGG
3030	Ogt	AGCATTATCGACATGCCTTG
3031	Ogt	ACAGTGCACCACTAGTCCCA
3032	Ogt	GAAAGTTTGTACCATCATCC
3033	Mthfd1	ACACCAACGATAGATTCCTG
3034	Mthfd1	CACTATGAATCCGTGCACAG
3035	Mthfd1	GATTGCCGGAAGGCACGCGG
3036	Mthfd1	GGTAGCGTCCAGTAAGAAAG

Number	Genes	Guide sequence
3037	Zdhhc15	TGGAACTTAGAGCGAACACT
3038	Zdhhc15	GAATCAAAAGGGCATACCAT
3039	Zdhhc15	GTGTACACAAGAACCGGGAG
3040	Zdhhc15	AGACTGTTGTAGCAATGTAC
3041	Atad3a	AAGCAGGAGGCCATACGGCG
3042	Atad3a	TTACCTGATAGACTCCAAGA
3043	Atad3a	TGCCACATCAACTCACACTG
3044	Atad3a	GCTGTCGAGCGAGCTTATCC
3045	B4gat1	CCGGGATTAATTATGCACTA
3046	B4gat1	GTAGACGCGATAATCGCCGC
3047	B4gat1	TTTACCTGGTCTACGGATCG
3048	B4gat1	CGAGGGGCACACGAGGTGCA
3049	Rars2	AAACCTGGTGGCATAGAGAG
3050	Rars2	TGTCACCCATTTCTAGTCGG
3051	Rars2	TCAGCTTAAGTGTGATACAG
3052	Rars2	ATTATCTTGATAGGTCTGCT
3053	Slc30a9	AAGGACTCGGTGTCATCGTG
3054	Slc30a9	ACTGAGACCGCTCTGGAACG
3055	Slc30a9	ATTATCTGATACTTGTAACC
3056	Slc30a9	CTACGAATGTCCAGAAAGGA
3057	Mmadhc	TCTGTGAGGCAGTCCCATTG
3058	Mmadhc	GTGTGGCCTGATGAAACTAT
3059	Mmadhc	TCACTAAAGAACAAAATCCT
3060	Mmadhc	TATGTAAATGAGTTTCAGGT
3061	Mmaa	CGACCTACTCGAAATGTGAG
3062	Mmaa	AGGACAGAGAGCTTGCCTAG
3063	Mmaa	TCAGGCCCTCTCCTACCAGT
3064	Mmaa	ACTTGAGTGAAGGAGCCATG
3065	Trip11	TACTGATCATAAACGAACCA
3066	Trip11	TTATTGAGTCAAGAAAAGGT
3067	Trip11	ATCCTGTGAGTAGGACGCGG
3068	Trip11	GAAGGAGAACCATGAACTGA
3069	Acy1	AATCTGACCAAGCTTGAAGG
3070	Acy1	TGTATCCTCAATGAAGCGTG
3071	Acy1	GACAGGTACCACATCTGTGT
3072	Acy1	AAAGACAGTAAAGGCATCCG
3073	Cyb5a	GTCCAAAACATACATCATCG
3074	Cyb5a	TCTGACCAAGTTTCTCGAAG
3075	Cyb5a	CTTATGATGCAGGATCACCC
3076	Cyb5a	GTCCTAAGAGAGCAAGCTGG
3077	Ampd2	CACTGCCTACGACTTAAGTG
3078	Ampd2	CAAATGCAAGGAGATCGCTG
3079	Ampd2	TCATAAGTTCGAGTCTCCAG
3080	Ampd2	ATATTGTAGAAGTCCCGGTG

Number	**Genes**	**Guide sequence**
3081	Cyb5r3	GTCATCATCGCTCGACACAG
3082	Cyb5r3	ACTTCACCGTCCTGACAACG
3083	Cyb5r3	GGAGACACCATTGAATTCCG
3084	Cyb5r3	AGGTCATCAGTCCTGACACT
3085	Blvra	TCTGAAACAGACGAGAACTT
3086	Blvra	TAAGAGAAAGCTCCCCAAAG
3087	Blvra	ATGCCATGGGGTATTCCACG
3088	Blvra	TATAGGCGACATCAACCTCT
3089	Pgm3	TACGGCCTCACATAACCCTG
3090	Pgm3	AACTTCTTCAAGGTACCGCG
3091	Pgm3	TACACCATGTAGTGCAACTG
3092	Pgm3	CTGCTATGACATACCCTGTG
3093	Asl	CTCGTGTCAGCGCAACAGCG
3094	Asl	TGGTTCCAATGAGCACCCGG
3095	Asl	AGATGCAGCAGATACTGCAA
3096	Asl	GCTGCAGGGAAGCTACACAC
3097	Gusb	GTATCTTGGGTCCATCGCCG
3098	Gusb	TGTTCGAATCCCGATAGGAA
3099	Gusb	GGAGCGCGCACCTCCCGTAG
3100	Gusb	GGTGTCAGTCTTGTAGACGA
3101	Phka2	GGGTCATAATGCAATCGGTG
3102	Phka2	ACAGTAGACCGAGTTCCACT
3103	Phka2	CACAGAAAGTATGTCCCGAG
3104	Phka2	CAAACAAATTGGTATCCCAG
3105	Pygl	AAACCAACGGGATTACCCCG
3106	Pygl	GGGCGAAGTAGTAGTCGCGG
3107	Pygl	CTTACAAAATGCCTGCGATG
3108	Pygl	AGGAGGCAAACGGATCAACA
3109	Cyp11b1	TTGCTATCCCATCCACCAAG
3110	Cyp11b1	ATAGTCCATAGAGAACTCCG
3111	Cyp11b1	CAAAGAAAGTCATTACCAAG
3112	Cyp11b1	GGCTCAGATCACGGCCAATG
3113	Mpi	TGGATGGGGACACACCCCCG
3114	Mpi	CGAAACATCCGATATCACCT
3115	Mpi	AGGGTGTGCCTGGATAGACA
3116	Mpi	CAGGTAGGCATGGGGTACGT
3117	Manba	GTCTGGTTCCCATGTCCACG
3118	Manba	AACCAACGGGATGAAAACCA
3119	Manba	GTTCACGTCTTTGACTACGT
3120	Manba	TTGAAGTAGAAACTCAGACC
3121	Fdps	AGATACACTGAAAAGAGGTG
3122	Fdps	CCAACTCACCATGTACATGG
3123	Fdps	ACAGATCTGCTGGTATCAGA
3124	Fdps	TTGCCCGGCTCAAGGAGGTG

Number	Genes	Guide sequence
3125	Cox6b1	AAGGCAATGACGGCCAAGGG
3126	Cox6b1	AACTGTTGGCAGAACTACCT
3127	Cox6b1	AGAACCAGACTAAGAACTGT
3128	Cox6b1	ACGCCGGTACCACTCACACA
3129	Qdpr	TGTCATCTTAACAACCACGC
3130	Qdpr	CTTACCAGGAGTCCCATCCA
3131	Qdpr	GGTGGATGCAATTCTCTGTG
3132	Qdpr	CACGCAGTGTTACCCAGTTG
3133	Pigh	CTTGTCCATCTCTATGAAGG
3134	Pigh	GGTCAATCTTCACAAAATGG
3135	Pigh	TGATGAAGATGGTGGCAGAG
3136	Pigh	TGAGTAGTAGCGGCACCGCA
3137	Acat1	GTCCCATACGTAATGAGCAG
3138	Acat1	AGTGCTATAAGAACTCCCAT
3139	Acat1	AGGCAAGCAACACTGGGCGC
3140	Acat1	GCCTCTCAAAGTCTTATGTG
3141	Acat2	CAAACCTGATGCGTTCGCTG
3142	Acat2	CTGAGAACAGGAGTCAGGAT
3143	Acat2	TCCTACTCGACAAGCCAGTG
3144	Acat2	TGCCTTTCACAACTACCACA
3145	Aldh7a1	GGGCTCCGCGAGGATAACGA
3146	Aldh7a1	TGGTGGAGCAGATATCGGGT
3147	Aldh7a1	ACACTAACGAGGGACGTAGT
3148	Aldh7a1	TAGATTCCTGCCCCAAAACG
3149	Nr3c2	GATGATTGGGCTCTTAACGA
3150	Nr3c2	CAAGGAACTTTCAGCCACGG
3151	Nr3c2	TCCACTAATGCATTGACAGG
3152	Nr3c2	GAATGGAAATGGGTTGACTG
3153	Pcca	CTGGACAATTATGTGATCCG
3154	Pcca	CCTGGATTTCTATATGACGA
3155	Pcca	GTAAACCGAAAGACTTGTAG
3156	Pcca	TTAGGTTCACGTGAAAATGG
3157	Etfb	CATCCACGTGGAGATACCAG
3158	Etfb	CCTGAGAGGCGAATGTACCC
3159	Etfb	AAAGCCGGACAAGTCTGGAG
3160	Etfb	CATGGCCAGAGCAGTTCGGA
3161	Etfa	TGGCGTAGCAAAGGTTCTGG
3162	Etfa	TTTGTGAGAACTATCTATGC
3163	Etfa	GGTAGTGCTAGTTCAGAAAA
3164	Etfa	AGTTACACACACATCTGTGC
3165	Hlcs	CAGCAATGTGAGAAGACACG
3166	Hlcs	ACAGTACCATTGACTCGGTG
3167	Hlcs	ATGGCCTATCTTTCTCAGGG
3168	Hlcs	CGGCGGCCTTGCAATCACCT

Number	Genes	Guide sequence
3169	Cldn16	GGCCACGATCAAAAACCCAG
3170	Cldn16	GAACGCTGATGACTCCCTGG
3171	Cldn16	AGTACCTGCAATGAGTAATG
3172	Cldn16	TATATTGTGTAAAACGAGAG
3173	Slc13a3	AGTTTCTTGCCAGTTCGGAA
3174	Slc13a3	TCCAGAGCCAGCCCACCAGT
3175	Slc13a3	GGCTAAAGCGGTGATCCAGG
3176	Slc13a3	CCACCGTACCTTGGGCGGCA
3177	Ddhd1	TCGTTGCGCTACTACAGCGA
3178	Ddhd1	TCAAAGCTTACTCTTGATGG
3179	Ddhd1	GATAAAATACCAGTAATGCG
3180	Ddhd1	ATAAGTGATTACACACCCCA
3181	Slc19a2	GGAGTAGTAGGCGATTTCGG
3182	Slc19a2	GACTCAGCCTGATTGTGACG
3183	Slc19a2	CAAGTGGTGAACTACGCGCA
3184	Slc19a2	GCAGGAACCAGCACTCGCGA
3185	Slc2a9	CGGAGAGGTTGTACCCGTAG
3186	Slc2a9	GCATGCCATCAGCAACGCTG
3187	Slc2a9	CCAACTATGTGGACTCAATG
3188	Slc2a9	TCTCAACGAGATCTCACCCA
3189	B3galt6	GCGCGCCAGGTACAACAGAG
3190	B3galt6	CCTGGTGGACCTACGCGCAC
3191	B3galt6	GTTCTCGTAGGCGTCGCGCA
3192	B3galt6	TGGCGGACCCGAGGACGTGT
3193	Mrps2	CTTGCGGTAGGCCACGTGCG
3194	Mrps2	CCTGTGCCAACTACCTATGG
3195	Mrps2	CACACCCGCTACTTCAAGGG
3196	Mrps2	GCGTATCTAGGATCCTGCTC
3197	Pofut1	TGTTGGTATTCAATCCATGG
3198	Pofut1	GCGCCTCCTACAAAGAACAA
3199	Pofut1	CCGGAGGCCTTACCCATGCA
3200	Pofut1	AGCTCCAGAAGTACATGGTG
3201	Slc2a10	CAGCCCCGTGGCGACCAAGG
3202	Slc2a10	AGAGGCGTAATACAGCACAT
3203	Slc2a10	TGTGCTGGTGTCCCTCTACG
3204	Slc2a10	AGCCAACAGATAAACGGCCC
3205	Bbox1	GTGGTGAGATCATAAAACTT
3206	Bbox1	TACACAGAATGTCAGTACTG
3207	Bbox1	GTTGAAGCTCACCTTACCCC
3208	Bbox1	CAAGATTGATGCCAACAATG
3209	Idh3b	TTCACCCTTATACTCCATTG
3210	Idh3b	TCGGCACAACAATCTAGACC
3211	Idh3b	ACAGGCACAAGATGTGAGGG
3212	Idh3b	TAAGGAGCATCATCTGAGCG

Number	Genes	Guide sequence
3213	Rtn4ip1	ATATTTATCTATCACCCAAG
3214	Rtn4ip1	TGAGGTCATTGATTACACGT
3215	Rtn4ip1	GCAGGTAATGAAAGCATGGG
3216	Rtn4ip1	GAGAGCCACATATGGCAAAG
3217	Mfn2	CCGAGGCAGACGCATCCCAG
3218	Mfn2	GTGGTATGACCAATCCCAGA
3219	Mfn2	ATAAACCTTGAGGACAACTG
3220	Mfn2	AGAACTGGACCCGGTTACCA
3221	Sugct	AAGATCTCCTAAATTCATCG
3222	Sugct	GGTGATGACACACGATCTTG
3223	Sugct	AGGAGTGAGAATCGTCAAAG
3224	Sugct	AATCTAAGGATACCTACCTC
3225	Mvd	CCCGCCGAGCCACTTCGGAG
3226	Mvd	CATCTGGCTGAATGGTCGCG
3227	Mvd	CCACGTGCACCTTATAGCTG
3228	Mvd	TGTTGTGCCTGAGCGCATGA
3229	Sardh	CCTTGACTACGACTACTACG
3230	Sardh	CGTCGTCACTGAGCGCATCG
3231	Sardh	AACCGAGTAGTTCTTGGCAT
3232	Sardh	CGGTGACTGGCATCCGTGTG
3233	Klf11	CAGTGTGATCCGTCACACCG
3234	Klf11	AGCTCACGGAGCCGTCAACA
3235	Klf11	ACCAGCATCACAGTTCCCTG
3236	Klf11	CCTTGCTTGCACAAGTCCGG
3237	Tmem199	TAGCCAATGAGGAGTATAAG
3238	Tmem199	CGGAATGAAACCAGGCGCCG
3239	Tmem199	TTTCTGTTACATACCCGGGG
3240	Tmem199	TGCTCTGGGAAAGAAACACG
3241	Alg11	GGAAACCAGCAAATGCCCTG
3242	Alg11	TTTCCTGGACTGATGATATG
3243	Alg11	AGTGAACATAGCTTCCGACT
3244	Alg11	TAAACCATATCCTCTCACTG
3245	Alg1	GTGAAGTTGACAGATCTGCG
3246	Alg1	TCTGGAAAGGAGAGTACGTG
3247	Alg1	TGTGACCAATGCTATGCGGG
3248	Alg1	TGAGAGGGATTGTCAGAGCG
3249	Alg3	AAGAAGGAATAGCAATCCCG
3250	Alg3	GGAAAAGAAACTGACGACCA
3251	Alg3	GCCACCAGCAATGTGTAGCG
3252	Alg3	ATTGATGAAACCCTCCACCT
3253	Slc25a38	TCCAGGGACACATCTCACAA
3254	Slc25a38	CTGAGAAGGGGGCATCACGG
3255	Slc25a38	AGAGGAAAGCCTTAATCACT
3256	Slc25a38	AGTGATCAAGACACGCTATG

Number	Genes	Guide sequence
3257	Akr1d1	TTGTCTGGGTGAAATACGGG
3258	Akr1d1	TGAAGACAGCTATTGATGAG
3259	Akr1d1	AACAAATCTGTGTGCCACGT
3260	Akr1d1	GGGCTGGGAGGACCATTGAT
3261	Zdhhc9	TGGAAATTCTTAATACGAGG
3262	Zdhhc9	GTGCTCGAGGAATCACTCCA
3263	Zdhhc9	AGAAGAGTGTACATGTCCCC
3264	Zdhhc9	AAGAGCATAGCGGCAAACAC
3265	Pycr1	CCGGGGTGTTAGTCATACAT
3266	Pycr1	TTGGGGCGAACATTGAGGAC
3267	Pycr1	CACAGGTACTCACGCTCAGG
3268	Pycr1	GGAGGGCCGAGACCGTAGCT
3269	Dhtkd1	CTGATGTTCCGTAAAATGCG
3270	Dhtkd1	GCCACGGTGAAGAGATACGG
3271	Dhtkd1	TCTTCTTTAGGAAAGCTCGT
3272	Dhtkd1	GATGGGGACTACTCCCCGAA
3273	Mtrr	GATGAAGCGGTTGTAATCAG
3274	Mtrr	GGTGAGCAAAATAGTCCGTG
3275	Mtrr	GAACAAAATGAGACAAACAG
3276	Mtrr	CTCGACCGTACTCATGTGCA
3277	Sepsecs	GAGGACGTCTAAGGACGGCG
3278	Sepsecs	TAAGCGTTGTTGACTACATG
3279	Sepsecs	CAGGACTTCTGGTCTATCCG
3280	Sepsecs	CACCGGATCGTCCAATTCCG
3281	Cln5	GACAAAATTCGAACAGTCGT
3282	Cln5	CCAGCGTTGCCCAGACGTCG
3283	Cln5	GCCCCTTGGTTACACCAGAA
3284	Cln5	ATATTTAAATTCCCAAATCG
3285	Suox	AGGGGGACATGCTATCTTCG
3286	Suox	TCCTCTTTAGAGTACATCCG
3287	Suox	AAACTTATGCAAATCATCCA
3288	Suox	CAGTCCTTCAAAACAGACAT
3289	Pde12	AGCTGTCGGAGAACACCGCG
3290	Pde12	AGCTTGGATCGAGACCGGTG
3291	Pde12	TCTTGGTGTACAGATGTCGA
3292	Pde12	AAGAACCGAGCCCACTCGAG
3293	Zfyve26	GAAGTCCTCACCTATCGCCG
3294	Zfyve26	CCTTCCCGAGGACTATGCCG
3295	Zfyve26	CTGAATCCTGATGGTATGCG
3296	Zfyve26	GGCCCTGGACATACTAACTG
3297	Aldh4a1	GTTCAACGCAAAGTTCGCCG
3298	Aldh4a1	CGCTCGGCATTCGAGTACGG
3299	Aldh4a1	CAACTGGTACTGTATATCGG
3300	Aldh4a1	ACCTTTATGACAGGGCAACG

Number	Genes	Guide sequence
3301	Mars2	ACTCGCAGACCATCTACGTG
3302	Mars2	GAGTGGACATAGATGCGATG
3303	Mars2	TCGATCGCACAGCTCGATCG
3304	Mars2	TGTCCCGTGTCTCTCGAGAG
3305	Dse	GTCAAAGTATAAGCATGACC
3306	Dse	CAGCACACAGAACATTGCCA
3307	Dse	AGTTTCATACATATAGCCCG
3308	Dse	TAATGAACGGCACACCATTG
3309	Kctd7	CGGTACTTCATCGATCGAGA
3310	Kctd7	CCGCAGAGTAGACAAGCGCG
3311	Kctd7	GTAATGCCGCCCGCTGAACA
3312	Kctd7	GAGAACATGCAGCCACTGAA
3313	Slc39a14	GAGCGAGCGATCTCAGATCG
3314	Slc39a14	GTAGAGGGTTCCAATCGCCA
3315	Slc39a14	TAAAATGGTTATGCCCGTGA
3316	Slc39a14	GTGACCGAGAAGCTACAGAA
3317	Slc18a2	CGAGCCATACGTACCTACGA
3318	Slc18a2	CCATCTGCTTTGCAAACATG
3319	Slc18a2	GTACATACCTAAGACCCCCA
3320	Slc18a2	ATGCAGAATCCAGCAAACAT
3321	Gnptg	GGCCTACCTAACAAAGAGTG
3322	Gnptg	CTGTGGAAAGATCAACCGAC
3323	Gnptg	TTACCCAAGGATCCCGCTGT
3324	Gnptg	ACAATACCTTCAAGGGCATG
3325	Aldh5a1	CCTCTGCCAAAGATAAGCGA
3326	Aldh5a1	ACTGTCAAAGACAATGAATG
3327	Aldh5a1	ACACCAATGGATCGGTACAC
3328	Aldh5a1	AGACACACCCTATTCCGCCC
3329	Spg11	TCCCCGGAAACACAACGCGT
3330	Spg11	ATTCCCGGGGATGTCCCACG
3331	Spg11	TCATTCCGCTCAACGACTGG
3332	Spg11	AGAGCTACAAATCCCGTGCA
3333	Pomgnt2	AAAGCCGTATTGGTACCAGG
3334	Pomgnt2	TCAACCACGGTAGCCCCGCG
3335	Pomgnt2	GTGGCTCTGCTACTCCAATG
3336	Pomgnt2	AGACGTGCATGAGGTTATCG
3337	Micu1	ATGGGATCTCCACTAGACCG
3338	Micu1	TTCTTGCTGTTAACGCATGG
3339	Micu1	TTGAAAGTAATCAACGAACC
3340	Micu1	CCGAACATAAGCCAGACTTG
3341	Iba57	CAGACTCCCAGAGTGTACGG
3342	Iba57	GAAGATCACAGACTCCCTCG
3343	Iba57	ACGGGCTAGGCAGTGACTCG
3344	Iba57	ACCCCCGGACTGCACGTATG

Number	Genes	Guide sequence
3345	Ptrh2	CTCAAAGAGTGGGAGTACTG
3346	Ptrh2	ACTGACCTTAAAATGGGGAA
3347	Ptrh2	CCCCCAGAACTCAACAAGTG
3348	Ptrh2	GTTGCTTGTGGCATGTGCCT
3349	Xylt2	GTATACAGATGACCCCCTCG
3350	Xylt2	GTGCCACTGACTATCCAACG
3351	Xylt2	TGTAGGCGATGCGTACTGGA
3352	Xylt2	GGACGTCGCTGAGTCCGCCA
3353	Nags	GGATGAACTAAGGCACAACG
3354	Nags	CAGCTACGGTGGCATCGTCG
3355	Nags	GACAGCCAGAAGGTGCCGTG
3356	Nags	GCTAGCGGCTGTAATGACTG
3357	Mgat2	GAAGTTCAACTGGTACACCA
3358	Mgat2	TGTAATGGCCGAAGGAGTCA
3359	Mgat2	AAAAGTCTGGGGCTAAGTAG
3360	Mgat2	CTGGACGCGGAGCCCGTACG
3361	L2hgdh	CGGACGCCGGTCCACTTGCG
3362	L2hgdh	AACAGCGGTGTCATACACAG
3363	L2hgdh	GCTATTGATTGTCCATACAC
3364	L2hgdh	GACCGTATTTCAGAGTTGAG
3365	Coq6	AGACACCGTGTACGACGTGG
3366	Coq6	GGCCTTGATAATGTTCGACA
3367	Coq6	CTAGGGTAATATGGACCCAA
3368	Coq6	GTGTGATGTGGACCAGACCA
3369	Pomt2	TGGACAGATCCAGTACGGTG
3370	Pomt2	GTAGTCCTTATGCAAATAGG
3371	Pomt2	CCTGCACAGTCACTATCATG
3372	Pomt2	TCTTTATCATCGTGCAAGTG
3373	B4galt7	CACTACAAGACCTATGTGGG
3374	B4galt7	CTACATCGCCATGCACGATG
3375	B4galt7	GGAAGATGGAGCATTTCCGG
3376	B4galt7	TCGGGCAGCACTCATCAATG
3377	Alg12	GTACCAAAGAAGACTGACGG
3378	Alg12	AAGCGAGAGCACATAAACCA
3379	Alg12	TGTAGGGACATATAACCAGG
3380	Alg12	CTGAACAAAAGTTCCAACTG
3381	Poglut1	ATGATATCATGTATCCTGCG
3382	Poglut1	ATTTCTTGACCAAATTAACA
3383	Poglut1	GGACCCCAGAGGATACCTGG
3384	Poglut1	GAGGACCTGACTCCTTTCCG
3385	Aars2	AGGACGCCATAACGACCTGG
3386	Aars2	CTACACTCTTCACCCCAACG
3387	Aars2	GATAGACACAGCGTACCGAG
3388	Aars2	GAGGCTACCTTGTCCGTACA

Number	**Genes**	**Guide sequence**
3389	Pex6	TGTAACTCTCGAGCAAACGG
3390	Pex6	AGGAAATGCCGTCTGCACAT
3391	Pex6	GCACGGGGAGGGTCTCCCCG
3392	Pex6	AGCACACAGCTCATTTACCA
3393	Ndufs8	ATGTGGACAGAACTCATCCG
3394	Ndufs8	TCAGTGGGCCCTTCTCAAAG
3395	Ndufs8	AAGCCTTCATAGCAGCGCAG
3396	Ndufs8	CCGAGCTGCATTGTCAGTTG
3397	Trpm6	AGAGTGCATACAGTTTAGCG
3398	Trpm6	TGTCAACAGTTATGGCCGAG
3399	Trpm6	AGGTCATGATGTAGCGATAG
3400	Trpm6	TATTCTATAGCTCGAGAGAA
3401	Cox15	AGAAAGGGTTGGCTCAACCG
3402	Cox15	AGGCGGTACTGACTGACCCG
3403	Cox15	GGTACATGGAATACTCACAC
3404	Cox15	TAGGGTGGCGTCCAGAACAC
3405	Lct	TGAGTTGTTCGATAGCTATG
3406	Lct	TCAGCCTATCAAATCGAAGG
3407	Lct	CTCCCGTGGATACGCCCCAG
3408	Lct	CTTAAACTTGTACATCAACG
3409	Dars2	GTTGCTCGGACCAACACATG
3410	Dars2	TCTTCTAAGAAAATGCCGAC
3411	Dars2	TAGACAGCCAGAGTTCACTC
3412	Dars2	AAAGCAATATGTGTTCATGA
3413	Ndufs2	GCGGCGTATATCCGACCTGG
3414	Ndufs2	TAGCACTCACCATTCCAAGG
3415	Ndufs2	CCTCGGGCACAGTGGATCCG
3416	Ndufs2	CACATCGGGCTCCTGCACCG
3417	Slc30a10	CCATGACAACAGTCAAACTG
3418	Slc30a10	AGCCGTGATGACCACAACCA
3419	Slc30a10	GCACAGCAGTGACTCTCCGG
3420	Slc30a10	TGCTGCAGATGGTCCCCAAG
3421	Hhat	CTGAGCCACGCAGAACGCGA
3422	Hhat	GCACAGACCCTGGATTGTCA
3423	Hhat	GACGGGATAATAGAAGACGT
3424	Hhat	AGAGGGCATGCATGTACATG
3425	Hibch	AGTCCATGGTCAATTCCGAG
3426	Hibch	CAGATGTTGCAGAATAACGC
3427	Hibch	CCTGCAACATCCTCAGCTGA
3428	Hibch	CTATTGCAGACCTTTAGCTG
3429	Ndufs1	AATGGATCTCTGATAAAACC
3430	Ndufs1	TGTCCTATTTGTGACCAGGG
3431	Ndufs1	TAGAGGTTAGGGCCCCTACA
3432	Ndufs1	TGATGGTCAGTCTGTCATGG

Number	**Genes**	**Guide sequence**
3433	Cps1	TGAGCCTCACAATTTCGTCG
3434	Cps1	ATGCAGACCGAATCATCACA
3435	Cps1	TACAGTATTCCATGGAAGTG
3436	Cps1	GTTGGTGGCATCTCGTGTCG
3437	Man1b1	GAGCACCATTCGCATCTTAG
3438	Man1b1	GGTTACCAAAAGTTTGCTTG
3439	Man1b1	GTGGACTTCAGACAGCACGG
3440	Man1b1	ATGTTCATCAACACGAACAG
3441	Coq4	TCATCGTCCACAAAGCGTGT
3442	Coq4	GCGTACGGGGCCGAAGACTG
3443	Coq4	CCAGGAAGCGAAGATACTCA
3444	Coq4	CTCTACAACCCCTATCGCCA
3445	Dolk	GGACCGATACTCCTGGTGCG
3446	Dolk	CAGTGTAGGCGAGGTGATCG
3447	Dolk	AAAGTATTTCCACTTCATTG
3448	Dolk	CCAGCAAAGACCAATAGGCA
3449	Agps	GTACCAATGAGTGCAAAGCG
3450	Agps	GTAAAACCAAGCCACTAAGT
3451	Agps	TCAGAGAAGGGATGTTTGAG
3452	Agps	TCCCTGGAATTCAGCACCGT
3453	Slc35c1	AGGGCACCCCTACGTACTTG
3454	Slc35c1	AGGTTAGGCGCCAGATACTG
3455	Slc35c1	CTCACCAATGATGACGCCGC
3456	Slc35c1	GCAGTGAGGTCACCAGGCAT
3457	Acad9	TCTGCCCAAACTGTCGTCTG
3458	Acad9	ATTTCCCGACTGCTCTATCG
3459	Acad9	GGACTCTCGAAAAATTGACC
3460	Acad9	GAGCATACATCGTGTTGGAG
3461	Gatb	GTTCATTTGATTATAAGCTG
3462	Gatb	GTGACCTCAGGTCGTCATGG
3463	Gatb	CTTCCCTAGATAGATACAGT
3464	Gatb	AATATATCTGTACATCACCC
3465	Msto1	CTGTTCTGTACAAGACGTCG
3466	Msto1	GGACAGACTACACTTCTATG
3467	Msto1	GGGCGGGGAGTCCTAACCTG
3468	Msto1	AGCCCCCATACCCATCATGG
3469	Ampd1	AATGACAAATACAATCCCGT
3470	Ampd1	CAAAGCACGACTCACCCCCG
3471	Ampd1	CGAGATCTCCCCCTTCGACG
3472	Ampd1	ATGGATGTGAGTATCCACCT
3473	Slc25a24	ATGAGAAAAAATCAGGACAG
3474	Slc25a24	AGAGACTGGACAATTTCAGA
3475	Slc25a24	AAGAAGTTGCTTACCGAGGA
3476	Slc25a24	ATCTTTGTTGACATCGCCAG

Number	Genes	Guide sequence
3477	Slc35a3	GCTGTAGAAGACAGATAACG
3478	Slc35a3	TGAAGCTCGCTATCCCGTCA
3479	Slc35a3	TCCTGCCATCAGAATTACTA
3480	Slc35a3	CAAACTGTGAGCCTGTTGAA
3481	Gba2	CTCACCTCAAGCCCATACCG
3482	Gba2	CGTCATCCCTCATGACATTG
3483	Gba2	ACCAAGCTACTGCAATTCAG
3484	Gba2	CATCGTATGTGTTGTACATG
3485	Aldob	TATCCACAGTTGGACCAAGG
3486	Aldob	AATTCCATTAGCCAGAGCAT
3487	Aldob	CCGCCTGCAAAGGATAAAGG
3488	Aldob	GGTCCCTATTGTTGAGCCAG
3489	Pigv	GAGGGCAAAAGGCATCTGCG
3490	Pigv	GTAGGCACGATACTGAAAGA
3491	Pigv	TTCCTGTTTATCGCTGAGCA
3492	Pigv	CAGGAGAAAATGCACCCCCA
3493	Slc30a2	CTGGTCGGGAAGACACCCAG
3494	Slc30a2	TGGAGATTATGAGATCAAAG
3495	Slc30a2	AGGCCACATAGAGTTTGCGT
3496	Slc30a2	GATGGAAAGCACGGACAACA
3497	Hadhb	ATATACAAGTCTTACCTCAG
3498	Hadhb	CTGACAGCAGAAATGGAATG
3499	Hadhb	GCATCGGACCAATATTCCAA
3500	Hadhb	TCAAACCAAGCCATGACCAC
3501	Slc26a1	ACAGGCCAACATATGTGATG
3502	Slc26a1	CCAGCCGGAGGATACCCATG
3503	Slc26a1	TACCAGACCCTAAGATAATG
3504	Slc26a1	GCCCACATTAACATGGCGGG
3505	Ap5z1	TGCGTCCAGTACCTTCCATG
3506	Ap5z1	TAGGTCCACACAGACTCCGT
3507	Ap5z1	ATAGCCCGGTCCCATCACTG
3508	Ap5z1	GGCCGCAGACAGCACAGACA
3509	Mat2a	CCTGATGCTAAAGTGGCTTG
3510	Mat2a	GTGCAATATATGCAAGATCG
3511	Mat2a	ACCAAGGCAATGTACCATTG
3512	Mat2a	ATTTACCACCTACAGCCAAG
3513	Cyp26b1	ACTGCTGGGTCCCAACACGG
3514	Cyp26b1	GCACCGGTCACACGAATCAG
3515	Cyp26b1	ACTGCTGGTATACCTCAAAG
3516	Cyp26b1	GGCCATCAATGTATATCAGG
3517	Slc6a1	CACCAACATGACCAGCGCCG
3518	Slc6a1	GCAGAAATACACGAGCACCC
3519	Slc6a1	TACCTCTGTGGGAAAAACGG
3520	Slc6a1	TCCATGTGTCCCGGTCAGGG

Number	**Genes**	**Guide sequence**
3521	Gys2	GCATAAGAGTAACGTCACCG
3522	Gys2	GTGGATGCGATGAATAAACA
3523	Gys2	GAGATAACGCCCAAGCAGTG
3524	Gys2	AAAACGACAGCCGATGAGTG
3525	Pgap2	AAACGCCACACGTAGCGTTG
3526	Pgap2	CATTAACTTCAGTCTCAATG
3527	Pgap2	GTAGTGGTTCCAATAGGCGA
3528	Pgap2	GACAACATCTACACACTGTG
3529	Xylt1	CCTGTACGGGAACTATCCTG
3530	Xylt1	CATGCGCTGTAGCTGTCGAG
3531	Xylt1	GTGCCAGTACAAGCATATCG
3532	Xylt1	GATGCCCAGGACAAACGACA
3533	Cog7	GTGCTATCAGACATTACCAG
3534	Cog7	TGAACGATGCTACGATCTGG
3535	Cog7	GTGGCACACACAAACCCAGT
3536	Cog7	GGTGCTGGTAGAGATTGACC
3537	Tufm	GAGGAAACTCCAGTCATCGT
3538	Tufm	CCGGTAGTTCTAGCCGAGGG
3539	Tufm	GTGACAGGTACATTAGAGCG
3540	Tufm	TCCACCCAGAATATGATCAC
3541	Csgalnact1	TTATTGTGCCCCTAGCGAGG
3542	Csgalnact1	CAGGGATTTACCGAACCGAA
3543	Csgalnact1	AGGGCTGTTTAGACTCTCCA
3544	Csgalnact1	CTTGACACCGGCATGTACCT
3545	Tat	ATGTTCGCGTCAATATTGGC
3546	Tat	GGCAAGCTTACCGATAGATG
3547	Tat	AACAACCCGTCCAATCCCTG
3548	Tat	TGAGCTGTGTCTAGCCGTGT
3549	Slc38a8	TCACGGTGCAATACTACCTG
3550	Slc38a8	ATTTCCCGAAGTGCTGACAG
3551	Slc38a8	GCTGGTCCCCGATCACTCTG
3552	Slc38a8	TCTTTGGTCTTCCTGATCAG
3553	Spg7	TTCCAAATGCAGTCAGACTG
3554	Spg7	GAACTCCCTCAGTACAAGTG
3555	Spg7	ATCAATGTACACTATGCAAG
3556	Spg7	GGATTCCCGTGTCCTACAAG
3557	Foxred1	ACTCCTTCTACGTTTATCCA
3558	Foxred1	CCCAATGAAGACCCCAACTG
3559	Foxred1	TGGAGCAGGACCACACGGTG
3560	Foxred1	TTGAACTGAAGTTCCACAGG
3561	Sc5d	CGTATGTATATCCAGCCACG
3562	Sc5d	CATGACTTGCAAACGGCGTG
3563	Sc5d	ATAGACAAAATAATAGCTGA
3564	Sc5d	AAGTAGACCACCTTGTGCAG

Number	Genes	Guide sequence
3565	Dlat	ACTACCGCAACGGACCGCAG
3566	Dlat	CAGGCTCTCAAACCCAACAG
3567	Dlat	CGACAAGGCCACCATAGGTG
3568	Dlat	TTCAGAACCACACCTACCGG
3569	Slc17a5	TCGTCACCCAGATTCCCGGT
3570	Slc17a5	TAGAACGTCTAAGGAGTGTG
3571	Slc17a5	GATCGTTATCTTACCCGCAT
3572	Slc17a5	GCTGGCCGCAGACTTAGGCG
3573	Glyctk	GGTGTGATCAGCGTACCCAA
3574	Glyctk	GCGGGAAAACCTCTACCTAG
3575	Glyctk	CTGTGCTCAACACCATGGCA
3576	Glyctk	AGTGATTGCCAGTGGCCCTA
3577	Phgdh	CCACACTGAGAGCCTACCTG
3578	Phgdh	CTCACTTCTGACCAGACTGT
3579	Phgdh	TAGTAGCAGACCGGACAATG
3580	Phgdh	CTGCGATTTCCTCCCCACAG
3581	Slc13a5	GATAGCCGCCAATACAGCTG
3582	Slc13a5	GGGTCCCGTCCCGGTCAAGG
3583	Slc13a5	AGTCCAGAACCTTCAAAAGT
3584	Slc13a5	AAGAAGGTGTGTTTACCGTG
3585	Apob	GCTGGTAGTGACATCAACAG
3586	Apob	AGTCTCACCTGTTAACTGCG
3587	Apob	ATGTTGCATGAGTATGCCAA
3588	Apob	GAATGGAATCATGCCCATTG
3589	Cog5	GGAGACTGTTACCAGTGTCG
3590	Cog5	GGAGGATTACGTCCTCCCGG
3591	Cog5	CAACTAGCAAAACTTGCCCA
3592	Cog5	TTTCACAGCATATAACTGGA
3593	Mtr	TCAGGTGCTCGATATCAACA
3594	Mtr	GGGGTCCGAATGAGACACGC
3595	Mtr	TGTGGATAGCATCATACACA
3596	Mtr	CTTCAAAAACACTAGCAGGG
3597	A4galt	TCTTCCTAGAGACATCGGAC
3598	A4galt	GCTGATGAAAGGGCTGCCTA
3599	A4galt	TCAGGGGCACCCCCAGACAG
3600	A4galt	ACTGTTTGAGGACACACCAC
3601	Pgap1	ATAGACAACAATATGCGACA
3602	Pgap1	ATATGTAACTTACCACACGA
3603	Pgap1	AGAATTTGCTCCTACAAGTG
3604	Pgap1	GTCGTCAGACTGTCAGTATG
3605	Impad1	ATTCCTGTGTAGCATCAAGT
3606	Impad1	TCCTTCACGAGAAGTCCAAG
3607	Impad1	CTCCCACTAGATAAATACTG
3608	Impad1	GCTTGGGCAATGGTAGATGG

Number	Genes	Guide sequence
3609	Gabbr2	CCTGCGACTCTACGACACCG
3610	Gabbr2	CATGGAAGGCTACATCGGAG
3611	Gabbr2	GCTGACAGGATGCTATACAG
3612	Gabbr2	CTTATCCGCAAGAACAGGCG
3613	Slc35d1	GGCGCCGGCCGAAACGCTAA
3614	Slc35d1	TGTGTGTGGAGGATTTCGCG
3615	Slc35d1	ACTGTATTTGCAATGATCAT
3616	Slc35d1	TGGTTCCCAAAATATAGTAG
3617	Cldn19	CCACACGGCTCTTGGCAGTG
3618	Cldn19	CTGGGCACTCACCTGCCAAG
3619	Cldn19	TGCTGACTGGATATGACCTG
3620	Cldn19	ACATCCACAGCCCTTCGTAG
3621	Slc45a1	GAGTACCGGAGTCACGTACG
3622	Slc45a1	AGGAGTACTCACCCGCCATG
3623	Slc45a1	GGAGTGACCGATGTACCTCA
3624	Slc45a1	CCACCCCGCACACTGTCAGG
3625	Ppm1k	CAGGTGGGCATAACTCGCGA
3626	Ppm1k	GCAGAATTGGCTCATCAATG
3627	Ppm1k	CTAGGATCAAGAAATTCGGT
3628	Ppm1k	AAAATTAGCCTGGAGAACGT
3629	Uroc1	TGTCACAACCCGTTCAATGG
3630	Uroc1	TCTGCCCCAGCATTGAGATG
3631	Uroc1	GGGAATCGTCCATGGCACAG
3632	Uroc1	CACCCCAATGCATCCAACGA
3633	Fkrp	GCTGGACTTGACCTTCGCCG
3634	Fkrp	CCAATGGCAGAAGTCCGGCG
3635	Fkrp	CCATCCAAAGCGTCGCAGCG
3636	Fkrp	CACAAACTCGGTGGCTACGT
3637	Nars2	TCACATCCAACGACTGTGAG
3638	Nars2	GGAACTCTTCAAGGCGACCA
3639	Nars2	CTCAGGGTCCAGGACGCGAG
3640	Nars2	TCAGTCCAAGAGGCAAAATG
3641	Cyp2r1	TAGGCATCAACAAAATGGTG
3642	Cyp2r1	GCAGAGCCGGGTGTATGGCG
3643	Cyp2r1	GATGCTATTGAAACATACAA
3644	Cyp2r1	AAAGGTAAGATGCCAATCCA
3645	Snx14	AGCTGTGCTGCCTAATTACG
3646	Snx14	CTTCAAGAGTTATTTCCGCA
3647	Snx14	GACAGATGCAAAAAACCGTA
3648	Snx14	TCAACATCGATACAAAACAC
3649	Slc36a2	TGACTAGGATGTGCATACAG
3650	Slc36a2	GGTAGTTCTGACGCCCACCA
3651	Slc36a2	AGCAAAGTACCTCCCCCAGT
3652	Slc36a2	AGCCCCGATAGCAATGTACA

Number	Genes	Guide sequence
3653	Fktn	GAGTCTATTCCATCTAGCCG
3654	Fktn	CACTCGATAAATCTGGAGTG
3655	Fktn	GACTCAAAGGACACATGGAT
3656	Fktn	TAATTGATTCCAGAATCCAT
3657	Atpaf2	ACAATGAATTAGCTACAGGG
3658	Atpaf2	AATGGGATCCCGTCATAGAG
3659	Atpaf2	CTATGTCCCGCCAACAGGTG
3660	Atpaf2	TGGCCCCGGCCATACTGAGA
3661	Slc5a2	ATGATTTATACTGTGACAGG
3662	Slc5a2	CTGGCACAAAAAGCCATCCG
3663	Slc5a2	GGTCTCTTCGACAAATACCT
3664	Slc5a2	ATTGGTTCTGAACATAGACT
3665	Acsf3	CACAGCGGCTAGGTTACGGT
3666	Acsf3	CATGAATACGGTAATCTGTG
3667	Acsf3	GGCCCACTGTGCTACAACGT
3668	Acsf3	ATATGGCCATCACACCTACA
3669	Gphn	GCTTTGTCCATAGACGTCAG
3670	Gphn	TGAAGGAGTAGTGCTAAGGG
3671	Gphn	ACCACGAGATGTCACTCCAG
3672	Gphn	ATCGGCCATGACATTAAGAG
3673	Sptlc1	AATGTGCCATAGAACCCTCG
3674	Sptlc1	CCCTCCAACCCACAACATCG
3675	Sptlc1	TCCTGCGTACTCTAAGAGAG
3676	Sptlc1	TTTGTCGTAGAATCCTCGCA
3677	Rnf31	GATGGATTGAGTTTCCCCGA
3678	Rnf31	GAACTATGAGTTGTTGGACG
3679	Rnf31	CTACCTCAACACCCTATCCA
3680	Rnf31	GGAGGAACCAAGGTGTTGTG
3681	Abat	GAGCAGAGGTAACTACCTAG
3682	Abat	GCTCCAGGAGTCCTTGATGT
3683	Abat	TTTCGGCAGAGTAAGGAACG
3684	Abat	AACGGTGGCTGGAATCATCG
3685	Ahcy	GCGCACCTGACAGAAGCTGT
3686	Ahcy	TGTCAACGATTCTGTCACCA
3687	Ahcy	TGACCCTATCATACCCTCCA
3688	Ahcy	TGTGATGATTGCGGGCAAGG
3689	Fbxl4	AGTTGTGCTGCATGGTACGA
3690	Fbxl4	TTGAGGTGGATATATTGCAG
3691	Fbxl4	ACAGTATGTCCTATACCATG
3692	Fbxl4	AGTGGCTGCAGGATAACTCA
3693	Vcp	ACTGTCTTCACAGACTCATG
3694	Vcp	TATAGGTCGCTTTGACAGAG
3695	Vcp	CCAATCGCCTTAAAGAGCGC
3696	Vcp	CTTCAGGAGTTGGTTCAGGT

Number	Genes	Guide sequence
3697	Chsy1	GGTGTAAGGTGATCGCTCGG
3698	Chsy1	GCGTGTGAACCCCATGTACG
3699	Chsy1	AAGAGAAAGTTCCTGTCGCG
3700	Chsy1	CAAGTACGAGTGGTTTATGA
3701	Gcdh	GATGATCATACCGGTAGCCG
3702	Gcdh	CAGGATCACCAACTCCCCTG
3703	Gcdh	GGTCCTTCCAGTCAAACACG
3704	Gcdh	CTCCTGGCAGTAGTTACGGA
3705	Clpx	AAGAATTCTCGAAAACTACG
3706	Clpx	TGGTGATTTGTGTACACACG
3707	Clpx	TCTCTTATAATGATTATACA
3708	Clpx	TGTTATTTACCTGACCCAGT
3709	Pigs	ACCATAATGCCACCCCAGCG
3710	Pigs	GGGCGACCTGGACTATGCGA
3711	Pigs	GATCTCTCGCTCATGCACAA
3712	Pigs	CTACCTAAGCTGGACTTGAG
3713	Flad1	ACAAACTCGCGGAGTCAGGT
3714	Flad1	TCACTCACGTCCTCACCGCG
3715	Flad1	GCTAAGCCTACGCCCAAAGT
3716	Flad1	GAAGCTGATTCTAGACTCCG
3717	Pik3r5	CCACAGGAATCTCCTACCAG
3718	Pik3r5	CGAGAGGCCTGAGACAAAGG
3719	Pik3r5	TGTACTTACACAGAGGACAG
3720	Pik3r5	GCTGAGCGGGACAGTCCAAG
3721	Alg6	TTTGCTCATTTACGTACCCG
3722	Alg6	TCTCATAGCCTCGTGATGTG
3723	Alg6	TAGTCGATAAGAATAAGACC
3724	Alg6	GCTTCATAATCACCAAACAT
3725	Ocrl	TTTCGAATCATATTTGTACG
3726	Ocrl	CCAATGCAGTAAATATCAGG
3727	Ocrl	ATTTACCCCAATATGGAACA
3728	Ocrl	ACGTGGAAGAGTTCGAACGA
3729	Pgap3	CATGCAGGTATGGTACATGG
3730	Pgap3	AGTCGCGGTACACGGGCTCG
3731	Pgap3	ACTGCAAGTATGAGTGTATG
3732	Pgap3	GGGACTACAGCACCCGTCTG
3733	Trappc11	GCAGGCCGGGACTTACATCG
3734	Trappc11	AGAGCTTGGAAAACCTAATG
3735	Trappc11	CGAGTGGTACATCCCTAAAG
3736	Trappc11	AGAGGAGTACTACTATGCAA
3737	Gfm2	GGATACACAAGATCATTGGG
3738	Gfm2	ACCAGCAGAGGCGTCAAACA
3739	Gfm2	GGAGCATGGAAAGAAGAGAG
3740	Gfm2	CCAATTACCTGTAAAATCAG

Number	Genes	Guide sequence
3741	Pisd	CAAACTTGCTAGTCACTGGG
3742	Pisd	GGTCCCCAGAAAATGGCGTG
3743	Pisd	GGGCCCTCGAGCCAATACAG
3744	Pisd	CGTATGTGGCTTGCACTGTG
3745	Rfx6	TGAGCATAAAGAATGCACCG
3746	Rfx6	GGACATAGGATGTCTCCACG
3747	Rfx6	GGTAAGATTATGCATCACGC
3748	Rfx6	TCAGAAATGCAGTTAAACAA
3749	Serac1	AGCCATAGTAAAGCATTCGG
3750	Serac1	AACCTGGACCGAGAAACTGT
3751	Serac1	CACCCTGCTATAGTCCACTC
3752	Serac1	GAGCAGCATTTAAAACCTGG
3753	Dna2	ACACGATGCGAAGGATACGG
3754	Dna2	GCCCTTCAGTCCAAACCTAG
3755	Dna2	TGCCTTGCCACAGATAATCG
3756	Dna2	CAGGCGTTAACCAGATACTC
3757	Pigl	CTTGTCAATAATCATTACAC
3758	Pigl	TTGATTGTAGTAGTTTCCTG
3759	Pigl	GTTCCGCTGAGTTCCAAACC
3760	Pigl	GCGTGCCAAGCCTAGCATGG
3761	Rft1	AGGACCAAAATATACCCAGT
3762	Rft1	GAATAATCTTGGCTCCCTTG
3763	Rft1	GGTTCTTGCTGAGAGCATGT
3764	Rft1	GGCAAAGCCAAAAACAGTCA
3765	Slc5a6	CTTACTTAATCCCAGAGATG
3766	Slc5a6	CAAACATGACCAGACCAATG
3767	Slc5a6	GCAGTTCACCAACGGTATGG
3768	Slc5a6	ATCCTATAGGTGATATACAT
3769	Gmppb	GTGGCTTCTCAACAAAACGG
3770	Gmppb	GTGCCGATGAAACTGCACCA
3771	Gmppb	TTCCCAGTTATGGCCAAGGA
3772	Gmppb	GAGCACTCCGAAGCCATTGG
3773	Cndp1	CACTCACTTATGGAACCCGG
3774	Cndp1	AGTCAGCCATTGGTTCGTTG
3775	Cndp1	CAGCTCAGAAGGACGACGGG
3776	Cndp1	AGCCGGTTCCATCGCCCTGG
3777	Fa2h	TTCGTGCGGCATCATCCGGG
3778	Fa2h	TCTTGAGCCACAGTTCAAAG
3779	Fa2h	CTACTACCGAACCCTCACCC
3780	Fa2h	GTGGATGACGTATTCCACAA
3781	Gars	AGTCAGCAAATTTGTCTACG
3782	Gars	GAGATATTCCAACCTTCGTG
3783	Gars	TAAGTTAAAAGGTACCGGAG
3784	Gars	CCAACAGTGAGTACCTGACT

Number	**Genes**	**Guide sequence**
3785	Lyrm4	ACAGATCTAAAACTTGTGCG
3786	Lyrm4	CCAGGGCTTGAATTTCTACA
3787	Lyrm4	TCATTAGAATGTATGCTGTC
3788	Lyrm4	CCCGGGTCACCTGTAATTGT
3789	Iars2	CCAAACTAAAACGCTAACAG
3790	Iars2	AAATCGGCGTTTGTCCGCTG
3791	Iars2	AGGCGGCAGATACCGTGACA
3792	Iars2	AATCGATTCCATATGATGAG
3793	Pdp1	GAGGTCAACACCATCTACAT
3794	Pdp1	GTGTACCTCAGACGATTCTG
3795	Pdp1	ACTGGAACACCCAAAAAATG
3796	Pdp1	TGCTTGTGCCACTGAAGGAT
3797	B3glct	TGAGGCAGAGTAGTCTACCG
3798	B3glct	TGGAACGTGGTGACGCAGCG
3799	B3glct	CATACAGCAAGAATTCAGCG
3800	B3glct	TGCCAAAAGATTAAAGAGTG
3801	Alg8	TTGTCCGCGTTACTTCCCTG
3802	Alg8	ACAGCCTCCCAATATCTCAG
3803	Alg8	CCGCAGCAGATAGACACCAT
3804	Alg8	AGTTTGGAGCCCAGTAGGCA
3805	Rrm2b	GAGAATGTACAAGCAAGCAC
3806	Rrm2b	TTGGAAAGATGACGAACCGT
3807	Rrm2b	GGAGATAAAATACTTCTCGT
3808	Rrm2b	TCTCCTAGGGGAAAGAGTGG
3809	Gatc	CAGATGCTCGATTACCGCGG
3810	Gatc	GCCCCTAGAGTCGGTACTGG
3811	Gatc	CAAAGCGAATCCACAGGGAA
3812	Gatc	GGCGTGCAGCTGATCCGCAA
3813	Ugt1a1	AGACAAACTCTTGGGCACGT
3814	Ugt1a1	CAGTGGCAAGTGACCCATAG
3815	Ugt1a1	ACTTTGTGAAAGATTACCCC
3816	Ugt1a1	ACACTAACAGCCTCCCAGCG
3817	Opa3	ATGCGCATAATGGGTTTCCG
3818	Opa3	AGGTCTTGAAGAACTCGCTG
3819	Opa3	TCCTTGATACGGTTGGCCAG
3820	Opa3	TCAGCAGCGCAATAAGGAGG
3821	Ndufs6	GGGGTTCAAGTGTCGCCGAG
3822	Ndufs6	CGAAACCCCGTGCAGCCCTG
3823	Ndufs6	TGGGGAGAGTCAACAGCCGG
3824	Ndufs6	TGATGAAAAAGACTACAGGA
3825	Gnptab	TGTTTGCAATGGACGCGTGG
3826	Gnptab	TCTGCCCATGCCAATCGACG
3827	Gnptab	AGGAGTGAAATATTTACCCG
3828	Gnptab	CATGCTGGACCGTTTAAGGG

Number	Genes	Guide sequence
3829	Pnpla1	TTTGTACGATGTGCTACCGG
3830	Pnpla1	CTGCAGAGATACATCGACGG
3831	Pnpla1	GGTTTCCGAGTACCGATCCA
3832	Pnpla1	AAATGTTCAAACTCCAAACC
3833	Pigg	AGGTGGATAAAAATGTCACA
3834	Pigg	ACCCCAGCGTCACTCCCATG
3835	Pigg	AAAGTACTCAGGCATTACCT
3836	Pigg	GATTCGAGGCATAGTAACTG
3837	Amt	AAATGGTGGCGTTTGCAGGG
3838	Amt	TTGTAAGCAATACTTCTGAG
3839	Amt	TGCGGAACTAAGGCCTAACC
3840	Amt	TGTAACACCTGTGTTGCCGT
3841	Cers3	TATCATGAATAAACATCACG
3842	Cers3	GTTTAGAAAATGGTTCTGGT
3843	Cers3	ACACCTCTAGCAAATGCACT
3844	Cers3	ATGGGCATATGACCTCTGGG
3845	Cyp26c1	CCCTTGGACGTACCGTTCAG
3846	Cyp26c1	GTCACACACACTACTTGGCG
3847	Cyp26c1	GTGCGCCGCCCAACGACCGG
3848	Cyp26c1	CTGTCCCGTAGCGCTCGCGG
3849	Lipt1	GGTTGATGTTACCCATGTCG
3850	Lipt1	CTGTAAAATGAGCCCATGTG
3851	Lipt1	TGAAGTTCTGATGAGTGCGG
3852	Lipt1	AGTCCGGCCGATCTTTGATG
3853	Gpx4	CGTGTGCATCGTCACCAACG
3854	Gpx4	CATGCCCGATATGCTGAGTG
3855	Gpx4	TGGTCTGGCAGGCACCATGG
3856	Gpx4	TAAGCCAGCACTGCTGTGCG
3857	Vps13b	TGTCCATACTACCCAAATCG
3858	Vps13b	TAAACACTGCAATACAAGCG
3859	Vps13b	GAAACCTCTTCCCGATACAG
3860	Vps13b	TGGCAGTAGTCCATGTACTG
3861	Pex10	CAGAAGGACGAGTACTACCT
3862	Pex10	ACCTGGCCAAGAGACTAGCA
3863	Pex10	GTACGTTGGGATCATCCAAG
3864	Pex10	TGGAGGACGCAGCCGATCAG
3865	Sco2	TTCAGCCTACTAGACCACAA
3866	Sco2	CTGTTCCTTCTCAGCCCTCG
3867	Sco2	GCTCATCGGGGCAAATATCA
3868	Sco2	GCATAGAAATTCCCGACACT
3869	Epg5	ACAGCCGACTCGTTGTAACA
3870	Epg5	TCGAGCCAGAAGAACCAATG
3871	Epg5	TGGGTACCATACCCATATTG
3872	Epg5	GAAACGCTGTCTTACACAAG

Number	Genes	Guide sequence
3873	Pet100	GGAGATCCAGAACATAACCA
3874	Pet100	CTGTGGCCAAGAGAGAAGGA
3875	Pet100	CTTTGATACCCACCTTACGC
3876	Pet100	GGATCTCCAATCAGGCTGAG
3877	Nt5c3	AGAGTAGAAGAAATTATCTG
3878	Nt5c3	CTCACCACTCTACCATGTAA
3879	Nt5c3	CCAGCAGAAAATATGAACAC
3880	Nt5c3	TCTCACTTACTATGACACGT
3881	Hprt	CTAGAATGATCAGTCAACGG
3882	Hprt	TATACCTAATCATTATGCCG
3883	Hprt	AACAAATCTAGGTCATAACC
3884	Hprt	AGCCCCCCTTGAGCACACAG
3885	Rnaset2a	CTCACCTTGCATACTGTTGG
3886	Rnaset2a	AAACATGAGTGGGTTAAACA
3887	Rnaset2a	AGAAGACCGGTGAATCACAT
3888	Rnaset2a	CAGAAGATTGTAACCAGTCC
3889	Oas1a	GGGAGGTACATTCCTCGATG
3890	Oas1a	GTTGGTACCAGTGCTTGACC
3891	Oas1a	AAAGACAGTGAGCAACTCTA
3892	Oas1a	GAGGATCAGTTAAACCGACG
3893	Car5a	ATTACAAGAAAGCCTCCGTG
3894	Car5a	GACACTGGGCCAGTCCAGAG
3895	Car5a	GGAGTTTGACGATTCCTGTG
3896	Car5a	AGTGTTTACGAACCTCAGCT
3897	Apoa1bp	TGTGGCCCCGGAAATAACGG
3898	Apoa1bp	TAACGAGTATCAGTTCAGCG
3899	Apoa1bp	CTCTTGGACATAGACGTGGG
3900	Apoa1bp	GAGTCACTAGCCCAGTGAAG
3901	Carkd	TAGGCCAGGTCCCACGACAA
3902	Carkd	CTGACGTCGAAGAAGCACAA
3903	Carkd	CATTCTCACCCCCAACCACG
3904	Carkd	CCATACAGCACATGCGACAA
3905	Ppat	ACCTTGGAATCGGACATACG
3906	Ppat	ATAAGACGCCCGATGCAGAG
3907	Ppat	TGATCACTCTGGGACTCGTG
3908	Ppat	AGGGGTGTATGCGAGTAACT
3909	Prosc	TATGCTGGAAACCGTAGACT
3910	Prosc	ATGGTCCAGATTAACACCAG
3911	Prosc	AGACCCACGAACTCCAGGCT
3912	Prosc	TTGCTGACCGCAACGAGCCG
3913	Ftl1	GCTGCTCACCAGAGAGAGGT
3914	Ftl1	TTGGCCGAGGAGAAGCGCGA
3915	Ftl1	GAGTTTCAGAACGATCGCGG
3916	Ftl1	TCGTCAGAATTATTCCACCG

Number	**Genes**	**Guide sequence**
3917	Sis	TCAGTCACGAATGACAACAG
3918	Sis	AATTTACCGGGAGTAAAAGG
3919	Sis	GGGAAGTAAAGTGTAGCGGA
3920	Sis	GTAATACGGATGGAATCCAT
3921	G6pdx	AGAGGTGGAAACTGACAACG
3922	G6pdx	TGCCCGCTCACGACTCACAG
3923	G6pdx	ATGACCCCACAGTACCCCAT
3924	G6pdx	AGAGATGGTCCAGAATCTCA
3925	Ins1	TAGAGAGCCTCTACCAGGTG
3926	Ins1	CTGGGAGCCCAAACCCACCC
3927	Ins1	ACCCAAGTCCCGCCGTGAAG
3928	Ins1	GTGGAACAACTGGAGCTGGG
3929	Gyg	AACAGCACAGGACTACTAGG
3930	Gyg	CTTACGCTTTAAATGCCGGG
3931	Gyg	CTGGTTATACGTTTCAATGG
3932	Gyg	CACTAAAATATGTATTCAGT
3933	Pcx	AGGCTGCCATCTCATACACG
3934	Pcx	ACGAGCAGAGAGTCATAGTG
3935	Pcx	GCGCATGGCAACGTCGAACG
3936	Pcx	GACTGGGGCTCACATTGACA
3937	Fh1	AATTGGGCGAACTCACACGC
3938	Fh1	CAGAGCTTCAAACTTATTCG
3939	Fh1	GCGACGTTCGGAGCACACCG
3940	Fh1	CTCGTAGATTCTTGGCATGG
3941	Atp5a1	TGGTCAGAAGCGGTCCACTG
3942	Atp5a1	GCTCCCGCACAGAGATTCGG
3943	Atp5a1	ACTGGGCGTGTGTTAAGCAT
3944	Atp5a1	CCAACAGCTCCTCGCCAACG
3945	Atp5d	TCAGGCGCGTACATACGCCG
3946	Atp5d	GTGAGTTCGTACCTGCGTCG
3947	Atp5d	CCAAAGGCTCCAGTCAGCGT
3948	Atp5d	CTCACCAAAGTACTTAGTCG
3949	Atp5e	GAGACACCATGGTGGCGTAC
3950	Atp5e	GTGGCGTACTGGCGACAGGC
3951	Atp5e	AGATCTGTGCAAAAGCAGTG
3952	Atp5e	CTGGGAAAACCGGATGTAGC
3953	Usmg5	TTACATTCATTCTACCTGTG
3954	Usmg5	TGTGTCCTGGCCACATATGG
3955	Usmg5	ATGGCTGGTGCAGAAAGTGA
3956	Usmg5	GATGGCCAATTCCAGTTCAC
3957	Peo1	CATGTGCACGTAAATACTGG
3958	Peo1	CTAACCAGAACACAATCCGA
3959	Peo1	ACGTGGCCTGAAGCTACTAG
3960	Peo1	AGGGCGGTACGAAGAATACG

Number	Genes	Guide sequence
3961	2810006K23Rik	TCCTGATCAGTGGTAGAGGG
3962	2810006K23Rik	GTGCCACCAAACAAGATCTG
3963	2810006K23Rik	CGTGAAAGGACATGGCCCAG
3964	2810006K23Rik	TACCTTGACCACAATGCCGG
3965	Timm8a1	TTCTGAACAGGAGAAGTGCA
3966	Timm8a1	TCAGCCCGACTGTCCAACTT
3967	Timm8a1	GCCCAGAGCCGAGCCCGAAG
3968	Timm8a1	GTTGCAGCATTTCATCGAGG
3969	Park2	CCAAACAGATCACGTGACGG
3970	Park2	TACACATAGTACAGAGACCA
3971	Park2	AAGTGGTTGCTAAGCGACAG
3972	Park2	TTAATTCCAAACCGGATGAG
3973	2410015M20Rik	GGGGCCTAGTGACAAGAGTG
3974	2410015M20Rik	TGGAAATTTAATCTTTGGAG
3975	2410015M20Rik	CTCGAGTGTGGTCGCTAATG
3976	2410015M20Rik	CAATATGTGTGCCAGCAGAC
3977	Clk1	TTCGCAGCACCATTCACACG
3978	Clk1	ATACTTACAAAGTACTATGG
3979	Clk1	ACTACATGGGCTACGAGCCA
3980	Clk1	CTGATATGATCCATTCGAAA
3981	Adck3	AGTTCAGTTCTCAACACCAC
3982	Adck3	CATGCCACTGAAACAGATGA
3983	Adck3	CCAGCGAAGATCCTTCCACC
3984	Adck3	CATTGTGAGTACACTGTGCA
3985	Adck4	GACCTTATGTACAGTCCGGG
3986	Adck4	ACTAAGAAGTCCTTGCCAGG
3987	Adck4	ATGAGTGTGGGCCTGCCAGA
3988	Adck4	GCTAAAGGATGGGACTGAGG
3989	Gyk	TCCATCTAGAGTTTAACAGG
3990	Gyk	GACCTTGTCCCAGACTACTG
3991	Gyk	TACAGCACCAGCTATAGCCA
3992	Gyk	CTACCTATAGGTATGGAACA
3993	Ept1	CAATTCCAGCACCCCGTTAG
3994	Ept1	GTGTACTCCATCTTTGGACG
3995	Ept1	TGACTGGGTTTGGATTGTCG
3996	Ept1	GGTCGAAGTATGTCAGGAGT
3997	Cyp4f39	GGGGAAAGAATTATCTGACG
3998	Cyp4f39	CTTCAGGACTTACCTAACCA
3999	Cyp4f39	TCAGCTTGCGACAGGTAATG
4000	Cyp4f39	TGTACTACCTCACAGCCGAT
4001	Cyp21a1	GCTTACCTTGCATCCCCAAG
4002	Cyp21a1	TACCATTTAGCATATGGGGT
4003	Cyp21a1	AGGAGATGATACTACAAGTG
4004	Cyp21a1	ATGATTGACTACATGCTCCA

Number	Genes	Guide sequence
4005	Akr1c21	AGGACTAACCAAGTCCATTG
4006	Akr1c21	GTATCTCATTCATTACCCAA
4007	Akr1c21	AGATGATTCTGAATAAGCCT
4008	Akr1c21	TACTGAAGATCATGTAGGAG
4009	Rab7	GGAAGTTCTCGGGATCCCGG
4010	Rab7	ACGGTTCCAGTCTCTTGGTG
4011	Rab7	CGACAGACTTGTTACCATGC
4012	Rab7	CACATACTGGTTCATGAGAG
4013	Tmem5	TGCATAAATTAACCACTGGG
4014	Tmem5	GCGCCCGAAGAAGACGTGGT
4015	Tmem5	ATGTCTGCACCATTAATCCA
4016	Tmem5	TCTTTACAGTGACTTACCAA
4017	Large	GATGTGTCTGATTTAAAGGT
4018	Large	CAGCAATAGAATCAGCAATG
4019	Large	GCAGGTAACAGCTCTGAGTG
4020	Large	ACAGCAGAGAGGGAACTCAT
4021	Chst5	GTAAGCCTCTGTGCGCAACG
4022	Chst5	GCGAAGGCTTCGCAGACCGG
4023	Chst5	CAGCCATGTGCGCATCGCAG
4024	Chst5	TGAGCGGATCAGGTCACGCA
4025	Hykk	CTCCGTATGCCGAACTAAAG
4026	Hykk	CCTGAGCCAAAGTCGAAACC
4027	Hykk	CCCAGGAAGACCAATAGCTG
4028	Hykk	TTTCGTGTTCACATTGCAAG
4029	Fdx1l	CGCCCGGGTCCTGTTACGGG
4030	Fdx1l	GTTTGTCCCCAGGGTCAACG
4031	Fdx1l	CTGGCAAGCGGATCCCGGTG
4032	Fdx1l	TCTAGGACGTTCGGGACTAC
4033	Zfp143	GCATTTCGGTGCAAATACGA
4034	Zfp143	CTAATTATAAAAACCATGTG
4035	Zfp143	CCTGACGGAGGCAGTAACCG
4036	Zfp143	AGTGTGAGCATTCAGGCTGT
4037	Cyp51	GCTGTCAAAAGAACCAGCTG
4038	Cyp51	ATGCAGAAGAAGTCTACGGT
4039	Cyp51	TAGAAGTCAACTCAACGAGA
4040	Cyp51	AGGAACATACTGCTTAAAGT
4041	Pigyl	GGGATGAGGACGGTCATGGT
4042	Pigyl	AGGCCTGCCAGCGAGACCAG
4043	Pigyl	TGGGAAGCCTTCCTCCACGG
4044	Pigyl	CCACGGAGGCGGAGTAGAGC
4045	Fmo3	GATGCTACAATGATTTGTTC
4046	Fmo3	TTCACAGGACCATATAGAAG
4047	Fmo3	TGTCACAGCCTGAGTTCCCC
4048	Fmo3	CTTGGGTGATGAGTCGAGTC

Number	Genes	Guide sequence
4049	Bckdhb	GCCAAGTATCGCTACCGCTC
4050	Bckdhb	CTCGTAAACCAACAGTGCAT
4051	Bckdhb	CCACACAACCCCACGGGGCC
4052	Bckdhb	CACCGGTGCTACAGCTATTG
4053	Agxt2	CATCACCATGGCCAGGTCGT
4054	Agxt2	TAGCAAAGGCTTCCGGAAAT
4055	Agxt2	AGACAGAACTTGTATGCCAC
4056	Agxt2	AAAAACAGATAGACCGCCTG
4057	Nnt	ACGAACGCTTCGTACTCACC
4058	Nnt	GTTATACATACCTTCGCAGG
4059	Nnt	TTCAATGTTGTCGTGGAATC
4060	Nnt	GCTTCGTGAGCGCCTAACGT
4061	Slc25a3	TGCGGCACTTTACTAAGTCC
4062	Slc25a3	TTCAACAGTACGTTCAAAGC
4063	Slc25a3	GCCTTATATAGCAACATACT
4064	Slc25a3	GCCCCGAAGTGAATGTACAA
4065	Ndufv1	GCCGCCTATATCTACATCCG
4066	Ndufv1	TGTACCAGTCACCCCGTCTC
4067	Ndufv1	GCCAATCAGACCTGCTTCAT
4068	Ndufv1	CCCACAGGTAGCTATCCGAG
4069	Ndufa12	CTTAAAGGGCAAATGATATA
4070	Ndufa12	CTGGTGGGAGAAGACAAATA
4071	Ndufa12	TGGTGTAGATGACCCATCGG
4072	Ndufa12	CCTACCTGAAGAAAACCCGT
4073	Ndufa12	TCCACCCTTAGAGATTGTTG
4074	Ndufa12	AGCAATTCCCCGCTGCCTCA
4075	Ndufa12	CATACAGGTGGGATCTCATC
4076	Ndufa12	ATCTGCGGAAATCGCGTGTT
4077	Bcs1l	TTGGTTATCCGCGCCGACGT
4078	Bcs1l	ACGTCGGCGCGGATAACCAA
4079	Bcs1l	TACCTTCTTTATGGGCCCCC
4080	Bcs1l	AAGAAGGTAGCCACGTCTGT
4081	Tymp	CACCAGGTGCCAATGATCAG
4082	Tymp	ATACTTAGGGGCCATGCTAA
4083	Tymp	TTCAGGTCACCTGTAATGAG
4084	Tymp	TCACATCTCGTGCAGCATAC
4085	Sacs	TTTGTAAACCTTCAATCAAA
4086	Sacs	TCTCCAATCTTGATCCAATC
4087	Sacs	ATATAAAAATTTAACCTCTG
4088	Sacs	GTCCGCGTGACCGTGCTCCG
4089	Tmlhe	AGTTGTTGCACCAACAAAGC
4090	Tmlhe	TATCTAGTCACATGACCATC
4091	Tmlhe	ATGCCGGTCTAGAGCTAGCT
4092	Tmlhe	CTCCGTAATTTGATGAAGAG

Number	Genes	Guide sequence
4093	Sbf2	TGTTGGCTGTTTCCGCTCTC
4094	Sbf2	GGATGACACGCCTTTCCCAC
4095	Sbf2	CTTACCAATTCAATTCCCTG
4096	Sbf2	CTAATCTGGATACCAACACC
4097	Pikfyve	CTGGCATCCAATATTGCTTC
4098	Pikfyve	TGTTGTAATCAAGAAATCCC
4099	Pikfyve	GGCTGGTTCTGCTTTCCTTC
4100	Pikfyve	CGAAGCTGAACAGCTGTACG
4101	Plcg2	TTGCCAAACTGAGCGTGCTG
4102	Plcg2	CGCTCACTTTGAAGTTGACC
4103	Plcg2	TAGATCAAACCCGAAGAAAC
4104	Plcg2	AGATAAAGGAAATCCGTCCG
4105	ApoE	GCCTCTGCGCGATCGCGCCC
4106	ApoE	CCGACTCGGAGCCGACATGG
4107	ApoE	CTACACAGGATGCCTAGCCG
4108	ApoE	GCTTCTGGGATTACCTGCGC
4109	Fdft1	AACCTTGTCCCAGTCCTGTT
4110	Fdft1	CTCTCAGTGAACCGCCACTC
4111	Fdft1	CTGCCATCCCACACCCCATC
4112	Fdft1	CAGTACTGCCACTACGTTGC
4113	Abcd1	TCATCCTGCTTGAGCGCCTA
4114	Abcd1	GTTCCAGCATGACATACCAT
4115	Abcd1	CAGGGTGTACGAGATGTTCC
4116	Abcd1	TCTCTCTACAGGCCAAGTTG
4117	Pex26	GCGCTCTGCGGCCTTCAGCG
4118	Pex26	TCTGGATCCGGCGGAAGAGC
4119	Pex26	CTGGTAGTACCGGAGGACCC
4120	Pex26	GGTCAAACCGTAGAATCAAG
4121	Tusc3	AAAAGCAGATGAATAACGCC
4122	Tusc3	CATTCTGAAGATCGAGCGCC
4123	Tusc3	TAACGAAGAATATCAAATCC
4124	Tusc3	CGCTCGATCTTCAGAATGAA
4125	Pigo	CAGGGGACTCATAGAACGCC
4126	Pigo	TCCGGGGAAGAGGTCTCTCC
4127	Pigo	CCCATCCCGTTTGGGAACAC
4128	Pigo	CCACAGTGGACGGCGGTTCG
4129	Atp6v0a2	TGAAGAGCTCGAACGAATAC
4130	Atp6v0a2	CAACAGAGAGTCGTTCTCTA
4131	Atp6v0a2	CTACAGCTGCATGCAGCGGC
4132	Atp6v0a2	TCTTCGTGACCCTCAGCATG
4133	Cers1	GCAGACGACACCGCTTGGCC
4134	Cers1	TGACGTCAGCGATGTGCAGC
4135	Cers1	ATGAACTCACCGGAAGGCGT
4136	Cers1	GTAAGCGCAGTAGCTCCAAC

Number	Genes	Guide sequence
4137	Cers2	TTGGGAGGGATATCCCATAC
4138	Cers2	GGCGGAACCAGCGTTCTACC
4139	Cers2	CATTGGGAGGTGCCCGCAGT
4140	Cers2	GCCCACTCTGCCGTGACAAA
4141	Ears2	TGCTATCCGCTTCCGTCTAG
4142	Ears2	AGGGGCAGATGAGCAAATCG
4143	Ears2	TTCAGAAGCTCCAGCCGCTG
4144	Ears2	AGTGGCAGGTGATCCGCGTC
4145	Hars2	GGAACCTTGATGACAAAATT
4146	Hars2	GCCTCCAGACCTTTCCAACT
4147	Hars2	GAAGTTGTCTTCATACTTCT
4148	Hars2	AACAGCTGATAATCTTATCG
4149	Stat2	AGTTCTTGGTGAGATCCATC
4150	Stat2	ATAACTTGCGAAAATTCAGC
4151	Stat2	CCTACTTAGACCTTTCCCAA
4152	Stat2	TGAGATTGAAAATCGAATCC
4153	BRDN0000737505	AAAAAGTCCGCGATTACGTC
4154	BRDN0000737693	AAAACGGCTCGATCGGTGAT
4155	BRDN0000737637	AAAACGTAATTATACCGAGC
4156	BRDN0000738185	AAAATTGCACCTTCCCGGCC
4157	BRDN0000737801	AAACCCCCGCGCGGAGCGTC
4158	BRDN0000737467	AAACCTAGCGTAGATTCGGC
4159	BRDN0000737848	AAACGAGGCTGTTCGTACAC
4160	BRDN0000737609	AAACTCATACGTAGCGAATC
4161	BRDN0000737434	AAACTCCCGTGTCAACCGAT
4162	BRDN0000738254	AAAGACGTGCATTCAGCGAG
4163	BRDN0000737777	AACATGTTAAGTCGCGTTAT
4164	BRDN0000737611	AACCAGCATTTGACCGCGCT
4165	BRDN0000737528	AACCCCGGCTGTCATCGCCG
4166	BRDN0000738228	AACCCGCCGGAACAATCAGC
4167	BRDN0000737727	AACCGGCTGCGCGTTTGCAA
4168	BRDN0000737483	AACCGTACTGCGAGGAGCAT
4169	BRDN0000737872	AACCTCGTCTCATGTACGAA
4170	BRDN0000737516	AACGCCCCGGATTTCGTTGA
4171	BRDN0000737844	AACGGCTGCGCCCGCGGCAA
4172	BRDN0000737412	AACGGGCGCAATACCCTTTT
4173	BRDN0000737631	AACGGTAGCGTACCCGTGAA
4174	BRDN0000737750	AACGGTCAAATCCGTGAGGG
4175	BRDN0000737875	AACGTCACCAACCTCGATCC
4176	BRDN0000738229	AACGTTATAGCTTCGTCTCT
4177	BRDN0000737806	AACTAACTCACTACGCACGA
4178	BRDN0000738366	AACTCCTCATCGTACGCTAA
4179	BRDN0000737593	AACTCGCGTGGGAAGTCCGG
4180	BRDN0000738128	AACTTATACGTAATCTGATC

Number	Genes	Guide sequence
4181	BRDN0000738307	AAGACTCCTACGTATCGAGC
4182	BRDN0000737391	AAGCACAAGAACGGTCCGCC
4183	BRDN0000737912	AAGCAGCGACTACTCGACGC
4184	BRDN0000738101	AAGCCTAACGGAGCTCGCGG
4185	BRDN0000738296	AAGCCTACTTCACCGGTCGG
4186	BRDN0000738095	AAGCGAGCCGCAGACCGTTT
4187	BRDN0000737714	AAGCGTACCCCACTCGTTAA
4188	BRDN0000738016	AAGCGTGAGATTCACCGCCG
4189	BRDN0000737416	AAGGCCTTAACACGTCGACC
4190	BRDN0000737993	AAGGCGTAAACGAGTACACG
4191	BRDN0000738351	AAGGGTAAGTACAGTATCGT
4192	BRDN0000738301	AAGTCCCCTTCGGGAACTCC
4193	BRDN0000737395	AAGTCTATGCGGGGCTCGTA
4194	BRDN0000737589	AATAAGCCTACCCGGCGAGA

Original Doc Name: IEM (All) Library (Andrew)

*Oligo name	Guide sequence
example 1	
Abca1	ACATGTCATCAACATAACAG
Abca1	GTGGACCCGTACTCTCGCAG
Abca1	CAAGCTGTCAAGCAACACTG
Abca1	GGTATACACAGAGCCATTTG
Abcb7	GATTAAATACTAACGCACTG
Abcb7	CGCTGGGACGAACTCCATCG
Abcb7	ACAGTTACTAGATGCTACAA
Abcb7	TCACAGTTGCAGTTACACGG
Acadl	AGGCGATCGAGCTTCACGGT
Acadl	AGAGCGTACTCCAATTGCAC
Acadl	AACATCGCAGAGAAACATGG
Acadl	CCGGAAAATGTCATGCTCCG
Acadm	AAGATGTGGATAACCAACGG
Acadm	CCCGGAATATGACAAAAGCG
Acadm	TCGAACACAACACTCGAAAG
Acadm	AGCAGGTTTCAAGATCGCAA
Acadvl	CAAAGCATCTAACACGTCAG
Acadvl	CAACAACGGAAGATTCGGGA
Acadvl	GCTACATCGGATCCACTCGA
Acadvl	CCAGCGACTTTATGCCAGGG
Acads	GGTGACTCATGGGTCCTCAA
Acads	GCTCATGATAACTCCCGTGG
Acads	GATGGGCTTCAAAATAGCCA
Acads	GCTCACCCATCTTCTTAACC
Slc33a1	GTGACTTACCTAAAGCCCCG
Slc33a1	ATGTTATCCCGGGAAAACGT
Slc33a1	GAAAGGGTAACGATTCCCCT
Slc33a1	AAATATTGATGGCAGAACAC
Aco2	AGATCCGTGCCACTATTGAG
Aco2	GCGTTTACGGCCCGACCGGG
Aco2	TGGGTGAGGTCCAACCAGAG
Aco2	GATTGAAATTAACCTCAATG
Acox1	CGATCCAGACTTCCAACATG
Acox1	AATGTCGGATGGCTTGCGGT
Acox1	CCTCACAGCACTGTATCGAA
Acox1	TCTCTTCATAACCAAACTTG
Aspa	ATTCATTACCAATCCAAGGG
Aspa	AGTGCAACCCATGTTAGAAG
Aspa	ACCAACAGGATACTTGGCAA
Aspa	CTTGCCATATGAAGTGAGAA
Ada	GTTGTGGATCTTGTGAACCA
Ada	ATTCATCGGACCGTCCACGC
Ada	CTTCATCTCCACAAACTCGT
Ada	GCTGCGCAACATTATCGGCA
Adk	TGTGCTGCGTGTATCACTGG

*Oligo name	Guide sequence
Adk	CACTTTCAATACCGACTCTG
Adk	ATAAGGCATGACGTCCATCA
Adk	CATTGGGATAGATAAGTTTG
Adsl	AAAGTGTGTGAAACCTAACG
Adsl	CCAGTGCGATGCCGTACAAG
Adsl	GCTGCGGGCATTATTCATCT
Adsl	TCACAGGACAGACGTACACA
Aga	CCAGATCCCTCAAAATACTG
Aga	AGGCCAAGTGTTGACGACCA
Aga	TGGTGGACATTGCTATCTGG
Aga	ATGGATTACAACCATGCCTA
Gla	CTAAACTCACGTAATTTGCG
Gla	CATAGGATCCAAAACTCCCG
Gla	TCATACAGGTTATAAGTACA
Gla	CATTGGACAATGGCTTGGCG
Agxt	AGCCCCTGTCAGTTCCTACG
Agxt	AGAACATTATACACTGCAGG
Agxt	ACATACTTGGCCAAATTGTG
Agxt	GTAGATAGGAACCCCGCCCA
Aicda	GTAGGAACAACAATTCCACG
Aicda	TTCACAGAAGTAGAGGCGCG
Aicda	ACCAGGTGACGCGGTAACAC
Aicda	TGAGACCTACCTCTGCTACG
Ak1	CTACACCCACCTGTCTACTG
Ak1	GATCGACGGCTACCCGAGGG
Ak1	GTCAGCTCTGGATCGGAGAG
Ak1	CTTTGGCTAACATAGCATCT
Ak2	TGAAGGCGACAATGGATGCA
Ak2	GGTAGGACCGGCCACTCTTG
Ak2	TCCGAACCGGAGATTCCGAA
Ak2	TCAGCCAGTTTGGGTGCCTG
Alpl	GGATAACGAGATGCCACCAG
Alpl	CTAGGAGGCAGGATTGACCA
Alpl	ACCTAAGAGGTAGTCCACCC
Alpl	GTTGCATCGCGTGCGCTCTG
Akt2	CATACTCCATCACAAAGCAT
Akt2	TACAGAGAAATTGTTCAGGG
Akt2	TGTGGTGTACCGTGACATCA
Akt2	AGTGGACCACAGTCATCGAG
Alas2	ATCCAAGGCATTCGCAACAG
Alas2	ACATCACACAATTCCTCCAG
Alas2	AATACTAAATAGGAACTGGT
Alas2	AGGTACCAGCAAGTTTCATG
Aldh3a2	CTGTATGCGATTGTTAATGG
Aldh3a2	GGAAATCTTAGCAGCCATCG
Aldh3a2	AGTCTCTGTCAATGTAACAA
Aldh3a2	TCTGGAGGGAGGCTTCGCAC

*Oligo name	Guide sequence
Aldoa	AATGGCGAGACAACTACCCA
Aldoa	CCTTGCCCGGAGCCACAATG
Aldoa	CCACGAGACACTGTACCAGA
Aldoa	GCCAGCATCTGCCAGCAGGT
Gfer	AGAATTGGGTCGCCACACCT
Gfer	ACGACCTGGTGACTGACGCG
Gfer	CCTGCGTGGACTTCAAGTCG
Gfer	TTCCCGTGCTCCAAACCTTG
Ampd3	TACCTGGTTCGCATGCACGG
Ampd3	GTCCTCGGGGACAGTAAACA
Ampd3	TGATCCGGGAGAAGTATGCA
Ampd3	AGTAGCTCCGGGAACCAGAG
Mat1a	ACAGGTATGGTGCTACTGTG
Mat1a	CTATGCTACTGATGAGACCG
Mat1a	GTGTTGCACAGAGATGACGA
Mat1a	GACACATTGGGCAATATCTG
Slc25a4	CAGTTTGACCCTCTCGATCG
Slc25a4	GGAAGATCCCTTGCCCACGT
Slc25a4	TTGTGTCGTGAGAATCCCCA
Slc25a4	GGGGAAGTACCGGATCACGT
Ap1s1	CCAAGAGCTCTACGTATCGG
Ap1s1	GAGCTCTTGGACAAGTACTT
Ap1s1	TCAGCCGGCAGGGAAAACTT
Ap1s1	TGGCCACCTCAGACAAGGAG
Atg5	AAGAGTCAGCTATTTGACGT
Atg5	AAATGTACTGTGATGTTCCA
Atg5	CCTTCTACACTGTCCATCCA
Atg5	AAGAAAAACTCACCATTTCA
Apoa1	GGAGCTCTACCGCCAGAAGG
Apoa1	CAAGGAGGAGGATTCAAACT
Apoa1	GTCCCAATGGGACAAAGTGA
Apoa1	CTGGAAAACTGGGACACTCT
Apoc2	AAGTTACTGGACCTCTGCCA
Apoc2	AGAGGTCCAGTAACTTAAGA
Apoc2	GGGAACCAGGAAGATGACTC
Apoc2	GAAGACATACCCGATCAGCA
Apoc3	GCAGGAGTCCGATATAGCTG
Apoc3	CATGGAACAAGCCTCCAAGA
Apoc3	GGATGCGCTAAGTAGCGTGC
Apoc3	GCCCCGGACGCTCCTCACTG
Aprt	GAGTCCGGGTCTTTCAAGAG
Aprt	CTAACAGGTCTAGACTCCAG
Aprt	TGTGTGCTCATCCGGAAACA
Aprt	CGCACCTGAACAGCACGCCC
Aqp7	GCCACTCACCATCATGACAT
Aqp7	AGTCACTGCGGCATTCATGT
Aqp7	ACACCCCAAGGACGGTAACA

*Oligo name	Guide sequence
Aqp7	TTCCTGAATACATGACACTG
Ar	GGTGGAAAGTAATAGTCGAT
Ar	ACCAGGATACCACACTTCGG
Ar	GACTTGGGTAGTCTACATGG
Ar	GCTCCTGGGAGGTCCACCCG
Arg1	AATAAACTTACTGTTCCCCA
Arg1	AGTATGACGTGAGAGACCAC
Arg1	AAATGACACATAGGTCAGGG
Arg1	AGATGTACCAGGATTCTCCT
Arsb	GGTGGGCAGACTAGGTCTGG
Arsb	GAATGTCTGCCGACACGCCG
Arsb	AGCACAGACGTATTTATGCA
Arsb	GCCAGCACGAAGACCACATG
Arsa	AAGCACGTTAGGTTCTGACA
Arsa	AGGAGTCCCCAAATGGCCCA
Arsa	GTGACCTGGCCAGTAGACCA
Arsa	TCGGGAGAAAGACACATACC
Asah1	GCAAGGTGTACGTTACCTAG
Asah1	TAACATTTATAACATACCGC
Asah1	AGTGATAAACCCTACCCACT
Asah1	GAATATAAATAATAACACTT
Ass1	TAACATCTTACCTTAATCTG
Ass1	TGGGATCCTGGAAAACCCCA
Ass1	AAGGCACTTCCTCACCAGGT
Ass1	TGCCTTCACCTGTAGCAACA
Fxyd2	ACCGGCTTACCGTACTCGAA
Fxyd2	TATGAAACCGTCCGCAAAGG
Fxyd2	GATGAGGAGGCCCACGACGA
Fxyd2	CCCACTTACTGAGAATGATG
Atp6v1a	TGACTGCTGATATCCGACAG
Atp6v1a	AGTCGGCCATCATACTGACG
Atp6v1a	ATGTTGCCCCCACGTAACAG
Atp6v1a	CTTACGGGAAAAGGGCATCG
Atp6v1e1	CCAACTTGATGAATCAAGCA
Atp6v1e1	TTTGTAGGATCTGCTAAATG
Atp6v1e1	TCAGTCTTTGCGTTTGCACA
Atp6v1e1	AGGCATCCAAGCATACCTGA
Atp7a	TCTATAGGGCAAAACCTCCG
Atp7a	ACACGGTATTGGTTAAGACA
Atp7a	CAATTATAATCCACACCAAG
Atp7a	AGGGATCTTCTACTGCTCTG
Atp7b	AAATATAGGCCAACTCCCGG
Atp7b	AAAATGGCTCCCGACACTAG
Atp7b	AGTTGTGTCATTACCCACAT
Atp7b	AGACCATCAATCCCATGACG
Slc7a2	AGGACGTCACTATTCCGATG
Slc7a2	GAACGGAACAAGCATCTACG

*Oligo name	Guide sequence
Slc7a2	GTATCTATACACTTACGTCA
Slc7a2	CCGAGACAACATATTTGGCG
Auh	CAATGTCATTGATCACCGAT
Auh	GGTTTAGTTATCAAAAGCGG
Auh	GAGGAGGGGCTACAGCTCGG
Auh	CCCTCCCTAACCAGGCATTG
Baat	AGGACCAGAAAAGGCCCATG
Baat	AGGCCCATTGATAAGTACAG
Baat	GTAAAGGAAAGCCGCATCCG
Baat	AAGGCACACCACCTGAAAGG
Bcat2	ACGGAACGAGCCTCTACGTG
Bcat2	CAGGAACTATGGACCCACTG
Bcat2	GTGGAGTGGAATAACAAGGC
Bcat2	GCACAGAATGACGTACAGGA
Bckdha	CATGACCAACTATGGCGAGG
Bckdha	CAGCGAAATTGAAACCGGCG
Bckdha	CTTGTCTACAAACTCTGCAG
Bckdha	CTGGCCACGCAGATCCCTCA
Bckdk	ACAGCACGAGCTATACATCC
Bckdk	AGTCCGCATCAACGGACATG
Bckdk	GCGACCGGAATAGAGCATCA
Bckdk	TGTCTTCATGTAGCGCCAAG
Glb1	GCGTAGGTAGTCGTAATCGC
Glb1	CTTCCCGAGATGTATCGGAA
Glb1	GGGTACTCACAAGTTCACGT
Glb1	GCAGGACCTGTACGCCACAG
Blk	TTATTACAAAAATAACATGA
Blk	ACTTGAATAGTGCTGCACCA
Blk	CGTGAAAGATATCACCACCC
Blk	AAGGTCCCTGTCATTCACAG
C1qbp	ATCAGTCAAGAATTCAACGA
C1qbp	CGTACGCTGAGCAAACCGAA
C1qbp	GTTGAAGTTACCAAGACTGA
C1qbp	TCCTCCTCACCATCAAATGT
Cat	AACTTAATATCATGACCGCG
Cat	TGGCATTGAAAAGATCTCGG
Cat	GGAGTATCTGGTGATATCGT
Cat	AGTGACCGAGGGATTCCCGA
Cbs	ACACTACGATGACACCGCCG
Cbs	TCGCCATGCCACTCCCACGT
Cbs	GTGAGTTCTTCAATGCGGGT
Cbs	ATAATGTGGGGAGTCCGCCA
Scarb2	ATAGAACAGGCCGAAATTCG
Scarb2	AAATAAAACTGGATGTACAC
Scarb2	AATATGATTAACGGGACAGA
Scarb2	ATAATGACACGTACCAACAG
Chkb	ATGGTCCCAAACAACCATCG

*Oligo name	Guide sequence
Chkb	GGTGCTGCTACGACTCTACG
Chkb	CGTGGTTCGGTAGTGAGCAT
Chkb	CAGAGCCAATCCCCAATCGG
Tpp1	TGAGTTTCATCGCTATGTAG
Tpp1	TTATGGTAGAAGGTTACCTG
Tpp1	AACCTGACAGCCAAAGATGT
Tpp1	GATCGAGGCCAGTCTAGATG
Cln3	ACACTCCGACTATCCAACCG
Cln3	AATCGAGATGAGCTGTTGTG
Cln3	GGACCCTGGAGGGGAAAACG
Cln3	CAGGAGTTTGATGACAAGGG
Abcc2	AAGACCCTGACTCATATCCG
Abcc2	GCATTCGGAAGAAAGAACTC
Abcc2	ACTCGGATCTTGGTTACACA
Abcc2	GTTTAAGACGATCATGACAA
Cox6a1	TGAGGGTAGGCAACGAACGG
Cox6a1	CCGTGGGCGCCACTCGACAT
Cox6a1	CGCCGCAGCTCGGATGTGGA
Cox6a1	TCAACGTGTTCCTCAAGTCG
Cox8a	GCCTGACCGGCTCGGCCCGG
Cox8a	TTCGAGTGGACCTGAGCCCG
Cox8a	TCTGTGTAGGATATCACCAT
Cox8a	GCTCCCGCGCCGGCTTCGAG
Cp	CATATAAGCATCAATTAGGG
Cp	GCTGTGAGGAGCGACCTGGT
Cp	ATGAAAAGTGTAGATCCTAG
Cp	GCTGAACAAATACCACACGA
Cpox	TGGGCGCATAAGGATTCTTG
Cpox	GAAGCAGCGAACCAAATGAG
Cpox	ACCGACATACTTGAACCAAG
Cpox	CGGACCCGCCTCTAGCCCAG
Cpt1a	CACATTGTCGTGTACCACAG
Cpt1a	CATACTGCTGTATCGTCGCA
Cpt1a	ACCTTGGACCCAAATTGCAG
Cpt1a	ACGTTGGACGAATCGGAACA
Cpt2	TCACTGGTCAAATAAGCCAG
Cpt2	TCGGGAAGTCATCTAAGCAG
Cpt2	AAATATTGGGACATATCCAG
Cpt2	TTAAATACATATCAAACCAG
Crat	ACCACCCACGCATATAACCG
Crat	GCAGGCCAGATGCTACATGG
Crat	TCCACAAGTGCAACTATGGG
Crat	TTTGCTGCCAAACTCATCGA
Pcyt1a	AATACGTATCTAATTGTGGG
Pcyt1a	ATGCAAGACGGAACCTACAG
Pcyt1a	GCACCACCTCGTCCACGTAG
Pcyt1a	CTTTAGTAAGCCCTATGTCA

*Oligo name	Guide sequence
Ctsc	CTGCAAGATACAACCTCCTG
Ctsc	GGCAGTAACTGATAGCTGTG
Ctsc	TCACAACCACAACTTTGTGA
Ctsc	CTGTATTTCATCAGTCATCG
Ctsd	TATCCGTCGGACTATGACGG
Ctsd	TGACTCCAAGTACTACCACG
Ctsd	GACTGTGAAACACTGCGGCG
Ctsd	ACGTCCTTTGACATCCACTA
Ctsk	AAGTTGTATGTATAACGCCA
Ctsk	CACTCTCTATACCCCAGAGT
Ctsk	CAATACGTGCAGCAGAACGG
Ctsk	AAGCCCAACAGGAACCACAC
Cyb561	ATGCCTATGACCATGCAGAG
Cyb561	GCACGACCAAGATCTTGCAT
Cyb561	TGCTGCACTGCCGTACTATG
Cyb561	GTTCAGGAACTCACCCACCA
Cycs	TCTTCCGCCCGAACAGACCG
Cycs	TTCTGTTTAGGCATCACCTG
Cycs	GTTCGGGCGGAAGACAGGCC
Cycs	CTGGGGAGAGGATACCCTGA
Cyp11a1	AGAGTATCGACGCATCCTTG
Cyp11a1	GTATTATCAGAGGCCCATTG
Cyp11a1	GGACCTAGGACTGCTAGTAG
Cyp11a1	CCTTACACTCAAAGGAAAAG
Cyp11b2	TGGAGAGTATGCTCCCCCGT
Cyp11b2	GACCGTGTCAACGCTCCCAG
Cyp11b2	AGGTGCTTCAAAATGCTCGT
Cyp11b2	TTCCGCCACAATGCCACTGT
Cyp17a1	GGAGCTACTACTATCCGCAA
Cyp17a1	AAACGGTAGACTACCCACCA
Cyp17a1	TAAAATTCGAGAAAAAACAC
Cyp17a1	TACCATACAGACCTTTACAG
Cyp19a1	AGTGACCGACATGGTGTCAG
Cyp19a1	AAGGGCGAATTGTTCTCCAA
Cyp19a1	GAGAGCTCGTCTTCAATACC
Cyp19a1	CCATCAAGCAGCATTTGGAC
Cyp24a1	TTCGTTGCGATGGTCCCGAT
Cyp24a1	CTTGCTGATAAATATCACAA
Cyp24a1	AGCGCCTCAACACCAAAGTG
Cyp24a1	GCTGGACAAGAAAATCAATG
Cyp27b1	GAGAGCGTATTGGATACCTG
Cyp27b1	TGCGACGACTAAGGCGCCAG
Cyp27b1	CTCAGGTGCATGGCGCTGCG
Cyp27b1	TTAGCAATCCGCAAGCACGC
Cyp7a1	GGTGAACCTCCTTTGGACAA
Cyp7a1	TTTGATTTAGGAAGGCCCGG
Cyp7a1	AGTATTTCCGGCACTAGTGG

*Oligo name	Guide sequence
Cyp7a1	AGCACAAGAACCTGTACATG
Cyp7b1	GTATGTCAGATACTAAGTAT
Cyp7b1	ACTGTCAATTTCGTCACGCA
Cyp7b1	TTTATCAAGGGTGGTTCACG
Cyp7b1	AGCAGAGCTTCTTACCCACA
Slc6a3	TAGATGATGAAGATCAACCC
Slc6a3	GCTCGTCAGGGAGTTAATGG
Slc6a3	CAGGGAGGGTGACTCCACGC
Slc6a3	TTACTCAAAATACTCAGCAG
Dbh	AGTGATATAGCACCAGTACG
Dbh	AACTTCCAGTCGGAGAAACG
Dbh	AGAGCTCTAAAATCCCTTCG
Dbh	CGTGCCGGCAGTAGTTGAGT
Dbt	TAGATGATATCGCTTATGTG
Dbt	TCATCACAATACCCGAAGTG
Dbt	CTGTGAAGTTCAAAGTGACA
Dbt	TGGAGGCTTTGCTATCGGCG
Pcbd1	AGCTGGACCACCATCCCGAG
Pcbd1	ACTGCTTGAAGATAGCATCT
Pcbd1	GGCACACAGGCTGAGCGCCG
Pcbd1	TGCCAAACCTGAGGGCTGTG
Ddc	CCTAGGTGGTCGCTACACTG
Ddc	TAACCCAGCTCTTTCTACAG
Ddc	CCGGTATCTTCTGAATGGTG
Ddc	AGCCAGTAGGGCCACCAAGG
Ddost	GAACTCCCCGTACTTAATGA
Ddost	CCCAGATAAACCAATCACCC
Ddost	AGGCAACTATGAACTAGCTG
Ddost	GGTCAGAAACATCATAGTTG
Dgat1	AGTGGTTTCAGCAATTATCG
Dgat1	AAAGCGCTTTCGTATTCGGG
Dgat1	ATACCCGGGACAAAGACGGG
Dgat1	GCTCACCAATAATCACGCAT
Slc25a1	ATGAACGAGCGAACCCACCG
Slc25a1	GAATAATCTCTCTAACCCCG
Slc25a1	ACTGCGACTGTACTGAAGCA
Slc25a1	CTTCACGTATTCGGTCGGGA
Dhcr7	CTGTAGCTATATCCAATGCG
Dhcr7	TGTTCTTCAATGGACGACCA
Dhcr7	GCCCTTGATCATTGCGAACG
Dhcr7	AGCCTAGGTACCACCCAAAG
Dhfr	GACATGGTTTGGATAGTCGG
Dhfr	AACCTCAGAGAACCACCACG
Dhfr	TCGCCGTGTCCCAAAATATG
Dhfr	CAGCCCGGCCAATACCTGAG
Dld	GGTGGAACATGCTTGAACGT
Dld	GCAGTAAAAGCATTAACAGG

*Oligo name	Guide sequence
Dld	AGAGAAGCTGGTTGTTATTG
Dld	CAAAAACATCCTTGTAGCTA
Dpagt1	CTTTGGCAATACAACCATCG
Dpagt1	TCCTGTACTACGTCTACATG
Dpagt1	CATGCCCGCAAAGTAACAGA
Dpagt1	AGCACCGCTGATCACTCCCT
Dpm1	ATGGAATCAAACACGCCACG
Dpm1	TCTCTGGAACTCGATACAAG
Dpm1	TGATTAATTTGGCAGCCGTG
Dpm1	GAGAAGCCCCTTCTACCTCT
Dpm2	TGATCAAGCTAACGGCGACA
Dpm2	CTTCACCTACTACACCACTT
Dpm2	ACCGGGACAGACCAAGCAGT
Dpm2	ACATGCTGGCTGTCAATGAA
Slc26a2	GAGCCGACACCATGACTCCG
Slc26a2	ATGGCCGGAGAGCTTTCCGT
Slc26a2	ACTGTGCCTTATGATTGGTG
Slc26a2	TCCAAAATGAGAAGCCAATG
Ebp	GAAAGGCAATCACTACCCAT
Ebp	GGGGCCTAATTGTGATCACG
Ebp	CCAGGATATGCGAAGTCGGG
Ebp	AAGCTGTAGGACAAAGCGGA
Egf	TCACCGTAACAGATATGACA
Egf	AGACTGTTCTGGACGGACGT
Egf	TGTTCATCGCCTGACAATGG
Egf	GTGTCACAAAGGATGGATGG
Eno3	AGCCGGTTACCCGGACAAGG
Eno3	GAGACAAAGCACGATACCTG
Eno3	CTTCCAGAAACTAAGTGTTG
Eno3	CTGCAAGATCTGCGATGTGT
Ephx1	CAGAAGTTCTACATTCAAGG
Ephx1	TGGAAGCGACTGCCCTCCAA
Ephx1	CCCCACCACCCATCTTCAAG
Ephx1	GGAGGAATGAGTTTGACTGG
Epm2a	TGTACCAGAACGTGTCAACG
Epm2a	CCGTTGCTGCACATATAATG
Epm2a	GCCCGGCCTGTGGCTCGCCG
Epm2a	GTCACATGTTCCAGTTGGCG
Esr1	GGCATACGGAAAGACCGCCG
Esr1	CACTGTGTTCAACTACCCCG
Esr1	TATTCAGAATAGATCATGGG
Esr1	AGAGGCATAGTCATTGCACA
Esr2	TGGCGCTTGGACTAGTAACA
Esr2	TTCGTGACGGCTCTCTACAT
Esr2	GAAGTAGGAATGGTCAAGTG
Esr2	CGGCTCACTAGCACATTGGG
Ext1	CTTATATCACGTCCATAACG

*Oligo name	Guide sequence
Ext1	GATTGTATTAACTACACTAG
Ext1	CTGACTACACTGAGGACGTG
Ext1	CAAAGGCAAGAAGTGCCGCA
Ext2	TGTTTCGATGTCTACCGCTG
Ext2	CTGGAGGACTCAATGGAGTG
Ext2	TCCTGCAGAACATCCCACAG
Ext2	AGGGCAGTGTTGTAATCTGG
Fah	CCCCGATTCGAAGACCCATG
Fah	CCGATGGCTACACCAATCCG
Fah	ACATCAACATGTCTTCGATG
Fah	AATGGGAGTACGTCCCACTT
Fbp1	CATGGCAAGGACCAACATGG
Fbp1	CACAAGAACACAGGTAGCGT
Fbp1	TGGCTCAACCAATGTGACTG
Fbp1	AACATCTACAGCCTTAATGA
Fdxr	CCAGAAAACAGACATCACAG
Fdxr	TCCATTGTACCAGCCCACAA
Fdxr	GCTTCTCGTAGATGTCTACG
Fdxr	CAGATGTCCCCCGTCCAAGG
Fech	CATTTACAGATACTATAACG
Fech	CGTACTTACAGACATCGGCA
Fech	GGCATGATGTACCTTCTCCG
Fech	GGCATATTGATGTTAAACAT
Lpin1	GGGGGTACGTTGAAATCGAG
Lpin1	CAGTCGCCAACAATGGCCCG
Lpin1	GACCACAGAGAGATCACCAA
Lpin1	CCATTTAAAACAGGCCACTG
Folr1	GACAATTTACACGACCAGGT
Folr1	AGTTCGGGGAACACTCATAG
Folr1	CCAGTTGAACCGGTACAGGT
Folr1	CTCCACCTACTCCTTACCCG
Fxn	AGGGAACCGATCGTAACCTG
Fxn	CGAAGCGCGTACTCACGGCG
Fxn	GCGCGGGTTCCCGACCCAGG
Fxn	TGGGGACATTGGACAACCCA
Ftcd	CAGGTTAAGAGCAATACGGT
Ftcd	CCGAACAAAACCGCGCAGTG
Ftcd	GCACTGTCTACACTTTCGTG
Ftcd	CACAGCTCAAACAGGCCGAG
Fth1	CACCATAGACAGATAGACGT
Fth1	AGTGCGCCAGAACTACCACC
Fth1	GGAGAGCGGGCTGAATGCAA
Fth1	TCTTCAGAGCCACATCATCT
Ganab	GATAAAGTTAGTCTCGCGCT
Ganab	CAGACCCATATAGAGCCATG
Ganab	AAGTCCAAACCTACAGACGT
Ganab	ACTCGGTATCGAGGCCGCCG

*Oligo name	Guide sequence
G6pc	GGTGTTTGAACGTCATCTTG
G6pc	GTTGTCCAAACAGAATCCTG
G6pc	GGTCAGCAATCACAGACACA
G6pc	ACAAGACTCCAGCCACGACC
Slc37a4	CTACGTTGACCAGACCAACC
Slc37a4	TCTTTACTCCGAAGACCACG
Slc37a4	CACAAACTTGCTGATGGCGT
Slc37a4	CAGAGCGATCTCATCCACCA
Gaa	ACCATCCCCACTTTACAGCG
Gaa	GAGTTACAGGCCCTACGACG
Gaa	CTAACCTGGAGGTCAACGGG
Gaa	ACCTGAGCTCTACAGAGTCG
Gabra1	CAGAGAGCCAGCCCGTTCAG
Gabra1	CAGTGTCACTTACCATATCG
Gabra1	AGAATAACTGTCATTATGCA
Gabra1	ACGCAGGAGCTTATTAGGCA
Gabra6	GGAAGTTAACCAATCTCATG
Gabra6	GGGACTTCTACTGAGTAAAG
Gabra6	TCTACTCTGAAAATGTCAGT
Gabra6	TTAAGCTCAGAATCTCAGCA
Gabrb1	TCTGTCCACAGGAATCACTA
Gabrb1	CACTTCAGATGGCTATACCA
Gabrb1	ATAGTCGTGGATATGCCCCT
Gabrb1	CAAGAAATCATTTGTGCATG
Gabrb2	ATGATTCGATTGCATCCCGA
Gabrb2	TAACCAGCGACATATTACTA
Gabrb2	CTTGACTTTGGACAACCGAG
Gabrb2	GATGAGTTTATAATCTACGA
Gabrb3	CCTCACGCTTGACAATCGAG
Gabrb3	CCTGGTAGATGGCTACACTA
Gabrb3	CGCCTGAGACCCGACTTCGG
Gabrb3	CGAAAACTCAATGAAAGTCG
Gabrd	TGTGGCGCTTGCCCTAGAGG
Gabrd	GTAACTGGTGATAGTGAACT
Gabrd	AACCATACCAACGAGACCTT
Gabrd	TATCCGCCTACAGCCTGATG
Gabrg2	AACAAACTTCGACCTGACAT
Gabrg2	GGTTGAATAGCAATATGGTG
Gabrg2	TCCTGCTATCGCTCTACCCA
Gabrg2	TACAACTGGAGAACTCCAGG
Gad1	CTATTCCATAAAGAAAGCCG
Gad1	GACATTTGATCGCTCCACCA
Gad1	GCGGTTGCATTGACATAAAG
Gad1	AGATGAGAGAGATCGTTGGA
Galc	AGTTGCCTTATGGACGAAGT
Galc	CTAGATGAGAATTATTTCCG
Galc	GTCGGAGTCGTCTAGCACGT

*Oligo name	Guide sequence
Galc	CATAGCGAGCGATAATCTCT
B4galnt1	TCTAGCAGATCGAGTCTCGG
B4galnt1	TGACCGTAGGGTAAAAGCGT
B4galnt1	GTTCGCAGGTCGGAACCTGG
B4galnt1	TGCAGTTGTGAATCCAAGGG
Galnt3	TACGGAAGCAACCATAACCG
Galnt3	AGCTGCCCCTAGCAACCGCG
Galnt3	AAAAACCGGCTTCAACTCCG
Galnt3	GTGGACGGTCCTAAGCAGCG
Galt	AGAAAGGTACCATCATAGTG
Galt	GCAGCGTCACATCCGACCAG
Galt	GGGTTGAGTGGGTCGTGGCG
Galt	GGACGAGTGGGTGTTAGTGT
Gamt	AGACGCGTCATAGGCCGCGG
Gamt	CTATATGCATGCGCTAGCGG
Gamt	GATTATTGAGTGCAATGATG
Gamt	ATCAAAGTGACCGTCAGGCA
Gata1	GTCACCGGCAGTGCTTACGG
Gata1	AGTATGGAGGGAATTCCTGG
Gata1	GAGCAACGGCTACTCCACTG
Gata1	GGCCTCAGCTTCTCTGTAGT
Gba	CGTTACGAGAGCACTCGACG
Gba	GGATAACTGGAAGTCGTTAG
Gba	GACTGGCAAAGAGTGAAATG
Gba	CGGAGAATGAACCTACAGCA
Gch1	GCACCAATGGGTTCTCCGAG
Gch1	CCCTTCCTACAAATGGAACA
Gch1	GGTGAACCTCCCCAAACTGG
Gch1	GTACTTCACCAAGGGATACC
Gdap1	TCCTTGTGGTTGCATAAGCG
Gdap1	AAGATAATCAATGATCTGAG
Gdap1	TGTGTAAGCATCCATTGGCA
Gdap1	AGAAAACCCTGACTTACAAG
Gpd1	GATGGGGTACCACAAAAACC
Gpd1	ACCCAACTTTCGCATCACTG
Gpd1	GTCTTCCTCAAACACCCACA
Gpd1	GTTGGAGCTCACCACATTGG
Gfpt1	TGTGGCACAAGTTACCACGC
Gfpt1	AAGCTGCGGTCTTTCCCGTG
Gfpt1	GGAGAGAGGAGCCTTAACTG
Gfpt1	TCTGTTGTGAACACAATGAG
Ggps1	GAGCCACTGGGAAACCACGT
Ggps1	AGCCCAAGTGTGTCAAGCAG
Ggps1	GGTGAGAAGCAAACTTTCAC
Ggps1	TGTCCCTCCAGTAAATATCG
B4galt1	GGCCAGAGAGGTAATAGACG
B4galt1	CAGGGCTGGAGTCGAGACCC

*Oligo name	Guide sequence
B4galt1	GCTCAATATTGGCTTTCAAG
B4galt1	TGATGTGGACCTCATTCCGA
Ggt1	ACTGACGTATCACCGTATCG
Ggt1	CGTACAGGGTCGCATCACCG
Ggt1	GAATTCAGGCTCATAGTAGG
Ggt1	CGACCACGTGTACTCCAGGG
Gif	ACGTGAGAGCCATAACGGTG
Gif	CCTGGCCGGCGCCTACAACG
Gif	TACTCAACGAGATTAAGCAA
Gif	TATGTACAACAAGATTCCTG
Gclc	TGTGCCGGTCCTTGACTGCG
Gclc	CAATATGAGGAAACGCCGGA
Gclc	AGAAACATCCGGCATCGGAG
Gclc	TGTAGATGATAGAACACGGG
Galk1	CTGGAAAGCCCACCCCCCAG
Galk1	GGGCCGCGTCAACCTCATCG
Galk1	AGTTGGTCCATGATGCCACA
Galk1	ACAGTGGGCCAATTATGTCA
Glul	GATTACGGGGACAAATGCGG
Glul	TGGAAGGCCAACCAAATGGG
Glul	CTTGCCCAGAGTTACCTGAG
Glul	TATTTCTAGAGACCAACTTG
Glra1	CCACTTCCACGAAATCACCA
Glra1	TTCCATCGCTGAGACAACCA
Glra1	ATGCTGCACCAGCTCGTGTG
Glra1	TCCTGGATAAGCTCATGGGG
Glrb	AGGTTACTACACTTGTGTGG
Glrb	GGAAACAGAGTTAAGTCTAG
Glrb	CACAGCGTACTCCACGAGGG
Glrb	CCACCATGTATAAGTGCTTG
Slc6a9	ATACCTCTGCTATCGCAACG
Slc6a9	GTAGTACATGATACCCGTGA
Slc6a9	ATGGTGGTGTCCACATACAT
Slc6a9	TGTGCTACCAGCGTCTACGC
Gm2a	GATCCAACCTGACCCCATTG
Gm2a	ATTCCTTGTGTAGAACAGCT
Gm2a	CCACCAAGTTGGGAAAGCTA
Gm2a	GTGACAGGTGGAGCTCACCG
Bscl2	GTTTCATGTTATACCAGAGG
Bscl2	CCTGGGCCCACAGTAAGGCG
Bscl2	CAAAGGATCAGACAAAGACG
Bscl2	AATGTCTCACTGGCTAAGAG
Gnmt	TGTGTGGCAGCTGTACATCG
Gnmt	AGAACATTGCAAGCATGGTG
Gnmt	GAGCCATCCTTTGACAATTG
Gnmt	GGGCTTCAGCGTGATGAGCG
Gnpat	CCTTCGGCTTAGGAACTCCG

*Oligo name	Guide sequence
Gnpat	TACACCCCGCCCTTGTATAG
Gnpat	CTCACCAAACTTAGGAGTCA
Gnpat	ATGAGCCACAAACTGCGCAT
Got2	TGGAGGTCCCATTTCAACAT
Got2	TTTCTGCCCAAACCATCCTG
Got2	CATCCTCCTCACCTTCACCA
Got2	AGCTCACCTTCCGGACACTG
Gpaa1	GTGGAGGCACTAACCCTACG
Gpaa1	CCGCAGGATGCCATACACGT
Gpaa1	GTCCCTCCACTGTCACATCG
Gpaa1	AGAGTCCGATGGAGACAAAG
Pigq	CAGGATATGCTCAATAAAGG
Pigq	TGACACAGTGGCACGCAGCG
Pigq	GAAGGCCAGTCAAGTACCAG
Pigq	CAATAACCGAATTGGACAGC
Gsr	GGCTATGCAACATTCGCAGA
Gsr	CGGCCCCCACGATGACGCTG
Gsr	GCTGTGAGGGTAAATTCAGT
Gsr	AACATCTGGAATCATGGTCG
Gria4	TGCATACATTGGTGTCAGCG
Gria4	GCATGTCAGTGCGATATGTG
Gria4	ACGTAGAGTTAATTACACAA
Gria4	TGCACCTCTGACAATCACGT
Grin1	AACATCACTGATCCACCGCG
Grin1	GTGGACATCTGGTATCCTCG
Grin1	CTGTCCTATGACAACAAGCG
Grin1	AACCAGGCCAATAAGCGACA
Grin2a	ATGGTAAAAGAAGGCCCATG
Grin2a	AGAAGAAATCGTAGCCGGTG
Grin2a	ATCTTGACAAACTTCCGACA
Grin2a	TGTGTGCGACCTCATGTCCG
Grin2b	TATCCTACGCTTGCTCCGAA
Grin2b	GGCACCGGTTGTAACCCACA
Grin2b	ACATCATGGAAGAATACGAC
Grin2b	TGACTGGCTACGGCTACACA
Nr3c1	CATTATGGGGTGCTGACGTG
Nr3c1	AGCTTGCCTGGCAATAAACC
Nr3c1	AAAGCCGTTTCACTGTCCAT
Nr3c1	AAAACTGGAATAGGTGCCAA
Grm1	GGGTGACAAATAGCGTCACG
Grm1	TAGTGTACAGCTGACACTAG
Grm1	ACTCTCCCACGACGCCAAGG
Grm1	AGATAAGATTAATGCGGACC
Grn	CCTATCCAAGAACTACACCA
Grn	CCCTGCACAAAAGACCAACA
Grn	GACACTGGACAGCACCCAAG
Grn	CACCTAGTGAAGTCATCACA

*Oligo name	Guide sequence
Gss	GTTCTCTGGACCAAAACCGA
Gss	AGTCAGTATAATTCACAGGT
Gss	ACAGCTGGCTGGGACTAAGA
Gss	TCAGATTACATGTTCCAGTG
Gstz1	GTCAGAAATCATGCGCACGA
Gstz1	AAGAGACTCGGCCTATCCCA
Gstz1	ATTTCTGACCTCATCGCTAG
Gstz1	TAATGACTCACCGTTAAAGC
Gys1	TTGGGACACCTGCAACATCG
Gys1	CAACGCCCAAAATACACCTG
Gys1	TGTTGTGGGTGCACACTGGT
Gys1	ATCCCAGATCACCGCAATCG
Hadh	CCTTTCAACCAGCACCGATG
Hadh	AGCAAATCGGTCTTGTCTGG
Hadh	AAGCATGTGACCGTCATCGG
Hadh	TGGCCATACAGTAGTATTGG
Hsd17b10	TGTTAATGATAACTCCACGT
Hsd17b10	GCTACGGCCAAAAGACTGGT
Hsd17b10	TTGGTCGCGGTAGTAACTGG
Hsd17b10	GTCACGACTCACATTTGCTG
Hal	ATGCTGTCCGACCTCACCGT
Hal	AAAAGATACAGGATTGTCTG
Hal	GGACAATGGTGGCTTCACTT
Hal	TCTTAGCCAAAGGTTACAGT
Hao1	CAGCATGCCAATATGTGTTG
Hao1	ACTGTGGACACCCCTTACCT
Hao1	GCAACGTTGCGAAGCATCCG
Hao1	GTATGACTATTACAGGTCTG
Hccs	CAAAGTAAATGGCTGATCTG
Hccs	TAGCTCTAGCACCAGTAACA
Hccs	TCCAGAACATCTGTTCAGAA
Hccs	ATCAGAATAATGAGCAAGCG
Hcfc1	GGTACCCTTCACAACCAATG
Hcfc1	ACAGCAGTATGTGACTCCCG
Hcfc1	TGGAAGGGCTAGTTGCACAA
Hcfc1	CCCAAGGTTAGCCACAACAG
Hexa	ACGCCCCGGTGAGGGAATCG
Hexa	AGGAGGTCATTGAATACGCA
Hexa	AGTGAAGCTCTCATATGGGA
Hexa	AGCAAGGTGTTAATAACCCA
Hexb	GCTCAGCTCGAAATCTAGCA
Hexb	TACACCAAACGATGTCCGGA
Hexb	GCGGAGATGTACAACAGCCG
Hexb	TAACGCTCCCCAAACGCTGT
Hfe	TGCTCCACGTACCCTTACTG
Hfe	TTCCTCCCGCACTCACGCGG
Hfe	GATCCGTGCCAAACAGAACA

*Oligo name	Guide sequence
Hfe	CATGAAGACAACAGTACCAG
Hgd	GAAGATCGTCGAGTGCCAGG
Hgd	CCCTTTGAGTCCATCGACCA
Hgd	GGAGACATCAAGTCTAACAA
Hgd	GATGTCTTTGAGGAGACCAG
Hk1	CCGACAATCCAAAATAGACG
Hk1	CGTAGCCGCCATTGAAACGT
Hk1	GGATCTTTACCAGTAGGACT
Hk1	CTCCCGGGATTATAACCCAA
Hmbs	AAGATGAGGGTGATTCGAGT
Hmbs	CCTGGTCGTTCACTCCCTGA
Hmbs	AGAGAAGAGCCTGTTTACCA
Hmbs	CTCAGTTGCTATGTCCACCA
Hmgcl	CACCTCAGCAACTTTAGCCG
Hmgcl	CTTGGGAGAAACAAAGCTGG
Hmgcl	CTTGGGGACACCATCGGCGT
Hmgcl	GGGGTGGGTACAATACTCTG
Hmgcs2	GACATTGCAGTCTACCCGAG
Hmgcs2	TTTATTACGAACCTTGCTCG
Hmgcs2	GAGGGATTGTAGAAAACCTG
Hmgcs2	TCATATACTGCACATCATCG
Hmox1	TCGTGCTCGAATGAACACTC
Hmox1	TCAGGACCTGACCCCCTGAG
Hmox1	ACGCTTTACATAGTGCTGTG
Hmox1	TTCCTTGTACCATATCTACA
Hnf4a	GCAATGACTACATCGTCCCT
Hnf4a	AATGTGCAGGTGTTGACCAT
Hnf4a	AGCGGGACCGGATCAGCACG
Hnf4a	GGCTCCGTAGTGTTTGCCGG
Hpd	GAAAGACATCGCATTCGAGG
Hpd	CATTGTGGTGACCAACTACG
Hpd	AGATACCACACACACCCTGG
Hpd	ATGATCTCAAGGTTACATCT
Hpgd	GCTGCTAACCTCATGAAAAG
Hpgd	TACATGAGTAAGCAAAACGG
Hpgd	CATAGGCAAAGCCTTCGCTG
Hpgd	GCTGACCAGAAACAACTGAG
Lipc	TTATCATGATCATCCACGGG
Lipc	AGGAGAAAGGCGCTCGTTGG
Lipc	CATAACCCAGAGTGTTGCAA
Lipc	GGTGTAGTGCTGGTATGCCA
Hsd11b1	CCTGGCAGTCAATACCACAT
Hsd11b1	ACAGCGAGGTCTGAGTGATG
Hsd11b1	AAAGAAAGTGATTGTCACTG
Hsd11b1	GTAGGGAGCAATCATAGGCT
Hsd11b2	CCACTCTTGCGTCACTCGAG
Hsd11b2	GGTGATGAGCACCGCGCGAG

*Oligo name	Guide sequence
Hsd11b2	GCTAAGAAACTGGATGCCAT
Hsd11b2	CGCTGGCCTCAATATCGTAG
Hsd17b3	CAACATTACCTCCGTAGTCA
Hsd17b3	AAGCCTATTCATTTGAGGTG
Hsd17b3	GCTGAGTACAGGCTGTAAAG
Hsd17b3	TTTCTGCCAGTCAACAACGT
Hsd17b4	TCTAACATAGGCTCTTCACG
Hsd17b4	ACCAAACCGTACCAGTCACG
Hsd17b4	TGGGCGCCATCGTCAGAAAG
Hsd17b4	TGCAGTGAACGACTTAGGAG
Hsd3b2	CTTCAGACCAGAAACAAGGA
Hsd3b2	GATTGTCTTGAATGGCCATG
Hsd3b2	ATATGTGGGCAATGTAGCCT
Hsd3b2	ATTATTATGTTAGAAATGAG
Hspd1	CGGAGAAGCTCTAAGCACGC
Hspd1	TCTTGAACTAGGTGTGATGT
Hspd1	AGGGACAATGGACTGAACAC
Hspd1	TGACTTAGGAAAAGTTGGGG
Hspa9	CAACTTGCCATACCTTACCA
Hspa9	CTCAACCCAAGCATCACCAT
Hspa9	GCCCTCCATAACAGCCACAC
Hspa9	GTGAATCATTGAAATAAGCA
Ndst1	CATCCAGGTTGACATACTTG
Ndst1	CTATGTGACACGGCCCAGTG
Ndst1	TTCTACAACGAGTACCCTGG
Ndst1	CCCCACAGATATGGGCTATG
Hyal1	TTGGCCAGAAACTTTAGTGG
Hyal1	CCCCTACTATACACCCACAG
Hyal1	CTGCAGGCAAATAAATACTG
Hyal1	TGAGAAGTCAGGTTCAGGCA
Ids	GTCTCCATAACAGCCCAGGG
Ids	CATTCTCCTTGAAGTATTGG
Ids	TCCCTTGGAAAACATAACCC
Ids	TCCCTATGGACCAATTCCTG
Idua	TACCCCTATTTACAATGACG
Idua	GTTGGACAGCAATCATACAG
Idua	GGTCCAAGAATGCATCCAAG
Idua	ACTATGATGCCTGCTCTGAG
Inppl1	AGAATCCGGTCACACCACGA
Inppl1	CCTGGATATCCATGTCTAAG
Inppl1	TCACACTGGACGTACTGACG
Inppl1	GCAGGGCACAAACAAGACCC
Insr	CGAGGATTACCTGCACAACG
Insr	GTGATACCAGAGCATAGGAG
Insr	CACACTGCACCTCTCATCTG
Insr	TATAGCCAGACGGGCACTCG
Stt3a	AAGGTGGTACGTAACGATGG

*Oligo name	Guide sequence
Stt3a	TACCATGTAGAAATAAGCGA
Stt3a	GTTTACCTGGAAACCAACAA
Stt3a	ACTTTAATTATCGGACTACC
Itpa	ATAGCAGTACTCACATGTAG
Itpa	TGATAAGTGCCTGAGTACCA
Itpa	AAACGCCAAGAAGCTGGAGG
Itpa	TGGCCTCTGAAGAGAAGCAC
Itpr1	CTGTGAAATATGCCCGACTG
Itpr1	ACACGAACGATGTCATCGAG
Itpr1	AAACGTGTCAATCTCTGCCG
Itpr1	GGAAGCTGAGAACTCCACAG
Itpr2	TCTGATACAGGATTCTACGG
Itpr2	CAAGTGCCTTAACCGCACGT
Itpr2	AATGCCGTAATCAACACCAG
Itpr2	TGTTGTGAGACTCTTTCATG
Kcna1	CGACACAATGGCAATAACCC
Kcna1	TTCTGAACACCCTTACCAAG
Kcna1	GGACTGGTAGTAATAAAGGA
Kcna1	CGCAGCATTCGTGGTCGTCG
Kcnj10	AGGTCGTCCATAGATCCTTG
Kcnj10	TGGCCCCAGGAATACGCCGG
Kcnj10	GCAACCCGGATCATAAGGCA
Kcnj10	CTGCGCAATAAGAAGCACGA
Kcnj11	CCAGGTACCGTACTCGAGAG
Kcnj11	GAGTGGATGCTTGTGACGCA
Kcnj11	CGGCGGGCGCATGGTGACAG
Kcnj11	GAGGCACAACTTCGCCCTCG
Khk	TCCGATGCATTCCGGCCCTG
Khk	AACTGGAAGAGCTCCTCACG
Khk	TGTGGTGGACAAATACCCAG
Khk	AAGAGCCCATGAAGGCACAG
Lamp2	GAGTGTAGTTGTAGTCGACG
Lamp2	CCTGACAAGGCGACACACGA
Lamp2	CACTTAAAGATGACATCCAA
Lamp2	GCTGCAGCTGAACATCACTG
Lcat	GATGTGCTACCGTAAGACAG
Lcat	CCTGTCCTAGGTGACAACCA
Lcat	GTGCAGAATCTGGTTAACAA
Lcat	GCGGGGGGAAGAGCACATTG
Ldha	CAAGCTGGTCATTATCACCG
Ldha	GTTGCAATCTGGATTCAGCG
Ldha	GGAGAACATGGCGACTCCAG
Ldha	GTCATGGAAGACAAACTCAA
Ldhb	AAATTGTGGCCGATAAAGGT
Ldhb	GTCTTCCAACACATCCACCA
Ldhb	GCTCGCCCAGGATCCATCCG
Ldhb	GGGCTGTACTTGACGATCTG

*Oligo name	Guide sequence
Cog1	GGGCTGGAACTCGATAATGG
Cog1	TGAGGATTGGAAATCTCGAG
Cog1	GTGGACATGCTTGTTCGATG
Cog1	CAGCAGCAGCTTAATCTGGG
Ldlr	AAAATGCATCGCTAGCAAGT
Ldlr	GGTGTCGTAGGACAAGTTAG
Ldlr	GCAGACTGGTGTACTCGCTG
Ldlr	TGACCGTGAACATGACTGCA
Lfng	GGCGATGAAGACGTCGCGAG
Lfng	AGACGCGGATCCACCGCCCG
Lfng	CACACCCAAGACGTGTACAT
Lfng	GGAGAGGCTATGCACCTCGC
Lipa	ACCGAGATAATCATGCGCTG
Lipa	GTATTCACCGAATCCCTCGT
Lipa	ACTTCAGCATCGCACTCTGA
Lipa	TGTAGTTAATTGAAGCAGGT
Lipe	GAGTATGTCACGCTACACAA
Lipe	CACTTAGAGAGTACGCTCAG
Lipe	TGCGGTTAGAAGCCACATAG
Lipe	AGAGCGGATATGCCTTGCAG
Phyh	CTCATTATAACGATCCCTGG
Phyh	CCCAAAGGATACAATCGTTG
Phyh	AAACAATTAGGTTGCTAGGT
Phyh	GAGCACATTGACAGAAACAA
Lpl	GAAAAACGTACCGTCTGCTG
Lpl	CCATCCATGGATCACCACGA
Lpl	TGGATTCCAATACTTCGACC
Lpl	TGACACTGGATAATGTTGCT
Ltc4s	CTTGCAACAGAACTCCCACG
Ltc4s	AGACGCGCTCGAACTCGGGA
Ltc4s	CGTATCCCTGGAAATAGCGG
Ltc4s	TACAGGTGATCTCTGCACGA
Alad	AAATGGAGCATTCCTAGCAG
Alad	ACGGACAGCCTCAATAGTTG
Alad	GCTCCGTCAGACATGATGGA
Alad	AAAACATGGACTTGGCAACA
Amacr	GCAGGTCATCGATTCAAGCA
Amacr	GGACAAAACATCTTAGATGG
Amacr	GCGGCGCATGTGCGCACGCG
Amacr	AAGCCAAATAGTTGATGTCA
Man2b1	ATGTTGTAAATGACTACGCG
Man2b1	TGAGTTCAATGCAAAAACGT
Man2b1	CTTGATAGTCAATGCGCCCA
Man2b1	AGCTCCCAGAGGTAACACGT
Man2b2	CAATGTCTACACTACCGTGG
Man2b2	TGGTGGCCAACGTTAAACAG
Man2b2	CAGGCCTTGTGTCTACCGAG

*Oligo name	Guide sequence
Man2b2	TCAAGTCATGCACGCCCGCG
Maoa	TCTTGGCAGTCAAAACCGGT
Maoa	TAGGAACGGAAATTTGTAGG
Maoa	GTTGTAATCCAAATATGCCA
Maoa	ATGGCAAGCAAGACATGCTG
Mc2r	ATGGGTTATCTTAAGCCTCG
Mc2r	ACAATCGGAGTTATTTCTTG
Mc2r	GGCGCATGGTCACAATGCTA
Mc2r	AGATAGAGCCCAGCAAAGAG
Rdh11	CCGGCAAGCTAAATACACAC
Rdh11	GCACCTTCTCATCAACAATG
Rdh11	GGAACAGTCAGGTCTTCGTA
Rdh11	TCCACTTCCATAACCTGCAG
Mocs2	ATCATCCCGCCAATCAGTGG
Mocs2	GAGACACTGCACCACACAGA
Mocs2	GAATACTGCTATGTGTCTCA
Mocs2	ATATGAAGCGTATGTACCGA
Mdh2	TCACGCACCTGAGAGATCAG
Mdh2	CGATATCGTAGAGGGTCAGG
Mdh2	GTTCGCTCTGACGATGTCAA
Mdh2	GTTGGCAATGATGCAAACCA
Mpv17	CATTGAGTATCCCGACCAGT
Mpv17	TGTACCAGCCTCCGACGACA
Mpv17	ACAGGATCACTGATGGGCGT
Mpv17	GGGATACCATGGTCAGAGTG
Mthfr	AGACCCTGTAGGTGACCACT
Mthfr	GACTGGGATGAGTTTCCTAA
Mthfr	AGGTAACATCTACGAAGAGG
Mthfr	CGAAGCTCTCTGCATCGGGG
Mtm1	AGGGAACCACCAAAAGAGCA
Mtm1	TTACCACTCATACCGACAAG
Mtm1	ATGGGAGGCGCGACAAGTAG
Mtm1	TCTGACCGGTGCCATTCAAG
Mttp	TGAGCGGTCTGGATTTACAA
Mttp	TGATCAAGTGATCCAAGTCA
Mttp	GATATACCACCAGAATCGTA
Mttp	ATCCTTTGCAGACACGCTCG
Mut	TTTGACTTGGCAACACATCG
Mut	TTATATGGCACACCCCAGAA
Mut	AGAGTTCGTATGCAAAGACT
Mut	ATCATGTACGACCCTCCCCA
Mvk	AGCGTCAATTTACCCAACAT
Mvk	GTGGTCGGAACTTCCCCCCG
Mvk	CAAGGTCCCGCGGAGTACCA
Mvk	TCTGAAGTCAATCAACAAGT
Naga	GCTAGGAAGGCAATCCCGTG
Naga	TGTTGAGGTATACATAGCCC

*Oligo name	Guide sequence
Naga	TCTCACAAACCAGTCCAGGA
Naga	TGTTCAGGTGAACTACACCG
Ndufa2	GCAGGGATTTCATCGTGCAA
Ndufa2	TCTGATCCGCGAATGCTCGG
Ndufa2	ATTCGCGGATCAGAATGGGC
Ndufa2	GGCTGCCGCTGCTAGCCGAG
Ndufa4	AAAGACCGTGAACTTACGCT
Ndufa4	AGCACTGTATGTGATGCGCT
Ndufa4	CACTGTTTAATCCAGATGTC
Ndufa4	TCTTCGTATTTATTGGAGCA
Ndufs4	CCTGGATGGAACTCTACAGA
Ndufs4	AGAGCACATCAAAACCAGAA
Ndufs4	GTTGATGCCCAACCCATCAA
Ndufs4	GTTGTCTGCCAGCTTCCAAG
Neu1	ACAGCCTTCATCGTAGACGA
Neu1	TTGGTTTGGAGTAAGGACGA
Neu1	TGTGTGTGGACACGGGACGC
Neu1	GAAAAAATCTGCATCCGATG
Neurod1	GAGCTGTCCATGGTGCCGTA
Neurod1	CCGGCGACCAAATTGGTAGT
Neurod1	AGCAAGGTACCACCTTGCGC
Neurod1	GTGTCTCAGTTCTCAGGACG
Nfs1	CTAGTGAAAATGATCTCCCG
Nfs1	TCACAGTCATAACGGAGACC
Nfs1	AGGGCCTCCACACGTACCCG
Nfs1	CCTCTGTTAGTCCTTACCAG
Npc1	GGGGAAGGTGATCACAAGCG
Npc1	CATCATGTGGGTCACCTACG
Npc1	CGGTTCGTAGATATGAACAC
Npc1	CCATCCCTACCTGAAAACAC
Slc11a2	ATGTCACCGTCAGTATCCCA
Slc11a2	AAACACAAAAGTGTCTGCGA
Slc11a2	TGAGAAAATCCCCATTCCTG
Slc11a2	CCTTGACTAAGGCAGAATGC
Nsdhl	TAGGCTTCATGGCGTAAGGG
Nsdhl	CTATAAAGAACTGCACCCGG
Nsdhl	CTTGGGCCGAAAATGCCATG
Nsdhl	CCTGTGTACCCACAGAAATG
Oat	CCGTTCAAAAATGTACTCGG
Oat	TGTACTCCTCGTATTCACCA
Oat	ATCATAACTGGTCGGATCTG
Oat	ACCCTGATGTACCTCCAGTG
Ogdh	TTGGCCCACTCATAGATACG
Ogdh	GACTAGTTCGAACTATGTGG
Ogdh	GTAAGTGGAAGACCTTGTCA
Ogdh	AAAGCTGAACAGTTCTACTG
Slc25a15	ACCTTTCCAGACCTCTACCG

*Oligo name	Guide sequence
Slc25a15	GCCCATGGTAGAAGCCCAAG
Slc25a15	GCACAGCATGCGTACTGACT
Slc25a15	GGACAGCACTTACTTCTGAC
Otc	CAGTCCATTGACAATTGGGA
Otc	CCTTCAAGCAGCTACTCCAA
Otc	TAGAAAGGGTCACACTTCTG
Otc	AAATTCAGGATCAAGCAGAA
Pah	CCTCTTCTGGAAAAGTACTG
Pah	CACTTACCTCAAATAAGCGC
Pah	GCAGCATCATCAAGAGCCTG
Pah	TCCTCGGGTGGAATACACAG
Pax4	TTGGAACCCAAGTGTATTGG
Pax4	AGGGTACTCATCCTTTAGCT
Pax4	ACTCAACTCAGATCACCAGG
Pax4	GTCTCTACAGAGTTTCAGCG
Pck1	ACTGACAGACTCGCCCTATG
Pck1	GTGGCCGAGACTAGCGATGG
Pck1	CCTTTGGAAGCGGATATGGT
Pck1	TCGCAGATGTGGATATACTC
Pdha1	AGAACAACCGCTATGGCATG
Pdha1	ATCACTGCCTATCGAGCACA
Pdha1	GCGCCGGATGGAGCTAAAGG
Pdha1	TGTTTGACATTATACGGCGA
Enpp1	TACAACGCAAGTTGCCACTG
Enpp1	GGTGACCGCTAATCATCAGG
Enpp1	ATGTGAAAGCATCGATACCC
Enpp1	AACGTCTTGGTAGGGTACAT
Pdx1	GACCCGTACTGCCTACACCC
Pdx1	ACTGCCAGCTCCACCCGGCG
Pdx1	AATCCACCAAAGCTCACGCG
Pdx1	CCATTCGGGAAAGGTCCGGG
Pepd	CACAAATCGGATCTCCAGCG
Pepd	CTGCTATGGTGTCATCGATG
Pepd	GCCCTGCAACACGACAGCTG
Pepd	CTTGCTAATGCCCTCGAAGG
Pex11b	CTCTACAAGTGCTACGCCTG
Pex11b	CAAAGTACAAGGCTCGGTTG
Pex11b	GGCGAATCTCATAAGCATCA
Pex11b	ATCTCAGAACGACATCTGAC
Pex16	GCTTCGAAAAAAGTTGCCTG
Pex16	TGAATCGGAGAAGCGACCTA
Pex16	TGAGAGCAATGACGAGCCAA
Pex16	GCCAGGAGCCATCATATGTG
Pex7	GATGCCGTAGTGCTGCGCCG
Pex7	ATGGGATCAAACTGTCAAAG
Pex7	CATCACCACTACAGGTGACA
Pex7	CTATAAAGAGCACACGCAGG

*Oligo name	Guide sequence
Pfkm	CCTCACGGTAGAGCGAACAG
Pfkm	GCGCCTTGGATATGACACCC
Pfkm	TTAGACCAAAGACGTGACCA
Pfkm	CATAGACACGCTCTCCCACG
Pgk1	TAAGGTGCTCAACAACATGG
Pgk1	TCAAGAACAGAACATCCCTG
Pgk1	GGACTGCACACCGAGCCCAT
Pgk1	CTTCCTCTACATGAAAGCGG
Pgr	CTCTGGCCGACTCATGAGCG
Pgr	AGGAGGAGTCGCAGCCAACG
Pgr	GGCGCGAACGAACCCTGCGT
Pgr	CAGTCTGGGAAGTCACCGCA
Abcb4	GATGACATCTGCGTTCCGGA
Abcb4	AGGACCGTGATAGCTTTCGG
Abcb4	TAGCGAAAGCATCAATACAG
Abcb4	TACTACTATTCGGGACTAGG
Phka1	GTAGAAAACCTACGATTCAG
Phka1	AGTGTAGTGAAGTTAATGAG
Phka1	GAGATAGGGAAAGTGATCGT
Phka1	CTAAACTAGCTCCTACCTCA
Piga	TCTTCCACGCCAAGACAATG
Piga	ATGGGTGCAGGTCCTATCGT
Piga	CAGACTGTGAAAGAGAGTCG
Piga	CCATGCTTATGGAAATCGAA
Pik3r1	GAGCTTTATAAGGAGAGGCG
Pik3r1	TCCATTAACCTTCAACTCTG
Pik3r1	TGGCTACAATGAAACCACTG
Pik3r1	CTGGAAATCTGAAAAGCACG
Pip5k1c	TGGTGGCAAGAACATCCGCG
Pip5k1c	CCGACGCATCCACGCCTCGG
Pip5k1c	TTACCAAATAGTCATCTGGA
Pip5k1c	GCCATGGAGTCTATCCAGGG
Pklr	TGTACGAAAAGCCAGTGATG
Pklr	GGGTTCACTCCAGACCTGTG
Pklr	GGGCGATGCAAAGACAGTGT
Pklr	CTGGTGACCGAAGTGGAACA
Plcb1	CAAATACTTACGAATCCACG
Plcb1	CCTGCACAGGCAATATCCGG
Plcb1	GGAACAGCGCATGATAACTG
Plcb1	TCCCAACTTTCTTATCAGAG
Plcb3	GAAGGTGGGCATCTACGTCG
Plcb3	CATACCGGGTATTTGTCGAG
Plcb3	TTGATAAAATATGCGCTCAG
Plcb3	CAGTGAGGTCAATGCCACGG
Plcb4	TGAAGTAATGAGCCAGCGGG
Plcb4	TAAGAAGATCGGGACATACG
Plcb4	CAAGTACGGATGGATGTTCG

*Oligo name	Guide sequence
Plcb4	CTTGGCGAATACTGTTGATG
Plcd1	ATTTGCCAGAGACATACCCG
Plcd1	GGGAAGAAGACACTAAGTAG
Plcd1	AGGTGGATGACAGCTACGCC
Plcd1	GTAGCGCTCAATGAGAGAGA
Pnp	AGATGCTGTGTGATGATGCA
Pnp	TCAGTGCCTGGAAACAAATG
Pnp	TGTGGCCAGAACCCTCTCCG
Pnp	CCTCAAGTGGCAGTGATCTG
Polg	TGCTCATAAACGTATCAGGT
Polg	CGGCGGGGAAATGCCCGACG
Polg	CCGTTGCCATGGTGATACGT
Polg	AGATCCTGGCCCGCCCAGCG
Por	TGGCTCCCAGACGGGAACCG
Por	ATGTCTCTAAACAATCTCGA
Por	AAGAGGATTTCATCACATGG
Por	TCCAAGACTACCCGTCCCTG
Ctsa	GTGGTGCTTTGGCTTAACGG
Ctsa	GGACTCGATATACAGCACGT
Ctsa	CTCCGGCTACCTCAGAGCAT
Ctsa	CATGACCAGTACAGCCAAGG
Ppox	CCAGCCGGCCTAATCCCTCG
Ppox	CCGGGCCTGACGAATTAGTG
Ppox	GTACTCAGGATTCGAGCTAG
Ppox	TAATAGTGAGGTGTTACCTG
Inpp5k	TTGTGCAGGAGAGTATAACG
Inpp5k	ACAGCGTACATGTTGTGACG
Inpp5k	AGGATGCGGTCAGTCCACGC
Inpp5k	TACCTTGACAAAGTTCAGTG
Ppt1	GGTACACACTCTCCTTGATA
Ppt1	TGTTAATGTCCAAGTCAACA
Ppt1	AGAGACAGGACGTAAATCCC
Ppt1	CCATGCCAGATCACCAGCGG
Prkcsh	AAGACCAGGTAGAAACACTG
Prkcsh	CAGGGACAAGTACCGCTCTG
Prkcsh	GGCACAGACGAGTACAACAG
Prkcsh	AACTTGACGACAACATGGAT
Prodh	AGGAGGCGTATCGCAGCCGG
Prodh	CCTGCTGTCACGGTTCACTG
Prodh	CAGGATAAAGCCAACACCAA
Prodh	TCTCCCAGGAGCAAATAAGA
Prps1	GATGACTGCAGTAACCCGGC
Prps1	TGCAGATCATATTATCACCA
Prps1	CATCTCCCACAAGTACCATG
Prps1	ATGTCTACATTGTTCAAAGT
Psap	CTACGTGGACCAGTATTCCG
Psap	GTCAACCACCTCCTTGCACG

*Oligo name	Guide sequence
Psap	CCTCAGCTAACCTTAGGTTG
Psap	TCTGGCATAAAATCACATTG
Pten	CCTCCAATTCAGGACCCACG
Pten	TGTGCATATTTATTGCATCG
Pten	ACTATTCCAATGTTCAGTGG
Pten	GGTTTGATAAGTTCTAGCTG
Pts	GGGAAATGCAACAATCCGAA
Pts	CGAGGCGCGACAGTCGCGCG
Pts	CGGGCACAACTATAAAGGTG
Pts	GTGATCAAGAGGCTTCATGA
Pex19	ACAGCACATCCTTAGACAGG
Pex19	GCTGGCTTCCCAAGCTACTG
Pex19	GATGGTCGGAGCATGTTCTG
Pex19	TGGAACTGCTCCACCAGATG
Abcd3	GCTCACACGGTACCTCTACG
Abcd3	AACCAGGTACCCGACGACAG
Abcd3	GTGAAATGACTAGATTGGCT
Abcd3	AGAATGGGACGCTCATTGAG
Abcd4	AGACTCCATAATACTGACTG
Abcd4	GGACGACATTGATAATCCGT
Abcd4	ATGTTGCCGGTTACACACAC
Abcd4	CATCTTTGGATATTTCATCG
Pex2	GTATGCTGTGTGCACCATTG
Pex2	TCCCAAAAGACGCTAAATGA
Pex2	GTTCTGGGGCTTGCAAAATA
Pex2	ATGAAAGCACTGAGTAAACT
Pex5	CTGGACTCACCATCGATCAG
Pex5	TCTTGTAAACTGATCAACCC
Pex5	TCGTGCGGCAGATTGGCGAG
Pex5	AGAAGGGCTGCATCGACTGG
Pygm	GTAGCCGCCAACATTGACTG
Pygm	ACTTGGAGGACTTGAAACGT
Pygm	GGATCCAGCGTCCCACGAGG
Pygm	GCAGCCTATCTACGTCCCCA
Rbp3	TAAGCAGGTACACTCCACGC
Rbp3	TTACGAGCCCAGTACCCTCG
Rbp3	CAGCACTGTATCTCTCCCCG
Rbp3	CTGCAATCTAAGTTGGCCCA
Rbp4	AACTTCGACAAGGCTCGTGT
Rbp4	CTTGCAAAAAGAGACCCTCG
Rbp4	AGGGACGAGTCCGTCTTCTG
Rbp4	CCCACTACTCACTTCCTCGC
Rdh5	TGATATCCAGTAGTGTTGTG
Rdh5	ATGGAGACTTGTACTCCGAA
Rdh5	AAATCATCCTGTGTTAGCCA
Rdh5	AAGTGGGTGAAGACACGTGT
Rlbp1	TCGGGACAAGTATGGTCGAG

*Oligo name	Guide sequence
Rlbp1	ATCCGGCCTCGATAGTGCAG
Rlbp1	CCGTGCCCGCAAGTTCGATG
Rlbp1	ACCTCACCTTCTGCAAAGTG
Rnaseh1	TGGGCGACAGACAAACCAGA
Rnaseh1	AGAGTCAGTCGTTGTCTACA
Rnaseh1	AGCAGGAAACCGGTCCACCT
Rnaseh1	AGGAGCTCTTCAAGCCCGGA
Rpe65	CAAAGAGCCCTGGCCCACAT
Rpe65	TCGAGTCCAATGAAAGCATG
Rpe65	CCTTGTAAATATCTACCCAG
Rpe65	TCAAGCCATCTTATGTACAC
Rpia	ACTGCACGTGGGAACCCGAG
Rpia	CGTGGTTCTCCACCGCCGTG
Rpia	ATGATGTACCTGGAAAGATG
Rpia	TGACCTGGATCAACACCCAG
Nr1h4	AAACGGGACATTGTTGTATG
Nr1h4	TGATGGACATGTACATGCGC
Nr1h4	TGTGACAAAGAAGCCGCGAA
Nr1h4	AGTGTAAATCTAAACGGCTA
Scp2	ACAGATCCCTTACTCCGCAG
Scp2	AAGTGGGTCATCAACCCTAG
Scp2	CTCCTCGCTGGACAGAATCG
Scp2	GCTGTATTCATCTTGGAACT
Sord	CAGTACTCATCTACTTCTCG
Sord	GTTACTAAAGATGCACTCGG
Sord	TGTGCTTGTAGAATCGGCAG
Sord	TCTTACCAGCGCCACACACA
Selenbp1	AGTCATGGTCAGCACCTTGG
Selenbp1	CATCTCCTCCCGCATCTACG
Selenbp1	TGCAGGAAGCGGATCTCCAG
Selenbp1	CCAGCCTCGACACAATGTCA
Sgpl1	ATATAAAATCCCACTCCATG
Sgpl1	AGGCTTATGGAGAATTCACG
Sgpl1	ATTGCACCAAATATGAGCCC
Sgpl1	GGGAACGGAAAGCATCCTGA
St3gal3	GCTGGACAAACCCTAGGCAC
St3gal3	CCTACGCATCACCTACCCTG
St3gal3	ACGACTATGACATTGTGATC
St3gal3	GATCCTAGCCCACTTGCGAA
St3gal5	GTTCGGGCAGCATATCCAAG
St3gal5	TAGTATTCAACGTCCGACAG
St3gal5	CGCCCTCAACCAGTTCGATG
St3gal5	AGCTGAGAAGTGATTGCTCA
Clpb	AGGACCGCGTTCCGACGAGG
Clpb	GGAGAACGGCTGGTACGATG
Clpb	CGTTGTCACCGGAGACCGCG
Clpb	CTCTCGAGTGACTAGGACTG

*Oligo name	Guide sequence
Slc10a1	TACAGCAAAGGAATCTACGA
Slc10a1	TTAACCCTCGGTCCTACCTG
Slc10a1	AGGACGTAGGGTACATAGTG
Slc10a1	GAGGGGCATGATACCGTACT
Slc10a2	CTATTGGATAGATGGCGACA
Slc10a2	GTTGCTCTCAGGTACTACGC
Slc10a2	TAGGACATATAAAGAGACCA
Slc10a2	GCTCACCATCCTCTTAGCCA
Slc12a3	AACCTGGTACCCGACTGGAG
Slc12a3	CGGTTACAACACCATAGACG
Slc12a3	TGTGGTCTTCCACCTCGTTG
Slc12a3	CACAGGCTAGCCCTTCGCAG
Slc16a1	ACTACTAAGAAAGACCAAAG
Slc16a1	CACCAGCGATCATTACTGGA
Slc16a1	GACTTGCAGCCAACACCAAG
Slc16a1	AGGCCCTATTGGTCTCATCA
Slc1a1	CGACTCACCTAGTACCACGG
Slc1a1	TAGGATTACAGCAATGACGG
Slc1a1	ATCATGCTGGATACGATCAG
Slc1a1	TCACCTGATCAGGTCCAACA
Slc1a2	CATGTTGATAGCCTTCCCGG
Slc1a2	CCATAGCTCTCGTGCCTAGG
Slc1a2	TAATTGCCCATAGGTCTGAT
Slc1a2	GTTCATGGTTTCATTCAACA
Slc1a3	GTATAAAATGAGCTACCGGG
Slc1a3	GACTCTGACCCGGATCCGGG
Slc1a3	GAGGCCGACAATGACTGTCA
Slc1a3	AGGCTTCTACCAGATTGGGA
Slc22a5	TTTATGATCTGATCCGAACA
Slc22a5	GGGTCAGATCTCCAACTACG
Slc22a5	CACAAGGCAACGGTGCTCCG
Slc22a5	CACACCCACGAAAAACAAGG
Slc22a12	GGGCCTGGGAGTTACATACC
Slc22a12	ACGGTAGGCAAGCTGGACCA
Slc22a12	GAGGTGCTATTGTCCAGGAG
Slc22a12	CATCACCAAAGGGCTACCCT
Slc2a1	CCTGCTCATCAATCGTAACG
Slc2a1	TCAGCATGGAGTTCCGCCTG
Slc2a1	GTGTCACCTACAGCTCTACG
Slc2a1	CAAACATGGAACCACCGCTA
Slc2a2	AGAGGGCTCCAGTCAATGAG
Slc2a2	TTACCGACAGCCCATCCTCG
Slc2a2	GGACTGGTTCCAATGTACAT
Slc2a2	TGTGATCAATGCACCTCAAG
Slc3a1	CCATATACCAGATCTACCCG
Slc3a1	ATCCTTGGTTCCAATCGAGT
Slc3a1	AGAGGAGCCTCACCTAAAGG

***Oligo name**	**Guide sequence**
Slc3a1	TGGCAAGCCATAGTACATCA
Slc5a1	AGGAAGAATGCTACACACCG
Slc5a1	GAGACATGTTCTTGGCCGAG
Slc5a1	CATCGCCTACCCCACGCTCG
Slc5a1	CCGGCCACCACACCATACTT
Slc7a5	GCCCTCCTCGCAGTACATCG
Slc7a5	ACCCCTACTTACGCACGCAG
Slc7a5	AGCGGCCTCTTCGCCTACGG
Slc7a5	GTAGCAGAGTGCGCCCACGA
Slc7a7	AAGAGATCAGGAACCCCGAG
Slc7a7	CAGCGCCAACACCTTAGCAT
Slc7a7	GGCCCCGGATTTCTTAATGG
Slc7a7	GAGACACACGCCATTAAGCA
Smpd1	AGGCTTTCTAGCGTTCGCAA
Smpd1	GAAGAGGACACGGCTGACAG
Smpd1	AGTCTCGCCAAGATCAGCTG
Smpd1	GCTGACTGGCACACATCTAG
Sms	ACTTACTAACATCCCCGCTG
Sms	TTACCACCCATAGTTCGCGG
Sms	CTTACACGAACAAGAATGGC
Sms	AAACAAGAAACTGACAGCGT
Spr	GCGTGCGCTTACGAGCATCA
Spr	GCGCAGTACGCGAGCTCCCG
Spr	AGCCTCGGTGCCCAGATCGG
Spr	TACAGACCCCAGCCTTTGTA
Sptlc2	GTTGTGTTTGAAGATTCGAA
Sptlc2	TGAGAGCAATCACTTCAGGA
Sptlc2	AATCTCGAAGATATCCAAAG
Sptlc2	ACAACTATCTTGGATTTGCG
Scarb1	GGGGCCGTGAAGCGATACGT
Scarb1	TGCGGTTCATAAAAGCACGC
Scarb1	GATGAACAACTCGAATTCTG
Scarb1	GAGGATTCGGGTGTCATGAA
Ssr4	TAGTAAGAAGGGGTGATCTG
Ssr4	AAACAATTTCCTGTAACCCG
Ssr4	TACAGAGACTGTATTCATCG
Ssr4	CACCTTCCTTAGGAGGCTAT
Star	AGAACTTGTGGACCGCATGG
Star	CGAACTTGACCCATCCACCC
Star	GAAGCTCCTATAGACATATG
Star	CGCACGCTCACGAAGTCTCG
Stra6	TCTTCAAGCACTACACCGAG
Stra6	CAAGTTGTACTGGATACCAA
Stra6	CCAGACCTGAACACCAAAGT
Stra6	GAAGCATCACCTATGGACTG
Sucla2	CAGAGCGTAACATACTGTCA
Sucla2	TGTGCACTTCCTATCAGTAC

*Oligo name	Guide sequence
Sucla2	GTAGAAGATTCTGACGGAAA
Sucla2	TCAAGTATTCATGCAGCGAA
Abcc8	ATGGCTGCTAAATGCCACGG
Abcc8	CAGACCAACGAGATGCTCCG
Abcc8	TGGACAATGAAGATCATCGG
Abcc8	GAAACTGGGATTAACCTGAG
Surf1	TGTTTCTATAGGTCCAACGT
Surf1	ATGGAAAGGAGTAACTACAT
Surf1	GTGGTCGCAATGGGCCTACG
Surf1	TTATGTACAACTCTTTAGAG
Taldo1	GCGCATCCTTGATTGGCATG
Taldo1	CTTCTTTGTAAAGCTCGATG
Taldo1	TTCTGAATTCAGGCCTCAAG
Taldo1	GCTTGTATTCATCGATGGCT
Tbxas1	TCACAGGCTTGGCTGATGAG
Tbxas1	CCACACTTACCATTTCAGGA
Tbxas1	ACAGAGGCCCGTATCGCTCT
Tbxas1	CTGCTGTTACACCATAGATG
Hnf1a	CCTATAACGGACCTCCACCG
Hnf1a	GACGTACCAGGTGTACAGAG
Hnf1a	TGCCAACTAAGAAGGGGCGT
Hnf1a	CGGACAGTCTGCAACCAGTG
Hnf1b	CAGCTTCACCCCGAAATTCG
Hnf1b	CTGGTTCGCAAACCGCCGGA
Hnf1b	GCCGCAACCGGTTTAAATGG
Hnf1b	CTTGGTACGTCAGAAAGCAA
Tcn2	GAAGCGGCTCCATGACAGCG
Tcn2	TCTGAGACCACGAATCACCA
Tcn2	GAGACTAGCAATACCGCAGG
Tcn2	GAATATCTATAGCACCCCAC
Tfam	TAAATGTTATATGCTGAACG
Tfam	GGAGCGTGCTAAAAGCACTG
Tfam	CTAACTCCAAGTCAGCTGAT
Tfam	GCTGTTCTGTGGAAAATCGA
Th	GGGTGAGCCAATTCCCCACG
Th	ACTGTGTGCACTGAAACACA
Th	CCCCAAGGTTCATTGGACGG
Th	GTGCGCTTCGAGGTGCCCAG
Tkt	CGTGGACGGACACAGCGTGG
Tkt	CAGCGCTGCAGCATGATGTG
Tkt	CCCACAGATAGCCACCCGGA
Tkt	CTCCGAGGGCTCCGTCTGGG
Tmem165	GGCATTAGAATGCTTCGGGA
Tmem165	ACATAGTATGTATACACCCT
Tmem165	GCAGCTGCCCAGACGAATCT
Tmem165	GTCATCATAGTGTCCGAACT
Tpi1	TGAAGGTCAGTACAAACGCA

*Oligo name	Guide sequence
Tpi1	AAGTCGATGTAAGCGGTGGG
Tpi1	AGTGAGCCACGCCCTAGCAG
Tpi1	CCAACGAAGAACTTCCTGGT
Tpmt	AAAGAACCAAGTACTAACCC
Tpmt	TTCTGCAGGTTCGCAGATCG
Tpmt	GCATTAGTGGCTATCAATCC
Tpmt	AAAACACTCGCAGTCCACTC
Trex1	TTTCCTCGAACCATTCCCTG
Trex1	ACACAGAAGGTACCATCTAG
Trex1	AGCTTGTCCACCACACGGGG
Trex1	GGAGCAGAGGAAAGTCATAG
Tfrc	CTACACGCTTACAATAGCCC
Tfrc	GAATACATACACTCCTCGTG
Tfrc	GGGCTCCTACTACAACATAA
Tfrc	AACCCTCGGGAGACTCCACT
Cmpk2	TCGGCCGCGGCGCTTCACTG
Cmpk2	GGTGTTCCAAGACCGGGACG
Cmpk2	AGTCGCGCCGAGTGTCCGGG
Cmpk2	AGTTGACCAGTGCCCAAAGG
Tyr	AGAAATTCGAGAACTAACTG
Tyr	TTTATGCGATGGAACACCTG
Tyr	ATGTTGATATCATTAAACAT
Tyr	ACCCCTTTGAAGGGGAACTG
Ucp2	TCTGGGTACCATCCTAACCA
Ucp2	GTCAAACAGTTCTACACCAA
Ucp2	AGACCATTGCACGAGAGGAA
Ucp2	CGGACCTTGGCGGTATCCAG
Slc35a2	TCACCCGCTGTAGTGGACCC
Slc35a2	CTGCTCTTCGCACAAAAGAG
Slc35a2	CTGCAAGGTATAGATGAGAG
Slc35a2	GGCCACTGGATCAGAACCCG
Ugcg	CGGCTACATACGGCAGCCCG
Ugcg	TGGCCAAAGCAATAGCCGAC
Ugcg	AAGGATGTGCTAGATCAGGC
Ugcg	CAGCCGTATAGCAAGCTCCC
Umps	GAGCAGATAACTGTCGCCAG
Umps	CCGCAGGTCGATGTAGACTG
Umps	AGAGCGTGCACACGGCGTGG
Umps	TCTGTCTGCCGATGTGTCGG
Ung	ACGGACCTAATCAAGCTCAC
Ung	TTGTCAGGGTGGGCCCGACA
Ung	CCAACCCCGACTCTGACTCC
Ung	CCACAAGGTCTATCCGCCCC
Uqcrq	GATCCCTACAGCGTTTGTAG
Uqcrq	CTCAAAGGGCGACAAGCTGT
Uqcrq	GCAGGATGCGCTCGCGAGTG
Uqcrq	TTTGCTGAAATAGCTTGGGA

*Oligo name	Guide sequence
Urod	CCATCACCCTTACTCGACAA
Urod	GTGGACCCTAATGACATACA
Urod	ACTGCCCTACATTCGTGATG
Urod	CAGCACCTGCCGATCTCCCG
Uros	TCTCCTTTGATAGTTCCACA
Uros	TGACAGCACAGGAATCAGTG
Uros	GCCAAGTCTGTGTACGTGGT
Uros	AGACATGCATGCTTTCCATG
Usp9x	GCAGATATGGAAACTCGAAG
Usp9x	ATGGGTATAGTATGACACAC
Usp9x	GAAGTTGATTGATTAAGTCA
Usp9x	TATCCAAACACATCATCCCT
Vdr	TGGAGATTGCCGCATCACCA
Vdr	AGCGTTGAAGTGGAAGCCCG
Vdr	TTCTTCATTCAGATCCATCG
Vdr	TTCGTGCAGACGTAAGTACA
Xdh	CCAGCATGCAACGTACAGGG
Xdh	CATACTCATGACAATACCAG
Xdh	TCAAAACGCAACGTCTTCCG
Xdh	GGAATTCCACCATCCCACCA
Nt5e	TCATGAATTTGATAACGGTG
Nt5e	TGAATAAGATCATCGCCCTG
Nt5e	TATGCCTTTGGCAAATACCT
Nt5e	CCTGAAGCGGCACGTCTGAG
Papss2	GAATATCCGCCGGATCGCGG
Papss2	AGTCGATCAAATCCGAGCTG
Papss2	CTTGATGTACGAAGGTCGGA
Papss2	GGTGCTAGAGAGAATAAGGT
Slco2a1	CCCACGGATGATCGGCATAG
Slco2a1	ACTCGGGGGATGGTTTGCAG
Slco2a1	CTTCGTGGACTACGGCAGAG
Slco2a1	CTCTGCAAAGTCGTCCACAT
Slc35a1	GAACACTCAGCAAATTACAG
Slc35a1	ATAGCACCAAAGCCTAACAA
Slc35a1	TGCACAGCATACACTAGTGA
Slc35a1	TCTTAAAGCTACGGTGTAAG
Mpdu1	TTCCTGGTCATGCACTACAG
Mpdu1	CTAGCTCCAGCATTACTGAC
Mpdu1	ACTACAGCCAGAGGCGTGAG
Mpdu1	ACGACCAGCTCTTCGTGCAA
Rbck1	TGCTTCATACCAGCCTGACG
Rbck1	AGTACGCCCGGATATGACAG
Rbck1	TGCATTCACACGGCATTCGG
Rbck1	ACCCGAGGTCTCCCCAACAC
Btd	CTTGCTGTTCATAGACGTCG
Btd	GTACCAAAAGGACTTGAGAG
Btd	ATACCAGTTTAACACAAATG

*Oligo name	Guide sequence
Btd	CCGCGAGGCTGAGTACTACG
Slc27a5	GTGGGCTTAATGAACTATGT
Slc27a5	TACCTCTGTACCATACGATA
Slc27a5	GTAACAGTGATCTTGTATGT
Slc27a5	CCTTTGTGGATGCTTTAGAG
Txnrd2	TATCCAGTCCAATTCCAGTG
Txnrd2	TGAGCACACAGTTCGCGGTG
Txnrd2	GGTGGCACCTGTGTCAACGT
Txnrd2	CGGTGGCCTAGCTTGTGCCA
Slc27a4	CAAACGGATAGGGTACACAA
Slc27a4	TCTACACATCGGGCACCACG
Slc27a4	TGACTTCAGGAAACATCGTG
Slc27a4	ACAGACCCACAAACTCATTG
Cln8	GCTCATCTCTAGGAGCAACG
Cln8	GTGTTGGTTTCACATCACCA
Cln8	AAAGGTGCGGAAGAACAGGT
Cln8	CTTTGTCGGCATAGAGCACG
Mecr	CGTGGCGGTACCAAGCCTCG
Mecr	AAGGATCTGACGTCCACGTG
Mecr	ATCCAGAATGCATCCAACAG
Mecr	AGCACTGATTGGAATCCCTA
Aifm1	CTGCCTAATATTGAGAACGG
Aifm1	ACCATGGAAAAAGTCAAACG
Aifm1	GTCAATTACAGTTATCGGCG
Aifm1	AAGTCTGTCTGCCATCGATA
Sgsh	CTGACCTAGAAGGCTCACGT
Sgsh	CGTTACGGAAGATAAGGCTG
Sgsh	TGTACCGGGCCAGTACAGGT
Sgsh	TCCTGAGGGTCGTAGATCTG
Asns	GCATGCCATCTATGACAGCG
Asns	GAATGCAGCCGATAAGAGTG
Asns	GCTGTGTGTTCAGAAGCTAA
Asns	ATTTGAATATCAGACCAATG
Sec23b	GCAACACCAGTGGACCGCAG
Sec23b	AATGGCGTTTGGTGCTACGT
Sec23b	AAAAGTGATGAGACCAACCA
Sec23b	GTGTTGGTGGCACAAGTCAG
Dguok	AGAAAGGGTCTGGAATGTGT
Dguok	TTTCATGAGTAACTTCACAA
Dguok	CGTGGACGCGCCACACGCCA
Dguok	TCCTGCAGGAGTTCGCAAAC
Slc25a10	CATGCGGGACTACATGACCA
Slc25a10	TACACGGTACAGACCATCCA
Slc25a10	GTCAGAGAGTAGGTCATCTG
Slc25a10	GACATTGACCAAATCTGCTG
Yme1l1	CAGGACGTATTAAGGCACTA
Yme1l1	TTAACTATTACCTCACTACT

*Oligo name	Guide sequence
Yme1l1	TCATCGATGAATATAACACA
Yme1l1	CTTGGAGGTAAACTTCCCAA
Pign	CCAGCTCCCCAAGTAACGAA
Pign	GTGTTGTTAAGATAACCCAC
Pign	TGCCACAAAACTGGATACGT
Pign	AAGTCAATAGTGATTCAACC
Pdhx	CTTTAGTGAAGATCCCGCGA
Pdhx	GTTAGACGAGATCTGGTCAA
Pdhx	TGTCTCCTACGATGGAGCAA
Pdhx	TCCTGGGCAACCGAATGCAG
Abcg5	GCTGATAGAGCAGCCCCACG
Abcg5	AGCTTGCCGAACATCCCAGG
Abcg5	CAATCATTTGGTCCGCCACG
Abcg5	GGATTGGAATGTTCAGGACA
Abcb11	TACGCACCATGCCTTCGCAG
Abcb11	ATGAAGGCGAGTACACACCA
Abcb11	CCACTGTTCGAATAGATGAG
Abcb11	AAGGTTGTGGGTAATCACTG
Naglu	TGCACACATTCTGGTAATAG
Naglu	GAGATCGATACGTACTTCAC
Naglu	AGGAAGAGGTTCCCGATGAG
Naglu	GCCCTCGAGGATGTGAACCG
Abcc6	GTGACCGCAACTCCTCGGCG
Abcc6	CCTCTGTGGAGGATCCACCA
Abcc6	AACAGGGTGTAGGTACAGAG
Abcc6	TGCACTGCATCGTTCAGGTG
Tango2	GTTTGCTACTATGGAAACCG
Tango2	GGCTGGGCATCAGCACACGT
Tango2	CCTGAAGAAGGTCTCTACAG
Tango2	TAGATGCCTTACCTCTACCA
Vkorc1	GTACGCACTGCACGTGAAGG
Vkorc1	GTGAGAGGGCTAAGCCAGCG
Vkorc1	GGTGGAGCACATGCTAGGAG
Vkorc1	CCATGTCTGCACGCACCGAG
Gfm1	GAACGGGTGCTATACTACAC
Gfm1	GAAGCACCATCTACAACACG
Gfm1	AGCAATGAGGCCTTCTAACA
Gfm1	TTACTCTGTAGCGAGCAATC
Tpk1	CTTGCCTGAATTCGTCAGTG
Tpk1	GAACTTGAAATACTGCCTTG
Tpk1	GACACTTGGTAAAGTCAGTG
Tpk1	CACTTATATGATCTCACTGA
Dnajc12	GAGCCCGCTATGACCATTGG
Dnajc12	GAGCTCATCGCATCCCAGCA
Dnajc12	TGTCAATGCCGTTCGAGCAG
Dnajc12	AATTTCTGAAAAGTCTCCAC
Angptl3	TGCTCTGCCGTTTATAACAG

*Oligo name	Guide sequence
Angptl3	TACACTACAAGTTAAAAACG
Angptl3	CATGGACATTAATTCAACAC
Angptl3	GAAGACAGCCCTTCAACACA
Aass	GAAACTTCTCTTAATTCGTG
Aass	GCAAATTATTCACGACAGGT
Aass	TAGGCAGTGATTACGTCCAA
Aass	GGATAGTGGCTTTCGGACAG
Slc7a9	GAGCACTTACCAACCATCGT
Slc7a9	CAAAGGCCTCCATCAGATAG
Slc7a9	GGACTGCAAGAGCTCCGTTG
Slc7a9	GCTGGCCAACACAGAATCCG
Hacd1	GCAACTCACCGATCAGACAA
Hacd1	CTGGCCCATTTAATGAAGTG
Hacd1	GATCCAGAATGAAGAGAGCG
Hacd1	CTTCTACAATATCGCCATGA
Ttpa	GAGGTGGAAACTCAACGCAA
Ttpa	CAGATCCAGATCGAAATCCC
Ttpa	GAAGTCCAAGGATACTTCTA
Ttpa	TTTATTTGTTGTAGCATACT
Mrps7	GGAATATTACCGCAAGCCGG
Mrps7	GGCCGCGACTGAAACCAGCT
Mrps7	CCCCTACAGGATCTTCCACG
Mrps7	GAGGCAACAAAGTTCTGGCC
Tfr2	GAGGTCGCTCCAGTACAACG
Tfr2	AGTGCGTGTCAGTCCACACG
Tfr2	TGGTGTACGCCCACTACGGG
Tfr2	ACCCCCAGTGAAGATTAGCA
Pnpla6	CTCCGTAGTGTCATCCAACG
Pnpla6	GCCATGTCAAAATCAGAACG
Pnpla6	AGGAGACTCCGACCCTACAA
Pnpla6	GGCCTGGCGCAGACAACGGA
Atp8a2	GCAAGCCCTCTTCATAAACT
Atp8a2	GGCCCTTATCCTATTGAAGG
Atp8a2	ACAACTTCGACTCTACTGCA
Atp8a2	CAGTGTTAAGAAATGGCATG
Polg2	GAAAGAACCTAGCCTCACAG
Polg2	TGTGGGAGTAAACCATACCA
Polg2	TGACGCCCCCGAGCATGCGG
Polg2	GCAATTAACATAGTGCTCCA
Hs6st1	GGCGCACGTTCTGCACTAGG
Hs6st1	ATGGCGACATGTACAGCGTG
Hs6st1	CTCATCCTTTACCAGTACGC
Hs6st1	CCTATAACCTGGCTAACAAC
Acsl4	GTCCAGGGATACGTTCACAC
Acsl4	GCCCATATCCCTGACCAATG
Acsl4	CAATAGAGCAGAGTACCCTG
Acsl4	GGAACAGCGGCCATAAGTGT

*Oligo name	Guide sequence
Gne	ACGTCCAACTCAAAGAACGC
Gne	TTGCAGCTCAAAGATATATG
Gne	GCTCCACACGATTGTTAGAG
Gne	CCTCTTGTTAAACGAGATCA
Slc25a13	GGGGCGACTCCCAGTAACTG
Slc25a13	CAGATTTATATGAGCCGAGG
Slc25a13	ACAAGGCATCCGGAGCACAC
Slc25a13	TACAAGATCGATAGGATACA
Galns	AGCAGTAGCACGATGTTGGG
Galns	CCCAATTAACCGGAAGACTG
Galns	GGCGTAAACTGGTGCATGAG
Galns	GAGAGACCCCAAATTTAGAC
Nus1	GTGGTCGTAGACGCTAATGT
Nus1	TCCAGGTGCCGAAGCGAACG
Nus1	ACAGCACCTTCACTGCCGAA
Nus1	CCAGCGCAGCCGAGGATGGG
Coq5	CTTCGGGTTTGAGACCGTGT
Coq5	GTTGTGCCTGAACGTAACTA
Coq5	ATGAATGACATGATGAGTCT
Coq5	GCCAGGATCTATGACACCCG
Hgsnat	CCTGCAGGTTAACTCCACCT
Hgsnat	ATGACTTCTATCCTGCAACG
Hgsnat	GATGTGTGGACACATTTAGG
Hgsnat	GTTGGGAGTGACATACTTCG
Slc46a1	AGAGCTAACATCTGCCACAG
Slc46a1	GGGCAATGGATCGATGATGG
Slc46a1	TGGACCAGAAGAGTCCCACC
Slc46a1	GAACTGTGGGAACCAAAGCG
Coa3	GATACAAATAGCTAACACCA
Coa3	CTCAGCGCATCGACCCGTCG
Coa3	GGGTCGATGCGCTGAGCGAA
Coa3	CATAAACTGCAACTGCGCTG
Trmt10c	CTTACGGTATCTGTATGGGA
Trmt10c	TTATTATGACAAGACAAAGA
Trmt10c	TTAGTTCTCTGGTTGAGGCG
Trmt10c	TAGGCCATGTCAAAAACCAA
Slc52a2	TGTTGTGGGTTCAGATGTCG
Slc52a2	ATGGGAGACACCTCGATCGG
Slc52a2	GGCCTCTCTGTGGAACCACG
Slc52a2	AAGACCGTAAAAAGGGGGGT
Sco1	AAATCAATACCCATTGACCC
Sco1	AAAAATGATTGAAGTCGTGG
Sco1	TTGGGAAGCCTTTACTAGGG
Sco1	CACTCACCCCAGGCTTCGGG
Pla2g6	AAATCCATGGCCTATATGCG
Pla2g6	GGCACCTGCATTAGCCCCGT
Pla2g6	AGTCTCCCCAAAGTCGTTTG

*Oligo name	Guide sequence
Pla2g6	CCATTGGGCCAAGAACGCCG
Chst3	CCACGAACGAGGAACCCGTG
Chst3	AACCTCGGGTCCTCAACTAG
Chst3	ACTCAGTTCCTGTTCCGCCG
Chst3	AAACTATGACCACAAATGCC
Fut8	TGAAACAGTAGACCACGTGA
Fut8	AAATGACAAAAACATTCAAG
Fut8	CCAGAAGGCCCCATTGACCA
Fut8	AATCAAGTATTTGACAAACT
Gria3	TGTGACGAAAGATGTATGCA
Gria3	GTACAATGTCAGTAAAACCC
Gria3	TACCTCTATGACACAGAACG
Gria3	AGGAATCCAAGTGGTCTACG
Porcn	ACAACTTCCACCATGGACCG
Porcn	GTGACATGGCACAAGATGCG
Porcn	CCACCTTCTTCAGCCATCGG
Porcn	GAAGGAGACAGCACTCTCGT
Clpp	GCGCTTATGACATATACTCG
Clpp	CCTGCAGATTGACGACAGTG
Clpp	CATATGTATATCAACAGCCC
Clpp	CAACACACCACGTGCAGATG
Slc40a1	CAGGGTACGCCTACACTCAG
Slc40a1	CCTTTGGATTGTGATCGCAG
Slc40a1	TCATCAGGATGATTCCGCAG
Slc40a1	CCCATCCATCTCGGAAAGTG
Pmm2	ATTCAATGAAAGTTCCCCTG
Pmm2	AAGACCAAAATTGGAGTGGT
Pmm2	GCTTGGTAGCGTACAAAGAT
Pmm2	AAAAGTTCGTAGCAGACCTG
Sult2b1	GGGAGACCACGACATCGCGG
Sult2b1	GGGCTCCGATCGGATCCACG
Sult2b1	AATGTTTCCGAAATGAGGTG
Sult2b1	AGGTGAGAGCTCATAATGCG
Cd320	TGGTCTCAGAACAGGCCTAG
Cd320	GCAACCACTGATGTTGTCAC
Cd320	CCATCACAGCGCCACGTGTG
Cd320	ACCTTCCAGTGTCTTACCAG
Elovl1	GGCTATTGGAAAAGTCTATG
Elovl1	GGGCAGACAATCCATAGTAG
Elovl1	TCCAAAGCTACCCTCTGATG
Elovl1	CGATAGGATGAAGTACACAT
Ndufa1	CATCCACAAATTCACCAACG
Ndufa1	TGTACGCAGTGGACACCCCG
Ndufa1	GAATTTGTGGATGTACGCAG
Ndufa1	CGCGTTCCATCAGATACCAC
Atp6ap1	GAGGATTTCACAGCATACGG
Atp6ap1	GATATGACCCTCATGTGTGT

*Oligo name	Guide sequence
Atp6ap1	TAGCTAGATCCACATGCAAG
Atp6ap1	GTGTCATTGTAACTCACAGG
Extl3	GCCCAAGCCTCGCGTCACAG
Extl3	TCAGACATAGCATGGACAAG
Extl3	CCACACAGTGCCCACTCAGT
Extl3	ATTGCGGAGGTATTTAGGTG
Wdr45	GACACTCGGGACAACCCCAA
Wdr45	AGGCGTCCGGATCTACAATG
Wdr45	AAGCTGGTAGAGCTTCGAAG
Wdr45	GTGTGGAAGTCTGCAACTTG
Atp8b1	AATGCCACACCGTCCTACCG
Atp8b1	AGCGTTGGATAAAGTGTACG
Atp8b1	GCTGATAAAATCCTGTTACG
Atp8b1	GATTTGCCATACGGTCATGG
Mpc1	ACTTCCGGGACTATCTCATG
Mpc1	GGCGGACTATGTCCGGAGCA
Mpc1	AAATCTCCAGAGATTATCAG
Mpc1	TGGGGCCCAGTTGCCAACTG
Slc1a4	GTCTGCAACCGATTACACAG
Slc1a4	TAGAGCCACTCCTAACACCA
Slc1a4	GATGCCACCCAGACGCCCGA
Slc1a4	ACCCACCAACACTCCCGACA
Pgam2	GGATGTTACGGACCAAATGT
Pgam2	AACCAAGAGAACCGTTTCTG
Pgam2	GCTTCAAGCCTGCATAGCGG
Pgam2	GTTTGACATCTGCTACACGT
Samhd1	ATCCTTACATTATGTCGATG
Samhd1	GCTTGATATAGCGAAGTCGC
Samhd1	CTTGGGCTGCCATCGCAGCG
Samhd1	TTAGGATCTTACCTAGGTCG
Pdss1	AGCCTTTAGACCGATTATTG
Pdss1	GAGGCGGCACGTGTTCCGAG
Pdss1	TATACTATGCATAGTTGGGG
Pdss1	GTTATTGAAGATTTGGTGCG
Dgke	TCTCGTAGTGGAACTAACAT
Dgke	GATCATGCTCAAGAACGACA
Dgke	GTCCACGACGAGTGCATGCG
Dgke	ACAAGAAAAATACATTCCAG
Pigp	TCTCTTGTGCAGATACTGGG
Pigp	TGCAGTACTTTATCTTGTGT
Pigp	AAGGAGTTTAACCAAGATTC
Pigp	ATGAATGGAGTCAAGTGGAG
Prodh2	TAGTCCATGAGTGACCAAAG
Prodh2	CCTGTGCCACTCGGTGCAAG
Prodh2	GGACTTATCCCGAGCCCTCG
Prodh2	GTTGGCAGTACCCACCGAGG
Pex14	CTTCACTGGGATCTGCCAGG

*Oligo name	Guide sequence
Pex14	ATGCTCTCCTGGTCGCAAGT
Pex14	GGAACAGGTGACTTACTGTA
Pex14	ATACTTACCAGTGGCTCTCG
Mrpl12	TCTTTGGGAGCATTATCCAG
Mrpl12	ATACCTTCAGGAGTTCGTTG
Mrpl12	TGCCCAGCGTCTGTGCAGCG
Mrpl12	GCCCCCCGGAGTCCAAGCCG
Ggcx	TGTGTGTATAAGAGGTCCCG
Ggcx	GCCTGCACGATGTCCACACG
Ggcx	AGAACTGTGTAGTTCCAAAG
Ggcx	GCTCGCCCGTGAGGCCGTCG
Timm22	GCTGGCATTGATACCAACGT
Timm22	AGAAGAAGGCTGTACTGCAA
Timm22	TGGGCGACAAGCGTCAGCCC
Timm22	CCTCTAGGGTTTGTCTTGGG
Ivd	AATATCGAGTGGGCCCGCCG
Ivd	CTCCTGGCTCAGGACGTTAG
Ivd	GGTAATGGAAGAGATATCCC
Ivd	TTCTTGGAGGTACTAAAACC
Pus1	CCTGCAAAGAGGGTCAAGGG
Pus1	CTTACCCAGAATCCGAATGT
Pus1	TACTCGGGCAAGGGCTACCA
Pus1	TCCAGGCCCTCACGTACGAA
Adar	ACTCCAACAAGCCGCCTACG
Adar	AGAGGTAACCCCAGTAACAG
Adar	TTCTTGTAGGGTGAACACCG
Adar	TGTATCCAGGAATTCCCTAG
Suclg1	GAGTACGGCACCAAACTCGT
Suclg1	AACAGAATGGGATACGACAC
Suclg1	TGACACGCCAGGGAACGACG
Suclg1	CATTAATGAAGCAATCGACG
Aldh18a1	CAAGTCTAGAGTGGGCCTAG
Aldh18a1	CGATGGGGACGATGTTCATG
Aldh18a1	CGTCCGAGAGGACAATCAAG
Aldh18a1	TGAGGGGTACCGTGATAAAG
Ctsf	ACAATTACGGCCGTGCTGCG
Ctsf	AAAGACAGTCAATCGCCACT
Ctsf	ACCAGGGGATCATTGCAAGG
Ctsf	CCTGAATCCCCTCTTACAGA
Tbk1	TGCCGTTTAGACCCTTCGAG
Tbk1	CTTCTCGCTACAACACATGA
Tbk1	CAACATCATGCGCGTCATAG
Tbk1	CGGGAACAACTCAATACCGT
Pex3	AAACAAGCTGGAAATATGGG
Pex3	TCATTAAACAAGCTGTACAA
Pex3	CATGCTGCCGACACTGAGAG
Pex3	TACTGCTGCTGTACATCCGG

*Oligo name	Guide sequence
Txn2	AGACCACCAGCATTGTACTG
Txn2	AGGGAAGCCCACACACCCTG
Txn2	GCGGTCCTAGGATCTTGCAG
Txn2	AAAGGTCGTCAAACAGACTC
Mlycd	GACTTCGTGAGCTTCTACGG
Mlycd	TGGAAGAGGCCGCGATACCG
Mlycd	CTCCGACTGAAACCGAGGAG
Mlycd	CCGCACAGCCGACGTCCCCG
Tdo2	GATAGCTCGGATGCATCGTG
Tdo2	TGATGAATAGGTGCTCGTCA
Tdo2	AATCCATTTGGCTCTAAACC
Tdo2	CACTATCGTGATAACTTTGG
Alg2	CAGAAAGACCATGCGCACGT
Alg2	GCTCTCGGTGCAATGCGCAG
Alg2	TCTCTATCAACCGATACGAA
Alg2	ACTGGCCAGACGGCGTAAGA
Mocs1	CACTTGGATTCCGAACACGG
Mocs1	TAGGTCTCGAGGGCTCCCCG
Mocs1	CGATGTCCACCACATCCGGT
Mocs1	AGGCCAGTATTGCATGCCCG
Nfu1	ACTGTACCTGTGTTACACAA
Nfu1	GAAACAGTACCTGGCCAGAG
Nfu1	GTGTAGTCCGGCTGTGCAGG
Nfu1	GCGCTACCTGCTTCTCCCGG
Dhodh	TTGATCCAGAGTCGGCGCAC
Dhodh	GTAGAAATGGTCGTCCCCCG
Dhodh	ATAAATTCCGAAATCCAGTA
Dhodh	GGTATGGATTCAACAGCCAC
Stap1	GTTGGCCAGTAAGGCACACG
Stap1	GGAGCCAGTACAAGACTATG
Stap1	CTTCATTCTTACAGTAACAG
Stap1	GGAGTACAAACACTATTGGA
Aldh1a3	CACCAGGCATGAGCCCATCG
Aldh1a3	TGCATCCAGCCGGCGCCACG
Aldh1a3	CCACCCGGCAAAATATCTGA
Aldh1a3	AACACTAGAGAAAATATGTG
Slc25a20	ATAGGGGTGACTCCAATGAT
Slc25a20	TCCAAGGTCCCAGAGTACAT
Slc25a20	TCAGGGGAGAACAAGTACAG
Slc25a20	TCCCAGCTGTAAACAGCTGT
Srd5a3	ACTGCTTGGTCTTCCCGTAG
Srd5a3	AGCACTCAAAGAGTCTCCGA
Srd5a3	ATCTACTGATACAAGCCCGG
Srd5a3	TCTACGTCATCTCAGTTGTG
Mogs	TCTAGGTCATTCTTCCCACG
Mogs	TCGGCAGCATATCCACGATG
Mogs	TGCCGAAATAGACGTGTGGG

*Oligo name	Guide sequence
Mogs	GAGGTCCTACTACCAGAGAT
Tk2	CTCCAATACAACAGACGTCG
Tk2	TTGAGGGCAATATTGCAAGT
Tk2	AGAATCGCGTAGTCAACCTC
Tk2	TACCATGATGCCAGCCGATG
Cldn10	GCCCGAGATGGAGACTACGA
Cldn10	CAGACCATCCAACGCCAGCA
Cldn10	TAGAGGACTAATGATCGCTG
Cldn10	ATCTGCGTTACCGATTCCAC
Chst11	AGCCAACGAAGCCCACGTGT
Chst11	GCAGACACCAGCCTCTCGAA
Chst11	AGCAGATGTCCACACCGAAG
Chst11	ACCTCCTTCCACAAGCGCTA
Treh	AGATTAGGGAGGACCTCTCG
Treh	AGCTACGGACATATCCCCAA
Treh	AGGGGACCGAGAGACTCTGT
Treh	AGGAACGCGTTCAGATCAGC
Hibadh	AGCTCCACAGTATACCACGT
Hibadh	GCTGCCCTCCAGTATGAATG
Hibadh	CGTGTTCCCTGATGTATGCA
Hibadh	GGAAACCTTACATTTATGGT
Sumf1	GCAGCCGCACGAGCCCGCAA
Sumf1	CTCGACTGGCTATTTGACAG
Sumf1	AGTGAAAACGCATATCCACC
Sumf1	AGCTAATTGGAGACACCCAG
Ngly1	GAGCTTCAAACCCTAATGCA
Ngly1	AGAGACTAGATCTAGAGATG
Ngly1	GCTACACTGTGATGCATGTG
Ngly1	GCTGGGTTAATACGGCACTC
Thap11	AGCCTGGTTGCTGTCTACGG
Thap11	GCTGCTACAACAATTCACAC
Thap11	GGGACACGTTCTTGAGCCAG
Thap11	CCACGCAGCGGGAAAATGGT
C1galt1c1	ATATGGACACAAATGACATG
C1galt1c1	TGTGCCTTGATCACTATGCT
C1galt1c1	CAAGAACTATACAGTATACC
C1galt1c1	CAATAACAGCGAAAGTAGTG
Bco1	GACATGATGGAAGACCACCA
Bco1	GAAGAGTCCCGTGAAGCACG
Bco1	TAACATGGGCACATCCGTCG
Bco1	GGGCACAGCAAACCTCCTGA
Slc29a1	GCTGATGCAGAAACGAGTTG
Slc29a1	GCATGATTGATCAGTGTCCG
Slc29a1	TACACAGCCCCCATCATGAG
Slc29a1	GGCCAAAATGACAACTGCAC
Inpp5e	GAGGTCCCTACGGATAAACA
Inpp5e	AGTGATCGTCACCAGCCAAG

*Oligo name	Guide sequence
Inpp5e	CACCGAGGCTGACTACACTC
Inpp5e	GGAGATACCTAAGTCCCGAA
Mrps22	CCGATGCTCTGCTCGCGACG
Mrps22	ATTTCTTTAGGCTACTAGAC
Mrps22	AATAAATGACGTATTAGCTG
Mrps22	TGGTATATACTCACCCGATG
Mrps23	TTATATATGTCATACCACAG
Mrps23	GCTTTGCCGTATCGCAAGCG
Mrps23	ACTTCAAGTCTACCTGTCAG
Mrps23	AGCTTTCTGACCAGATCCAT
Htra2	AAACGGATCAGGATTCGTAG
Htra2	GCCTCATAAGTATCCCCGCT
Htra2	GTACAATTTCATCGCAGATG
Htra2	CGGAGGTCAGGAGCTAACAG
Dpys	GTGTGCGTGTCGATGCCCCC
Dpys	GTGGCGATTTGACCACAACA
Dpys	CGAAGGTGGTAGCCGATGCG
Dpys	GAAAGGCAGCTCCCTCATCG
Lpin2	GGATACTCACGTTTCTAATG
Lpin2	GGTTATATATCCGGATCACG
Lpin2	TGCAGGTCACCAAAAGAGAA
Lpin2	AACCTGGATCCGTGTCACTG
Cubn	GTGTATCTGGAACATTCGCG
Cubn	AGTTATCAACTTCACCCACG
Cubn	ACAGCTCCGAATGCTACTGG
Cubn	CCACCTGTGTGAACACTATG
Sdhc	TACTTGTAGATAGTCAAATG
Sdhc	TCTGGAATAGCCTTGAGTGG
Sdhc	TTTGGGAACCACAGCTAAGG
Sdhc	CAGGAAGCAGCAGTGCCGAC
Ethe1	GGGCTCAAGCTGTTGTACGC
Ethe1	AACTCACAAAGCGTCCAAAG
Ethe1	TCCACACCCTCGGATCAGCA
Ethe1	GGGTGACCGGGAGTCAAGAG
Sdhaf2	CTCTATGAGAGCAGAAAGAG
Sdhaf2	CGTTAATCAGGCGATCATAG
Sdhaf2	AATGATGTCACACTAGGCAA
Sdhaf2	GCAGATACTCTTTAGCAAAC
Rmnd1	CGGGTCCGGGATGCTTTCAG
Rmnd1	GAAGTGACAAGCCTGCCTAG
Rmnd1	GAAAGTACAACATGCCACAA
Rmnd1	GGACAATCAAAACTGCACAG
Ndufa9	GGTTAACAACGTATCGACCC
Ndufa9	CCAGGTCACCCATCAGACGA
Ndufa9	GATGCCTGAGCTATTGCTCG
Ndufa9	GTCATACCTCACGGGAAAGG
Apoa5	CAAACTCACACGTAAGGCGA

*Oligo name	Guide sequence
Apoa5	TCACCAAGCGTTCTGCGTAA
Apoa5	GCAGTTGAAACCCTACACGG
Apoa5	AAAAGCTGGGACCCTTGAGA
Cox7b	TTATCTGCTCACCTTGGAGA
Cox7b	GGGAATGCTATATTAGCAGG
Cox7b	AACTAGGTGCCCTCTTCTGG
Cox7b	TAGCATTCCCATATTTGTCA
Acer3	ACAGAACTCAGCGACGAACA
Acer3	ATACAGTTTAACAGTAACTA
Acer3	TCAGGTCATGTATGGAATGT
Acer3	TGAATTGCACCAAAAATTGG
Ndufb9	TGTGGATACACCATGACTCG
Ndufb9	GTAGCACTCATATCTCTCGA
Ndufb9	AGAATGAGAAGGATATGATG
Ndufb9	AGGATACATTGCTTTCTCAG
Msmo1	TAGTATGTTCCACAAATCAG
Msmo1	AAAGTTCCAGATCGCAACCT
Msmo1	GATAAACCAGAAACCTTCGA
Msmo1	ACAGGTACTTAACTTTGGCA
Mrps16	TGCTCACAACAAGTGCCCCA
Mrps16	GCCACCCAAAGCAAGGCGTA
Mrps16	AAAACTAGTTGCCCTCAACC
Mrps16	GGCCGATTTGTGGAGCAGTT
Tmem126a	TTTGGCTATACCCGTCAATG
Tmem126a	AACTAGTGCACCCCGTGTTG
Tmem126a	TAAAACATACCTGTACTCAA
Tmem126a	AACAACTTCCAGAATCAGAC
Cox20	CGCCCCGGAGCCCCACGAGA
Cox20	TAGCGAAATTATACCTACAG
Cox20	AGTATAGATTCTCGAGCACA
Cox20	ATTAGAAGATCATGTGATGT
Cox14	CACAGTGAGGAGCATCATCG
Cox14	GGTAACCCCCATACACAGTG
Cox14	GCGCAGCTGGAGGTAACGGT
Cox14	GCCAAGCAGCTAGCCGATAT
Iscu	TATGAAAACCCTCGGAACGT
Iscu	CCAGCTCCTTAGCCACAGAG
Iscu	TTCATGACGTCACCACATGC
Iscu	GGCCAGGCTCTACCACAAGA
Sar1b	AAGAATTAGAATAGGCACGT
Sar1b	ACTTACTGGGATGTAGCGTT
Sar1b	TCCCGGCATTATCCAATCCA
Sar1b	CAATGCCATTGATAGCAGGA
Tsfm	CAGATACTCACCAATCGCTA
Tsfm	CCATGGCTCACGTTTCACGC
Tsfm	ACTGTCAGAACCTGACGGAT
Tsfm	AGGAGCTCCTTATGAAACTG

*Oligo name	Guide sequence
Cyc1	TAGCTCGAACGATGTAGCTG
Cyc1	GGTGGGAGTGTGCTACACGG
Cyc1	AGCTACCCATGGTCTCATCG
Cyc1	GGTCCCGGCAGCTTCCATTG
Pam16	TCACCTTCTGGACCTCCTCG
Pam16	CCTGGCCCAGATCATTGTGA
Pam16	AGGCAGCCGCTGACGCTCGA
Pam16	CCGTGTATCCACAGCCAGCC
Nmnat1	AAAGGCATTATCTCACCGGT
Nmnat1	GAACAGCCTGAGGTGCATGT
Nmnat1	GTTCTGCCATGATGATTCGG
Nmnat1	GGAGGACATCACGCAAATCG
Ndufb3	GCTGGACATGGACATGAACA
Ndufb3	AACTTCCAGATTACAGACAG
Ndufb3	GACTCATCTTACCGAGCCCA
Ndufb3	CATGGACATGAACATGGACA
Timm50	GACGCCACCAGATATATGGA
Timm50	GGGTCCACACTATCAATGAG
Timm50	ACTGGTCCTGGAGCTTACCG
Timm50	ATTCCTGATGAATTCGACAG
Pgm1	CATTACCGATGGACGCGCTG
Pgm1	ATCATCTCTCCCCACGATCG
Pgm1	TGGGGGTTATATCAGAGAAG
Pgm1	AGGCCAACTGCACAAACTCG
Alg14	TGTCCAATGCCTATTCACCA
Alg14	CCGAATTCCGAGAAGCCGGG
Alg14	AAGAGTCTGAGAGACTCTCG
Alg14	GCTTTATTCGGAGAACCAGT
Taz	TTTGGAGAAGCTTAACCATG
Taz	GGTCATCCATGCAAGACTGG
Taz	AGCAGCTCACCTCGACACAC
Taz	TATGAGCTCATTGAGAACCG
Etfdh	GGTACGGATTCTGATAGTCG
Etfdh	GAGTAGATCACACTGTTGGT
Etfdh	GGCGGGAAGAGGATAGCCTA
Etfdh	GGCAATTACATCGTACGCCT
Pnpla2	GGCAGGAGGCCACGCCAATG
Pnpla2	TGTTCTTGCAAAGCGCTATG
Pnpla2	AGCAGGTGCCAACATTATTG
Pnpla2	CCTGTTTGCACATCTCTCGG
Pmpca	AGAGCTCACACACATCATGG
Pmpca	AGAAATTGAGATGACGAGGA
Pmpca	TGAAACCAAAGTTACCACTC
Pmpca	TCAGTGGCACAGTACACTGG
Acadsb	GAGGATTTGAGGACACGAGG
Acadsb	CATAGCGAAAGAGTCGCTAC
Acadsb	AAGTTGAAGCACAATATGGA

*Oligo name	Guide sequence
Acadsb	TTCAAATGTTAACTGACAGG
Pccb	GGAAATTGAAGAATTCACGC
Pccb	GGAGTCCTTGGCTGGCTACG
Pccb	GCTTGTGCTGCGCGTCGATG
Pccb	TGTGAAGTCTGTTACCAATG
Sdhd	GCAGAGAGGACATACAGTGG
Sdhd	AGGACCAGCCTACCCAAGGA
Sdhd	TGCAGTGGCCAAGGAGCTCG
Sdhd	AGGGATTCAAGTACCCAGCA
Sdha	GTCAGTTACCTCAACCACAG
Sdha	TTCTACTCAATACCCAGTGG
Sdha	TGCACAGTGCAATGACACCA
Sdha	ACTGTGCATTACAACATGGG
Acad8	TGGCTCCCAATATGGCGGAG
Acad8	CCAACAGGATTGGGACCGAG
Acad8	TCTCCATGGTACAGAGCGGT
Acad8	GTGGATGCTTATATAGGCAG
Trit1	GCCACTTGTAGTGATTCTCG
Trit1	TGAGCGCTTGGATAAAAGAG
Trit1	CCATAAACGGCTAAGCCAGG
Trit1	TGTGACCAGCTACACCGTGG
Plin5	AGGGACTTAGACTCACACTG
Plin5	GCAGAGCAAACACCGTACCC
Plin5	GAATGTGGTGAATCGAGTGG
Plin5	ATGGTGGACCTGGCCCAAAG
Uqcrc2	AACAAGCCGATTCTTGACAG
Uqcrc2	ACAGTACAAAGGATTAGCCA
Uqcrc2	CATCTTTCAAGATAACCCGT
Uqcrc2	GCAAAAGCCAAATACCGTGG
Oxct1	GAAGCGTTTATCACTCCGAA
Oxct1	CATTGCCAGCAAGCCACGAG
Oxct1	AGCTGCAGGAACTACCGTGG
Oxct1	TCTAGGGCACACTTGCCGAG
Magt1	TGTGTGTGCGATCGCAGCGG
Magt1	CAGCTGAGCAGATTGCCCGG
Magt1	TTATGCTGGACCCCTAATGT
Magt1	GTGGAGCTTTAACAAGACGA
Gatm	ATCAAAGACTACTTCCATCG
Gatm	ATTCGTTGTAAGAGGAGACA
Gatm	ACTTGAGTGACCAGTCGATG
Gatm	ACAACCATCAGGATGTCTCG
Trak1	GTGGAAGTAATTCTGGACGG
Trak1	TCCGCTCTTAGCTTGTAATG
Trak1	TTAGGCGGCTATCCCTACGC
Trak1	TTACCATGTTTAGTGCGCGG
Mmachc	CAAACCAGCCCCCAAATCGG
Mmachc	CCAAACACTGAGAGACCCGG

*Oligo name	Guide sequence
Mmachc	GAAGTTTATCCCTTCCAGGT
Mmachc	ACTATGAGGTACACCCCAAT
Ndufa6	GCACCTCCCGATACCAAGCG
Ndufa6	ATATCACGGTGAAACAAGGA
Ndufa6	ACTGAAAATGGGCTTCACCG
Ndufa6	ACCTGAACGAGGCCAAGCGG
Rnaseh2b	CTCCTAGGTCAACCAAACTG
Rnaseh2b	TCAGCCCTTGGACCAAGTCG
Rnaseh2b	CAGCCTTTAGGAGATAGTGA
Rnaseh2b	TGGCCAGCTTTACGAACAGG
Lipt2	TACACGGGCGGGCTACGCGG
Lipt2	ACCCGCTTTGGTCCCCGACA
Lipt2	CCGAAGTTCGCACAGTCGCA
Lipt2	CAGACGCCAGTGTAGGGCGG
Pdzk1ip1	CGGCGAAGACGATTGCAACA
Pdzk1ip1	AGAACACAGCGACAGCAATG
Pdzk1ip1	GCACCTGCCAGCTGTCAACA
Pdzk1ip1	CAACCACTTCTGGTGCCAGG
Ndufa13	GGTTCCGCTTGTAGTCGATG
Ndufa13	ACTGACCCGACAGTCCCCGG
Ndufa13	GATTCTCCGGGAAAACCTGG
Ndufa13	GTGGAACCAGGAGCGCAGGT
Ndufb8	GGGGTCCTAGGATATGACCC
Ndufb8	CAAGAAGTATAACATGCGAG
Ndufb8	CATGTACATCAGGAATCGTG
Ndufb8	CAACCGATCACAGCATGAGA
Uqcc2	CCAGTGGACGAGACCAAACG
Uqcc2	TTCAAACTACTACAAGCACA
Uqcc2	GCTCTCGTACATCTGATCAC
Uqcc2	CACAGAGCTTAAGGAAACGC
Ndufa10	TCGATATAGATGACTGCGTG
Ndufa10	CCACTAAACTCTATGTCGAG
Ndufa10	TGGGAAAAACAAGCTCGCAA
Ndufa10	CTGGAGGCAATGTACAACCA
Slc25a19	ACGGACCATGTATAAGACCG
Slc25a19	TCAGCGCACTTTGTGTGCGG
Slc25a19	GACCCCAATGCCAAATACCA
Slc25a19	AGAACTGCAGGCCCGCGTAG
Pigc	TGTACTGACAGACTCCGTCA
Pigc	GAATAAAACATACCCAACCA
Pigc	TCCGGAAAAACATCTATGCC
Pigc	GGCCGACCTGAAGAGTACTC
Far1	CTCTCGAACAGGCCTTCAGA
Far1	ACATAGACAGAATTCACCCT
Far1	CGTCGATCGTCGGCGCCAGT
Far1	TCTCGTTCCTGTAGATGTAG
Dhdds	GGATGTCGGGATGAGGAGAG

*Oligo name	Guide sequence
Dhdds	CTATGCCAAGAAGTGTCAGG
Dhdds	CTTCAAACGTTCCAAGAGTG
Dhdds	GCAGCAGATGCAGATCACCC
Hoga1	GCGGCCACGATAGTAACAAG
Hoga1	ACAGTGTCCCAGCCAATACG
Hoga1	TGGGTATGGCCTGGCGCACG
Hoga1	CTTCCCTCTTACCTCGAAAG
Mtpap	TTTGCCAAATGTGTTCACTG
Mtpap	CAGTTGTCCAGGGACTATTG
Mtpap	TGTTAGCAGTCAGATCACAC
Mtpap	ATGTATCAAAACAGTCCGCT
Pnpla8	GAAGGCGTACAAGCCTTAGT
Pnpla8	AGTAATACAGAGCTTTGGGT
Pnpla8	CTTAGCACTTCTGCTCCCAA
Pnpla8	CATGCCGCTGGATGAATGTG
Slc25a46	GTGAATTTACACCTTTACCG
Slc25a46	TGAGATGGTAATGCCGAGCA
Slc25a46	GCGGAACCCTCGAGCGTCGG
Slc25a46	AATTGGACGAGTGATAGGCT
Abhd5	AGTTTGGATCAGGGCCCTAG
Abhd5	TTGAAGATCTAAGCACCGAT
Abhd5	CGGCAGCCAAGAACCCTCCC
Abhd5	GAGCCTGTGCGCATATCCAA
Abcg8	GCGCCGACGAGTGAGCATTG
Abcg8	GGTTGCTATAGCGAGGACAA
Abcg8	AGTCTGTACTTCACCTACAG
Abcg8	TGTGATCACGTCGAGTAGTG
Agpat2	TGATTAGAGATGATGACACA
Agpat2	GGGTACACGCAACGACAATG
Agpat2	AGCGTGAGCTAATGTTCACA
Agpat2	GCCGCACCGTGGATAACATG
Uqcrb	ATGCCTCATAGTCAGGTCCA
Uqcrb	GCTGCAGGATTCAATAAACT
Uqcrb	TAGTTTCAGCATCAAGCAAG
Uqcrb	AGCCATAAGAAGGCTTCCTG
Cog6	AGTCGTTGGGCATATCACCG
Cog6	TTGTGCAGCTTACGCGACAG
Cog6	CGGACTCGAAGAAATTTACG
Cog6	GGTCAATCACTATACCTCAG
Slc39a8	TCAGCTGCTGTAAGATCGCG
Slc39a8	AGGGGGTTAAAATCAATCCC
Slc39a8	CGTTAGGCTCAGTGACAGCG
Slc39a8	CGGCGCCAACCGGAGCCTGT
Pigm	GTTTGTACGACTTCCTGAGG
Pigm	CCGCGCGCTTCGTCACGGAA
Pigm	CGCGAAGCCATAGAACACCG
Pigm	AGTACGGAGAGAAATTATGG

*Oligo name	Guide sequence
Alg13	GATCTTGTCATTAGCCACGC
Alg13	GTGAATGACTCAGTACGGAA
Alg13	GGTTGTAACCCAGACTCTCG
Alg13	TTTCGACGAGCTCGTCGCAC
Slc25a26	GGCATTCAAGGACTGTACCG
Slc25a26	AACACCCTTACCGTTAGGAA
Slc25a26	CCAGCCTTGTTAAATCCCTG
Slc25a26	ACTTTCAAGGATTCCCACAA
Sdhb	TGCGCCATGAACATCAACGG
Sdhb	ACAGTATCTGCAGTCCATCG
Sdhb	ACCTCGAATGCAGACGTACG
Sdhb	TAGAAGTTACTCAAATCCTG
Dnajc19	AATTTCTTTCAGGCATTCGG
Dnajc19	TTAGCCCTACTGCCAATAAA
Dnajc19	TTTACAAGCCATGAAGCATG
Dnajc19	CCAGCACAGTGGTAGCAGTC
Jagn1	GCACTACCAGATGAGGTACG
Jagn1	GTACCTCATCTGGTAGTGCA
Jagn1	AGTGCATGGCGACGCGCTCC
Jagn1	CCGTCGGTGCCGGCCGCTCG
Dcxr	TATGGTTGGTCAGTGCACGT
Dcxr	GGCGGTGAGTCGGACGCGAG
Dcxr	GCCAAGGGCATGATAGCTCG
Dcxr	CCTAAGCAATGTGGGACCCG
Coa6	CAGCCCCTTCCATGAAGGAA
Coa6	GCGGGACTTACCCACTGCTG
Coa6	CGTCCAGGCAGCGCCAGTAC
Coa6	GCGCTGCCTGGACGACAACG
Coq9	CTCAGGTACACAGACCAGAG
Coq9	GTGCCTTCCACACTGCCGTG
Coq9	GGGGCCAGTGCTCAATGTAG
Coq9	GTTGAGGCGAGCATTGCACT
Npc2	GTCAACATCACCTTTACCAG
Npc2	TAAGGTGGGAGTTATAAAGG
Npc2	CCCCTGCACTTCAAGGACTG
Npc2	GTCAGGCTCAGGAATAGGGA
Atad1	TACGCACATGCATATTAAGA
Atad1	TAGATGCCATTGACCCCACC
Atad1	AAGGCTGTAGCTTTATGGCA
Atad1	CACTTATCAGTCAGTGTCGA
Apopt1	TGAGCGCCCTACGGATCACA
Apopt1	TGTGAAAATGAACGGGACGA
Apopt1	CAGTCTTGCCATGATTGGAT
Apopt1	AGAATGGAATCAACAGTTCT
Gcsh	GCGGCGGCGCTCGGTACACA
Gcsh	AGAGGAAGGTATTGGAACGG
Gcsh	AATTCACAGAGAAACATGAG

*Oligo name	Guide sequence
Gcsh	GGGACAAAATTGAAAAAACA
Rnaseh2c	CGTGAAGAAGCGATCTACCG
Rnaseh2c	CGGCTGACTAGAACGTCGCA
Rnaseh2c	AGGGTTTGCGGGATTCGTGA
Rnaseh2c	ACCGTCTGCATCGTGGCGGA
Pdhb	TCTTAATTGTAGGTTAGCAG
Pdhb	GGGCACAGGCTGAAGGCCAG
Pdhb	TGAAGCTATTAATCAAGGTA
Pdhb	GCCATTCGTGATAATAACCC
Slc25a22	GTGTCTTAGCCAGGTCGATG
Slc25a22	ATACATGCCGAAGTAGCCCT
Slc25a22	TGATTCAGGTTGGCAAACAG
Slc25a22	GACACCAGCTCTCTAAGGAT
Pomgnt1	GCCTTCGTGGGACGAAAAGG
Pomgnt1	CACTCGGAGAGCAATCAGCG
Pomgnt1	GCTGTGTGTTCATACCCCTA
Pomgnt1	GGGCTGAACTCAATAGGCGT
Mto1	TTCGACGTGGTAGTTATCGG
Mto1	AGTGTAACAGATAACCCTTG
Mto1	ATGGACTCTTTAGCGAGTCG
Mto1	ACTTTATAAACAGAACATGC
Stt3b	AGGGTACATATCTCGGTCAG
Stt3b	CGACAGCATGCAGACGACCG
Stt3b	GTCATCTATCTGACATACAC
Stt3b	TACAGCAAGAGAGTCTACAT
Sdhaf1	CGGACCCCGCGGGCGCACGA
Sdhaf1	GCAGCACGTCGGTTCGCGGA
Sdhaf1	GTATCGAGTATCTGTATCGC
Sdhaf1	AGGTACCCATGGCCGTGGCG
Ndufs3	TTGTGGGTCACATCACTCCG
Ndufs3	TACGTGCTGCCACAGCACGG
Ndufs3	CAGCGTTGGGATGACTCCAT
Ndufs3	GGGTGTCAGCTCATCTGCAT
G6pc3	TAGGCCGACTGCCAATAGGA
G6pc3	TTCCCGGGCTAGAGAATATG
G6pc3	GGGGCTCATTAGCCAGCCAA
G6pc3	TAAAGAGAGTCCAATACATG
Lmbrd1	TTACAAACAGCAACGCAACG
Lmbrd1	AAGGCACGTCTATCCCTCGC
Lmbrd1	CATCATCTGTTTCAGGCGTA
Lmbrd1	AACGGTATTCTCAATCTGTA
Slc39a13	ATAAAGAAAGCGAGTCCTGG
Slc39a13	TACACCTGTAACATCACCCC
Slc39a13	CTCACCTTCTGACTGTAACA
Slc39a13	CTGGGGCTATGGGTCATCGC
Gpihbp1	GCAGGTATCAGTACACCACA
Gpihbp1	CACTGTGCAATATTCCACCC

*Oligo name	Guide sequence
Gpihbp1	CTGTCAAGTGCTTCACAGCG
Gpihbp1	CCTGCTTCCAGGGATCATGT
Tmem126b	AAGATGGCACTTTATAAACA
Tmem126b	AAAGAGCTTGTAAGAAACGA
Tmem126b	GCACTAATTGGCATGGCATG
Tmem126b	CCGTCTAGGTGACATAAGCA
Ndufaf4	TAACGTATACATTACCGGCA
Ndufaf4	AATATCACGGACATTCCCAA
Ndufaf4	AAGGAATTCAGACTGCCGAT
Ndufaf4	CGCCTTAAGGAACTTCAACG
Dpm3	AAGTTAACACAGTGGCTTTG
Dpm3	GCGATAGCCCACCGTGCCCA
Dpm3	GGCCACAGGACCTCTCGGCA
Dpm3	ACCAACAGGTAGGCAGGCAG
Mocos	GCTTCAGCGCTATTACATCG
Mocos	GCTGTAAATGCGCACCACAG
Mocos	GGTGTGGAAGCTGACAGTCG
Mocos	CAAACTCACCCACGACACTG
Pmvk	AGCTGGTGAGTGACACACGG
Pmvk	CTACAAGGAGACCTATCGGA
Pmvk	GCTCTCTGGTCCACTCAAGG
Pmvk	TGTCTGTATCACAGCCCCAT
Elac2	TGTGCTGCGCAGGTGAACGG
Elac2	GGGAAGAGTATCACTTACGA
Elac2	CTCAGCGTGCCAACAGTTCG
Elac2	ATGCATTGGTCAAATGTTGG
Nadk2	GCCTTACGGAGGTTCTCTCG
Nadk2	CCTCCGAGAGCTCCGCGTAG
Nadk2	ACTTCATTGAGCGCTCTCAC
Nadk2	GGTGGTAGCCCCGCCGACGG
Elovl5	CTGCCAGGGAACACGCAGCG
Elovl5	AGATGTTGAGCATGGTAGCG
Elovl5	GACCATAGTACGAGTACATG
Elovl5	ATCCTGCAGTTGTATAACCT
Vars2	ATCCCCGGGTCTGATCACGC
Vars2	TCCAGATGACCCGAGATACA
Vars2	CCAACCCACGTCACCTCTCG
Vars2	TGCAGATGGGCAGTACCATG
Pink1	CATGGTGGCTTCATACACAG
Pink1	GTCGGACTTGAGATCCCGAT
Pink1	CGAGGAACAGTGTGCGACCG
Pink1	CCAGCCCAGCTACCGACTGG
Phkg2	AATGTGCATCTCTCGCCGTG
Phkg2	CGGTAGCTCGATGGACACAG
Phkg2	CATGAAGCTAGAAGACTCGT
Phkg2	GTAGCATCAGGATTTGGCGC
Isca1	CTTGCTCACAGCCCGCACGG

*Oligo name	Guide sequence
Isca1	GAGGTGACTCACCAGTGTGA
Isca1	AAAGTTGGCGTGCGAACCAG
Isca1	CAACAGTTACTTACATGCTC
Pycr2	GGTGCCCGTGGCATACACGG
Pycr2	GATGTGCCTCTCCTGCACGT
Pycr2	CGTGGGCAGGTCCATATCCG
Pycr2	GATGCTATCACCGGGCTCAG
Gmppa	GGAGCCAGATCAAGTCTGCA
Gmppa	TGGAAGGTTAAACTCCTGCT
Gmppa	AGGACACAATCCCTCAACTA
Gmppa	ATCAGTGACATCATCAACTG
Mrpl44	AAACTGGGATTACCATGCGG
Mrpl44	TAGACTCTCAGTGCCTTCGG
Mrpl44	TTCTTCACTCCCCGAACCGG
Mrpl44	TGAGGCAGTTGTCTGTCACG
Ndufaf5	GCGACACACTCTATGAACTC
Ndufaf5	TCAGGTAGTCAAATTTCATG
Ndufaf5	ATCGAGCGGCAGTCGCAGGG
Ndufaf5	TCAGCTAAAATATTCACAGT
Hfe2	GGCTCACCGGACACGCCGCG
Hfe2	GTTGGCTCCCGACGAAACCG
Hfe2	CTATGCCATGCACCGCAGAG
Hfe2	ACAAACTCGAGCCCCCAGGT
Afg3l2	AAAAGCGATAATGAGTACGG
Afg3l2	GTTCGTGTGACCTTTACACC
Afg3l2	GCCTGCCAGGATGACCACAT
Afg3l2	GTGAAGTTTAAAGATGTGGC
Mtfmt	GTGTACGAGTGGCCCGACGT
Mtfmt	GTGCCTTCGCTATCCCCCAA
Mtfmt	ACCGTGTGGATTATCGGAGC
Mtfmt	GTCAAAACTTGGTGCCAACA
Pitrm1	TTGGGTGATAATGAGTAGCG
Pitrm1	ATATAATGGCTATACACGGG
Pitrm1	AGGGAATTCCATATAACATG
Pitrm1	GGTGAATTCTCTCTCCCCGG
Ccdc115	AGCTGACGCCCAGACCCCCG
Ccdc115	ACAGCTGCTCAGTGACCTGG
Ccdc115	CTAACTCTTTGGTCTTGGTG
Ccdc115	GACCTGAGGCTCCATACGCG
Slc52a3	GTGACCTCCTGGATACAGGG
Slc52a3	TGTCTCCGTGACATTGACAC
Slc52a3	GCTGGTGACTGAGTTGCCCG
Slc52a3	GGGTCGGAAGCGGTGCATCA
Ndufaf1	AGACGGCCGCCCATTACAAG
Ndufaf1	GAACAGGCCACACCTACCCG
Ndufaf1	TCTGTATCTCCGAGTTCGTG
Ndufaf1	ACTTCTGATAAGACAATTGG

*Oligo name	Guide sequence
Cad	CGCAGGGGTACCCGACCGTG
Cad	AGGATTAGAACCTTTCGTGG
Cad	ATGGTGAGTGCCCACCACAA
Cad	CTCAGAAACTCTGTTACGGG
Rnaseh2a	TGTCACACGATACAGCTGCG
Rnaseh2a	GTAACAGATGGCGTAGACCA
Rnaseh2a	AGACCTTGACAGAGAACGAG
Rnaseh2a	GGCTCCTTGAGACACACAGC
Ndufa11	CAACCCCGCAGATTCCACCC
Ndufa11	TCTTACCATGAGGTCCCCGA
Ndufa11	GGCCGGTACACATTCACTGC
Ndufa11	AGCGGAGCCGATTATGCCTG
Coa7	GTTGAATCCTGTCACAACGT
Coa7	CTACCAATGCTACCGCGAGA
Coa7	AACTGTGAGAAATACGGGCA
Coa7	AGGATGGCCAGCCTGACCTG
Slc25a32	CGGATCTTCACGAGGTCGAG
Slc25a32	GGTTCTCGTACCGGACGTGG
Slc25a32	GGAGTAACCCCGAATGTGTG
Slc25a32	AGGTGTGCGTGGATTATACA
Agk	ATATTGCAGACGGATTATGA
Agk	CTCTGAAAGATCCCCACCGG
Agk	GAAATACCCTTTGCAAGCTG
Agk	AGTACTGAGAAGAACAGATG
Fars2	CACACACATCAGCGCATCAG
Fars2	ACCTTAAACAAGTACTGACT
Fars2	TGGAGGAAGCTGGTCATAGA
Fars2	ACTTGGTAAATCCTACCCTC
Trnt1	CATGAATTAAGAATAGCAGG
Trnt1	ATTCGCATGATCAACAACAA
Trnt1	AACCTGTTCTCACCTATGTG
Trnt1	GGCAGAATTGTCGACAGACC
Sdr9c7	CACCGCCGAATATAGCCACA
Sdr9c7	AGGTCAGCATCATTGAGCCA
Sdr9c7	CCGACTTGGTGACATCTAGG
Sdr9c7	GCCAAACAACTGGTTGATAG
Yars2	CCACGAGCGCGATCACGTTG
Yars2	TCCCCCCAGACGGTGTACTG
Yars2	CTGGGCGGATCAGATCAGTT
Yars2	AGAACTCCTTGAACAAGCCG
Taco1	GCGATGCCTCGGGTTCCGCG
Taco1	GCTGACTCGATGGTTGACTT
Taco1	ATTGAGGCGTTATCAAACAG
Taco1	CCACTTATTGTGTCCCGCCG
Pigw	TGTGGCTGTCAGCATAACTG
Pigw	ACAGTCAGAGTGATCACTAG
Pigw	TGTTGTATCAGATATACCAC

*Oligo name	Guide sequence
Pigw	GTTCCAGTGAATGCCGTACT
Gtpbp3	GTGGAGTTTCACGTACACGG
Gtpbp3	CCACAACATTTGCCCCCGAG
Gtpbp3	GTCAATGTAGGCCTCCACAT
Gtpbp3	AGTCTCCAGCACGTCACGGG
Cox10	TCTGTCCCGGAAGCCAAATG
Cox10	GGGAGTGAATCCACTCACAG
Cox10	TATACAGGGATTGCCACACA
Cox10	AGTTGGCAGCACAGGATGCG
Tmem70	CGGGATCGCTTTCTGGCGTG
Tmem70	GAAGGTACGGCAAGAATGCA
Tmem70	GCTGATTTATACTGGAAACC
Tmem70	GTAAGAAGGTGAAGCAGCGT
Mipep	TCCACGTTTGTATTCAACCT
Mipep	GATTGCCACTTCACCATCCG
Mipep	TGGGACCCTCCCTACTACAG
Mipep	CTGGGGCTTGACGTTGAAGG
Atp6ap2	TTAGCATATTAAGATCGCCA
Atp6ap2	TGAACTTGGGAAGCGTTATG
Atp6ap2	CCGGTGGAATAGGTTACCCA
Atp6ap2	TGGACAGTGCAGCTACGTCT
Wars2	GAGCTGGGTGAACTTACAGG
Wars2	CACACACGTTCCTGTCGGGG
Wars2	CAGAAGCATGATGGGACCGT
Wars2	TGGTGTAAATGCTGCAATCG
Kynu	GCGGATGGTAAAGCCACGAG
Kynu	CAAACGCCCTTGGATTGTAG
Kynu	TCTTTAAGCCTACTCCAAAG
Kynu	CAACACCCCAGTCATGTAAG
Slc29a3	AATGATGGCCATGCACGCGA
Slc29a3	GGGAAACTGCGCAGAACCCG
Slc29a3	CAAGGAAGACTGCTGCCATG
Slc29a3	ACCAGAAAACACTCGAACTG
Pdss2	ATGATATTGGAATCTCGACC
Pdss2	TGCGTGTCAGAACTACGACA
Pdss2	CGGCATAACCTACAACTGCG
Pdss2	AGCTCTTCTACAGAACACCA
Pex1	TTGGTCCCAAGGAAATACGT
Pex1	TATTACCAAAGGAAGCATCG
Pex1	GCAGCTTCATACGAACTCAG
Pex1	AGTGTTGTGAAGAATAAACT
Cyp2u1	GCTCCTTAAATGGACCAAAG
Cyp2u1	CAGGCGCAGCAGCTTCGACG
Cyp2u1	GAAATGACGAAGCGTCGAGT
Cyp2u1	AAGTGTTCAGTGACCGCCCG
Fuca1	ACTGCCGAGCTGGTTCGATG
Fuca1	GTTCGGCCCACTGATCCGGG

*Oligo name	Guide sequence
Fuca1	CCAACTCACCGACCAAATCA
Fuca1	GTGATAGTGAATGACCGGTG
Pnpt1	AATGTGTCGTTAACCCAACA
Pnpt1	ACCAACGGCATGAATTGGGA
Pnpt1	GAAGAGATCTGACTTCACTT
Pnpt1	TTGCCATGCTATCAAAGTTG
Ubiad1	GGCTTCCCGAACGATCCTGG
Ubiad1	CCAAATCGAACAACATCCTG
Ubiad1	CCAGCGGGCCGAAAGTGATG
Ubiad1	TCAGAGCGGACAGGTAGTAG
Tmprss6	GGTTCGATGCCTACGCACTG
Tmprss6	GGAAAGCAATAGACTCCCGT
Tmprss6	AAGACCTCATGATCAAAGTG
Tmprss6	CCTTGATCCCGTCACACGCA
Tars2	CTTTAAGCTTCATCTGATCG
Tars2	AAGAGTCTATAATGCCCTGG
Tars2	CTACTGCTACAGTGTAACAC
Tars2	TCCCCAAAGTAGAGTTACTG
Coq2	ACCAGTCTGGAAAACAACCT
Coq2	ATGCGCCTGGACAAGCCCAT
Coq2	AGGGCCAATGGGAGCCCGCG
Coq2	CTGTCCCCCAAGGAAGACGA
Cars2	TTAGATTTGACATTATCCGG
Cars2	TCAGATCATTGCTTTCATCG
Cars2	GCACATCGAGTGCTCTACCA
Cars2	ACAGCAGCGACTTCGCCCTG
Sars2	CCGGTCCTATTACCTGCGTG
Sars2	CTGTACGAACACGCACGAGA
Sars2	TCGCTTCGAAGACCTTAACC
Sars2	ACGGTCCCAGACCTTCTGAG
Trmu	AGGGGTATTTATGAAGAACT
Trmu	GTGATGGAGGCTATTCTCCG
Trmu	GCTTATTGCAGTTGATGTCG
Trmu	ATTCCAATACTCCTTCACAT
Slc39a4	GGTCCTGAATACGGATAGTG
Slc39a4	CAGTTGGGGAAGATCTACAC
Slc39a4	CATGCAGCGTGATATTGGGA
Slc39a4	TGGAGAGGGTCACACCCATG
Mccc1	GTTATGATCAAAGCAGTCCG
Mccc1	AACAGGAGGAAGTATTACCA
Mccc1	CAGGAAGAAATCCCTCTGCA
Mccc1	GCAGTACCTCAGCTTCGACA
Ddhd2	AGAAAATGAGCAGATCGGAA
Ddhd2	TATTGTATTACACAACCCAA
Ddhd2	GTCCACAATAGTCTGACAGT
Ddhd2	TACCACAGTGAATATCAACA
Pex13	AGATGAGATAAGGACCGCCA

*Oligo name	Guide sequence
Pex13	TGGGAGGAAGATCATCTACA
Pex13	GGCCTGGGAAGAATAGGCGG
Pex13	AGCCCTGAAACTGTTATAGA
Chst14	GAAACACCAAGTCACTGCGG
Chst14	CGGACCTTGAGGGCCGTGTG
Chst14	GCTGATGTTCGCTGTAATCG
Chst14	TGTTACGGTAAGCAGACAGG
Cep89	AACTGTCTGCCCAGTCAACG
Cep89	TGAGATGTTAGGCTACGGGG
Cep89	ACACTCTGTTCTGAATCTAG
Cep89	GTTTCACTTACCAACCAGGG
Mfsd8	AGCAATGTATGATCGGACAA
Mfsd8	TGGACCGAGAATAAAGCCCA
Mfsd8	GGATATGTACGCCTGGACCC
Mfsd8	GAGCATCGTGTGGATGACTT
Lrpprc	AGCTGATAGACTACTGTCGG
Lrpprc	GAATAGCCGAAGCATCTAAG
Lrpprc	CCGAACTGAGTCTCGCCGAG
Lrpprc	GAAAGACCTTCCGATCACAG
B3gat3	GGACTCGCGGTGTCTCAGTG
B3gat3	TCTACACTGGCTGCTAGTGG
B3gat3	AATGACATAGATAGTAGGCA
B3gat3	ACGGAGATCAGCTTGCAACT
Ttc19	CAGGTCATAAGTGTACGTGA
Ttc19	TCTGCATTTCAACTCTAGAG
Ttc19	AAGAGTCTAAGCACATACCA
Ttc19	GCAACGATGAGTTATCTGCT
Ndufv2	ATTCAATACCTTGTTCATAG
Ndufv2	AAGGTGTAGTAGTGCAGACC
Ndufv2	TAGTAAAAAACTACCCAGAA
Ndufv2	CTCTTACCCACTGAGCAGCG
Phykpl	AGACTAGCTCGACAGTACAC
Phykpl	CCAGAAGGAATGGGTCCATG
Phykpl	AGTACCTGTACGATGAGCAA
Phykpl	CGTGTTGAAGTATTCTACAC
Appl1	CCGACTGTACCTATTAATTG
Appl1	AACTTAATGAGTCAAGCCCG
Appl1	GCCTGCATGTATCCCAGTAG
Appl1	AATTGTATCAAGCTATGCAT
Glrx5	GCACGGTGTTCGCGACTATG
Glrx5	GCGTTGCTGAAGCCGCACTG
Glrx5	AGGTGGTGGTGTTCCTCAAG
Glrx5	GGAGTAGTCTTTAATACCTG
Pmpcb	GAAATATAACTAACCTCCGG
Pmpcb	GGACCGACTAAGAAGCACAC
Pmpcb	GAGACAGATCGTGTCTGGAT
Pmpcb	CTTCCAGTGAACTTGCAGGG

*Oligo name	Guide sequence
Slc25a42	GCTGGGTGTCATTCCCTATG
Slc25a42	AGGAATCACTCGCACCATGG
Slc25a42	GTACGTGAGGGAAGCCGCAG
Slc25a42	CTTCATCCGAATCTCGAGAG
Mcee	TGGAACTGCTTCATCCACTG
Mcee	TTCAAGAATCCAGTCCTGTG
Mcee	AACATCCCTGTAAAATGACG
Mcee	TGCAACTGAAGTTTGGACTC
Dnm1l	AATCGTGTTACAATACTCTG
Dnm1l	GCACAAATAAAGCAGGACGG
Dnm1l	GATGCCATGGATGTATTGAT
Dnm1l	GTGACCACACCAGTTCCTCT
Plce1	CAGGTATTCATCGCGCAGCG
Plce1	GTGACTCCTCGGATCCATGG
Plce1	CACCGGCCATCAGCTCAAGG
Plce1	GTGCAGTAATCTATTGTCCG
Abcb6	CTCCAGAGGTCACATAACGC
Abcb6	TGAAGTAGACCGCTATCGAG
Abcb6	GTGCAGCAGTTTACGTCCCG
Abcb6	TAGGTGCCAAACCAGTTGAG
Dmgdh	TTAGCCGGACTGTATAACCC
Dmgdh	AGGATCCTTCCAGGTCGCGG
Dmgdh	TGGGATGTGGAGACTCCACA
Dmgdh	ACAGCATCAAACTTTACGAG
Lonp1	TCATTCGCAACTTGTCTCCG
Lonp1	GGCAGCGACGAGACCTCCGA
Lonp1	GCGCTTTATCAAGATCGTGG
Lonp1	CAAGGCGATGATATCCCGAA
Opa1	GCGCCTGCGAGAGCTCGACA
Opa1	AGGTTGTACTGTTAGCCCCG
Opa1	AGAGCGTGTCATCATCTCGC
Opa1	AAGTGACAAGCATTACAGGA
Ehhadh	TTCATATGGATGCTTCACGG
Ehhadh	CCACATCATGAGGTTACTAG
Ehhadh	GTAAACCCATAGAACCCCGC
Ehhadh	TCACTATGGCTCTAACCGTA
Acbd5	AGTGTATGAAACCAGATTTG
Acbd5	CCAGGCCGTGAAAGTTTACA
Acbd5	GGAGCAATTTGGACAAGAAG
Acbd5	AAAGCTACCTTTATAGCCAT
Gbe1	GGCTATGAACCACATCTAGG
Gbe1	AATCCCCCCTGATACCTCAT
Gbe1	AGACTCGATAACAATAGCAG
Gbe1	GAACTATGATTGGATACACT
Gale	ATCTTCACCGATGCGCCCAG
Gale	AGAACTTGGACTTGCCGTAG
Gale	TTAACTCTATAGTAGTCCAG

*Oligo name	Guide sequence
Gale	CTGGGGGTTCCCGTACACGG
Isca2	CTTGTCCCTAACTGCCGAGG
Isca2	TCATTCCTAGGCGCTCGGGA
Isca2	GTCCTCCTTGCCTGTCGTCG
Isca2	CTCAGGCTGCAAGTAGAGGG
Slc6a19	ATCGGTCAGAGGCTACGCAA
Slc6a19	ACAGTCATCAAAGCGCTCAG
Slc6a19	AGCTGAGCAACCCCAACACG
Slc6a19	TCCGTGGCATCGAGACCACT
Pank2	GTCCGCAGACTCGCCGACCG
Pank2	GGATCCGTAAGCCACATTGG
Pank2	AAAGCAGGCATGTCATGGGT
Pank2	CGAGTAGCGCGGCGCCGTCG
Mgme1	AAAGTGGAGAAACTCACAGG
Mgme1	GGAGAAGAGCACCCCCAGTG
Mgme1	CTAAACGAGAGTACTTCGCT
Mgme1	CAAACAGTTCCATAAAGCCT
Pck2	TGCGTATTATGACCCGCCTG
Pck2	TGATTGTAACTCCTTCGCAG
Pck2	AGGGTTTGGATGCTACGGCA
Pck2	ATGGAAGCACATACATAATG
Shpk	CATGGTTTGAAATCCCAAAG
Shpk	GACCAGAATGCCGCTAGCTG
Shpk	GCAGGCTGTGAATGGATGGA
Shpk	GTAAGGGAAGAAGGCAACTG
Pomk	CCCATTCTGAAGTAGCCCGG
Pomk	GAGTGAGCACGTGGTCACGC
Pomk	CACATGACCCTCGTGCCCAG
Pomk	CGCCACGTTCATAAGGGCCA
Dhcr24	ACCTGACCCATAGACACCAA
Dhcr24	GTAAGACCTTCATGTGCACG
Dhcr24	AGATGCTGCGCGTGTGTCGG
Dhcr24	GTCTGCCAGGATCAGCTCGT
Atp13a2	CGTCATCACAGGTACGACCG
Atp13a2	CCAGCTACATGACACCCCGG
Atp13a2	GGGACCCCGTGTGCTAGCAG
Atp13a2	TGTGGTAGTGACATGGCCAG
Ppa2	TGGTTGTGGAAATACCTCGG
Ppa2	CCGAACATCTTCCCTCACAA
Ppa2	TACAGGGACATGACGCGGCG
Ppa2	TAAGAGCACCGACTGCTGTG
Ndufs7	AAGCGGTCCATGTCATAGCG
Ndufs7	CATCAGAGTGTAGCCACTGA
Ndufs7	TGGCACGCTTACCAACAAGA
Ndufs7	CCCGGCGTGCCCAGTTGATG
Secisbp2	AGTACGACTACAGCCAAGCA
Secisbp2	CTGTACAAATGGATAGTAGG

*Oligo name	Guide sequence
Secisbp2	ACCGTCAGGACTTCATAACT
Secisbp2	TGCCGAACAATATAACCCAT
Oplah	TGGTGCGGATTGTTCCTCGG
Oplah	TGACTGTCATCACACCGGTG
Oplah	CTGTGCTTCGTGAACCACAT
Oplah	GCTCCAAAGTCACCAGCACG
Lyrm7	TCTTAACAGATGATGAAACT
Lyrm7	AATGATAAGAGAGCATTGGA
Lyrm7	AGCTCTTTAAAACACTGCAC
Lyrm7	GATGAAACTAGGTTCTGATG
Ndufaf2	CAGGAGACATCCCAACCGAG
Ndufaf2	ATTCTTACCTCCATAGTGGG
Ndufaf2	ACGTGGGCACGGACCATCTG
Ndufaf2	TTGGAGCGCCTTGTCCAGGG
Gns	CCAAAGTGTTGTTAACGACG
Gns	TGCTGGGAAGTATTTAAACG
Gns	TCAGACAACGGCTACCACAC
Gns	CAGAGGAACCTACCGTCCCG
Fastkd2	ATGTGAATGCGCTTCGAGCA
Fastkd2	TGAAAGAGGTATCTAACAGA
Fastkd2	TAGCATTAAGGCTGAACAAG
Fastkd2	ATAAGCTTGTCCATCAAACC
Mff	GGATAAGCGACAAAATGCCA
Mff	GCAAGTCCCAGAGAGGATCG
Mff	AGGTATTAGTCAGCGAATGA
Mff	TGTTCGCCAAAATGGACAGT
Ispd	CGGCGGCCACGGTTCCAGGG
Ispd	TAAGCGCATCTCACTAGCTG
Ispd	TGGTCACTTAGACCACTCAC
Ispd	TCTTAGCAGCTAAGGAACAT
Cant1	GGAGTGGGATAAAGACCACG
Cant1	CAGCACCCACAAAGGACGTG
Cant1	CCATCAGAAAGGATCACCCA
Cant1	GGAGTGGACCACCACGACAG
Coa5	CCGGTATTATGAGGACAAGC
Coa5	ATCCGCTACCTGGAGCACAC
Coa5	GCGGGCGTGAAGGAGGATCT
Coa5	GCCGGAGGGCGGCGCGTGTG
Abhd12	TGACTCAGTAGGAACACCAT
Abhd12	GATAATCCTGTGTATATTTG
Abhd12	GCCGCACAGCGCATCCGACG
Abhd12	GCAGGTATAGTATGATGGCA
Grhpr	TGGAGCCCATTATGGATGTG
Grhpr	TCCAGAGATTTCTTTACACG
Grhpr	CTTTGGATGAAATCAAGAAG
Grhpr	AAGAAACTTCTGGATGCCGC
Cog2	GACGGTGTGCCAACAAAGGT

*Oligo name	Guide sequence
Cog2	TGCCACCATTGATAAGACAC
Cog2	TCTTCTCGTAACTGTCCCAA
Cog2	GTGATGCCAGCTATACGCTG
Trmt5	AGAGGAAAATATGCTGACCA
Trmt5	CAGCAGTAAGCATCCTGTAG
Trmt5	ATTCCTCGAACGTCAGAGGG
Trmt5	TTTCCTAAGTCTCGGCACCA
Lmf1	GATCTGCCCTACGTTGACCA
Lmf1	CTTCAGAATCATGCTTGGAG
Lmf1	GGTGGCATTCAATCAGAACA
Lmf1	CCTATGCACCAACCATTATG
Cln6	CCTGCACGAACGCGACACCG
Cln6	CTGACATAGACTATAGACCG
Cln6	TGGATCGGGAATACCAGCTG
Cln6	ATAGTAGTACAACAGCTCAA
Qrsl1	ACGTCCATTGAATTCACCAG
Qrsl1	ATCAGGGTGCCCTACTCATG
Qrsl1	TTACGCAAAGCAGGTGAACG
Qrsl1	GCTGTGTATAGGAATCCCAA
Mfsd2a	TCAGGGACGGAAAGTTCACA
Mfsd2a	GCAGCCGGTCAACTGGTACG
Mfsd2a	GAGGGACTTACTGTATGCCG
Mfsd2a	TCTCTACTTACCAGGGCATG
Alpi	AAACTAAGGTATTACCCATG
Alpi	AAGGCCAACTACAAGACCAT
Alpi	AGCCGGCACCTACGCACACA
Alpi	ACAGTAACCAGTCTGGAACC
Slc10a7	CCGTCGGTCGGAGTGAACGG
Slc10a7	GTTGAAGAATATCGTTGCGA
Slc10a7	GAAGAAGCCACCATTTGGTG
Slc10a7	AACTGCCTTGGTTAAAATCA
Nubpl	CCCAAAGCTCGGCACCCCCG
Nubpl	GTGGAGACAATCACAGCACC
Nubpl	TCAGCTGGACTATTTAGTTG
Nubpl	ACACCTTACAATACCTGCGG
Timmdc1	ATCCGGATTCCAGGGAACCG
Timmdc1	GGAAATTGACTATATCTACA
Timmdc1	ATACCGGATGAAGCCCCTTG
Timmdc1	CACCGGCAGCAAAGACTCGG
Ndufaf6	AATTATGCTGAGAATACGCA
Ndufaf6	ACACGTTCCCACGCATCCCG
Ndufaf6	AACATAACCTAACTAAAAGG
Ndufaf6	GCAGTTCTGGAAAAAAGCTG
Mrap	GAGAAAGAGGAGCACCACGA
Mrap	GTCCATGAACATATTGGCTG
Mrap	CAACCACAGGGCGATGACAA
Mrap	GGTGAGCGGGACAGAGGCGT

*Oligo name	Guide sequence
Mtmr2	TGCTCGGCCAAGTGTCAATG
Mtmr2	GCCTTCTGTACTCTAGAAGG
Mtmr2	GTGGCATCCTTTAGGTCACG
Mtmr2	GTAATGATTCTCTCATAACA
Agl	ACTGGTCTACCGGTACGGAG
Agl	AGAAATGGCCTTATCCGCAG
Agl	TGGTCATCACTTAAGTACGC
Agl	AACAGACTGGTGGATGCTCG
Vps33a	GCAAGAGGTTATCAAACACG
Vps33a	TAATTGCTGAGAATGTACTC
Vps33a	ACACAACGCTAAGACAGTCG
Vps33a	GCCTGTACCACGCAGCCAAG
Mboat7	TGATCAGAGAATGCAAACTG
Mboat7	ATAGCAGTCGATGTTACGGA
Mboat7	AGCTATAGCTACTGTTACGT
Mboat7	GCCTGGATTGCGGCCGAGTG
Mmab	CAGTGCATGCTACAGGACGT
Mmab	ATCAAGTATTTGAAGCCGTG
Mmab	GAAGCTCTTCGGCAAACATG
Mmab	TGTCCCCGTTTCCAGAGCCG
Rdh12	GGAAAGGTTGACCACCCGTG
Rdh12	CAATTTCCGCACTAGCACCT
Rdh12	TGCTAGGAAGCGTTCAGCAA
Rdh12	CCCAAAGATACTTACCCAGG
Sbf1	ATTGTGCCCTCATCTAGCCG
Sbf1	AGAGCAGGGCTACACTACAG
Sbf1	ATTGTTGCTGATCTTGACGG
Sbf1	TGTGTCGTGACAGGAGACTG
Mccc2	TTACCAGTTATATGGCGACG
Mccc2	GAGGAGCTTTGATGTCCGAG
Mccc2	TGACTGTGAAAAAGCACGTG
Mccc2	GGTGGTCGTCCAAAGCATAG
Cpt1c	CCACTCGGACAGGAGTATGT
Cpt1c	TCATACTGGGCGGAACACAA
Cpt1c	CATTTGCCAGCGCTGTAGCG
Cpt1c	TGGGAGAGTGAGTCCCTACA
Bola3	GCGAATGTTTGCCTCTCAGA
Bola3	GCTGCGCACAGTGCCACAGA
Bola3	CCCGCGCAGCAGAGGCGCAG
Bola3	GTATGAAATTAAAATCGAAT
Ak7	TCTCCCTTAGGACGACAACG
Ak7	GGAGGCGATTGTCGCACCCA
Ak7	CTCCAAACACGGGTAGTGCG
Ak7	GGAGAACTTTAACATCCGCT
Slc25a12	ACCCGGATGCAAAACCAGCG
Slc25a12	ATAGCACTTTAGCAGGCACG
Slc25a12	CTCTTGATAGGAGATCAACC

*Oligo name	Guide sequence
Slc25a12	TCACTGGAAGTCTTACCCTG
Pigt	GATCCGAATCCCAACGCGTG
Pigt	AAACAAGTCATAGACGGCAT
Pigt	GGTAACTGGTGTGGAACAAG
Pigt	TGAGAGTCCGGGAGAACATG
Mrps34	TGGGTACCAAACGCCAATCG
Mrps34	AGTCGGGCCTCACACGCGTG
Mrps34	GCGGCTCTCGCGACGCACGT
Mrps34	ACGCTGACCCGGCCGCACTC
Lrat	GAAATCAGCTCTTTCGTCCG
Lrat	TCCTAGTCAATCACCTAGAC
Lrat	CAAGGTGGCTAGCATCCGTG
Lrat	TCTAATGCCTGACATCCTGT
Lias	AGGTTGCCTTACCATGATCG
Lias	GCAGTCACCTCTGTAACTCG
Lias	ATAAACTGAAAAATACATTG
Lias	GGATTATGTTGTCCTGACGT
Slc19a3	CTGTCGGAGTATCACACTGG
Slc19a3	TGCCAATTCAAAGAATCTAG
Slc19a3	ACCAGAGGGACCAGTAAACA
Slc19a3	ACAACGTGTAGCATGATGAC
Ctns	AGGCATCATTACTGTCGACG
Ctns	TGGAGGGCCATGACACACGC
Ctns	TAACAGGTTATAGTGCCTCG
Ctns	CCCAAGGGTGATGTCGACGT
Elovl4	TTCATGGGATCATACAACGC
Elovl4	ACACCGTGGAGTTCTATCGC
Elovl4	TGCAGTGGTGGTACACGTGA
Elovl4	CGATACAAAATACCACCACA
Hamp	CACCTGTTGATGGAGATAGG
Hamp	AGATACCAATGCAGAAGAGA
Hamp	AGAGCTGCAGCCTTTGCACG
Hamp	AGAAAGCAGGGCAGACATTG
Cox4i2	GGGCGTAGCAGTCAACGTAG
Cox4i2	CCAGCGCTCCTATCCCATGC
Cox4i2	GGACAGGACTCAGAACTAGA
Cox4i2	CTTCTGCACAGAGCTCAGCG
Kars	CTCATCTTCTATGACCTGCG
Kars	GGAGCGTTGTGAAAGGAGCA
Kars	TGTATGTGATGATCTTAGAG
Kars	TGTGGCTATTGACTACCTTG
Acox2	TAGGCCGAAGACGAGACTGG
Acox2	GATGAGCAGATTGCTAAATG
Acox2	CTTGAGTGACCAGTGTCGGT
Acox2	ATGCCAAGATAATTGCTCTG
Echs1	AGTCGGCAAATCGCTAGCAA
Echs1	GACAGCCAGAAATCCTCCTG

*Oligo name	Guide sequence
Echs1	GATGACCGGTTTCTTGACCC
Echs1	GTGCATTGAGTGCTTTGGGG
Amn	GCAGACGTTCTCGCGCGACG
Amn	ACAGACGCAGCCCGACGCGT
Amn	CCAGAACCGGACCCCGTGCG
Amn	GCGCGATGGATCTTTCCGCG
Mrpl3	GGAGACCAGTTGCTTAACAA
Mrpl3	TGTGTTAAAATACACTCCCA
Mrpl3	CCCACCTTCTCTCTAAGCCG
Mrpl3	GAAAACCTTTACCAATACTG
Mcoln1	GACATAGGCATACCGGCCCA
Mcoln1	TTTGACAATAAAGCGCACAG
Mcoln1	ATACCTTTGACATTGATCCA
Mcoln1	TGGCCCGGAACTTGTCACAT
Nans	TATGTGACGTTCCAACACCT
Nans	TATACTTCGAAGCATTCATG
Nans	TCGTGCCCGGAATACCCGAT
Nans	GAGATCACCATAGGACGACC
Cnnm2	ACCGTCGTGGTAAATCCAGG
Cnnm2	CGGCGATTGAGAATGATGTG
Cnnm2	TGCTAACCGGATAAGAAGCG
Cnnm2	CTGCTTCATGATAACCGGCG
Srd5a2	CCCAGCAGCACATTCCCCGG
Srd5a2	ACAGACATGCGGTTTAGCGT
Srd5a2	CATCCCTACCGACACCACAA
Srd5a2	GGTATTCCGCGCAATAAACC
Sfxn4	TTAAGCCAAAAGTTATTCGG
Sfxn4	AGCACATGAGACATACCACT
Sfxn4	TGCAGTCAGGAACTCACCAT
Sfxn4	CCATCGAGGAATTGAGGTGA
Hadha	ACACTTTGTGCTTTACACCG
Hadha	TATTAATTATGGCGTCAAAG
Hadha	TTAAAGACACCACAGTGACG
Hadha	AAGGACAATTGAATACCTAG
Cog8	CTACAAGACGTTCATTCGCG
Cog8	ACACACGTGTCCATAAGCTG
Cog8	TGGCGTGAGAAGCCCGACGT
Cog8	AGGTGGCTACCTGGATAACG
B3galnt2	TAGTGGCTAAATTTCCAGTG
B3galnt2	ACACCTTCCATGAATTCATG
B3galnt2	ACCCACCGTTGACTTAATGT
B3galnt2	GGAACAGTTCATCTTACCAG
Kmo	GCTGTCGAAATGCATTCCGG
Kmo	GATGTGTACGAAGCTAGGGA
Kmo	GACAATTCCACCTAAGAATG
Kmo	TTGCCCAAAAAATGGGACAA
D2hgdh	GGCTCACAGAGCATACTCCG

*Oligo name	Guide sequence
D2hgdh	AGGCCTGGGTGGGCACACAA
D2hgdh	GGATACTGAATGCATGCAGT
D2hgdh	GACTGGCTGAAGACCGTCCG
Lbr	TTCAAGTGACCACTCCACAG
Lbr	GCGCCCTGGATTGATTGGAT
Lbr	GAAGTAAGTACCAACACAAG
Lbr	GAGCTTGAACGAAAAACCAG
Pomt1	TGTGAACAGAGAGTCCAACC
Pomt1	ATAGTCGGGTAAGTAGTCCC
Pomt1	GGGGCACTCACGTGTTAAGG
Pomt1	GTCCACGCGTGGAATCTGAT
Dpyd	CTATAACCTTCCGTGGCGAG
Dpyd	GAGGCACAGCTTATACTCGC
Dpyd	TTTGTCCAGGGCCATACAAG
Dpyd	AGAGCTAAGAGTCATTTCAT
Ldlrap1	GCTCCACCAGCGTCATACCA
Ldlrap1	TCGGTCAGGATGATCCCCCG
Ldlrap1	TGCAGACAAGATGCACGACA
Ldlrap1	CAGAGAACTGGACGGACACG
Pcsk9	GCTGCCAGGAACCTACATTG
Pcsk9	TGGAGCGAATTATCCCAGCA
Pcsk9	AGGACCAGCCAGTTACCTTG
Pcsk9	CATGCTTCATGTCACAGAGT
H6pd	TAGGCGTAGTAATCAGACAG
H6pd	CTTGAAGGAGACCATAGATG
H6pd	AGTTCCACGCCCATACCCAG
H6pd	ATGTCTGCGTAGGCAAAGGG
Psph	TTCGTACATTTCAGACACTG
Psph	CTTATGCCAGGAGTCAGATG
Psph	CCTGGACATTACGCTCCTGG
Psph	CAGCCTATTGGCAAACACAT
Acacb	AGAACAACGATATCGACACG
Acacb	CCAGTGTGCCGACCACATGG
Acacb	GTGGCCGTACATGTCGATGG
Acacb	TTCATTACGGAACATCTCGT
Eogt	GTCGACATAGCTGCAAACGG
Eogt	GAGGCTGGAGTAGTCATACA
Eogt	ACATCAAGAGAAACCACGAC
Eogt	AACAGCCCGTACCGCATGCG
Hsd3b7	CCTTCACCATAAATGCCCGT
Hsd3b7	TGCTTGGATGCACATACTGG
Hsd3b7	ATCCACAAAGTCAACGTGCA
Hsd3b7	ATGTGGTCATCCATACAGCT
Phkb	TCGGCCATAAAGTGTATGAG
Phkb	AAGCGGTTTCCAAGTAACTG
Phkb	CCGTGTTATAGATTATCTGG
Phkb	AACGCAGGGTAACTGATGCA

*Oligo name	Guide sequence
Cog4	GGAAACTCACCAACCCATCG
Cog4	GCTGTGTACGAACGACTCTG
Cog4	GCACAAGTAACGATGAATGT
Cog4	CAACAGAAAAAATTGAACCA
Lars2	GGTTAGCCATGATAACGATG
Lars2	TCTTAATGAACCACTGTCGG
Lars2	CAAATGCATCCCACCCCATG
Lars2	CATCTATGGCATCTCCCACG
Alg9	ATGAGCGGATGGCATACACG
Alg9	ATACAAAACAATGTTGAGAG
Alg9	TCCCGTCATGGCGATCAGCG
Alg9	TCAAGTGTCTGCTCTCAGCG
Slc6a8	GGAAGCGCCACACGTTACCG
Slc6a8	GCATCAGTGTGACAGCCCGT
Slc6a8	GCACAACGAGGACCACGTAG
Slc6a8	ACTCGATGACAGGGGACCGG
Upb1	TCTCGTGTACAAAAAGCGAA
Upb1	CTGTACATGAGCCAGTTGAG
Upb1	GTAGAGAATTCGCTTCACCT
Upb1	ACTGAAGGGATATGCCTTCG
Fig4	CTTGGTGGTAATCGACGACA
Fig4	AAATCCGAACAGAGTCATTG
Fig4	GAAGGATTAATTACACAGGG
Fig4	CACAGGTGGAATGAACTAGG
Pnpo	AATGCGCAAGAGTTACCGCG
Pnpo	ACTAACTACGAGAGCCGGAA
Pnpo	GGTAGCCACACACATAGCAT
Pnpo	CTGAACAGCCTCGTCAAACC
Pex12	TTTCATCAAACCACCGCCAG
Pex12	TTATGGCTTAAAGCGGATTG
Pex12	GGAACATGGCAGATTTCCAG
Pex12	GGCCATGTTAACAAAAGGGT
Plin1	ACAGCCCTGCCCAACCCGAG
Plin1	GTCATGGCTCTCATCCTGAG
Plin1	ATACCTGACTCCTTGTCTGG
Plin1	GGTGTGTCGAGAAAGAGTGT
Gck	TTCTGGGGTGGAACGCACGT
Gck	AAGGCACGAAGACATAGACA
Gck	CCATCCGGTCGTACTCCAGG
Gck	CCAGATGTATTCCATCCCCG
Synj1	TATGTCAATCAAGGCAACGA
Synj1	GGGACAAGGTTCAATGTCCG
Synj1	TAAAATATATGCAGGCACCG
Synj1	GAAGAGCATCCGAATTGCAA
Cyp27a1	CTACACGGATGCCTTAAACG
Cyp27a1	AGACCAAGTATGGTCCAATG
Cyp27a1	GAGGACGCGTCCATTTGGGA

*Oligo name	Guide sequence
Cyp27a1	GGTCCTTCCACTGATCCATG
Ndufb11	TGTAATCGCCCCATCCGGTG
Ndufb11	GGACGAAAACGTCTACGCGA
Ndufb11	TATTCCAGACGTCCACCACA
Ndufb11	GTCGCTGCCTGTCAGCAGCG
Gldc	CCACTGAAATCCATTTCGTG
Gldc	TTTACTCAACTACCAGACCA
Gldc	CTTGATCCAGGGATGCCACA
Gldc	AGGCCACAAACAGCTACCAG
Slc6a5	GGGATGGTCACCGATAACAC
Slc6a5	GTGTACGCATCACTGGCGAA
Slc6a5	GCTTACCGGTATGGTAGTGG
Slc6a5	GAGGACGCGAACGTGAGTGT
Aldh6a1	TAGATGTGTCTGCCCACGCA
Aldh6a1	TAAGTTACTTACCACTGATG
Aldh6a1	TTCAACAGCCATCCTCGTAG
Aldh6a1	AATGTTCAGTGTTCCGTCAG
Tecpr2	AGCAGACATCCTGACCCATG
Tecpr2	GTGGCAAAGTCACCATCAAG
Tecpr2	TCTCGCCTGAGAAACACCTG
Tecpr2	AGCAGATTGGATCCCAACCA
Nhlrc1	GCACGACGTGAAGTACCCAC
Nhlrc1	ACTGTGCCCCAAGACCGGAC
Nhlrc1	GGAGATCACCCCTCACAATG
Nhlrc1	TCCCTGAAGGGGTCCTTCGG
Tecr	TACGTCCAGTCGGCATACGG
Tecr	ACTCTACTTCCGGGACCTCG
Tecr	TGTCTGGACCCACTTACTAG
Tecr	ACTTTGAAGATGTTTCGCAA
Ppcs	ATAGAAATCTGACACTGCCG
Ppcs	ATGCAGATAATCCGCCAAAG
Ppcs	AACTTCAGTAGCGGGCGACG
Ppcs	GTTCTTGTACCGAGCGCGCT
Uqcc3	AGATGCCGGAAAGGGACTCG
Uqcc3	GGACGAAGCAGTCAGGACCA
Uqcc3	GGTGGCTCGTAAAGCACTTG
Uqcc3	GCAGTTGCAGTGCTAGGCGG
Psat1	TGGAAGGAGTGCTGACTACG
Psat1	TGCAAACGAGACTGTGCACG
Psat1	CAATACAGAGAATCTTGTGA
Psat1	CTTTGTAGTCAAGGACTGAT
Acaca	GCCATTCATTATCACTACGT
Acaca	AATGCATGCGATCTATCCGT
Acaca	TTGATTCATAGGTACCGAAG
Acaca	AAGCCCTTCGAACATACACC
Haao	TGGGTGCTAACTGCGTGCCA
Haao	AGAGGTTTGCCAACACCATG

*Oligo name	Guide sequence
Haao	GCAAACCGGAGGCTGAAAGG
Haao	CGGGACGTGCCTATACGGCA
Cth	TGCATGGATGAAGTGTATGG
Cth	GCAATGGAATTCTCGTGCCG
Cth	TTCCAAAACCAAATTGCTAG
Cth	TTTGTGGACAATTTGTGCGC
Mthfs	TTGCTCTGGAATTGGTACCG
Mthfs	CTTCTCGCACCTTCTGCGTG
Mthfs	GATGAGGTCAAGTCCACCTG
Mthfs	ATCTTGCATGCTTAGAAAGA
Grm6	ATTCTCATTGAACATCACTG
Grm6	GGAGTCAGGAGGCACCACTC
Grm6	CCGGTGTGCGACTAGGCGCG
Grm6	GTGGTCAGGCGACCCCCATG
Prkag2	GGGACGAGGAAGCATAGATG
Prkag2	AAGAACATAAGATTGAAACG
Prkag2	CCACTGAAGCTCATCCGGCG
Prkag2	GCGTTTATATGCGATTCATG
Atic	AGACGACTGTCACTCGAGCG
Atic	GAGATGTGTCTGAGCTAACA
Atic	AATTGCTTCATCGTATTGAG
Atic	TTCTTTCAAGCACGTCAGCC
Ogt	TTTGAGCCCAAATCATGCGG
Ogt	AGCATTATCGACATGCCTTG
Ogt	ACAGTGCACCACTAGTCCCA
Ogt	GAAAGTTTGTACCATCATCC
Mthfd1	ACACCAACGATAGATTCCTG
Mthfd1	CACTATGAATCCGTGCACAG
Mthfd1	GATTGCCGGAAGGCACGCGG
Mthfd1	GGTAGCGTCCAGTAAGAAAG
Zdhhc15	TGGAACTTAGAGCGAACACT
Zdhhc15	GAATCAAAAGGGCATACCAT
Zdhhc15	GTGTACACAAGAACCGGGAG
Zdhhc15	AGACTGTTGTAGCAATGTAC
Atad3a	AAGCAGGAGGCCATACGGCG
Atad3a	TTACCTGATAGACTCCAAGA
Atad3a	TGCCACATCAACTCACACTG
Atad3a	GCTGTCGAGCGAGCTTATCC
B4gat1	CCGGGATTAATTATGCACTA
B4gat1	GTAGACGCGATAATCGCCGC
B4gat1	TTTACCTGGTCTACGGATCG
B4gat1	CGAGGGGCACACGAGGTGCA
Rars2	AAACCTGGTGGCATAGAGAG
Rars2	TGTCACCCATTTCTAGTCGG
Rars2	TCAGCTTAAGTGTGATACAG
Rars2	ATTATCTTGATAGGTCTGCT
Slc30a9	AAGGACTCGGTGTCATCGTG

*Oligo name	Guide sequence
Slc30a9	ACTGAGACCGCTCTGGAACG
Slc30a9	ATTATCTGATACTTGTAACC
Slc30a9	CTACGAATGTCCAGAAAGGA
Mmadhc	TCTGTGAGGCAGTCCCATTG
Mmadhc	GTGTGGCCTGATGAAACTAT
Mmadhc	TCACTAAAGAACAAAATCCT
Mmadhc	TATGTAAATGAGTTTCAGGT
Mmaa	CGACCTACTCGAAATGTGAG
Mmaa	AGGACAGAGAGCTTGCCTAG
Mmaa	TCAGGCCCTCTCCTACCAGT
Mmaa	ACTTGAGTGAAGGAGCCATG
Trip11	TACTGATCATAAACGAACCA
Trip11	TTATTGAGTCAAGAAAAGGT
Trip11	ATCCTGTGAGTAGGACGCGG
Trip11	GAAGGAGAACCATGAACTGA
Acy1	AATCTGACCAAGCTTGAAGG
Acy1	TGTATCCTCAATGAAGCGTG
Acy1	GACAGGTACCACATCTGTGT
Acy1	AAAGACAGTAAAGGCATCCG
Cyb5a	GTCCAAAACATACATCATCG
Cyb5a	TCTGACCAAGTTTCTCGAAG
Cyb5a	CTTATGATGCAGGATCACCC
Cyb5a	GTCCTAAGAGAGCAAGCTGG
Ampd2	CACTGCCTACGACTTAAGTG
Ampd2	CAAATGCAAGGAGATCGCTG
Ampd2	TCATAAGTTCGAGTCTCCAG
Ampd2	ATATTGTAGAAGTCCCGGTG
Cyb5r3	GTCATCATCGCTCGACACAG
Cyb5r3	ACTTCACCGTCCTGACAACG
Cyb5r3	GGAGACACCATTGAATTCCG
Cyb5r3	AGGTCATCAGTCCTGACACT
Blvra	TCTGAAACAGACGAGAACTT
Blvra	TAAGAGAAAGCTCCCCAAAG
Blvra	ATGCCATGGGGTATTCCACG
Blvra	TATAGGCGACATCAACCTCT
Pgm3	TACGGCCTCACATAACCCTG
Pgm3	AACTTCTTCAAGGTACCGCG
Pgm3	TACACCATGTAGTGCAACTG
Pgm3	CTGCTATGACATACCCTGTG
Asl	CTCGTGTCAGCGCAACAGCG
Asl	TGGTTCCAATGAGCACCCGG
Asl	AGATGCAGCAGATACTGCAA
Asl	GCTGCAGGGAAGCTACACAC
Gusb	GTATCTTGGGTCCATCGCCG
Gusb	TGTTCGAATCCCGATAGGAA
Gusb	GGAGCGCGCACCTCCCGTAG
Gusb	GGTGTCAGTCTTGTAGACGA

*Oligo name	Guide sequence
Phka2	GGGTCATAATGCAATCGGTG
Phka2	ACAGTAGACCGAGTTCCACT
Phka2	CACAGAAAGTATGTCCCGAG
Phka2	CAAACAAATTGGTATCCCAG
Pygl	AAACCAACGGGATTACCCCG
Pygl	GGGCGAAGTAGTAGTCGCGG
Pygl	CTTACAAAATGCCTGCGATG
Pygl	AGGAGGCAAACGGATCAACA
Cyp11b1	TTGCTATCCCATCCACCAAG
Cyp11b1	ATAGTCCATAGAGAACTCCG
Cyp11b1	CAAAGAAAGTCATTACCAAG
Cyp11b1	GGCTCAGATCACGGCCAATG
Mpi	TGGATGGGGACACACCCCCG
Mpi	CGAAACATCCGATATCACCT
Mpi	AGGGTGTGCCTGGATAGACA
Mpi	CAGGTAGGCATGGGGTACGT
Manba	GTCTGGTTCCCATGTCCACG
Manba	AACCAACGGGATGAAAACCA
Manba	GTTCACGTCTTTGACTACGT
Manba	TTGAAGTAGAAACTCAGACC
Fdps	AGATACACTGAAAAGAGGTG
Fdps	CCAACTCACCATGTACATGG
Fdps	ACAGATCTGCTGGTATCAGA
Fdps	TTGCCCGGCTCAAGGAGGTG
Cox6b1	AAGGCAATGACGGCCAAGGG
Cox6b1	AACTGTTGGCAGAACTACCT
Cox6b1	AGAACCAGACTAAGAACTGT
Cox6b1	ACGCCGGTACCACTCACACA
Qdpr	TGTCATCTTAACAACCACGC
Qdpr	CTTACCAGGAGTCCCATCCA
Qdpr	GGTGGATGCAATTCTCTGTG
Qdpr	CACGCAGTGTTACCCAGTTG
Pigh	CTTGTCCATCTCTATGAAGG
Pigh	GGTCAATCTTCACAAAATGG
Pigh	TGATGAAGATGGTGGCAGAG
Pigh	TGAGTAGTAGCGGCACCGCA
Acat1	GTCCCATACGTAATGAGCAG
Acat1	AGTGCTATAAGAACTCCCAT
Acat1	AGGCAAGCAACACTGGGCGC
Acat1	GCCTCTCAAAGTCTTATGTG
Acat2	CAAACCTGATGCGTTCGCTG
Acat2	CTGAGAACAGGAGTCAGGAT
Acat2	TCCTACTCGACAAGCCAGTG
Acat2	TGCCTTTCACAACTACCACA
Aldh7a1	GGGCTCCGCGAGGATAACGA
Aldh7a1	TGGTGGAGCAGATATCGGGT
Aldh7a1	ACACTAACGAGGGACGTAGT

*Oligo name	Guide sequence
Aldh7a1	TAGATTCCTGCCCCAAAACG
Nr3c2	GATGATTGGGCTCTTAACGA
Nr3c2	CAAGGAACTTTCAGCCACGG
Nr3c2	TCCACTAATGCATTGACAGG
Nr3c2	GAATGGAAATGGGTTGACTG
Pcca	CTGGACAATTATGTGATCCG
Pcca	CCTGGATTTCTATATGACGA
Pcca	GTAAACCGAAAGACTTGTAG
Pcca	TTAGGTTCACGTGAAAATGG
Etfb	CATCCACGTGGAGATACCAG
Etfb	CCTGAGAGGCGAATGTACCC
Etfb	AAAGCCGGACAAGTCTGGAG
Etfb	CATGGCCAGAGCAGTTCGGA
Etfa	TGGCGTAGCAAAGGTTCTGG
Etfa	TTTGTGAGAACTATCTATGC
Etfa	GGTAGTGCTAGTTCAGAAAA
Etfa	AGTTACACACACATCTGTGC
Hlcs	CAGCAATGTGAGAAGACACG
Hlcs	ACAGTACCATTGACTCGGTG
Hlcs	ATGGCCTATCTTTCTCAGGG
Hlcs	CGGCGGCCTTGCAATCACCT
Cldn16	GGCCACGATCAAAAACCCAG
Cldn16	GAACGCTGATGACTCCCTGG
Cldn16	AGTACCTGCAATGAGTAATG
Cldn16	TATATTGTGTAAAACGAGAG
Slc13a3	AGTTTCTTGCCAGTTCGGAA
Slc13a3	TCCAGAGCCAGCCCACCAGT
Slc13a3	GGCTAAAGCGGTGATCCAGG
Slc13a3	CCACCGTACCTTGGGCGGCA
Ddhd1	TCGTTGCGCTACTACAGCGA
Ddhd1	TCAAAGCTTACTCTTGATGG
Ddhd1	GATAAAATACCAGTAATGCG
Ddhd1	ATAAGTGATTACACACCCCA
Slc19a2	GGAGTAGTAGGCGATTTCGG
Slc19a2	GACTCAGCCTGATTGTGACG
Slc19a2	CAAGTGGTGAACTACGCGCA
Slc19a2	GCAGGAACCAGCACTCGCGA
Slc2a9	CGGAGAGGTTGTACCCGTAG
Slc2a9	GCATGCCATCAGCAACGCTG
Slc2a9	CCAACTATGTGGACTCAATG
Slc2a9	TCTCAACGAGATCTCACCCA
B3galt6	GCGCGCCAGGTACAACAGAG
B3galt6	CCTGGTGGACCTACGCGCAC
B3galt6	GTTCTCGTAGGCGTCGCGCA
B3galt6	TGGCGGACCCGAGGACGTGT
Mrps2	CTTGCGGTAGGCCACGTGCG
Mrps2	CCTGTGCCAACTACCTATGG

*Oligo name	Guide sequence
Mrps2	CACACCCGCTACTTCAAGGG
Mrps2	GCGTATCTAGGATCCTGCTC
Pofut1	TGTTGGTATTCAATCCATGG
Pofut1	GCGCCTCCTACAAAGAACAA
Pofut1	CCGGAGGCCTTACCCATGCA
Pofut1	AGCTCCAGAAGTACATGGTG
Slc2a10	CAGCCCCGTGGCGACCAAGG
Slc2a10	AGAGGCGTAATACAGCACAT
Slc2a10	TGTGCTGGTGTCCCTCTACG
Slc2a10	AGCCAACAGATAAACGGCCC
Bbox1	GTGGTGAGATCATAAAACTT
Bbox1	TACACAGAATGTCAGTACTG
Bbox1	GTTGAAGCTCACCTTACCCC
Bbox1	CAAGATTGATGCCAACAATG
Idh3b	TTCACCCTTATACTCCATTG
Idh3b	TCGGCACAACAATCTAGACC
Idh3b	ACAGGCACAAGATGTGAGGG
Idh3b	TAAGGAGCATCATCTGAGCG
Rtn4ip1	ATATTTATCTATCACCCAAG
Rtn4ip1	TGAGGTCATTGATTACACGT
Rtn4ip1	GCAGGTAATGAAAGCATGGG
Rtn4ip1	GAGAGCCACATATGGCAAAG
Mfn2	CCGAGGCAGACGCATCCCAG
Mfn2	GTGGTATGACCAATCCCAGA
Mfn2	ATAAACCTTGAGGACAACTG
Mfn2	AGAACTGGACCCGGTTACCA
Sugct	AAGATCTCCTAAATTCATCG
Sugct	GGTGATGACACACGATCTTG
Sugct	AGGAGTGAGAATCGTCAAAG
Sugct	AATCTAAGGATACCTACCTC
Mvd	CCCGCCGAGCCACTTCGGAG
Mvd	CATCTGGCTGAATGGTCGCG
Mvd	CCACGTGCACCTTATAGCTG
Mvd	TGTTGTGCCTGAGCGCATGA
Sardh	CCTTGACTACGACTACTACG
Sardh	CGTCGTCACTGAGCGCATCG
Sardh	AACCGAGTAGTTCTTGGCAT
Sardh	CGGTGACTGGCATCCGTGTG
Klf11	CAGTGTGATCCGTCACACCG
Klf11	AGCTCACGGAGCCGTCAACA
Klf11	ACCAGCATCACAGTTCCCTG
Klf11	CCTTGCTTGCACAAGTCCGG
Tmem199	TAGCCAATGAGGAGTATAAG
Tmem199	CGGAATGAAACCAGGCGCCG
Tmem199	TTTCTGTTACATACCCGGGG
Tmem199	TGCTCTGGGAAAGAAACACG
Alg11	GGAAACCAGCAAATGCCCTG

*Oligo name	Guide sequence
Alg11	TTTCCTGGACTGATGATATG
Alg11	AGTGAACATAGCTTCCGACT
Alg11	TAAACCATATCCTCTCACTG
Alg1	GTGAAGTTGACAGATCTGCG
Alg1	TCTGGAAAGGAGAGTACGTG
Alg1	TGTGACCAATGCTATGCGGG
Alg1	TGAGAGGGATTGTCAGAGCG
Alg3	AAGAAGGAATAGCAATCCCG
Alg3	GGAAAAGAAACTGACGACCA
Alg3	GCCACCAGCAATGTGTAGCG
Alg3	ATTGATGAAACCCTCCACCT
Slc25a38	TCCAGGGACACATCTCACAA
Slc25a38	CTGAGAAGGGGGCATCACGG
Slc25a38	AGAGGAAAGCCTTAATCACT
Slc25a38	AGTGATCAAGACACGCTATG
Akr1d1	TTGTCTGGGTGAAATACGGG
Akr1d1	TGAAGACAGCTATTGATGAG
Akr1d1	AACAAATCTGTGTGCCACGT
Akr1d1	GGGCTGGGAGGACCATTGAT
Zdhhc9	TGGAAATTCTTAATACGAGG
Zdhhc9	GTGCTCGAGGAATCACTCCA
Zdhhc9	AGAAGAGTGTACATGTCCCC
Zdhhc9	AAGAGCATAGCGGCAAACAC
Pycr1	CCGGGGTGTTAGTCATACAT
Pycr1	TTGGGGCGAACATTGAGGAC
Pycr1	CACAGGTACTCACGCTCAGG
Pycr1	GGAGGGCCGAGACCGTAGCT
Dhtkd1	CTGATGTTCCGTAAAATGCG
Dhtkd1	GCCACGGTGAAGAGATACGG
Dhtkd1	TCTTCTTTAGGAAAGCTCGT
Dhtkd1	GATGGGGACTACTCCCCGAA
Mtrr	GATGAAGCGGTTGTAATCAG
Mtrr	GGTGAGCAAAATAGTCCGTG
Mtrr	GAACAAAATGAGACAAACAG
Mtrr	CTCGACCGTACTCATGTGCA
Sepsecs	GAGGACGTCTAAGGACGGCG
Sepsecs	TAAGCGTTGTTGACTACATG
Sepsecs	CAGGACTTCTGGTCTATCCG
Sepsecs	CACCGGATCGTCCAATTCCG
Cln5	GACAAAATTCGAACAGTCGT
Cln5	CCAGCGTTGCCCAGACGTCG
Cln5	GCCCCTTGGTTACACCAGAA
Cln5	ATATTTAAATTCCCAAATCG
Suox	AGGGGGACATGCTATCTTCG
Suox	TCCTCTTTAGAGTACATCCG
Suox	AAACTTATGCAAATCATCCA
Suox	CAGTCCTTCAAAACAGACAT

*Oligo name	Guide sequence
Pde12	AGCTGTCGGAGAACACCGCG
Pde12	AGCTTGGATCGAGACCGGTG
Pde12	TCTTGGTGTACAGATGTCGA
Pde12	AAGAACCGAGCCCACTCGAG
Zfyve26	GAAGTCCTCACCTATCGCCG
Zfyve26	CCTTCCCGAGGACTATGCCG
Zfyve26	CTGAATCCTGATGGTATGCG
Zfyve26	GGCCCTGGACATACTAACTG
Aldh4a1	GTTCAACGCAAAGTTCGCCG
Aldh4a1	CGCTCGGCATTCGAGTACGG
Aldh4a1	CAACTGGTACTGTATATCGG
Aldh4a1	ACCTTTATGACAGGGCAACG
Mars2	ACTCGCAGACCATCTACGTG
Mars2	GAGTGGACATAGATGCGATG
Mars2	TCGATCGCACAGCTCGATCG
Mars2	TGTCCCGTGTCTCTCGAGAG
Dse	GTCAAAGTATAAGCATGACC
Dse	CAGCACACAGAACATTGCCA
Dse	AGTTTCATACATATAGCCCG
Dse	TAATGAACGGCACACCATTG
Kctd7	CGGTACTTCATCGATCGAGA
Kctd7	CCGCAGAGTAGACAAGCGCG
Kctd7	GTAATGCCGCCCGCTGAACA
Kctd7	GAGAACATGCAGCCACTGAA
Slc39a14	GAGCGAGCGATCTCAGATCG
Slc39a14	GTAGAGGGTTCCAATCGCCA
Slc39a14	TAAAATGGTTATGCCCGTGA
Slc39a14	GTGACCGAGAAGCTACAGAA
Slc18a2	CGAGCCATACGTACCTACGA
Slc18a2	CCATCTGCTTTGCAAACATG
Slc18a2	GTACATACCTAAGACCCCCA
Slc18a2	ATGCAGAATCCAGCAAACAT
Gnptg	GGCCTACCTAACAAAGAGTG
Gnptg	CTGTGGAAAGATCAACCGAC
Gnptg	TTACCCAAGGATCCCGCTGT
Gnptg	ACAATACCTTCAAGGGCATG
Aldh5a1	CCTCTGCCAAAGATAAGCGA
Aldh5a1	ACTGTCAAAGACAATGAATG
Aldh5a1	ACACCAATGGATCGGTACAC
Aldh5a1	AGACACACCCTATTCCGCCC
Spg11	TCCCCGGAAACACAACGCGT
Spg11	ATTCCCGGGGATGTCCCACG
Spg11	TCATTCCGCTCAACGACTGG
Spg11	AGAGCTACAAATCCCGTGCA
Pomgnt2	AAAGCCGTATTGGTACCAGG
Pomgnt2	TCAACCACGGTAGCCCCGCG
Pomgnt2	GTGGCTCTGCTACTCCAATG

*Oligo name	**Guide sequence**
Pomgnt2	AGACGTGCATGAGGTTATCG
Micu1	ATGGGATCTCCACTAGACCG
Micu1	TTCTTGCTGTTAACGCATGG
Micu1	TTGAAAGTAATCAACGAACC
Micu1	CCGAACATAAGCCAGACTTG
Iba57	CAGACTCCCAGAGTGTACGG
Iba57	GAAGATCACAGACTCCCTCG
Iba57	ACGGGCTAGGCAGTGACTCG
Iba57	ACCCCCGGACTGCACGTATG
Ptrh2	CTCAAAGAGTGGGAGTACTG
Ptrh2	ACTGACCTTAAAATGGGGAA
Ptrh2	CCCCCAGAACTCAACAAGTG
Ptrh2	GTTGCTTGTGGCATGTGCCT
Xylt2	GTATACAGATGACCCCCTCG
Xylt2	GTGCCACTGACTATCCAACG
Xylt2	TGTAGGCGATGCGTACTGGA
Xylt2	GGACGTCGCTGAGTCCGCCA
Nags	GGATGAACTAAGGCACAACG
Nags	CAGCTACGGTGGCATCGTCG
Nags	GACAGCCAGAAGGTGCCGTG
Nags	GCTAGCGGCTGTAATGACTG
Mgat2	GAAGTTCAACTGGTACACCA
Mgat2	TGTAATGGCCGAAGGAGTCA
Mgat2	AAAAGTCTGGGGCTAAGTAG
Mgat2	CTGGACGCGGAGCCCGTACG
L2hgdh	CGGACGCCGGTCCACTTGCG
L2hgdh	AACAGCGGTGTCATACACAG
L2hgdh	GCTATTGATTGTCCATACAC
L2hgdh	GACCGTATTTCAGAGTTGAG
Coq6	AGACACCGTGTACGACGTGG
Coq6	GGCCTTGATAATGTTCGACA
Coq6	CTAGGGTAATATGGACCCAA
Coq6	GTGTGATGTGGACCAGACCA
Pomt2	TGGACAGATCCAGTACGGTG
Pomt2	GTAGTCCTTATGCAAATAGG
Pomt2	CCTGCACAGTCACTATCATG
Pomt2	TCTTTATCATCGTGCAAGTG
B4galt7	CACTACAAGACCTATGTGGG
B4galt7	CTACATCGCCATGCACGATG
B4galt7	GGAAGATGGAGCATTTCCGG
B4galt7	TCGGGCAGCACTCATCAATG
Alg12	GTACCAAAGAAGACTGACGG
Alg12	AAGCGAGAGCACATAAACCA
Alg12	TGTAGGGACATATAACCAGG
Alg12	CTGAACAAAAGTTCCAACTG
Poglut1	ATGATATCATGTATCCTGCG
Poglut1	ATTTCTTGACCAAATTAACA

*Oligo name	Guide sequence
Poglut1	GGACCCCAGAGGATACCTGG
Poglut1	GAGGACCTGACTCCTTTCCG
Aars2	AGGACGCCATAACGACCTGG
Aars2	CTACACTCTTCACCCCAACG
Aars2	GATAGACACAGCGTACCGAG
Aars2	GAGGCTACCTTGTCCGTACA
Pex6	TGTAACTCTCGAGCAAACGG
Pex6	AGGAAATGCCGTCTGCACAT
Pex6	GCACGGGGAGGGTCTCCCCG
Pex6	AGCACACAGCTCATTTACCA
Ndufs8	ATGTGGACAGAACTCATCCG
Ndufs8	TCAGTGGGCCCTTCTCAAAG
Ndufs8	AAGCCTTCATAGCAGCGCAG
Ndufs8	CCGAGCTGCATTGTCAGTTG
Trpm6	AGAGTGCATACAGTTTAGCG
Trpm6	TGTCAACAGTTATGGCCGAG
Trpm6	AGGTCATGATGTAGCGATAG
Trpm6	TATTCTATAGCTCGAGAGAA
Cox15	AGAAAGGGTTGGCTCAACCG
Cox15	AGGCGGTACTGACTGACCCG
Cox15	GGTACATGGAATACTCACAC
Cox15	TAGGGTGGCGTCCAGAACAC
Lct	TGAGTTGTTCGATAGCTATG
Lct	TCAGCCTATCAAATCGAAGG
Lct	CTCCCGTGGATACGCCCCAG
Lct	CTTAAACTTGTACATCAACG
Dars2	GTTGCTCGGACCAACACATG
Dars2	TCTTCTAAGAAAATGCCGAC
Dars2	TAGACAGCCAGAGTTCACTC
Dars2	AAAGCAATATGTGTTCATGA
Ndufs2	GCGGCGTATATCCGACCTGG
Ndufs2	TAGCACTCACCATTCCAAGG
Ndufs2	CCTCGGGCACAGTGGATCCG
Ndufs2	CACATCGGGCTCCTGCACCG
Slc30a10	CCATGACAACAGTCAAACTG
Slc30a10	AGCCGTGATGACCACAACCA
Slc30a10	GCACAGCAGTGACTCTCCGG
Slc30a10	TGCTGCAGATGGTCCCCAAG
Hhat	CTGAGCCACGCAGAACGCGA
Hhat	GCACAGACCCTGGATTGTCA
Hhat	GACGGGATAATAGAAGACGT
Hhat	AGAGGGCATGCATGTACATG
Hibch	AGTCCATGGTCAATTCCGAG
Hibch	CAGATGTTGCAGAATAACGC
Hibch	CCTGCAACATCCTCAGCTGA
Hibch	CTATTGCAGACCTTTAGCTG
Ndufs1	AATGGATCTCTGATAAAACC

*Oligo name	Guide sequence
Ndufs1	TGTCCTATTTGTGACCAGGG
Ndufs1	TAGAGGTTAGGGCCCCTACA
Ndufs1	TGATGGTCAGTCTGTCATGG
Cps1	TGAGCCTCACAATTTCGTCG
Cps1	ATGCAGACCGAATCATCACA
Cps1	TACAGTATTCCATGGAAGTG
Cps1	GTTGGTGGCATCTCGTGTCG
Man1b1	GAGCACCATTCGCATCTTAG
Man1b1	GGTTACCAAAAGTTTGCTTG
Man1b1	GTGGACTTCAGACAGCACGG
Man1b1	ATGTTCATCAACACGAACAG
Coq4	TCATCGTCCACAAAGCGTGT
Coq4	GCGTACGGGGCCGAAGACTG
Coq4	CCAGGAAGCGAAGATACTCA
Coq4	CTCTACAACCCCTATCGCCA
Dolk	GGACCGATACTCCTGGTGCG
Dolk	CAGTGTAGGCGAGGTGATCG
Dolk	AAAGTATTTCCACTTCATTG
Dolk	CCAGCAAAGACCAATAGGCA
Agps	GTACCAATGAGTGCAAAGCG
Agps	GTAAAACCAAGCCACTAAGT
Agps	TCAGAGAAGGGATGTTTGAG
Agps	TCCCTGGAATTCAGCACCGT
Slc35c1	AGGGCACCCCTACGTACTTG
Slc35c1	AGGTTAGGCGCCAGATACTG
Slc35c1	CTCACCAATGATGACGCCGC
Slc35c1	GCAGTGAGGTCACCAGGCAT
Acad9	TCTGCCCAAACTGTCGTCTG
Acad9	ATTTCCCGACTGCTCTATCG
Acad9	GGACTCTCGAAAAATTGACC
Acad9	GAGCATACATCGTGTTGGAG
Gatb	GTTCATTTGATTATAAGCTG
Gatb	GTGACCTCAGGTCGTCATGG
Gatb	CTTCCCTAGATAGATACAGT
Gatb	AATATATCTGTACATCACCC
Msto1	CTGTTCTGTACAAGACGTCG
Msto1	GGACAGACTACACTTCTATG
Msto1	GGGCGGGGAGTCCTAACCTG
Msto1	AGCCCCCATACCCATCATGG
Ampd1	AATGACAAATACAATCCCGT
Ampd1	CAAAGCACGACTCACCCCCG
Ampd1	CGAGATCTCCCCCTTCGACG
Ampd1	ATGGATGTGAGTATCCACCT
Slc25a24	ATGAGAAAAAATCAGGACAG
Slc25a24	AGAGACTGGACAATTTCAGA
Slc25a24	AAGAAGTTGCTTACCGAGGA
Slc25a24	ATCTTTGTTGACATCGCCAG

*Oligo name	Guide sequence
Slc35a3	GCTGTAGAAGACAGATAACG
Slc35a3	TGAAGCTCGCTATCCCGTCA
Slc35a3	TCCTGCCATCAGAATTACTA
Slc35a3	CAAACTGTGAGCCTGTTGAA
Gba2	CTCACCTCAAGCCCATACCG
Gba2	CGTCATCCCTCATGACATTG
Gba2	ACCAAGCTACTGCAATTCAG
Gba2	CATCGTATGTGTTGTACATG
Aldob	TATCCACAGTTGGACCAAGG
Aldob	AATTCCATTAGCCAGAGCAT
Aldob	CCGCCTGCAAAGGATAAAGG
Aldob	GGTCCCTATTGTTGAGCCAG
Pigv	GAGGGCAAAAGGCATCTGCG
Pigv	GTAGGCACGATACTGAAAGA
Pigv	TTCCTGTTTATCGCTGAGCA
Pigv	CAGGAGAAAATGCACCCCCA
Slc30a2	CTGGTCGGGAAGACACCCAG
Slc30a2	TGGAGATTATGAGATCAAAG
Slc30a2	AGGCCACATAGAGTTTGCGT
Slc30a2	GATGGAAAGCACGGACAACA
Hadhb	ATATACAAGTCTTACCTCAG
Hadhb	CTGACAGCAGAAATGGAATG
Hadhb	GCATCGGACCAATATTCCAA
Hadhb	TCAAACCAAGCCATGACCAC
Slc26a1	ACAGGCCAACATATGTGATG
Slc26a1	CCAGCCGGAGGATACCCATG
Slc26a1	TACCAGACCCTAAGATAATG
Slc26a1	GCCCACATTAACATGGCGGG
Ap5z1	TGCGTCCAGTACCTTCCATG
Ap5z1	TAGGTCCACACAGACTCCGT
Ap5z1	ATAGCCCGGTCCCATCACTG
Ap5z1	GGCCGCAGACAGCACAGACA
Mat2a	CCTGATGCTAAAGTGGCTTG
Mat2a	GTGCAATATATGCAAGATCG
Mat2a	ACCAAGGCAATGTACCATTG
Mat2a	ATTTACCACCTACAGCCAAG
Cyp26b1	ACTGCTGGGTCCCAACACGG
Cyp26b1	GCACCGGTCACACGAATCAG
Cyp26b1	ACTGCTGGTATACCTCAAAG
Cyp26b1	GGCCATCAATGTATATCAGG
Slc6a1	CACCAACATGACCAGCGCCG
Slc6a1	GCAGAAATACACGAGCACCC
Slc6a1	TACCTCTGTGGGAAAAACGG
Slc6a1	TCCATGTGTCCCGGTCAGGG
Gys2	GCATAAGAGTAACGTCACCG
Gys2	GTGGATGCGATGAATAAACA
Gys2	GAGATAACGCCCAAGCAGTG

*Oligo name	Guide sequence
Gys2	AAAACGACAGCCGATGAGTG
Pgap2	AAACGCCACACGTAGCGTTG
Pgap2	CATTAACTTCAGTCTCAATG
Pgap2	GTAGTGGTTCCAATAGGCGA
Pgap2	GACAACATCTACACACTGTG
Xylt1	CCTGTACGGGAACTATCCTG
Xylt1	CATGCGCTGTAGCTGTCGAG
Xylt1	GTGCCAGTACAAGCATATCG
Xylt1	GATGCCCAGGACAAACGACA
Cog7	GTGCTATCAGACATTACCAG
Cog7	TGAACGATGCTACGATCTGG
Cog7	GTGGCACACACAAACCCAGT
Cog7	GGTGCTGGTAGAGATTGACC
Tufm	GAGGAAACTCCAGTCATCGT
Tufm	CCGGTAGTTCTAGCCGAGGG
Tufm	GTGACAGGTACATTAGAGCG
Tufm	TCCACCCAGAATATGATCAC
Csgalnact1	TTATTGTGCCCCTAGCGAGG
Csgalnact1	CAGGGATTTACCGAACCGAA
Csgalnact1	AGGGCTGTTTAGACTCTCCA
Csgalnact1	CTTGACACCGGCATGTACCT
Tat	ATGTTCGCGTCAATATTGGC
Tat	GGCAAGCTTACCGATAGATG
Tat	AACAACCCGTCCAATCCCTG
Tat	TGAGCTGTGTCTAGCCGTGT
Slc38a8	TCACGGTGCAATACTACCTG
Slc38a8	ATTTCCCGAAGTGCTGACAG
Slc38a8	GCTGGTCCCCGATCACTCTG
Slc38a8	TCTTTGGTCTTCCTGATCAG
Spg7	TTCCAAATGCAGTCAGACTG
Spg7	GAACTCCCTCAGTACAAGTG
Spg7	ATCAATGTACACTATGCAAG
Spg7	GGATTCCCGTGTCCTACAAG
Foxred1	ACTCCTTCTACGTTTATCCA
Foxred1	CCCAATGAAGACCCCAACTG
Foxred1	TGGAGCAGGACCACACGGTG
Foxred1	TTGAACTGAAGTTCCACAGG
Sc5d	CGTATGTATATCCAGCCACG
Sc5d	CATGACTTGCAAACGGCGTG
Sc5d	ATAGACAAAATAATAGCTGA
Sc5d	AAGTAGACCACCTTGTGCAG
Dlat	ACTACCGCAACGGACCGCAG
Dlat	CAGGCTCTCAAACCCAACAG
Dlat	CGACAAGGCCACCATAGGTG
Dlat	TTCAGAACCACACCTACCGG
Slc17a5	TCGTCACCCAGATTCCCGGT
Slc17a5	TAGAACGTCTAAGGAGTGTG

*Oligo name	Guide sequence
Slc17a5	GATCGTTATCTTACCCGCAT
Slc17a5	GCTGGCCGCAGACTTAGGCG
Glyctk	GGTGTGATCAGCGTACCCAA
Glyctk	GCGGGAAAACCTCTACCTAG
Glyctk	CTGTGCTCAACACCATGGCA
Glyctk	AGTGATTGCCAGTGGCCCTA
Phgdh	CCACACTGAGAGCCTACCTG
Phgdh	CTCACTTCTGACCAGACTGT
Phgdh	TAGTAGCAGACCGGACAATG
Phgdh	CTGCGATTTCCTCCCCACAG
Slc13a5	GATAGCCGCCAATACAGCTG
Slc13a5	GGGTCCCGTCCCGGTCAAGG
Slc13a5	AGTCCAGAACCTTCAAAAGT
Slc13a5	AAGAAGGTGTGTTTACCGTG
Apob	GCTGGTAGTGACATCAACAG
Apob	AGTCTCACCTGTTAACTGCG
Apob	ATGTTGCATGAGTATGCCAA
Apob	GAATGGAATCATGCCCATTG
Cog5	GGAGACTGTTACCAGTGTCG
Cog5	GGAGGATTACGTCCTCCCGG
Cog5	CAACTAGCAAAACTTGCCCA
Cog5	TTTCACAGCATATAACTGGA
Mtr	TCAGGTGCTCGATATCAACA
Mtr	GGGGTCCGAATGAGACACGC
Mtr	TGTGGATAGCATCATACACA
Mtr	CTTCAAAAACACTAGCAGGG
A4galt	TCTTCCTAGAGACATCGGAC
A4galt	GCTGATGAAAGGGCTGCCTA
A4galt	TCAGGGGCACCCCCAGACAG
A4galt	ACTGTTTGAGGACACACCAC
Pgap1	ATAGACAACAATATGCGACA
Pgap1	ATATGTAACTTACCACACGA
Pgap1	AGAATTTGCTCCTACAAGTG
Pgap1	GTCGTCAGACTGTCAGTATG
Impad1	ATTCCTGTGTAGCATCAAGT
Impad1	TCCTTCACGAGAAGTCCAAG
Impad1	CTCCCACTAGATAAATACTG
Impad1	GCTTGGGCAATGGTAGATGG
Gabbr2	CCTGCGACTCTACGACACCG
Gabbr2	CATGGAAGGCTACATCGGAG
Gabbr2	GCTGACAGGATGCTATACAG
Gabbr2	CTTATCCGCAAGAACAGGCG
Slc35d1	GGCGCCGGCCGAAACGCTAA
Slc35d1	TGTGTGTGGAGGATTTCGCG
Slc35d1	ACTGTATTTGCAATGATCAT
Slc35d1	TGGTTCCCAAAATATAGTAG
Cldn19	CCACACGGCTCTTGGCAGTG

*Oligo name	Guide sequence
Cldn19	CTGGGCACTCACCTGCCAAG
Cldn19	TGCTGACTGGATATGACCTG
Cldn19	ACATCCACAGCCCTTCGTAG
Slc45a1	GAGTACCGGAGTCACGTACG
Slc45a1	AGGAGTACTCACCCGCCATG
Slc45a1	GGAGTGACCGATGTACCTCA
Slc45a1	CCACCCCGCACACTGTCAGG
Ppm1k	CAGGTGGGCATAACTCGCGA
Ppm1k	GCAGAATTGGCTCATCAATG
Ppm1k	CTAGGATCAAGAAATTCGGT
Ppm1k	AAAATTAGCCTGGAGAACGT
Uroc1	TGTCACAACCCGTTCAATGG
Uroc1	TCTGCCCCAGCATTGAGATG
Uroc1	GGGAATCGTCCATGGCACAG
Uroc1	CACCCCAATGCATCCAACGA
Fkrp	GCTGGACTTGACCTTCGCCG
Fkrp	CCAATGGCAGAAGTCCGGCG
Fkrp	CCATCCAAAGCGTCGCAGCG
Fkrp	CACAAACTCGGTGGCTACGT
Nars2	TCACATCCAACGACTGTGAG
Nars2	GGAACTCTTCAAGGCGACCA
Nars2	CTCAGGGTCCAGGACGCGAG
Nars2	TCAGTCCAAGAGGCAAAATG
Cyp2r1	TAGGCATCAACAAAATGGTG
Cyp2r1	GCAGAGCCGGGTGTATGGCG
Cyp2r1	GATGCTATTGAAACATACAA
Cyp2r1	AAAGGTAAGATGCCAATCCA
Snx14	AGCTGTGCTGCCTAATTACG
Snx14	CTTCAAGAGTTATTTCCGCA
Snx14	GACAGATGCAAAAAACCGTA
Snx14	TCAACATCGATACAAAACAC
Slc36a2	TGACTAGGATGTGCATACAG
Slc36a2	GGTAGTTCTGACGCCCACCA
Slc36a2	AGCAAAGTACCTCCCCCAGT
Slc36a2	AGCCCCGATAGCAATGTACA
Fktn	GAGTCTATTCCATCTAGCCG
Fktn	CACTCGATAAATCTGGAGTG
Fktn	GACTCAAAGGACACATGGAT
Fktn	TAATTGATTCCAGAATCCAT
Atpaf2	ACAATGAATTAGCTACAGGG
Atpaf2	AATGGGATCCCGTCATAGAG
Atpaf2	CTATGTCCCGCCAACAGGTG
Atpaf2	TGGCCCCGGCCATACTGAGA
Slc5a2	ATGATTTATACTGTGACAGG
Slc5a2	CTGGCACAAAAAGCCATCCG
Slc5a2	GGTCTCTTCGACAAATACCT
Slc5a2	ATTGGTTCTGAACATAGACT

*Oligo name	Guide sequence
Acsf3	CACAGCGGCTAGGTTACGGT
Acsf3	CATGAATACGGTAATCTGTG
Acsf3	GGCCCACTGTGCTACAACGT
Acsf3	ATATGGCCATCACACCTACA
Gphn	GCTTTGTCCATAGACGTCAG
Gphn	TGAAGGAGTAGTGCTAAGGG
Gphn	ACCACGAGATGTCACTCCAG
Gphn	ATCGGCCATGACATTAAGAG
Sptlc1	AATGTGCCATAGAACCCTCG
Sptlc1	CCCTCCAACCCACAACATCG
Sptlc1	TCCTGCGTACTCTAAGAGAG
Sptlc1	TTTGTCGTAGAATCCTCGCA
Rnf31	GATGGATTGAGTTTCCCCGA
Rnf31	GAACTATGAGTTGTTGGACG
Rnf31	CTACCTCAACACCCTATCCA
Rnf31	GGAGGAACCAAGGTGTTGTG
Abat	GAGCAGAGGTAACTACCTAG
Abat	GCTCCAGGAGTCCTTGATGT
Abat	TTTCGGCAGAGTAAGGAACG
Abat	AACGGTGGCTGGAATCATCG
Ahcy	GCGCACCTGACAGAAGCTGT
Ahcy	TGTCAACGATTCTGTCACCA
Ahcy	TGACCCTATCATACCCTCCA
Ahcy	TGTGATGATTGCGGGCAAGG
Fbxl4	AGTTGTGCTGCATGGTACGA
Fbxl4	TTGAGGTGGATATATTGCAG
Fbxl4	ACAGTATGTCCTATACCATG
Fbxl4	AGTGGCTGCAGGATAACTCA
Vcp	ACTGTCTTCACAGACTCATG
Vcp	TATAGGTCGCTTTGACAGAG
Vcp	CCAATCGCCTTAAAGAGCGC
Vcp	CTTCAGGAGTTGGTTCAGGT
Chsy1	GGTGTAAGGTGATCGCTCGG
Chsy1	GCGTGTGAACCCCATGTACG
Chsy1	AAGAGAAAGTTCCTGTCGCG
Chsy1	CAAGTACGAGTGGTTTATGA
Gcdh	GATGATCATACCGGTAGCCG
Gcdh	CAGGATCACCAACTCCCCTG
Gcdh	GGTCCTTCCAGTCAAACACG
Gcdh	CTCCTGGCAGTAGTTACGGA
Clpx	AAGAATTCTCGAAAACTACG
Clpx	TGGTGATTTGTGTACACACG
Clpx	TCTCTTATAATGATTATACA
Clpx	TGTTATTTACCTGACCCAGT
Pigs	ACCATAATGCCACCCCAGCG
Pigs	GGGCGACCTGGACTATGCGA
Pigs	GATCTCTCGCTCATGCACAA

*Oligo name	Guide sequence
Pigs	CTACCTAAGCTGGACTTGAG
Flad1	ACAAACTCGCGGAGTCAGGT
Flad1	TCACTCACGTCCTCACCGCG
Flad1	GCTAAGCCTACGCCCAAAGT
Flad1	GAAGCTGATTCTAGACTCCG
Pik3r5	CCACAGGAATCTCCTACCAG
Pik3r5	CGAGAGGCCTGAGACAAAGG
Pik3r5	TGTACTTACACAGAGGACAG
Pik3r5	GCTGAGCGGGACAGTCCAAG
Alg6	TTTGCTCATTTACGTACCCG
Alg6	TCTCATAGCCTCGTGATGTG
Alg6	TAGTCGATAAGAATAAGACC
Alg6	GCTTCATAATCACCAAACAT
Ocrl	TTTCGAATCATATTTGTACG
Ocrl	CCAATGCAGTAAATATCAGG
Ocrl	ATTTACCCCAATATGGAACA
Ocrl	ACGTGGAAGAGTTCGAACGA
Pgap3	CATGCAGGTATGGTACATGG
Pgap3	AGTCGCGGTACACGGGCTCG
Pgap3	ACTGCAAGTATGAGTGTATG
Pgap3	GGGACTACAGCACCCGTCTG
Trappc11	GCAGGCCGGGACTTACATCG
Trappc11	AGAGCTTGGAAAACCTAATG
Trappc11	CGAGTGGTACATCCCTAAAG
Trappc11	AGAGGAGTACTACTATGCAA
Gfm2	GGATACACAAGATCATTGGG
Gfm2	ACCAGCAGAGGCGTCAAACA
Gfm2	GGAGCATGGAAAGAAGAGAG
Gfm2	CCAATTACCTGTAAAATCAG
Pisd	CAAACTTGCTAGTCACTGGG
Pisd	GGTCCCCAGAAAATGGCGTG
Pisd	GGGCCCTCGAGCCAATACAG
Pisd	CGTATGTGGCTTGCACTGTG
Rfx6	TGAGCATAAAGAATGCACCG
Rfx6	GGACATAGGATGTCTCCACG
Rfx6	GGTAAGATTATGCATCACGC
Rfx6	TCAGAAATGCAGTTAAACAA
Serac1	AGCCATAGTAAAGCATTCGG
Serac1	AACCTGGACCGAGAAACTGT
Serac1	CACCCTGCTATAGTCCACTC
Serac1	GAGCAGCATTTAAAACCTGG
Dna2	ACACGATGCGAAGGATACGG
Dna2	GCCCTTCAGTCCAAACCTAG
Dna2	TGCCTTGCCACAGATAATCG
Dna2	CAGGCGTTAACCAGATACTC
Pigl	CTTGTCAATAATCATTACAC
Pigl	TTGATTGTAGTAGTTTCCTG

*Oligo name	Guide sequence
Pigl	GTTCCGCTGAGTTCCAAACC
Pigl	GCGTGCCAAGCCTAGCATGG
Rft1	AGGACCAAAATATACCCAGT
Rft1	GAATAATCTTGGCTCCCTTG
Rft1	GGTTCTTGCTGAGAGCATGT
Rft1	GGCAAAGCCAAAAACAGTCA
Slc5a6	CTTACTTAATCCCAGAGATG
Slc5a6	CAAACATGACCAGACCAATG
Slc5a6	GCAGTTCACCAACGGTATGG
Slc5a6	ATCCTATAGGTGATATACAT
Gmppb	GTGGCTTCTCAACAAAACGG
Gmppb	GTGCCGATGAAACTGCACCA
Gmppb	TTCCCAGTTATGGCCAAGGA
Gmppb	GAGCACTCCGAAGCCATTGG
Cndp1	CACTCACTTATGGAACCCGG
Cndp1	AGTCAGCCATTGGTTCGTTG
Cndp1	CAGCTCAGAAGGACGACGGG
Cndp1	AGCCGGTTCCATCGCCCTGG
Fa2h	TTCGTGCGGCATCATCCGGG
Fa2h	TCTTGAGCCACAGTTCAAAG
Fa2h	CTACTACCGAACCCTCACCC
Fa2h	GTGGATGACGTATTCCACAA
Gars	AGTCAGCAAATTTGTCTACG
Gars	GAGATATTCCAACCTTCGTG
Gars	TAAGTTAAAAGGTACCGGAG
Gars	CCAACAGTGAGTACCTGACT
Lyrm4	ACAGATCTAAAACTTGTGCG
Lyrm4	CCAGGGCTTGAATTTCTACA
Lyrm4	TCATTAGAATGTATGCTGTC
Lyrm4	CCCGGGTCACCTGTAATTGT
Iars2	CCAAACTAAAACGCTAACAG
Iars2	AAATCGGCGTTTGTCCGCTG
Iars2	AGGCGGCAGATACCGTGACA
Iars2	AATCGATTCCATATGATGAG
Pdp1	GAGGTCAACACCATCTACAT
Pdp1	GTGTACCTCAGACGATTCTG
Pdp1	ACTGGAACACCCAAAAAATG
Pdp1	TGCTTGTGCCACTGAAGGAT
B3glct	TGAGGCAGAGTAGTCTACCG
B3glct	TGGAACGTGGTGACGCAGCG
B3glct	CATACAGCAAGAATTCAGCG
B3glct	TGCCAAAAGATTAAAGAGTG
Alg8	TTGTCCGCGTTACTTCCCTG
Alg8	ACAGCCTCCCAATATCTCAG
Alg8	CCGCAGCAGATAGACACCAT
Alg8	AGTTTGGAGCCCAGTAGGCA
Rrm2b	GAGAATGTACAAGCAAGCAC

*Oligo name	Guide sequence
Rrm2b	TTGGAAAGATGACGAACCGT
Rrm2b	GGAGATAAAATACTTCTCGT
Rrm2b	TCTCCTAGGGGAAAGAGTGG
Gatc	CAGATGCTCGATTACCGCGG
Gatc	GCCCCTAGAGTCGGTACTGG
Gatc	CAAAGCGAATCCACAGGGAA
Gatc	GGCGTGCAGCTGATCCGCAA
Ugt1a1	AGACAAACTCTTGGGCACGT
Ugt1a1	CAGTGGCAAGTGACCCATAG
Ugt1a1	ACTTTGTGAAAGATTACCCC
Ugt1a1	ACACTAACAGCCTCCCAGCG
Opa3	ATGCGCATAATGGGTTTCCG
Opa3	AGGTCTTGAAGAACTCGCTG
Opa3	TCCTTGATACGGTTGGCCAG
Opa3	TCAGCAGCGCAATAAGGAGG
Ndufs6	GGGGTTCAAGTGTCGCCGAG
Ndufs6	CGAAACCCCGTGCAGCCCTG
Ndufs6	TGGGGAGAGTCAACAGCCGG
Ndufs6	TGATGAAAAAGACTACAGGA
Gnptab	TGTTTGCAATGGACGCGTGG
Gnptab	TCTGCCCATGCCAATCGACG
Gnptab	AGGAGTGAAATATTTACCCG
Gnptab	CATGCTGGACCGTTTAAGGG
Pnpla1	TTTGTACGATGTGCTACCGG
Pnpla1	CTGCAGAGATACATCGACGG
Pnpla1	GGTTTCCGAGTACCGATCCA
Pnpla1	AAATGTTCAAACTCCAAACC
Pigg	AGGTGGATAAAAATGTCACA
Pigg	ACCCCAGCGTCACTCCCATG
Pigg	AAAGTACTCAGGCATTACCT
Pigg	GATTCGAGGCATAGTAACTG
Amt	AAATGGTGGCGTTTGCAGGG
Amt	TTGTAAGCAATACTTCTGAG
Amt	TGCGGAACTAAGGCCTAACC
Amt	TGTAACACCTGTGTTGCCGT
Cers3	TATCATGAATAAACATCACG
Cers3	GTTTAGAAAATGGTTCTGGT
Cers3	ACACCTCTAGCAAATGCACT
Cers3	ATGGGCATATGACCTCTGGG
Cyp26c1	CCCTTGGACGTACCGTTCAG
Cyp26c1	GTCACACACACTACTTGGCG
Cyp26c1	GTGCGCCGCCCAACGACCGG
Cyp26c1	CTGTCCCGTAGCGCTCGCGG
Lipt1	GGTTGATGTTACCCATGTCG
Lipt1	CTGTAAAATGAGCCCATGTG
Lipt1	TGAAGTTCTGATGAGTGCGG
Lipt1	AGTCCGGCCGATCTTTGATG

*Oligo name	Guide sequence
Gpx4	CGTGTGCATCGTCACCAACG
Gpx4	CATGCCCGATATGCTGAGTG
Gpx4	TGGTCTGGCAGGCACCATGG
Gpx4	TAAGCCAGCACTGCTGTGCG
Vps13b	TGTCCATACTACCCAAATCG
Vps13b	TAAACACTGCAATACAAGCG
Vps13b	GAAACCTCTTCCCGATACAG
Vps13b	TGGCAGTAGTCCATGTACTG
Pex10	CAGAAGGACGAGTACTACCT
Pex10	ACCTGGCCAAGAGACTAGCA
Pex10	GTACGTTGGGATCATCCAAG
Pex10	TGGAGGACGCAGCCGATCAG
Sco2	TTCAGCCTACTAGACCACAA
Sco2	CTGTTCCTTCTCAGCCCTCG
Sco2	GCTCATCGGGGCAAATATCA
Sco2	GCATAGAAATTCCCGACACT
Epg5	ACAGCCGACTCGTTGTAACA
Epg5	TCGAGCCAGAAGAACCAATG
Epg5	TGGGTACCATACCCATATTG
Epg5	GAAACGCTGTCTTACACAAG
Pet100	GGAGATCCAGAACATAACCA
Pet100	CTGTGGCCAAGAGAGAAGGA
Pet100	CTTTGATACCCACCTTACGC
Pet100	GGATCTCCAATCAGGCTGAG
Nt5c3	AGAGTAGAAGAAATTATCTG
Nt5c3	CTCACCACTCTACCATGTAA
Nt5c3	CCAGCAGAAAATATGAACAC
Nt5c3	TCTCACTTACTATGACACGT
Hprt	CTAGAATGATCAGTCAACGG
Hprt	TATACCTAATCATTATGCCG
Hprt	AACAAATCTAGGTCATAACC
Hprt	AGCCCCCCTTGAGCACACAG
Rnaset2a	CTCACCTTGCATACTGTTGG
Rnaset2a	AAACATGAGTGGGTTAAACA
Rnaset2a	AGAAGACCGGTGAATCACAT
Rnaset2a	CAGAAGATTGTAACCAGTCC
Oas1a	GGGAGGTACATTCCTCGATG
Oas1a	GTTGGTACCAGTGCTTGACC
Oas1a	AAAGACAGTGAGCAACTCTA
Oas1a	GAGGATCAGTTAAACCGACG
Car5a	ATTACAAGAAAGCCTCCGTG
Car5a	GACACTGGGCCAGTCCAGAG
Car5a	GGAGTTTGACGATTCCTGTG
Car5a	AGTGTTTACGAACCTCAGCT
Apoa1bp	TGTGGCCCCGGAAATAACGG
Apoa1bp	TAACGAGTATCAGTTCAGCG
Apoa1bp	CTCTTGGACATAGACGTGGG

*Oligo name	Guide sequence
Apoa1bp	GAGTCACTAGCCCAGTGAAG
Carkd	TAGGCCAGGTCCCACGACAA
Carkd	CTGACGTCGAAGAAGCACAA
Carkd	CATTCTCACCCCCAACCACG
Carkd	CCATACAGCACATGCGACAA
Ppat	ACCTTGGAATCGGACATACG
Ppat	ATAAGACGCCCGATGCAGAG
Ppat	TGATCACTCTGGGACTCGTG
Ppat	AGGGGTGTATGCGAGTAACT
Prosc	TATGCTGGAAACCGTAGACT
Prosc	ATGGTCCAGATTAACACCAG
Prosc	AGACCCACGAACTCCAGGCT
Prosc	TTGCTGACCGCAACGAGCCG
Ftl1	GCTGCTCACCAGAGAGAGGT
Ftl1	TTGGCCGAGGAGAAGCGCGA
Ftl1	GAGTTTCAGAACGATCGCGG
Ftl1	TCGTCAGAATTATTCCACCG
Sis	TCAGTCACGAATGACAACAG
Sis	AATTTACCGGGAGTAAAAGG
Sis	GGGAAGTAAAGTGTAGCGGA
Sis	GTAATACGGATGGAATCCAT
G6pdx	AGAGGTGGAAACTGACAACG
G6pdx	TGCCCGCTCACGACTCACAG
G6pdx	ATGACCCCACAGTACCCCAT
G6pdx	AGAGATGGTCCAGAATCTCA
Ins1	TAGAGAGCCTCTACCAGGTG
Ins1	CTGGGAGCCCAAACCCACCC
Ins1	ACCCAAGTCCCGCCGTGAAG
Ins1	GTGGAACAACTGGAGCTGGG
Gyg	AACAGCACAGGACTACTAGG
Gyg	CTTACGCTTTAAATGCCGGG
Gyg	CTGGTTATACGTTTCAATGG
Gyg	CACTAAAATATGTATTCAGT
Pcx	AGGCTGCCATCTCATACACG
Pcx	ACGAGCAGAGAGTCATAGTG
Pcx	GCGCATGGCAACGTCGAACG
Pcx	GACTGGGGCTCACATTGACA
Fh1	AATTGGGCGAACTCACACGC
Fh1	CAGAGCTTCAAACTTATTCG
Fh1	GCGACGTTCGGAGCACACCG
Fh1	CTCGTAGATTCTTGGCATGG
Atp5a1	TGGTCAGAAGCGGTCCACTG
Atp5a1	GCTCCCGCACAGAGATTCGG
Atp5a1	ACTGGGCGTGTGTTAAGCAT
Atp5a1	CCAACAGCTCCTCGCCAACG
Atp5d	TCAGGCGCGTACATACGCCG
Atp5d	GTGAGTTCGTACCTGCGTCG

*Oligo name	Guide sequence
Atp5d	CCAAAGGCTCCAGTCAGCGT
Atp5d	CTCACCAAAGTACTTAGTCG
Atp5e	GAGACACCATGGTGGCGTAC
Atp5e	GTGGCGTACTGGCGACAGGC
Atp5e	AGATCTGTGCAAAAGCAGTG
Atp5e	CTGGGAAAACCGGATGTAGC
Usmg5	TTACATTCATTCTACCTGTG
Usmg5	TGTGTCCTGGCCACATATGG
Usmg5	ATGGCTGGTGCAGAAAGTGA
Usmg5	GATGGCCAATTCCAGTTCAC
Peo1	CATGTGCACGTAAATACTGG
Peo1	CTAACCAGAACACAATCCGA
Peo1	ACGTGGCCTGAAGCTACTAG
Peo1	AGGGCGGTACGAAGAATACG
2810006K23Rik	TCCTGATCAGTGGTAGAGGG
2810006K23Rik	GTGCCACCAAACAAGATCTG
2810006K23Rik	CGTGAAAGGACATGGCCCAG
2810006K23Rik	TACCTTGACCACAATGCCGG
Timm8a1	TTCTGAACAGGAGAAGTGCA
Timm8a1	TCAGCCCGACTGTCCAACTT
Timm8a1	GCCCAGAGCCGAGCCCGAAG
Timm8a1	GTTGCAGCATTTCATCGAGG
Park2	CCAAACAGATCACGTGACGG
Park2	TACACATAGTACAGAGACCA
Park2	AAGTGGTTGCTAAGCGACAG
Park2	TTAATTCCAAACCGGATGAG
2410015M20Rik	GGGGCCTAGTGACAAGAGTG
2410015M20Rik	TGGAAATTTAATCTTTGGAG
2410015M20Rik	CTCGAGTGTGGTCGCTAATG
2410015M20Rik	CAATATGTGTGCCAGCAGAC
Clk1	TTCGCAGCACCATTCACACG
Clk1	ATACTTACAAAGTACTATGG
Clk1	ACTACATGGGCTACGAGCCA
Clk1	CTGATATGATCCATTCGAAA
Adck3	AGTTCAGTTCTCAACACCAC
Adck3	CATGCCACTGAAACAGATGA
Adck3	CCAGCGAAGATCCTTCCACC
Adck3	CATTGTGAGTACACTGTGCA
Adck4	GACCTTATGTACAGTCCGGG
Adck4	ACTAAGAAGTCCTTGCCAGG
Adck4	ATGAGTGTGGGCCTGCCAGA
Adck4	GCTAAAGGATGGGACTGAGG
Gyk	TCCATCTAGAGTTTAACAGG
Gyk	GACCTTGTCCCAGACTACTG
Gyk	TACAGCACCAGCTATAGCCA
Gyk	CTACCTATAGGTATGGAACA
Ept1	CAATTCCAGCACCCCGTTAG

*Oligo name	Guide sequence
Ept1	GTGTACTCCATCTTTGGACG
Ept1	TGACTGGGTTTGGATTGTCG
Ept1	GGTCGAAGTATGTCAGGAGT
Cyp4f39	GGGGAAAGAATTATCTGACG
Cyp4f39	CTTCAGGACTTACCTAACCA
Cyp4f39	TCAGCTTGCGACAGGTAATG
Cyp4f39	TGTACTACCTCACAGCCGAT
Cyp21a1	GCTTACCTTGCATCCCCAAG
Cyp21a1	TACCATTTAGCATATGGGGT
Cyp21a1	AGGAGATGATACTACAAGTG
Cyp21a1	ATGATTGACTACATGCTCCA
Akr1c21	AGGACTAACCAAGTCCATTG
Akr1c21	GTATCTCATTCATTACCCAA
Akr1c21	AGATGATTCTGAATAAGCCT
Akr1c21	TACTGAAGATCATGTAGGAG
Rab7	GGAAGTTCTCGGGATCCCGG
Rab7	ACGGTTCCAGTCTCTTGGTG
Rab7	CGACAGACTTGTTACCATGC
Rab7	CACATACTGGTTCATGAGAG
Tmem5	TGCATAAATTAACCACTGGG
Tmem5	GCGCCCGAAGAAGACGTGGT
Tmem5	ATGTCTGCACCATTAATCCA
Tmem5	TCTTTACAGTGACTTACCAA
Large	GATGTGTCTGATTTAAAGGT
Large	CAGCAATAGAATCAGCAATG
Large	GCAGGTAACAGCTCTGAGTG
Large	ACAGCAGAGAGGGAACTCAT
Chst5	GTAAGCCTCTGTGCGCAACG
Chst5	GCGAAGGCTTCGCAGACCGG
Chst5	CAGCCATGTGCGCATCGCAG
Chst5	TGAGCGGATCAGGTCACGCA
Hykk	CTCCGTATGCCGAACTAAAG
Hykk	CCTGAGCCAAAGTCGAAACC
Hykk	CCCAGGAAGACCAATAGCTG
Hykk	TTTCGTGTTCACATTGCAAG
Fdx1l	CGCCCGGGTCCTGTTACGGG
Fdx1l	GTTTGTCCCCAGGGTCAACG
Fdx1l	CTGGCAAGCGGATCCCGGTG
Fdx1l	TCTAGGACGTTCGGGACTAC
Zfp143	GCATTTCGGTGCAAATACGA
Zfp143	CTAATTATAAAAACCATGTG
Zfp143	CCTGACGGAGGCAGTAACCG
Zfp143	AGTGTGAGCATTCAGGCTGT
Cyp51	GCTGTCAAAAGAACCAGCTG
Cyp51	ATGCAGAAGAAGTCTACGGT
Cyp51	TAGAAGTCAACTCAACGAGA
Cyp51	AGGAACATACTGCTTAAAGT

*Oligo name	Guide sequence
Pigyl	GGGATGAGGACGGTCATGGT
Pigyl	AGGCCTGCCAGCGAGACCAG
Pigyl	TGGGAAGCCTTCCTCCACGG
Pigyl	CCACGGAGGCGGAGTAGAGC
Fmo3	GATGCTACAATGATTTGTTC
Fmo3	TTCACAGGACCATATAGAAG
Fmo3	TGTCACAGCCTGAGTTCCCC
Fmo3	CTTGGGTGATGAGTCGAGTC
Bckdhb	GCCAAGTATCGCTACCGCTC
Bckdhb	CTCGTAAACCAACAGTGCAT
Bckdhb	CCACACAACCCCACGGGGCC
Bckdhb	CACCGGTGCTACAGCTATTG
Agxt2	CATCACCATGGCCAGGTCGT
Agxt2	TAGCAAAGGCTTCCGGAAAT
Agxt2	AGACAGAACTTGTATGCCAC
Agxt2	AAAAACAGATAGACCGCCTG
Nnt	ACGAACGCTTCGTACTCACC
Nnt	GTTATACATACCTTCGCAGG
Nnt	TTCAATGTTGTCGTGGAATC
Nnt	GCTTCGTGAGCGCCTAACGT
Slc25a3	TGCGGCACTTTACTAAGTCC
Slc25a3	TTCAACAGTACGTTCAAAGC
Slc25a3	GCCTTATATAGCAACATACT
Slc25a3	GCCCCGAAGTGAATGTACAA
Ndufv1	GCCGCCTATATCTACATCCG
Ndufv1	TGTACCAGTCACCCCGTCTC
Ndufv1	GCCAATCAGACCTGCTTCAT
Ndufv1	CCCACAGGTAGCTATCCGAG
Ndufa12	CTTAAAGGGCAAATGATATA
Ndufa12	CTGGTGGGAGAAGACAAATA
Ndufa12	TGGTGTAGATGACCCATCGG
Ndufa12	CCTACCTGAAGAAAACCCGT
Ndufa12	TCCACCCTTAGAGATTGTTG
Ndufa12	AGCAATTCCCCGCTGCCTCA
Ndufa12	CATACAGGTGGGATCTCATC
Ndufa12	ATCTGCGGAAATCGCGTGTT
Bcs1l	TTGGTTATCCGCGCCGACGT
Bcs1l	ACGTCGGCGCGGATAACCAA
Bcs1l	TACCTTCTTTATGGGCCCCC
Bcs1l	AAGAAGGTAGCCACGTCTGT
Tymp	CACCAGGTGCCAATGATCAG
Tymp	ATACTTAGGGGCCATGCTAA
Tymp	TTCAGGTCACCTGTAATGAG
Tymp	TCACATCTCGTGCAGCATAC
Sacs	TTTGTAAACCTTCAATCAAA
Sacs	TCTCCAATCTTGATCCAATC
Sacs	ATATAAAAATTTAACCTCTG

*Oligo name	Guide sequence
Sacs	GTCCGCGTGACCGTGCTCCG
Tmlhe	AGTTGTTGCACCAACAAAGC
Tmlhe	TATCTAGTCACATGACCATC
Tmlhe	ATGCCGGTCTAGAGCTAGCT
Tmlhe	CTCCGTAATTTGATGAAGAG
Sbf2	TGTTGGCTGTTTCCGCTCTC
Sbf2	GGATGACACGCCTTTCCCAC
Sbf2	CTTACCAATTCAATTCCCTG
Sbf2	CTAATCTGGATACCAACACC
Pikfyve	CTGGCATCCAATATTGCTTC
Pikfyve	TGTTGTAATCAAGAAATCCC
Pikfyve	GGCTGGTTCTGCTTTCCTTC
Pikfyve	CGAAGCTGAACAGCTGTACG
Plcg2	TTGCCAAACTGAGCGTGCTG
Plcg2	CGCTCACTTTGAAGTTGACC
Plcg2	TAGATCAAACCCGAAGAAAC
Plcg2	AGATAAAGGAAATCCGTCCG
ApoE	GCCTCTGCGCGATCGCGCCC
ApoE	CCGACTCGGAGCCGACATGG
ApoE	CTACACAGGATGCCTAGCCG
ApoE	GCTTCTGGGATTACCTGCGC
Fdft1	AACCTTGTCCCAGTCCTGTT
Fdft1	CTCTCAGTGAACCGCCACTC
Fdft1	CTGCCATCCCACACCCCATC
Fdft1	CAGTACTGCCACTACGTTGC
Abcd1	TCATCCTGCTTGAGCGCCTA
Abcd1	GTTCCAGCATGACATACCAT
Abcd1	CAGGGTGTACGAGATGTTCC
Abcd1	TCTCTCTACAGGCCAAGTTG
Pex26	GCGCTCTGCGGCCTTCAGCG
Pex26	TCTGGATCCGGCGGAAGAGC
Pex26	CTGGTAGTACCGGAGGACCC
Pex26	GGTCAAACCGTAGAATCAAG
Tusc3	AAAAGCAGATGAATAACGCC
Tusc3	CATTCTGAAGATCGAGCGCC
Tusc3	TAACGAAGAATATCAAATCC
Tusc3	CGCTCGATCTTCAGAATGAA
Pigo	CAGGGGACTCATAGAACGCC
Pigo	TCCGGGGAAGAGGTCTCTCC
Pigo	CCCATCCCGTTTGGGAACAC
Pigo	CCACAGTGGACGGCGGTTCG
Atp6v0a2	TGAAGAGCTCGAACGAATAC
Atp6v0a2	CAACAGAGAGTCGTTCTCTA
Atp6v0a2	CTACAGCTGCATGCAGCGGC
Atp6v0a2	TCTTCGTGACCCTCAGCATG
Cers1	GCAGACGACACCGCTTGGCC
Cers1	TGACGTCAGCGATGTGCAGC

*Oligo name	Guide sequence
Cers1	ATGAACTCACCGGAAGGCGT
Cers1	GTAAGCGCAGTAGCTCCAAC
Cers2	TTGGGAGGGATATCCCATAC
Cers2	GGCGGAACCAGCGTTCTACC
Cers2	CATTGGGAGGTGCCCGCAGT
Cers2	GCCCACTCTGCCGTGACAAA
Ears2	TGCTATCCGCTTCCGTCTAG
Ears2	AGGGGCAGATGAGCAAATCG
Ears2	TTCAGAAGCTCCAGCCGCTG
Ears2	AGTGGCAGGTGATCCGCGTC
Hars2	GGAACCTTGATGACAAAATT
Hars2	GCCTCCAGACCTTTCCAACT
Hars2	GAAGTTGTCTTCATACTTCT
Hars2	AACAGCTGATAATCTTATCG
Stat2	AGTTCTTGGTGAGATCCATC
Stat2	ATAACTTGCGAAAATTCAGC
Stat2	CCTACTTAGACCTTTCCCAA
Stat2	TGAGATTGAAAATCGAATCC
BRDN0000737505	AAAAAGTCCGCGATTACGTC
BRDN0000737693	AAAACGGCTCGATCGGTGAT
BRDN0000737637	AAAACGTAATTATACCGAGC
BRDN0000738185	AAAATTGCACCTTCCCGGCC
BRDN0000737801	AAACCCCCGCGCGGAGCGTC
BRDN0000737467	AAACCTAGCGTAGATTCGGC
BRDN0000737848	AAACGAGGCTGTTCGTACAC
BRDN0000737609	AAACTCATACGTAGCGAATC
BRDN0000737434	AAACTCCCGTGTCAACCGAT
BRDN0000738254	AAAGACGTGCATTCAGCGAG
BRDN0000737777	AACATGTTAAGTCGCGTTAT
BRDN0000737611	AACCAGCATTTGACCGCGCT
BRDN0000737528	AACCCCGGCTGTCATCGCCG
BRDN0000738228	AACCCGCCGGAACAATCAGC
BRDN0000737727	AACCGGCTGCGCGTTTGCAA
BRDN0000737483	AACCGTACTGCGAGGAGCAT
BRDN0000737872	AACCTCGTCTCATGTACGAA
BRDN0000737516	AACGCCCCGGATTTCGTTGA
BRDN0000737844	AACGGCTGCGCCCGCGGCAA
BRDN0000737412	AACGGGCGCAATACCCTTTT
BRDN0000737631	AACGGTAGCGTACCCGTGAA
BRDN0000737750	AACGGTCAAATCCGTGAGGG
BRDN0000737875	AACGTCACCAACCTCGATCC
BRDN0000738229	AACGTTATAGCTTCGTCTCT
BRDN0000737806	AACTAACTCACTACGCACGA
BRDN0000738366	AACTCCTCATCGTACGCTAA
BRDN0000737593	AACTCGCGTGGGAAGTCCGG
BRDN0000738128	AACTTATACGTAATCTGATC
BRDN0000738307	AAGACTCCTACGTATCGAGC

*Oligo name	Guide sequence
BRDN0000737391	AAGCACAAGAACGGTCCGCC
BRDN0000737912	AAGCAGCGACTACTCGACGC
BRDN0000738101	AAGCCTAACGGAGCTCGCGG
BRDN0000738296	AAGCCTACTTCACCGGTCGG
BRDN0000738095	AAGCGAGCCGCAGACCGTTT
BRDN0000737714	AAGCGTACCCCACTCGTTAA
BRDN0000738016	AAGCGTGAGATTCACCGCCG
BRDN0000737416	AAGGCCTTAACACGTCGACC
BRDN0000737993	AAGGCGTAAACGAGTACACG
BRDN0000738351	AAGGGTAAGTACAGTATCGT
BRDN0000738301	AAGTCCCCTTCGGGAACTCC
BRDN0000737395	AAGTCTATGCGGGGCTCGTA
BRDN0000737589	AATAAGCCTACCCGGCGAGA

Original Doc Name: IEM (All) Library (Andrew)

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
Example row, don't delete	example 1	example 1	AATATTTAAGGTCTGCCTTAACGTGATCCCCATTGCTGAATTTTACCTCCTGACTCCAA	59		GGAAAGGACGAAACACCG		GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
1	Abca1	Abca1_1	GGAAAGGACGAAACACCGACATGTCATCAACATAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATGTCATCAACATAACAG	
2	Abca1	Abca1_2	GGAAAGGACGAAACACCGGTGGACCCGTACTCTCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACCCGTACTCTCGCAG	
3	Abca1	Abca1_3	GGAAAGGACGAAACACCGCAAGCTGTCAAGCAACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGCTGTCAAGCAACACTG	
4	Abca1	Abca1_4	GGAAAGGACGAAACACCGGGTATACACAGAGCCATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTATACACAGAGCCATTTG	
5	Abcb7	Abcb7_5	GGAAAGGACGAAACACCGGATTAAATACTAACGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTAAATACTAACGCACTG	
6	Abcb7	Abcb7_6	GGAAAGGACGAAACACCGCGCTGGGACGAACTCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCTGGGACGAACTCCATCG	
7	Abcb7	Abcb7_7	GGAAAGGACGAAACACCGACAGTTACTAGATGCTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTTACTAGATGCTACAA	
8	Abcb7	Abcb7_8	GGAAAGGACGAAACACCGTCACAGTTGCAGTTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACAGTTGCAGTTACACGG	
9	Acadl	Acadl_9	GGAAAGGACGAAACACCGAGGCGATCGAGCTTCACGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCGATCGAGCTTCACGGT	
10	Acadl	Acadl_10	GGAAAGGACGAAACACCGAGAGCGTACTCCAATTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCGTACTCCAATTGCAC	
11	Acadl	Acadl_11	GGAAAGGACGAAACACCGAACATCGCAGAGAAACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATCGCAGAGAAACATGG	
12	Acadl	Acadl_12	GGAAAGGACGAAACACCGCCGGAAAATGTCATGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGAAAATGTCATGCTCCG	
13	Acadm	Acadm_13	GGAAAGGACGAAACACCGAAGATGTGGATAACCAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGATGTGGATAACCAACGG	
14	Acadm	Acadm_14	GGAAAGGACGAAACACCGCCCGGAATATGACAAAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCGGAATATGACAAAAGCG	
15	Acadm	Acadm_15	GGAAAGGACGAAACACCGTCGAACACAACACTCGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGAACACAACACTCGAAAG	
16	Acadm	Acadm_16	GGAAAGGACGAAACACCGAGCAGGTTTCAAGATCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGGTTTCAAGATCGCAA	
17	Acadvl	Acadvl_17	GGAAAGGACGAAACACCGCAAAGCATCTAACACGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGCATCTAACACGTCAG	
18	Acadvl	Acadvl_18	GGAAAGGACGAAACACCGCAACAACGGAAGATTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACAACGGAAGATTCGGGA	
19	Acadvl	Acadvl_19	GGAAAGGACGAAACACCGGCTACATCGGATCCACTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTACATCGGATCCACTCGA	
20	Acadvl	Acadvl_20	GGAAAGGACGAAACACCGCCAGCGACTTTATGCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGACTTTATGCCAGGG	
21	Acads	Acads_21	GGAAAGGACGAAACACCGGGTGACTCATGGGTCCTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGACTCATGGGTCCTCAA	
22	Acads	Acads_22	GGAAAGGACGAAACACCGGCTCATGATAACTCCCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCATGATAACTCCCGTGG	
23	Acads	Acads_23	GGAAAGGACGAAACACCGGATGGGCTTCAAAATAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGGCTTCAAAATAGCCA	
24	Acads	Acads_24	GGAAAGGACGAAACACCGGCTCACCCATCTTCTTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCACCCATCTTCTTAACC	
25	Slc33a1	Slc33a1_25	GGAAAGGACGAAACACCGGTGACTTACCTAAAGCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACTTACCTAAAGCCCCG	
26	Slc33a1	Slc33a1_26	GGAAAGGACGAAACACCGATGTTATCCCGGGAAAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTATCCCGGGAAAACGT	
27	Slc33a1	Slc33a1_27	GGAAAGGACGAAACACCGGAAAGGGTAACGATTCCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGGGTAACGATTCCCCT	
28	Slc33a1	Slc33a1_28	GGAAAGGACGAAACACCGAAATATTGATGGCAGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATATTGATGGCAGAACAC	
29	Aco2	Aco2_29	GGAAAGGACGAAACACCGAGATCCGTGCCACTATTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATCCGTGCCACTATTGAG	
30	Aco2	Aco2_30	GGAAAGGACGAAACACCGGCGTTTACGGCCCGACCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTTTACGGCCCGACCGGG	
31	Aco2	Aco2_31	GGAAAGGACGAAACACCGTGGGTGAGGTCCAACCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGTGAGGTCCAACCAGAG	
32	Aco2	Aco2_32	GGAAAGGACGAAACACCGGATTGAAATTAACCTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTGAAATTAACCTCAATG	
33	Acox1	Acox1_33	GGAAAGGACGAAACACCGCGATCCAGACTTCCAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATCCAGACTTCCAACATG	
34	Acox1	Acox1_34	GGAAAGGACGAAACACCGAATGTCGGATGGCTTGCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTCGGATGGCTTGCGGT	
35	Acox1	Acox1_35	GGAAAGGACGAAACACCGCCTCACAGCACTGTATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCACAGCACTGTATCGAA	
36	Acox1	Acox1_36	GGAAAGGACGAAACACCGTCTCTTCATAACCAAACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTTCATAACCAAACTTG	
37	Aspa	Aspa_37	GGAAAGGACGAAACACCGATTCATTACCAATCCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCATTACCAATCCAAGGG	
38	Aspa	Aspa_38	GGAAAGGACGAAACACCGAGTGCAACCCATGTTAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGCAACCCATGTTAGAAG	
39	Aspa	Aspa_39	GGAAAGGACGAAACACCGACCAACAGGATACTTGGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAACAGGATACTTGGCAA	
40	Aspa	Aspa_40	GGAAAGGACGAAACACCGCTTGCCATATGAAGTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCCATATGAAGTGAGAA	
41	Ada	Ada_41	GGAAAGGACGAAACACCGGTTGTGGATCTTGTGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTGGATCTTGTGAACCA	
42	Ada	Ada_42	GGAAAGGACGAAACACCGATTCATCGGACCGTCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCATCGGACCGTCCACGC	
43	Ada	Ada_43	GGAAAGGACGAAACACCGCTTCATCTCCACAAACTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCATCTCCACAAACTCGT	
44	Ada	Ada_44	GGAAAGGACGAAACACCGGCTGCGCAACATTATCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCGCAACATTATCGGCA	
45	Adk	Adk_45	GGAAAGGACGAAACACCGTGTGCTGCGTGTATCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCTGCGTGTATCACTGG	
46	Adk	Adk_46	GGAAAGGACGAAACACCGCACTTTCAATACCGACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTTCAATACCGACTCTG	
47	Adk	Adk_47	GGAAAGGACGAAACACCGATAAGGCATGACGTCCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAGGCATGACGTCCATCA	
48	Adk	Adk_48	GGAAAGGACGAAACACCGCATTGGGATAGATAAGTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGGGATAGATAAGTTTG	
49	Adsl	Adsl_49	GGAAAGGACGAAACACCGAAAGTGTGTGAAACCTAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTGTGTGAAACCTAACG	
50	Adsl	Adsl_50	GGAAAGGACGAAACACCGCCAGTGCGATGCCGTACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGTGCGATGCCGTACAAG	
51	Adsl	Adsl_51	GGAAAGGACGAAACACCGGCTGCGGGCATTATTCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCGGGCATTATTCATCT	
52	Adsl	Adsl_52	GGAAAGGACGAAACACCGTCACAGGACAGACGTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACAGGACAGACGTACACA	
53	Aga	Aga_53	GGAAAGGACGAAACACCGCCAGATCCCTCAAAATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGATCCCTCAAAATACTG	
54	Aga	Aga_54	GGAAAGGACGAAACACCGAGGCCAAGTGTTGACGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCAAGTGTTGACGACCA	
55	Aga	Aga_55	GGAAAGGACGAAACACCGTGGTGGACATTGCTATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGGACATTGCTATCTGG	
56	Aga	Aga_56	GGAAAGGACGAAACACCGATGGATTACAACCATGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGATTACAACCATGCCTA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
57	Gla	Gla_57	GGAAAGGACGAAACACCGCTAAACTCACGTAATTTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAAACTCACGTAATTTGCG	
58	Gla	Gla_58	GGAAAGGACGAAACACCGCATAGGATCCAAAACTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAGGATCCAAAACTCCCG	
59	Gla	Gla_59	GGAAAGGACGAAACACCGTCATACAGGTTATAAGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATACAGGTTATAAGTACA	
60	Gla	Gla_60	GGAAAGGACGAAACACCGCATTGGACAATGGCTTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGGACAATGGCTTGGCG	
61	Agxt	Agxt_61	GGAAAGGACGAAACACCGAGCCCCTGTCAGTTCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCCTGTCAGTTCCTACG	
62	Agxt	Agxt_62	GGAAAGGACGAAACACCGAGAACATTATACACTGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACATTATACACTGCAGG	
63	Agxt	Agxt_63	GGAAAGGACGAAACACCGACATACTTGGCCAAATTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATACTTGGCCAAATTGTG	
64	Agxt	Agxt_64	GGAAAGGACGAAACACCGGTAGATAGGAACCCCGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGATAGGAACCCCGCCCA	
65	Aicda	Aicda_65	GGAAAGGACGAAACACCGGTAGGAACAACAATTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGGAACAACAATTCCACG	
66	Aicda	Aicda_66	GGAAAGGACGAAACACCGTTCACAGAAGTAGAGGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCACAGAAGTAGAGGCGCG	
67	Aicda	Aicda_67	GGAAAGGACGAAACACCGACCAGGTGACGCGGTAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGGTGACGCGGTAACAC	
68	Aicda	Aicda_68	GGAAAGGACGAAACACCGTGAGACCTACCTCTGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGACCTACCTCTGCTACG	
69	Ak1	Ak1_69	GGAAAGGACGAAACACCGCTACACCCACCTGTCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACACCCACCTGTCTACTG	
70	Ak1	Ak1_70	GGAAAGGACGAAACACCGGATCGACGGCTACCCGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCGACGGCTACCCGAGGG	
71	Ak1	Ak1_71	GGAAAGGACGAAACACCGGTCAGCTCTGGATCGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAGCTCTGGATCGGAGAG	
72	Ak1	Ak1_72	GGAAAGGACGAAACACCGCTTTGGCTAACATAGCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGGCTAACATAGCATCT	
73	Ak2	Ak2_73	GGAAAGGACGAAACACCGTGAAGGCGACAATGGATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGGCGACAATGGATGCA	
74	Ak2	Ak2_74	GGAAAGGACGAAACACCGGGTAGGACCGGCCACTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAGGACCGGCCACTCTTG	
75	Ak2	Ak2_75	GGAAAGGACGAAACACCGTCCGAACCGGAGATTCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGAACCGGAGATTCCGAA	
76	Ak2	Ak2_76	GGAAAGGACGAAACACCGTCAGCCAGTTTGGGTGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCCAGTTTGGGTGCCTG	
77	Alpl	Alpl_77	GGAAAGGACGAAACACCGGGATAACGAGATGCCACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATAACGAGATGCCACCAG	
78	Alpl	Alpl_78	GGAAAGGACGAAACACCGCTAGGAGGCAGGATTGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGGAGGCAGGATTGACCA	
79	Alpl	Alpl_79	GGAAAGGACGAAACACCGACCTAAGAGGTAGTCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTAAGAGGTAGTCCACCC	
80	Alpl	Alpl_80	GGAAAGGACGAAACACCGGTTGCATCGCGTGCGCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCATCGCGTGCGCTCTG	
81	Akt2	Akt2_81	GGAAAGGACGAAACACCGCATACTCCATCACAAAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACTCCATCACAAAGCAT	
82	Akt2	Akt2_82	GGAAAGGACGAAACACCGTACAGAGAAATTGTTCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGAGAAATTGTTCAGGG	
83	Akt2	Akt2_83	GGAAAGGACGAAACACCGTGTGGTGTACCGTGACATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGTGTACCGTGACATCA	
84	Akt2	Akt2_84	GGAAAGGACGAAACACCGAGTGGACCACAGTCATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGGACCACAGTCATCGAG	
85	Alas2	Alas2_85	GGAAAGGACGAAACACCGATCCAAGGCATTCGCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCAAGGCATTCGCAACAG	
86	Alas2	Alas2_86	GGAAAGGACGAAACACCGACATCACACAATTCCTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATCACACAATTCCTCCAG	
87	Alas2	Alas2_87	GGAAAGGACGAAACACCGAATACTAAATAGGAACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATACTAAATAGGAACTGGT	
88	Alas2	Alas2_88	GGAAAGGACGAAACACCGAGGTACCAGCAAGTTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTACCAGCAAGTTTCATG	
89	Aldh3a2	Aldh3a2_89	GGAAAGGACGAAACACCGCTGTATGCGATTGTTAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTATGCGATTGTTAATGG	
90	Aldh3a2	Aldh3a2_90	GGAAAGGACGAAACACCGGGAAATCTTAGCAGCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAATCTTAGCAGCCATCG	
91	Aldh3a2	Aldh3a2_91	GGAAAGGACGAAACACCGAGTCTCTGTCAATGTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTCTGTCAATGTAACAA	
92	Aldh3a2	Aldh3a2_92	GGAAAGGACGAAACACCGTCTGGAGGGAGGCTTCGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGAGGGAGGCTTCGCAC	
93	Aldoa	Aldoa_93	GGAAAGGACGAAACACCGAATGGCGAGACAACTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGGCGAGACAACTACCCA	
94	Aldoa	Aldoa_94	GGAAAGGACGAAACACCGCCTTGCCCGGAGCCACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGCCCGGAGCCACAATG	
95	Aldoa	Aldoa_95	GGAAAGGACGAAACACCGCCACGAGACACTGTACCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGAGACACTGTACCAGA	
96	Aldoa	Aldoa_96	GGAAAGGACGAAACACCGGCCAGCATCTGCCAGCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAGCATCTGCCAGCAGGT	
97	Gfer	Gfer_97	GGAAAGGACGAAACACCGAGAATTGGGTCGCCACACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATTGGGTCGCCACACCT	
98	Gfer	Gfer_98	GGAAAGGACGAAACACCGACGACCTGGTGACTGACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGACCTGGTGACTGACGCG	
99	Gfer	Gfer_99	GGAAAGGACGAAACACCGCCTGCGTGGACTTCAAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCGTGGACTTCAAGTCG	
100	Gfer	Gfer_100	GGAAAGGACGAAACACCGTTCCCGTGCTCCAAACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCCGTGCTCCAAACCTTG	
101	Ampd3	Ampd3_101	GGAAAGGACGAAACACCGTACCTGGTTCGCATGCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTGGTTCGCATGCACGG	
102	Ampd3	Ampd3_102	GGAAAGGACGAAACACCGGTCCTCGGGGACAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCTCGGGGACAGTAAACA	
103	Ampd3	Ampd3_103	GGAAAGGACGAAACACCGTGATCCGGGAGAAGTATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATCCGGGAGAAGTATGCA	
104	Ampd3	Ampd3_104	GGAAAGGACGAAACACCGAGTAGCTCCGGGAACCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTAGCTCCGGGAACCAGAG	
105	Mat1a	Mat1a_105	GGAAAGGACGAAACACCGACAGGTATGGTGCTACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGGTATGGTGCTACTGTG	
106	Mat1a	Mat1a_106	GGAAAGGACGAAACACCGCTATGCTACTGATGAGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATGCTACTGATGAGACCG	
107	Mat1a	Mat1a_107	GGAAAGGACGAAACACCGGTGTTGCACAGAGATGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTTGCACAGAGATGACGA	
108	Mat1a	Mat1a_108	GGAAAGGACGAAACACCGGACACATTGGGCAATATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACATTGGGCAATATCTG	
109	Slc25a4	Slc25a4_109	GGAAAGGACGAAACACCGCAGTTTGACCCTCTCGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTTTGACCCTCTCGATCG	
110	Slc25a4	Slc25a4_110	GGAAAGGACGAAACACCGGGAAGATCCCTTGCCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGATCCCTTGCCCACGT	
111	Slc25a4	Slc25a4_111	GGAAAGGACGAAACACCGTTGTGTCGTGAGAATCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTGTCGTGAGAATCCCCA	
112	Slc25a4	Slc25a4_112	GGAAAGGACGAAACACCGGGGGAAGTACCGGATCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGAAGTACCGGATCACGT	
113	Ap1s1	Ap1s1_113	GGAAAGGACGAAACACCGCCAAGAGCTCTACGTATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAGAGCTCTACGTATCGG	
114	Ap1s1	Ap1s1_114	GGAAAGGACGAAACACCGGAGCTCTTGGACAAGTACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTCTTGGACAAGTACTT	
115	Ap1s1	Ap1s1_115	GGAAAGGACGAAACACCGTCAGCCGGCAGGGAAAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCCGGCAGGGAAAACTT	

No.	*Oligo name	*Oligo name	*Sequence(5' to3')	nt#	Remarks	5'	guide sequence	3'
116	Ap1s1	Ap1s1_116	GGAAAGGACGAAACACCGTGGCCACCTCAGACAAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCACCTCAGACAAGGAG	
117	Atg5	Atg5_117	GGAAAGGACGAAACACCGAAGAGTCAGCTATTTGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGTCAGCTATTTGACGT	
118	Atg5	Atg5_118	GGAAAGGACGAAACACCGAAATGTACTGTGATGTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGTACTGTGATGTTCCA	
119	Atg5	Atg5_119	GGAAAGGACGAAACACCGCCTTCTACACTGTCCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTCTACACTGTCCATCCA	
120	Atg5	Atg5_120	GGAAAGGACGAAACACCGAAGAAAAACTCACCATTTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAAAACTCACCATTTCA	
121	Apoa1	Apoa1_121	GGAAAGGACGAAACACCGGGAGCTCTACCGCCAGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCTCTACCGCCAGAAGG	
122	Apoa1	Apoa1_122	GGAAAGGACGAAACACCGCAAGGAGGAGGATTCAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGAGGAGGATTCAAACT	
123	Apoa1	Apoa1_123	GGAAAGGACGAAACACCGGTCCCAATGGGACAAAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCCAATGGGACAAAGTGA	
124	Apoa1	Apoa1_124	GGAAAGGACGAAACACCGCTGGAAAACTGGGACACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGAAAACTGGGACACTCT	
125	Apoc2	Apoc2_125	GGAAAGGACGAAACACCGAAGTTACTGGACCTCTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTTACTGGACCTCTGCCA	
126	Apoc2	Apoc2_126	GGAAAGGACGAAACACCGAGAGGTCCAGTAACTTAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGTCCAGTAACTTAAGA	
127	Apoc2	Apoc2_127	GGAAAGGACGAAACACCGGGGAACCAGGAAGATGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAACCAGGAAGATGACTC	
128	Apoc2	Apoc2_128	GGAAAGGACGAAACACCGGAAGACATACCCGATCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGACATACCCGATCAGCA	
129	Apoc3	Apoc3_129	GGAAAGGACGAAACACCGGCAGGAGTCCGATATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGAGTCCGATATAGCTG	
130	Apoc3	Apoc3_130	GGAAAGGACGAAACACCGCATGGAACAAGCCTCCAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGAACAAGCCTCCAAGA	
131	Apoc3	Apoc3_131	GGAAAGGACGAAACACCGGGATGCGCTAAGTAGCGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATGCGCTAAGTAGCGTGC	
132	Apoc3	Apoc3_132	GGAAAGGACGAAACACCGGCCCCGGACGCTCCTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCCGGACGCTCCTCACTG	
133	Aprt	Aprt_133	GGAAAGGACGAAACACCGGAGTCCGGGTCTTTCAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTCCGGGTCTTTCAAGAG	
134	Aprt	Aprt_134	GGAAAGGACGAAACACCGCTAACAGGTCTAGACTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAACAGGTCTAGACTCCAG	
135	Aprt	Aprt_135	GGAAAGGACGAAACACCGTGTGTGCTCATCCGGAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGCTCATCCGGAAACA	
136	Aprt	Aprt_136	GGAAAGGACGAAACACCGCGCACCTGAACAGCACGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCACCTGAACAGCACGCCC	
137	Aqp7	Aqp7_137	GGAAAGGACGAAACACCGGCCACTCACCATCATGACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCACTCACCATCATGACAT	
138	Aqp7	Aqp7_138	GGAAAGGACGAAACACCGAGTCACTGCGGCATTCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCACTGCGGCATTCATGT	
139	Aqp7	Aqp7_139	GGAAAGGACGAAACACCGACACCCCAAGGACGGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCCCAAGGACGGTAACA	
140	Aqp7	Aqp7_140	GGAAAGGACGAAACACCGTTCCTGAATACATGACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCTGAATACATGACACTG	
141	Ar	Ar_141	GGAAAGGACGAAACACCGGGTGGAAAGTAATAGTCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGAAAGTAATAGTCGAT	
142	Ar	Ar_142	GGAAAGGACGAAACACCGACCAGGATACCACACTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGGATACCACACTTCGG	
143	Ar	Ar_143	GGAAAGGACGAAACACCGGACTTGGGTAGTCTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTTGGGTAGTCTACATGG	
144	Ar	Ar_144	GGAAAGGACGAAACACCGGCTCCTGGGAGGTCCACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCTGGGAGGTCCACCCG	
145	Arg1	Arg1_145	GGAAAGGACGAAACACCGAATAAACTTACTGTTCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATAAACTTACTGTTCCCCA	
146	Arg1	Arg1_146	GGAAAGGACGAAACACCGAGTATGACGTGAGAGACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTATGACGTGAGAGACCAC	
147	Arg1	Arg1_147	GGAAAGGACGAAACACCGAAATGACACATAGGTCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGACACATAGGTCAGGG	
148	Arg1	Arg1_148	GGAAAGGACGAAACACCGAGATGTACCAGGATTCTCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGTACCAGGATTCTCCT	
149	Arsb	Arsb_149	GGAAAGGACGAAACACCGGGTGGGCAGACTAGGTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGGCAGACTAGGTCTGG	
150	Arsb	Arsb_150	GGAAAGGACGAAACACCGGAATGTCTGCCGACACGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATGTCTGCCGACACGCCG	
151	Arsb	Arsb_151	GGAAAGGACGAAACACCGAGCACAGACGTATTTATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACAGACGTATTTATGCA	
152	Arsb	Arsb_152	GGAAAGGACGAAACACCGGCCAGCACGAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAGCACGAAGACCACATG	
153	Arsa	Arsa_153	GGAAAGGACGAAACACCGAAGCACGTTAGGTTCTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCACGTTAGGTTCTGACA	
154	Arsa	Arsa_154	GGAAAGGACGAAACACCGAGGAGTCCCCAAATGGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGTCCCCAAATGGCCCA	
155	Arsa	Arsa_155	GGAAAGGACGAAACACCGGTGACCTGGCCAGTAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCTGGCCAGTAGACCA	
156	Arsa	Arsa_156	GGAAAGGACGAAACACCGTCGGGAGAAAGACACATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGGAGAAAGACACATACC	
157	Asah1	Asah1_157	GGAAAGGACGAAACACCGGCAAGGTGTACGTTACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAGGTGTACGTTACCTAG	
158	Asah1	Asah1_158	GGAAAGGACGAAACACCGTAACATTTATAACATACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACATTTATAACATACCGC	
159	Asah1	Asah1_159	GGAAAGGACGAAACACCGAGTGATAAACCCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGATAAACCCTACCCACT	
160	Asah1	Asah1_160	GGAAAGGACGAAACACCGGAATATAAATAATAACACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATATAAATAATAACACTT	
161	Ass1	Ass1_161	GGAAAGGACGAAACACCGTAACATCTTACCTTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACATCTTACCTTAATCTG	
162	Ass1	Ass1_162	GGAAAGGACGAAACACCGTGGGATCCTGGAAAACCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGATCCTGGAAAACCCCA	
163	Ass1	Ass1_163	GGAAAGGACGAAACACCGAAGGCACTTCCTCACCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCACTTCCTCACCAGGT	
164	Ass1	Ass1_164	GGAAAGGACGAAACACCGTGCCTTCACCTGTAGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCTTCACCTGTAGCAACA	
165	Fxyd2	Fxyd2_165	GGAAAGGACGAAACACCGACCGGCTTACCGTACTCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGGCTTACCGTACTCGAA	
166	Fxyd2	Fxyd2_166	GGAAAGGACGAAACACCGTATGAAACCGTCCGCAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGAAACCGTCCGCAAAGG	
167	Fxyd2	Fxyd2_167	GGAAAGGACGAAACACCGGATGAGGAGGCCCACGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAGGAGGCCCACGACGA	
168	Fxyd2	Fxyd2_168	GGAAAGGACGAAACACCGCCCACTTACTGAGAATGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACTTACTGAGAATGATG	
169	Atp6v1a	Atp6v1a_169	GGAAAGGACGAAACACCGTGACTGCTGATATCCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTGCTGATATCCGACAG	
170	Atp6v1a	Atp6v1a_170	GGAAAGGACGAAACACCGAGTCGGCCATCATACTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGGCCATCATACTGACG	
171	Atp6v1a	Atp6v1a_171	GGAAAGGACGAAACACCGATGTTGCCCCCACGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTGCCCCCACGTAACAG	
172	Atp6v1a	Atp6v1a_172	GGAAAGGACGAAACACCGCTTACGGGAAAAGGGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACGGGAAAAGGGCATCG	
173	Atp6v1e1	Atp6v1e1_173	GGAAAGGACGAAACACCGCCAACTTGATGAATCAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACTTGATGAATCAAGCA	
174	Atp6v1e1	Atp6v1e1_174	GGAAAGGACGAAACACCGTTTGTAGGATCTGCTAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTAGGATCTGCTAAATG	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
175	Atp6v1e1	Atp6v1e1_175	GGAAAGGACGAAACACCGTCAGTCTTTGCGTTTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTCTTTGCGTTTGCACA	
176	Atp6v1e1	Atp6v1e1_176	GGAAAGGACGAAACACCGAGGCATCCAAGCATACCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCATCCAAGCATACCTGA	
177	Atp7a	Atp7a_177	GGAAAGGACGAAACACCGTCTATAGGGCAAAACCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTATAGGGCAAAACCTCCG	
178	Atp7a	Atp7a_178	GGAAAGGACGAAACACCGACACGGTATTGGTTAAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACGGTATTGGTTAAGACA	
179	Atp7a	Atp7a_179	GGAAAGGACGAAACACCGCAATTATAATCCACACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATTATAATCCACACCAAG	
180	Atp7a	Atp7a_180	GGAAAGGACGAAACACCGAGGGATCTTCTACTGCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGATCTTCTACTGCTCTG	
181	Atp7b	Atp7b_181	GGAAAGGACGAAACACCGAAATATAGGCCAACTCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATATAGGCCAACTCCCGG	
182	Atp7b	Atp7b_182	GGAAAGGACGAAACACCGAAAATGGCTCCCGACACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAATGGCTCCCGACACTAG	
183	Atp7b	Atp7b_183	GGAAAGGACGAAACACCGAGTTGTGTCATTACCCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGTGTCATTACCCACAT	
184	Atp7b	Atp7b_184	GGAAAGGACGAAACACCGAGACCATCAATCCCATGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCATCAATCCCATGACG	
185	Slc7a2	Slc7a2_185	GGAAAGGACGAAACACCGAGGACGTCACTATTCCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACGTCACTATTCCGATG	
186	Slc7a2	Slc7a2_186	GGAAAGGACGAAACACCGGAACGGAACAAGCATCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACGGAACAAGCATCTACG	
187	Slc7a2	Slc7a2_187	GGAAAGGACGAAACACCGGTATCTATACACTTACGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATCTATACACTTACGTCA	
188	Slc7a2	Slc7a2_188	GGAAAGGACGAAACACCGCCGAGACAACATATTTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAGACAACATATTTGGCG	
189	Auh	Auh_189	GGAAAGGACGAAACACCGCAATGTCATTGATCACCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATGTCATTGATCACCGAT	
190	Auh	Auh_190	GGAAAGGACGAAACACCGGGTTTAGTTATCAAAAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTTAGTTATCAAAAGCGG	
191	Auh	Auh_191	GGAAAGGACGAAACACCGGAGGAGGGGCTACAGCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGAGGGGCTACAGCTCGG	
192	Auh	Auh_192	GGAAAGGACGAAACACCGCCCTCCCTAACCAGGCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTCCCTAACCAGGCATTG	
193	Baat	Baat_193	GGAAAGGACGAAACACCGAGGACCAGAAAAGGCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCAGAAAAGGCCCATG	
194	Baat	Baat_194	GGAAAGGACGAAACACCGAGGCCCATTGATAAGTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCCATTGATAAGTACAG	
195	Baat	Baat_195	GGAAAGGACGAAACACCGGTAAAGGAAAGCCGCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAAGGAAAGCCGCATCCG	
196	Baat	Baat_196	GGAAAGGACGAAACACCGAAGGCACACCACCTGAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCACACCACCTGAAAGG	
197	Bcat2	Bcat2_197	GGAAAGGACGAAACACCGACGGAACGAGCCTCTACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGAACGAGCCTCTACGTG	
198	Bcat2	Bcat2_198	GGAAAGGACGAAACACCGCAGGAACTATGGACCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAACTATGGACCCACTG	
199	Bcat2	Bcat2_199	GGAAAGGACGAAACACCGGTGGAGTGGAATAACAAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAGTGGAATAACAAGGC	
200	Bcat2	Bcat2_200	GGAAAGGACGAAACACCGGCACAGAATGACGTACAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAGAATGACGTACAGGA	
201	Bckdha	Bckdha_201	GGAAAGGACGAAACACCGCATGACCAACTATGGCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGACCAACTATGGCGAGG	
202	Bckdha	Bckdha_202	GGAAAGGACGAAACACCGCAGCGAAATTGAAACCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCGAAATTGAAACCGGCG	
203	Bckdha	Bckdha_203	GGAAAGGACGAAACACCGCTTGTCTACAAACTCTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGTCTACAAACTCTGCAG	
204	Bckdha	Bckdha_204	GGAAAGGACGAAACACCGCTGGCCACGCAGATCCCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGCCACGCAGATCCCTCA	
205	Bckdk	Bckdk_205	GGAAAGGACGAAACACCGACAGCACGAGCTATACATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCACGAGCTATACATCC	
206	Bckdk	Bckdk_206	GGAAAGGACGAAACACCGAGTCCGCATCAACGGACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCCGCATCAACGGACATG	
207	Bckdk	Bckdk_207	GGAAAGGACGAAACACCGGCGACCGGAATAGAGCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGACCGGAATAGAGCATCA	
208	Bckdk	Bckdk_208	GGAAAGGACGAAACACCGTGTCTTCATGTAGCGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCTTCATGTAGCGCCAAG	
209	Glb1	Glb1_209	GGAAAGGACGAAACACCGGCGTAGGTAGTCGTAATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTAGGTAGTCGTAATCGC	
210	Glb1	Glb1_210	GGAAAGGACGAAACACCGCTTCCCGAGATGTATCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCCGAGATGTATCGGAA	
211	Glb1	Glb1_211	GGAAAGGACGAAACACCGGGGTACTCACAAGTTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTACTCACAAGTTCACGT	
212	Glb1	Glb1_212	GGAAAGGACGAAACACCGGCAGGACCTGTACGCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGACCTGTACGCCACAG	
213	Blk	Blk_213	GGAAAGGACGAAACACCGTTATTACAAAAATAACATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATTACAAAAATAACATGA	
214	Blk	Blk_214	GGAAAGGACGAAACACCGACTTGAATAGTGCTGCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTGAATAGTGCTGCACCA	
215	Blk	Blk_215	GGAAAGGACGAAACACCGCGTGAAAGATATCACCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGAAAGATATCACCACCC	
216	Blk	Blk_216	GGAAAGGACGAAACACCGAAGGTCCCTGTCATTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGTCCCTGTCATTCACAG	
217	C1qbp	C1qbp_217	GGAAAGGACGAAACACCGATCAGTCAAGAATTCAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAGTCAAGAATTCAACGA	
218	C1qbp	C1qbp_218	GGAAAGGACGAAACACCGCGTACGCTGAGCAAACCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTACGCTGAGCAAACCGAA	
219	C1qbp	C1qbp_219	GGAAAGGACGAAACACCGGTTGAAGTTACCAAGACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGAAGTTACCAAGACTGA	
220	C1qbp	C1qbp_220	GGAAAGGACGAAACACCGTCCTCCTCACCATCAAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTCCTCACCATCAAATGT	
221	Cat	Cat_221	GGAAAGGACGAAACACCGAACTTAATATCATGACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTAATATCATGACCGCG	
222	Cat	Cat_222	GGAAAGGACGAAACACCGTGGCATTGAAAAGATCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCATTGAAAAGATCTCGG	
223	Cat	Cat_223	GGAAAGGACGAAACACCGGGAGTATCTGGTGATATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTATCTGGTGATATCGT	
224	Cat	Cat_224	GGAAAGGACGAAACACCGAGTGACCGAGGGATTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGACCGAGGGATTCCCGA	
225	Cbs	Cbs_225	GGAAAGGACGAAACACCGACACTACGATGACACCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTACGATGACACCGCCG	
226	Cbs	Cbs_226	GGAAAGGACGAAACACCGTCGCCATGCCACTCCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGCCATGCCACTCCCACGT	
227	Cbs	Cbs_227	GGAAAGGACGAAACACCGGTGAGTTCTTCAATGCGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAGTTCTTCAATGCGGGT	
228	Cbs	Cbs_228	GGAAAGGACGAAACACCGATAATGTGGGGAGTCCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAATGTGGGGAGTCCGCCA	
229	Scarb2	Scarb2_229	GGAAAGGACGAAACACCGATAGAACAGGCCGAAATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGAACAGGCCGAAATTCG	
230	Scarb2	Scarb2_230	GGAAAGGACGAAACACCGAAATAAAACTGGATGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATAAAACTGGATGTACAC	
231	Scarb2	Scarb2_231	GGAAAGGACGAAACACCGAATATGATTAACGGGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATATGATTAACGGGACAGA	
232	Scarb2	Scarb2_232	GGAAAGGACGAAACACCGATAATGACACGTACCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAATGACACGTACCAACAG	
233	Chkb	Chkb_233	GGAAAGGACGAAACACCGATGGTCCCAAACAACCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTCCCAAACAACCATCG	

No.	*Oligo name	*Oligo name	*Sequence(5’ to3’)	nt#	Remarks	5'	guide sequence	3'
234	Chkb	Chkb_234	GGAAAGGACGAAACACCGGGTGCTGCTACGACTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGCTGCTACGACTCTACG	
235	Chkb	Chkb_235	GGAAAGGACGAAACACCGCGTGGTTCGGTAGTGAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGTTCGGTAGTGAGCAT	
236	Chkb	Chkb_236	GGAAAGGACGAAACACCGCAGAGCCAATCCCCAATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGCCAATCCCCAATCGG	
237	Tpp1	Tpp1_237	GGAAAGGACGAAACACCGTGAGTTTCATCGCTATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGTTTCATCGCTATGTAG	
238	Tpp1	Tpp1_238	GGAAAGGACGAAACACCGTTATGGTAGAAGGTTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATGGTAGAAGGTTACCTG	
239	Tpp1	Tpp1_239	GGAAAGGACGAAACACCGAACCTGACAGCCAAAGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTGACAGCCAAAGATGT	
240	Tpp1	Tpp1_240	GGAAAGGACGAAACACCGGATCGAGGCCAGTCTAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCGAGGCCAGTCTAGATG	
241	Cln3	Cln3_241	GGAAAGGACGAAACACCGACACTCCGACTATCCAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTCCGACTATCCAACCG	
242	Cln3	Cln3_242	GGAAAGGACGAAACACCGAATCGAGATGAGCTGTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCGAGATGAGCTGTTGTG	
243	Cln3	Cln3_243	GGAAAGGACGAAACACCGGGACCCTGGAGGGGAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACCCTGGAGGGGAAAACG	
244	Cln3	Cln3_244	GGAAAGGACGAAACACCGCAGGAGTTTGATGACAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAGTTTGATGACAAGGG	
245	Abcc2	Abcc2_245	GGAAAGGACGAAACACCGAAGACCCTGACTCATATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACCCTGACTCATATCCG	
246	Abcc2	Abcc2_246	GGAAAGGACGAAACACCGGCATTCGGAAGAAAGAACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATTCGGAAGAAAGAACTC	
247	Abcc2	Abcc2_247	GGAAAGGACGAAACACCGACTCGGATCTTGGTTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCGGATCTTGGTTACACA	
248	Abcc2	Abcc2_248	GGAAAGGACGAAACACCGGTTTAAGACGATCATGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTAAGACGATCATGACAA	
249	Cox6a1	Cox6a1_249	GGAAAGGACGAAACACCGTGAGGGTAGGCAACGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGGTAGGCAACGAACGG	
250	Cox6a1	Cox6a1_250	GGAAAGGACGAAACACCGCCGTGGGCGCCACTCGACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTGGGCGCCACTCGACAT	
251	Cox6a1	Cox6a1_251	GGAAAGGACGAAACACCGCGCCGCAGCTCGGATGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCGCAGCTCGGATGTGGA	
252	Cox6a1	Cox6a1_252	GGAAAGGACGAAACACCGTCAACGTGTTCCTCAAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAACGTGTTCCTCAAGTCG	
253	Cox8a	Cox8a_253	GGAAAGGACGAAACACCGGCCTGACCGGCTCGGCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGACCGGCTCGGCCCGG	
254	Cox8a	Cox8a_254	GGAAAGGACGAAACACCGTTCGAGTGGACCTGAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGAGTGGACCTGAGCCCG	
255	Cox8a	Cox8a_255	GGAAAGGACGAAACACCGTCTGTGTAGGATATCACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTGTAGGATATCACCAT	
256	Cox8a	Cox8a_256	GGAAAGGACGAAACACCGGCTCCCGCGCCGGCTTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCCGCGCCGGCTTCGAG	
257	Cp	Cp_257	GGAAAGGACGAAACACCGCATATAAGCATCAATTAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATATAAGCATCAATTAGGG	
258	Cp	Cp_258	GGAAAGGACGAAACACCGGCTGTGAGGAGCGACCTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGAGGAGCGACCTGGT	
259	Cp	Cp_259	GGAAAGGACGAAACACCGATGAAAAGTGTAGATCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAAAAGTGTAGATCCTAG	
260	Cp	Cp_260	GGAAAGGACGAAACACCGGCTGAACAAATACCACACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGAACAAATACCACACGA	
261	Cpox	Cpox_261	GGAAAGGACGAAACACCGTGGGCGCATAAGGATTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGCGCATAAGGATTCTTG	
262	Cpox	Cpox_262	GGAAAGGACGAAACACCGGAAGCAGCGAACCAAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCAGCGAACCAAATGAG	
263	Cpox	Cpox_263	GGAAAGGACGAAACACCGACCGACATACTTGAACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGACATACTTGAACCAAG	
264	Cpox	Cpox_264	GGAAAGGACGAAACACCGCGGACCCGCCTCTAGCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACCCGCCTCTAGCCCAG	
265	Cpt1a	Cpt1a_265	GGAAAGGACGAAACACCGCACATTGTCGTGTACCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACATTGTCGTGTACCACAG	
266	Cpt1a	Cpt1a_266	GGAAAGGACGAAACACCGCATACTGCTGTATCGTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACTGCTGTATCGTCGCA	
267	Cpt1a	Cpt1a_267	GGAAAGGACGAAACACCGACCTTGGACCCAAATTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTGGACCCAAATTGCAG	
268	Cpt1a	Cpt1a_268	GGAAAGGACGAAACACCGACGTTGGACGAATCGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTTGGACGAATCGGAACA	
269	Cpt2	Cpt2_269	GGAAAGGACGAAACACCGTCACTGGTCAAATAAGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACTGGTCAAATAAGCCAG	
270	Cpt2	Cpt2_270	GGAAAGGACGAAACACCGTCGGGAAGTCATCTAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGGAAGTCATCTAAGCAG	
271	Cpt2	Cpt2_271	GGAAAGGACGAAACACCGAAATATTGGGACATATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATATTGGGACATATCCAG	
272	Cpt2	Cpt2_272	GGAAAGGACGAAACACCGTTAAATACATATCAAACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAAATACATATCAAACCAG	
273	Crat	Crat_273	GGAAAGGACGAAACACCGACCACCCACGCATATAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCACCCACGCATATAACCG	
274	Crat	Crat_274	GGAAAGGACGAAACACCGGCAGGCCAGATGCTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGCCAGATGCTACATGG	
275	Crat	Crat_275	GGAAAGGACGAAACACCGTCCACAAGTGCAACTATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACAAGTGCAACTATGGG	
276	Crat	Crat_276	GGAAAGGACGAAACACCGTTTGCTGCCAAACTCATCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGCTGCCAAACTCATCGA	
277	Pcyt1a	Pcyt1a_277	GGAAAGGACGAAACACCGAATACGTATCTAATTGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATACGTATCTAATTGTGGG	
278	Pcyt1a	Pcyt1a_278	GGAAAGGACGAAACACCGATGCAAGACGGAACCTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCAAGACGGAACCTACAG	
279	Pcyt1a	Pcyt1a_279	GGAAAGGACGAAACACCGGCACCACCTCGTCCACGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCACCTCGTCCACGTAG	
280	Pcyt1a	Pcyt1a_280	GGAAAGGACGAAACACCGCTTTAGTAAGCCCTATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTAGTAAGCCCTATGTCA	
281	Ctsc	Ctsc_281	GGAAAGGACGAAACACCGCTGCAAGATACAACCTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAAGATACAACCTCCTG	
282	Ctsc	Ctsc_282	GGAAAGGACGAAACACCGGGCAGTAACTGATAGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAGTAACTGATAGCTGTG	
283	Ctsc	Ctsc_283	GGAAAGGACGAAACACCGTCACAACCACAACTTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACAACCACAACTTTGTGA	
284	Ctsc	Ctsc_284	GGAAAGGACGAAACACCGCTGTATTTCATCAGTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTATTTCATCAGTCATCG	
285	Ctsd	Ctsd_285	GGAAAGGACGAAACACCGTATCCGTCGGACTATGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCGTCGGACTATGACGG	
286	Ctsd	Ctsd_286	GGAAAGGACGAAACACCGTGACTCCAAGTACTACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTCCAAGTACTACCACG	
287	Ctsd	Ctsd_287	GGAAAGGACGAAACACCGGACTGTGAAACACTGCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTGTGAAACACTGCGGCG	
288	Ctsd	Ctsd_288	GGAAAGGACGAAACACCGACGTCCTTTGACATCCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTCCTTTGACATCCACTA	
289	Ctsk	Ctsk_289	GGAAAGGACGAAACACCGAAGTTGTATGTATAACGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTTGTATGTATAACGCCA	
290	Ctsk	Ctsk_290	GGAAAGGACGAAACACCGCACTCTCTATACCCCAGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTCTCTATACCCCAGAGT	
291	Ctsk	Ctsk_291	GGAAAGGACGAAACACCGCAATACGTGCAGCAGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATACGTGCAGCAGAACGG	
292	Ctsk	Ctsk_292	GGAAAGGACGAAACACCGAAGCCCAACAGGAACCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCCAACAGGAACCACAC	

No.	*Oligo name	*Oligo name	*Sequence(5’ to3’)	nt#	Remarks	5'	guide sequence	3'
293	Cyb561	Cyb561_293	GGAAAGGACGAAACACCGATGCCTATGACCATGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCCTATGACCATGCAGAG	
294	Cyb561	Cyb561_294	GGAAAGGACGAAACACCGGCACGACCAAGATCTTGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACGACCAAGATCTTGCAT	
295	Cyb561	Cyb561_295	GGAAAGGACGAAACACCGTGCTGCACTGCCGTACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTGCACTGCCGTACTATG	
296	Cyb561	Cyb561_296	GGAAAGGACGAAACACCGGTTCAGGAACTCACCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCAGGAACTCACCCACCA	
297	Cycs	Cycs_297	GGAAAGGACGAAACACCGTCTTCCGCCCGAACAGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCCGCCCGAACAGACCG	
298	Cycs	Cycs_298	GGAAAGGACGAAACACCGTTCTGTTTAGGCATCACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGTTTAGGCATCACCTG	
299	Cycs	Cycs_299	GGAAAGGACGAAACACCGGTTCGGGCGGAAGACAGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGGGCGGAAGACAGGCC	
300	Cycs	Cycs_300	GGAAAGGACGAAACACCGCTGGGGAGAGGATACCCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGGAGAGGATACCCTGA	
301	Cyp11a1	Cyp11a1_301	GGAAAGGACGAAACACCGAGAGTATCGACGCATCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTATCGACGCATCCTTG	
302	Cyp11a1	Cyp11a1_302	GGAAAGGACGAAACACCGGTATTATCAGAGGCCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATTATCAGAGGCCCATTG	
303	Cyp11a1	Cyp11a1_303	GGAAAGGACGAAACACCGGGACCTAGGACTGCTAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACCTAGGACTGCTAGTAG	
304	Cyp11a1	Cyp11a1_304	GGAAAGGACGAAACACCGCCTTACACTCAAAGGAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTACACTCAAAGGAAAAG	
305	Cyp11b2	Cyp11b2_305	GGAAAGGACGAAACACCGTGGAGAGTATGCTCCCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGAGTATGCTCCCCCGT	
306	Cyp11b2	Cyp11b2_306	GGAAAGGACGAAACACCGGACCGTGTCAACGCTCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCGTGTCAACGCTCCCAG	
307	Cyp11b2	Cyp11b2_307	GGAAAGGACGAAACACCGAGGTGCTTCAAAATGCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGCTTCAAAATGCTCGT	
308	Cyp11b2	Cyp11b2_308	GGAAAGGACGAAACACCGTTCCGCCACAATGCCACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCGCCACAATGCCACTGT	
309	Cyp17a1	Cyp17a1_309	GGAAAGGACGAAACACCGGGAGCTACTACTATCCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCTACTACTATCCGCAA	
310	Cyp17a1	Cyp17a1_310	GGAAAGGACGAAACACCGAAACGGTAGACTACCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGGTAGACTACCCACCA	
311	Cyp17a1	Cyp17a1_311	GGAAAGGACGAAACACCGTAAAATTCGAGAAAAAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAAATTCGAGAAAAAACAC	
312	Cyp17a1	Cyp17a1_312	GGAAAGGACGAAACACCGTACCATACAGACCTTTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCATACAGACCTTTACAG	
313	Cyp19a1	Cyp19a1_313	GGAAAGGACGAAACACCGAGTGACCGACATGGTGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGACCGACATGGTGTCAG	
314	Cyp19a1	Cyp19a1_314	GGAAAGGACGAAACACCGAAGGGCGAATTGTTCTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGGCGAATTGTTCTCCAA	
315	Cyp19a1	Cyp19a1_315	GGAAAGGACGAAACACCGGAGAGCTCGTCTTCAATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAGCTCGTCTTCAATACC	
316	Cyp19a1	Cyp19a1_316	GGAAAGGACGAAACACCGCCATCAAGCAGCATTTGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCAAGCAGCATTTGGAC	
317	Cyp24a1	Cyp24a1_317	GGAAAGGACGAAACACCGTTCGTTGCGATGGTCCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGTTGCGATGGTCCCGAT	
318	Cyp24a1	Cyp24a1_318	GGAAAGGACGAAACACCGCTTGCTGATAAATATCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCTGATAAATATCACAA	
319	Cyp24a1	Cyp24a1_319	GGAAAGGACGAAACACCGAGCGCCTCAACACCAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGCCTCAACACCAAAGTG	
320	Cyp24a1	Cyp24a1_320	GGAAAGGACGAAACACCGGCTGGACAAGAAAATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGACAAGAAAATCAATG	
321	Cyp27b1	Cyp27b1_321	GGAAAGGACGAAACACCGGAGAGCGTATTGGATACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAGCGTATTGGATACCTG	
322	Cyp27b1	Cyp27b1_322	GGAAAGGACGAAACACCGTGCGACGACTAAGGCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGACGACTAAGGCGCCAG	
323	Cyp27b1	Cyp27b1_323	GGAAAGGACGAAACACCGCTCAGGTGCATGGCGCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGGTGCATGGCGCTGCG	
324	Cyp27b1	Cyp27b1_324	GGAAAGGACGAAACACCGTTAGCAATCCGCAAGCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGCAATCCGCAAGCACGC	
325	Cyp7a1	Cyp7a1_325	GGAAAGGACGAAACACCGGGTGAACCTCCTTTGGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAACCTCCTTTGGACAA	
326	Cyp7a1	Cyp7a1_326	GGAAAGGACGAAACACCGTTTGATTTAGGAAGGCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGATTTAGGAAGGCCCGG	
327	Cyp7a1	Cyp7a1_327	GGAAAGGACGAAACACCGAGTATTTCCGGCACTAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTATTTCCGGCACTAGTGG	
328	Cyp7a1	Cyp7a1_328	GGAAAGGACGAAACACCGAGCACAAGAACCTGTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACAAGAACCTGTACATG	
329	Cyp7b1	Cyp7b1_329	GGAAAGGACGAAACACCGGTATGTCAGATACTAAGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATGTCAGATACTAAGTAT	
330	Cyp7b1	Cyp7b1_330	GGAAAGGACGAAACACCGACTGTCAATTTCGTCACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTCAATTTCGTCACGCA	
331	Cyp7b1	Cyp7b1_331	GGAAAGGACGAAACACCGTTTATCAAGGGTGGTTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTATCAAGGGTGGTTCACG	
332	Cyp7b1	Cyp7b1_332	GGAAAGGACGAAACACCGAGCAGAGCTTCTTACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGAGCTTCTTACCCACA	
333	Slc6a3	Slc6a3_333	GGAAAGGACGAAACACCGTAGATGATGAAGATCAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATGATGAAGATCAACCC	
334	Slc6a3	Slc6a3_334	GGAAAGGACGAAACACCGGCTCGTCAGGGAGTTAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCGTCAGGGAGTTAATGG	
335	Slc6a3	Slc6a3_335	GGAAAGGACGAAACACCGCAGGGAGGGTGACTCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGAGGGTGACTCCACGC	
336	Slc6a3	Slc6a3_336	GGAAAGGACGAAACACCGTTACTCAAAATACTCAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACTCAAAATACTCAGCAG	
337	Dbh	Dbh_337	GGAAAGGACGAAACACCGAGTGATATAGCACCAGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGATATAGCACCAGTACG	
338	Dbh	Dbh_338	GGAAAGGACGAAACACCGAACTTCCAGTCGGAGAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTCCAGTCGGAGAAACG	
339	Dbh	Dbh_339	GGAAAGGACGAAACACCGAGAGCTCTAAAATCCCTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTCTAAAATCCCTTCG	
340	Dbh	Dbh_340	GGAAAGGACGAAACACCGCGTGCCGGCAGTAGTTGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGCCGGCAGTAGTTGAGT	
341	Dbt	Dbt_341	GGAAAGGACGAAACACCGTAGATGATATCGCTTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATGATATCGCTTATGTG	
342	Dbt	Dbt_342	GGAAAGGACGAAACACCGTCATCACAATACCCGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATCACAATACCCGAAGTG	
343	Dbt	Dbt_343	GGAAAGGACGAAACACCGCTGTGAAGTTCAAAGTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGAAGTTCAAAGTGACA	
344	Dbt	Dbt_344	GGAAAGGACGAAACACCGTGGAGGCTTTGCTATCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGGCTTTGCTATCGGCG	
345	Pcbd1	Pcbd1_345	GGAAAGGACGAAACACCGAGCTGGACCACCATCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGGACCACCATCCCGAG	
346	Pcbd1	Pcbd1_346	GGAAAGGACGAAACACCGACTGCTTGAAGATAGCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCTTGAAGATAGCATCT	
347	Pcbd1	Pcbd1_347	GGAAAGGACGAAACACCGGGCACACAGGCTGAGCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCACACAGGCTGAGCGCCG	
348	Pcbd1	Pcbd1_348	GGAAAGGACGAAACACCGTGCCAAACCTGAGGGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCAAACCTGAGGGCTGTG	
349	Ddc	Ddc_349	GGAAAGGACGAAACACCGCCTAGGTGGTCGCTACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTAGGTGGTCGCTACACTG	
350	Ddc	Ddc_350	GGAAAGGACGAAACACCGTAACCCAGCTCTTTCTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACCCAGCTCTTTCTACAG	
351	Ddc	Ddc_351	GGAAAGGACGAAACACCGCCGGTATCTTCTGAATGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTATCTTCTGAATGGTG	

No.	*Oligo name	*Oligo name	*Sequence(5' to3')	nt#	Remarks	5'	guide sequence	3'
352	Ddc	Ddc_352	GGAAAGGACGAAACACCGAGCCAGTAGGGCCACCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCAGTAGGGCCACCAAGG	
353	Ddost	Ddost_353	GGAAAGGACGAAACACCGGAACTCCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTCCCCGTACTTAATGA	
354	Ddost	Ddost_354	GGAAAGGACGAAACACCGCCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAGATAAACCAATCACCC	
355	Ddost	Ddost_355	GGAAAGGACGAAACACCGAGGCAACTATGAACTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCAACTATGAACTAGCTG	
356	Ddost	Ddost_356	GGAAAGGACGAAACACCGGGTCAGAAACATCATAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCAGAAACATCATAGTTG	
357	Dgat1	Dgat1_357	GGAAAGGACGAAACACCGAGTGGTTTCAGCAATTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGGTTTCAGCAATTATCG	
358	Dgat1	Dgat1_358	GGAAAGGACGAAACACCGAAAGCGCTTTCGTATTCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCGCTTTCGTATTCGGG	
359	Dgat1	Dgat1_359	GGAAAGGACGAAACACCGATACCCGGGACAAAGACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCCGGGACAAAGACGGG	
360	Dgat1	Dgat1_360	GGAAAGGACGAAACACCGGCTCACCAATAATCACGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCACCAATAATCACGCAT	
361	Slc25a1	Slc25a1_361	GGAAAGGACGAAACACCGATGAACGAGCGAACCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAACGAGCGAACCCACCG	
362	Slc25a1	Slc25a1_362	GGAAAGGACGAAACACCGGAATAATCTCTCTAACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATAATCTCTCTAACCCCG	
363	Slc25a1	Slc25a1_363	GGAAAGGACGAAACACCGACTGCGACTGTACTGAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCGACTGTACTGAAGCA	
364	Slc25a1	Slc25a1_364	GGAAAGGACGAAACACCGCTTCACGTATTCGGTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCACGTATTCGGTCGGGA	
365	Dhcr7	Dhcr7_365	GGAAAGGACGAAACACCGCTGTAGCTATATCCAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTAGCTATATCCAATGCG	
366	Dhcr7	Dhcr7_366	GGAAAGGACGAAACACCGTGTTCTTCAATGGACGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCTTCAATGGACGACCA	
367	Dhcr7	Dhcr7_367	GGAAAGGACGAAACACCGGCCCTTGATCATTGCGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTTGATCATTGCGAACG	
368	Dhcr7	Dhcr7_368	GGAAAGGACGAAACACCGAGCCTAGGTACCACCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCTAGGTACCACCCAAAG	
369	Dhfr	Dhfr_369	GGAAAGGACGAAACACCGGACATGGTTTGGATAGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATGGTTTGGATAGTCGG	
370	Dhfr	Dhfr_370	GGAAAGGACGAAACACCGAACCTCAGAGAACCACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTCAGAGAACCACCACG	
371	Dhfr	Dhfr_371	GGAAAGGACGAAACACCGTCGCCGTGTCCCAAAATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGCCGTGTCCCAAAATATG	
372	Dhfr	Dhfr_372	GGAAAGGACGAAACACCGCAGCCCGGCCAATACCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCCGGCCAATACCTGAG	
373	Dld	Dld_373	GGAAAGGACGAAACACCGGGTGGAACATGCTTGAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGAACATGCTTGAACGT	
374	Dld	Dld_374	GGAAAGGACGAAACACCGGCAGTAAAAGCATTAACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTAAAAGCATTAACAGG	
375	Dld	Dld_375	GGAAAGGACGAAACACCGAGAGAAGCTGGTTGTTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGAAGCTGGTTGTTATTG	
376	Dld	Dld_376	GGAAAGGACGAAACACCGCAAAAACATCCTTGTAGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAAACATCCTTGTAGCTA	
377	Dpagt1	Dpagt1_377	GGAAAGGACGAAACACCGCTTTGGCAATACAACCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGGCAATACAACCATCG	
378	Dpagt1	Dpagt1_378	GGAAAGGACGAAACACCGTCCTGTACTACGTCTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGTACTACGTCTACATG	
379	Dpagt1	Dpagt1_379	GGAAAGGACGAAACACCGCATGCCCGCAAAGTAACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCCCGCAAAGTAACAGA	
380	Dpagt1	Dpagt1_380	GGAAAGGACGAAACACCGAGCACCGCTGATCACTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACCGCTGATCACTCCCT	
381	Dpm1	Dpm1_381	GGAAAGGACGAAACACCGATGGAATCAAACACGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGAATCAAACACGCCACG	
382	Dpm1	Dpm1_382	GGAAAGGACGAAACACCGTCTCTGGAACTCGATACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTGGAACTCGATACAAG	
383	Dpm1	Dpm1_383	GGAAAGGACGAAACACCGTGATTAATTTGGCAGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATTAATTTGGCAGCCGTG	
384	Dpm1	Dpm1_384	GGAAAGGACGAAACACCGGAGAAGCCCCTTCTACCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAAGCCCCTTCTACCTCT	
385	Dpm2	Dpm2_385	GGAAAGGACGAAACACCGTGATCAAGCTAACGGCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATCAAGCTAACGGCGACA	
386	Dpm2	Dpm2_386	GGAAAGGACGAAACACCGCTTCACCTACTACACCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCACCTACTACACCACTT	
387	Dpm2	Dpm2_387	GGAAAGGACGAAACACCGACCGGGACAGACCAAGCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGGGACAGACCAAGCAGT	
388	Dpm2	Dpm2_388	GGAAAGGACGAAACACCGACATGCTGGCTGTCAATGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATGCTGGCTGTCAATGAA	
389	Slc26a2	Slc26a2_389	GGAAAGGACGAAACACCGGAGCCGACACCATGACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCCGACACCATGACTCCG	
390	Slc26a2	Slc26a2_390	GGAAAGGACGAAACACCGATGGCCGGAGAGCTTTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCCGGAGAGCTTTCCGT	
391	Slc26a2	Slc26a2_391	GGAAAGGACGAAACACCGACTGTGCCTTATGATTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTGCCTTATGATTGGTG	
392	Slc26a2	Slc26a2_392	GGAAAGGACGAAACACCGTCCAAAATGAGAAGCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAAAATGAGAAGCCAATG	
393	Ebp	Ebp_393	GGAAAGGACGAAACACCGGAAAGGCAATCACTACCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGGCAATCACTACCCAT	
394	Ebp	Ebp_394	GGAAAGGACGAAACACCGGGGGCCTAATTGTGATCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCCTAATTGTGATCACG	
395	Ebp	Ebp_395	GGAAAGGACGAAACACCGCCAGGATATGCGAAGTCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGATATGCGAAGTCGGG	
396	Ebp	Ebp_396	GGAAAGGACGAAACACCGAAGCTGTAGGACAAAGCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCTGTAGGACAAAGCGGA	
397	Egf	Egf_397	GGAAAGGACGAAACACCGTCACCGTAACAGATATGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACCGTAACAGATATGACA	
398	Egf	Egf_398	GGAAAGGACGAAACACCGAGACTGTTCTGGACGGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACTGTTCTGGACGGACGT	
399	Egf	Egf_399	GGAAAGGACGAAACACCGTGTTCATCGCCTGACAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCATCGCCTGACAATGG	
400	Egf	Egf_400	GGAAAGGACGAAACACCGGTGTCACAAAGGATGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTCACAAAGGATGGATGG	
401	Eno3	Eno3_401	GGAAAGGACGAAACACCGAGCCGGTTACCCGGACAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCGGTTACCCGGACAAGG	
402	Eno3	Eno3_402	GGAAAGGACGAAACACCGGAGACAAAGCACGATACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACAAAGCACGATACCTG	
403	Eno3	Eno3_403	GGAAAGGACGAAACACCGCTTCCAGAAACTAAGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCAGAAACTAAGTGTTG	
404	Eno3	Eno3_404	GGAAAGGACGAAACACCGCTGCAAGATCTGCGATGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAAGATCTGCGATGTGT	
405	Ephx1	Ephx1_405	GGAAAGGACGAAACACCGCAGAAGTTCTACATTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAAGTTCTACATTCAAGG	
406	Ephx1	Ephx1_406	GGAAAGGACGAAACACCGTGGAAGCGACTGCCCTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGCGACTGCCCTCCAA	
407	Ephx1	Ephx1_407	GGAAAGGACGAAACACCGCCCCACCACCCATCTTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCACCACCCATCTTCAAG	
408	Ephx1	Ephx1_408	GGAAAGGACGAAACACCGGGAGGAATGAGTTTGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGAATGAGTTTGACTGG	
409	Epm2a	Epm2a_409	GGAAAGGACGAAACACCGTGTACCAGAACGTGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACCAGAACGTGTCAACG	
410	Epm2a	Epm2a_410	GGAAAGGACGAAACACCGCCGTTGCTGCACATATAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTTGCTGCACATATAATG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
411	Epm2a	Epm2a_411	GGAAAGGACGAAACACCGGCCCGGCCTGTGGCTCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCGGCCTGTGGCTCGCCG	
412	Epm2a	Epm2a_412	GGAAAGGACGAAACACCGGTCACATGTTCCAGTTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCACATGTTCCAGTTGGCG	
413	Esr1	Esr1_413	GGAAAGGACGAAACACCGGGCATACGGAAAGACCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCATACGGAAAGACCGCCG	
414	Esr1	Esr1_414	GGAAAGGACGAAACACCGCACTGTGTTCAACTACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTGTGTTCAACTACCCCG	
415	Esr1	Esr1_415	GGAAAGGACGAAACACCGTATTCAGAATAGATCATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTCAGAATAGATCATGGG	
416	Esr1	Esr1_416	GGAAAGGACGAAACACCGAGAGGCATAGTCATTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGCATAGTCATTGCACA	
417	Esr2	Esr2_417	GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCGCTTGGACTAGTAACA	
418	Esr2	Esr2_418	GGAAAGGACGAAACACCGTTCGTGACGGCTCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGTGACGGCTCTCTACAT	
419	Esr2	Esr2_419	GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTAGGAATGGTCAAGTG	
420	Esr2	Esr2_420	GGAAAGGACGAAACACCGCGGCTCACTAGCACATTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCTCACTAGCACATTGGG	
421	Ext1	Ext1_421	GGAAAGGACGAAACACCGCTTATATCACGTCCATAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTATATCACGTCCATAACG	
422	Ext1	Ext1_422	GGAAAGGACGAAACACCGGATTGTATTAACTACACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTGTATTAACTACACTAG	
423	Ext1	Ext1_423	GGAAAGGACGAAACACCGCTGACTACACTGAGGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGACTACACTGAGGACGTG	
424	Ext1	Ext1_424	GGAAAGGACGAAACACCGCAAAGGCAAGAAGTGCCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGGCAAGAAGTGCCGCA	
425	Ext2	Ext2_425	GGAAAGGACGAAACACCGTGTTTCGATGTCTACCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTTCGATGTCTACCGCTG	
426	Ext2	Ext2_426	GGAAAGGACGAAACACCGCTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGAGGACTCAATGGAGTG	
427	Ext2	Ext2_427	GGAAAGGACGAAACACCGTCCTGCAGAACATCCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGCAGAACATCCCACAG	
428	Ext2	Ext2_428	GGAAAGGACGAAACACCGAGGGCAGTGTTGTAATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCAGTGTTGTAATCTGG	
429	Fah	Fah_429	GGAAAGGACGAAACACCGCCCCGATTCGAAGACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCGATTCGAAGACCCATG	
430	Fah	Fah_430	GGAAAGGACGAAACACCGCCGATGGCTACACCAATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGATGGCTACACCAATCCG	
431	Fah	Fah_431	GGAAAGGACGAAACACCGACATCAACATGTCTTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATCAACATGTCTTCGATG	
432	Fah	Fah_432	GGAAAGGACGAAACACCGAATGGGAGTACGTCCCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGGGAGTACGTCCCACTT	
433	Fbp1	Fbp1_433	GGAAAGGACGAAACACCGCATGGCAAGGACCAACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGCAAGGACCAACATGG	
434	Fbp1	Fbp1_434	GGAAAGGACGAAACACCGCACAAGAACACAGGTAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAAGAACACAGGTAGCGT	
435	Fbp1	Fbp1_435	GGAAAGGACGAAACACCGTGGCTCAACCAATGTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCTCAACCAATGTGACTG	
436	Fbp1	Fbp1_436	GGAAAGGACGAAACACCGAACATCTACAGCCTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATCTACAGCCTTAATGA	
437	Fdxr	Fdxr_437	GGAAAGGACGAAACACCGCCAGAAAACAGACATCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGAAAACAGACATCACAG	
438	Fdxr	Fdxr_438	GGAAAGGACGAAACACCGTCCATTGTACCAGCCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCATTGTACCAGCCCACAA	
439	Fdxr	Fdxr_439	GGAAAGGACGAAACACCGGCTTCTCGTAGATGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCTCGTAGATGTCTACG	
440	Fdxr	Fdxr_440	GGAAAGGACGAAACACCGCAGATGTCCCCCGTCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATGTCCCCCGTCCAAGG	
441	Fech	Fech_441	GGAAAGGACGAAACACCGCATTTACAGATACTATAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTTACAGATACTATAACG	
442	Fech	Fech_442	GGAAAGGACGAAACACCGCGTACTTACAGACATCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTACTTACAGACATCGGCA	
443	Fech	Fech_443	GGAAAGGACGAAACACCGGGCATGATGTACCTTCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCATGATGTACCTTCTCCG	
444	Fech	Fech_444	GGAAAGGACGAAACACCGGGCATATTGATGTTAAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCATATTGATGTTAAACAT	
445	Lpin1	Lpin1_445	GGAAAGGACGAAACACCGGGGGGTACGTTGAAATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGGTACGTTGAAATCGAG	
446	Lpin1	Lpin1_446	GGAAAGGACGAAACACCGCAGTCGCCAACAATGGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTCGCCAACAATGGCCCG	
447	Lpin1	Lpin1_447	GGAAAGGACGAAACACCGGACCACAGAGAGATCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCACAGAGAGATCACCAA	
448	Lpin1	Lpin1_448	GGAAAGGACGAAACACCGCCATTTAAAACAGGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATTTAAAACAGGCCACTG	
449	Folr1	Folr1_449	GGAAAGGACGAAACACCGGACAATTTACACGACCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAATTTACACGACCAGGT	
450	Folr1	Folr1_450	GGAAAGGACGAAACACCGAGTTCGGGGAACACTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTCGGGGAACACTCATAG	
451	Folr1	Folr1_451	GGAAAGGACGAAACACCGCCAGTTGAACCGGTACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGTTGAACCGGTACAGGT	
452	Folr1	Folr1_452	GGAAAGGACGAAACACCGCTCCACCTACTCCTTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCACCTACTCCTTACCCG	
453	Fxn	Fxn_453	GGAAAGGACGAAACACCGAGGGAACCGATCGTAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGAACCGATCGTAACCTG	
454	Fxn	Fxn_454	GGAAAGGACGAAACACCGCGAAGCGCGTACTCACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAGCGCGTACTCACGGCG	
455	Fxn	Fxn_455	GGAAAGGACGAAACACCGGCGCGGGTTCCCGACCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCGGGTTCCCGACCCAGG	
456	Fxn	Fxn_456	GGAAAGGACGAAACACCGTGGGGACATTGGACAACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGGACATTGGACAACCCA	
457	Ftcd	Ftcd_457	GGAAAGGACGAAACACCGCAGGTTAAGAGCAATACGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGTTAAGAGCAATACGGT	
458	Ftcd	Ftcd_458	GGAAAGGACGAAACACCGCCGAACAAAACCGCGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAACAAAACCGCGCAGTG	
459	Ftcd	Ftcd_459	GGAAAGGACGAAACACCGGCACTGTCTACACTTTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACTGTCTACACTTTCGTG	
460	Ftcd	Ftcd_460	GGAAAGGACGAAACACCGCACAGCTCAAACAGGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGCTCAAACAGGCCGAG	
461	Fth1	Fth1_461	GGAAAGGACGAAACACCGCACCATAGACAGATAGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCATAGACAGATAGACGT	
462	Fth1	Fth1_462	GGAAAGGACGAAACACCGAGTGCGCCAGAACTACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGCGCCAGAACTACCACC	
463	Fth1	Fth1_463	GGAAAGGACGAAACACCGGGAGAGCGGGCTGAATGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAGCGGGCTGAATGCAA	
464	Fth1	Fth1_464	GGAAAGGACGAAACACCGTCTTCAGAGCCACATCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCAGAGCCACATCATCT	
465	Ganab	Ganab_465	GGAAAGGACGAAACACCGGATAAAGTTAGTCTCGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAAAGTTAGTCTCGCGCT	
466	Ganab	Ganab_466	GGAAAGGACGAAACACCGCAGACCCATATAGAGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACCCATATAGAGCCATG	
467	Ganab	Ganab_467	GGAAAGGACGAAACACCGAAGTCCAAACCTACAGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCCAAACCTACAGACGT	
468	Ganab	Ganab_468	GGAAAGGACGAAACACCGACTCGGTATCGAGGCCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCGGTATCGAGGCCGCCG	
469	G6pc	G6pc_469	GGAAAGGACGAAACACCGGGTGTTTGAACGTCATCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTTTGAACGTCATCTTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
470	G6pc	G6pc_470	GGAAAGGACGAAACACCGGTTGTCCAAACAGAATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTCCAAACAGAATCCTG	
471	G6pc	G6pc_471	GGAAAGGACGAAACACCGGGTCAGCAATCACAGACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCAGCAATCACAGACACA	
472	G6pc	G6pc_472	GGAAAGGACGAAACACCGACAAGACTCCAGCCACGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAAGACTCCAGCCACGACC	
473	Slc37a4	Slc37a4_473	GGAAAGGACGAAACACCGCTACGTTGACCAGACCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACGTTGACCAGACCAACC	
474	Slc37a4	Slc37a4_474	GGAAAGGACGAAACACCGTCTTTACTCCGAAGACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTACTCCGAAGACCACG	
475	Slc37a4	Slc37a4_475	GGAAAGGACGAAACACCGCACAAACTTGCTGATGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAAACTTGCTGATGGCGT	
476	Slc37a4	Slc37a4_476	GGAAAGGACGAAACACCGCAGAGCGATCTCATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGCGATCTCATCCACCA	
477	Gaa	Gaa_477	GGAAAGGACGAAACACCGACCATCCCCACTTTACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCATCCCCACTTTACAGCG	
478	Gaa	Gaa_478	GGAAAGGACGAAACACCGGAGTTACAGGCCCTACGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTTACAGGCCCTACGACG	
479	Gaa	Gaa_479	GGAAAGGACGAAACACCGCTAACCTGGAGGTCAACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAACCTGGAGGTCAACGGG	
480	Gaa	Gaa_480	GGAAAGGACGAAACACCGACCTGAGCTCTACAGAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTGAGCTCTACAGAGTCG	
481	Gabra1	Gabra1_481	GGAAAGGACGAAACACCGCAGAGAGCCAGCCCGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGAGCCAGCCCGTTCAG	
482	Gabra1	Gabra1_482	GGAAAGGACGAAACACCGCAGTGTCACTTACCATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGTCACTTACCATATCG	
483	Gabra1	Gabra1_483	GGAAAGGACGAAACACCGAGAATAACTGTCATTATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATAACTGTCATTATGCA	
484	Gabra1	Gabra1_484	GGAAAGGACGAAACACCGACGCAGGAGCTTATTAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGCAGGAGCTTATTAGGCA	
485	Gabra6	Gabra6_485	GGAAAGGACGAAACACCGGGAAGTTAACCAATCTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGTTAACCAATCTCATG	
486	Gabra6	Gabra6_486	GGAAAGGACGAAACACCGGGGACTTCTACTGAGTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACTTCTACTGAGTAAAG	
487	Gabra6	Gabra6_487	GGAAAGGACGAAACACCGTCTACTCTGAAAATGTCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTACTCTGAAAATGTCAGT	
488	Gabra6	Gabra6_488	GGAAAGGACGAAACACCGTTAAGCTCAGAATCTCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAAGCTCAGAATCTCAGCA	
489	Gabrb1	Gabrb1_489	GGAAAGGACGAAACACCGTCTGTCCACAGGAATCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTCCACAGGAATCACTA	
490	Gabrb1	Gabrb1_490	GGAAAGGACGAAACACCGCACTTCAGATGGCTATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTCAGATGGCTATACCA	
491	Gabrb1	Gabrb1_491	GGAAAGGACGAAACACCGATAGTCGTGGATATGCCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGTCGTGGATATGCCCCT	
492	Gabrb1	Gabrb1_492	GGAAAGGACGAAACACCGCAAGAAATCATTTGTGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGAAATCATTTGTGCATG	
493	Gabrb2	Gabrb2_493	GGAAAGGACGAAACACCGATGATTCGATTGCATCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATTCGATTGCATCCCGA	
494	Gabrb2	Gabrb2_494	GGAAAGGACGAAACACCGTAACCAGCGACATATTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACCAGCGACATATTACTA	
495	Gabrb2	Gabrb2_495	GGAAAGGACGAAACACCGCTTGACTTTGGACAACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGACTTTGGACAACCGAG	
496	Gabrb2	Gabrb2_496	GGAAAGGACGAAACACCGGATGAGTTTATAATCTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAGTTTATAATCTACGA	
497	Gabrb3	Gabrb3_497	GGAAAGGACGAAACACCGCCTCACGCTTGACAATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCACGCTTGACAATCGAG	
498	Gabrb3	Gabrb3_498	GGAAAGGACGAAACACCGCCTGGTAGATGGCTACACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGTAGATGGCTACACTA	
499	Gabrb3	Gabrb3_499	GGAAAGGACGAAACACCGCGCCTGAGACCCGACTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCTGAGACCCGACTTCGG	
500	Gabrb3	Gabrb3_500	GGAAAGGACGAAACACCGCGAAAACTCAATGAAAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAAACTCAATGAAAGTCG	
501	Gabrd	Gabrd_501	GGAAAGGACGAAACACCGTGTGGCGCTTGCCCTAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCGCTTGCCCTAGAGG	
502	Gabrd	Gabrd_502	GGAAAGGACGAAACACCGGTAACTGGTGATAGTGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAACTGGTGATAGTGAACT	
503	Gabrd	Gabrd_503	GGAAAGGACGAAACACCGAACCATACCAACGAGACCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCATACCAACGAGACCTT	
504	Gabrd	Gabrd_504	GGAAAGGACGAAACACCGTATCCGCCTACAGCCTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCGCCTACAGCCTGATG	
505	Gabrg2	Gabrg2_505	GGAAAGGACGAAACACCGAACAAACTTCGACCTGACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAAACTTCGACCTGACAT	
506	Gabrg2	Gabrg2_506	GGAAAGGACGAAACACCGGGTTGAATAGCAATATGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTGAATAGCAATATGGTG	
507	Gabrg2	Gabrg2_507	GGAAAGGACGAAACACCGTCCTGCTATCGCTCTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGCTATCGCTCTACCCA	
508	Gabrg2	Gabrg2_508	GGAAAGGACGAAACACCGTACAACTGGAGAACTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAACTGGAGAACTCCAGG	
509	Gad1	Gad1_509	GGAAAGGACGAAACACCGCTATTCCATAAAGAAAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATTCCATAAAGAAAGCCG	
510	Gad1	Gad1_510	GGAAAGGACGAAACACCGGACATTTGATCGCTCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATTTGATCGCTCCACCA	
511	Gad1	Gad1_511	GGAAAGGACGAAACACCGGCGGTTGCATTGACATAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGTTGCATTGACATAAAG	
512	Gad1	Gad1_512	GGAAAGGACGAAACACCGAGATGAGAGAGATCGTTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGAGAGAGATCGTTGGA	
513	Galc	Galc_513	GGAAAGGACGAAACACCGAGTTGCCTTATGGACGAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGCCTTATGGACGAAGT	
514	Galc	Galc_514	GGAAAGGACGAAACACCGCTAGATGAGAATTATTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGATGAGAATTATTTCCG	
515	Galc	Galc_515	GGAAAGGACGAAACACCGGTCGGAGTCGTCTAGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCGGAGTCGTCTAGCACGT	
516	Galc	Galc_516	GGAAAGGACGAAACACCGCATAGCGAGCGATAATCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAGCGAGCGATAATCTCT	
517	B4galnt1	B4galnt1_517	GGAAAGGACGAAACACCGTCTAGCAGATCGAGTCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAGCAGATCGAGTCTCGG	
518	B4galnt1	B4galnt1_518	GGAAAGGACGAAACACCGTGACCGTAGGGTAAAAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACCGTAGGGTAAAAGCGT	
519	B4galnt1	B4galnt1_519	GGAAAGGACGAAACACCGGTTCGCAGGTCGGAACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGCAGGTCGGAACCTGG	
520	B4galnt1	B4galnt1_520	GGAAAGGACGAAACACCGTGCAGTTGTGAATCCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTTGTGAATCCAAGGG	
521	Galnt3	Galnt3_521	GGAAAGGACGAAACACCGTACGGAAGCAACCATAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGGAAGCAACCATAACCG	
522	Galnt3	Galnt3_522	GGAAAGGACGAAACACCGAGCTGCCCCTAGCAACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGCCCCTAGCAACCGCG	
523	Galnt3	Galnt3_523	GGAAAGGACGAAACACCGAAAAACCGGCTTCAACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAACCGGCTTCAACTCCG	
524	Galnt3	Galnt3_524	GGAAAGGACGAAACACCGGTGGACGGTCCTAAGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACGGTCCTAAGCAGCG	
525	Galt	Galt_525	GGAAAGGACGAAACACCGAGAAAGGTACCATCATAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAGGTACCATCATAGTG	
526	Galt	Galt_526	GGAAAGGACGAAACACCGGCAGCGTCACATCCGACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCGTCACATCCGACCAG	
527	Galt	Galt_527	GGAAAGGACGAAACACCGGGGTTGAGTGGGTCGTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTTGAGTGGGTCGTGGCG	
528	Galt	Galt_528	GGAAAGGACGAAACACCGGGACGAGTGGGTGTTAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACGAGTGGGTGTTAGTGT	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
529	Gamt	Gamt_529	GGAAAGGACGAAACACCGAGACGCGTCATAGGCCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGCGTCATAGGCCGCGG	
530	Gamt	Gamt_530	GGAAAGGACGAAACACCGCTATATGCATGCGCTAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATATGCATGCGCTAGCGG	
531	Gamt	Gamt_531	GGAAAGGACGAAACACCGGATTATTGAGTGCAATGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTATTGAGTGCAATGATG	
532	Gamt	Gamt_532	GGAAAGGACGAAACACCGATCAAAGTGACCGTCAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAAAGTGACCGTCAGGCA	
533	Gata1	Gata1_533	GGAAAGGACGAAACACCGGTCACCGGCAGTGCTTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCACCGGCAGTGCTTACGG	
534	Gata1	Gata1_534	GGAAAGGACGAAACACCGAGTATGGAGGGAATTCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTATGGAGGGAATTCCTGG	
535	Gata1	Gata1_535	GGAAAGGACGAAACACCGGAGCAACGGCTACTCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCAACGGCTACTCCACTG	
536	Gata1	Gata1_536	GGAAAGGACGAAACACCGGGCCTCAGCTTCTCTGTAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTCAGCTTCTCTGTAGT	
537	Gba	Gba_537	GGAAAGGACGAAACACCGCGTTACGAGAGCACTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTTACGAGAGCACTCGACG	
538	Gba	Gba_538	GGAAAGGACGAAACACCGGGATAACTGGAAGTCGTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATAACTGGAAGTCGTTAG	
539	Gba	Gba_539	GGAAAGGACGAAACACCGGACTGGCAAAGAGTGAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTGGCAAAGAGTGAAATG	
540	Gba	Gba_540	GGAAAGGACGAAACACCGCGGAGAATGAACCTACAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGAGAATGAACCTACAGCA	
541	Gch1	Gch1_541	GGAAAGGACGAAACACCGGCACCAATGGGTTCTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCAATGGGTTCTCCGAG	
542	Gch1	Gch1_542	GGAAAGGACGAAACACCGCCCTTCCTACAAATGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTTCCTACAAATGGAACA	
543	Gch1	Gch1_543	GGAAAGGACGAAACACCGGGTGAACCTCCCCAAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAACCTCCCCAAACTGG	
544	Gch1	Gch1_544	GGAAAGGACGAAACACCGGTACTTCACCAAGGGATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACTTCACCAAGGGATACC	
545	Gdap1	Gdap1_545	GGAAAGGACGAAACACCGTCCTTGTGGTTGCATAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTTGTGGTTGCATAAGCG	
546	Gdap1	Gdap1_546	GGAAAGGACGAAACACCGAAGATAATCAATGATCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGATAATCAATGATCTGAG	
547	Gdap1	Gdap1_547	GGAAAGGACGAAACACCGTGTGTAAGCATCCATTGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTAAGCATCCATTGGCA	
548	Gdap1	Gdap1_548	GGAAAGGACGAAACACCGAGAAAACCCTGACTTACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAACCCTGACTTACAAG	
549	Gpd1	Gpd1_549	GGAAAGGACGAAACACCGGATGGGGTACCACAAAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGGGTACCACAAAAACC	
550	Gpd1	Gpd1_550	GGAAAGGACGAAACACCGACCCAACTTTCGCATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCAACTTTCGCATCACTG	
551	Gpd1	Gpd1_551	GGAAAGGACGAAACACCGGTCTTCCTCAAACACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTTCCTCAAACACCCACA	
552	Gpd1	Gpd1_552	GGAAAGGACGAAACACCGGTTGGAGCTCACCACATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGAGCTCACCACATTGG	
553	Gfpt1	Gfpt1_553	GGAAAGGACGAAACACCGTGTGGCACAAGTTACCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCACAAGTTACCACGC	
554	Gfpt1	Gfpt1_554	GGAAAGGACGAAACACCGAAGCTGCGGTCTTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCTGCGGTCTTTCCCGTG	
555	Gfpt1	Gfpt1_555	GGAAAGGACGAAACACCGGGAGAGAGGAGCCTTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAGAGGAGCCTTAACTG	
556	Gfpt1	Gfpt1_556	GGAAAGGACGAAACACCGTCTGTTGTGAACACAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTTGTGAACACAATGAG	
557	Ggps1	Ggps1_557	GGAAAGGACGAAACACCGGAGCCACTGGGAAACCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCCACTGGGAAACCACGT	
558	Ggps1	Ggps1_558	GGAAAGGACGAAACACCGAGCCCAAGTGTGTCAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCAAGTGTGTCAAGCAG	
559	Ggps1	Ggps1_559	GGAAAGGACGAAACACCGGGTGAGAAGCAAACTTTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAGAAGCAAACTTTCAC	
560	Ggps1	Ggps1_560	GGAAAGGACGAAACACCGTGTCCCTCCAGTAAATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCCTCCAGTAAATATCG	
561	B4galt1	B4galt1_561	GGAAAGGACGAAACACCGGGCCAGAGAGGTAATAGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCAGAGAGGTAATAGACG	
562	B4galt1	B4galt1_562	GGAAAGGACGAAACACCGCAGGGCTGGAGTCGAGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGCTGGAGTCGAGACCC	
563	B4galt1	B4galt1_563	GGAAAGGACGAAACACCGGCTCAATATTGGCTTTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCAATATTGGCTTTCAAG	
564	B4galt1	B4galt1_564	GGAAAGGACGAAACACCGTGATGTGGACCTCATTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGTGGACCTCATTCCGA	
565	Ggt1	Ggt1_565	GGAAAGGACGAAACACCGACTGACGTATCACCGTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGACGTATCACCGTATCG	
566	Ggt1	Ggt1_566	GGAAAGGACGAAACACCGCGTACAGGGTCGCATCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTACAGGGTCGCATCACCG	
567	Ggt1	Ggt1_567	GGAAAGGACGAAACACCGGAATTCAGGCTCATAGTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATTCAGGCTCATAGTAGG	
568	Ggt1	Ggt1_568	GGAAAGGACGAAACACCGCGACCACGTGTACTCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACCACGTGTACTCCAGGG	
569	Gif	Gif_569	GGAAAGGACGAAACACCGACGTGAGAGCCATAACGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTGAGAGCCATAACGGTG	
570	Gif	Gif_570	GGAAAGGACGAAACACCGCCTGGCCGGCGCCTACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGCCGGCGCCTACAACG	
571	Gif	Gif_571	GGAAAGGACGAAACACCGTACTCAACGAGATTAAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTCAACGAGATTAAGCAA	
572	Gif	Gif_572	GGAAAGGACGAAACACCGTATGTACAACAAGATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGTACAACAAGATTCCTG	
573	Gclc	Gclc_573	GGAAAGGACGAAACACCGTGTGCCGGTCCTTGACTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCCGGTCCTTGACTGCG	
574	Gclc	Gclc_574	GGAAAGGACGAAACACCGCAATATGAGGAAACGCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATATGAGGAAACGCCGGA	
575	Gclc	Gclc_575	GGAAAGGACGAAACACCGAGAAACATCCGGCATCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAACATCCGGCATCGGAG	
576	Gclc	Gclc_576	GGAAAGGACGAAACACCGTGTAGATGATAGAACACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAGATGATAGAACACGGG	
577	Galk1	Galk1_577	GGAAAGGACGAAACACCGCTGGAAAGCCCACCCCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGAAAGCCCACCCCCCAG	
578	Galk1	Galk1_578	GGAAAGGACGAAACACCGGGGCCGCGTCAACCTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCCGCGTCAACCTCATCG	
579	Galk1	Galk1_579	GGAAAGGACGAAACACCGAGTTGGTCCATGATGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGGTCCATGATGCCACA	
580	Galk1	Galk1_580	GGAAAGGACGAAACACCGACAGTGGGCCAATTATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTGGGCCAATTATGTCA	
581	Glul	Glul_581	GGAAAGGACGAAACACCGGATTACGGGGACAAATGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTACGGGGACAAATGCGG	
582	Glul	Glul_582	GGAAAGGACGAAACACCGTGGAAGGCCAACCAAATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGGCCAACCAAATGGG	
583	Glul	Glul_583	GGAAAGGACGAAACACCGCTTGCCCAGAGTTACCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCCCAGAGTTACCTGAG	
584	Glul	Glul_584	GGAAAGGACGAAACACCGTATTTCTAGAGACCAACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTTCTAGAGACCAACTTG	
585	Glra1	Glra1_585	GGAAAGGACGAAACACCGCCACTTCCACGAAATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTTCCACGAAATCACCA	
586	Glra1	Glra1_586	GGAAAGGACGAAACACCGTTCCATCGCTGAGACAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCATCGCTGAGACAACCA	
587	Glra1	Glra1_587	GGAAAGGACGAAACACCGATGCTGCACCAGCTCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCTGCACCAGCTCGTGTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
588	Glra1	Glra1_588	GGAAAGGACGAAACACCGTCCTGGATAAGCTCATGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGGATAAGCTCATGGGG	
589	Glrb	Glrb_589	GGAAAGGACGAAACACCGAGGTTACTACACTTGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTTACTACACTTGTGTGG	
590	Glrb	Glrb_590	GGAAAGGACGAAACACCGGGAAACAGAGTTAAGTCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAACAGAGTTAAGTCTAG	
591	Glrb	Glrb_591	GGAAAGGACGAAACACCGCACAGCGTACTCCACGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGCGTACTCCACGAGGG	
592	Glrb	Glrb_592	GGAAAGGACGAAACACCGCCACCATGTATAAGTGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCATGTATAAGTGCTTG	
593	Slc6a9	Slc6a9_593	GGAAAGGACGAAACACCGATACCTCTGCTATCGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCTCTGCTATCGCAACG	
594	Slc6a9	Slc6a9_594	GGAAAGGACGAAACACCGGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGTACATGATACCCGTGA	
595	Slc6a9	Slc6a9_595	GGAAAGGACGAAACACCGATGGTGGTGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTGGTGTCCACATACAT	
596	Slc6a9	Slc6a9_596	GGAAAGGACGAAACACCGTGTGCTACCAGCGTCTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCTACCAGCGTCTACGC	
597	Gm2a	Gm2a_597	GGAAAGGACGAAACACCGGATCCAACCTGACCCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCAACCTGACCCCATTG	
598	Gm2a	Gm2a_598	GGAAAGGACGAAACACCGATTCCTTGTGTAGAACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCTTGTGTAGAACAGCT	
599	Gm2a	Gm2a_599	GGAAAGGACGAAACACCGCCACCAAGTTGGGAAAGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCAAGTTGGGAAAGCTA	
600	Gm2a	Gm2a_600	GGAAAGGACGAAACACCGGTGACAGGTGGAGCTCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACAGGTGGAGCTCACCG	
601	Bscl2	Bscl2_601	GGAAAGGACGAAACACCGGTTTCATGTTATACCAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTCATGTTATACCAGAGG	
602	Bscl2	Bscl2_602	GGAAAGGACGAAACACCGCCTGGGCCCACAGTAAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGGCCCACAGTAAGGCG	
603	Bscl2	Bscl2_603	GGAAAGGACGAAACACCGCAAAGGATCAGACAAAGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGGATCAGACAAAGACG	
604	Bscl2	Bscl2_604	GGAAAGGACGAAACACCGAATGTCTCACTGGCTAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTCTCACTGGCTAAGAG	
605	Gnmt	Gnmt_605	GGAAAGGACGAAACACCGTGTGTGGCAGCTGTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGGCAGCTGTACATCG	
606	Gnmt	Gnmt_606	GGAAAGGACGAAACACCGAGAACATTGCAAGCATGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACATTGCAAGCATGGTG	
607	Gnmt	Gnmt_607	GGAAAGGACGAAACACCGGAGCCATCCTTTGACAATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCCATCCTTTGACAATTG	
608	Gnmt	Gnmt_608	GGAAAGGACGAAACACCGGGGCTTCAGCGTGATGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTTCAGCGTGATGAGCG	
609	Gnpat	Gnpat_609	GGAAAGGACGAAACACCGCCTTCGGCTTAGGAACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTCGGCTTAGGAACTCCG	
610	Gnpat	Gnpat_610	GGAAAGGACGAAACACCGTACACCCCGCCCTTGTATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACCCCGCCCTTGTATAG	
611	Gnpat	Gnpat_611	GGAAAGGACGAAACACCGCTCACCAAACTTAGGAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCAAACTTAGGAGTCA	
612	Gnpat	Gnpat_612	GGAAAGGACGAAACACCGATGAGCCACAAACTGCGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAGCCACAAACTGCGCAT	
613	Got2	Got2_613	GGAAAGGACGAAACACCGTGGAGGTCCCATTTCAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGGTCCCATTTCAACAT	
614	Got2	Got2_614	GGAAAGGACGAAACACCGTTTCTGCCCAAACCATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCTGCCCAAACCATCCTG	
615	Got2	Got2_615	GGAAAGGACGAAACACCGCATCCTCCTCACCTTCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCCTCCTCACCTTCACCA	
616	Got2	Got2_616	GGAAAGGACGAAACACCGAGCTCACCTTCCGGACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCACCTTCCGGACACTG	
617	Gpaa1	Gpaa1_617	GGAAAGGACGAAACACCGGTGGAGGCACTAACCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAGGCACTAACCCTACG	
618	Gpaa1	Gpaa1_618	GGAAAGGACGAAACACCGCCGCAGGATGCCATACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCAGGATGCCATACACGT	
619	Gpaa1	Gpaa1_619	GGAAAGGACGAAACACCGGTCCCTCCACTGTCACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCCTCCACTGTCACATCG	
620	Gpaa1	Gpaa1_620	GGAAAGGACGAAACACCGAGAGTCCGATGGAGACAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTCCGATGGAGACAAAG	
621	Pigq	Pigq_621	GGAAAGGACGAAACACCGCAGGATATGCTCAATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGATATGCTCAATAAAGG	
622	Pigq	Pigq_622	GGAAAGGACGAAACACCGTGACACAGTGGCACGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACACAGTGGCACGCAGCG	
623	Pigq	Pigq_623	GGAAAGGACGAAACACCGGAAGGCCAGTCAAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGCCAGTCAAGTACCAG	
624	Pigq	Pigq_624	GGAAAGGACGAAACACCGCAATAACCGAATTGGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATAACCGAATTGGACAGC	
625	Gsr	Gsr_625	GGAAAGGACGAAACACCGGGCTATGCAACATTCGCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTATGCAACATTCGCAGA	
626	Gsr	Gsr_626	GGAAAGGACGAAACACCGCGGCCCCCACGATGACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCCCCCACGATGACGCTG	
627	Gsr	Gsr_627	GGAAAGGACGAAACACCGGCTGTGAGGGTAAATTCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGAGGGTAAATTCAGT	
628	Gsr	Gsr_628	GGAAAGGACGAAACACCGAACATCTGGAATCATGGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATCTGGAATCATGGTCG	
629	Gria4	Gria4_629	GGAAAGGACGAAACACCGTGCATACATTGGTGTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCATACATTGGTGTCAGCG	
630	Gria4	Gria4_630	GGAAAGGACGAAACACCGGCATGTCAGTGCGATATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATGTCAGTGCGATATGTG	
631	Gria4	Gria4_631	GGAAAGGACGAAACACCGACGTAGAGTTAATTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTAGAGTTAATTACACAA	
632	Gria4	Gria4_632	GGAAAGGACGAAACACCGTGCACCTCTGACAATCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCACCTCTGACAATCACGT	
633	Grin1	Grin1_633	GGAAAGGACGAAACACCGAACATCACTGATCCACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATCACTGATCCACCGCG	
634	Grin1	Grin1_634	GGAAAGGACGAAACACCGGTGGACATCTGGTATCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACATCTGGTATCCTCG	
635	Grin1	Grin1_635	GGAAAGGACGAAACACCGCTGTCCTATGACAACAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTCCTATGACAACAAGCG	
636	Grin1	Grin1_636	GGAAAGGACGAAACACCGAACCAGGCCAATAAGCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCAGGCCAATAAGCGACA	
637	Grin2a	Grin2a_637	GGAAAGGACGAAACACCGATGGTAAAAGAAGGCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTAAAAGAAGGCCCATG	
638	Grin2a	Grin2a_638	GGAAAGGACGAAACACCGAGAAGAAATCGTAGCCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAGAAATCGTAGCCGGTG	
639	Grin2a	Grin2a_639	GGAAAGGACGAAACACCGATCTTGACAAACTTCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTTGACAAACTTCCGACA	
640	Grin2a	Grin2a_640	GGAAAGGACGAAACACCGTGTGTGCGACCTCATGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGCGACCTCATGTCCG	
641	Grin2b	Grin2b_641	GGAAAGGACGAAACACCGTATCCTACGCTTGCTCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCTACGCTTGCTCCGAA	
642	Grin2b	Grin2b_642	GGAAAGGACGAAACACCGGGCACCGGTTGTAACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCACCGGTTGTAACCCACA	
643	Grin2b	Grin2b_643	GGAAAGGACGAAACACCGACATCATGGAAGAATACGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATCATGGAAGAATACGAC	
644	Grin2b	Grin2b_644	GGAAAGGACGAAACACCGTGACTGGCTACGGCTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTGGCTACGGCTACACA	
645	Nr3c1	Nr3c1_645	GGAAAGGACGAAACACCGCATTATGGGGTGCTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTATGGGGTGCTGACGTG	
646	Nr3c1	Nr3c1_646	GGAAAGGACGAAACACCGAGCTTGCCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTTGCCTGGCAATAAACC	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
647	Nr3c1	Nr3c1_647	GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCCGTTTCACTGTCCAT	
648	Nr3c1	Nr3c1_648	GGAAAGGACGAAACACCGAAAACTGGAATAGGTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACTGGAATAGGTGCCAA	
649	Grm1	Grm1_649	GGAAAGGACGAAACACCGGGGTGACAAATAGCGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTGACAAATAGCGTCACG	
650	Grm1	Grm1_650	GGAAAGGACGAAACACCGTAGTGTACAGCTGACACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTGTACAGCTGACACTAG	
651	Grm1	Grm1_651	GGAAAGGACGAAACACCGACTCTCCCACGACGCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCTCCCACGACGCCAAGG	
652	Grm1	Grm1_652	GGAAAGGACGAAACACCGAGATAAGATTAATGCGGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATAAGATTAATGCGGACC	
653	Grn	Grn_653	GGAAAGGACGAAACACCGCCTATCCAAGAACTACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTATCCAAGAACTACACCA	
654	Grn	Grn_654	GGAAAGGACGAAACACCGCCCTGCACAAAAGACCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTGCACAAAAGACCAACA	
655	Grn	Grn_655	GGAAAGGACGAAACACCGGACACTGGACAGCACCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACTGGACAGCACCCAAG	
656	Grn	Grn_656	GGAAAGGACGAAACACCGCACCTAGTGAAGTCATCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCTAGTGAAGTCATCACA	
657	Gss	Gss_657	GGAAAGGACGAAACACCGGTTCTCTGGACCAAAACCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCTCTGGACCAAAACCGA	
658	Gss	Gss_658	GGAAAGGACGAAACACCGAGTCAGTATAATTCACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCAGTATAATTCACAGGT	
659	Gss	Gss_659	GGAAAGGACGAAACACCGACAGCTGGCTGGGACTAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCTGGCTGGGACTAAGA	
660	Gss	Gss_660	GGAAAGGACGAAACACCGTCAGATTACATGTTCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGATTACATGTTCCAGTG	
661	Gstz1	Gstz1_661	GGAAAGGACGAAACACCGGTCAGAAATCATGCGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAGAAATCATGCGCACGA	
662	Gstz1	Gstz1_662	GGAAAGGACGAAACACCGAAGAGACTCGGCCTATCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGACTCGGCCTATCCCA	
663	Gstz1	Gstz1_663	GGAAAGGACGAAACACCGATTTCTGACCTCATCGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTCTGACCTCATCGCTAG	
664	Gstz1	Gstz1_664	GGAAAGGACGAAACACCGTAATGACTCACCGTTAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATGACTCACCGTTAAAGC	
665	Gys1	Gys1_665	GGAAAGGACGAAACACCGTTGGGACACCTGCAACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGGACACCTGCAACATCG	
666	Gys1	Gys1_666	GGAAAGGACGAAACACCGCAACGCCCAAAATACACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACGCCCAAAATACACCTG	
667	Gys1	Gys1_667	GGAAAGGACGAAACACCGTGTTGTGGGTGCACACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTGGGTGCACACTGGT	
668	Gys1	Gys1_668	GGAAAGGACGAAACACCGATCCCAGATCACCGCAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCCAGATCACCGCAATCG	
669	Hadh	Hadh_669	GGAAAGGACGAAACACCGCCTTTCAACCAGCACCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTTCAACCAGCACCGATG	
670	Hadh	Hadh_670	GGAAAGGACGAAACACCGAGCAAATCGGTCTTGTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAAATCGGTCTTGTCTGG	
671	Hadh	Hadh_671	GGAAAGGACGAAACACCGAAGCATGTGACCGTCATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCATGTGACCGTCATCGG	
672	Hadh	Hadh_672	GGAAAGGACGAAACACCGTGGCCATACAGTAGTATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCATACAGTAGTATTGG	
673	Hsd17b10	Hsd17b10_673	GGAAAGGACGAAACACCGTGTTAATGATAACTCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTAATGATAACTCCACGT	
674	Hsd17b10	Hsd17b10_674	GGAAAGGACGAAACACCGGCTACGGCCAAAAGACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTACGGCCAAAAGACTGGT	
675	Hsd17b10	Hsd17b10_675	GGAAAGGACGAAACACCGTTGGTCGCGGTAGTAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGTCGCGGTAGTAACTGG	
676	Hsd17b10	Hsd17b10_676	GGAAAGGACGAAACACCGGTCACGACTCACATTTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCACGACTCACATTTGCTG	
677	Hal	Hal_677	GGAAAGGACGAAACACCGATGCTGTCCGACCTCACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCTGTCCGACCTCACCGT	
678	Hal	Hal_678	GGAAAGGACGAAACACCGAAAAGATACAGGATTGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGATACAGGATTGTCTG	
679	Hal	Hal_679	GGAAAGGACGAAACACCGGGACAATGGTGGCTTCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAATGGTGGCTTCACTT	
680	Hal	Hal_680	GGAAAGGACGAAACACCGTCTTAGCCAAAGGTTACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAGCCAAAGGTTACAGT	
681	Hao1	Hao1_681	GGAAAGGACGAAACACCGCAGCATGCCAATATGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCATGCCAATATGTGTTG	
682	Hao1	Hao1_682	GGAAAGGACGAAACACCGACTGTGGACACCCCTTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTGGACACCCCTTACCT	
683	Hao1	Hao1_683	GGAAAGGACGAAACACCGGCAACGTTGCGAAGCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACGTTGCGAAGCATCCG	
684	Hao1	Hao1_684	GGAAAGGACGAAACACCGGTATGACTATTACAGGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATGACTATTACAGGTCTG	
685	Hccs	Hccs_685	GGAAAGGACGAAACACCGCAAAGTAAATGGCTGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGTAAATGGCTGATCTG	
686	Hccs	Hccs_686	GGAAAGGACGAAACACCGTAGCTCTAGCACCAGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCTCTAGCACCAGTAACA	
687	Hccs	Hccs_687	GGAAAGGACGAAACACCGTCCAGAACATCTGTTCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGAACATCTGTTCAGAA	
688	Hccs	Hccs_688	GGAAAGGACGAAACACCGATCAGAATAATGAGCAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAGAATAATGAGCAAGCG	
689	Hcfc1	Hcfc1_689	GGAAAGGACGAAACACCGGGTACCCTTCACAACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTACCCTTCACAACCAATG	
690	Hcfc1	Hcfc1_690	GGAAAGGACGAAACACCGACAGCAGTATGTGACTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCAGTATGTGACTCCCG	
691	Hcfc1	Hcfc1_691	GGAAAGGACGAAACACCGTGGAAGGGCTAGTTGCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGGGCTAGTTGCACAA	
692	Hcfc1	Hcfc1_692	GGAAAGGACGAAACACCGCCCAAGGTTAGCCACAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAAGGTTAGCCACAACAG	
693	Hexa	Hexa_693	GGAAAGGACGAAACACCGACGCCCCGGTGAGGGAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGCCCCGGTGAGGGAATCG	
694	Hexa	Hexa_694	GGAAAGGACGAAACACCGAGGAGGTCATTGAATACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGGTCATTGAATACGCA	
695	Hexa	Hexa_695	GGAAAGGACGAAACACCGAGTGAAGCTCTCATATGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGAAGCTCTCATATGGGA	
696	Hexa	Hexa_696	GGAAAGGACGAAACACCGAGCAAGGTGTTAATAACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAAGGTGTTAATAACCCA	
697	Hexb	Hexb_697	GGAAAGGACGAAACACCGGCTCAGCTCGAAATCTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCAGCTCGAAATCTAGCA	
698	Hexb	Hexb_698	GGAAAGGACGAAACACCGTACACCAAACGATGTCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACCAAACGATGTCCGGA	
699	Hexb	Hexb_699	GGAAAGGACGAAACACCGGCGGAGATGTACAACAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGAGATGTACAACAGCCG	
700	Hexb	Hexb_700	GGAAAGGACGAAACACCGTAACGCTCCCCAAACGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACGCTCCCCAAACGCTGT	
701	Hfe	Hfe_701	GGAAAGGACGAAACACCGTGCTCCACGTACCCTTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCCACGTACCCTTACTG	
702	Hfe	Hfe_702	GGAAAGGACGAAACACCGTTCCTCCCGCACTCACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCTCCCGCACTCACGCGG	
703	Hfe	Hfe_703	GGAAAGGACGAAACACCGGATCCGTGCCAAACAGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCGTGCCAAACAGAACA	
704	Hfe	Hfe_704	GGAAAGGACGAAACACCGCATGAAGACAACAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGAAGACAACAGTACCAG	
705	Hgd	Hgd_705	GGAAAGGACGAAACACCGGAAGATCGTCGAGTGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGATCGTCGAGTGCCAGG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
706	Hgd	Hgd_706	GGAAAGGACGAAACACCGCCCTTTGAGTCCATCGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTTTGAGTCCATCGACCA	
707	Hgd	Hgd_707	GGAAAGGACGAAACACCGGGAGACATCAAGTCTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGACATCAAGTCTAACAA	
708	Hgd	Hgd_708	GGAAAGGACGAAACACCGGATGTCTTTGAGGAGACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTCTTTGAGGAGACCAG	
709	Hk1	Hk1_709	GGAAAGGACGAAACACCGCCGACAATCCAAAATAGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGACAATCCAAAATAGACG	
710	Hk1	Hk1_710	GGAAAGGACGAAACACCGCGTAGCCGCCATTGAAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTAGCCGCCATTGAAACGT	
711	Hk1	Hk1_711	GGAAAGGACGAAACACCGGGATCTTTACCAGTAGGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATCTTTACCAGTAGGACT	
712	Hk1	Hk1_712	GGAAAGGACGAAACACCGCTCCCGGGATTATAACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCCGGGATTATAACCCAA	
713	Hmbs	Hmbs_713	GGAAAGGACGAAACACCGAAGATGAGGGTGATTCGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGATGAGGGTGATTCGAGT	
714	Hmbs	Hmbs_714	GGAAAGGACGAAACACCGCCTGGTCGTTCACTCCCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGTCGTTCACTCCCTGA	
715	Hmbs	Hmbs_715	GGAAAGGACGAAACACCGAGAGAAGAGCCTGTTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGAAGAGCCTGTTTACCA	
716	Hmbs	Hmbs_716	GGAAAGGACGAAACACCGCTCAGTTGCTATGTCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGTTGCTATGTCCACCA	
717	Hmgcl	Hmgcl_717	GGAAAGGACGAAACACCGCACCTCAGCAACTTTAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCTCAGCAACTTTAGCCG	
718	Hmgcl	Hmgcl_718	GGAAAGGACGAAACACCGCTTGGGAGAAACAAAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGGAGAAACAAAGCTGG	
719	Hmgcl	Hmgcl_719	GGAAAGGACGAAACACCGCTTGGGGACACCATCGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGGGACACCATCGGCGT	
720	Hmgcl	Hmgcl_720	GGAAAGGACGAAACACCGGGGGTGGGTACAATACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGTGGGTACAATACTCTG	
721	Hmgcs2	Hmgcs2_721	GGAAAGGACGAAACACCGGACATTGCAGTCTACCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATTGCAGTCTACCCGAG	
722	Hmgcs2	Hmgcs2_722	GGAAAGGACGAAACACCGTTTATTACGAACCTTGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTATTACGAACCTTGCTCG	
723	Hmgcs2	Hmgcs2_723	GGAAAGGACGAAACACCGGAGGGATTGTAGAAAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGGATTGTAGAAAACCTG	
724	Hmgcs2	Hmgcs2_724	GGAAAGGACGAAACACCGTCATATACTGCACATCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATATACTGCACATCATCG	
725	Hmox1	Hmox1_725	GGAAAGGACGAAACACCGTCGTGCTCGAATGAACACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTGCTCGAATGAACACTC	
726	Hmox1	Hmox1_726	GGAAAGGACGAAACACCGTCAGGACCTGACCCCCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGACCTGACCCCCTGAG	
727	Hmox1	Hmox1_727	GGAAAGGACGAAACACCGACGCTTTACATAGTGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGCTTTACATAGTGCTGTG	
728	Hmox1	Hmox1_728	GGAAAGGACGAAACACCGTTCCTTGTACCATATCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCTTGTACCATATCTACA	
729	Hnf4a	Hnf4a_729	GGAAAGGACGAAACACCGGCAATGACTACATCGTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAATGACTACATCGTCCCT	
730	Hnf4a	Hnf4a_730	GGAAAGGACGAAACACCGAATGTGCAGGTGTTGACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTGCAGGTGTTGACCAT	
731	Hnf4a	Hnf4a_731	GGAAAGGACGAAACACCGAGCGGGACCGGATCAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGGGACCGGATCAGCACG	
732	Hnf4a	Hnf4a_732	GGAAAGGACGAAACACCGGGCTCCGTAGTGTTTGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTCCGTAGTGTTTGCCGG	
733	Hpd	Hpd_733	GGAAAGGACGAAACACCGGAAAGACATCGCATTCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGACATCGCATTCGAGG	
734	Hpd	Hpd_734	GGAAAGGACGAAACACCGCATTGTGGTGACCAACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGTGGTGACCAACTACG	
735	Hpd	Hpd_735	GGAAAGGACGAAACACCGAGATACCACACACACCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATACCACACACACCCTGG	
736	Hpd	Hpd_736	GGAAAGGACGAAACACCGATGATCTCAAGGTTACATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATCTCAAGGTTACATCT	
737	Hpgd	Hpgd_737	GGAAAGGACGAAACACCGGCTGCTAACCTCATGAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCTAACCTCATGAAAAG	
738	Hpgd	Hpgd_738	GGAAAGGACGAAACACCGTACATGAGTAAGCAAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACATGAGTAAGCAAAACGG	
739	Hpgd	Hpgd_739	GGAAAGGACGAAACACCGCATAGGCAAAGCCTTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAGGCAAAGCCTTCGCTG	
740	Hpgd	Hpgd_740	GGAAAGGACGAAACACCGGCTGACCAGAAACAACTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGACCAGAAACAACTGAG	
741	Lipc	Lipc_741	GGAAAGGACGAAACACCGTTATCATGATCATCCACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATCATGATCATCCACGGG	
742	Lipc	Lipc_742	GGAAAGGACGAAACACCGAGGAGAAAGGCGCTCGTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGAAAGGCGCTCGTTGG	
743	Lipc	Lipc_743	GGAAAGGACGAAACACCGCATAACCCAGAGTGTTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAACCCAGAGTGTTGCAA	
744	Lipc	Lipc_744	GGAAAGGACGAAACACCGGGTGTAGTGCTGGTATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTAGTGCTGGTATGCCA	
745	Hsd11b1	Hsd11b1_745	GGAAAGGACGAAACACCGCCTGGCAGTCAATACCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGCAGTCAATACCACAT	
746	Hsd11b1	Hsd11b1_746	GGAAAGGACGAAACACCGACAGCGAGGTCTGAGTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCGAGGTCTGAGTGATG	
747	Hsd11b1	Hsd11b1_747	GGAAAGGACGAAACACCGAAAGAAAGTGATTGTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGAAAGTGATTGTCACTG	
748	Hsd11b1	Hsd11b1_748	GGAAAGGACGAAACACCGGTAGGGAGCAATCATAGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGGGAGCAATCATAGGCT	
749	Hsd11b2	Hsd11b2_749	GGAAAGGACGAAACACCGCCACTCTTGCGTCACTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTCTTGCGTCACTCGAG	
750	Hsd11b2	Hsd11b2_750	GGAAAGGACGAAACACCGGGTGATGAGCACCGCGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGATGAGCACCGCGCGAG	
751	Hsd11b2	Hsd11b2_751	GGAAAGGACGAAACACCGGCTAAGAAACTGGATGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTAAGAAACTGGATGCCAT	
752	Hsd11b2	Hsd11b2_752	GGAAAGGACGAAACACCGCGCTGGCCTCAATATCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCTGGCCTCAATATCGTAG	
753	Hsd17b3	Hsd17b3_753	GGAAAGGACGAAACACCGCAACATTACCTCCGTAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACATTACCTCCGTAGTCA	
754	Hsd17b3	Hsd17b3_754	GGAAAGGACGAAACACCGAAGCCTATTCATTTGAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCTATTCATTTGAGGTG	
755	Hsd17b3	Hsd17b3_755	GGAAAGGACGAAACACCGGCTGAGTACAGGCTGTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGAGTACAGGCTGTAAAG	
756	Hsd17b3	Hsd17b3_756	GGAAAGGACGAAACACCGTTTCTGCCAGTCAACAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCTGCCAGTCAACAACGT	
757	Hsd17b4	Hsd17b4_757	GGAAAGGACGAAACACCGTCTAACATAGGCTCTTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAACATAGGCTCTTCACG	
758	Hsd17b4	Hsd17b4_758	GGAAAGGACGAAACACCGACCAAACCGTACCAGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAAACCGTACCAGTCACG	
759	Hsd17b4	Hsd17b4_759	GGAAAGGACGAAACACCGTGGGCGCCATCGTCAGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGCGCCATCGTCAGAAAG	
760	Hsd17b4	Hsd17b4_760	GGAAAGGACGAAACACCGTGCAGTGAACGACTTAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTGAACGACTTAGGAG	
761	Hsd3b2	Hsd3b2_761	GGAAAGGACGAAACACCGCTTCAGACCAGAAACAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAGACCAGAAACAAGGA	
762	Hsd3b2	Hsd3b2_762	GGAAAGGACGAAACACCGGATTGTCTTGAATGGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTGTCTTGAATGGCCATG	
763	Hsd3b2	Hsd3b2_763	GGAAAGGACGAAACACCGATATGTGGGCAATGTAGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATGTGGGCAATGTAGCCT	
764	Hsd3b2	Hsd3b2_764	GGAAAGGACGAAACACCGATTATTATGTTAGAAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTATTATGTTAGAAATGAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
765	Hspd1	Hspd1_765	GGAAAGGACGAAACACCGCGGAGAAGCTCTAAGCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGAGAAGCTCTAAGCACGC	
766	Hspd1	Hspd1_766	GGAAAGGACGAAACACCGTCTTGAACTAGGTGTGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTGAACTAGGTGTGATGT	
767	Hspd1	Hspd1_767	GGAAAGGACGAAACACCGAGGGACAATGGACTGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGACAATGGACTGAACAC	
768	Hspd1	Hspd1_768	GGAAAGGACGAAACACCGTGACTTAGGAAAAGTTGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTTAGGAAAAGTTGGGG	
769	Hspa9	Hspa9_769	GGAAAGGACGAAACACCGCAACTTGCCATACCTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACTTGCCATACCTTACCA	
770	Hspa9	Hspa9_770	GGAAAGGACGAAACACCGCTCAACCCAAGCATCACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAACCCAAGCATCACCAT	
771	Hspa9	Hspa9_771	GGAAAGGACGAAACACCGGCCCTCCATAACAGCCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTCCATAACAGCCACAC	
772	Hspa9	Hspa9_772	GGAAAGGACGAAACACCGGTGAATCATTGAAATAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAATCATTGAAATAAGCA	
773	Ndst1	Ndst1_773	GGAAAGGACGAAACACCGCATCCAGGTTGACATACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCCAGGTTGACATACTTG	
774	Ndst1	Ndst1_774	GGAAAGGACGAAACACCGCTATGTGACACGGCCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATGTGACACGGCCCAGTG	
775	Ndst1	Ndst1_775	GGAAAGGACGAAACACCGTTCTACAACGAGTACCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTACAACGAGTACCCTGG	
776	Ndst1	Ndst1_776	GGAAAGGACGAAACACCGCCCCACAGATATGGGCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCACAGATATGGGCTATG	
777	Hyal1	Hyal1_777	GGAAAGGACGAAACACCGTTGGCCAGAAACTTTAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGCCAGAAACTTTAGTGG	
778	Hyal1	Hyal1_778	GGAAAGGACGAAACACCGCCCCTACTATACACCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCTACTATACACCCACAG	
779	Hyal1	Hyal1_779	GGAAAGGACGAAACACCGCTGCAGGCAAATAAATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAGGCAAATAAATACTG	
780	Hyal1	Hyal1_780	GGAAAGGACGAAACACCGTGAGAAGTCAGGTTCAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAAGTCAGGTTCAGGCA	
781	Ids	Ids_781	GGAAAGGACGAAACACCGGTCTCCATAACAGCCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTCCATAACAGCCCAGGG	
782	Ids	Ids_782	GGAAAGGACGAAACACCGCATTCTCCTTGAAGTATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTCTCCTTGAAGTATTGG	
783	Ids	Ids_783	GGAAAGGACGAAACACCGTCCCTTGGAAAACATAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCTTGGAAAACATAACCC	
784	Ids	Ids_784	GGAAAGGACGAAACACCGTCCCTATGGACCAATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCTATGGACCAATTCCTG	
785	Idua	Idua_785	GGAAAGGACGAAACACCGTACCCCTATTTACAATGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCCCTATTTACAATGACG	
786	Idua	Idua_786	GGAAAGGACGAAACACCGGTTGGACAGCAATCATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGACAGCAATCATACAG	
787	Idua	Idua_787	GGAAAGGACGAAACACCGGGTCCAAGAATGCATCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCAAGAATGCATCCAAG	
788	Idua	Idua_788	GGAAAGGACGAAACACCGACTATGATGCCTGCTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTATGATGCCTGCTCTGAG	
789	Inppl1	Inppl1_789	GGAAAGGACGAAACACCGAGAATCCGGTCACACCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATCCGGTCACACCACGA	
790	Inppl1	Inppl1_790	GGAAAGGACGAAACACCGCCTGGATATCCATGTCTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGATATCCATGTCTAAG	
791	Inppl1	Inppl1_791	GGAAAGGACGAAACACCGTCACACTGGACGTACTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACACTGGACGTACTGACG	
792	Inppl1	Inppl1_792	GGAAAGGACGAAACACCGGCAGGGCACAAACAAGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGGCACAAACAAGACCC	
793	Insr	Insr_793	GGAAAGGACGAAACACCGCGAGGATTACCTGCACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGGATTACCTGCACAACG	
794	Insr	Insr_794	GGAAAGGACGAAACACCGGTGATACCAGAGCATAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGATACCAGAGCATAGGAG	
795	Insr	Insr_795	GGAAAGGACGAAACACCGCACACTGCACCTCTCATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACTGCACCTCTCATCTG	
796	Insr	Insr_796	GGAAAGGACGAAACACCGTATAGCCAGACGGGCACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATAGCCAGACGGGCACTCG	
797	Stt3a	Stt3a_797	GGAAAGGACGAAACACCGAAGGTGGTACGTAACGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGTGGTACGTAACGATGG	
798	Stt3a	Stt3a_798	GGAAAGGACGAAACACCGTACCATGTAGAAATAAGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCATGTAGAAATAAGCGA	
799	Stt3a	Stt3a_799	GGAAAGGACGAAACACCGGTTTACCTGGAAACCAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTACCTGGAAACCAACAA	
800	Stt3a	Stt3a_800	GGAAAGGACGAAACACCGACTTTAATTATCGGACTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTTAATTATCGGACTACC	
801	Itpa	Itpa_801	GGAAAGGACGAAACACCGATAGCAGTACTCACATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGCAGTACTCACATGTAG	
802	Itpa	Itpa_802	GGAAAGGACGAAACACCGTGATAAGTGCCTGAGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATAAGTGCCTGAGTACCA	
803	Itpa	Itpa_803	GGAAAGGACGAAACACCGAAACGCCAAGAAGCTGGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGCCAAGAAGCTGGAGG	
804	Itpa	Itpa_804	GGAAAGGACGAAACACCGTGGCCTCTGAAGAGAAGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCTCTGAAGAGAAGCAC	
805	Itpr1	Itpr1_805	GGAAAGGACGAAACACCGCTGTGAAATATGCCCGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGAAATATGCCCGACTG	
806	Itpr1	Itpr1_806	GGAAAGGACGAAACACCGACACGAACGATGTCATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACGAACGATGTCATCGAG	
807	Itpr1	Itpr1_807	GGAAAGGACGAAACACCGAAACGTGTCAATCTCTGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGTGTCAATCTCTGCCG	
808	Itpr1	Itpr1_808	GGAAAGGACGAAACACCGGGAAGCTGAGAACTCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGCTGAGAACTCCACAG	
809	Itpr2	Itpr2_809	GGAAAGGACGAAACACCGTCTGATACAGGATTCTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGATACAGGATTCTACGG	
810	Itpr2	Itpr2_810	GGAAAGGACGAAACACCGCAAGTGCCTTAACCGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTGCCTTAACCGCACGT	
811	Itpr2	Itpr2_811	GGAAAGGACGAAACACCGAATGCCGTAATCAACACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGCCGTAATCAACACCAG	
812	Itpr2	Itpr2_812	GGAAAGGACGAAACACCGTGTTGTGAGACTCTTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTGAGACTCTTTCATG	
813	Kcna1	Kcna1_813	GGAAAGGACGAAACACCGCGACACAATGGCAATAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACACAATGGCAATAACCC	
814	Kcna1	Kcna1_814	GGAAAGGACGAAACACCGTTCTGAACACCCTTACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGAACACCCTTACCAAG	
815	Kcna1	Kcna1_815	GGAAAGGACGAAACACCGGGACTGGTAGTAATAAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTGGTAGTAATAAAGGA	
816	Kcna1	Kcna1_816	GGAAAGGACGAAACACCGCGCAGCATTCGTGGTCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCAGCATTCGTGGTCGTCG	
817	Kcnj10	Kcnj10_817	GGAAAGGACGAAACACCGAGGTCGTCCATAGATCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTCGTCCATAGATCCTTG	
818	Kcnj10	Kcnj10_818	GGAAAGGACGAAACACCGTGGCCCCAGGAATACGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCCCAGGAATACGCCGG	
819	Kcnj10	Kcnj10_819	GGAAAGGACGAAACACCGGCAACCCGGATCATAAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACCCGGATCATAAGGCA	
820	Kcnj10	Kcnj10_820	GGAAAGGACGAAACACCGCTGCGCAATAAGAAGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCGCAATAAGAAGCACGA	
821	Kcnj11	Kcnj11_821	GGAAAGGACGAAACACCGCCAGGTACCGTACTCGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGTACCGTACTCGAGAG	
822	Kcnj11	Kcnj11_822	GGAAAGGACGAAACACCGGAGTGGATGCTTGTGACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTGGATGCTTGTGACGCA	
823	Kcnj11	Kcnj11_823	GGAAAGGACGAAACACCGCGGCGGGCGCATGGTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGGGCGCATGGTGACAG	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
824	Kcnj11	Kcnj11_824	GGAAAGGACGAAACACCGGAGGCACAACTTCGCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCACAACTTCGCCCTCG	
825	Khk	Khk_825	GGAAAGGACGAAACACCGTCCGATGCATTCCGGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGATGCATTCCGGCCCTG	
826	Khk	Khk_826	GGAAAGGACGAAACACCGAACTGGAAGAGCTCCTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTGGAAGAGCTCCTCACG	
827	Khk	Khk_827	GGAAAGGACGAAACACCGTGTGGTGGACAAATACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGTGGACAAATACCCAG	
828	Khk	Khk_828	GGAAAGGACGAAACACCGAAGAGCCCATGAAGGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGCCCATGAAGGCACAG	
829	Lamp2	Lamp2_829	GGAAAGGACGAAACACCGGAGTGTAGTTGTAGTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTGTAGTTGTAGTCGACG	
830	Lamp2	Lamp2_830	GGAAAGGACGAAACACCGCCTGACAAGGCGACACACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGACAAGGCGACACACGA	
831	Lamp2	Lamp2_831	GGAAAGGACGAAACACCGCACTTAAAGATGACATCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTAAAGATGACATCCAA	
832	Lamp2	Lamp2_832	GGAAAGGACGAAACACCGGCTGCAGCTGAACATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCAGCTGAACATCACTG	
833	Lcat	Lcat_833	GGAAAGGACGAAACACCGGATGTGCTACCGTAAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTGCTACCGTAAGACAG	
834	Lcat	Lcat_834	GGAAAGGACGAAACACCGCCTGTCCTAGGTGACAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTCCTAGGTGACAACCA	
835	Lcat	Lcat_835	GGAAAGGACGAAACACCGGTGCAGAATCTGGTTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCAGAATCTGGTTAACAA	
836	Lcat	Lcat_836	GGAAAGGACGAAACACCGGCGGGGGGAAGAGCACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGGGGGAAGAGCACATTG	
837	Ldha	Ldha_837	GGAAAGGACGAAACACCGCAAGCTGGTCATTATCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGCTGGTCATTATCACCG	
838	Ldha	Ldha_838	GGAAAGGACGAAACACCGGTTGCAATCTGGATTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCAATCTGGATTCAGCG	
839	Ldha	Ldha_839	GGAAAGGACGAAACACCGGGAGAACATGGCGACTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAACATGGCGACTCCAG	
840	Ldha	Ldha_840	GGAAAGGACGAAACACCGGTCATGGAAGACAAACTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATGGAAGACAAACTCAA	
841	Ldhb	Ldhb_841	GGAAAGGACGAAACACCGAAATTGTGGCCGATAAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATTGTGGCCGATAAAGGT	
842	Ldhb	Ldhb_842	GGAAAGGACGAAACACCGGTCTTCCAACACATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTTCCAACACATCCACCA	
843	Ldhb	Ldhb_843	GGAAAGGACGAAACACCGGCTCGCCCAGGATCCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCGCCCAGGATCCATCCG	
844	Ldhb	Ldhb_844	GGAAAGGACGAAACACCGGGGCTGTACTTGACGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTGTACTTGACGATCTG	
845	Cog1	Cog1_845	GGAAAGGACGAAACACCGGGGCTGGAACTCGATAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTGGAACTCGATAATGG	
846	Cog1	Cog1_846	GGAAAGGACGAAACACCGTGAGGATTGGAAATCTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGATTGGAAATCTCGAG	
847	Cog1	Cog1_847	GGAAAGGACGAAACACCGGTGGACATGCTTGTTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACATGCTTGTTCGATG	
848	Cog1	Cog1_848	GGAAAGGACGAAACACCGCAGCAGCAGCTTAATCTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCAGCAGCTTAATCTGGG	
849	Ldlr	Ldlr_849	GGAAAGGACGAAACACCGAAAATGCATCGCTAGCAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAATGCATCGCTAGCAAGT	
850	Ldlr	Ldlr_850	GGAAAGGACGAAACACCGGGTGTCGTAGGACAAGTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTCGTAGGACAAGTTAG	
851	Ldlr	Ldlr_851	GGAAAGGACGAAACACCGGCAGACTGGTGTACTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGACTGGTGTACTCGCTG	
852	Ldlr	Ldlr_852	GGAAAGGACGAAACACCGTGACCGTGAACATGACTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACCGTGAACATGACTGCA	
853	Lfng	Lfng_853	GGAAAGGACGAAACACCGGGCGATGAAGACGTCGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGATGAAGACGTCGCGAG	
854	Lfng	Lfng_854	GGAAAGGACGAAACACCGAGACGCGGATCCACCGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGCGGATCCACCGCCCG	
855	Lfng	Lfng_855	GGAAAGGACGAAACACCGCACACCCAAGACGTGTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACCCAAGACGTGTACAT	
856	Lfng	Lfng_856	GGAAAGGACGAAACACCGGGAGAGGCTATGCACCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAGGCTATGCACCTCGC	
857	Lipa	Lipa_857	GGAAAGGACGAAACACCGACCGAGATAATCATGCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGAGATAATCATGCGCTG	
858	Lipa	Lipa_858	GGAAAGGACGAAACACCGGTATTCACCGAATCCCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATTCACCGAATCCCTCGT	
859	Lipa	Lipa_859	GGAAAGGACGAAACACCGACTTCAGCATCGCACTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCAGCATCGCACTCTGA	
860	Lipa	Lipa_860	GGAAAGGACGAAACACCGTGTAGTTAATTGAAGCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAGTTAATTGAAGCAGGT	
861	Lipe	Lipe_861	GGAAAGGACGAAACACCGGAGTATGTCACGCTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTATGTCACGCTACACAA	
862	Lipe	Lipe_862	GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTAGAGAGTACGCTCAG	
863	Lipe	Lipe_863	GGAAAGGACGAAACACCGTGCGGTTAGAAGCCACATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGGTTAGAAGCCACATAG	
864	Lipe	Lipe_864	GGAAAGGACGAAACACCGAGAGCGGATATGCCTTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCGGATATGCCTTGCAG	
865	Phyh	Phyh_865	GGAAAGGACGAAACACCGCTCATTATAACGATCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCATTATAACGATCCCTGG	
866	Phyh	Phyh_866	GGAAAGGACGAAACACCGCCCAAAGGATACAATCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAAAGGATACAATCGTTG	
867	Phyh	Phyh_867	GGAAAGGACGAAACACCGAAACAATTAGGTTGCTAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACAATTAGGTTGCTAGGT	
868	Phyh	Phyh_868	GGAAAGGACGAAACACCGGAGCACATTGACAGAAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCACATTGACAGAAACAA	
869	Lpl	Lpl_869	GGAAAGGACGAAACACCGGAAAAACGTACCGTCTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAAACGTACCGTCTGCTG	
870	Lpl	Lpl_870	GGAAAGGACGAAACACCGCCATCCATGGATCACCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCCATGGATCACCACGA	
871	Lpl	Lpl_871	GGAAAGGACGAAACACCGTGGATTCCAATACTTCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGATTCCAATACTTCGACC	
872	Lpl	Lpl_872	GGAAAGGACGAAACACCGTGACACTGGATAATGTTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACACTGGATAATGTTGCT	
873	Ltc4s	Ltc4s_873	GGAAAGGACGAAACACCGCTTGCAACAGAACTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCAACAGAACTCCCACG	
874	Ltc4s	Ltc4s_874	GGAAAGGACGAAACACCGAGACGCGCTCGAACTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGCGCTCGAACTCGGGA	
875	Ltc4s	Ltc4s_875	GGAAAGGACGAAACACCGCGTATCCCTGGAAATAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTATCCCTGGAAATAGCGG	
876	Ltc4s	Ltc4s_876	GGAAAGGACGAAACACCGTACAGGTGATCTCTGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGGTGATCTCTGCACGA	
877	Alad	Alad_877	GGAAAGGACGAAACACCGAAATGGAGCATTCCTAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGGAGCATTCCTAGCAG	
878	Alad	Alad_878	GGAAAGGACGAAACACCGACGGACAGCCTCAATAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGACAGCCTCAATAGTTG	
879	Alad	Alad_879	GGAAAGGACGAAACACCGGCTCCGTCAGACATGATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCGTCAGACATGATGGA	
880	Alad	Alad_880	GGAAAGGACGAAACACCGAAAACATGGACTTGGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACATGGACTTGGCAACA	
881	Amacr	Amacr_881	GGAAAGGACGAAACACCGGCAGGTCATCGATTCAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGTCATCGATTCAAGCA	
882	Amacr	Amacr_882	GGAAAGGACGAAACACCGGGACAAAACATCTTAGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAAAACATCTTAGATGG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
883	Amacr	Amacr_883	GGAAAGGACGAAACACCGGCGGCGCATGTGCGCACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGCGCATGTGCGCACGCG	
884	Amacr	Amacr_884	GGAAAGGACGAAACACCGAAGCCAAATAGTTGATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCAAATAGTTGATGTCA	
885	Man2b1	Man2b1_885	GGAAAGGACGAAACACCGATGTTGTAAATGACTACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTGTAAATGACTACGCG	
886	Man2b1	Man2b1_886	GGAAAGGACGAAACACCGTGAGTTCAATGCAAAAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGTTCAATGCAAAAACGT	
887	Man2b1	Man2b1_887	GGAAAGGACGAAACACCGCTTGATAGTCAATGCGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGATAGTCAATGCGCCCA	
888	Man2b1	Man2b1_888	GGAAAGGACGAAACACCGAGCTCCCAGAGGTAACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCCCAGAGGTAACACGT	
889	Man2b2	Man2b2_889	GGAAAGGACGAAACACCGCAATGTCTACACTACCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATGTCTACACTACCGTGG	
890	Man2b2	Man2b2_890	GGAAAGGACGAAACACCGTGGTGGCCAACGTTAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGGCCAACGTTAAACAG	
891	Man2b2	Man2b2_891	GGAAAGGACGAAACACCGCAGGCCTTGTGTCTACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGCCTTGTGTCTACCGAG	
892	Man2b2	Man2b2_892	GGAAAGGACGAAACACCGTCAAGTCATGCACGCCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAGTCATGCACGCCCGCG	
893	Maoa	Maoa_893	GGAAAGGACGAAACACCGTCTTGGCAGTCAAAACCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTGGCAGTCAAAACCGGT	
894	Maoa	Maoa_894	GGAAAGGACGAAACACCGTAGGAACGGAAATTTGTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGAACGGAAATTTGTAGG	
895	Maoa	Maoa_895	GGAAAGGACGAAACACCGGTTGTAATCCAAATATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTAATCCAAATATGCCA	
896	Maoa	Maoa_896	GGAAAGGACGAAACACCGATGGCAAGCAAGACATGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCAAGCAAGACATGCTG	
897	Mc2r	Mc2r_897	GGAAAGGACGAAACACCGATGGGTTATCTTAAGCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGTTATCTTAAGCCTCG	
898	Mc2r	Mc2r_898	GGAAAGGACGAAACACCGACAATCGGAGTTATTTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAATCGGAGTTATTTCTTG	
899	Mc2r	Mc2r_899	GGAAAGGACGAAACACCGGGCGCATGGTCACAATGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGCATGGTCACAATGCTA	
900	Mc2r	Mc2r_900	GGAAAGGACGAAACACCGAGATAGAGCCCAGCAAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATAGAGCCCAGCAAAGAG	
901	Rdh11	Rdh11_901	GGAAAGGACGAAACACCGCCGGCAAGCTAAATACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGCAAGCTAAATACACAC	
902	Rdh11	Rdh11_902	GGAAAGGACGAAACACCGGCACCTTCTCATCAACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCTTCTCATCAACAATG	
903	Rdh11	Rdh11_903	GGAAAGGACGAAACACCGGGAACAGTCAGGTCTTCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACAGTCAGGTCTTCGTA	
904	Rdh11	Rdh11_904	GGAAAGGACGAAACACCGTCCACTTCCATAACCTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACTTCCATAACCTGCAG	
905	Mocs2	Mocs2_905	GGAAAGGACGAAACACCGATCATCCCGCCAATCAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCATCCCGCCAATCAGTGG	
906	Mocs2	Mocs2_906	GGAAAGGACGAAACACCGGAGACACTGCACCACACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACACTGCACCACACAGA	
907	Mocs2	Mocs2_907	GGAAAGGACGAAACACCGGAATACTGCTATGTGTCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATACTGCTATGTGTCTCA	
908	Mocs2	Mocs2_908	GGAAAGGACGAAACACCGATATGAAGCGTATGTACCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATGAAGCGTATGTACCGA	
909	Mdh2	Mdh2_909	GGAAAGGACGAAACACCGTCACGCACCTGAGAGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACGCACCTGAGAGATCAG	
910	Mdh2	Mdh2_910	GGAAAGGACGAAACACCGCGATATCGTAGAGGGTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATATCGTAGAGGGTCAGG	
911	Mdh2	Mdh2_911	GGAAAGGACGAAACACCGGTTCGCTCTGACGATGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGCTCTGACGATGTCAA	
912	Mdh2	Mdh2_912	GGAAAGGACGAAACACCGGTTGGCAATGATGCAAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGCAATGATGCAAACCA	
913	Mpv17	Mpv17_913	GGAAAGGACGAAACACCGCATTGAGTATCCCGACCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGAGTATCCCGACCAGT	
914	Mpv17	Mpv17_914	GGAAAGGACGAAACACCGTGTACCAGCCTCCGACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACCAGCCTCCGACGACA	
915	Mpv17	Mpv17_915	GGAAAGGACGAAACACCGACAGGATCACTGATGGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGGATCACTGATGGGCGT	
916	Mpv17	Mpv17_916	GGAAAGGACGAAACACCGGGGATACCATGGTCAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGATACCATGGTCAGAGTG	
917	Mthfr	Mthfr_917	GGAAAGGACGAAACACCGAGACCCTGTAGGTGACCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCCTGTAGGTGACCACT	
918	Mthfr	Mthfr_918	GGAAAGGACGAAACACCGGACTGGGATGAGTTTCCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTGGGATGAGTTTCCTAA	
919	Mthfr	Mthfr_919	GGAAAGGACGAAACACCGAGGTAACATCTACGAAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTAACATCTACGAAGAGG	
920	Mthfr	Mthfr_920	GGAAAGGACGAAACACCGCGAAGCTCTCTGCATCGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAGCTCTCTGCATCGGGG	
921	Mtm1	Mtm1_921	GGAAAGGACGAAACACCGAGGGAACCACCAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGAACCACCAAAAGAGCA	
922	Mtm1	Mtm1_922	GGAAAGGACGAAACACCGTTACCACTCATACCGACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCACTCATACCGACAAG	
923	Mtm1	Mtm1_923	GGAAAGGACGAAACACCGATGGGAGGCGCGACAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGAGGCGCGACAAGTAG	
924	Mtm1	Mtm1_924	GGAAAGGACGAAACACCGTCTGACCGGTGCCATTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGACCGGTGCCATTCAAG	
925	Mttp	Mttp_925	GGAAAGGACGAAACACCGTGAGCGGTCTGGATTTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCGGTCTGGATTTACAA	
926	Mttp	Mttp_926	GGAAAGGACGAAACACCGTGATCAAGTGATCCAAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATCAAGTGATCCAAGTCA	
927	Mttp	Mttp_927	GGAAAGGACGAAACACCGGATATACCACCAGAATCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATATACCACCAGAATCGTA	
928	Mttp	Mttp_928	GGAAAGGACGAAACACCGATCCTTTGCAGACACGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTTTGCAGACACGCTCG	
929	Mut	Mut_929	GGAAAGGACGAAACACCGTTTGACTTGGCAACACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGACTTGGCAACACATCG	
930	Mut	Mut_930	GGAAAGGACGAAACACCGTTATATGGCACACCCCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATATGGCACACCCCAGAA	
931	Mut	Mut_931	GGAAAGGACGAAACACCGAGAGTTCGTATGCAAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTTCGTATGCAAAGACT	
932	Mut	Mut_932	GGAAAGGACGAAACACCGATCATGTACGACCCTCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCATGTACGACCCTCCCCA	
933	Mvk	Mvk_933	GGAAAGGACGAAACACCGAGCGTCAATTTACCCAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGTCAATTTACCCAACAT	
934	Mvk	Mvk_934	GGAAAGGACGAAACACCGGTGGTCGGAACTTCCCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTCGGAACTTCCCCCCG	
935	Mvk	Mvk_935	GGAAAGGACGAAACACCGCAAGGTCCCGCGGAGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGTCCCGCGGAGTACCA	
936	Mvk	Mvk_936	GGAAAGGACGAAACACCGTCTGAAGTCAATCAACAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGAAGTCAATCAACAAGT	
937	Naga	Naga_937	GGAAAGGACGAAACACCGGCTAGGAAGGCAATCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTAGGAAGGCAATCCCGTG	
938	Naga	Naga_938	GGAAAGGACGAAACACCGTGTTGAGGTATACATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGAGGTATACATAGCCC	
939	Naga	Naga_939	GGAAAGGACGAAACACCGTCTCACAAACCAGTCCAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCACAAACCAGTCCAGGA	
940	Naga	Naga_940	GGAAAGGACGAAACACCGTGTTCAGGTGAACTACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCAGGTGAACTACACCG	
941	Ndufa2	Ndufa2_941	GGAAAGGACGAAACACCGGCAGGGATTTCATCGTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGGATTTCATCGTGCAA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
942	Ndufa2	Ndufa2_942	GGAAAGGACGAAACACCGTCTGATCCGCGAATGCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGATCCGCGAATGCTCGG	
943	Ndufa2	Ndufa2_943	GGAAAGGACGAAACACCGATTCGCGGATCAGAATGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCGCGGATCAGAATGGGC	
944	Ndufa2	Ndufa2_944	GGAAAGGACGAAACACCGGGCTGCCGCTGCTAGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTGCCGCTGCTAGCCGAG	
945	Ndufa4	Ndufa4_945	GGAAAGGACGAAACACCGAAAGACCGTGAACTTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGACCGTGAACTTACGCT	
946	Ndufa4	Ndufa4_946	GGAAAGGACGAAACACCGAGCACTGTATGTGATGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACTGTATGTGATGCGCT	
947	Ndufa4	Ndufa4_947	GGAAAGGACGAAACACCGCACTGTTTAATCCAGATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTGTTTAATCCAGATGTC	
948	Ndufa4	Ndufa4_948	GGAAAGGACGAAACACCGTCTTCGTATTTATTGGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCGTATTTATTGGAGCA	
949	Ndufs4	Ndufs4_949	GGAAAGGACGAAACACCGCCTGGATGGAACTCTACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGATGGAACTCTACAGA	
950	Ndufs4	Ndufs4_950	GGAAAGGACGAAACACCGAGAGCACATCAAAACCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCACATCAAAACCAGAA	
951	Ndufs4	Ndufs4_951	GGAAAGGACGAAACACCGGTTGATGCCCAACCCATCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGATGCCCAACCCATCAA	
952	Ndufs4	Ndufs4_952	GGAAAGGACGAAACACCGGTTGTCTGCCAGCTTCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTCTGCCAGCTTCCAAG	
953	Neu1	Neu1_953	GGAAAGGACGAAACACCGACAGCCTTCATCGTAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCCTTCATCGTAGACGA	
954	Neu1	Neu1_954	GGAAAGGACGAAACACCGTTGGTTTGGAGTAAGGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGTTTGGAGTAAGGACGA	
955	Neu1	Neu1_955	GGAAAGGACGAAACACCGTGTGTGTGGACACGGGACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGTGGACACGGGACGC	
956	Neu1	Neu1_956	GGAAAGGACGAAACACCGGAAAAAATCTGCATCCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAAAATCTGCATCCGATG	
957	Neurod1	Neurod1_957	GGAAAGGACGAAACACCGGAGCTGTCCATGGTGCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTGTCCATGGTGCCGTA	
958	Neurod1	Neurod1_958	GGAAAGGACGAAACACCGCCGGCGACCAAATTGGTAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGCGACCAAATTGGTAGT	
959	Neurod1	Neurod1_959	GGAAAGGACGAAACACCGAGCAAGGTACCACCTTGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAAGGTACCACCTTGCGC	
960	Neurod1	Neurod1_960	GGAAAGGACGAAACACCGGTGTCTCAGTTCTCAGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTCTCAGTTCTCAGGACG	
961	Nfs1	Nfs1_961	GGAAAGGACGAAACACCGCTAGTGAAAATGATCTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGTGAAAATGATCTCCCG	
962	Nfs1	Nfs1_962	GGAAAGGACGAAACACCGTCACAGTCATAACGGAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACAGTCATAACGGAGACC	
963	Nfs1	Nfs1_963	GGAAAGGACGAAACACCGAGGGCCTCCACACGTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCCTCCACACGTACCCG	
964	Nfs1	Nfs1_964	GGAAAGGACGAAACACCGCCTCTGTTAGTCCTTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTGTTAGTCCTTACCAG	
965	Npc1	Npc1_965	GGAAAGGACGAAACACCGGGGGAAGGTGATCACAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGAAGGTGATCACAAGCG	
966	Npc1	Npc1_966	GGAAAGGACGAAACACCGCATCATGTGGGTCACCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCATGTGGGTCACCTACG	
967	Npc1	Npc1_967	GGAAAGGACGAAACACCGCGGTTCGTAGATATGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTTCGTAGATATGAACAC	
968	Npc1	Npc1_968	GGAAAGGACGAAACACCGCCATCCCTACCTGAAAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCCCTACCTGAAAACAC	
969	Slc11a2	Slc11a2_969	GGAAAGGACGAAACACCGATGTCACCGTCAGTATCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTCACCGTCAGTATCCCA	
970	Slc11a2	Slc11a2_970	GGAAAGGACGAAACACCGAAACACAAAAGTGTCTGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACACAAAAGTGTCTGCGA	
971	Slc11a2	Slc11a2_971	GGAAAGGACGAAACACCGTGAGAAAATCCCCATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAAAATCCCCATTCCTG	
972	Slc11a2	Slc11a2_972	GGAAAGGACGAAACACCGCCTTGACTAAGGCAGAATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGACTAAGGCAGAATGC	
973	Nsdhl	Nsdhl_973	GGAAAGGACGAAACACCGTAGGCTTCATGGCGTAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCTTCATGGCGTAAGGG	
974	Nsdhl	Nsdhl_974	GGAAAGGACGAAACACCGCTATAAAGAACTGCACCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATAAAGAACTGCACCCGG	
975	Nsdhl	Nsdhl_975	GGAAAGGACGAAACACCGCTTGGGCCGAAAATGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGGCCGAAAATGCCATG	
976	Nsdhl	Nsdhl_976	GGAAAGGACGAAACACCGCCTGTGTACCCACAGAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTGTACCCACAGAAATG	
977	Oat	Oat_977	GGAAAGGACGAAACACCGCCGTTCAAAAATGTACTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTTCAAAAATGTACTCGG	
978	Oat	Oat_978	GGAAAGGACGAAACACCGTGTACTCCTCGTATTCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACTCCTCGTATTCACCA	
979	Oat	Oat_979	GGAAAGGACGAAACACCGATCATAACTGGTCGGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCATAACTGGTCGGATCTG	
980	Oat	Oat_980	GGAAAGGACGAAACACCGACCCTGATGTACCTCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCTGATGTACCTCCAGTG	
981	Ogdh	Ogdh_981	GGAAAGGACGAAACACCGTTGGCCCACTCATAGATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGCCCACTCATAGATACG	
982	Ogdh	Ogdh_982	GGAAAGGACGAAACACCGGACTAGTTCGAACTATGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTAGTTCGAACTATGTGG	
983	Ogdh	Ogdh_983	GGAAAGGACGAAACACCGGTAAGTGGAAGACCTTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGTGGAAGACCTTGTCA	
984	Ogdh	Ogdh_984	GGAAAGGACGAAACACCGAAAGCTGAACAGTTCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCTGAACAGTTCTACTG	
985	Slc25a15	Slc25a15_985	GGAAAGGACGAAACACCGACCTTTCCAGACCTCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTTCCAGACCTCTACCG	
986	Slc25a15	Slc25a15_986	GGAAAGGACGAAACACCGGCCCATGGTAGAAGCCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCATGGTAGAAGCCCAAG	
987	Slc25a15	Slc25a15_987	GGAAAGGACGAAACACCGGCACAGCATGCGTACTGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAGCATGCGTACTGACT	
988	Slc25a15	Slc25a15_988	GGAAAGGACGAAACACCGGGACAGCACTTACTTCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAGCACTTACTTCTGAC	
989	Otc	Otc_989	GGAAAGGACGAAACACCGCAGTCCATTGACAATTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTCCATTGACAATTGGGA	
990	Otc	Otc_990	GGAAAGGACGAAACACCGCCTTCAAGCAGCTACTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTCAAGCAGCTACTCCAA	
991	Otc	Otc_991	GGAAAGGACGAAACACCGTAGAAAGGGTCACACTTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAAAGGGTCACACTTCTG	
992	Otc	Otc_992	GGAAAGGACGAAACACCGAAATTCAGGATCAAGCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATTCAGGATCAAGCAGAA	
993	Pah	Pah_993	GGAAAGGACGAAACACCGCCTCTTCTGGAAAAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTTCTGGAAAAGTACTG	
994	Pah	Pah_994	GGAAAGGACGAAACACCGCACTTACCTCAAATAAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTACCTCAAATAAGCGC	
995	Pah	Pah_995	GGAAAGGACGAAACACCGGCAGCATCATCAAGAGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCATCATCAAGAGCCTG	
996	Pah	Pah_996	GGAAAGGACGAAACACCGTCCTCGGGTGGAATACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTCGGGTGGAATACACAG	
997	Pax4	Pax4_997	GGAAAGGACGAAACACCGTTGGAACCCAAGTGTATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGAACCCAAGTGTATTGG	
998	Pax4	Pax4_998	GGAAAGGACGAAACACCGAGGGTACTCATCCTTTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGTACTCATCCTTTAGCT	
999	Pax4	Pax4_999	GGAAAGGACGAAACACCGACTCAACTCAGATCACCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCAACTCAGATCACCAGG	
1000	Pax4	Pax4_1000	GGAAAGGACGAAACACCGGTCTCTACAGAGTTTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTCTACAGAGTTTCAGCG	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
1001	Pck1	Pck1_1001	GGAAAGGACGAAACACCGACTGACAGACTCGCCCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGACAGACTCGCCCTATG	
1002	Pck1	Pck1_1002	GGAAAGGACGAAACACCGGTGGCCGAGACTAGCGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCCGAGACTAGCGATGG	
1003	Pck1	Pck1_1003	GGAAAGGACGAAACACCGCCTTTGGAAGCGGATATGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTTGGAAGCGGATATGGT	
1004	Pck1	Pck1_1004	GGAAAGGACGAAACACCGTCGCAGATGTGGATATACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGCAGATGTGGATATACTC	
1005	Pdha1	Pdha1_1005	GGAAAGGACGAAACACCGAGAACAACCGCTATGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACAACCGCTATGGCATG	
1006	Pdha1	Pdha1_1006	GGAAAGGACGAAACACCGATCACTGCCTATCGAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCACTGCCTATCGAGCACA	
1007	Pdha1	Pdha1_1007	GGAAAGGACGAAACACCGGCGCCGGATGGAGCTAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCGGATGGAGCTAAAGG	
1008	Pdha1	Pdha1_1008	GGAAAGGACGAAACACCGTGTTTGACATTATACGGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTTGACATTATACGGCGA	
1009	Enpp1	Enpp1_1009	GGAAAGGACGAAACACCGTACAACGCAAGTTGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAACGCAAGTTGCCACTG	
1010	Enpp1	Enpp1_1010	GGAAAGGACGAAACACCGGGTGACCGCTAATCATCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGACCGCTAATCATCAGG	
1011	Enpp1	Enpp1_1011	GGAAAGGACGAAACACCGATGTGAAAGCATCGATACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTGAAAGCATCGATACCC	
1012	Enpp1	Enpp1_1012	GGAAAGGACGAAACACCGAACGTCTTGGTAGGGTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGTCTTGGTAGGGTACAT	
1013	Pdx1	Pdx1_1013	GGAAAGGACGAAACACCGGACCCGTACTGCCTACACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCCGTACTGCCTACACCC	
1014	Pdx1	Pdx1_1014	GGAAAGGACGAAACACCGACTGCCAGCTCCACCCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCCAGCTCCACCCGGCG	
1015	Pdx1	Pdx1_1015	GGAAAGGACGAAACACCGAATCCACCAAAGCTCACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCCACCAAAGCTCACGCG	
1016	Pdx1	Pdx1_1016	GGAAAGGACGAAACACCGCCATTCGGGAAAGGTCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATTCGGGAAAGGTCCGGG	
1017	Pepd	Pepd_1017	GGAAAGGACGAAACACCGCACAAATCGGATCTCCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAAATCGGATCTCCAGCG	
1018	Pepd	Pepd_1018	GGAAAGGACGAAACACCGCTGCTATGGTGTCATCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCTATGGTGTCATCGATG	
1019	Pepd	Pepd_1019	GGAAAGGACGAAACACCGGCCCTGCAACACGACAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTGCAACACGACAGCTG	
1020	Pepd	Pepd_1020	GGAAAGGACGAAACACCGCTTGCTAATGCCCTCGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCTAATGCCCTCGAAGG	
1021	Pex11b	Pex11b_1021	GGAAAGGACGAAACACCGCTCTACAAGTGCTACGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTACAAGTGCTACGCCTG	
1022	Pex11b	Pex11b_1022	GGAAAGGACGAAACACCGCAAAGTACAAGGCTCGGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGTACAAGGCTCGGTTG	
1023	Pex11b	Pex11b_1023	GGAAAGGACGAAACACCGGGCGAATCTCATAAGCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGAATCTCATAAGCATCA	
1024	Pex11b	Pex11b_1024	GGAAAGGACGAAACACCGATCTCAGAACGACATCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTCAGAACGACATCTGAC	
1025	Pex16	Pex16_1025	GGAAAGGACGAAACACCGGCTTCGAAAAAAGTTGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCGAAAAAAGTTGCCTG	
1026	Pex16	Pex16_1026	GGAAAGGACGAAACACCGTGAATCGGAGAAGCGACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAATCGGAGAAGCGACCTA	
1027	Pex16	Pex16_1027	GGAAAGGACGAAACACCGTGAGAGCAATGACGAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAGCAATGACGAGCCAA	
1028	Pex16	Pex16_1028	GGAAAGGACGAAACACCGGCCAGGAGCCATCATATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAGGAGCCATCATATGTG	
1029	Pex7	Pex7_1029	GGAAAGGACGAAACACCGGATGCCGTAGTGCTGCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCCGTAGTGCTGCGCCG	
1030	Pex7	Pex7_1030	GGAAAGGACGAAACACCGATGGGATCAAACTGTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGATCAAACTGTCAAAG	
1031	Pex7	Pex7_1031	GGAAAGGACGAAACACCGCATCACCACTACAGGTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCACCACTACAGGTGACA	
1032	Pex7	Pex7_1032	GGAAAGGACGAAACACCGCTATAAAGAGCACACGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATAAAGAGCACACGCAGG	
1033	Pfkm	Pfkm_1033	GGAAAGGACGAAACACCGCCTCACGGTAGAGCGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCACGGTAGAGCGAACAG	
1034	Pfkm	Pfkm_1034	GGAAAGGACGAAACACCGGCGCCTTGGATATGACACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCTTGGATATGACACCC	
1035	Pfkm	Pfkm_1035	GGAAAGGACGAAACACCGTTAGACCAAAGACGTGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGACCAAAGACGTGACCA	
1036	Pfkm	Pfkm_1036	GGAAAGGACGAAACACCGCATAGACACGCTCTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAGACACGCTCTCCCACG	
1037	Pgk1	Pgk1_1037	GGAAAGGACGAAACACCGTAAGGTGCTCAACAACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGGTGCTCAACAACATGG	
1038	Pgk1	Pgk1_1038	GGAAAGGACGAAACACCGTCAAGAACAGAACATCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAGAACAGAACATCCCTG	
1039	Pgk1	Pgk1_1039	GGAAAGGACGAAACACCGGGACTGCACACCGAGCCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTGCACACCGAGCCCAT	
1040	Pgk1	Pgk1_1040	GGAAAGGACGAAACACCGCTTCCTCTACATGAAAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCTCTACATGAAAGCGG	
1041	Pgr	Pgr_1041	GGAAAGGACGAAACACCGCTCTGGCCGACTCATGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTGGCCGACTCATGAGCG	
1042	Pgr	Pgr_1042	GGAAAGGACGAAACACCGAGGAGGAGTCGCAGCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGGAGTCGCAGCCAACG	
1043	Pgr	Pgr_1043	GGAAAGGACGAAACACCGGGCGCGAACGAACCCTGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGCGAACGAACCCTGCGT	
1044	Pgr	Pgr_1044	GGAAAGGACGAAACACCGCAGTCTGGGAAGTCACCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTCTGGGAAGTCACCGCA	
1045	Abcb4	Abcb4_1045	GGAAAGGACGAAACACCGGATGACATCTGCGTTCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGACATCTGCGTTCCGGA	
1046	Abcb4	Abcb4_1046	GGAAAGGACGAAACACCGAGGACCGTGATAGCTTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCGTGATAGCTTTCGG	
1047	Abcb4	Abcb4_1047	GGAAAGGACGAAACACCGTAGCGAAAGCATCAATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCGAAAGCATCAATACAG	
1048	Abcb4	Abcb4_1048	GGAAAGGACGAAACACCGTACTACTATTCGGGACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTACTATTCGGGACTAGG	
1049	Phka1	Phka1_1049	GGAAAGGACGAAACACCGGTAGAAAACCTACGATTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGAAAACCTACGATTCAG	
1050	Phka1	Phka1_1050	GGAAAGGACGAAACACCGAGTGTAGTGAAGTTAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTAGTGAAGTTAATGAG	
1051	Phka1	Phka1_1051	GGAAAGGACGAAACACCGGAGATAGGGAAAGTGATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATAGGGAAAGTGATCGT	
1052	Phka1	Phka1_1052	GGAAAGGACGAAACACCGCTAAACTAGCTCCTACCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAAACTAGCTCCTACCTCA	
1053	Piga	Piga_1053	GGAAAGGACGAAACACCGTCTTCCACGCCAAGACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCCACGCCAAGACAATG	
1054	Piga	Piga_1054	GGAAAGGACGAAACACCGATGGGTGCAGGTCCTATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGTGCAGGTCCTATCGT	
1055	Piga	Piga_1055	GGAAAGGACGAAACACCGCAGACTGTGAAAGAGAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACTGTGAAAGAGAGTCG	
1056	Piga	Piga_1056	GGAAAGGACGAAACACCGCCATGCTTATGGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATGCTTATGGAAATCGAA	
1057	Pik3r1	Pik3r1_1057	GGAAAGGACGAAACACCGGAGCTTTATAAGGAGAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTTTATAAGGAGAGGCG	
1058	Pik3r1	Pik3r1_1058	GGAAAGGACGAAACACCGTCCATTAACCTTCAACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCATTAACCTTCAACTCTG	
1059	Pik3r1	Pik3r1_1059	GGAAAGGACGAAACACCGTGGCTACAATGAAACCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCTACAATGAAACCACTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1060	Pik3r1	Pik3r1_1060	GGAAAGGACGAAACACCGCTGGAAATCTGAAAAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGAAATCTGAAAAGCACG	
1061	Pip5k1c	Pip5k1c_1061	GGAAAGGACGAAACACCGTGGTGGCAAGAACATCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGGCAAGAACATCCGCG	
1062	Pip5k1c	Pip5k1c_1062	GGAAAGGACGAAACACCGCCGACGCATCCACGCCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGACGCATCCACGCCTCGG	
1063	Pip5k1c	Pip5k1c_1063	GGAAAGGACGAAACACCGTTACCAAATAGTCATCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCAAATAGTCATCTGGA	
1064	Pip5k1c	Pip5k1c_1064	GGAAAGGACGAAACACCGGCCATGGAGTCTATCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCATGGAGTCTATCCAGGG	
1065	Pklr	Pklr_1065	GGAAAGGACGAAACACCGTGTACGAAAAGCCAGTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACGAAAAGCCAGTGATG	
1066	Pklr	Pklr_1066	GGAAAGGACGAAACACCGGGGTTCACTCCAGACCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTTCACTCCAGACCTGTG	
1067	Pklr	Pklr_1067	GGAAAGGACGAAACACCGGGGCGATGCAAAGACAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCGATGCAAAGACAGTGT	
1068	Pklr	Pklr_1068	GGAAAGGACGAAACACCGCTGGTGACCGAAGTGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTGACCGAAGTGGAACA	
1069	Plcb1	Plcb1_1069	GGAAAGGACGAAACACCGCAAATACTTACGAATCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAATACTTACGAATCCACG	
1070	Plcb1	Plcb1_1070	GGAAAGGACGAAACACCGCCTGCACAGGCAATATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCACAGGCAATATCCGG	
1071	Plcb1	Plcb1_1071	GGAAAGGACGAAACACCGGGAACAGCGCATGATAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACAGCGCATGATAACTG	
1072	Plcb1	Plcb1_1072	GGAAAGGACGAAACACCGTCCCAACTTTCTTATCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCAACTTTCTTATCAGAG	
1073	Plcb3	Plcb3_1073	GGAAAGGACGAAACACCGGAAGGTGGGCATCTACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGTGGGCATCTACGTCG	
1074	Plcb3	Plcb3_1074	GGAAAGGACGAAACACCGCATACCGGGTATTTGTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACCGGGTATTTGTCGAG	
1075	Plcb3	Plcb3_1075	GGAAAGGACGAAACACCGTTGATAAAATATGCGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGATAAAATATGCGCTCAG	
1076	Plcb3	Plcb3_1076	GGAAAGGACGAAACACCGCAGTGAGGTCAATGCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGAGGTCAATGCCACGG	
1077	Plcb4	Plcb4_1077	GGAAAGGACGAAACACCGTGAAGTAATGAGCCAGCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGTAATGAGCCAGCGGG	
1078	Plcb4	Plcb4_1078	GGAAAGGACGAAACACCGTAAGAAGATCGGGACATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGAAGATCGGGACATACG	
1079	Plcb4	Plcb4_1079	GGAAAGGACGAAACACCGCAAGTACGGATGGATGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTACGGATGGATGTTCG	
1080	Plcb4	Plcb4_1080	GGAAAGGACGAAACACCGCTTGGCGAATACTGTTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGCGAATACTGTTGATG	
1081	Plcd1	Plcd1_1081	GGAAAGGACGAAACACCGATTTGCCAGAGACATACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTGCCAGAGACATACCCG	
1082	Plcd1	Plcd1_1082	GGAAAGGACGAAACACCGGGGAAGAAGACACTAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAAGAAGACACTAAGTAG	
1083	Plcd1	Plcd1_1083	GGAAAGGACGAAACACCGAGGTGGATGACAGCTACGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGGATGACAGCTACGCC	
1084	Plcd1	Plcd1_1084	GGAAAGGACGAAACACCGGTAGCGCTCAATGAGAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGCGCTCAATGAGAGAGA	
1085	Pnp	Pnp_1085	GGAAAGGACGAAACACCGAGATGCTGTGTGATGATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGCTGTGTGATGATGCA	
1086	Pnp	Pnp_1086	GGAAAGGACGAAACACCGTCAGTGCCTGGAAACAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTGCCTGGAAACAAATG	
1087	Pnp	Pnp_1087	GGAAAGGACGAAACACCGTGTGGCCAGAACCCTCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCCAGAACCCTCTCCG	
1088	Pnp	Pnp_1088	GGAAAGGACGAAACACCGCCTCAAGTGGCAGTGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCAAGTGGCAGTGATCTG	
1089	Polg	Polg_1089	GGAAAGGACGAAACACCGTGCTCATAAACGTATCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCATAAACGTATCAGGT	
1090	Polg	Polg_1090	GGAAAGGACGAAACACCGCGGCGGGGAAATGCCCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGGGGAAATGCCCGACG	
1091	Polg	Polg_1091	GGAAAGGACGAAACACCGCCGTTGCCATGGTGATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTTGCCATGGTGATACGT	
1092	Polg	Polg_1092	GGAAAGGACGAAACACCGAGATCCTGGCCCGCCCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATCCTGGCCCGCCCAGCG	
1093	Por	Por_1093	GGAAAGGACGAAACACCGTGGCTCCCAGACGGGAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCTCCCAGACGGGAACCG	
1094	Por	Por_1094	GGAAAGGACGAAACACCGATGTCTCTAAACAATCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTCTCTAAACAATCTCGA	
1095	Por	Por_1095	GGAAAGGACGAAACACCGAAGAGGATTTCATCACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGGATTTCATCACATGG	
1096	Por	Por_1096	GGAAAGGACGAAACACCGTCCAAGACTACCCGTCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAAGACTACCCGTCCCTG	
1097	Ctsa	Ctsa_1097	GGAAAGGACGAAACACCGGTGGTGCTTTGGCTTAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTGCTTTGGCTTAACGG	
1098	Ctsa	Ctsa_1098	GGAAAGGACGAAACACCGGGACTCGATATACAGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTCGATATACAGCACGT	
1099	Ctsa	Ctsa_1099	GGAAAGGACGAAACACCGCTCCGGCTACCTCAGAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGGCTACCTCAGAGCAT	
1100	Ctsa	Ctsa_1100	GGAAAGGACGAAACACCGCATGACCAGTACAGCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGACCAGTACAGCCAAGG	
1101	Ppox	Ppox_1101	GGAAAGGACGAAACACCGCCAGCCGGCCTAATCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCCGGCCTAATCCCTCG	
1102	Ppox	Ppox_1102	GGAAAGGACGAAACACCGCCGGGCCTGACGAATTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGGCCTGACGAATTAGTG	
1103	Ppox	Ppox_1103	GGAAAGGACGAAACACCGGTACTCAGGATTCGAGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACTCAGGATTCGAGCTAG	
1104	Ppox	Ppox_1104	GGAAAGGACGAAACACCGTAATAGTGAGGTGTTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATAGTGAGGTGTTACCTG	
1105	Inpp5k	Inpp5k_1105	GGAAAGGACGAAACACCGTTGTGCAGGAGAGTATAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTGCAGGAGAGTATAACG	
1106	Inpp5k	Inpp5k_1106	GGAAAGGACGAAACACCGACAGCGTACATGTTGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCGTACATGTTGTGACG	
1107	Inpp5k	Inpp5k_1107	GGAAAGGACGAAACACCGAGGATGCGGTCAGTCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGATGCGGTCAGTCCACGC	
1108	Inpp5k	Inpp5k_1108	GGAAAGGACGAAACACCGTACCTTGACAAAGTTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTTGACAAAGTTCAGTG	
1109	Ppt1	Ppt1_1109	GGAAAGGACGAAACACCGGGTACACACTCTCCTTGATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTACACACTCTCCTTGATA	
1110	Ppt1	Ppt1_1110	GGAAAGGACGAAACACCGTGTTAATGTCCAAGTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTAATGTCCAAGTCAACA	
1111	Ppt1	Ppt1_1111	GGAAAGGACGAAACACCGAGAGACAGGACGTAAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGACAGGACGTAAATCCC	
1112	Ppt1	Ppt1_1112	GGAAAGGACGAAACACCGCCATGCCAGATCACCAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATGCCAGATCACCAGCGG	
1113	Prkcsh	Prkcsh_1113	GGAAAGGACGAAACACCGAAGACCAGGTAGAAACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACCAGGTAGAAACACTG	
1114	Prkcsh	Prkcsh_1114	GGAAAGGACGAAACACCGCAGGGACAAGTACCGCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGACAAGTACCGCTCTG	
1115	Prkcsh	Prkcsh_1115	GGAAAGGACGAAACACCGGGCACAGACGAGTACAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCACAGACGAGTACAACAG	
1116	Prkcsh	Prkcsh_1116	GGAAAGGACGAAACACCGAACTTGACGACAACATGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTGACGACAACATGGAT	
1117	Prodh	Prodh_1117	GGAAAGGACGAAACACCGAGGAGGCGTATCGCAGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGGCGTATCGCAGCCGG	
1118	Prodh	Prodh_1118	GGAAAGGACGAAACACCGCCTGCTGTCACGGTTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCTGTCACGGTTCACTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1119	Prodh	Prodh_1119	GGAAAGGACGAAACACCGCAGGATAAAGCCAACACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGATAAAGCCAACACCAA	
1120	Prodh	Prodh_1120	GGAAAGGACGAAACACCGTCTCCCAGGAGCAAATAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCCAGGAGCAAATAAGA	
1121	Prps1	Prps1_1121	GGAAAGGACGAAACACCGGATGACTGCAGTAACCCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGACTGCAGTAACCCGGC	
1122	Prps1	Prps1_1122	GGAAAGGACGAAACACCGTGCAGATCATATTATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGATCATATTATCACCA	
1123	Prps1	Prps1_1123	GGAAAGGACGAAACACCGCATCTCCCACAAGTACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTCCCACAAGTACCATG	
1124	Prps1	Prps1_1124	GGAAAGGACGAAACACCGATGTCTACATTGTTCAAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTCTACATTGTTCAAAGT	
1125	Psap	Psap_1125	GGAAAGGACGAAACACCGCTACGTGGACCAGTATTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACGTGGACCAGTATTCCG	
1126	Psap	Psap_1126	GGAAAGGACGAAACACCGGTCAACCACCTCCTTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAACCACCTCCTTGCACG	
1127	Psap	Psap_1127	GGAAAGGACGAAACACCGCCTCAGCTAACCTTAGGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCAGCTAACCTTAGGTTG	
1128	Psap	Psap_1128	GGAAAGGACGAAACACCGTCTGGCATAAAATCACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGCATAAAATCACATTG	
1129	Pten	Pten_1129	GGAAAGGACGAAACACCGCCTCCAATTCAGGACCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCCAATTCAGGACCCACG	
1130	Pten	Pten_1130	GGAAAGGACGAAACACCGTGTGCATATTTATTGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCATATTTATTGCATCG	
1131	Pten	Pten_1131	GGAAAGGACGAAACACCGACTATTCCAATGTTCAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTATTCCAATGTTCAGTGG	
1132	Pten	Pten_1132	GGAAAGGACGAAACACCGGGTTTGATAAGTTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTTGATAAGTTCTAGCTG	
1133	Pts	Pts_1133	GGAAAGGACGAAACACCGGGGAAATGCAACAATCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAAATGCAACAATCCGAA	
1134	Pts	Pts_1134	GGAAAGGACGAAACACCGCGAGGCGCGACAGTCGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGGCGCGACAGTCGCGCG	
1135	Pts	Pts_1135	GGAAAGGACGAAACACCGCGGGCACAACTATAAAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGGCACAACTATAAAGGTG	
1136	Pts	Pts_1136	GGAAAGGACGAAACACCGGTGATCAAGAGGCTTCATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGATCAAGAGGCTTCATGA	
1137	Pex19	Pex19_1137	GGAAAGGACGAAACACCGACAGCACATCCTTAGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCACATCCTTAGACAGG	
1138	Pex19	Pex19_1138	GGAAAGGACGAAACACCGGCTGGCTTCCCAAGCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGCTTCCCAAGCTACTG	
1139	Pex19	Pex19_1139	GGAAAGGACGAAACACCGGATGGTCGGAGCATGTTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGTCGGAGCATGTTCTG	
1140	Pex19	Pex19_1140	GGAAAGGACGAAACACCGTGGAACTGCTCCACCAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAACTGCTCCACCAGATG	
1141	Abcd3	Abcd3_1141	GGAAAGGACGAAACACCGGCTCACACGGTACCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCACACGGTACCTCTACG	
1142	Abcd3	Abcd3_1142	GGAAAGGACGAAACACCGAACCAGGTACCCGACGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCAGGTACCCGACGACAG	
1143	Abcd3	Abcd3_1143	GGAAAGGACGAAACACCGGTGAAATGACTAGATTGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAAATGACTAGATTGGCT	
1144	Abcd3	Abcd3_1144	GGAAAGGACGAAACACCGAGAATGGGACGCTCATTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATGGGACGCTCATTGAG	
1145	Abcd4	Abcd4_1145	GGAAAGGACGAAACACCGAGACTCCATAATACTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACTCCATAATACTGACTG	
1146	Abcd4	Abcd4_1146	GGAAAGGACGAAACACCGGGACGACATTGATAATCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACGACATTGATAATCCGT	
1147	Abcd4	Abcd4_1147	GGAAAGGACGAAACACCGATGTTGCCGGTTACACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTGCCGGTTACACACAC	
1148	Abcd4	Abcd4_1148	GGAAAGGACGAAACACCGCATCTTTGGATATTTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTTTGGATATTTCATCG	
1149	Pex2	Pex2_1149	GGAAAGGACGAAACACCGGTATGCTGTGTGCACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATGCTGTGTGCACCATTG	
1150	Pex2	Pex2_1150	GGAAAGGACGAAACACCGTCCCAAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCAAAAGACGCTAAATGA	
1151	Pex2	Pex2_1151	GGAAAGGACGAAACACCGGTTCTGGGGCTTGCAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCTGGGGCTTGCAAAATA	
1152	Pex2	Pex2_1152	GGAAAGGACGAAACACCGATGAAAGCACTGAGTAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAAAGCACTGAGTAAACT	
1153	Pex5	Pex5_1153	GGAAAGGACGAAACACCGCTGGACTCACCATCGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGACTCACCATCGATCAG	
1154	Pex5	Pex5_1154	GGAAAGGACGAAACACCGTCTTGTAAACTGATCAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTGTAAACTGATCAACCC	
1155	Pex5	Pex5_1155	GGAAAGGACGAAACACCGTCGTGCGGCAGATTGGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTGCGGCAGATTGGCGAG	
1156	Pex5	Pex5_1156	GGAAAGGACGAAACACCGAGAAGGGCTGCATCGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAGGGCTGCATCGACTGG	
1157	Pygm	Pygm_1157	GGAAAGGACGAAACACCGGTAGCCGCCAACATTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGCCGCCAACATTGACTG	
1158	Pygm	Pygm_1158	GGAAAGGACGAAACACCGACTTGGAGGACTTGAAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTGGAGGACTTGAAACGT	
1159	Pygm	Pygm_1159	GGAAAGGACGAAACACCGGGATCCAGCGTCCCACGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATCCAGCGTCCCACGAGG	
1160	Pygm	Pygm_1160	GGAAAGGACGAAACACCGGCAGCCTATCTACGTCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCCTATCTACGTCCCCA	
1161	Rbp3	Rbp3_1161	GGAAAGGACGAAACACCGTAAGCAGGTACACTCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGCAGGTACACTCCACGC	
1162	Rbp3	Rbp3_1162	GGAAAGGACGAAACACCGTTACGAGCCCAGTACCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACGAGCCCAGTACCCTCG	
1163	Rbp3	Rbp3_1163	GGAAAGGACGAAACACCGCAGCACTGTATCTCTCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCACTGTATCTCTCCCCG	
1164	Rbp3	Rbp3_1164	GGAAAGGACGAAACACCGCTGCAATCTAAGTTGGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAATCTAAGTTGGCCCA	
1165	Rbp4	Rbp4_1165	GGAAAGGACGAAACACCGAACTTCGACAAGGCTCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTCGACAAGGCTCGTGT	
1166	Rbp4	Rbp4_1166	GGAAAGGACGAAACACCGCTTGCAAAAAGAGACCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCAAAAAGAGACCCTCG	
1167	Rbp4	Rbp4_1167	GGAAAGGACGAAACACCGAGGGACGAGTCCGTCTTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGACGAGTCCGTCTTCTG	
1168	Rbp4	Rbp4_1168	GGAAAGGACGAAACACCGCCCACTACTCACTTCCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACTACTCACTTCCTCGC	
1169	Rdh5	Rdh5_1169	GGAAAGGACGAAACACCGTGATATCCAGTAGTGTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATATCCAGTAGTGTTGTG	
1170	Rdh5	Rdh5_1170	GGAAAGGACGAAACACCGATGGAGACTTGTACTCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGAGACTTGTACTCCGAA	
1171	Rdh5	Rdh5_1171	GGAAAGGACGAAACACCGAAATCATCCTGTGTTAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCATCCTGTGTTAGCCA	
1172	Rdh5	Rdh5_1172	GGAAAGGACGAAACACCGAAGTGGGTGAAGACACGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTGGGTGAAGACACGTGT	
1173	Rlbp1	Rlbp1_1173	GGAAAGGACGAAACACCGTCGGGACAAGTATGGTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGGACAAGTATGGTCGAG	
1174	Rlbp1	Rlbp1_1174	GGAAAGGACGAAACACCGATCCGGCCTCGATAGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCGGCCTCGATAGTGCAG	
1175	Rlbp1	Rlbp1_1175	GGAAAGGACGAAACACCGCCGTGCCCGCAAGTTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTGCCCGCAAGTTCGATG	
1176	Rlbp1	Rlbp1_1176	GGAAAGGACGAAACACCGACCTCACCTTCTGCAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTCACCTTCTGCAAAGTG	
1177	Rnaseh1	Rnaseh1_1177	GGAAAGGACGAAACACCGTGGGCGACAGACAAACCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGCGACAGACAAACCAGA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1178	Rnaseh1	Rnaseh1_1178	GGAAAGGACGAAACACCGAGAGTCAGTCGTTGTCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTCAGTCGTTGTCTACA	
1179	Rnaseh1	Rnaseh1_1179	GGAAAGGACGAAACACCGAGCAGGAAACCGGTCCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGGAAACCGGTCCACCT	
1180	Rnaseh1	Rnaseh1_1180	GGAAAGGACGAAACACCGAGGAGCTCTTCAAGCCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGCTCTTCAAGCCCGGA	
1181	Rpe65	Rpe65_1181	GGAAAGGACGAAACACCGCAAAGAGCCCTGGCCCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGAGCCCTGGCCCACAT	
1182	Rpe65	Rpe65_1182	GGAAAGGACGAAACACCGTCGAGTCCAATGAAAGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGAGTCCAATGAAAGCATG	
1183	Rpe65	Rpe65_1183	GGAAAGGACGAAACACCGCCTTGTAAATATCTACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGTAAATATCTACCCAG	
1184	Rpe65	Rpe65_1184	GGAAAGGACGAAACACCGTCAAGCCATCTTATGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAGCCATCTTATGTACAC	
1185	Rpia	Rpia_1185	GGAAAGGACGAAACACCGACTGCACGTGGGAACCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCACGTGGGAACCCGAG	
1186	Rpia	Rpia_1186	GGAAAGGACGAAACACCGCGTGGTTCTCCACCGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGTTCTCCACCGCCGTG	
1187	Rpia	Rpia_1187	GGAAAGGACGAAACACCGATGATGTACCTGGAAAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATGTACCTGGAAAGATG	
1188	Rpia	Rpia_1188	GGAAAGGACGAAACACCGTGACCTGGATCAACACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACCTGGATCAACACCCAG	
1189	Nr1h4	Nr1h4_1189	GGAAAGGACGAAACACCGAAACGGGACATTGTTGTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGGGACATTGTTGTATG	
1190	Nr1h4	Nr1h4_1190	GGAAAGGACGAAACACCGTGATGGACATGTACATGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGGACATGTACATGCGC	
1191	Nr1h4	Nr1h4_1191	GGAAAGGACGAAACACCGTGTGACAAAGAAGCCGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGACAAAGAAGCCGCGAA	
1192	Nr1h4	Nr1h4_1192	GGAAAGGACGAAACACCGAGTGTAAATCTAAACGGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTAAATCTAAACGGCTA	
1193	Scp2	Scp2_1193	GGAAAGGACGAAACACCGACAGATCCCTTACTCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGATCCCTTACTCCGCAG	
1194	Scp2	Scp2_1194	GGAAAGGACGAAACACCGAAGTGGGTCATCAACCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTGGGTCATCAACCCTAG	
1195	Scp2	Scp2_1195	GGAAAGGACGAAACACCGCTCCTCGCTGGACAGAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCTCGCTGGACAGAATCG	
1196	Scp2	Scp2_1196	GGAAAGGACGAAACACCGGCTGTATTCATCTTGGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTATTCATCTTGGAACT	
1197	Sord	Sord_1197	GGAAAGGACGAAACACCGCAGTACTCATCTACTTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTACTCATCTACTTCTCG	
1198	Sord	Sord_1198	GGAAAGGACGAAACACCGGTTACTAAAGATGCACTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTACTAAAGATGCACTCGG	
1199	Sord	Sord_1199	GGAAAGGACGAAACACCGTGTGCTTGTAGAATCGGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCTTGTAGAATCGGCAG	
1200	Sord	Sord_1200	GGAAAGGACGAAACACCGTCTTACCAGCGCCACACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTACCAGCGCCACACACA	
1201	Selenbp1	Selenbp1_1201	GGAAAGGACGAAACACCGAGTCATGGTCAGCACCTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCATGGTCAGCACCTTGG	
1202	Selenbp1	Selenbp1_1202	GGAAAGGACGAAACACCGCATCTCCTCCCGCATCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTCCTCCCGCATCTACG	
1203	Selenbp1	Selenbp1_1203	GGAAAGGACGAAACACCGTGCAGGAAGCGGATCTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGGAAGCGGATCTCCAG	
1204	Selenbp1	Selenbp1_1204	GGAAAGGACGAAACACCGCCAGCCTCGACACAATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCCTCGACACAATGTCA	
1205	Sgpl1	Sgpl1_1205	GGAAAGGACGAAACACCGATATAAAATCCCACTCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATAAAATCCCACTCCATG	
1206	Sgpl1	Sgpl1_1206	GGAAAGGACGAAACACCGAGGCTTATGGAGAATTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCTTATGGAGAATTCACG	
1207	Sgpl1	Sgpl1_1207	GGAAAGGACGAAACACCGATTGCACCAAATATGAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGCACCAAATATGAGCCC	
1208	Sgpl1	Sgpl1_1208	GGAAAGGACGAAACACCGGGGAACGGAAAGCATCCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAACGGAAAGCATCCTGA	
1209	St3gal3	St3gal3_1209	GGAAAGGACGAAACACCGGCTGGACAAACCCTAGGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGACAAACCCTAGGCAC	
1210	St3gal3	St3gal3_1210	GGAAAGGACGAAACACCGCCTACGCATCACCTACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTACGCATCACCTACCCTG	
1211	St3gal3	St3gal3_1211	GGAAAGGACGAAACACCGACGACTATGACATTGTGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGACTATGACATTGTGATC	
1212	St3gal3	St3gal3_1212	GGAAAGGACGAAACACCGGATCCTAGCCCACTTGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCTAGCCCACTTGCGAA	
1213	St3gal5	St3gal5_1213	GGAAAGGACGAAACACCGGTTCGGGCAGCATATCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGGGCAGCATATCCAAG	
1214	St3gal5	St3gal5_1214	GGAAAGGACGAAACACCGTAGTATTCAACGTCCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTATTCAACGTCCGACAG	
1215	St3gal5	St3gal5_1215	GGAAAGGACGAAACACCGCGCCCTCAACCAGTTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCCTCAACCAGTTCGATG	
1216	St3gal5	St3gal5_1216	GGAAAGGACGAAACACCGAGCTGAGAAGTGATTGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGAGAAGTGATTGCTCA	
1217	Clpb	Clpb_1217	GGAAAGGACGAAACACCGAGGACCGCGTTCCGACGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCGCGTTCCGACGAGG	
1218	Clpb	Clpb_1218	GGAAAGGACGAAACACCGGGAGAACGGCTGGTACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAACGGCTGGTACGATG	
1219	Clpb	Clpb_1219	GGAAAGGACGAAACACCGCGTTGTCACCGGAGACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTTGTCACCGGAGACCGCG	
1220	Clpb	Clpb_1220	GGAAAGGACGAAACACCGCTCTCGAGTGACTAGGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTCGAGTGACTAGGACTG	
1221	Slc10a1	Slc10a1_1221	GGAAAGGACGAAACACCGTACAGCAAAGGAATCTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGCAAAGGAATCTACGA	
1222	Slc10a1	Slc10a1_1222	GGAAAGGACGAAACACCGTTAACCCTCGGTCCTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAACCCTCGGTCCTACCTG	
1223	Slc10a1	Slc10a1_1223	GGAAAGGACGAAACACCGAGGACGTAGGGTACATAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACGTAGGGTACATAGTG	
1224	Slc10a1	Slc10a1_1224	GGAAAGGACGAAACACCGGAGGGGCATGATACCGTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGGGCATGATACCGTACT	
1225	Slc10a2	Slc10a2_1225	GGAAAGGACGAAACACCGCTATTGGATAGATGGCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATTGGATAGATGGCGACA	
1226	Slc10a2	Slc10a2_1226	GGAAAGGACGAAACACCGGTTGCTCTCAGGTACTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCTCTCAGGTACTACGC	
1227	Slc10a2	Slc10a2_1227	GGAAAGGACGAAACACCGTAGGACATATAAAGAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGACATATAAAGAGACCA	
1228	Slc10a2	Slc10a2_1228	GGAAAGGACGAAACACCGGCTCACCATCCTCTTAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCACCATCCTCTTAGCCA	
1229	Slc12a3	Slc12a3_1229	GGAAAGGACGAAACACCGAACCTGGTACCCGACTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTGGTACCCGACTGGAG	
1230	Slc12a3	Slc12a3_1230	GGAAAGGACGAAACACCGCGGTTACAACACCATAGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTTACAACACCATAGACG	
1231	Slc12a3	Slc12a3_1231	GGAAAGGACGAAACACCGTGTGGTCTTCCACCTCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGTCTTCCACCTCGTTG	
1232	Slc12a3	Slc12a3_1232	GGAAAGGACGAAACACCGCACAGGCTAGCCCTTCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGGCTAGCCCTTCGCAG	
1233	Slc16a1	Slc16a1_1233	GGAAAGGACGAAACACCGACTACTAAGAAAGACCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTACTAAGAAAGACCAAAG	
1234	Slc16a1	Slc16a1_1234	GGAAAGGACGAAACACCGCACCAGCGATCATTACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCAGCGATCATTACTGGA	
1235	Slc16a1	Slc16a1_1235	GGAAAGGACGAAACACCGGACTTGCAGCCAACACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTTGCAGCCAACACCAAG	
1236	Slc16a1	Slc16a1_1236	GGAAAGGACGAAACACCGAGGCCCTATTGGTCTCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCCTATTGGTCTCATCA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1237	Slc1a1	Slc1a1_1237	GGAAAGGACGAAACACCGCGACTCACCTAGTACCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACTCACCTAGTACCACGG	
1238	Slc1a1	Slc1a1_1238	GGAAAGGACGAAACACCGTAGGATTACAGCAATGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGATTACAGCAATGACGG	
1239	Slc1a1	Slc1a1_1239	GGAAAGGACGAAACACCGATCATGCTGGATACGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCATGCTGGATACGATCAG	
1240	Slc1a1	Slc1a1_1240	GGAAAGGACGAAACACCGTCACCTGATCAGGTCCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACCTGATCAGGTCCAACA	
1241	Slc1a2	Slc1a2_1241	GGAAAGGACGAAACACCGCATGTTGATAGCCTTCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGTTGATAGCCTTCCCGG	
1242	Slc1a2	Slc1a2_1242	GGAAAGGACGAAACACCGCCATAGCTCTCGTGCCTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATAGCTCTCGTGCCTAGG	
1243	Slc1a2	Slc1a2_1243	GGAAAGGACGAAACACCGTAATTGCCCATAGGTCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATTGCCCATAGGTCTGAT	
1244	Slc1a2	Slc1a2_1244	GGAAAGGACGAAACACCGGTTCATGGTTTCATTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCATGGTTTCATTCAACA	
1245	Slc1a3	Slc1a3_1245	GGAAAGGACGAAACACCGGTATAAAATGAGCTACCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATAAAATGAGCTACCGGG	
1246	Slc1a3	Slc1a3_1246	GGAAAGGACGAAACACCGGACTCTGACCCGGATCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTCTGACCCGGATCCGGG	
1247	Slc1a3	Slc1a3_1247	GGAAAGGACGAAACACCGGAGGCCGACAATGACTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCCGACAATGACTGTCA	
1248	Slc1a3	Slc1a3_1248	GGAAAGGACGAAACACCGAGGCTTCTACCAGATTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCTTCTACCAGATTGGGA	
1249	Slc22a5	Slc22a5_1249	GGAAAGGACGAAACACCGTTTATGATCTGATCCGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTATGATCTGATCCGAACA	
1250	Slc22a5	Slc22a5_1250	GGAAAGGACGAAACACCGGGGTCAGATCTCCAACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCAGATCTCCAACTACG	
1251	Slc22a5	Slc22a5_1251	GGAAAGGACGAAACACCGCACAAGGCAACGGTGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAAGGCAACGGTGCTCCG	
1252	Slc22a5	Slc22a5_1252	GGAAAGGACGAAACACCGCACACCCACGAAAAACAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACCCACGAAAAACAAGG	
1253	Slc22a12	Slc22a12_1253	GGAAAGGACGAAACACCGGGGCCTGGGAGTTACATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCCTGGGAGTTACATACC	
1254	Slc22a12	Slc22a12_1254	GGAAAGGACGAAACACCGACGGTAGGCAAGCTGGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGTAGGCAAGCTGGACCA	
1255	Slc22a12	Slc22a12_1255	GGAAAGGACGAAACACCGGAGGTGCTATTGTCCAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTGCTATTGTCCAGGAG	
1256	Slc22a12	Slc22a12_1256	GGAAAGGACGAAACACCGCATCACCAAAGGGCTACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCACCAAAGGGCTACCCT	
1257	Slc2a1	Slc2a1_1257	GGAAAGGACGAAACACCGCCTGCTCATCAATCGTAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCTCATCAATCGTAACG	
1258	Slc2a1	Slc2a1_1258	GGAAAGGACGAAACACCGTCAGCATGGAGTTCCGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCATGGAGTTCCGCCTG	
1259	Slc2a1	Slc2a1_1259	GGAAAGGACGAAACACCGGTGTCACCTACAGCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTCACCTACAGCTCTACG	
1260	Slc2a1	Slc2a1_1260	GGAAAGGACGAAACACCGCAAACATGGAACCACCGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACATGGAACCACCGCTA	
1261	Slc2a2	Slc2a2_1261	GGAAAGGACGAAACACCGAGAGGGCTCCAGTCAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGGCTCCAGTCAATGAG	
1262	Slc2a2	Slc2a2_1262	GGAAAGGACGAAACACCGTTACCGACAGCCCATCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCGACAGCCCATCCTCG	
1263	Slc2a2	Slc2a2_1263	GGAAAGGACGAAACACCGGGACTGGTTCCAATGTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTGGTTCCAATGTACAT	
1264	Slc2a2	Slc2a2_1264	GGAAAGGACGAAACACCGTGTGATCAATGCACCTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGATCAATGCACCTCAAG	
1265	Slc3a1	Slc3a1_1265	GGAAAGGACGAAACACCGCCATATACCAGATCTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATATACCAGATCTACCCG	
1266	Slc3a1	Slc3a1_1266	GGAAAGGACGAAACACCGATCCTTGGTTCCAATCGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTTGGTTCCAATCGAGT	
1267	Slc3a1	Slc3a1_1267	GGAAAGGACGAAACACCGAGAGGAGCCTCACCTAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGAGCCTCACCTAAAGG	
1268	Slc3a1	Slc3a1_1268	GGAAAGGACGAAACACCGTGGCAAGCCATAGTACATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCAAGCCATAGTACATCA	
1269	Slc5a1	Slc5a1_1269	GGAAAGGACGAAACACCGAGGAAGAATGCTACACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAAGAATGCTACACACCG	
1270	Slc5a1	Slc5a1_1270	GGAAAGGACGAAACACCGGAGACATGTTCTTGGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACATGTTCTTGGCCGAG	
1271	Slc5a1	Slc5a1_1271	GGAAAGGACGAAACACCGCATCGCCTACCCCACGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCGCCTACCCCACGCTCG	
1272	Slc5a1	Slc5a1_1272	GGAAAGGACGAAACACCGCCGGCCACCACACCATACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGCCACCACACCATACTT	
1273	Slc7a5	Slc7a5_1273	GGAAAGGACGAAACACCGGCCCTCCTCGCAGTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTCCTCGCAGTACATCG	
1274	Slc7a5	Slc7a5_1274	GGAAAGGACGAAACACCGACCCCTACTTACGCACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCCTACTTACGCACGCAG	
1275	Slc7a5	Slc7a5_1275	GGAAAGGACGAAACACCGAGCGGCCTCTTCGCCTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGGCCTCTTCGCCTACGG	
1276	Slc7a5	Slc7a5_1276	GGAAAGGACGAAACACCGGTAGCAGAGTGCGCCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGCAGAGTGCGCCCACGA	
1277	Slc7a7	Slc7a7_1277	GGAAAGGACGAAACACCGAAGAGATCAGGAACCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGATCAGGAACCCCGAG	
1278	Slc7a7	Slc7a7_1278	GGAAAGGACGAAACACCGCAGCGCCAACACCTTAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCGCCAACACCTTAGCAT	
1279	Slc7a7	Slc7a7_1279	GGAAAGGACGAAACACCGGGCCCCGGATTTCTTAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCCCGGATTTCTTAATGG	
1280	Slc7a7	Slc7a7_1280	GGAAAGGACGAAACACCGGAGACACACGCCATTAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACACACGCCATTAAGCA	
1281	Smpd1	Smpd1_1281	GGAAAGGACGAAACACCGAGGCTTTCTAGCGTTCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCTTTCTAGCGTTCGCAA	
1282	Smpd1	Smpd1_1282	GGAAAGGACGAAACACCGGAAGAGGACACGGCTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGAGGACACGGCTGACAG	
1283	Smpd1	Smpd1_1283	GGAAAGGACGAAACACCGAGTCTCGCCAAGATCAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTCGCCAAGATCAGCTG	
1284	Smpd1	Smpd1_1284	GGAAAGGACGAAACACCGGCTGACTGGCACACATCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGACTGGCACACATCTAG	
1285	Sms	Sms_1285	GGAAAGGACGAAACACCGACTTACTAACATCCCCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTACTAACATCCCCGCTG	
1286	Sms	Sms_1286	GGAAAGGACGAAACACCGTTACCACCCATAGTTCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCACCCATAGTTCGCGG	
1287	Sms	Sms_1287	GGAAAGGACGAAACACCGCTTACACGAACAAGAATGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACACGAACAAGAATGGC	
1288	Sms	Sms_1288	GGAAAGGACGAAACACCGAAACAAGAAACTGACAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACAAGAAACTGACAGCGT	
1289	Spr	Spr_1289	GGAAAGGACGAAACACCGGCGTGCGCTTACGAGCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTGCGCTTACGAGCATCA	
1290	Spr	Spr_1290	GGAAAGGACGAAACACCGGCGCAGTACGCGAGCTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCAGTACGCGAGCTCCCG	
1291	Spr	Spr_1291	GGAAAGGACGAAACACCGAGCCTCGGTGCCCAGATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCTCGGTGCCCAGATCGG	
1292	Spr	Spr_1292	GGAAAGGACGAAACACCGTACAGACCCCAGCCTTTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGACCCCAGCCTTTGTA	
1293	Sptlc2	Sptlc2_1293	GGAAAGGACGAAACACCGGTTGTGTTTGAAGATTCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTGTTTGAAGATTCGAA	
1294	Sptlc2	Sptlc2_1294	GGAAAGGACGAAACACCGTGAGAGCAATCACTTCAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAGCAATCACTTCAGGA	
1295	Sptlc2	Sptlc2_1295	GGAAAGGACGAAACACCGAATCTCGAAGATATCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCTCGAAGATATCCAAAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1296	Sptlc2	Sptlc2_1296	GGAAAGGACGAAACACCGACAACTATCTTGGATTTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAACTATCTTGGATTTGCG	
1297	Scarb1	Scarb1_1297	GGAAAGGACGAAACACCGGGGGCCGTGAAGCGATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCCGTGAAGCGATACGT	
1298	Scarb1	Scarb1_1298	GGAAAGGACGAAACACCGTGCGGTTCATAAAAGCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGGTTCATAAAAGCACGC	
1299	Scarb1	Scarb1_1299	GGAAAGGACGAAACACCGGATGAACAACTCGAATTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAACAACTCGAATTCTG	
1300	Scarb1	Scarb1_1300	GGAAAGGACGAAACACCGGAGGATTCGGGTGTCATGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGATTCGGGTGTCATGAA	
1301	Ssr4	Ssr4_1301	GGAAAGGACGAAACACCGTAGTAAGAAGGGGTGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTAAGAAGGGGTGATCTG	
1302	Ssr4	Ssr4_1302	GGAAAGGACGAAACACCGAAACAATTTCCTGTAACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACAATTTCCTGTAACCCG	
1303	Ssr4	Ssr4_1303	GGAAAGGACGAAACACCGTACAGAGACTGTATTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGAGACTGTATTCATCG	
1304	Ssr4	Ssr4_1304	GGAAAGGACGAAACACCGCACCTTCCTTAGGAGGCTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCTTCCTTAGGAGGCTAT	
1305	Star	Star_1305	GGAAAGGACGAAACACCGAGAACTTGTGGACCGCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTTGTGGACCGCATGG	
1306	Star	Star_1306	GGAAAGGACGAAACACCGCGAACTTGACCCATCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAACTTGACCCATCCACCC	
1307	Star	Star_1307	GGAAAGGACGAAACACCGGAAGCTCCTATAGACATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCTCCTATAGACATATG	
1308	Star	Star_1308	GGAAAGGACGAAACACCGCGCACGCTCACGAAGTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCACGCTCACGAAGTCTCG	
1309	Stra6	Stra6_1309	GGAAAGGACGAAACACCGTCTTCAAGCACTACACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCAAGCACTACACCGAG	
1310	Stra6	Stra6_1310	GGAAAGGACGAAACACCGCAAGTTGTACTGGATACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTTGTACTGGATACCAA	
1311	Stra6	Stra6_1311	GGAAAGGACGAAACACCGCCAGACCTGAACACCAAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGACCTGAACACCAAAGT	
1312	Stra6	Stra6_1312	GGAAAGGACGAAACACCGGAAGCATCACCTATGGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCATCACCTATGGACTG	
1313	Sucla2	Sucla2_1313	GGAAAGGACGAAACACCGCAGAGCGTAACATACTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGCGTAACATACTGTCA	
1314	Sucla2	Sucla2_1314	GGAAAGGACGAAACACCGTGTGCACTTCCTATCAGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCACTTCCTATCAGTAC	
1315	Sucla2	Sucla2_1315	GGAAAGGACGAAACACCGGTAGAAGATTCTGACGGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGAAGATTCTGACGGAAA	
1316	Sucla2	Sucla2_1316	GGAAAGGACGAAACACCGTCAAGTATTCATGCAGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAGTATTCATGCAGCGAA	
1317	Abcc8	Abcc8_1317	GGAAAGGACGAAACACCGATGGCTGCTAAATGCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCTGCTAAATGCCACGG	
1318	Abcc8	Abcc8_1318	GGAAAGGACGAAACACCGCAGACCAACGAGATGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACCAACGAGATGCTCCG	
1319	Abcc8	Abcc8_1319	GGAAAGGACGAAACACCGTGGACAATGAAGATCATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGACAATGAAGATCATCGG	
1320	Abcc8	Abcc8_1320	GGAAAGGACGAAACACCGGAAACTGGGATTAACCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACTGGGATTAACCTGAG	
1321	Surf1	Surf1_1321	GGAAAGGACGAAACACCGTGTTTCTATAGGTCCAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTTCTATAGGTCCAACGT	
1322	Surf1	Surf1_1322	GGAAAGGACGAAACACCGATGGAAAGGAGTAACTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGAAAGGAGTAACTACAT	
1323	Surf1	Surf1_1323	GGAAAGGACGAAACACCGGTGGTCGCAATGGGCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTCGCAATGGGCCTACG	
1324	Surf1	Surf1_1324	GGAAAGGACGAAACACCGTTATGTACAACTCTTTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATGTACAACTCTTTAGAG	
1325	Taldo1	Taldo1_1325	GGAAAGGACGAAACACCGGCGCATCCTTGATTGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCATCCTTGATTGGCATG	
1326	Taldo1	Taldo1_1326	GGAAAGGACGAAACACCGCTTCTTTGTAAAGCTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCTTTGTAAAGCTCGATG	
1327	Taldo1	Taldo1_1327	GGAAAGGACGAAACACCGTTCTGAATTCAGGCCTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGAATTCAGGCCTCAAG	
1328	Taldo1	Taldo1_1328	GGAAAGGACGAAACACCGGCTTGTATTCATCGATGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTGTATTCATCGATGGCT	
1329	Tbxas1	Tbxas1_1329	GGAAAGGACGAAACACCGTCACAGGCTTGGCTGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACAGGCTTGGCTGATGAG	
1330	Tbxas1	Tbxas1_1330	GGAAAGGACGAAACACCGCCACACTTACCATTTCAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACACTTACCATTTCAGGA	
1331	Tbxas1	Tbxas1_1331	GGAAAGGACGAAACACCGACAGAGGCCCGTATCGCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGAGGCCCGTATCGCTCT	
1332	Tbxas1	Tbxas1_1332	GGAAAGGACGAAACACCGCTGCTGTTACACCATAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCTGTTACACCATAGATG	
1333	Hnf1a	Hnf1a_1333	GGAAAGGACGAAACACCGCCTATAACGGACCTCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTATAACGGACCTCCACCG	
1334	Hnf1a	Hnf1a_1334	GGAAAGGACGAAACACCGGACGTACCAGGTGTACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACGTACCAGGTGTACAGAG	
1335	Hnf1a	Hnf1a_1335	GGAAAGGACGAAACACCGTGCCAACTAAGAAGGGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCAACTAAGAAGGGGCGT	
1336	Hnf1a	Hnf1a_1336	GGAAAGGACGAAACACCGCGGACAGTCTGCAACCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACAGTCTGCAACCAGTG	
1337	Hnf1b	Hnf1b_1337	GGAAAGGACGAAACACCGCAGCTTCACCCCGAAATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCTTCACCCCGAAATTCG	
1338	Hnf1b	Hnf1b_1338	GGAAAGGACGAAACACCGCTGGTTCGCAAACCGCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTTCGCAAACCGCCGGA	
1339	Hnf1b	Hnf1b_1339	GGAAAGGACGAAACACCGGCCGCAACCGGTTTAAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCGCAACCGGTTTAAATGG	
1340	Hnf1b	Hnf1b_1340	GGAAAGGACGAAACACCGCTTGGTACGTCAGAAAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGTACGTCAGAAAGCAA	
1341	Tcn2	Tcn2_1341	GGAAAGGACGAAACACCGGAAGCGGCTCCATGACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCGGCTCCATGACAGCG	
1342	Tcn2	Tcn2_1342	GGAAAGGACGAAACACCGTCTGAGACCACGAATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGAGACCACGAATCACCA	
1343	Tcn2	Tcn2_1343	GGAAAGGACGAAACACCGGAGACTAGCAATACCGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACTAGCAATACCGCAGG	
1344	Tcn2	Tcn2_1344	GGAAAGGACGAAACACCGGAATATCTATAGCACCCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATATCTATAGCACCCCAC	
1345	Tfam	Tfam_1345	GGAAAGGACGAAACACCGTAAATGTTATATGCTGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAATGTTATATGCTGAACG	
1346	Tfam	Tfam_1346	GGAAAGGACGAAACACCGGGAGCGTGCTAAAAGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCGTGCTAAAAGCACTG	
1347	Tfam	Tfam_1347	GGAAAGGACGAAACACCGCTAACTCCAAGTCAGCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAACTCCAAGTCAGCTGAT	
1348	Tfam	Tfam_1348	GGAAAGGACGAAACACCGGCTGTTCTGTGGAAAATCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTTCTGTGGAAAATCGA	
1349	Th	Th_1349	GGAAAGGACGAAACACCGGGGTGAGCCAATTCCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTGAGCCAATTCCCCACG	
1350	Th	Th_1350	GGAAAGGACGAAACACCGACTGTGTGCACTGAAACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTGTGCACTGAAACACA	
1351	Th	Th_1351	GGAAAGGACGAAACACCGCCCCAAGGTTCATTGGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCAAGGTTCATTGGACGG	
1352	Th	Th_1352	GGAAAGGACGAAACACCGGTGCGCTTCGAGGTGCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCGCTTCGAGGTGCCCAG	
1353	Tkt	Tkt_1353	GGAAAGGACGAAACACCGCGTGGACGGACACAGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGACGGACACAGCGTGG	
1354	Tkt	Tkt_1354	GGAAAGGACGAAACACCGCAGCGCTGCAGCATGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCGCTGCAGCATGATGTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1355	Tkt	Tkt_1355	GGAAAGGACGAAACACCGCCCACAGATAGCCACCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACAGATAGCCACCCGGA	
1356	Tkt	Tkt_1356	GGAAAGGACGAAACACCGCTCCGAGGGCTCCGTCTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGAGGGCTCCGTCTGGG	
1357	Tmem165	Tmem165_1357	GGAAAGGACGAAACACCGGGCATTAGAATGCTTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCATTAGAATGCTTCGGGA	
1358	Tmem165	Tmem165_1358	GGAAAGGACGAAACACCGACATAGTATGTATACACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATAGTATGTATACACCCT	
1359	Tmem165	Tmem165_1359	GGAAAGGACGAAACACCGGCAGCTGCCCAGACGAATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCTGCCCAGACGAATCT	
1360	Tmem165	Tmem165_1360	GGAAAGGACGAAACACCGGTCATCATAGTGTCCGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATCATAGTGTCCGAACT	
1361	Tpi1	Tpi1_1361	GGAAAGGACGAAACACCGTGAAGGTCAGTACAAACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGGTCAGTACAAACGCA	
1362	Tpi1	Tpi1_1362	GGAAAGGACGAAACACCGAAGTCGATGTAAGCGGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCGATGTAAGCGGTGGG	
1363	Tpi1	Tpi1_1363	GGAAAGGACGAAACACCGAGTGAGCCACGCCCTAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGAGCCACGCCCTAGCAG	
1364	Tpi1	Tpi1_1364	GGAAAGGACGAAACACCGCCAACGAAGAACTTCCTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACGAAGAACTTCCTGGT	
1365	Tpmt	Tpmt_1365	GGAAAGGACGAAACACCGAAAGAACCAAGTACTAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGAACCAAGTACTAACCC	
1366	Tpmt	Tpmt_1366	GGAAAGGACGAAACACCGTTCTGCAGGTTCGCAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGCAGGTTCGCAGATCG	
1367	Tpmt	Tpmt_1367	GGAAAGGACGAAACACCGGCATTAGTGGCTATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATTAGTGGCTATCAATCC	
1368	Tpmt	Tpmt_1368	GGAAAGGACGAAACACCGAAAACACTCGCAGTCCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACACTCGCAGTCCACTC	
1369	Trex1	Trex1_1369	GGAAAGGACGAAACACCGTTTCCTCGAACCATTCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCCTCGAACCATTCCCTG	
1370	Trex1	Trex1_1370	GGAAAGGACGAAACACCGACACAGAAGGTACCATCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACAGAAGGTACCATCTAG	
1371	Trex1	Trex1_1371	GGAAAGGACGAAACACCGAGCTTGTCCACCACACGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTTGTCCACCACACGGGG	
1372	Trex1	Trex1_1372	GGAAAGGACGAAACACCGGGAGCAGAGGAAAGTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCAGAGGAAAGTCATAG	
1373	Tfrc	Tfrc_1373	GGAAAGGACGAAACACCGCTACACGCTTACAATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACACGCTTACAATAGCCC	
1374	Tfrc	Tfrc_1374	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATACATACACTCCTCGTG	
1375	Tfrc	Tfrc_1375	GGAAAGGACGAAACACCGGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTCCTACTACAACATAA	
1376	Tfrc	Tfrc_1376	GGAAAGGACGAAACACCGAACCCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCCTCGGGAGACTCCACT	
1377	Cmpk2	Cmpk2_1377	GGAAAGGACGAAACACCGTCGGCCGCGGCGCTTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGCCGCGGCGCTTCACTG	
1378	Cmpk2	Cmpk2_1378	GGAAAGGACGAAACACCGGGTGTTCCAAGACCGGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTTCCAAGACCGGGACG	
1379	Cmpk2	Cmpk2_1379	GGAAAGGACGAAACACCGAGTCGCGCCGAGTGTCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGCGCCGAGTGTCCGGG	
1380	Cmpk2	Cmpk2_1380	GGAAAGGACGAAACACCGAGTTGACCAGTGCCCAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGACCAGTGCCCAAAGG	
1381	Tyr	Tyr_1381	GGAAAGGACGAAACACCGAGAAATTCGAGAACTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAATTCGAGAACTAACTG	
1382	Tyr	Tyr_1382	GGAAAGGACGAAACACCGTTTATGCGATGGAACACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTATGCGATGGAACACCTG	
1383	Tyr	Tyr_1383	GGAAAGGACGAAACACCGATGTTGATATCATTAAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTGATATCATTAAACAT	
1384	Tyr	Tyr_1384	GGAAAGGACGAAACACCGACCCCTTTGAAGGGGAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCCTTTGAAGGGGAACTG	
1385	Ucp2	Ucp2_1385	GGAAAGGACGAAACACCGTCTGGGTACCATCCTAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGGTACCATCCTAACCA	
1386	Ucp2	Ucp2_1386	GGAAAGGACGAAACACCGGTCAAACAGTTCTACACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAAACAGTTCTACACCAA	
1387	Ucp2	Ucp2_1387	GGAAAGGACGAAACACCGAGACCATTGCACGAGAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCATTGCACGAGAGGAA	
1388	Ucp2	Ucp2_1388	GGAAAGGACGAAACACCGCGGACCTTGGCGGTATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACCTTGGCGGTATCCAG	
1389	Slc35a2	Slc35a2_1389	GGAAAGGACGAAACACCGTCACCCGCTGTAGTGGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACCCGCTGTAGTGGACCC	
1390	Slc35a2	Slc35a2_1390	GGAAAGGACGAAACACCGCTGCTCTTCGCACAAAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCTCTTCGCACAAAAGAG	
1391	Slc35a2	Slc35a2_1391	GGAAAGGACGAAACACCGCTGCAAGGTATAGATGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAAGGTATAGATGAGAG	
1392	Slc35a2	Slc35a2_1392	GGAAAGGACGAAACACCGGGCCACTGGATCAGAACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCACTGGATCAGAACCCG	
1393	Ugcg	Ugcg_1393	GGAAAGGACGAAACACCGCGGCTACATACGGCAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCTACATACGGCAGCCCG	
1394	Ugcg	Ugcg_1394	GGAAAGGACGAAACACCGTGGCCAAAGCAATAGCCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCAAAGCAATAGCCGAC	
1395	Ugcg	Ugcg_1395	GGAAAGGACGAAACACCGAAGGATGTGCTAGATCAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGATGTGCTAGATCAGGC	
1396	Ugcg	Ugcg_1396	GGAAAGGACGAAACACCGCAGCCGTATAGCAAGCTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCGTATAGCAAGCTCCC	
1397	Umps	Umps_1397	GGAAAGGACGAAACACCGGAGCAGATAACTGTCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCAGATAACTGTCGCCAG	
1398	Umps	Umps_1398	GGAAAGGACGAAACACCGCCGCAGGTCGATGTAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCAGGTCGATGTAGACTG	
1399	Umps	Umps_1399	GGAAAGGACGAAACACCGAGAGCGTGCACACGGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCGTGCACACGGCGTGG	
1400	Umps	Umps_1400	GGAAAGGACGAAACACCGTCTGTCTGCCGATGTGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTCTGCCGATGTGTCGG	
1401	Ung	Ung_1401	GGAAAGGACGAAACACCGACGGACCTAATCAAGCTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGACCTAATCAAGCTCAC	
1402	Ung	Ung_1402	GGAAAGGACGAAACACCGTTGTCAGGGTGGGCCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTCAGGGTGGGCCCGACA	
1403	Ung	Ung_1403	GGAAAGGACGAAACACCGCCAACCCCGACTCTGACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACCCCGACTCTGACTCC	
1404	Ung	Ung_1404	GGAAAGGACGAAACACCGCCACAAGGTCTATCCGCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACAAGGTCTATCCGCCCC	
1405	Uqcrq	Uqcrq_1405	GGAAAGGACGAAACACCGGATCCCTACAGCGTTTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCCTACAGCGTTTGTAG	
1406	Uqcrq	Uqcrq_1406	GGAAAGGACGAAACACCGCTCAAAGGGCGACAAGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAAAGGGCGACAAGCTGT	
1407	Uqcrq	Uqcrq_1407	GGAAAGGACGAAACACCGGCAGGATGCGCTCGCGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGATGCGCTCGCGAGTG	
1408	Uqcrq	Uqcrq_1408	GGAAAGGACGAAACACCGTTTGCTGAAATAGCTTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGCTGAAATAGCTTGGGA	
1409	Urod	Urod_1409	GGAAAGGACGAAACACCGCCATCACCCTTACTCGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCACCCTTACTCGACAA	
1410	Urod	Urod_1410	GGAAAGGACGAAACACCGGTGGACCCTAATGACATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACCCTAATGACATACA	
1411	Urod	Urod_1411	GGAAAGGACGAAACACCGACTGCCCTACATTCGTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCCCTACATTCGTGATG	
1412	Urod	Urod_1412	GGAAAGGACGAAACACCGCAGCACCTGCCGATCTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCACCTGCCGATCTCCCG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1413	Uros	Uros_1413	GGAAAGGACGAAACACCGTCTCCTTTGATAGTTCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCTTTGATAGTTCCACA	
1414	Uros	Uros_1414	GGAAAGGACGAAACACCGTGACAGCACAGGAATCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACAGCACAGGAATCAGTG	
1415	Uros	Uros_1415	GGAAAGGACGAAACACCGGCCAAGTCTGTGTACGTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAAGTCTGTGTACGTGGT	
1416	Uros	Uros_1416	GGAAAGGACGAAACACCGAGACATGCATGCTTTCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACATGCATGCTTTCCATG	
1417	Usp9x	Usp9x_1417	GGAAAGGACGAAACACCGGCAGATATGGAAACTCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGATATGGAAACTCGAAG	
1418	Usp9x	Usp9x_1418	GGAAAGGACGAAACACCGATGGGTATAGTATGACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGTATAGTATGACACAC	
1419	Usp9x	Usp9x_1419	GGAAAGGACGAAACACCGGAAGTTGATTGATTAAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTTGATTGATTAAGTCA	
1420	Usp9x	Usp9x_1420	GGAAAGGACGAAACACCGTATCCAAACACATCATCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCAAACACATCATCCCT	
1421	Vdr	Vdr_1421	GGAAAGGACGAAACACCGTGGAGATTGCCGCATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGATTGCCGCATCACCA	
1422	Vdr	Vdr_1422	GGAAAGGACGAAACACCGAGCGTTGAAGTGGAAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGTTGAAGTGGAAGCCCG	
1423	Vdr	Vdr_1423	GGAAAGGACGAAACACCGTTCTTCATTCAGATCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTCATTCAGATCCATCG	
1424	Vdr	Vdr_1424	GGAAAGGACGAAACACCGTTCGTGCAGACGTAAGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGTGCAGACGTAAGTACA	
1425	Xdh	Xdh_1425	GGAAAGGACGAAACACCGCCAGCATGCAACGTACAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCATGCAACGTACAGGG	
1426	Xdh	Xdh_1426	GGAAAGGACGAAACACCGCATACTCATGACAATACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACTCATGACAATACCAG	
1427	Xdh	Xdh_1427	GGAAAGGACGAAACACCGTCAAAACGCAACGTCTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAAACGCAACGTCTTCCG	
1428	Xdh	Xdh_1428	GGAAAGGACGAAACACCGGGAATTCCACCATCCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAATTCCACCATCCCACCA	
1429	Nt5e	Nt5e_1429	GGAAAGGACGAAACACCGTCATGAATTTGATAACGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATGAATTTGATAACGGTG	
1430	Nt5e	Nt5e_1430	GGAAAGGACGAAACACCGTGAATAAGATCATCGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAATAAGATCATCGCCCTG	
1431	Nt5e	Nt5e_1431	GGAAAGGACGAAACACCGTATGCCTTTGGCAAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGCCTTTGGCAAATACCT	
1432	Nt5e	Nt5e_1432	GGAAAGGACGAAACACCGCCTGAAGCGGCACGTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGAAGCGGCACGTCTGAG	
1433	Papss2	Papss2_1433	GGAAAGGACGAAACACCGGAATATCCGCCGGATCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATATCCGCCGGATCGCGG	
1434	Papss2	Papss2_1434	GGAAAGGACGAAACACCGAGTCGATCAAATCCGAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGATCAAATCCGAGCTG	
1435	Papss2	Papss2_1435	GGAAAGGACGAAACACCGCTTGATGTACGAAGGTCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGATGTACGAAGGTCGGA	
1436	Papss2	Papss2_1436	GGAAAGGACGAAACACCGGGTGCTAGAGAGAATAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGCTAGAGAGAATAAGGT	
1437	Slco2a1	Slco2a1_1437	GGAAAGGACGAAACACCGCCCACGGATGATCGGCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACGGATGATCGGCATAG	
1438	Slco2a1	Slco2a1_1438	GGAAAGGACGAAACACCGACTCGGGGGATGGTTTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCGGGGGATGGTTTGCAG	
1439	Slco2a1	Slco2a1_1439	GGAAAGGACGAAACACCGCTTCGTGGACTACGGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCGTGGACTACGGCAGAG	
1440	Slco2a1	Slco2a1_1440	GGAAAGGACGAAACACCGCTCTGCAAAGTCGTCCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTGCAAAGTCGTCCACAT	
1441	Slc35a1	Slc35a1_1441	GGAAAGGACGAAACACCGGAACACTCAGCAAATTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACACTCAGCAAATTACAG	
1442	Slc35a1	Slc35a1_1442	GGAAAGGACGAAACACCGATAGCACCAAAGCCTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGCACCAAAGCCTAACAA	
1443	Slc35a1	Slc35a1_1443	GGAAAGGACGAAACACCGTGCACAGCATACACTAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCACAGCATACACTAGTGA	
1444	Slc35a1	Slc35a1_1444	GGAAAGGACGAAACACCGTCTTAAAGCTACGGTGTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAAAGCTACGGTGTAAG	
1445	Mpdu1	Mpdu1_1445	GGAAAGGACGAAACACCGTTCCTGGTCATGCACTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCTGGTCATGCACTACAG	
1446	Mpdu1	Mpdu1_1446	GGAAAGGACGAAACACCGCTAGCTCCAGCATTACTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGCTCCAGCATTACTGAC	
1447	Mpdu1	Mpdu1_1447	GGAAAGGACGAAACACCGACTACAGCCAGAGGCGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTACAGCCAGAGGCGTGAG	
1448	Mpdu1	Mpdu1_1448	GGAAAGGACGAAACACCGACGACCAGCTCTTCGTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGACCAGCTCTTCGTGCAA	
1449	Rbck1	Rbck1_1449	GGAAAGGACGAAACACCGTGCTTCATACCAGCCTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTTCATACCAGCCTGACG	
1450	Rbck1	Rbck1_1450	GGAAAGGACGAAACACCGAGTACGCCCGGATATGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACGCCCGGATATGACAG	
1451	Rbck1	Rbck1_1451	GGAAAGGACGAAACACCGTGCATTCACACGGCATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCATTCACACGGCATTCGG	
1452	Rbck1	Rbck1_1452	GGAAAGGACGAAACACCGACCCGAGGTCTCCCCAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCGAGGTCTCCCCAACAC	
1453	Btd	Btd_1453	GGAAAGGACGAAACACCGCTTGCTGTTCATAGACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCTGTTCATAGACGTCG	
1454	Btd	Btd_1454	GGAAAGGACGAAACACCGGTACCAAAAGGACTTGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACCAAAAGGACTTGAGAG	
1455	Btd	Btd_1455	GGAAAGGACGAAACACCGATACCAGTTTAACACAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCAGTTTAACACAAATG	
1456	Btd	Btd_1456	GGAAAGGACGAAACACCGCCGCGAGGCTGAGTACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCGAGGCTGAGTACTACG	
1457	Slc27a5	Slc27a5_1457	GGAAAGGACGAAACACCGGTGGGCTTAATGAACTATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGGCTTAATGAACTATGT	
1458	Slc27a5	Slc27a5_1458	GGAAAGGACGAAACACCGTACCTCTGTACCATACGATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTCTGTACCATACGATA	
1459	Slc27a5	Slc27a5_1459	GGAAAGGACGAAACACCGGTAACAGTGATCTTGTATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAACAGTGATCTTGTATGT	
1460	Slc27a5	Slc27a5_1460	GGAAAGGACGAAACACCGCCTTTGTGGATGCTTTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTTGTGGATGCTTTAGAG	
1461	Txnrd2	Txnrd2_1461	GGAAAGGACGAAACACCGTATCCAGTCCAATTCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCAGTCCAATTCCAGTG	
1462	Txnrd2	Txnrd2_1462	GGAAAGGACGAAACACCGTGAGCACACAGTTCGCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCACACAGTTCGCGGTG	
1463	Txnrd2	Txnrd2_1463	GGAAAGGACGAAACACCGGGTGGCACCTGTGTCAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGCACCTGTGTCAACGT	
1464	Txnrd2	Txnrd2_1464	GGAAAGGACGAAACACCGCGGTGGCCTAGCTTGTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTGGCCTAGCTTGTGCCA	
1465	Slc27a4	Slc27a4_1465	GGAAAGGACGAAACACCGCAAACGGATAGGGTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACGGATAGGGTACACAA	
1466	Slc27a4	Slc27a4_1466	GGAAAGGACGAAACACCGTCTACACATCGGGCACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTACACATCGGGCACCACG	
1467	Slc27a4	Slc27a4_1467	GGAAAGGACGAAACACCGTGACTTCAGGAAACATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTTCAGGAAACATCGTG	
1468	Slc27a4	Slc27a4_1468	GGAAAGGACGAAACACCGACAGACCCACAAACTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGACCCACAAACTCATTG	
1469	Cln8	Cln8_1469	GGAAAGGACGAAACACCGGCTCATCTCTAGGAGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCATCTCTAGGAGCAACG	
1470	Cln8	Cln8_1470	GGAAAGGACGAAACACCGGTGTTGGTTTCACATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTTGGTTTCACATCACCA	
1471	Cln8	Cln8_1471	GGAAAGGACGAAACACCGAAAGGTGCGGAAGAACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGGTGCGGAAGAACAGGT	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
1472	Cln8	Cln8_1472	GGAAAGGACGAAACACCGCTTTGTCGGCATAGAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGTCGGCATAGAGCACG	
1473	Mecr	Mecr_1473	GGAAAGGACGAAACACCGCGTGGCGGTACCAAGCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGCGGTACCAAGCCTCG	
1474	Mecr	Mecr_1474	GGAAAGGACGAAACACCGAAGGATCTGACGTCCACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGATCTGACGTCCACGTG	
1475	Mecr	Mecr_1475	GGAAAGGACGAAACACCGATCCAGAATGCATCCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCAGAATGCATCCAACAG	
1476	Mecr	Mecr_1476	GGAAAGGACGAAACACCGAGCACTGATTGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACTGATTGGAATCCCTA	
1477	Aifm1	Aifm1_1477	GGAAAGGACGAAACACCGCTGCCTAATATTGAGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCCTAATATTGAGAACGG	
1478	Aifm1	Aifm1_1478	GGAAAGGACGAAACACCGACCATGGAAAAAGTCAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCATGGAAAAAGTCAAACG	
1479	Aifm1	Aifm1_1479	GGAAAGGACGAAACACCGGTCAATTACAGTTATCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAATTACAGTTATCGGCG	
1480	Aifm1	Aifm1_1480	GGAAAGGACGAAACACCGAAGTCTGTCTGCCATCGATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCTGTCTGCCATCGATA	
1481	Sgsh	Sgsh_1481	GGAAAGGACGAAACACCGCTGACCTAGAAGGCTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGACCTAGAAGGCTCACGT	
1482	Sgsh	Sgsh_1482	GGAAAGGACGAAACACCGCGTTACGGAAGATAAGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTTACGGAAGATAAGGCTG	
1483	Sgsh	Sgsh_1483	GGAAAGGACGAAACACCGTGTACCGGGCCAGTACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACCGGGCCAGTACAGGT	
1484	Sgsh	Sgsh_1484	GGAAAGGACGAAACACCGTCCTGAGGGTCGTAGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGAGGGTCGTAGATCTG	
1485	Asns	Asns_1485	GGAAAGGACGAAACACCGGCATGCCATCTATGACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATGCCATCTATGACAGCG	
1486	Asns	Asns_1486	GGAAAGGACGAAACACCGGAATGCAGCCGATAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATGCAGCCGATAAGAGTG	
1487	Asns	Asns_1487	GGAAAGGACGAAACACCGGCTGTGTGTTCAGAAGCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGTGTTCAGAAGCTAA	
1488	Asns	Asns_1488	GGAAAGGACGAAACACCGATTTGAATATCAGACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTGAATATCAGACCAATG	
1489	Sec23b	Sec23b_1489	GGAAAGGACGAAACACCGGCAACACCAGTGGACCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACACCAGTGGACCGCAG	
1490	Sec23b	Sec23b_1490	GGAAAGGACGAAACACCGAATGGCGTTTGGTGCTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGGCGTTTGGTGCTACGT	
1491	Sec23b	Sec23b_1491	GGAAAGGACGAAACACCGAAAAGTGATGAGACCAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGTGATGAGACCAACCA	
1492	Sec23b	Sec23b_1492	GGAAAGGACGAAACACCGGTGTTGGTGGCACAAGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTTGGTGGCACAAGTCAG	
1493	Dguok	Dguok_1493	GGAAAGGACGAAACACCGAGAAAGGGTCTGGAATGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAGGGTCTGGAATGTGT	
1494	Dguok	Dguok_1494	GGAAAGGACGAAACACCGTTTCATGAGTAACTTCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCATGAGTAACTTCACAA	
1495	Dguok	Dguok_1495	GGAAAGGACGAAACACCGCGTGGACGCGCCACACGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGACGCGCCACACGCCA	
1496	Dguok	Dguok_1496	GGAAAGGACGAAACACCGTCCTGCAGGAGTTCGCAAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGCAGGAGTTCGCAAAC	
1497	Slc25a10	Slc25a10_1497	GGAAAGGACGAAACACCGCATGCGGGACTACATGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCGGGACTACATGACCA	
1498	Slc25a10	Slc25a10_1498	GGAAAGGACGAAACACCGTACACGGTACAGACCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACGGTACAGACCATCCA	
1499	Slc25a10	Slc25a10_1499	GGAAAGGACGAAACACCGGTCAGAGAGTAGGTCATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAGAGAGTAGGTCATCTG	
1500	Slc25a10	Slc25a10_1500	GGAAAGGACGAAACACCGGACATTGACCAAATCTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATTGACCAAATCTGCTG	
1501	Yme1l1	Yme1l1_1501	GGAAAGGACGAAACACCGCAGGACGTATTAAGGCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGACGTATTAAGGCACTA	
1502	Yme1l1	Yme1l1_1502	GGAAAGGACGAAACACCGTTAACTATTACCTCACTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAACTATTACCTCACTACT	
1503	Yme1l1	Yme1l1_1503	GGAAAGGACGAAACACCGTCATCGATGAATATAACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATCGATGAATATAACACA	
1504	Yme1l1	Yme1l1_1504	GGAAAGGACGAAACACCGCTTGGAGGTAAACTTCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGAGGTAAACTTCCCAA	
1505	Pign	Pign_1505	GGAAAGGACGAAACACCGCCAGCTCCCCAAGTAACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCTCCCCAAGTAACGAA	
1506	Pign	Pign_1506	GGAAAGGACGAAACACCGGTGTTGTTAAGATAACCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTTGTTAAGATAACCCAC	
1507	Pign	Pign_1507	GGAAAGGACGAAACACCGTGCCACAAAACTGGATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCACAAAACTGGATACGT	
1508	Pign	Pign_1508	GGAAAGGACGAAACACCGAAGTCAATAGTGATTCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCAATAGTGATTCAACC	
1509	Pdhx	Pdhx_1509	GGAAAGGACGAAACACCGCTTTAGTGAAGATCCCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTAGTGAAGATCCCGCGA	
1510	Pdhx	Pdhx_1510	GGAAAGGACGAAACACCGGTTAGACGAGATCTGGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTAGACGAGATCTGGTCAA	
1511	Pdhx	Pdhx_1511	GGAAAGGACGAAACACCGTGTCTCCTACGATGGAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCTCCTACGATGGAGCAA	
1512	Pdhx	Pdhx_1512	GGAAAGGACGAAACACCGTCCTGGGCAACCGAATGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGGGCAACCGAATGCAG	
1513	Abcg5	Abcg5_1513	GGAAAGGACGAAACACCGGCTGATAGAGCAGCCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATAGAGCAGCCCCACG	
1514	Abcg5	Abcg5_1514	GGAAAGGACGAAACACCGAGCTTGCCGAACATCCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTTGCCGAACATCCCAGG	
1515	Abcg5	Abcg5_1515	GGAAAGGACGAAACACCGCAATCATTTGGTCCGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATCATTTGGTCCGCCACG	
1516	Abcg5	Abcg5_1516	GGAAAGGACGAAACACCGGGATTGGAATGTTCAGGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATTGGAATGTTCAGGACA	
1517	Abcb11	Abcb11_1517	GGAAAGGACGAAACACCGTACGCACCATGCCTTCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGCACCATGCCTTCGCAG	
1518	Abcb11	Abcb11_1518	GGAAAGGACGAAACACCGATGAAGGCGAGTACACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAAGGCGAGTACACACCA	
1519	Abcb11	Abcb11_1519	GGAAAGGACGAAACACCGCCACTGTTCGAATAGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTGTTCGAATAGATGAG	
1520	Abcb11	Abcb11_1520	GGAAAGGACGAAACACCGAAGGTTGTGGGTAATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGTTGTGGGTAATCACTG	
1521	Naglu	Naglu_1521	GGAAAGGACGAAACACCGTGCACACATTCTGGTAATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCACACATTCTGGTAATAG	
1522	Naglu	Naglu_1522	GGAAAGGACGAAACACCGGAGATCGATACGTACTTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATCGATACGTACTTCAC	
1523	Naglu	Naglu_1523	GGAAAGGACGAAACACCGAGGAAGAGGTTCCCGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAAGAGGTTCCCGATGAG	
1524	Naglu	Naglu_1524	GGAAAGGACGAAACACCGGCCCTCGAGGATGTGAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTCGAGGATGTGAACCG	
1525	Abcc6	Abcc6_1525	GGAAAGGACGAAACACCGGTGACCGCAACTCCTCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCGCAACTCCTCGGCG	
1526	Abcc6	Abcc6_1526	GGAAAGGACGAAACACCGCCTCTGTGGAGGATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTGTGGAGGATCCACCA	
1527	Abcc6	Abcc6_1527	GGAAAGGACGAAACACCGAACAGGGTGTAGGTACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGGGTGTAGGTACAGAG	
1528	Abcc6	Abcc6_1528	GGAAAGGACGAAACACCGTGCACTGCATCGTTCAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCACTGCATCGTTCAGGTG	
1529	Tango2	Tango2_1529	GGAAAGGACGAAACACCGGTTTGCTACTATGGAAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTGCTACTATGGAAACCG	
1530	Tango2	Tango2_1530	GGAAAGGACGAAACACCGGGCTGGGCATCAGCACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTGGGCATCAGCACACGT	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
1531	Tango2	Tango2_1531	GGAAAGGACGAAACACCGCCTGAAGAAGGTCTCTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGAAGAAGGTCTCTACAG	
1532	Tango2	Tango2_1532	GGAAAGGACGAAACACCGTAGATGCCTTACCTCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATGCCTTACCTCTACCA	
1533	Vkorc1	Vkorc1_1533	GGAAAGGACGAAACACCGGTACGCACTGCACGTGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACGCACTGCACGTGAAGG	
1534	Vkorc1	Vkorc1_1534	GGAAAGGACGAAACACCGGTGAGAGGGCTAAGCCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAGAGGGCTAAGCCAGCG	
1535	Vkorc1	Vkorc1_1535	GGAAAGGACGAAACACCGGGTGGAGCACATGCTAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGAGCACATGCTAGGAG	
1536	Vkorc1	Vkorc1_1536	GGAAAGGACGAAACACCGCCATGTCTGCACGCACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATGTCTGCACGCACCGAG	
1537	Gfm1	Gfm1_1537	GGAAAGGACGAAACACCGGAACGGGTGCTATACTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACGGGTGCTATACTACAC	
1538	Gfm1	Gfm1_1538	GGAAAGGACGAAACACCGGAAGCACCATCTACAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCACCATCTACAACACG	
1539	Gfm1	Gfm1_1539	GGAAAGGACGAAACACCGAGCAATGAGGCCTTCTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAATGAGGCCTTCTAACA	
1540	Gfm1	Gfm1_1540	GGAAAGGACGAAACACCGTTACTCTGTAGCGAGCAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACTCTGTAGCGAGCAATC	
1541	Tpk1	Tpk1_1541	GGAAAGGACGAAACACCGCTTGCCTGAATTCGTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCCTGAATTCGTCAGTG	
1542	Tpk1	Tpk1_1542	GGAAAGGACGAAACACCGGAACTTGAAATACTGCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTTGAAATACTGCCTTG	
1543	Tpk1	Tpk1_1543	GGAAAGGACGAAACACCGGACACTTGGTAAAGTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACTTGGTAAAGTCAGTG	
1544	Tpk1	Tpk1_1544	GGAAAGGACGAAACACCGCACTTATATGATCTCACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTATATGATCTCACTGA	
1545	Dnajc12	Dnajc12_1545	GGAAAGGACGAAACACCGGAGCCCGCTATGACCATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCCCGCTATGACCATTGG	
1546	Dnajc12	Dnajc12_1546	GGAAAGGACGAAACACCGGAGCTCATCGCATCCCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTCATCGCATCCCAGCA	
1547	Dnajc12	Dnajc12_1547	GGAAAGGACGAAACACCGTGTCAATGCCGTTCGAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCAATGCCGTTCGAGCAG	
1548	Dnajc12	Dnajc12_1548	GGAAAGGACGAAACACCGAATTTCTGAAAAGTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTTCTGAAAAGTCTCCAC	
1549	Angptl3	Angptl3_1549	GGAAAGGACGAAACACCGTGCTCTGCCGTTTATAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCTGCCGTTTATAACAG	
1550	Angptl3	Angptl3_1550	GGAAAGGACGAAACACCGTACACTACAAGTTAAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACTACAAGTTAAAAACG	
1551	Angptl3	Angptl3_1551	GGAAAGGACGAAACACCGCATGGACATTAATTCAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGACATTAATTCAACAC	
1552	Angptl3	Angptl3_1552	GGAAAGGACGAAACACCGGAAGACAGCCCTTCAACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGACAGCCCTTCAACACA	
1553	Aass	Aass_1553	GGAAAGGACGAAACACCGGAAACTTCTCTTAATTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACTTCTCTTAATTCGTG	
1554	Aass	Aass_1554	GGAAAGGACGAAACACCGGCAAATTATTCACGACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAATTATTCACGACAGGT	
1555	Aass	Aass_1555	GGAAAGGACGAAACACCGTAGGCAGTGATTACGTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCAGTGATTACGTCCAA	
1556	Aass	Aass_1556	GGAAAGGACGAAACACCGGGATAGTGGCTTTCGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATAGTGGCTTTCGGACAG	
1557	Slc7a9	Slc7a9_1557	GGAAAGGACGAAACACCGGAGCACTTACCAACCATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCACTTACCAACCATCGT	
1558	Slc7a9	Slc7a9_1558	GGAAAGGACGAAACACCGCAAAGGCCTCCATCAGATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGGCCTCCATCAGATAG	
1559	Slc7a9	Slc7a9_1559	GGAAAGGACGAAACACCGGGACTGCAAGAGCTCCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTGCAAGAGCTCCGTTG	
1560	Slc7a9	Slc7a9_1560	GGAAAGGACGAAACACCGGCTGGCCAACACAGAATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGCCAACACAGAATCCG	
1561	Hacd1	Hacd1_1561	GGAAAGGACGAAACACCGGCAACTCACCGATCAGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACTCACCGATCAGACAA	
1562	Hacd1	Hacd1_1562	GGAAAGGACGAAACACCGCTGGCCCATTTAATGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGCCCATTTAATGAAGTG	
1563	Hacd1	Hacd1_1563	GGAAAGGACGAAACACCGGATCCAGAATGAAGAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCAGAATGAAGAGAGCG	
1564	Hacd1	Hacd1_1564	GGAAAGGACGAAACACCGCTTCTACAATATCGCCATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCTACAATATCGCCATGA	
1565	Ttpa	Ttpa_1565	GGAAAGGACGAAACACCGGAGGTGGAAACTCAACGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTGGAAACTCAACGCAA	
1566	Ttpa	Ttpa_1566	GGAAAGGACGAAACACCGCAGATCCAGATCGAAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATCCAGATCGAAATCCC	
1567	Ttpa	Ttpa_1567	GGAAAGGACGAAACACCGGAAGTCCAAGGATACTTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTCCAAGGATACTTCTA	
1568	Ttpa	Ttpa_1568	GGAAAGGACGAAACACCGTTTATTTGTTGTAGCATACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTATTTGTTGTAGCATACT	
1569	Mrps7	Mrps7_1569	GGAAAGGACGAAACACCGGGAATATTACCGCAAGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAATATTACCGCAAGCCGG	
1570	Mrps7	Mrps7_1570	GGAAAGGACGAAACACCGGGCCGCGACTGAAACCAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCGCGACTGAAACCAGCT	
1571	Mrps7	Mrps7_1571	GGAAAGGACGAAACACCGCCCCTACAGGATCTTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCTACAGGATCTTCCACG	
1572	Mrps7	Mrps7_1572	GGAAAGGACGAAACACCGGAGGCAACAAAGTTCTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCAACAAAGTTCTGGCC	
1573	Tfr2	Tfr2_1573	GGAAAGGACGAAACACCGGAGGTCGCTCCAGTACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTCGCTCCAGTACAACG	
1574	Tfr2	Tfr2_1574	GGAAAGGACGAAACACCGAGTGCGTGTCAGTCCACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGCGTGTCAGTCCACACG	
1575	Tfr2	Tfr2_1575	GGAAAGGACGAAACACCGTGGTGTACGCCCACTACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGTACGCCCACTACGGG	
1576	Tfr2	Tfr2_1576	GGAAAGGACGAAACACCGACCCCCAGTGAAGATTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCCCAGTGAAGATTAGCA	
1577	Pnpla6	Pnpla6_1577	GGAAAGGACGAAACACCGCTCCGTAGTGTCATCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGTAGTGTCATCCAACG	
1578	Pnpla6	Pnpla6_1578	GGAAAGGACGAAACACCGGCCATGTCAAAATCAGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCATGTCAAAATCAGAACG	
1579	Pnpla6	Pnpla6_1579	GGAAAGGACGAAACACCGAGGAGACTCCGACCCTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGACTCCGACCCTACAA	
1580	Pnpla6	Pnpla6_1580	GGAAAGGACGAAACACCGGGCCTGGCGCAGACAACGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTGGCGCAGACAACGGA	
1581	Atp8a2	Atp8a2_1581	GGAAAGGACGAAACACCGGCAAGCCCTCTTCATAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAGCCCTCTTCATAAACT	
1582	Atp8a2	Atp8a2_1582	GGAAAGGACGAAACACCGGGCCCTTATCCTATTGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCCTTATCCTATTGAAGG	
1583	Atp8a2	Atp8a2_1583	GGAAAGGACGAAACACCGACAACTTCGACTCTACTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAACTTCGACTCTACTGCA	
1584	Atp8a2	Atp8a2_1584	GGAAAGGACGAAACACCGCAGTGTTAAGAAATGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGTTAAGAAATGGCATG	
1585	Polg2	Polg2_1585	GGAAAGGACGAAACACCGGAAAGAACCTAGCCTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGAACCTAGCCTCACAG	
1586	Polg2	Polg2_1586	GGAAAGGACGAAACACCGTGTGGGAGTAAACCATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGGAGTAAACCATACCA	
1587	Polg2	Polg2_1587	GGAAAGGACGAAACACCGTGACGCCCCCGAGCATGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACGCCCCCGAGCATGCGG	
1588	Polg2	Polg2_1588	GGAAAGGACGAAACACCGGCAATTAACATAGTGCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAATTAACATAGTGCTCCA	
1589	Hs6st1	Hs6st1_1589	GGAAAGGACGAAACACCGGGCGCACGTTCTGCACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGCACGTTCTGCACTAGG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1590	Hs6st1	Hs6st1_1590	GGAAAGGACGAAACACCGATGGCGACATGTACAGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCGACATGTACAGCGTG	
1591	Hs6st1	Hs6st1_1591	GGAAAGGACGAAACACCGCTCATCCTTTACCAGTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCATCCTTTACCAGTACGC	
1592	Hs6st1	Hs6st1_1592	GGAAAGGACGAAACACCGCCTATAACCTGGCTAACAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTATAACCTGGCTAACAAC	
1593	Acsl4	Acsl4_1593	GGAAAGGACGAAACACCGGTCCAGGGATACGTTCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCAGGGATACGTTCACAC	
1594	Acsl4	Acsl4_1594	GGAAAGGACGAAACACCGGCCCATATCCCTGACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCATATCCCTGACCAATG	
1595	Acsl4	Acsl4_1595	GGAAAGGACGAAACACCGCAATAGAGCAGAGTACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATAGAGCAGAGTACCCTG	
1596	Acsl4	Acsl4_1596	GGAAAGGACGAAACACCGGGAACAGCGGCCATAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACAGCGGCCATAAGTGT	
1597	Gne	Gne_1597	GGAAAGGACGAAACACCGACGTCCAACTCAAAGAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTCCAACTCAAAGAACGC	
1598	Gne	Gne_1598	GGAAAGGACGAAACACCGTTGCAGCTCAAAGATATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCAGCTCAAAGATATATG	
1599	Gne	Gne_1599	GGAAAGGACGAAACACCGGCTCCACACGATTGTTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCACACGATTGTTAGAG	
1600	Gne	Gne_1600	GGAAAGGACGAAACACCGCCTCTTGTTAAACGAGATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTTGTTAAACGAGATCA	
1601	Slc25a13	Slc25a13_1601	GGAAAGGACGAAACACCGGGGGCGACTCCCAGTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCGACTCCCAGTAACTG	
1602	Slc25a13	Slc25a13_1602	GGAAAGGACGAAACACCGCAGATTTATATGAGCCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATTTATATGAGCCGAGG	
1603	Slc25a13	Slc25a13_1603	GGAAAGGACGAAACACCGACAAGGCATCCGGAGCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAAGGCATCCGGAGCACAC	
1604	Slc25a13	Slc25a13_1604	GGAAAGGACGAAACACCGTACAAGATCGATAGGATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAAGATCGATAGGATACA	
1605	Galns	Galns_1605	GGAAAGGACGAAACACCGAGCAGTAGCACGATGTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGTAGCACGATGTTGGG	
1606	Galns	Galns_1606	GGAAAGGACGAAACACCGCCCAATTAACCGGAAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAATTAACCGGAAGACTG	
1607	Galns	Galns_1607	GGAAAGGACGAAACACCGGGCGTAAACTGGTGCATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGTAAACTGGTGCATGAG	
1608	Galns	Galns_1608	GGAAAGGACGAAACACCGGAGAGACCCCAAATTTAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAGACCCCAAATTTAGAC	
1609	Nus1	Nus1_1609	GGAAAGGACGAAACACCGGTGGTCGTAGACGCTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTCGTAGACGCTAATGT	
1610	Nus1	Nus1_1610	GGAAAGGACGAAACACCGTCCAGGTGCCGAAGCGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGGTGCCGAAGCGAACG	
1611	Nus1	Nus1_1611	GGAAAGGACGAAACACCGACAGCACCTTCACTGCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCACCTTCACTGCCGAA	
1612	Nus1	Nus1_1612	GGAAAGGACGAAACACCGCCAGCGCAGCCGAGGATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGCAGCCGAGGATGGG	
1613	Coq5	Coq5_1613	GGAAAGGACGAAACACCGCTTCGGGTTTGAGACCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCGGGTTTGAGACCGTGT	
1614	Coq5	Coq5_1614	GGAAAGGACGAAACACCGGTTGTGCCTGAACGTAACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGTGCCTGAACGTAACTA	
1615	Coq5	Coq5_1615	GGAAAGGACGAAACACCGATGAATGACATGATGAGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAATGACATGATGAGTCT	
1616	Coq5	Coq5_1616	GGAAAGGACGAAACACCGGCCAGGATCTATGACACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAGGATCTATGACACCCG	
1617	Hgsnat	Hgsnat_1617	GGAAAGGACGAAACACCGCCTGCAGGTTAACTCCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCAGGTTAACTCCACCT	
1618	Hgsnat	Hgsnat_1618	GGAAAGGACGAAACACCGATGACTTCTATCCTGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGACTTCTATCCTGCAACG	
1619	Hgsnat	Hgsnat_1619	GGAAAGGACGAAACACCGGATGTGTGGACACATTTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTGTGGACACATTTAGG	
1620	Hgsnat	Hgsnat_1620	GGAAAGGACGAAACACCGGTTGGGAGTGACATACTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGGAGTGACATACTTCG	
1621	Slc46a1	Slc46a1_1621	GGAAAGGACGAAACACCGAGAGCTAACATCTGCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTAACATCTGCCACAG	
1622	Slc46a1	Slc46a1_1622	GGAAAGGACGAAACACCGGGGCAATGGATCGATGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCAATGGATCGATGATGG	
1623	Slc46a1	Slc46a1_1623	GGAAAGGACGAAACACCGTGGACCAGAAGAGTCCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGACCAGAAGAGTCCCACC	
1624	Slc46a1	Slc46a1_1624	GGAAAGGACGAAACACCGGAACTGTGGGAACCAAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTGTGGGAACCAAAGCG	
1625	Coa3	Coa3_1625	GGAAAGGACGAAACACCGGATACAAATAGCTAACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATACAAATAGCTAACACCA	
1626	Coa3	Coa3_1626	GGAAAGGACGAAACACCGCTCAGCGCATCGACCCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGCGCATCGACCCGTCG	
1627	Coa3	Coa3_1627	GGAAAGGACGAAACACCGGGGTCGATGCGCTGAGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCGATGCGCTGAGCGAA	
1628	Coa3	Coa3_1628	GGAAAGGACGAAACACCGCATAAACTGCAACTGCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAAACTGCAACTGCGCTG	
1629	Trmt10c	Trmt10c_1629	GGAAAGGACGAAACACCGCTTACGGTATCTGTATGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACGGTATCTGTATGGGA	
1630	Trmt10c	Trmt10c_1630	GGAAAGGACGAAACACCGTTATTATGACAAGACAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATTATGACAAGACAAAGA	
1631	Trmt10c	Trmt10c_1631	GGAAAGGACGAAACACCGTTAGTTCTCTGGTTGAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGTTCTCTGGTTGAGGCG	
1632	Trmt10c	Trmt10c_1632	GGAAAGGACGAAACACCGTAGGCCATGTCAAAAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCCATGTCAAAAACCAA	
1633	Slc52a2	Slc52a2_1633	GGAAAGGACGAAACACCGTGTTGTGGGTTCAGATGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTGGGTTCAGATGTCG	
1634	Slc52a2	Slc52a2_1634	GGAAAGGACGAAACACCGATGGGAGACACCTCGATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGAGACACCTCGATCGG	
1635	Slc52a2	Slc52a2_1635	GGAAAGGACGAAACACCGGGCCTCTCTGTGGAACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTCTCTGTGGAACCACG	
1636	Slc52a2	Slc52a2_1636	GGAAAGGACGAAACACCGAAGACCGTAAAAAGGGGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACCGTAAAAAGGGGGGT	
1637	Sco1	Sco1_1637	GGAAAGGACGAAACACCGAAATCAATACCCATTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCAATACCCATTGACCC	
1638	Sco1	Sco1_1638	GGAAAGGACGAAACACCGAAAAATGATTGAAGTCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAATGATTGAAGTCGTGG	
1639	Sco1	Sco1_1639	GGAAAGGACGAAACACCGTTGGGAAGCCTTTACTAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGGAAGCCTTTACTAGGG	
1640	Sco1	Sco1_1640	GGAAAGGACGAAACACCGCACTCACCCCAGGCTTCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTCACCCCAGGCTTCGGG	
1641	Pla2g6	Pla2g6_1641	GGAAAGGACGAAACACCGAAATCCATGGCCTATATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCCATGGCCTATATGCG	
1642	Pla2g6	Pla2g6_1642	GGAAAGGACGAAACACCGGGCACCTGCATTAGCCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCACCTGCATTAGCCCCGT	
1643	Pla2g6	Pla2g6_1643	GGAAAGGACGAAACACCGAGTCTCCCCAAAGTCGTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTCCCCAAAGTCGTTTG	
1644	Pla2g6	Pla2g6_1644	GGAAAGGACGAAACACCGCCATTGGGCCAAGAACGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATTGGGCCAAGAACGCCG	
1645	Chst3	Chst3_1645	GGAAAGGACGAAACACCGCCACGAACGAGGAACCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGAACGAGGAACCCGTG	
1646	Chst3	Chst3_1646	GGAAAGGACGAAACACCGAACCTCGGGTCCTCAACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTCGGGTCCTCAACTAG	
1647	Chst3	Chst3_1647	GGAAAGGACGAAACACCGACTCAGTTCCTGTTCCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCAGTTCCTGTTCCGCCG	
1648	Chst3	Chst3_1648	GGAAAGGACGAAACACCGAAACTATGACCACAAATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTATGACCACAAATGCC	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1649	Fut8	Fut8_1649	GGAAAGGACGAAACACCGTGAAACAGTAGACCACGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAACAGTAGACCACGTGA	
1650	Fut8	Fut8_1650	GGAAAGGACGAAACACCGAAATGACAAAAACATTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGACAAAAACATTCAAG	
1651	Fut8	Fut8_1651	GGAAAGGACGAAACACCGCCAGAAGGCCCCATTGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGAAGGCCCCATTGACCA	
1652	Fut8	Fut8_1652	GGAAAGGACGAAACACCGAATCAAGTATTTGACAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCAAGTATTTGACAAACT	
1653	Gria3	Gria3_1653	GGAAAGGACGAAACACCGTGTGACGAAAGATGTATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGACGAAAGATGTATGCA	
1654	Gria3	Gria3_1654	GGAAAGGACGAAACACCGGTACAATGTCAGTAAAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACAATGTCAGTAAAACCC	
1655	Gria3	Gria3_1655	GGAAAGGACGAAACACCGTACCTCTATGACACAGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTCTATGACACAGAACG	
1656	Gria3	Gria3_1656	GGAAAGGACGAAACACCGAGGAATCCAAGTGGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAATCCAAGTGGTCTACG	
1657	Porcn	Porcn_1657	GGAAAGGACGAAACACCGACAACTTCCACCATGGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAACTTCCACCATGGACCG	
1658	Porcn	Porcn_1658	GGAAAGGACGAAACACCGGTGACATGGCACAAGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACATGGCACAAGATGCG	
1659	Porcn	Porcn_1659	GGAAAGGACGAAACACCGCCACCTTCTTCAGCCATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCTTCTTCAGCCATCGG	
1660	Porcn	Porcn_1660	GGAAAGGACGAAACACCGGAAGGAGACAGCACTCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGAGACAGCACTCTCGT	
1661	Clpp	Clpp_1661	GGAAAGGACGAAACACCGGCGCTTATGACATATACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCTTATGACATATACTCG	
1662	Clpp	Clpp_1662	GGAAAGGACGAAACACCGCCTGCAGATTGACGACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCAGATTGACGACAGTG	
1663	Clpp	Clpp_1663	GGAAAGGACGAAACACCGCATATGTATATCAACAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATATGTATATCAACAGCCC	
1664	Clpp	Clpp_1664	GGAAAGGACGAAACACCGCAACACACCACGTGCAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACACACCACGTGCAGATG	
1665	Slc40a1	Slc40a1_1665	GGAAAGGACGAAACACCGCAGGGTACGCCTACACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGTACGCCTACACTCAG	
1666	Slc40a1	Slc40a1_1666	GGAAAGGACGAAACACCGCCTTTGGATTGTGATCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTTGGATTGTGATCGCAG	
1667	Slc40a1	Slc40a1_1667	GGAAAGGACGAAACACCGTCATCAGGATGATTCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATCAGGATGATTCCGCAG	
1668	Slc40a1	Slc40a1_1668	GGAAAGGACGAAACACCGCCCATCCATCTCGGAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCATCCATCTCGGAAAGTG	
1669	Pmm2	Pmm2_1669	GGAAAGGACGAAACACCGATTCAATGAAAGTTCCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCAATGAAAGTTCCCCTG	
1670	Pmm2	Pmm2_1670	GGAAAGGACGAAACACCGAAGACCAAAATTGGAGTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACCAAAATTGGAGTGGT	
1671	Pmm2	Pmm2_1671	GGAAAGGACGAAACACCGGCTTGGTAGCGTACAAAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTGGTAGCGTACAAAGAT	
1672	Pmm2	Pmm2_1672	GGAAAGGACGAAACACCGAAAAGTTCGTAGCAGACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGTTCGTAGCAGACCTG	
1673	Sult2b1	Sult2b1_1673	GGAAAGGACGAAACACCGGGGAGACCACGACATCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAGACCACGACATCGCGG	
1674	Sult2b1	Sult2b1_1674	GGAAAGGACGAAACACCGGGGCTCCGATCGGATCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTCCGATCGGATCCACG	
1675	Sult2b1	Sult2b1_1675	GGAAAGGACGAAACACCGAATGTTTCCGAAATGAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTTTCCGAAATGAGGTG	
1676	Sult2b1	Sult2b1_1676	GGAAAGGACGAAACACCGAGGTGAGAGCTCATAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGAGAGCTCATAATGCG	
1677	Cd320	Cd320_1677	GGAAAGGACGAAACACCGTGGTCTCAGAACAGGCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTCTCAGAACAGGCCTAG	
1678	Cd320	Cd320_1678	GGAAAGGACGAAACACCGGCAACCACTGATGTTGTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACCACTGATGTTGTCAC	
1679	Cd320	Cd320_1679	GGAAAGGACGAAACACCGCCATCACAGCGCCACGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCACAGCGCCACGTGTG	
1680	Cd320	Cd320_1680	GGAAAGGACGAAACACCGACCTTCCAGTGTCTTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTCCAGTGTCTTACCAG	
1681	Elovl1	Elovl1_1681	GGAAAGGACGAAACACCGGGCTATTGGAAAAGTCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTATTGGAAAAGTCTATG	
1682	Elovl1	Elovl1_1682	GGAAAGGACGAAACACCGGGGCAGACAATCCATAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCAGACAATCCATAGTAG	
1683	Elovl1	Elovl1_1683	GGAAAGGACGAAACACCGTCCAAAGCTACCCTCTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAAAGCTACCCTCTGATG	
1684	Elovl1	Elovl1_1684	GGAAAGGACGAAACACCGCGATAGGATGAAGTACACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATAGGATGAAGTACACAT	
1685	Ndufa1	Ndufa1_1685	GGAAAGGACGAAACACCGCATCCACAAATTCACCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCCACAAATTCACCAACG	
1686	Ndufa1	Ndufa1_1686	GGAAAGGACGAAACACCGTGTACGCAGTGGACACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACGCAGTGGACACCCCG	
1687	Ndufa1	Ndufa1_1687	GGAAAGGACGAAACACCGGAATTTGTGGATGTACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATTTGTGGATGTACGCAG	
1688	Ndufa1	Ndufa1_1688	GGAAAGGACGAAACACCGCGCGTTCCATCAGATACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCGTTCCATCAGATACCAC	
1689	Atp6ap1	Atp6ap1_1689	GGAAAGGACGAAACACCGGAGGATTTCACAGCATACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGATTTCACAGCATACGG	
1690	Atp6ap1	Atp6ap1_1690	GGAAAGGACGAAACACCGGATATGACCCTCATGTGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATATGACCCTCATGTGTGT	
1691	Atp6ap1	Atp6ap1_1691	GGAAAGGACGAAACACCGTAGCTAGATCCACATGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCTAGATCCACATGCAAG	
1692	Atp6ap1	Atp6ap1_1692	GGAAAGGACGAAACACCGGTGTCATTGTAACTCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTCATTGTAACTCACAGG	
1693	Extl3	Extl3_1693	GGAAAGGACGAAACACCGGCCCAAGCCTCGCGTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCAAGCCTCGCGTCACAG	
1694	Extl3	Extl3_1694	GGAAAGGACGAAACACCGTCAGACATAGCATGGACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGACATAGCATGGACAAG	
1695	Extl3	Extl3_1695	GGAAAGGACGAAACACCGCCACACAGTGCCCACTCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACACAGTGCCCACTCAGT	
1696	Extl3	Extl3_1696	GGAAAGGACGAAACACCGATTGCGGAGGTATTTAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGCGGAGGTATTTAGGTG	
1697	Wdr45	Wdr45_1697	GGAAAGGACGAAACACCGGACACTCGGGACAACCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACTCGGGACAACCCCAA	
1698	Wdr45	Wdr45_1698	GGAAAGGACGAAACACCGAGGCGTCCGGATCTACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCGTCCGGATCTACAATG	
1699	Wdr45	Wdr45_1699	GGAAAGGACGAAACACCGAAGCTGGTAGAGCTTCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCTGGTAGAGCTTCGAAG	
1700	Wdr45	Wdr45_1700	GGAAAGGACGAAACACCGGTGTGGAAGTCTGCAACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTGGAAGTCTGCAACTTG	
1701	Atp8b1	Atp8b1_1701	GGAAAGGACGAAACACCGAATGCCACACCGTCCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGCCACACCGTCCTACCG	
1702	Atp8b1	Atp8b1_1702	GGAAAGGACGAAACACCGAGCGTTGGATAAAGTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGTTGGATAAAGTGTACG	
1703	Atp8b1	Atp8b1_1703	GGAAAGGACGAAACACCGGCTGATAAAATCCTGTTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATAAAATCCTGTTACG	
1704	Atp8b1	Atp8b1_1704	GGAAAGGACGAAACACCGGATTTGCCATACGGTCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTTGCCATACGGTCATGG	
1705	Mpc1	Mpc1_1705	GGAAAGGACGAAACACCGACTTCCGGGACTATCTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCCGGGACTATCTCATG	
1706	Mpc1	Mpc1_1706	GGAAAGGACGAAACACCGGGCGGACTATGTCCGGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGGACTATGTCCGGAGCA	
1707	Mpc1	Mpc1_1707	GGAAAGGACGAAACACCGAAATCTCCAGAGATTATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCTCCAGAGATTATCAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1708	Mpc1	Mpc1_1708	GGAAAGGACGAAACACCGTGGGGCCCAGTTGCCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGGCCCAGTTGCCAACTG	
1709	Slc1a4	Slc1a4_1709	GGAAAGGACGAAACACCGGTCTGCAACCGATTACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTGCAACCGATTACACAG	
1710	Slc1a4	Slc1a4_1710	GGAAAGGACGAAACACCGTAGAGCCACTCCTAACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAGCCACTCCTAACACCA	
1711	Slc1a4	Slc1a4_1711	GGAAAGGACGAAACACCGGATGCCACCCAGACGCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCCACCCAGACGCCCGA	
1712	Slc1a4	Slc1a4_1712	GGAAAGGACGAAACACCGACCCACCAACACTCCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCACCAACACTCCCGACA	
1713	Pgam2	Pgam2_1713	GGAAAGGACGAAACACCGGGATGTTACGGACCAAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATGTTACGGACCAAATGT	
1714	Pgam2	Pgam2_1714	GGAAAGGACGAAACACCGAACCAAGAGAACCGTTTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCAAGAGAACCGTTTCTG	
1715	Pgam2	Pgam2_1715	GGAAAGGACGAAACACCGGCTTCAAGCCTGCATAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCAAGCCTGCATAGCGG	
1716	Pgam2	Pgam2_1716	GGAAAGGACGAAACACCGGTTTGACATCTGCTACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTGACATCTGCTACACGT	
1717	Samhd1	Samhd1_1717	GGAAAGGACGAAACACCGATCCTTACATTATGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTTACATTATGTCGATG	
1718	Samhd1	Samhd1_1718	GGAAAGGACGAAACACCGGCTTGATATAGCGAAGTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTGATATAGCGAAGTCGC	
1719	Samhd1	Samhd1_1719	GGAAAGGACGAAACACCGCTTGGGCTGCCATCGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGGCTGCCATCGCAGCG	
1720	Samhd1	Samhd1_1720	GGAAAGGACGAAACACCGTTAGGATCTTACCTAGGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGGATCTTACCTAGGTCG	
1721	Pdss1	Pdss1_1721	GGAAAGGACGAAACACCGAGCCTTTAGACCGATTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCTTTAGACCGATTATTG	
1722	Pdss1	Pdss1_1722	GGAAAGGACGAAACACCGGAGGCGGCACGTGTTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCGGCACGTGTTCCGAG	
1723	Pdss1	Pdss1_1723	GGAAAGGACGAAACACCGTATACTATGCATAGTTGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATACTATGCATAGTTGGGG	
1724	Pdss1	Pdss1_1724	GGAAAGGACGAAACACCGGTTATTGAAGATTTGGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTATTGAAGATTTGGTGCG	
1725	Dgke	Dgke_1725	GGAAAGGACGAAACACCGTCTCGTAGTGGAACTAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCGTAGTGGAACTAACAT	
1726	Dgke	Dgke_1726	GGAAAGGACGAAACACCGGATCATGCTCAAGAACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCATGCTCAAGAACGACA	
1727	Dgke	Dgke_1727	GGAAAGGACGAAACACCGGTCCACGACGAGTGCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCACGACGAGTGCATGCG	
1728	Dgke	Dgke_1728	GGAAAGGACGAAACACCGACAAGAAAAATACATTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAAGAAAAATACATTCCAG	
1729	Pigp	Pigp_1729	GGAAAGGACGAAACACCGTCTCTTGTGCAGATACTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTTGTGCAGATACTGGG	
1730	Pigp	Pigp_1730	GGAAAGGACGAAACACCGTGCAGTACTTTATCTTGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTACTTTATCTTGTGT	
1731	Pigp	Pigp_1731	GGAAAGGACGAAACACCGAAGGAGTTTAACCAAGATTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGAGTTTAACCAAGATTC	
1732	Pigp	Pigp_1732	GGAAAGGACGAAACACCGATGAATGGAGTCAAGTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAATGGAGTCAAGTGGAG	
1733	Prodh2	Prodh2_1733	GGAAAGGACGAAACACCGTAGTCCATGAGTGACCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTCCATGAGTGACCAAAG	
1734	Prodh2	Prodh2_1734	GGAAAGGACGAAACACCGCCTGTGCCACTCGGTGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTGCCACTCGGTGCAAG	
1735	Prodh2	Prodh2_1735	GGAAAGGACGAAACACCGGGACTTATCCCGAGCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTTATCCCGAGCCCTCG	
1736	Prodh2	Prodh2_1736	GGAAAGGACGAAACACCGGTTGGCAGTACCCACCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGCAGTACCCACCGAGG	
1737	Pex14	Pex14_1737	GGAAAGGACGAAACACCGCTTCACTGGGATCTGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCACTGGGATCTGCCAGG	
1738	Pex14	Pex14_1738	GGAAAGGACGAAACACCGATGCTCTCCTGGTCGCAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCTCTCCTGGTCGCAAGT	
1739	Pex14	Pex14_1739	GGAAAGGACGAAACACCGGGAACAGGTGACTTACTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACAGGTGACTTACTGTA	
1740	Pex14	Pex14_1740	GGAAAGGACGAAACACCGATACTTACCAGTGGCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACTTACCAGTGGCTCTCG	
1741	Mrpl12	Mrpl12_1741	GGAAAGGACGAAACACCGTCTTTGGGAGCATTATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTGGGAGCATTATCCAG	
1742	Mrpl12	Mrpl12_1742	GGAAAGGACGAAACACCGATACCTTCAGGAGTTCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCTTCAGGAGTTCGTTG	
1743	Mrpl12	Mrpl12_1743	GGAAAGGACGAAACACCGTGCCCAGCGTCTGTGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCCAGCGTCTGTGCAGCG	
1744	Mrpl12	Mrpl12_1744	GGAAAGGACGAAACACCGGCCCCCCGGAGTCCAAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCCCCGGAGTCCAAGCCG	
1745	Ggcx	Ggcx_1745	GGAAAGGACGAAACACCGTGTGTGTATAAGAGGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGTATAAGAGGTCCCG	
1746	Ggcx	Ggcx_1746	GGAAAGGACGAAACACCGGCCTGCACGATGTCCACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGCACGATGTCCACACG	
1747	Ggcx	Ggcx_1747	GGAAAGGACGAAACACCGAGAACTGTGTAGTTCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTGTGTAGTTCCAAAG	
1748	Ggcx	Ggcx_1748	GGAAAGGACGAAACACCGGCTCGCCCGTGAGGCCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCGCCCGTGAGGCCGTCG	
1749	Timm22	Timm22_1749	GGAAAGGACGAAACACCGGCTGGCATTGATACCAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGCATTGATACCAACGT	
1750	Timm22	Timm22_1750	GGAAAGGACGAAACACCGAGAAGAAGGCTGTACTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAGAAGGCTGTACTGCAA	
1751	Timm22	Timm22_1751	GGAAAGGACGAAACACCGTGGGCGACAAGCGTCAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGCGACAAGCGTCAGCCC	
1752	Timm22	Timm22_1752	GGAAAGGACGAAACACCGCCTCTAGGGTTTGTCTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTAGGGTTTGTCTTGGG	
1753	Ivd	Ivd_1753	GGAAAGGACGAAACACCGAATATCGAGTGGGCCCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATATCGAGTGGGCCCGCCG	
1754	Ivd	Ivd_1754	GGAAAGGACGAAACACCGCTCCTGGCTCAGGACGTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCTGGCTCAGGACGTTAG	
1755	Ivd	Ivd_1755	GGAAAGGACGAAACACCGGGTAATGGAAGAGATATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAATGGAAGAGATATCCC	
1756	Ivd	Ivd_1756	GGAAAGGACGAAACACCGTTCTTGGAGGTACTAAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTGGAGGTACTAAAACC	
1757	Pus1	Pus1_1757	GGAAAGGACGAAACACCGCCTGCAAAGAGGGTCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCAAAGAGGGTCAAGGG	
1758	Pus1	Pus1_1758	GGAAAGGACGAAACACCGCTTACCCAGAATCCGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACCCAGAATCCGAATGT	
1759	Pus1	Pus1_1759	GGAAAGGACGAAACACCGTACTCGGGCAAGGGCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTCGGGCAAGGGCTACCA	
1760	Pus1	Pus1_1760	GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGGCCCTCACGTACGAA	
1761	Adar	Adar_1761	GGAAAGGACGAAACACCGACTCCAACAAGCCGCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCCAACAAGCCGCCTACG	
1762	Adar	Adar_1762	GGAAAGGACGAAACACCGAGAGGTAACCCCAGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGTAACCCCAGTAACAG	
1763	Adar	Adar_1763	GGAAAGGACGAAACACCGTTCTTGTAGGGTGAACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTGTAGGGTGAACACCG	
1764	Adar	Adar_1764	GGAAAGGACGAAACACCGTGTATCCAGGAATTCCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTATCCAGGAATTCCCTAG	
1765	Suclg1	Suclg1_1765	GGAAAGGACGAAACACCGGAGTACGGCACCAAACTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTACGGCACCAAACTCGT	
1766	Suclg1	Suclg1_1766	GGAAAGGACGAAACACCGAACAGAATGGGATACGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGAATGGGATACGACAC	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
1767	Suclg1	Suclg1_1767	GGAAAGGACGAAACACCGTGACACGCCAGGGAACGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACACGCCAGGGAACGACG	
1768	Suclg1	Suclg1_1768	GGAAAGGACGAAACACCGCATTAATGAAGCAATCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTAATGAAGCAATCGACG	
1769	Aldh18a1	Aldh18a1_1769	GGAAAGGACGAAACACCGCAAGTCTAGAGTGGGCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTCTAGAGTGGGCCTAG	
1770	Aldh18a1	Aldh18a1_1770	GGAAAGGACGAAACACCGCGATGGGGACGATGTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATGGGGACGATGTTCATG	
1771	Aldh18a1	Aldh18a1_1771	GGAAAGGACGAAACACCGCGTCCGAGAGGACAATCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCCGAGAGGACAATCAAG	
1772	Aldh18a1	Aldh18a1_1772	GGAAAGGACGAAACACCGTGAGGGGTACCGTGATAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGGGTACCGTGATAAAG	
1773	Ctsf	Ctsf_1773	GGAAAGGACGAAACACCGACAATTACGGCCGTGCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAATTACGGCCGTGCTGCG	
1774	Ctsf	Ctsf_1774	GGAAAGGACGAAACACCGAAAGACAGTCAATCGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGACAGTCAATCGCCACT	
1775	Ctsf	Ctsf_1775	GGAAAGGACGAAACACCGACCAGGGGATCATTGCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGGGGATCATTGCAAGG	
1776	Ctsf	Ctsf_1776	GGAAAGGACGAAACACCGCCTGAATCCCCTCTTACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGAATCCCCTCTTACAGA	
1777	Tbk1	Tbk1_1777	GGAAAGGACGAAACACCGTGCCGTTTAGACCCTTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCGTTTAGACCCTTCGAG	
1778	Tbk1	Tbk1_1778	GGAAAGGACGAAACACCGCTTCTCGCTACAACACATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCTCGCTACAACACATGA	
1779	Tbk1	Tbk1_1779	GGAAAGGACGAAACACCGCAACATCATGCGCGTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACATCATGCGCGTCATAG	
1780	Tbk1	Tbk1_1780	GGAAAGGACGAAACACCGCGGGAACAACTCAATACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGGAACAACTCAATACCGT	
1781	Pex3	Pex3_1781	GGAAAGGACGAAACACCGAAACAAGCTGGAAATATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACAAGCTGGAAATATGGG	
1782	Pex3	Pex3_1782	GGAAAGGACGAAACACCGTCATTAAACAAGCTGTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATTAAACAAGCTGTACAA	
1783	Pex3	Pex3_1783	GGAAAGGACGAAACACCGCATGCTGCCGACACTGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCTGCCGACACTGAGAG	
1784	Pex3	Pex3_1784	GGAAAGGACGAAACACCGTACTGCTGCTGTACATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTGCTGCTGTACATCCGG	
1785	Txn2	Txn2_1785	GGAAAGGACGAAACACCGAGACCACCAGCATTGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCACCAGCATTGTACTG	
1786	Txn2	Txn2_1786	GGAAAGGACGAAACACCGAGGGAAGCCCACACACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGAAGCCCACACACCCTG	
1787	Txn2	Txn2_1787	GGAAAGGACGAAACACCGGCGGTCCTAGGATCTTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGTCCTAGGATCTTGCAG	
1788	Txn2	Txn2_1788	GGAAAGGACGAAACACCGAAAGGTCGTCAAACAGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGGTCGTCAAACAGACTC	
1789	Mlycd	Mlycd_1789	GGAAAGGACGAAACACCGGACTTCGTGAGCTTCTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTTCGTGAGCTTCTACGG	
1790	Mlycd	Mlycd_1790	GGAAAGGACGAAACACCGTGGAAGAGGCCGCGATACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGAGGCCGCGATACCG	
1791	Mlycd	Mlycd_1791	GGAAAGGACGAAACACCGCTCCGACTGAAACCGAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGACTGAAACCGAGGAG	
1792	Mlycd	Mlycd_1792	GGAAAGGACGAAACACCGCCGCACAGCCGACGTCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCACAGCCGACGTCCCCG	
1793	Tdo2	Tdo2_1793	GGAAAGGACGAAACACCGGATAGCTCGGATGCATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAGCTCGGATGCATCGTG	
1794	Tdo2	Tdo2_1794	GGAAAGGACGAAACACCGTGATGAATAGGTGCTCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGAATAGGTGCTCGTCA	
1795	Tdo2	Tdo2_1795	GGAAAGGACGAAACACCGAATCCATTTGGCTCTAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCCATTTGGCTCTAAACC	
1796	Tdo2	Tdo2_1796	GGAAAGGACGAAACACCGCACTATCGTGATAACTTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTATCGTGATAACTTTGG	
1797	Alg2	Alg2_1797	GGAAAGGACGAAACACCGCAGAAAGACCATGCGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAAAGACCATGCGCACGT	
1798	Alg2	Alg2_1798	GGAAAGGACGAAACACCGGCTCTCGGTGCAATGCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCTCGGTGCAATGCGCAG	
1799	Alg2	Alg2_1799	GGAAAGGACGAAACACCGTCTCTATCAACCGATACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTATCAACCGATACGAA	
1800	Alg2	Alg2_1800	GGAAAGGACGAAACACCGACTGGCCAGACGGCGTAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGGCCAGACGGCGTAAGA	
1801	Mocs1	Mocs1_1801	GGAAAGGACGAAACACCGCACTTGGATTCCGAACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTGGATTCCGAACACGG	
1802	Mocs1	Mocs1_1802	GGAAAGGACGAAACACCGTAGGTCTCGAGGGCTCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGTCTCGAGGGCTCCCCG	
1803	Mocs1	Mocs1_1803	GGAAAGGACGAAACACCGCGATGTCCACCACATCCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATGTCCACCACATCCGGT	
1804	Mocs1	Mocs1_1804	GGAAAGGACGAAACACCGAGGCCAGTATTGCATGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCAGTATTGCATGCCCG	
1805	Nfu1	Nfu1_1805	GGAAAGGACGAAACACCGACTGTACCTGTGTTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTACCTGTGTTACACAA	
1806	Nfu1	Nfu1_1806	GGAAAGGACGAAACACCGGAAACAGTACCTGGCCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACAGTACCTGGCCAGAG	
1807	Nfu1	Nfu1_1807	GGAAAGGACGAAACACCGGTGTAGTCCGGCTGTGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTAGTCCGGCTGTGCAGG	
1808	Nfu1	Nfu1_1808	GGAAAGGACGAAACACCGGCGCTACCTGCTTCTCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCTACCTGCTTCTCCCGG	
1809	Dhodh	Dhodh_1809	GGAAAGGACGAAACACCGTTGATCCAGAGTCGGCGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGATCCAGAGTCGGCGCAC	
1810	Dhodh	Dhodh_1810	GGAAAGGACGAAACACCGGTAGAAATGGTCGTCCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGAAATGGTCGTCCCCCG	
1811	Dhodh	Dhodh_1811	GGAAAGGACGAAACACCGATAAATTCCGAAATCCAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAATTCCGAAATCCAGTA	
1812	Dhodh	Dhodh_1812	GGAAAGGACGAAACACCGGGTATGGATTCAACAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTATGGATTCAACAGCCAC	
1813	Stap1	Stap1_1813	GGAAAGGACGAAACACCGGTTGGCCAGTAAGGCACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGCCAGTAAGGCACACG	
1814	Stap1	Stap1_1814	GGAAAGGACGAAACACCGGGAGCCAGTACAAGACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCCAGTACAAGACTATG	
1815	Stap1	Stap1_1815	GGAAAGGACGAAACACCGCTTCATTCTTACAGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCATTCTTACAGTAACAG	
1816	Stap1	Stap1_1816	GGAAAGGACGAAACACCGGGAGTACAAACACTATTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTACAAACACTATTGGA	
1817	Aldh1a3	Aldh1a3_1817	GGAAAGGACGAAACACCGCACCAGGCATGAGCCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCAGGCATGAGCCCATCG	
1818	Aldh1a3	Aldh1a3_1818	GGAAAGGACGAAACACCGTGCATCCAGCCGGCGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCATCCAGCCGGCGCCACG	
1819	Aldh1a3	Aldh1a3_1819	GGAAAGGACGAAACACCGCCACCCGGCAAAATATCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCCGGCAAAATATCTGA	
1820	Aldh1a3	Aldh1a3_1820	GGAAAGGACGAAACACCGAACACTAGAGAAAATATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACACTAGAGAAAATATGTG	
1821	Slc25a20	Slc25a20_1821	GGAAAGGACGAAACACCGATAGGGGTGACTCCAATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGGGGTGACTCCAATGAT	
1822	Slc25a20	Slc25a20_1822	GGAAAGGACGAAACACCGTCCAAGGTCCCAGAGTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAAGGTCCCAGAGTACAT	
1823	Slc25a20	Slc25a20_1823	GGAAAGGACGAAACACCGTCAGGGGAGAACAAGTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGGGAGAACAAGTACAG	
1824	Slc25a20	Slc25a20_1824	GGAAAGGACGAAACACCGTCCCAGCTGTAAACAGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCAGCTGTAAACAGCTGT	
1825	Srd5a3	Srd5a3_1825	GGAAAGGACGAAACACCGACTGCTTGGTCTTCCCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCTTGGTCTTCCCGTAG	

No.	*Oligo name	*Oligo name	*Sequence(5' to3')	nt#	Remarks	5'	guide sequence	3'
1826	Srd5a3	Srd5a3_1826	GGAAAGGACGAAACACCGAGCACTCAAAGAGTCTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACTCAAAGAGTCTCCGA	
1827	Srd5a3	Srd5a3_1827	GGAAAGGACGAAACACCGATCTACTGATACAAGCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTACTGATACAAGCCCGG	
1828	Srd5a3	Srd5a3_1828	GGAAAGGACGAAACACCGTCTACGTCATCTCAGTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTACGTCATCTCAGTTGTG	
1829	Mogs	Mogs_1829	GGAAAGGACGAAACACCGTCTAGGTCATTCTTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAGGTCATTCTTCCCACG	
1830	Mogs	Mogs_1830	GGAAAGGACGAAACACCGTCGGCAGCATATCCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGCAGCATATCCACGATG	
1831	Mogs	Mogs_1831	GGAAAGGACGAAACACCGTGCCGAAATAGACGTGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCGAAATAGACGTGTGGG	
1832	Mogs	Mogs_1832	GGAAAGGACGAAACACCGGAGGTCCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTCCTACTACCAGAGAT	
1833	Tk2	Tk2_1833	GGAAAGGACGAAACACCGCTCCAATACAACAGACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCAATACAACAGACGTCG	
1834	Tk2	Tk2_1834	GGAAAGGACGAAACACCGTTGAGGGCAATATTGCAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAGGGCAATATTGCAAGT	
1835	Tk2	Tk2_1835	GGAAAGGACGAAACACCGAGAATCGCGTAGTCAACCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATCGCGTAGTCAACCTC	
1836	Tk2	Tk2_1836	GGAAAGGACGAAACACCGTACCATGATGCCAGCCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCATGATGCCAGCCGATG	
1837	Cldn10	Cldn10_1837	GGAAAGGACGAAACACCGGCCCGAGATGGAGACTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCGAGATGGAGACTACGA	
1838	Cldn10	Cldn10_1838	GGAAAGGACGAAACACCGCAGACCATCCAACGCCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACCATCCAACGCCAGCA	
1839	Cldn10	Cldn10_1839	GGAAAGGACGAAACACCGTAGAGGACTAATGATCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAGGACTAATGATCGCTG	
1840	Cldn10	Cldn10_1840	GGAAAGGACGAAACACCGATCTGCGTTACCGATTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTGCGTTACCGATTCCAC	
1841	Chst11	Chst11_1841	GGAAAGGACGAAACACCGAGCCAACGAAGCCCACGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCAACGAAGCCCACGTGT	
1842	Chst11	Chst11_1842	GGAAAGGACGAAACACCGGCAGACACCAGCCTCTCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGACACCAGCCTCTCGAA	
1843	Chst11	Chst11_1843	GGAAAGGACGAAACACCGAGCAGATGTCCACACCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGATGTCCACACCGAAG	
1844	Chst11	Chst11_1844	GGAAAGGACGAAACACCGACCTCCTTCCACAAGCGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTCCTTCCACAAGCGCTA	
1845	Treh	Treh_1845	GGAAAGGACGAAACACCGAGATTAGGGAGGACCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATTAGGGAGGACCTCTCG	
1846	Treh	Treh_1846	GGAAAGGACGAAACACCGAGCTACGGACATATCCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTACGGACATATCCCCAA	
1847	Treh	Treh_1847	GGAAAGGACGAAACACCGAGGGGACCGAGAGACTCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGACCGAGAGACTCTGT	
1848	Treh	Treh_1848	GGAAAGGACGAAACACCGAGGAACGCGTTCAGATCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAACGCGTTCAGATCAGC	
1849	Hibadh	Hibadh_1849	GGAAAGGACGAAACACCGAGCTCCACAGTATACCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCCACAGTATACCACGT	
1850	Hibadh	Hibadh_1850	GGAAAGGACGAAACACCGGCTGCCCTCCAGTATGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCCCTCCAGTATGAATG	
1851	Hibadh	Hibadh_1851	GGAAAGGACGAAACACCGCGTGTTCCCTGATGTATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGTTCCCTGATGTATGCA	
1852	Hibadh	Hibadh_1852	GGAAAGGACGAAACACCGGGAAACCTTACATTTATGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAACCTTACATTTATGGT	
1853	Sumf1	Sumf1_1853	GGAAAGGACGAAACACCGGCAGCCGCACGAGCCCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCCGCACGAGCCCGCAA	
1854	Sumf1	Sumf1_1854	GGAAAGGACGAAACACCGCTCGACTGGCTATTTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGACTGGCTATTTGACAG	
1855	Sumf1	Sumf1_1855	GGAAAGGACGAAACACCGAGTGAAAACGCATATCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGAAAACGCATATCCACC	
1856	Sumf1	Sumf1_1856	GGAAAGGACGAAACACCGAGCTAATTGGAGACACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTAATTGGAGACACCCAG	
1857	Ngly1	Ngly1_1857	GGAAAGGACGAAACACCGGAGCTTCAAACCCTAATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTTCAAACCCTAATGCA	
1858	Ngly1	Ngly1_1858	GGAAAGGACGAAACACCGAGAGACTAGATCTAGAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGACTAGATCTAGAGATG	
1859	Ngly1	Ngly1_1859	GGAAAGGACGAAACACCGGCTACACTGTGATGCATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTACACTGTGATGCATGTG	
1860	Ngly1	Ngly1_1860	GGAAAGGACGAAACACCGGCTGGGTTAATACGGCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGGTTAATACGGCACTC	
1861	Thap11	Thap11_1861	GGAAAGGACGAAACACCGAGCCTGGTTGCTGTCTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCTGGTTGCTGTCTACGG	
1862	Thap11	Thap11_1862	GGAAAGGACGAAACACCGGCTGCTACAACAATTCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCTACAACAATTCACAC	
1863	Thap11	Thap11_1863	GGAAAGGACGAAACACCGGGGACACGTTCTTGAGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACACGTTCTTGAGCCAG	
1864	Thap11	Thap11_1864	GGAAAGGACGAAACACCGCCACGCAGCGGGAAAATGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGCAGCGGGAAAATGGT	
1865	C1galt1c1	C1galt1c1_1865	GGAAAGGACGAAACACCGATATGGACACAAATGACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATGGACACAAATGACATG	
1866	C1galt1c1	C1galt1c1_1866	GGAAAGGACGAAACACCGTGTGCCTTGATCACTATGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCCTTGATCACTATGCT	
1867	C1galt1c1	C1galt1c1_1867	GGAAAGGACGAAACACCGCAAGAACTATACAGTATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGAACTATACAGTATACC	
1868	C1galt1c1	C1galt1c1_1868	GGAAAGGACGAAACACCGCAATAACAGCGAAAGTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATAACAGCGAAAGTAGTG	
1869	Bco1	Bco1_1869	GGAAAGGACGAAACACCGGACATGATGGAAGACCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATGATGGAAGACCACCA	
1870	Bco1	Bco1_1870	GGAAAGGACGAAACACCGGAAGAGTCCCGTGAAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGAGTCCCGTGAAGCACG	
1871	Bco1	Bco1_1871	GGAAAGGACGAAACACCGTAACATGGGCACATCCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACATGGGCACATCCGTCG	
1872	Bco1	Bco1_1872	GGAAAGGACGAAACACCGGGGCACAGCAAACCTCCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCACAGCAAACCTCCTGA	
1873	Slc29a1	Slc29a1_1873	GGAAAGGACGAAACACCGGCTGATGCAGAAACGAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATGCAGAAACGAGTTG	
1874	Slc29a1	Slc29a1_1874	GGAAAGGACGAAACACCGGCATGATTGATCAGTGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATGATTGATCAGTGTCCG	
1875	Slc29a1	Slc29a1_1875	GGAAAGGACGAAACACCGTACACAGCCCCCATCATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACAGCCCCCATCATGAG	
1876	Slc29a1	Slc29a1_1876	GGAAAGGACGAAACACCGGGCCAAAATGACAACTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCAAAATGACAACTGCAC	
1877	Inpp5e	Inpp5e_1877	GGAAAGGACGAAACACCGGAGGTCCCTACGGATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTCCCTACGGATAAACA	
1878	Inpp5e	Inpp5e_1878	GGAAAGGACGAAACACCGAGTGATCGTCACCAGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGATCGTCACCAGCCAAG	
1879	Inpp5e	Inpp5e_1879	GGAAAGGACGAAACACCGCACCGAGGCTGACTACACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGAGGCTGACTACACTC	
1880	Inpp5e	Inpp5e_1880	GGAAAGGACGAAACACCGGGAGATACCTAAGTCCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGATACCTAAGTCCCGAA	
1881	Mrps22	Mrps22_1881	GGAAAGGACGAAACACCGCCGATGCTCTGCTCGCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGATGCTCTGCTCGCGACG	
1882	Mrps22	Mrps22_1882	GGAAAGGACGAAACACCGATTTCTTTAGGCTACTAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTCTTTAGGCTACTAGAC	
1883	Mrps22	Mrps22_1883	GGAAAGGACGAAACACCGAATAAATGACGTATTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATAAATGACGTATTAGCTG	
1884	Mrps22	Mrps22_1884	GGAAAGGACGAAACACCGTGGTATATACTCACCCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTATATACTCACCCGATG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1885	Mrps23	Mrps23_1885	GGAAAGGACGAAACACCGTTATATATGTCATACCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATATATGTCATACCACAG	
1886	Mrps23	Mrps23_1886	GGAAAGGACGAAACACCGGCTTTGCCGTATCGCAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTTGCCGTATCGCAAGCG	
1887	Mrps23	Mrps23_1887	GGAAAGGACGAAACACCGACTTCAAGTCTACCTGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCAAGTCTACCTGTCAG	
1888	Mrps23	Mrps23_1888	GGAAAGGACGAAACACCGAGCTTTCTGACCAGATCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTTTCTGACCAGATCCAT	
1889	Htra2	Htra2_1889	GGAAAGGACGAAACACCGAAACGGATCAGGATTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGGATCAGGATTCGTAG	
1890	Htra2	Htra2_1890	GGAAAGGACGAAACACCGGCCTCATAAGTATCCCCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTCATAAGTATCCCCGCT	
1891	Htra2	Htra2_1891	GGAAAGGACGAAACACCGGTACAATTTCATCGCAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACAATTTCATCGCAGATG	
1892	Htra2	Htra2_1892	GGAAAGGACGAAACACCGCGGAGGTCAGGAGCTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGAGGTCAGGAGCTAACAG	
1893	Dpys	Dpys_1893	GGAAAGGACGAAACACCGGTGTGCGTGTCGATGCCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTGCGTGTCGATGCCCCC	
1894	Dpys	Dpys_1894	GGAAAGGACGAAACACCGGTGGCGATTTGACCACAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCGATTTGACCACAACA	
1895	Dpys	Dpys_1895	GGAAAGGACGAAACACCGCGAAGGTGGTAGCCGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAGGTGGTAGCCGATGCG	
1896	Dpys	Dpys_1896	GGAAAGGACGAAACACCGGAAAGGCAGCTCCCTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGGCAGCTCCCTCATCG	
1897	Lpin2	Lpin2_1897	GGAAAGGACGAAACACCGGGATACTCACGTTTCTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATACTCACGTTTCTAATG	
1898	Lpin2	Lpin2_1898	GGAAAGGACGAAACACCGGGTTATATATCCGGATCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTATATATCCGGATCACG	
1899	Lpin2	Lpin2_1899	GGAAAGGACGAAACACCGTGCAGGTCACCAAAAGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGGTCACCAAAAGAGAA	
1900	Lpin2	Lpin2_1900	GGAAAGGACGAAACACCGAACCTGGATCCGTGTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTGGATCCGTGTCACTG	
1901	Cubn	Cubn_1901	GGAAAGGACGAAACACCGGTGTATCTGGAACATTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTATCTGGAACATTCGCG	
1902	Cubn	Cubn_1902	GGAAAGGACGAAACACCGAGTTATCAACTTCACCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTATCAACTTCACCCACG	
1903	Cubn	Cubn_1903	GGAAAGGACGAAACACCGACAGCTCCGAATGCTACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCTCCGAATGCTACTGG	
1904	Cubn	Cubn_1904	GGAAAGGACGAAACACCGCCACCTGTGTGAACACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCTGTGTGAACACTATG	
1905	Sdhc	Sdhc_1905	GGAAAGGACGAAACACCGTACTTGTAGATAGTCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTTGTAGATAGTCAAATG	
1906	Sdhc	Sdhc_1906	GGAAAGGACGAAACACCGTCTGGAATAGCCTTGAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGAATAGCCTTGAGTGG	
1907	Sdhc	Sdhc_1907	GGAAAGGACGAAACACCGTTTGGGAACCACAGCTAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGGGAACCACAGCTAAGG	
1908	Sdhc	Sdhc_1908	GGAAAGGACGAAACACCGCAGGAAGCAGCAGTGCCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAAGCAGCAGTGCCGAC	
1909	Ethe1	Ethe1_1909	GGAAAGGACGAAACACCGGGGCTCAAGCTGTTGTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTCAAGCTGTTGTACGC	
1910	Ethe1	Ethe1_1910	GGAAAGGACGAAACACCGAACTCACAAAGCGTCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTCACAAAGCGTCCAAAG	
1911	Ethe1	Ethe1_1911	GGAAAGGACGAAACACCGTCCACACCCTCGGATCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACACCCTCGGATCAGCA	
1912	Ethe1	Ethe1_1912	GGAAAGGACGAAACACCGGGGTGACCGGGAGTCAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTGACCGGGAGTCAAGAG	
1913	Sdhaf2	Sdhaf2_1913	GGAAAGGACGAAACACCGCTCTATGAGAGCAGAAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTATGAGAGCAGAAAGAG	
1914	Sdhaf2	Sdhaf2_1914	GGAAAGGACGAAACACCGCGTTAATCAGGCGATCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTTAATCAGGCGATCATAG	
1915	Sdhaf2	Sdhaf2_1915	GGAAAGGACGAAACACCGAATGATGTCACACTAGGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGATGTCACACTAGGCAA	
1916	Sdhaf2	Sdhaf2_1916	GGAAAGGACGAAACACCGGCAGATACTCTTTAGCAAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGATACTCTTTAGCAAAC	
1917	Rmnd1	Rmnd1_1917	GGAAAGGACGAAACACCGCGGGTCCGGGATGCTTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGGTCCGGGATGCTTTCAG	
1918	Rmnd1	Rmnd1_1918	GGAAAGGACGAAACACCGGAAGTGACAAGCCTGCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTGACAAGCCTGCCTAG	
1919	Rmnd1	Rmnd1_1919	GGAAAGGACGAAACACCGGAAAGTACAACATGCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGTACAACATGCCACAA	
1920	Rmnd1	Rmnd1_1920	GGAAAGGACGAAACACCGGGACAATCAAAACTGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAATCAAAACTGCACAG	
1921	Ndufa9	Ndufa9_1921	GGAAAGGACGAAACACCGGGTTAACAACGTATCGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTAACAACGTATCGACCC	
1922	Ndufa9	Ndufa9_1922	GGAAAGGACGAAACACCGCCAGGTCACCCATCAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGTCACCCATCAGACGA	
1923	Ndufa9	Ndufa9_1923	GGAAAGGACGAAACACCGGATGCCTGAGCTATTGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCCTGAGCTATTGCTCG	
1924	Ndufa9	Ndufa9_1924	GGAAAGGACGAAACACCGGTCATACCTCACGGGAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATACCTCACGGGAAAGG	
1925	Apoa5	Apoa5_1925	GGAAAGGACGAAACACCGCAAACTCACACGTAAGGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACTCACACGTAAGGCGA	
1926	Apoa5	Apoa5_1926	GGAAAGGACGAAACACCGTCACCAAGCGTTCTGCGTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACCAAGCGTTCTGCGTAA	
1927	Apoa5	Apoa5_1927	GGAAAGGACGAAACACCGGCAGTTGAAACCCTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTTGAAACCCTACACGG	
1928	Apoa5	Apoa5_1928	GGAAAGGACGAAACACCGAAAAGCTGGGACCCTTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGCTGGGACCCTTGAGA	
1929	Cox7b	Cox7b_1929	GGAAAGGACGAAACACCGTTATCTGCTCACCTTGGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATCTGCTCACCTTGGAGA	
1930	Cox7b	Cox7b_1930	GGAAAGGACGAAACACCGGGGAATGCTATATTAGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAATGCTATATTAGCAGG	
1931	Cox7b	Cox7b_1931	GGAAAGGACGAAACACCGAACTAGGTGCCCTCTTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTAGGTGCCCTCTTCTGG	
1932	Cox7b	Cox7b_1932	GGAAAGGACGAAACACCGTAGCATTCCCATATTTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCATTCCCATATTTGTCA	
1933	Acer3	Acer3_1933	GGAAAGGACGAAACACCGACAGAACTCAGCGACGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGAACTCAGCGACGAACA	
1934	Acer3	Acer3_1934	GGAAAGGACGAAACACCGATACAGTTTAACAGTAACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACAGTTTAACAGTAACTA	
1935	Acer3	Acer3_1935	GGAAAGGACGAAACACCGTCAGGTCATGTATGGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGTCATGTATGGAATGT	
1936	Acer3	Acer3_1936	GGAAAGGACGAAACACCGTGAATTGCACCAAAAATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAATTGCACCAAAAATTGG	
1937	Ndufb9	Ndufb9_1937	GGAAAGGACGAAACACCGTGTGGATACACCATGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGATACACCATGACTCG	
1938	Ndufb9	Ndufb9_1938	GGAAAGGACGAAACACCGGTAGCACTCATATCTCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGCACTCATATCTCTCGA	
1939	Ndufb9	Ndufb9_1939	GGAAAGGACGAAACACCGAGAATGAGAAGGATATGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATGAGAAGGATATGATG	
1940	Ndufb9	Ndufb9_1940	GGAAAGGACGAAACACCGAGGATACATTGCTTTCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGATACATTGCTTTCTCAG	
1941	Msmo1	Msmo1_1941	GGAAAGGACGAAACACCGTAGTATGTTCCACAAATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTATGTTCCACAAATCAG	
1942	Msmo1	Msmo1_1942	GGAAAGGACGAAACACCGAAAGTTCCAGATCGCAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTTCCAGATCGCAACCT	
1943	Msmo1	Msmo1_1943	GGAAAGGACGAAACACCGGATAAACCAGAAACCTTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAAACCAGAAACCTTCGA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
1944	Msmo1	Msmo1_1944	GGAAAGGACGAAACACCGACAGGTACTTAACTTTGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGGTACTTAACTTTGGCA	
1945	Mrps16	Mrps16_1945	GGAAAGGACGAAACACCGTGCTCACAACAAGTGCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCACAACAAGTGCCCCA	
1946	Mrps16	Mrps16_1946	GGAAAGGACGAAACACCGGCCACCCAAAGCAAGGCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCACCCAAAGCAAGGCGTA	
1947	Mrps16	Mrps16_1947	GGAAAGGACGAAACACCGAAAACTAGTTGCCCTCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACTAGTTGCCCTCAACC	
1948	Mrps16	Mrps16_1948	GGAAAGGACGAAACACCGGGCCGATTTGTGGAGCAGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCGATTTGTGGAGCAGTT	
1949	Tmem126a	Tmem126a_1949	GGAAAGGACGAAACACCGTTTGGCTATACCCGTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGGCTATACCCGTCAATG	
1950	Tmem126a	Tmem126a_1950	GGAAAGGACGAAACACCGAACTAGTGCACCCCGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTAGTGCACCCCGTGTTG	
1951	Tmem126a	Tmem126a_1951	GGAAAGGACGAAACACCGTAAAACATACCTGTACTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAAACATACCTGTACTCAA	
1952	Tmem126a	Tmem126a_1952	GGAAAGGACGAAACACCGAACAACTTCCAGAATCAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAACTTCCAGAATCAGAC	
1953	Cox20	Cox20_1953	GGAAAGGACGAAACACCGCGCCCCGGAGCCCCACGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCCCGGAGCCCCACGAGA	
1954	Cox20	Cox20_1954	GGAAAGGACGAAACACCGTAGCGAAATTATACCTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCGAAATTATACCTACAG	
1955	Cox20	Cox20_1955	GGAAAGGACGAAACACCGAGTATAGATTCTCGAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTATAGATTCTCGAGCACA	
1956	Cox20	Cox20_1956	GGAAAGGACGAAACACCGATTAGAAGATCATGTGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTAGAAGATCATGTGATGT	
1957	Cox14	Cox14_1957	GGAAAGGACGAAACACCGCACAGTGAGGAGCATCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGTGAGGAGCATCATCG	
1958	Cox14	Cox14_1958	GGAAAGGACGAAACACCGGGTAACCCCCATACACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAACCCCCATACACAGTG	
1959	Cox14	Cox14_1959	GGAAAGGACGAAACACCGGCGCAGCTGGAGGTAACGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCAGCTGGAGGTAACGGT	
1960	Cox14	Cox14_1960	GGAAAGGACGAAACACCGGCCAAGCAGCTAGCCGATATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAAGCAGCTAGCCGATAT	
1961	Iscu	Iscu_1961	GGAAAGGACGAAACACCGTATGAAAACCCTCGGAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGAAAACCCTCGGAACGT	
1962	Iscu	Iscu_1962	GGAAAGGACGAAACACCGCCAGCTCCTTAGCCACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCTCCTTAGCCACAGAG	
1963	Iscu	Iscu_1963	GGAAAGGACGAAACACCGTTCATGACGTCACCACATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCATGACGTCACCACATGC	
1964	Iscu	Iscu_1964	GGAAAGGACGAAACACCGGGCCAGGCTCTACCACAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCAGGCTCTACCACAAGA	
1965	Sar1b	Sar1b_1965	GGAAAGGACGAAACACCGAAGAATTAGAATAGGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAATTAGAATAGGCACGT	
1966	Sar1b	Sar1b_1966	GGAAAGGACGAAACACCGACTTACTGGGATGTAGCGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTACTGGGATGTAGCGTT	
1967	Sar1b	Sar1b_1967	GGAAAGGACGAAACACCGTCCCGGCATTATCCAATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCGGCATTATCCAATCCA	
1968	Sar1b	Sar1b_1968	GGAAAGGACGAAACACCGCAATGCCATTGATAGCAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATGCCATTGATAGCAGGA	
1969	Tsfm	Tsfm_1969	GGAAAGGACGAAACACCGCAGATACTCACCAATCGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATACTCACCAATCGCTA	
1970	Tsfm	Tsfm_1970	GGAAAGGACGAAACACCGCCATGGCTCACGTTTCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATGGCTCACGTTTCACGC	
1971	Tsfm	Tsfm_1971	GGAAAGGACGAAACACCGACTGTCAGAACCTGACGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTCAGAACCTGACGGAT	
1972	Tsfm	Tsfm_1972	GGAAAGGACGAAACACCGAGGAGCTCCTTATGAAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGCTCCTTATGAAACTG	
1973	Cyc1	Cyc1_1973	GGAAAGGACGAAACACCGTAGCTCGAACGATGTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCTCGAACGATGTAGCTG	
1974	Cyc1	Cyc1_1974	GGAAAGGACGAAACACCGGGTGGGAGTGTGCTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGGAGTGTGCTACACGG	
1975	Cyc1	Cyc1_1975	GGAAAGGACGAAACACCGAGCTACCCATGGTCTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTACCCATGGTCTCATCG	
1976	Cyc1	Cyc1_1976	GGAAAGGACGAAACACCGGGTCCCGGCAGCTTCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCCGGCAGCTTCCATTG	
1977	Pam16	Pam16_1977	GGAAAGGACGAAACACCGTCACCTTCTGGACCTCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACCTTCTGGACCTCCTCG	
1978	Pam16	Pam16_1978	GGAAAGGACGAAACACCGCCTGGCCCAGATCATTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGCCCAGATCATTGTGA	
1979	Pam16	Pam16_1979	GGAAAGGACGAAACACCGAGGCAGCCGCTGACGCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCAGCCGCTGACGCTCGA	
1980	Pam16	Pam16_1980	GGAAAGGACGAAACACCGCCGTGTATCCACAGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTGTATCCACAGCCAGCC	
1981	Nmnat1	Nmnat1_1981	GGAAAGGACGAAACACCGAAAGGCATTATCTCACCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGGCATTATCTCACCGGT	
1982	Nmnat1	Nmnat1_1982	GGAAAGGACGAAACACCGGAACAGCCTGAGGTGCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACAGCCTGAGGTGCATGT	
1983	Nmnat1	Nmnat1_1983	GGAAAGGACGAAACACCGGTTCTGCCATGATGATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCTGCCATGATGATTCGG	
1984	Nmnat1	Nmnat1_1984	GGAAAGGACGAAACACCGGGAGGACATCACGCAAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGACATCACGCAAATCG	
1985	Ndufb3	Ndufb3_1985	GGAAAGGACGAAACACCGGCTGGACATGGACATGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGACATGGACATGAACA	
1986	Ndufb3	Ndufb3_1986	GGAAAGGACGAAACACCGAACTTCCAGATTACAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTCCAGATTACAGACAG	
1987	Ndufb3	Ndufb3_1987	GGAAAGGACGAAACACCGGACTCATCTTACCGAGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTCATCTTACCGAGCCCA	
1988	Ndufb3	Ndufb3_1988	GGAAAGGACGAAACACCGCATGGACATGAACATGGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGACATGAACATGGACA	
1989	Timm50	Timm50_1989	GGAAAGGACGAAACACCGGACGCCACCAGATATATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACGCCACCAGATATATGGA	
1990	Timm50	Timm50_1990	GGAAAGGACGAAACACCGGGGTCCACACTATCAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCCACACTATCAATGAG	
1991	Timm50	Timm50_1991	GGAAAGGACGAAACACCGACTGGTCCTGGAGCTTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGGTCCTGGAGCTTACCG	
1992	Timm50	Timm50_1992	GGAAAGGACGAAACACCGATTCCTGATGAATTCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCTGATGAATTCGACAG	
1993	Pgm1	Pgm1_1993	GGAAAGGACGAAACACCGCATTACCGATGGACGCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTACCGATGGACGCGCTG	
1994	Pgm1	Pgm1_1994	GGAAAGGACGAAACACCGATCATCTCTCCCCACGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCATCTCTCCCCACGATCG	
1995	Pgm1	Pgm1_1995	GGAAAGGACGAAACACCGTGGGGGTTATATCAGAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGGGTTATATCAGAGAAG	
1996	Pgm1	Pgm1_1996	GGAAAGGACGAAACACCGAGGCCAACTGCACAAACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCAACTGCACAAACTCG	
1997	Alg14	Alg14_1997	GGAAAGGACGAAACACCGTGTCCAATGCCTATTCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCAATGCCTATTCACCA	
1998	Alg14	Alg14_1998	GGAAAGGACGAAACACCGCCGAATTCCGAGAAGCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAATTCCGAGAAGCCGGG	
1999	Alg14	Alg14_1999	GGAAAGGACGAAACACCGAAGAGTCTGAGAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGTCTGAGAGACTCTCG	
2000	Alg14	Alg14_2000	GGAAAGGACGAAACACCGGCTTTATTCGGAGAACCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTTATTCGGAGAACCAGT	
2001	Taz	Taz_2001	GGAAAGGACGAAACACCGTTTGGAGAAGCTTAACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGGAGAAGCTTAACCATG	
2002	Taz	Taz_2002	GGAAAGGACGAAACACCGGGTCATCCATGCAAGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCATCCATGCAAGACTGG	

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2003	Taz	Taz_2003	GGAAAGGACGAAACACCGAGCAGCTCACCTCGACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGCTCACCTCGACACAC	
2004	Taz	Taz_2004	GGAAAGGACGAAACACCGTATGAGCTCATTGAGAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGAGCTCATTGAGAACCG	
2005	Etfdh	Etfdh_2005	GGAAAGGACGAAACACCGGGTACGGATTCTGATAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTACGGATTCTGATAGTCG	
2006	Etfdh	Etfdh_2006	GGAAAGGACGAAACACCGGAGTAGATCACACTGTTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTAGATCACACTGTTGGT	
2007	Etfdh	Etfdh_2007	GGAAAGGACGAAACACCGGGCGGGAAGAGGATAGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGGGAAGAGGATAGCCTA	
2008	Etfdh	Etfdh_2008	GGAAAGGACGAAACACCGGGCAATTACATCGTACGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAATTACATCGTACGCCT	
2009	Pnpla2	Pnpla2_2009	GGAAAGGACGAAACACCGGGCAGGAGGCCACGCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAGGAGGCCACGCCAATG	
2010	Pnpla2	Pnpla2_2010	GGAAAGGACGAAACACCGTGTTCTTGCAAAGCGCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCTTGCAAAGCGCTATG	
2011	Pnpla2	Pnpla2_2011	GGAAAGGACGAAACACCGAGCAGGTGCCAACATTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGGTGCCAACATTATTG	
2012	Pnpla2	Pnpla2_2012	GGAAAGGACGAAACACCGCCTGTTTGCACATCTCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTTTGCACATCTCTCGG	
2013	Pmpca	Pmpca_2013	GGAAAGGACGAAACACCGAGAGCTCACACACATCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTCACACACATCATGG	
2014	Pmpca	Pmpca_2014	GGAAAGGACGAAACACCGAGAAATTGAGATGACGAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAATTGAGATGACGAGGA	
2015	Pmpca	Pmpca_2015	GGAAAGGACGAAACACCGTGAAACCAAAGTTACCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAACCAAAGTTACCACTC	
2016	Pmpca	Pmpca_2016	GGAAAGGACGAAACACCGTCAGTGGCACAGTACACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTGGCACAGTACACTGG	
2017	Acadsb	Acadsb_2017	GGAAAGGACGAAACACCGGAGGATTTGAGGACACGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGATTTGAGGACACGAGG	
2018	Acadsb	Acadsb_2018	GGAAAGGACGAAACACCGCATAGCGAAAGAGTCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATAGCGAAAGAGTCGCTAC	
2019	Acadsb	Acadsb_2019	GGAAAGGACGAAACACCGAAGTTGAAGCACAATATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTTGAAGCACAATATGGA	
2020	Acadsb	Acadsb_2020	GGAAAGGACGAAACACCGTTCAAATGTTAACTGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAAATGTTAACTGACAGG	
2021	Pccb	Pccb_2021	GGAAAGGACGAAACACCGGGAAATTGAAGAATTCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAATTGAAGAATTCACGC	
2022	Pccb	Pccb_2022	GGAAAGGACGAAACACCGGGAGTCCTTGGCTGGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTCCTTGGCTGGCTACG	
2023	Pccb	Pccb_2023	GGAAAGGACGAAACACCGGCTTGTGCTGCGCGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTGTGCTGCGCGTCGATG	
2024	Pccb	Pccb_2024	GGAAAGGACGAAACACCGTGTGAAGTCTGTTACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGAAGTCTGTTACCAATG	
2025	Sdhd	Sdhd_2025	GGAAAGGACGAAACACCGGCAGAGAGGACATACAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGAGAGGACATACAGTGG	
2026	Sdhd	Sdhd_2026	GGAAAGGACGAAACACCGAGGACCAGCCTACCCAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCAGCCTACCCAAGGA	
2027	Sdhd	Sdhd_2027	GGAAAGGACGAAACACCGTGCAGTGGCCAAGGAGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTGGCCAAGGAGCTCG	
2028	Sdhd	Sdhd_2028	GGAAAGGACGAAACACCGAGGGATTCAAGTACCCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGATTCAAGTACCCAGCA	
2029	Sdha	Sdha_2029	GGAAAGGACGAAACACCGGTCAGTTACCTCAACCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAGTTACCTCAACCACAG	
2030	Sdha	Sdha_2030	GGAAAGGACGAAACACCGTTCTACTCAATACCCAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTACTCAATACCCAGTGG	
2031	Sdha	Sdha_2031	GGAAAGGACGAAACACCGTGCACAGTGCAATGACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCACAGTGCAATGACACCA	
2032	Sdha	Sdha_2032	GGAAAGGACGAAACACCGACTGTGCATTACAACATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTGCATTACAACATGGG	
2033	Acad8	Acad8_2033	GGAAAGGACGAAACACCGTGGCTCCCAATATGGCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCTCCCAATATGGCGGAG	
2034	Acad8	Acad8_2034	GGAAAGGACGAAACACCGCCAACAGGATTGGGACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACAGGATTGGGACCGAG	
2035	Acad8	Acad8_2035	GGAAAGGACGAAACACCGTCTCCATGGTACAGAGCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCATGGTACAGAGCGGT	
2036	Acad8	Acad8_2036	GGAAAGGACGAAACACCGGTGGATGCTTATATAGGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGATGCTTATATAGGCAG	
2037	Trit1	Trit1_2037	GGAAAGGACGAAACACCGGCCACTTGTAGTGATTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCACTTGTAGTGATTCTCG	
2038	Trit1	Trit1_2038	GGAAAGGACGAAACACCGTGAGCGCTTGGATAAAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCGCTTGGATAAAAGAG	
2039	Trit1	Trit1_2039	GGAAAGGACGAAACACCGCCATAAACGGCTAAGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATAAACGGCTAAGCCAGG	
2040	Trit1	Trit1_2040	GGAAAGGACGAAACACCGTGTGACCAGCTACACCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGACCAGCTACACCGTGG	
2041	Plin5	Plin5_2041	GGAAAGGACGAAACACCGAGGGACTTAGACTCACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGACTTAGACTCACACTG	
2042	Plin5	Plin5_2042	GGAAAGGACGAAACACCGGCAGAGCAAACACCGTACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGAGCAAACACCGTACCC	
2043	Plin5	Plin5_2043	GGAAAGGACGAAACACCGGAATGTGGTGAATCGAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATGTGGTGAATCGAGTGG	
2044	Plin5	Plin5_2044	GGAAAGGACGAAACACCGATGGTGGACCTGGCCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTGGACCTGGCCCAAAG	
2045	Uqcrc2	Uqcrc2_2045	GGAAAGGACGAAACACCGAACAAGCCGATTCTTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAAGCCGATTCTTGACAG	
2046	Uqcrc2	Uqcrc2_2046	GGAAAGGACGAAACACCGACAGTACAAAGGATTAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTACAAAGGATTAGCCA	
2047	Uqcrc2	Uqcrc2_2047	GGAAAGGACGAAACACCGCATCTTTCAAGATAACCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTTTCAAGATAACCCGT	
2048	Uqcrc2	Uqcrc2_2048	GGAAAGGACGAAACACCGGCAAAAGCCAAATACCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAAAGCCAAATACCGTGG	
2049	Oxct1	Oxct1_2049	GGAAAGGACGAAACACCGGAAGCGTTTATCACTCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCGTTTATCACTCCGAA	
2050	Oxct1	Oxct1_2050	GGAAAGGACGAAACACCGCATTGCCAGCAAGCCACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGCCAGCAAGCCACGAG	
2051	Oxct1	Oxct1_2051	GGAAAGGACGAAACACCGAGCTGCAGGAACTACCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGCAGGAACTACCGTGG	
2052	Oxct1	Oxct1_2052	GGAAAGGACGAAACACCGTCTAGGGCACACTTGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAGGGCACACTTGCCGAG	
2053	Magt1	Magt1_2053	GGAAAGGACGAAACACCGTGTGTGTGCGATCGCAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGTGCGATCGCAGCGG	
2054	Magt1	Magt1_2054	GGAAAGGACGAAACACCGCAGCTGAGCAGATTGCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCTGAGCAGATTGCCCGG	
2055	Magt1	Magt1_2055	GGAAAGGACGAAACACCGTTATGCTGGACCCCTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATGCTGGACCCCTAATGT	
2056	Magt1	Magt1_2056	GGAAAGGACGAAACACCGGTGGAGCTTTAACAAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAGCTTTAACAAGACGA	
2057	Gatm	Gatm_2057	GGAAAGGACGAAACACCGATCAAAGACTACTTCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAAAGACTACTTCCATCG	
2058	Gatm	Gatm_2058	GGAAAGGACGAAACACCGATTCGTTGTAAGAGGAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCGTTGTAAGAGGAGACA	
2059	Gatm	Gatm_2059	GGAAAGGACGAAACACCGACTTGAGTGACCAGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTGAGTGACCAGTCGATG	
2060	Gatm	Gatm_2060	GGAAAGGACGAAACACCGACAACCATCAGGATGTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAACCATCAGGATGTCTCG	
2061	Trak1	Trak1_2061	GGAAAGGACGAAACACCGGTGGAAGTAATTCTGGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAAGTAATTCTGGACGG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2062	Trak1	Trak1_2062	GGAAAGGACGAAACACCGTCCGCTCTTAGCTTGTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGCTCTTAGCTTGTAATG	
2063	Trak1	Trak1_2063	GGAAAGGACGAAACACCGTTAGGCGGCTATCCCTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGGCGGCTATCCCTACGC	
2064	Trak1	Trak1_2064	GGAAAGGACGAAACACCGTTACCATGTTTAGTGCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCATGTTTAGTGCGCGG	
2065	Mmachc	Mmachc_2065	GGAAAGGACGAAACACCGCAAACCAGCCCCCAAATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACCAGCCCCCAAATCGG	
2066	Mmachc	Mmachc_2066	GGAAAGGACGAAACACCGCCAAACACTGAGAGACCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAACACTGAGAGACCCGG	
2067	Mmachc	Mmachc_2067	GGAAAGGACGAAACACCGGAAGTTTATCCCTTCCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTTTATCCCTTCCAGGT	
2068	Mmachc	Mmachc_2068	GGAAAGGACGAAACACCGACTATGAGGTACACCCCAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTATGAGGTACACCCCAAT	
2069	Ndufa6	Ndufa6_2069	GGAAAGGACGAAACACCGGCACCTCCCGATACCAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCTCCCGATACCAAGCG	
2070	Ndufa6	Ndufa6_2070	GGAAAGGACGAAACACCGATATCACGGTGAAACAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATCACGGTGAAACAAGGA	
2071	Ndufa6	Ndufa6_2071	GGAAAGGACGAAACACCGACTGAAAATGGGCTTCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGAAAATGGGCTTCACCG	
2072	Ndufa6	Ndufa6_2072	GGAAAGGACGAAACACCGACCTGAACGAGGCCAAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTGAACGAGGCCAAGCGG	
2073	Rnaseh2b	Rnaseh2b_2073	GGAAAGGACGAAACACCGCTCCTAGGTCAACCAAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCTAGGTCAACCAAACTG	
2074	Rnaseh2b	Rnaseh2b_2074	GGAAAGGACGAAACACCGTCAGCCCTTGGACCAAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCCCTTGGACCAAGTCG	
2075	Rnaseh2b	Rnaseh2b_2075	GGAAAGGACGAAACACCGCAGCCTTTAGGAGATAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCTTTAGGAGATAGTGA	
2076	Rnaseh2b	Rnaseh2b_2076	GGAAAGGACGAAACACCGTGGCCAGCTTTACGAACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCAGCTTTACGAACAGG	
2077	Lipt2	Lipt2_2077	GGAAAGGACGAAACACCGTACACGGGCGGGCTACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACGGGCGGGCTACGCGG	
2078	Lipt2	Lipt2_2078	GGAAAGGACGAAACACCGACCCGCTTTGGTCCCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCGCTTTGGTCCCCGACA	
2079	Lipt2	Lipt2_2079	GGAAAGGACGAAACACCGCCGAAGTTCGCACAGTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAAGTTCGCACAGTCGCA	
2080	Lipt2	Lipt2_2080	GGAAAGGACGAAACACCGCAGACGCCAGTGTAGGGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACGCCAGTGTAGGGCGG	
2081	Pdzk1ip1	Pdzk1ip1_2081	GGAAAGGACGAAACACCGCGGCGAAGACGATTGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGAAGACGATTGCAACA	
2082	Pdzk1ip1	Pdzk1ip1_2082	GGAAAGGACGAAACACCGAGAACACAGCGACAGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACACAGCGACAGCAATG	
2083	Pdzk1ip1	Pdzk1ip1_2083	GGAAAGGACGAAACACCGGCACCTGCCAGCTGTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCTGCCAGCTGTCAACA	
2084	Pdzk1ip1	Pdzk1ip1_2084	GGAAAGGACGAAACACCGCAACCACTTCTGGTGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACCACTTCTGGTGCCAGG	
2085	Ndufa13	Ndufa13_2085	GGAAAGGACGAAACACCGGGTTCCGCTTGTAGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTCCGCTTGTAGTCGATG	
2086	Ndufa13	Ndufa13_2086	GGAAAGGACGAAACACCGACTGACCCGACAGTCCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGACCCGACAGTCCCCGG	
2087	Ndufa13	Ndufa13_2087	GGAAAGGACGAAACACCGGATTCTCCGGGAAAACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTCTCCGGGAAAACCTGG	
2088	Ndufa13	Ndufa13_2088	GGAAAGGACGAAACACCGGTGGAACCAGGAGCGCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAACCAGGAGCGCAGGT	
2089	Ndufb8	Ndufb8_2089	GGAAAGGACGAAACACCGGGGGTCCTAGGATATGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGTCCTAGGATATGACCC	
2090	Ndufb8	Ndufb8_2090	GGAAAGGACGAAACACCGCAAGAAGTATAACATGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGAAGTATAACATGCGAG	
2091	Ndufb8	Ndufb8_2091	GGAAAGGACGAAACACCGCATGTACATCAGGAATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGTACATCAGGAATCGTG	
2092	Ndufb8	Ndufb8_2092	GGAAAGGACGAAACACCGCAACCGATCACAGCATGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACCGATCACAGCATGAGA	
2093	Uqcc2	Uqcc2_2093	GGAAAGGACGAAACACCGCCAGTGGACGAGACCAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGTGGACGAGACCAAACG	
2094	Uqcc2	Uqcc2_2094	GGAAAGGACGAAACACCGTTCAAACTACTACAAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAAACTACTACAAGCACA	
2095	Uqcc2	Uqcc2_2095	GGAAAGGACGAAACACCGGCTCTCGTACATCTGATCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCTCGTACATCTGATCAC	
2096	Uqcc2	Uqcc2_2096	GGAAAGGACGAAACACCGCACAGAGCTTAAGGAAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGAGCTTAAGGAAACGC	
2097	Ndufa10	Ndufa10_2097	GGAAAGGACGAAACACCGTCGATATAGATGACTGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGATATAGATGACTGCGTG	
2098	Ndufa10	Ndufa10_2098	GGAAAGGACGAAACACCGCCACTAAACTCTATGTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTAAACTCTATGTCGAG	
2099	Ndufa10	Ndufa10_2099	GGAAAGGACGAAACACCGTGGGAAAAACAAGCTCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGAAAAACAAGCTCGCAA	
2100	Ndufa10	Ndufa10_2100	GGAAAGGACGAAACACCGCTGGAGGCAATGTACAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGAGGCAATGTACAACCA	
2101	Slc25a19	Slc25a19_2101	GGAAAGGACGAAACACCGACGGACCATGTATAAGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGACCATGTATAAGACCG	
2102	Slc25a19	Slc25a19_2102	GGAAAGGACGAAACACCGTCAGCGCACTTTGTGTGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCGCACTTTGTGTGCGG	
2103	Slc25a19	Slc25a19_2103	GGAAAGGACGAAACACCGGACCCCAATGCCAAATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCCCAATGCCAAATACCA	
2104	Slc25a19	Slc25a19_2104	GGAAAGGACGAAACACCGAGAACTGCAGGCCCGCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTGCAGGCCCGCGTAG	
2105	Pigc	Pigc_2105	GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACTGACAGACTCCGTCA	
2106	Pigc	Pigc_2106	GGAAAGGACGAAACACCGGAATAAAACATACCCAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATAAAACATACCCAACCA	
2107	Pigc	Pigc_2107	GGAAAGGACGAAACACCGTCCGGAAAAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGGAAAAACATCTATGCC	
2108	Pigc	Pigc_2108	GGAAAGGACGAAACACCGGGCCGACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCGACCTGAAGAGTACTC	
2109	Far1	Far1_2109	GGAAAGGACGAAACACCGCTCTCGAACAGGCCTTCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTCGAACAGGCCTTCAGA	
2110	Far1	Far1_2110	GGAAAGGACGAAACACCGACATAGACAGAATTCACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATAGACAGAATTCACCCT	
2111	Far1	Far1_2111	GGAAAGGACGAAACACCGCGTCGATCGTCGGCGCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCGATCGTCGGCGCCAGT	
2112	Far1	Far1_2112	GGAAAGGACGAAACACCGTCTCGTTCCTGTAGATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCGTTCCTGTAGATGTAG	
2113	Dhdds	Dhdds_2113	GGAAAGGACGAAACACCGGGATGTCGGGATGAGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATGTCGGGATGAGGAGAG	
2114	Dhdds	Dhdds_2114	GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATGCCAAGAAGTGTCAGG	
2115	Dhdds	Dhdds_2115	GGAAAGGACGAAACACCGCTTCAAACGTTCCAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAAACGTTCCAAGAGTG	
2116	Dhdds	Dhdds_2116	GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCAGATGCAGATCACCC	
2117	Hoga1	Hoga1_2117	GGAAAGGACGAAACACCGGCGGCCACGATAGTAACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGCCACGATAGTAACAAG	
2118	Hoga1	Hoga1_2118	GGAAAGGACGAAACACCGACAGTGTCCCAGCCAATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTGTCCCAGCCAATACG	
2119	Hoga1	Hoga1_2119	GGAAAGGACGAAACACCGTGGGTATGGCCTGGCGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGTATGGCCTGGCGCACG	
2120	Hoga1	Hoga1_2120	GGAAAGGACGAAACACCGCTTCCCTCTTACCTCGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCCTCTTACCTCGAAAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2121	Mtpap	Mtpap_2121	GGAAAGGACGAAACACCGTTTGCCAAATGTGTTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGCCAAATGTGTTCACTG	
2122	Mtpap	Mtpap_2122	GGAAAGGACGAAACACCGCAGTTGTCCAGGGACTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTTGTCCAGGGACTATTG	
2123	Mtpap	Mtpap_2123	GGAAAGGACGAAACACCGTGTTAGCAGTCAGATCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTAGCAGTCAGATCACAC	
2124	Mtpap	Mtpap_2124	GGAAAGGACGAAACACCGATGTATCAAAACAGTCCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTATCAAAACAGTCCGCT	
2125	Pnpla8	Pnpla8_2125	GGAAAGGACGAAACACCGGAAGGCGTACAAGCCTTAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGCGTACAAGCCTTAGT	
2126	Pnpla8	Pnpla8_2126	GGAAAGGACGAAACACCGAGTAATACAGAGCTTTGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTAATACAGAGCTTTGGGT	
2127	Pnpla8	Pnpla8_2127	GGAAAGGACGAAACACCGCTTAGCACTTCTGCTCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTAGCACTTCTGCTCCCAA	
2128	Pnpla8	Pnpla8_2128	GGAAAGGACGAAACACCGCATGCCGCTGGATGAATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCCGCTGGATGAATGTG	
2129	Slc25a46	Slc25a46_2129	GGAAAGGACGAAACACCGGTGAATTTACACCTTTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAATTTACACCTTTACCG	
2130	Slc25a46	Slc25a46_2130	GGAAAGGACGAAACACCGTGAGATGGTAATGCCGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGATGGTAATGCCGAGCA	
2131	Slc25a46	Slc25a46_2131	GGAAAGGACGAAACACCGGCGGAACCCTCGAGCGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGAACCCTCGAGCGTCGG	
2132	Slc25a46	Slc25a46_2132	GGAAAGGACGAAACACCGAATTGGACGAGTGATAGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTGGACGAGTGATAGGCT	
2133	Abhd5	Abhd5_2133	GGAAAGGACGAAACACCGAGTTTGGATCAGGGCCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTTGGATCAGGGCCCTAG	
2134	Abhd5	Abhd5_2134	GGAAAGGACGAAACACCGTTGAAGATCTAAGCACCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAAGATCTAAGCACCGAT	
2135	Abhd5	Abhd5_2135	GGAAAGGACGAAACACCGCGGCAGCCAAGAACCCTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCAGCCAAGAACCCTCCC	
2136	Abhd5	Abhd5_2136	GGAAAGGACGAAACACCGGAGCCTGTGCGCATATCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCCTGTGCGCATATCCAA	
2137	Abcg8	Abcg8_2137	GGAAAGGACGAAACACCGGCGCCGACGAGTGAGCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCGACGAGTGAGCATTG	
2138	Abcg8	Abcg8_2138	GGAAAGGACGAAACACCGGGTTGCTATAGCGAGGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTGCTATAGCGAGGACAA	
2139	Abcg8	Abcg8_2139	GGAAAGGACGAAACACCGAGTCTGTACTTCACCTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTGTACTTCACCTACAG	
2140	Abcg8	Abcg8_2140	GGAAAGGACGAAACACCGTGTGATCACGTCGAGTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGATCACGTCGAGTAGTG	
2141	Agpat2	Agpat2_2141	GGAAAGGACGAAACACCGTGATTAGAGATGATGACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATTAGAGATGATGACACA	
2142	Agpat2	Agpat2_2142	GGAAAGGACGAAACACCGGGGTACACGCAACGACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTACACGCAACGACAATG	
2143	Agpat2	Agpat2_2143	GGAAAGGACGAAACACCGAGCGTGAGCTAATGTTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGTGAGCTAATGTTCACA	
2144	Agpat2	Agpat2_2144	GGAAAGGACGAAACACCGGCCGCACCGTGGATAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCGCACCGTGGATAACATG	
2145	Uqcrb	Uqcrb_2145	GGAAAGGACGAAACACCGATGCCTCATAGTCAGGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCCTCATAGTCAGGTCCA	
2146	Uqcrb	Uqcrb_2146	GGAAAGGACGAAACACCGGCTGCAGGATTCAATAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCAGGATTCAATAAACT	
2147	Uqcrb	Uqcrb_2147	GGAAAGGACGAAACACCGTAGTTTCAGCATCAAGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTTTCAGCATCAAGCAAG	
2148	Uqcrb	Uqcrb_2148	GGAAAGGACGAAACACCGAGCCATAAGAAGGCTTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCATAAGAAGGCTTCCTG	
2149	Cog6	Cog6_2149	GGAAAGGACGAAACACCGAGTCGTTGGGCATATCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGTTGGGCATATCACCG	
2150	Cog6	Cog6_2150	GGAAAGGACGAAACACCGTTGTGCAGCTTACGCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTGCAGCTTACGCGACAG	
2151	Cog6	Cog6_2151	GGAAAGGACGAAACACCGCGGACTCGAAGAAATTTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACTCGAAGAAATTTACG	
2152	Cog6	Cog6_2152	GGAAAGGACGAAACACCGGGTCAATCACTATACCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCAATCACTATACCTCAG	
2153	Slc39a8	Slc39a8_2153	GGAAAGGACGAAACACCGTCAGCTGCTGTAAGATCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCTGCTGTAAGATCGCG	
2154	Slc39a8	Slc39a8_2154	GGAAAGGACGAAACACCGAGGGGGTTAAAATCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGGTTAAAATCAATCCC	
2155	Slc39a8	Slc39a8_2155	GGAAAGGACGAAACACCGCGTTAGGCTCAGTGACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTTAGGCTCAGTGACAGCG	
2156	Slc39a8	Slc39a8_2156	GGAAAGGACGAAACACCGCGGCGCCAACCGGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGCCAACCGGAGCCTGT	
2157	Pigm	Pigm_2157	GGAAAGGACGAAACACCGGTTTGTACGACTTCCTGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTGTACGACTTCCTGAGG	
2158	Pigm	Pigm_2158	GGAAAGGACGAAACACCGCCGCGCGCTTCGTCACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCGCGCTTCGTCACGGAA	
2159	Pigm	Pigm_2159	GGAAAGGACGAAACACCGCGCGAAGCCATAGAACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCGAAGCCATAGAACACCG	
2160	Pigm	Pigm_2160	GGAAAGGACGAAACACCGAGTACGGAGAGAAATTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACGGAGAGAAATTATGG	
2161	Alg13	Alg13_2161	GGAAAGGACGAAACACCGGATCTTGTCATTAGCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCTTGTCATTAGCCACGC	
2162	Alg13	Alg13_2162	GGAAAGGACGAAACACCGGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAATGACTCAGTACGGAA	
2163	Alg13	Alg13_2163	GGAAAGGACGAAACACCGGGTTGTAACCCAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTGTAACCCAGACTCTCG	
2164	Alg13	Alg13_2164	GGAAAGGACGAAACACCGTTTCGACGAGCTCGTCGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCGACGAGCTCGTCGCAC	
2165	Slc25a26	Slc25a26_2165	GGAAAGGACGAAACACCGGGCATTCAAGGACTGTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCATTCAAGGACTGTACCG	
2166	Slc25a26	Slc25a26_2166	GGAAAGGACGAAACACCGAACACCCTTACCGTTAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACACCCTTACCGTTAGGAA	
2167	Slc25a26	Slc25a26_2167	GGAAAGGACGAAACACCGCCAGCCTTGTTAAATCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCCTTGTTAAATCCCTG	
2168	Slc25a26	Slc25a26_2168	GGAAAGGACGAAACACCGACTTTCAAGGATTCCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTTCAAGGATTCCCACAA	
2169	Sdhb	Sdhb_2169	GGAAAGGACGAAACACCGTGCGCCATGAACATCAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGCCATGAACATCAACGG	
2170	Sdhb	Sdhb_2170	GGAAAGGACGAAACACCGACAGTATCTGCAGTCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTATCTGCAGTCCATCG	
2171	Sdhb	Sdhb_2171	GGAAAGGACGAAACACCGACCTCGAATGCAGACGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTCGAATGCAGACGTACG	
2172	Sdhb	Sdhb_2172	GGAAAGGACGAAACACCGTAGAAGTTACTCAAATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAAGTTACTCAAATCCTG	
2173	Dnajc19	Dnajc19_2173	GGAAAGGACGAAACACCGAATTTCTTTCAGGCATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTTCTTTCAGGCATTCGG	
2174	Dnajc19	Dnajc19_2174	GGAAAGGACGAAACACCGTTAGCCCTACTGCCAATAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGCCCTACTGCCAATAAA	
2175	Dnajc19	Dnajc19_2175	GGAAAGGACGAAACACCGTTTACAAGCCATGAAGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTACAAGCCATGAAGCATG	
2176	Dnajc19	Dnajc19_2176	GGAAAGGACGAAACACCGCCAGCACAGTGGTAGCAGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCACAGTGGTAGCAGTC	
2177	Jagn1	Jagn1_2177	GGAAAGGACGAAACACCGGCACTACCAGATGAGGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACTACCAGATGAGGTACG	
2178	Jagn1	Jagn1_2178	GGAAAGGACGAAACACCGGTACCTCATCTGGTAGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACCTCATCTGGTAGTGCA	
2179	Jagn1	Jagn1_2179	GGAAAGGACGAAACACCGAGTGCATGGCGACGCGCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGCATGGCGACGCGCTCC	

No.	✱Oligo name	✱Oligo name	✱Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2180	Jagn1	Jagn1_2180	GGAAAGGACGAAACACCGCCGTCGGTGCCGGCCGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTCGGTGCCGGCCGCTCG	
2181	Dcxr	Dcxr_2181	GGAAAGGACGAAACACCGTATGGTTGGTCAGTGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGGTTGGTCAGTGCACGT	
2182	Dcxr	Dcxr_2182	GGAAAGGACGAAACACCGGGCGGTGAGTCGGACGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGGTGAGTCGGACGCGAG	
2183	Dcxr	Dcxr_2183	GGAAAGGACGAAACACCGGCCAAGGGCATGATAGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAAGGGCATGATAGCTCG	
2184	Dcxr	Dcxr_2184	GGAAAGGACGAAACACCGCCTAAGCAATGTGGGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTAAGCAATGTGGGACCCG	
2185	Coa6	Coa6_2185	GGAAAGGACGAAACACCGCAGCCCCTTCCATGAAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCCCTTCCATGAAGGAA	
2186	Coa6	Coa6_2186	GGAAAGGACGAAACACCGGCGGGACTTACCCACTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGGACTTACCCACTGCTG	
2187	Coa6	Coa6_2187	GGAAAGGACGAAACACCGCGTCCAGGCAGCGCCAGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCCAGGCAGCGCCAGTAC	
2188	Coa6	Coa6_2188	GGAAAGGACGAAACACCGGCGCTGCCTGGACGACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCTGCCTGGACGACAACG	
2189	Coq9	Coq9_2189	GGAAAGGACGAAACACCGCTCAGGTACACAGACCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGGTACACAGACCAGAG	
2190	Coq9	Coq9_2190	GGAAAGGACGAAACACCGGTGCCTTCCACACTGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCTTCCACACTGCCGTG	
2191	Coq9	Coq9_2191	GGAAAGGACGAAACACCGGGGGCCAGTGCTCAATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCCAGTGCTCAATGTAG	
2192	Coq9	Coq9_2192	GGAAAGGACGAAACACCGGTTGAGGCGAGCATTGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGAGGCGAGCATTGCACT	
2193	Npc2	Npc2_2193	GGAAAGGACGAAACACCGGTCAACATCACCTTTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAACATCACCTTTACCAG	
2194	Npc2	Npc2_2194	GGAAAGGACGAAACACCGTAAGGTGGGAGTTATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGGTGGGAGTTATAAAGG	
2195	Npc2	Npc2_2195	GGAAAGGACGAAACACCGCCCCTGCACTTCAAGGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCTGCACTTCAAGGACTG	
2196	Npc2	Npc2_2196	GGAAAGGACGAAACACCGGTCAGGCTCAGGAATAGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAGGCTCAGGAATAGGGA	
2197	Atad1	Atad1_2197	GGAAAGGACGAAACACCGTACGCACATGCATATTAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGCACATGCATATTAAGA	
2198	Atad1	Atad1_2198	GGAAAGGACGAAACACCGTAGATGCCATTGACCCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATGCCATTGACCCCACC	
2199	Atad1	Atad1_2199	GGAAAGGACGAAACACCGAAGGCTGTAGCTTTATGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCTGTAGCTTTATGGCA	
2200	Atad1	Atad1_2200	GGAAAGGACGAAACACCGCACTTATCAGTCAGTGTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTTATCAGTCAGTGTCGA	
2201	Apopt1	Apopt1_2201	GGAAAGGACGAAACACCGTGAGCGCCCTACGGATCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCGCCCTACGGATCACA	
2202	Apopt1	Apopt1_2202	GGAAAGGACGAAACACCGTGTGAAAATGAACGGGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGAAAATGAACGGGACGA	
2203	Apopt1	Apopt1_2203	GGAAAGGACGAAACACCGCAGTCTTGCCATGATTGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTCTTGCCATGATTGGAT	
2204	Apopt1	Apopt1_2204	GGAAAGGACGAAACACCGAGAATGGAATCAACAGTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATGGAATCAACAGTTCT	
2205	Gcsh	Gcsh_2205	GGAAAGGACGAAACACCGGCGGCGGCGCTCGGTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGCGGCGCTCGGTACACA	
2206	Gcsh	Gcsh_2206	GGAAAGGACGAAACACCGAGAGGAAGGTATTGGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGAAGGTATTGGAACGG	
2207	Gcsh	Gcsh_2207	GGAAAGGACGAAACACCGAATTCACAGAGAAACATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTCACAGAGAAACATGAG	
2208	Gcsh	Gcsh_2208	GGAAAGGACGAAACACCGGGGACAAAATTGAAAAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACAAAATTGAAAAAACA	
2209	Rnaseh2c	Rnaseh2c_2209	GGAAAGGACGAAACACCGCGTGAAGAAGCGATCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGAAGAAGCGATCTACCG	
2210	Rnaseh2c	Rnaseh2c_2210	GGAAAGGACGAAACACCGCGGCTGACTAGAACGTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCTGACTAGAACGTCGCA	
2211	Rnaseh2c	Rnaseh2c_2211	GGAAAGGACGAAACACCGAGGGTTTGCGGGATTCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGTTTGCGGGATTCGTGA	
2212	Rnaseh2c	Rnaseh2c_2212	GGAAAGGACGAAACACCGACCGTCTGCATCGTGGCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGTCTGCATCGTGGCGGA	
2213	Pdhb	Pdhb_2213	GGAAAGGACGAAACACCGTCTTAATTGTAGGTTAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAATTGTAGGTTAGCAG	
2214	Pdhb	Pdhb_2214	GGAAAGGACGAAACACCGGGGCACAGGCTGAAGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCACAGGCTGAAGGCCAG	
2215	Pdhb	Pdhb_2215	GGAAAGGACGAAACACCGTGAAGCTATTAATCAAGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGCTATTAATCAAGGTA	
2216	Pdhb	Pdhb_2216	GGAAAGGACGAAACACCGGCCATTCGTGATAATAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCATTCGTGATAATAACCC	
2217	Slc25a22	Slc25a22_2217	GGAAAGGACGAAACACCGGTGTCTTAGCCAGGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTCTTAGCCAGGTCGATG	
2218	Slc25a22	Slc25a22_2218	GGAAAGGACGAAACACCGATACATGCCGAAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACATGCCGAAGTAGCCCT	
2219	Slc25a22	Slc25a22_2219	GGAAAGGACGAAACACCGTGATTCAGGTTGGCAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATTCAGGTTGGCAAACAG	
2220	Slc25a22	Slc25a22_2220	GGAAAGGACGAAACACCGGACACCAGCTCTCTAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACCAGCTCTCTAAGGAT	
2221	Pomgnt1	Pomgnt1_2221	GGAAAGGACGAAACACCGGCCTTCGTGGGACGAAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTTCGTGGGACGAAAAGG	
2222	Pomgnt1	Pomgnt1_2222	GGAAAGGACGAAACACCGCACTCGGAGAGCAATCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTCGGAGAGCAATCAGCG	
2223	Pomgnt1	Pomgnt1_2223	GGAAAGGACGAAACACCGGCTGTGTGTTCATACCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGTGTTCATACCCCTA	
2224	Pomgnt1	Pomgnt1_2224	GGAAAGGACGAAACACCGGGGCTGAACTCAATAGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTGAACTCAATAGGCGT	
2225	Mto1	Mto1_2225	GGAAAGGACGAAACACCGTTCGACGTGGTAGTTATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGACGTGGTAGTTATCGG	
2226	Mto1	Mto1_2226	GGAAAGGACGAAACACCGAGTGTAACAGATAACCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTAACAGATAACCCTTG	
2227	Mto1	Mto1_2227	GGAAAGGACGAAACACCGATGGACTCTTTAGCGAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGACTCTTTAGCGAGTCG	
2228	Mto1	Mto1_2228	GGAAAGGACGAAACACCGACTTTATAAACAGAACATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTTATAAACAGAACATGC	
2229	Stt3b	Stt3b_2229	GGAAAGGACGAAACACCGAGGGTACATATCTCGGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGTACATATCTCGGTCAG	
2230	Stt3b	Stt3b_2230	GGAAAGGACGAAACACCGCGACAGCATGCAGACGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACAGCATGCAGACGACCG	
2231	Stt3b	Stt3b_2231	GGAAAGGACGAAACACCGGTCATCTATCTGACATACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATCTATCTGACATACAC	
2232	Stt3b	Stt3b_2232	GGAAAGGACGAAACACCGTACAGCAAGAGAGTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGCAAGAGAGTCTACAT	
2233	Sdhaf1	Sdhaf1_2233	GGAAAGGACGAAACACCGCGGACCCCGCGGGCGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACCCCGCGGGCGCACGA	
2234	Sdhaf1	Sdhaf1_2234	GGAAAGGACGAAACACCGGCAGCACGTCGGTTCGCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCACGTCGGTTCGCGGA	
2235	Sdhaf1	Sdhaf1_2235	GGAAAGGACGAAACACCGGTATCGAGTATCTGTATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATCGAGTATCTGTATCGC	
2236	Sdhaf1	Sdhaf1_2236	GGAAAGGACGAAACACCGAGGTACCCATGGCCGTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTACCCATGGCCGTGGCG	
2237	Ndufs3	Ndufs3_2237	GGAAAGGACGAAACACCGTTGTGGGTCACATCACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTGGGTCACATCACTCCG	
2238	Ndufs3	Ndufs3_2238	GGAAAGGACGAAACACCGTACGTGCTGCCACAGCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGTGCTGCCACAGCACGG	

No.	*Oligo name	*Oligo name	*Sequence(5’ to3’)	nt#	Remarks	5'	guide sequence	3'
2239	Ndufs3	Ndufs3_2239	GGAAAGGACGAAACACCGCAGCGTTGGGATGACTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCGTTGGGATGACTCCAT	
2240	Ndufs3	Ndufs3_2240	GGAAAGGACGAAACACCGGGGTGTCAGCTCATCTGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTGTCAGCTCATCTGCAT	
2241	G6pc3	G6pc3_2241	GGAAAGGACGAAACACCGTAGGCCGACTGCCAATAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCCGACTGCCAATAGGA	
2242	G6pc3	G6pc3_2242	GGAAAGGACGAAACACCGTTCCCGGGCTAGAGAATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCCGGGCTAGAGAATATG	
2243	G6pc3	G6pc3_2243	GGAAAGGACGAAACACCGGGGGCTCATTAGCCAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCTCATTAGCCAGCCAA	
2244	G6pc3	G6pc3_2244	GGAAAGGACGAAACACCGTAAAGAGAGTCCAATACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAAGAGAGTCCAATACATG	
2245	Lmbrd1	Lmbrd1_2245	GGAAAGGACGAAACACCGTTACAAACAGCAACGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACAAACAGCAACGCAACG	
2246	Lmbrd1	Lmbrd1_2246	GGAAAGGACGAAACACCGAAGGCACGTCTATCCCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCACGTCTATCCCTCGC	
2247	Lmbrd1	Lmbrd1_2247	GGAAAGGACGAAACACCGCATCATCTGTTTCAGGCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCATCTGTTTCAGGCGTA	
2248	Lmbrd1	Lmbrd1_2248	GGAAAGGACGAAACACCGAACGGTATTCTCAATCTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGTATTCTCAATCTGTA	
2249	Slc39a13	Slc39a13_2249	GGAAAGGACGAAACACCGATAAAGAAAGCGAGTCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAAGAAAGCGAGTCCTGG	
2250	Slc39a13	Slc39a13_2250	GGAAAGGACGAAACACCGTACACCTGTAACATCACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACCTGTAACATCACCCC	
2251	Slc39a13	Slc39a13_2251	GGAAAGGACGAAACACCGCTCACCTTCTGACTGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCTTCTGACTGTAACA	
2252	Slc39a13	Slc39a13_2252	GGAAAGGACGAAACACCGCTGGGGCTATGGGTCATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGGCTATGGGTCATCGC	
2253	Gpihbp1	Gpihbp1_2253	GGAAAGGACGAAACACCGGCAGGTATCAGTACACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGTATCAGTACACCACA	
2254	Gpihbp1	Gpihbp1_2254	GGAAAGGACGAAACACCGCACTGTGCAATATTCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTGTGCAATATTCCACCC	
2255	Gpihbp1	Gpihbp1_2255	GGAAAGGACGAAACACCGCTGTCAAGTGCTTCACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTCAAGTGCTTCACAGCG	
2256	Gpihbp1	Gpihbp1_2256	GGAAAGGACGAAACACCGCCTGCTTCCAGGGATCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCTTCCAGGGATCATGT	
2257	Tmem126b	Tmem126b_2257	GGAAAGGACGAAACACCGAAGATGGCACTTTATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGATGGCACTTTATAAACA	
2258	Tmem126b	Tmem126b_2258	GGAAAGGACGAAACACCGAAAGAGCTTGTAAGAAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGAGCTTGTAAGAAACGA	
2259	Tmem126b	Tmem126b_2259	GGAAAGGACGAAACACCGGCACTAATTGGCATGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACTAATTGGCATGGCATG	
2260	Tmem126b	Tmem126b_2260	GGAAAGGACGAAACACCGCCGTCTAGGTGACATAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTCTAGGTGACATAAGCA	
2261	Ndufaf4	Ndufaf4_2261	GGAAAGGACGAAACACCGTAACGTATACATTACCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACGTATACATTACCGGCA	
2262	Ndufaf4	Ndufaf4_2262	GGAAAGGACGAAACACCGAATATCACGGACATTCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATATCACGGACATTCCCAA	
2263	Ndufaf4	Ndufaf4_2263	GGAAAGGACGAAACACCGAAGGAATTCAGACTGCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGAATTCAGACTGCCGAT	
2264	Ndufaf4	Ndufaf4_2264	GGAAAGGACGAAACACCGCGCCTTAAGGAACTTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCTTAAGGAACTTCAACG	
2265	Dpm3	Dpm3_2265	GGAAAGGACGAAACACCGAAGTTAACACAGTGGCTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTTAACACAGTGGCTTTG	
2266	Dpm3	Dpm3_2266	GGAAAGGACGAAACACCGGCGATAGCCCACCGTGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGATAGCCCACCGTGCCCA	
2267	Dpm3	Dpm3_2267	GGAAAGGACGAAACACCGGGCCACAGGACCTCTCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCACAGGACCTCTCGGCA	
2268	Dpm3	Dpm3_2268	GGAAAGGACGAAACACCGACCAACAGGTAGGCAGGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAACAGGTAGGCAGGCAG	
2269	Mocos	Mocos_2269	GGAAAGGACGAAACACCGGCTTCAGCGCTATTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCAGCGCTATTACATCG	
2270	Mocos	Mocos_2270	GGAAAGGACGAAACACCGGCTGTAAATGCGCACCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTAAATGCGCACCACAG	
2271	Mocos	Mocos_2271	GGAAAGGACGAAACACCGGGTGTGGAAGCTGACAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTGGAAGCTGACAGTCG	
2272	Mocos	Mocos_2272	GGAAAGGACGAAACACCGCAAACTCACCCACGACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACTCACCCACGACACTG	
2273	Pmvk	Pmvk_2273	GGAAAGGACGAAACACCGAGCTGGTGAGTGACACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGGTGAGTGACACACGG	
2274	Pmvk	Pmvk_2274	GGAAAGGACGAAACACCGCTACAAGGAGACCTATCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACAAGGAGACCTATCGGA	
2275	Pmvk	Pmvk_2275	GGAAAGGACGAAACACCGGCTCTCTGGTCCACTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCTCTGGTCCACTCAAGG	
2276	Pmvk	Pmvk_2276	GGAAAGGACGAAACACCGTGTCTGTATCACAGCCCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCTGTATCACAGCCCCAT	
2277	Elac2	Elac2_2277	GGAAAGGACGAAACACCGTGTGCTGCGCAGGTGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCTGCGCAGGTGAACGG	
2278	Elac2	Elac2_2278	GGAAAGGACGAAACACCGGGGAAGAGTATCACTTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAAGAGTATCACTTACGA	
2279	Elac2	Elac2_2279	GGAAAGGACGAAACACCGCTCAGCGTGCCAACAGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGCGTGCCAACAGTTCG	
2280	Elac2	Elac2_2280	GGAAAGGACGAAACACCGATGCATTGGTCAAATGTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCATTGGTCAAATGTTGG	
2281	Nadk2	Nadk2_2281	GGAAAGGACGAAACACCGGCCTTACGGAGGTTCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTTACGGAGGTTCTCTCG	
2282	Nadk2	Nadk2_2282	GGAAAGGACGAAACACCGCCTCCGAGAGCTCCGCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCCGAGAGCTCCGCGTAG	
2283	Nadk2	Nadk2_2283	GGAAAGGACGAAACACCGACTTCATTGAGCGCTCTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCATTGAGCGCTCTCAC	
2284	Nadk2	Nadk2_2284	GGAAAGGACGAAACACCGGGTGGTAGCCCCGCCGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGTAGCCCCGCCGACGG	
2285	Elovl5	Elovl5_2285	GGAAAGGACGAAACACCGCTGCCAGGGAACACGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCCAGGGAACACGCAGCG	
2286	Elovl5	Elovl5_2286	GGAAAGGACGAAACACCGAGATGTTGAGCATGGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGTTGAGCATGGTAGCG	
2287	Elovl5	Elovl5_2287	GGAAAGGACGAAACACCGGACCATAGTACGAGTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCATAGTACGAGTACATG	
2288	Elovl5	Elovl5_2288	GGAAAGGACGAAACACCGATCCTGCAGTTGTATAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTGCAGTTGTATAACCT	
2289	Vars2	Vars2_2289	GGAAAGGACGAAACACCGATCCCCGGGTCTGATCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCCCGGGTCTGATCACGC	
2290	Vars2	Vars2_2290	GGAAAGGACGAAACACCGTCCAGATGACCCGAGATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGATGACCCGAGATACA	
2291	Vars2	Vars2_2291	GGAAAGGACGAAACACCGCCAACCCACGTCACCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACCCACGTCACCTCTCG	
2292	Vars2	Vars2_2292	GGAAAGGACGAAACACCGTGCAGATGGGCAGTACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGATGGGCAGTACCATG	
2293	Pink1	Pink1_2293	GGAAAGGACGAAACACCGCATGGTGGCTTCATACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGTGGCTTCATACACAG	
2294	Pink1	Pink1_2294	GGAAAGGACGAAACACCGGTCGGACTTGAGATCCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCGGACTTGAGATCCCGAT	
2295	Pink1	Pink1_2295	GGAAAGGACGAAACACCGCGAGGAACAGTGTGCGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGGAACAGTGTGCGACCG	
2296	Pink1	Pink1_2296	GGAAAGGACGAAACACCGCCAGCCCAGCTACCGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCCCAGCTACCGACTGG	
2297	Phkg2	Phkg2_2297	GGAAAGGACGAAACACCGAATGTGCATCTCTCGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTGCATCTCTCGCCGTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2298	Phkg2	Phkg2_2298	GGAAAGGACGAAACACCGCGGTAGCTCGATGGACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTAGCTCGATGGACACAG	
2299	Phkg2	Phkg2_2299	GGAAAGGACGAAACACCGCATGAAGCTAGAAGACTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGAAGCTAGAAGACTCGT	
2300	Phkg2	Phkg2_2300	GGAAAGGACGAAACACCGGTAGCATCAGGATTTGGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGCATCAGGATTTGGCGC	
2301	Isca1	Isca1_2301	GGAAAGGACGAAACACCGCTTGCTCACAGCCCGCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCTCACAGCCCGCACGG	
2302	Isca1	Isca1_2302	GGAAAGGACGAAACACCGGAGGTGACTCACCAGTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTGACTCACCAGTGTGA	
2303	Isca1	Isca1_2303	GGAAAGGACGAAACACCGAAAGTTGGCGTGCGAACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTTGGCGTGCGAACCAG	
2304	Isca1	Isca1_2304	GGAAAGGACGAAACACCGCAACAGTTACTTACATGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACAGTTACTTACATGCTC	
2305	Pycr2	Pycr2_2305	GGAAAGGACGAAACACCGGGTGCCCGTGGCATACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGCCCGTGGCATACACGG	
2306	Pycr2	Pycr2_2306	GGAAAGGACGAAACACCGGATGTGCCTCTCCTGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTGCCTCTCCTGCACGT	
2307	Pycr2	Pycr2_2307	GGAAAGGACGAAACACCGCGTGGGCAGGTCCATATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGGGCAGGTCCATATCCG	
2308	Pycr2	Pycr2_2308	GGAAAGGACGAAACACCGGATGCTATCACCGGGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCTATCACCGGGCTCAG	
2309	Gmppa	Gmppa_2309	GGAAAGGACGAAACACCGGGAGCCAGATCAAGTCTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCCAGATCAAGTCTGCA	
2310	Gmppa	Gmppa_2310	GGAAAGGACGAAACACCGTGGAAGGTTAAACTCCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGGTTAAACTCCTGCT	
2311	Gmppa	Gmppa_2311	GGAAAGGACGAAACACCGAGGACACAATCCCTCAACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACACAATCCCTCAACTA	
2312	Gmppa	Gmppa_2312	GGAAAGGACGAAACACCGATCAGTGACATCATCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAGTGACATCATCAACTG	
2313	Mrpl44	Mrpl44_2313	GGAAAGGACGAAACACCGAAACTGGGATTACCATGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTGGGATTACCATGCGG	
2314	Mrpl44	Mrpl44_2314	GGAAAGGACGAAACACCGTAGACTCTCAGTGCCTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGACTCTCAGTGCCTTCGG	
2315	Mrpl44	Mrpl44_2315	GGAAAGGACGAAACACCGTTCTTCACTCCCCGAACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTCACTCCCCGAACCGG	
2316	Mrpl44	Mrpl44_2316	GGAAAGGACGAAACACCGTGAGGCAGTTGTCTGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGCAGTTGTCTGTCACG	
2317	Ndufaf5	Ndufaf5_2317	GGAAAGGACGAAACACCGGCGACACACTCTATGAACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGACACACTCTATGAACTC	
2318	Ndufaf5	Ndufaf5_2318	GGAAAGGACGAAACACCGTCAGGTAGTCAAATTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGTAGTCAAATTTCATG	
2319	Ndufaf5	Ndufaf5_2319	GGAAAGGACGAAACACCGATCGAGCGGCAGTCGCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCGAGCGGCAGTCGCAGGG	
2320	Ndufaf5	Ndufaf5_2320	GGAAAGGACGAAACACCGTCAGCTAAAATATTCACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCTAAAATATTCACAGT	
2321	Hfe2	Hfe2_2321	GGAAAGGACGAAACACCGGGCTCACCGGACACGCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTCACCGGACACGCCGCG	
2322	Hfe2	Hfe2_2322	GGAAAGGACGAAACACCGGTTGGCTCCCGACGAAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGCTCCCGACGAAACCG	
2323	Hfe2	Hfe2_2323	GGAAAGGACGAAACACCGCTATGCCATGCACCGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATGCCATGCACCGCAGAG	
2324	Hfe2	Hfe2_2324	GGAAAGGACGAAACACCGACAAACTCGAGCCCCCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAAACTCGAGCCCCCAGGT	
2325	Afg3l2	Afg3l2_2325	GGAAAGGACGAAACACCGAAAAGCGATAATGAGTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGCGATAATGAGTACGG	
2326	Afg3l2	Afg3l2_2326	GGAAAGGACGAAACACCGGTTCGTGTGACCTTTACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGTGTGACCTTTACACC	
2327	Afg3l2	Afg3l2_2327	GGAAAGGACGAAACACCGGCCTGCCAGGATGACCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGCCAGGATGACCACAT	
2328	Afg3l2	Afg3l2_2328	GGAAAGGACGAAACACCGGTGAAGTTTAAAGATGTGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAAGTTTAAAGATGTGGC	
2329	Mtfmt	Mtfmt_2329	GGAAAGGACGAAACACCGGTGTACGAGTGGCCCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTACGAGTGGCCCGACGT	
2330	Mtfmt	Mtfmt_2330	GGAAAGGACGAAACACCGGTGCCTTCGCTATCCCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCTTCGCTATCCCCCAA	
2331	Mtfmt	Mtfmt_2331	GGAAAGGACGAAACACCGACCGTGTGGATTATCGGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGTGTGGATTATCGGAGC	
2332	Mtfmt	Mtfmt_2332	GGAAAGGACGAAACACCGGTCAAAACTTGGTGCCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAAAACTTGGTGCCAACA	
2333	Pitrm1	Pitrm1_2333	GGAAAGGACGAAACACCGTTGGGTGATAATGAGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGGTGATAATGAGTAGCG	
2334	Pitrm1	Pitrm1_2334	GGAAAGGACGAAACACCGATATAATGGCTATACACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATAATGGCTATACACGGG	
2335	Pitrm1	Pitrm1_2335	GGAAAGGACGAAACACCGAGGGAATTCCATATAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGAATTCCATATAACATG	
2336	Pitrm1	Pitrm1_2336	GGAAAGGACGAAACACCGGGTGAATTCTCTCTCCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAATTCTCTCTCCCCGG	
2337	Ccdc115	Ccdc115_2337	GGAAAGGACGAAACACCGAGCTGACGCCCAGACCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGACGCCCAGACCCCCG	
2338	Ccdc115	Ccdc115_2338	GGAAAGGACGAAACACCGACAGCTGCTCAGTGACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCTGCTCAGTGACCTGG	
2339	Ccdc115	Ccdc115_2339	GGAAAGGACGAAACACCGCTAACTCTTTGGTCTTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAACTCTTTGGTCTTGGTG	
2340	Ccdc115	Ccdc115_2340	GGAAAGGACGAAACACCGGACCTGAGGCTCCATACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCTGAGGCTCCATACGCG	
2341	Slc52a3	Slc52a3_2341	GGAAAGGACGAAACACCGGTGACCTCCTGGATACAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCTCCTGGATACAGGG	
2342	Slc52a3	Slc52a3_2342	GGAAAGGACGAAACACCGTGTCTCCGTGACATTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCTCCGTGACATTGACAC	
2343	Slc52a3	Slc52a3_2343	GGAAAGGACGAAACACCGGCTGGTGACTGAGTTGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGTGACTGAGTTGCCCG	
2344	Slc52a3	Slc52a3_2344	GGAAAGGACGAAACACCGGGGTCGGAAGCGGTGCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCGGAAGCGGTGCATCA	
2345	Ndufaf1	Ndufaf1_2345	GGAAAGGACGAAACACCGAGACGGCCGCCCATTACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGGCCGCCCATTACAAG	
2346	Ndufaf1	Ndufaf1_2346	GGAAAGGACGAAACACCGGAACAGGCCACACCTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACAGGCCACACCTACCCG	
2347	Ndufaf1	Ndufaf1_2347	GGAAAGGACGAAACACCGTCTGTATCTCCGAGTTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTATCTCCGAGTTCGTG	
2348	Ndufaf1	Ndufaf1_2348	GGAAAGGACGAAACACCGACTTCTGATAAGACAATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCTGATAAGACAATTGG	
2349	Cad	Cad_2349	GGAAAGGACGAAACACCGCGCAGGGGTACCCGACCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCAGGGGTACCCGACCGTG	
2350	Cad	Cad_2350	GGAAAGGACGAAACACCGAGGATTAGAACCTTTCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGATTAGAACCTTTCGTGG	
2351	Cad	Cad_2351	GGAAAGGACGAAACACCGATGGTGAGTGCCCACCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTGAGTGCCCACCACAA	
2352	Cad	Cad_2352	GGAAAGGACGAAACACCGCTCAGAAACTCTGTTACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGAAACTCTGTTACGGG	
2353	Rnaseh2a	Rnaseh2a_2353	GGAAAGGACGAAACACCGTGTCACACGATACAGCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCACACGATACAGCTGCG	
2354	Rnaseh2a	Rnaseh2a_2354	GGAAAGGACGAAACACCGGTAACAGATGGCGTAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAACAGATGGCGTAGACCA	
2355	Rnaseh2a	Rnaseh2a_2355	GGAAAGGACGAAACACCGAGACCTTGACAGAGAACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCTTGACAGAGAACGAG	
2356	Rnaseh2a	Rnaseh2a_2356	GGAAAGGACGAAACACCGGGCTCCTTGAGACACACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTCCTTGAGACACACAGC	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
2357	Ndufa11	Ndufa11_2357	GGAAAGGACGAAACACCGCAACCCCGCAGATTCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACCCCGCAGATTCCACCC	
2358	Ndufa11	Ndufa11_2358	GGAAAGGACGAAACACCGTCTTACCATGAGGTCCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTACCATGAGGTCCCCGA	
2359	Ndufa11	Ndufa11_2359	GGAAAGGACGAAACACCGGGCCGGTACACATTCACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCGGTACACATTCACTGC	
2360	Ndufa11	Ndufa11_2360	GGAAAGGACGAAACACCGAGCGGAGCCGATTATGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCGGAGCCGATTATGCCTG	
2361	Coa7	Coa7_2361	GGAAAGGACGAAACACCGGTTGAATCCTGTCACAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGAATCCTGTCACAACGT	
2362	Coa7	Coa7_2362	GGAAAGGACGAAACACCGCTACCAATGCTACCGCGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACCAATGCTACCGCGAGA	
2363	Coa7	Coa7_2363	GGAAAGGACGAAACACCGAACTGTGAGAAATACGGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTGTGAGAAATACGGGCA	
2364	Coa7	Coa7_2364	GGAAAGGACGAAACACCGAGGATGGCCAGCCTGACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGATGGCCAGCCTGACCTG	
2365	Slc25a32	Slc25a32_2365	GGAAAGGACGAAACACCGCGGATCTTCACGAGGTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGATCTTCACGAGGTCGAG	
2366	Slc25a32	Slc25a32_2366	GGAAAGGACGAAACACCGGGTTCTCGTACCGGACGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTCTCGTACCGGACGTGG	
2367	Slc25a32	Slc25a32_2367	GGAAAGGACGAAACACCGGGAGTAACCCCGAATGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTAACCCCGAATGTGTG	
2368	Slc25a32	Slc25a32_2368	GGAAAGGACGAAACACCGAGGTGTGCGTGGATTATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGTGCGTGGATTATACA	
2369	Agk	Agk_2369	GGAAAGGACGAAACACCGATATTGCAGACGGATTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATTGCAGACGGATTATGA	
2370	Agk	Agk_2370	GGAAAGGACGAAACACCGCTCTGAAAGATCCCCACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTGAAAGATCCCCACCGG	
2371	Agk	Agk_2371	GGAAAGGACGAAACACCGGAAATACCCTTTGCAAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAATACCCTTTGCAAGCTG	
2372	Agk	Agk_2372	GGAAAGGACGAAACACCGAGTACTGAGAAGAACAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACTGAGAAGAACAGATG	
2373	Fars2	Fars2_2373	GGAAAGGACGAAACACCGCACACACATCAGCGCATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACACATCAGCGCATCAG	
2374	Fars2	Fars2_2374	GGAAAGGACGAAACACCGACCTTAAACAAGTACTGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTAAACAAGTACTGACT	
2375	Fars2	Fars2_2375	GGAAAGGACGAAACACCGTGGAGGAAGCTGGTCATAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGGAAGCTGGTCATAGA	
2376	Fars2	Fars2_2376	GGAAAGGACGAAACACCGACTTGGTAAATCCTACCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTGGTAAATCCTACCCTC	
2377	Trnt1	Trnt1_2377	GGAAAGGACGAAACACCGCATGAATTAAGAATAGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGAATTAAGAATAGCAGG	
2378	Trnt1	Trnt1_2378	GGAAAGGACGAAACACCGATTCGCATGATCAACAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCGCATGATCAACAACAA	
2379	Trnt1	Trnt1_2379	GGAAAGGACGAAACACCGAACCTGTTCTCACCTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTGTTCTCACCTATGTG	
2380	Trnt1	Trnt1_2380	GGAAAGGACGAAACACCGGGCAGAATTGTCGACAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAGAATTGTCGACAGACC	
2381	Sdr9c7	Sdr9c7_2381	GGAAAGGACGAAACACCGCACCGCCGAATATAGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGCCGAATATAGCCACA	
2382	Sdr9c7	Sdr9c7_2382	GGAAAGGACGAAACACCGAGGTCAGCATCATTGAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTCAGCATCATTGAGCCA	
2383	Sdr9c7	Sdr9c7_2383	GGAAAGGACGAAACACCGCCGACTTGGTGACATCTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGACTTGGTGACATCTAGG	
2384	Sdr9c7	Sdr9c7_2384	GGAAAGGACGAAACACCGGCCAAACAACTGGTTGATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAAACAACTGGTTGATAG	
2385	Yars2	Yars2_2385	GGAAAGGACGAAACACCGCCACGAGCGCGATCACGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGAGCGCGATCACGTTG	
2386	Yars2	Yars2_2386	GGAAAGGACGAAACACCGTCCCCCCAGACGGTGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCCCCAGACGGTGTACTG	
2387	Yars2	Yars2_2387	GGAAAGGACGAAACACCGCTGGGCGGATCAGATCAGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGCGGATCAGATCAGTT	
2388	Yars2	Yars2_2388	GGAAAGGACGAAACACCGAGAACTCCTTGAACAAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTCCTTGAACAAGCCG	
2389	Taco1	Taco1_2389	GGAAAGGACGAAACACCGGCGATGCCTCGGGTTCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGATGCCTCGGGTTCCGCG	
2390	Taco1	Taco1_2390	GGAAAGGACGAAACACCGGCTGACTCGATGGTTGACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGACTCGATGGTTGACTT	
2391	Taco1	Taco1_2391	GGAAAGGACGAAACACCGATTGAGGCGTTATCAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGAGGCGTTATCAAACAG	
2392	Taco1	Taco1_2392	GGAAAGGACGAAACACCGCCACTTATTGTGTCCCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTTATTGTGTCCCGCCG	
2393	Pigw	Pigw_2393	GGAAAGGACGAAACACCGTGTGGCTGTCAGCATAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCTGTCAGCATAACTG	
2394	Pigw	Pigw_2394	GGAAAGGACGAAACACCGACAGTCAGAGTGATCACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTCAGAGTGATCACTAG	
2395	Pigw	Pigw_2395	GGAAAGGACGAAACACCGTGTTGTATCAGATATACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTATCAGATATACCAC	
2396	Pigw	Pigw_2396	GGAAAGGACGAAACACCGGTTCCAGTGAATGCCGTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCCAGTGAATGCCGTACT	
2397	Gtpbp3	Gtpbp3_2397	GGAAAGGACGAAACACCGGTGGAGTTTCACGTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAGTTTCACGTACACGG	
2398	Gtpbp3	Gtpbp3_2398	GGAAAGGACGAAACACCGCCACAACATTTGCCCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACAACATTTGCCCCCGAG	
2399	Gtpbp3	Gtpbp3_2399	GGAAAGGACGAAACACCGGTCAATGTAGGCCTCCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAATGTAGGCCTCCACAT	
2400	Gtpbp3	Gtpbp3_2400	GGAAAGGACGAAACACCGAGTCTCCAGCACGTCACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTCCAGCACGTCACGGG	
2401	Cox10	Cox10_2401	GGAAAGGACGAAACACCGTCTGTCCCGGAAGCCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTCCCGGAAGCCAAATG	
2402	Cox10	Cox10_2402	GGAAAGGACGAAACACCGGGGAGTGAATCCACTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAGTGAATCCACTCACAG	
2403	Cox10	Cox10_2403	GGAAAGGACGAAACACCGTATACAGGGATTGCCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATACAGGGATTGCCACACA	
2404	Cox10	Cox10_2404	GGAAAGGACGAAACACCGAGTTGGCAGCACAGGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGGCAGCACAGGATGCG	
2405	Tmem70	Tmem70_2405	GGAAAGGACGAAACACCGCGGGATCGCTTTCTGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGGATCGCTTTCTGGCGTG	
2406	Tmem70	Tmem70_2406	GGAAAGGACGAAACACCGGAAGGTACGGCAAGAATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGTACGGCAAGAATGCA	
2407	Tmem70	Tmem70_2407	GGAAAGGACGAAACACCGGCTGATTTATACTGGAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATTTATACTGGAAACC	
2408	Tmem70	Tmem70_2408	GGAAAGGACGAAACACCGGTAAGAAGGTGAAGCAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGAAGGTGAAGCAGCGT	
2409	Mipep	Mipep_2409	GGAAAGGACGAAACACCGTCCACGTTTGTATTCAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACGTTTGTATTCAACCT	
2410	Mipep	Mipep_2410	GGAAAGGACGAAACACCGGATTGCCACTTCACCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTGCCACTTCACCATCCG	
2411	Mipep	Mipep_2411	GGAAAGGACGAAACACCGTGGGACCCTCCCTACTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGACCCTCCCTACTACAG	
2412	Mipep	Mipep_2412	GGAAAGGACGAAACACCGCTGGGGCTTGACGTTGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGGCTTGACGTTGAAGG	
2413	Atp6ap2	Atp6ap2_2413	GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGCATATTAAGATCGCCA	
2414	Atp6ap2	Atp6ap2_2414	GGAAAGGACGAAACACCGTGAACTTGGGAAGCGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAACTTGGGAAGCGTTATG	
2415	Atp6ap2	Atp6ap2_2415	GGAAAGGACGAAACACCGCCGGTGGAATAGGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTGGAATAGGTTACCCA	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
2416	Atp6ap2	Atp6ap2_2416	GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGACAGTGCAGCTACGTCT	
2417	Wars2	Wars2_2417	GGAAAGGACGAAACACCGGAGCTGGGTGAACTTACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTGGGTGAACTTACAGG	
2418	Wars2	Wars2_2418	GGAAAGGACGAAACACCGCACACACGTTCCTGTCGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACACGTTCCTGTCGGGG	
2419	Wars2	Wars2_2419	GGAAAGGACGAAACACCGCAGAAGCATGATGGGACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAAGCATGATGGGACCGT	
2420	Wars2	Wars2_2420	GGAAAGGACGAAACACCGTGGTGTAAATGCTGCAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGTAAATGCTGCAATCG	
2421	Kynu	Kynu_2421	GGAAAGGACGAAACACCGGCGGATGGTAAAGCCACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGATGGTAAAGCCACGAG	
2422	Kynu	Kynu_2422	GGAAAGGACGAAACACCGCAAACGCCCTTGGATTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACGCCCTTGGATTGTAG	
2423	Kynu	Kynu_2423	GGAAAGGACGAAACACCGTCTTTAAGCCTACTCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTAAGCCTACTCCAAAG	
2424	Kynu	Kynu_2424	GGAAAGGACGAAACACCGCAACACCCCAGTCATGTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACACCCCAGTCATGTAAG	
2425	Slc29a3	Slc29a3_2425	GGAAAGGACGAAACACCGAATGATGGCCATGCACGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGATGGCCATGCACGCGA	
2426	Slc29a3	Slc29a3_2426	GGAAAGGACGAAACACCGGGGAAACTGCGCAGAACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAAACTGCGCAGAACCCG	
2427	Slc29a3	Slc29a3_2427	GGAAAGGACGAAACACCGCAAGGAAGACTGCTGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGAAGACTGCTGCCATG	
2428	Slc29a3	Slc29a3_2428	GGAAAGGACGAAACACCGACCAGAAAACACTCGAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGAAAACACTCGAACTG	
2429	Pdss2	Pdss2_2429	GGAAAGGACGAAACACCGATGATATTGGAATCTCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATATTGGAATCTCGACC	
2430	Pdss2	Pdss2_2430	GGAAAGGACGAAACACCGTGCGTGTCAGAACTACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGTGTCAGAACTACGACA	
2431	Pdss2	Pdss2_2431	GGAAAGGACGAAACACCGCGGCATAACCTACAACTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCATAACCTACAACTGCG	
2432	Pdss2	Pdss2_2432	GGAAAGGACGAAACACCGAGCTCTTCTACAGAACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCTTCTACAGAACACCA	
2433	Pex1	Pex1_2433	GGAAAGGACGAAACACCGTTGGTCCCAAGGAAATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGTCCCAAGGAAATACGT	
2434	Pex1	Pex1_2434	GGAAAGGACGAAACACCGTATTACCAAAGGAAGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTACCAAAGGAAGCATCG	
2435	Pex1	Pex1_2435	GGAAAGGACGAAACACCGGCAGCTTCATACGAACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCTTCATACGAACTCAG	
2436	Pex1	Pex1_2436	GGAAAGGACGAAACACCGAGTGTTGTGAAGAATAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTTGTGAAGAATAAACT	
2437	Cyp2u1	Cyp2u1_2437	GGAAAGGACGAAACACCGGCTCCTTAAATGGACCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCTTAAATGGACCAAAG	
2438	Cyp2u1	Cyp2u1_2438	GGAAAGGACGAAACACCGCAGGCGCAGCAGCTTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGCGCAGCAGCTTCGACG	
2439	Cyp2u1	Cyp2u1_2439	GGAAAGGACGAAACACCGGAAATGACGAAGCGTCGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAATGACGAAGCGTCGAGT	
2440	Cyp2u1	Cyp2u1_2440	GGAAAGGACGAAACACCGAAGTGTTCAGTGACCGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTGTTCAGTGACCGCCCG	
2441	Fuca1	Fuca1_2441	GGAAAGGACGAAACACCGACTGCCGAGCTGGTTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCCGAGCTGGTTCGATG	
2442	Fuca1	Fuca1_2442	GGAAAGGACGAAACACCGGTTCGGCCCACTGATCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCGGCCCACTGATCCGGG	
2443	Fuca1	Fuca1_2443	GGAAAGGACGAAACACCGCCAACTCACCGACCAAATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACTCACCGACCAAATCA	
2444	Fuca1	Fuca1_2444	GGAAAGGACGAAACACCGGTGATAGTGAATGACCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGATAGTGAATGACCGGTG	
2445	Pnpt1	Pnpt1_2445	GGAAAGGACGAAACACCGAATGTGTCGTTAACCCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTGTCGTTAACCCAACA	
2446	Pnpt1	Pnpt1_2446	GGAAAGGACGAAACACCGACCAACGGCATGAATTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAACGGCATGAATTGGGA	
2447	Pnpt1	Pnpt1_2447	GGAAAGGACGAAACACCGGAAGAGATCTGACTTCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGAGATCTGACTTCACTT	
2448	Pnpt1	Pnpt1_2448	GGAAAGGACGAAACACCGTTGCCATGCTATCAAAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCCATGCTATCAAAGTTG	
2449	Ubiad1	Ubiad1_2449	GGAAAGGACGAAACACCGGGCTTCCCGAACGATCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTTCCCGAACGATCCTGG	
2450	Ubiad1	Ubiad1_2450	GGAAAGGACGAAACACCGCCAAATCGAACAACATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAATCGAACAACATCCTG	
2451	Ubiad1	Ubiad1_2451	GGAAAGGACGAAACACCGCCAGCGGGCCGAAAGTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGGGCCGAAAGTGATG	
2452	Ubiad1	Ubiad1_2452	GGAAAGGACGAAACACCGTCAGAGCGGACAGGTAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGAGCGGACAGGTAGTAG	
2453	Tmprss6	Tmprss6_2453	GGAAAGGACGAAACACCGGGTTCGATGCCTACGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTCGATGCCTACGCACTG	
2454	Tmprss6	Tmprss6_2454	GGAAAGGACGAAACACCGGGAAAGCAATAGACTCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAAGCAATAGACTCCCGT	
2455	Tmprss6	Tmprss6_2455	GGAAAGGACGAAACACCGAAGACCTCATGATCAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACCTCATGATCAAAGTG	
2456	Tmprss6	Tmprss6_2456	GGAAAGGACGAAACACCGCCTTGATCCCGTCACACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGATCCCGTCACACGCA	
2457	Tars2	Tars2_2457	GGAAAGGACGAAACACCGCTTTAAGCTTCATCTGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTAAGCTTCATCTGATCG	
2458	Tars2	Tars2_2458	GGAAAGGACGAAACACCGAAGAGTCTATAATGCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGTCTATAATGCCCTGG	
2459	Tars2	Tars2_2459	GGAAAGGACGAAACACCGCTACTGCTACAGTGTAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACTGCTACAGTGTAACAC	
2460	Tars2	Tars2_2460	GGAAAGGACGAAACACCGTCCCCAAAGTAGAGTTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCCAAAGTAGAGTTACTG	
2461	Coq2	Coq2_2461	GGAAAGGACGAAACACCGACCAGTCTGGAAAACAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGTCTGGAAAACAACCT	
2462	Coq2	Coq2_2462	GGAAAGGACGAAACACCGATGCGCCTGGACAAGCCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCGCCTGGACAAGCCCAT	
2463	Coq2	Coq2_2463	GGAAAGGACGAAACACCGAGGGCCAATGGGAGCCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCCAATGGGAGCCCGCG	
2464	Coq2	Coq2_2464	GGAAAGGACGAAACACCGCTGTCCCCCAAGGAAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTCCCCCAAGGAAGACGA	
2465	Cars2	Cars2_2465	GGAAAGGACGAAACACCGTTAGATTTGACATTATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGATTTGACATTATCCGG	
2466	Cars2	Cars2_2466	GGAAAGGACGAAACACCGTCAGATCATTGCTTTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGATCATTGCTTTCATCG	
2467	Cars2	Cars2_2467	GGAAAGGACGAAACACCGGCACATCGAGTGCTCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACATCGAGTGCTCTACCA	
2468	Cars2	Cars2_2468	GGAAAGGACGAAACACCGACAGCAGCGACTTCGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCAGCGACTTCGCCCTG	
2469	Sars2	Sars2_2469	GGAAAGGACGAAACACCGCCGGTCCTATTACCTGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTCCTATTACCTGCGTG	
2470	Sars2	Sars2_2470	GGAAAGGACGAAACACCGCTGTACGAACACGCACGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTACGAACACGCACGAGA	
2471	Sars2	Sars2_2471	GGAAAGGACGAAACACCGTCGCTTCGAAGACCTTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGCTTCGAAGACCTTAACC	
2472	Sars2	Sars2_2472	GGAAAGGACGAAACACCGACGGTCCCAGACCTTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGTCCCAGACCTTCTGAG	
2473	Trmu	Trmu_2473	GGAAAGGACGAAACACCGAGGGGTATTTATGAAGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGTATTTATGAAGAACT	
2474	Trmu	Trmu_2474	GGAAAGGACGAAACACCGGTGATGGAGGCTATTCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGATGGAGGCTATTCTCCG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2475	Trmu	Trmu_2475	GGAAAGGACGAAACACCGGCTTATTGCAGTTGATGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTATTGCAGTTGATGTCG	
2476	Trmu	Trmu_2476	GGAAAGGACGAAACACCGATTCCAATACTCCTTCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCAATACTCCTTCACAT	
2477	Slc39a4	Slc39a4_2477	GGAAAGGACGAAACACCGGGTCCTGAATACGGATAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCTGAATACGGATAGTG	
2478	Slc39a4	Slc39a4_2478	GGAAAGGACGAAACACCGCAGTTGGGGAAGATCTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTTGGGGAAGATCTACAC	
2479	Slc39a4	Slc39a4_2479	GGAAAGGACGAAACACCGCATGCAGCGTGATATTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCAGCGTGATATTGGGA	
2480	Slc39a4	Slc39a4_2480	GGAAAGGACGAAACACCGTGGAGAGGGTCACACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGAGGGTCACACCCATG	
2481	Mccc1	Mccc1_2481	GGAAAGGACGAAACACCGGTTATGATCAAAGCAGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTATGATCAAAGCAGTCCG	
2482	Mccc1	Mccc1_2482	GGAAAGGACGAAACACCGAACAGGAGGAAGTATTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGGAGGAAGTATTACCA	
2483	Mccc1	Mccc1_2483	GGAAAGGACGAAACACCGCAGGAAGAAATCCCTCTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAAGAAATCCCTCTGCA	
2484	Mccc1	Mccc1_2484	GGAAAGGACGAAACACCGGCAGTACCTCAGCTTCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTACCTCAGCTTCGACA	
2485	Ddhd2	Ddhd2_2485	GGAAAGGACGAAACACCGAGAAAATGAGCAGATCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAATGAGCAGATCGGAA	
2486	Ddhd2	Ddhd2_2486	GGAAAGGACGAAACACCGTATTGTATTACACAACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTGTATTACACAACCCAA	
2487	Ddhd2	Ddhd2_2487	GGAAAGGACGAAACACCGGTCCACAATAGTCTGACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCACAATAGTCTGACAGT	
2488	Ddhd2	Ddhd2_2488	GGAAAGGACGAAACACCGTACCACAGTGAATATCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCACAGTGAATATCAACA	
2489	Pex13	Pex13_2489	GGAAAGGACGAAACACCGAGATGAGATAAGGACCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGAGATAAGGACCGCCA	
2490	Pex13	Pex13_2490	GGAAAGGACGAAACACCGTGGGAGGAAGATCATCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGAGGAAGATCATCTACA	
2491	Pex13	Pex13_2491	GGAAAGGACGAAACACCGGGCCTGGGAAGAATAGGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTGGGAAGAATAGGCGG	
2492	Pex13	Pex13_2492	GGAAAGGACGAAACACCGAGCCCTGAAACTGTTATAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCTGAAACTGTTATAGA	
2493	Chst14	Chst14_2493	GGAAAGGACGAAACACCGGAAACACCAAGTCACTGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACACCAAGTCACTGCGG	
2494	Chst14	Chst14_2494	GGAAAGGACGAAACACCGCGGACCTTGAGGGCCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACCTTGAGGGCCGTGTG	
2495	Chst14	Chst14_2495	GGAAAGGACGAAACACCGGCTGATGTTCGCTGTAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATGTTCGCTGTAATCG	
2496	Chst14	Chst14_2496	GGAAAGGACGAAACACCGTGTTACGGTAAGCAGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTACGGTAAGCAGACAGG	
2497	Cep89	Cep89_2497	GGAAAGGACGAAACACCGAACTGTCTGCCCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTGTCTGCCCAGTCAACG	
2498	Cep89	Cep89_2498	GGAAAGGACGAAACACCGTGAGATGTTAGGCTACGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGATGTTAGGCTACGGGG	
2499	Cep89	Cep89_2499	GGAAAGGACGAAACACCGACACTCTGTTCTGAATCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTCTGTTCTGAATCTAG	
2500	Cep89	Cep89_2500	GGAAAGGACGAAACACCGGTTTCACTTACCAACCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTCACTTACCAACCAGGG	
2501	Mfsd8	Mfsd8_2501	GGAAAGGACGAAACACCGAGCAATGTATGATCGGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAATGTATGATCGGACAA	
2502	Mfsd8	Mfsd8_2502	GGAAAGGACGAAACACCGTGGACCGAGAATAAAGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGACCGAGAATAAAGCCCA	
2503	Mfsd8	Mfsd8_2503	GGAAAGGACGAAACACCGGGATATGTACGCCTGGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATATGTACGCCTGGACCC	
2504	Mfsd8	Mfsd8_2504	GGAAAGGACGAAACACCGGAGCATCGTGTGGATGACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCATCGTGTGGATGACTT	
2505	Lrpprc	Lrpprc_2505	GGAAAGGACGAAACACCGAGCTGATAGACTACTGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGATAGACTACTGTCGG	
2506	Lrpprc	Lrpprc_2506	GGAAAGGACGAAACACCGGAATAGCCGAAGCATCTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATAGCCGAAGCATCTAAG	
2507	Lrpprc	Lrpprc_2507	GGAAAGGACGAAACACCGCCGAACTGAGTCTCGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAACTGAGTCTCGCCGAG	
2508	Lrpprc	Lrpprc_2508	GGAAAGGACGAAACACCGGAAAGACCTTCCGATCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGACCTTCCGATCACAG	
2509	B3gat3	B3gat3_2509	GGAAAGGACGAAACACCGGGACTCGCGGTGTCTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTCGCGGTGTCTCAGTG	
2510	B3gat3	B3gat3_2510	GGAAAGGACGAAACACCGTCTACACTGGCTGCTAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTACACTGGCTGCTAGTGG	
2511	B3gat3	B3gat3_2511	GGAAAGGACGAAACACCGAATGACATAGATAGTAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGACATAGATAGTAGGCA	
2512	B3gat3	B3gat3_2512	GGAAAGGACGAAACACCGACGGAGATCAGCTTGCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGAGATCAGCTTGCAACT	
2513	Ttc19	Ttc19_2513	GGAAAGGACGAAACACCGCAGGTCATAAGTGTACGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGTCATAAGTGTACGTGA	
2514	Ttc19	Ttc19_2514	GGAAAGGACGAAACACCGTCTGCATTTCAACTCTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGCATTTCAACTCTAGAG	
2515	Ttc19	Ttc19_2515	GGAAAGGACGAAACACCGAAGAGTCTAAGCACATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGTCTAAGCACATACCA	
2516	Ttc19	Ttc19_2516	GGAAAGGACGAAACACCGGCAACGATGAGTTATCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAACGATGAGTTATCTGCT	
2517	Ndufv2	Ndufv2_2517	GGAAAGGACGAAACACCGATTCAATACCTTGTTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCAATACCTTGTTCATAG	
2518	Ndufv2	Ndufv2_2518	GGAAAGGACGAAACACCGAAGGTGTAGTAGTGCAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGTGTAGTAGTGCAGACC	
2519	Ndufv2	Ndufv2_2519	GGAAAGGACGAAACACCGTAGTAAAAAACTACCCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTAAAAAACTACCCAGAA	
2520	Ndufv2	Ndufv2_2520	GGAAAGGACGAAACACCGCTCTTACCCACTGAGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTTACCCACTGAGCAGCG	
2521	Phykpl	Phykpl_2521	GGAAAGGACGAAACACCGAGACTAGCTCGACAGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACTAGCTCGACAGTACAC	
2522	Phykpl	Phykpl_2522	GGAAAGGACGAAACACCGCCAGAAGGAATGGGTCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGAAGGAATGGGTCCATG	
2523	Phykpl	Phykpl_2523	GGAAAGGACGAAACACCGAGTACCTGTACGATGAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACCTGTACGATGAGCAA	
2524	Phykpl	Phykpl_2524	GGAAAGGACGAAACACCGCGTGTTGAAGTATTCTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGTTGAAGTATTCTACAC	
2525	Appl1	Appl1_2525	GGAAAGGACGAAACACCGCCGACTGTACCTATTAATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGACTGTACCTATTAATTG	
2526	Appl1	Appl1_2526	GGAAAGGACGAAACACCGAACTTAATGAGTCAAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTAATGAGTCAAGCCCG	
2527	Appl1	Appl1_2527	GGAAAGGACGAAACACCGGCCTGCATGTATCCCAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGCATGTATCCCAGTAG	
2528	Appl1	Appl1_2528	GGAAAGGACGAAACACCGAATTGTATCAAGCTATGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTGTATCAAGCTATGCAT	
2529	Glrx5	Glrx5_2529	GGAAAGGACGAAACACCGGCACGGTGTTCGCGACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACGGTGTTCGCGACTATG	
2530	Glrx5	Glrx5_2530	GGAAAGGACGAAACACCGGCGTTGCTGAAGCCGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTTGCTGAAGCCGCACTG	
2531	Glrx5	Glrx5_2531	GGAAAGGACGAAACACCGAGGTGGTGGTGTTCCTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGGTGGTGTTCCTCAAG	
2532	Glrx5	Glrx5_2532	GGAAAGGACGAAACACCGGGAGTAGTCTTTAATACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTAGTCTTTAATACCTG	
2533	Pmpcb	Pmpcb_2533	GGAAAGGACGAAACACCGGAAATATAACTAACCTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAATATAACTAACCTCCGG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2534	Pmpcb	Pmpcb_2534	GGAAAGGACGAAACACCGGGACCGACTAAGAAGCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACCGACTAAGAAGCACAC	
2535	Pmpcb	Pmpcb_2535	GGAAAGGACGAAACACCGGAGACAGATCGTGTCTGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACAGATCGTGTCTGGAT	
2536	Pmpcb	Pmpcb_2536	GGAAAGGACGAAACACCGCTTCCAGTGAACTTGCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCAGTGAACTTGCAGGG	
2537	Slc25a42	Slc25a42_2537	GGAAAGGACGAAACACCGGCTGGGTGTCATTCCCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGGTGTCATTCCCTATG	
2538	Slc25a42	Slc25a42_2538	GGAAAGGACGAAACACCGAGGAATCACTCGCACCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAATCACTCGCACCATGG	
2539	Slc25a42	Slc25a42_2539	GGAAAGGACGAAACACCGGTACGTGAGGGAAGCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACGTGAGGGAAGCCGCAG	
2540	Slc25a42	Slc25a42_2540	GGAAAGGACGAAACACCGCTTCATCCGAATCTCGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCATCCGAATCTCGAGAG	
2541	Mcee	Mcee_2541	GGAAAGGACGAAACACCGTGGAACTGCTTCATCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAACTGCTTCATCCACTG	
2542	Mcee	Mcee_2542	GGAAAGGACGAAACACCGTTCAAGAATCCAGTCCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAAGAATCCAGTCCTGTG	
2543	Mcee	Mcee_2543	GGAAAGGACGAAACACCGAACATCCCTGTAAAATGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATCCCTGTAAAATGACG	
2544	Mcee	Mcee_2544	GGAAAGGACGAAACACCGTGCAACTGAAGTTTGGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAACTGAAGTTTGGACTC	
2545	Dnm1l	Dnm1l_2545	GGAAAGGACGAAACACCGAATCGTGTTACAATACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCGTGTTACAATACTCTG	
2546	Dnm1l	Dnm1l_2546	GGAAAGGACGAAACACCGGCACAAATAAAGCAGGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAAATAAAGCAGGACGG	
2547	Dnm1l	Dnm1l_2547	GGAAAGGACGAAACACCGGATGCCATGGATGTATTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCCATGGATGTATTGAT	
2548	Dnm1l	Dnm1l_2548	GGAAAGGACGAAACACCGGTGACCACACCAGTTCCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCACACCAGTTCCTCT	
2549	Plce1	Plce1_2549	GGAAAGGACGAAACACCGCAGGTATTCATCGCGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGTATTCATCGCGCAGCG	
2550	Plce1	Plce1_2550	GGAAAGGACGAAACACCGGTGACTCCTCGGATCCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACTCCTCGGATCCATGG	
2551	Plce1	Plce1_2551	GGAAAGGACGAAACACCGCACCGGCCATCAGCTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGGCCATCAGCTCAAGG	
2552	Plce1	Plce1_2552	GGAAAGGACGAAACACCGGTGCAGTAATCTATTGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCAGTAATCTATTGTCCG	
2553	Abcb6	Abcb6_2553	GGAAAGGACGAAACACCGCTCCAGAGGTCACATAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCAGAGGTCACATAACGC	
2554	Abcb6	Abcb6_2554	GGAAAGGACGAAACACCGTGAAGTAGACCGCTATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGTAGACCGCTATCGAG	
2555	Abcb6	Abcb6_2555	GGAAAGGACGAAACACCGGTGCAGCAGTTTACGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCAGCAGTTTACGTCCCG	
2556	Abcb6	Abcb6_2556	GGAAAGGACGAAACACCGTAGGTGCCAAACCAGTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGTGCCAAACCAGTTGAG	
2557	Dmgdh	Dmgdh_2557	GGAAAGGACGAAACACCGTTAGCCGGACTGTATAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGCCGGACTGTATAACCC	
2558	Dmgdh	Dmgdh_2558	GGAAAGGACGAAACACCGAGGATCCTTCCAGGTCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGATCCTTCCAGGTCGCGG	
2559	Dmgdh	Dmgdh_2559	GGAAAGGACGAAACACCGTGGGATGTGGAGACTCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGATGTGGAGACTCCACA	
2560	Dmgdh	Dmgdh_2560	GGAAAGGACGAAACACCGACAGCATCAAACTTTACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCATCAAACTTTACGAG	
2561	Lonp1	Lonp1_2561	GGAAAGGACGAAACACCGTCATTCGCAACTTGTCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATTCGCAACTTGTCTCCG	
2562	Lonp1	Lonp1_2562	GGAAAGGACGAAACACCGGGCAGCGACGAGACCTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAGCGACGAGACCTCCGA	
2563	Lonp1	Lonp1_2563	GGAAAGGACGAAACACCGGCGCTTTATCAAGATCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCTTTATCAAGATCGTGG	
2564	Lonp1	Lonp1_2564	GGAAAGGACGAAACACCGCAAGGCGATGATATCCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGCGATGATATCCCGAA	
2565	Opa1	Opa1_2565	GGAAAGGACGAAACACCGGCGCCTGCGAGAGCTCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCTGCGAGAGCTCGACA	
2566	Opa1	Opa1_2566	GGAAAGGACGAAACACCGAGGTTGTACTGTTAGCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTTGTACTGTTAGCCCCG	
2567	Opa1	Opa1_2567	GGAAAGGACGAAACACCGAGAGCGTGTCATCATCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCGTGTCATCATCTCGC	
2568	Opa1	Opa1_2568	GGAAAGGACGAAACACCGAAGTGACAAGCATTACAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTGACAAGCATTACAGGA	
2569	Ehhadh	Ehhadh_2569	GGAAAGGACGAAACACCGTTCATATGGATGCTTCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCATATGGATGCTTCACGG	
2570	Ehhadh	Ehhadh_2570	GGAAAGGACGAAACACCGCCACATCATGAGGTTACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACATCATGAGGTTACTAG	
2571	Ehhadh	Ehhadh_2571	GGAAAGGACGAAACACCGGTAAACCCATAGAACCCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAACCCATAGAACCCCGC	
2572	Ehhadh	Ehhadh_2572	GGAAAGGACGAAACACCGTCACTATGGCTCTAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACTATGGCTCTAACCGTA	
2573	Acbd5	Acbd5_2573	GGAAAGGACGAAACACCGAGTGTATGAAACCAGATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTATGAAACCAGATTTG	
2574	Acbd5	Acbd5_2574	GGAAAGGACGAAACACCGCCAGGCCGTGAAAGTTTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGCCGTGAAAGTTTACA	
2575	Acbd5	Acbd5_2575	GGAAAGGACGAAACACCGGGAGCAATTTGGACAAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCAATTTGGACAAGAAG	
2576	Acbd5	Acbd5_2576	GGAAAGGACGAAACACCGAAAGCTACCTTTATAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCTACCTTTATAGCCAT	
2577	Gbe1	Gbe1_2577	GGAAAGGACGAAACACCGGGCTATGAACCACATCTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTATGAACCACATCTAGG	
2578	Gbe1	Gbe1_2578	GGAAAGGACGAAACACCGAATCCCCCCTGATACCTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCCCCCCTGATACCTCAT	
2579	Gbe1	Gbe1_2579	GGAAAGGACGAAACACCGAGACTCGATAACAATAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACTCGATAACAATAGCAG	
2580	Gbe1	Gbe1_2580	GGAAAGGACGAAACACCGGAACTATGATTGGATACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTATGATTGGATACACT	
2581	Gale	Gale_2581	GGAAAGGACGAAACACCGATCTTCACCGATGCGCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTTCACCGATGCGCCCAG	
2582	Gale	Gale_2582	GGAAAGGACGAAACACCGAGAACTTGGACTTGCCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTTGGACTTGCCGTAG	
2583	Gale	Gale_2583	GGAAAGGACGAAACACCGTTAACTCTATAGTAGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAACTCTATAGTAGTCCAG	
2584	Gale	Gale_2584	GGAAAGGACGAAACACCGCTGGGGGTTCCCGTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGGGTTCCCGTACACGG	
2585	Isca2	Isca2_2585	GGAAAGGACGAAACACCGCTTGTCCCTAACTGCCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGTCCCTAACTGCCGAGG	
2586	Isca2	Isca2_2586	GGAAAGGACGAAACACCGTCATTCCTAGGCGCTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATTCCTAGGCGCTCGGGA	
2587	Isca2	Isca2_2587	GGAAAGGACGAAACACCGGTCCTCCTTGCCTGTCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCTCCTTGCCTGTCGTCG	
2588	Isca2	Isca2_2588	GGAAAGGACGAAACACCGCTCAGGCTGCAAGTAGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGGCTGCAAGTAGAGGG	
2589	Slc6a19	Slc6a19_2589	GGAAAGGACGAAACACCGATCGGTCAGAGGCTACGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCGGTCAGAGGCTACGCAA	
2590	Slc6a19	Slc6a19_2590	GGAAAGGACGAAACACCGACAGTCATCAAAGCGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTCATCAAAGCGCTCAG	
2591	Slc6a19	Slc6a19_2591	GGAAAGGACGAAACACCGAGCTGAGCAACCCCAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGAGCAACCCCAACACG	
2592	Slc6a19	Slc6a19_2592	GGAAAGGACGAAACACCGTCCGTGGCATCGAGACCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGTGGCATCGAGACCACT	

No.	*Oligo name	*Oligo name	*Sequence(5' to3')	nt#	Remarks	5'	guide sequence	3'
2593	Pank2	Pank2_2593	GGAAAGGACGAAACACCGGTCCGCAGACTCGCCGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCGCAGACTCGCCGACCG	
2594	Pank2	Pank2_2594	GGAAAGGACGAAACACCGGGATCCGTAAGCCACATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATCCGTAAGCCACATTGG	
2595	Pank2	Pank2_2595	GGAAAGGACGAAACACCGAAAGCAGGCATGTCATGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCAGGCATGTCATGGGT	
2596	Pank2	Pank2_2596	GGAAAGGACGAAACACCGCGAGTAGCGCGGCGCCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGTAGCGCGGCGCCGTCG	
2597	Mgme1	Mgme1_2597	GGAAAGGACGAAACACCGAAAGTGGAGAAACTCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTGGAGAAACTCACAGG	
2598	Mgme1	Mgme1_2598	GGAAAGGACGAAACACCGGGAGAAGAGCACCCCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAAGAGCACCCCCAGTG	
2599	Mgme1	Mgme1_2599	GGAAAGGACGAAACACCGCTAAACGAGAGTACTTCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAAACGAGAGTACTTCGCT	
2600	Mgme1	Mgme1_2600	GGAAAGGACGAAACACCGCAAACAGTTCCATAAAGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACAGTTCCATAAAGCCT	
2601	Pck2	Pck2_2601	GGAAAGGACGAAACACCGTGCGTATTATGACCCGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGTATTATGACCCGCCTG	
2602	Pck2	Pck2_2602	GGAAAGGACGAAACACCGTGATTGTAACTCCTTCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATTGTAACTCCTTCGCAG	
2603	Pck2	Pck2_2603	GGAAAGGACGAAACACCGAGGGTTTGGATGCTACGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGTTTGGATGCTACGGCA	
2604	Pck2	Pck2_2604	GGAAAGGACGAAACACCGATGGAAGCACATACATAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGAAGCACATACATAATG	
2605	Shpk	Shpk_2605	GGAAAGGACGAAACACCGCATGGTTTGAAATCCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGTTTGAAATCCCAAAG	
2606	Shpk	Shpk_2606	GGAAAGGACGAAACACCGGACCAGAATGCCGCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCAGAATGCCGCTAGCTG	
2607	Shpk	Shpk_2607	GGAAAGGACGAAACACCGGCAGGCTGTGAATGGATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGCTGTGAATGGATGGA	
2608	Shpk	Shpk_2608	GGAAAGGACGAAACACCGGTAAGGGAAGAAGGCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGGGAAGAAGGCAACTG	
2609	Pomk	Pomk_2609	GGAAAGGACGAAACACCGCCCATTCTGAAGTAGCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCATTCTGAAGTAGCCCGG	
2610	Pomk	Pomk_2610	GGAAAGGACGAAACACCGGAGTGAGCACGTGGTCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTGAGCACGTGGTCACGC	
2611	Pomk	Pomk_2611	GGAAAGGACGAAACACCGCACATGACCCTCGTGCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACATGACCCTCGTGCCCAG	
2612	Pomk	Pomk_2612	GGAAAGGACGAAACACCGCGCCACGTTCATAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCACGTTCATAAGGGCCA	
2613	Dhcr24	Dhcr24_2613	GGAAAGGACGAAACACCGACCTGACCCATAGACACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTGACCCATAGACACCAA	
2614	Dhcr24	Dhcr24_2614	GGAAAGGACGAAACACCGGTAAGACCTTCATGTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGACCTTCATGTGCACG	
2615	Dhcr24	Dhcr24_2615	GGAAAGGACGAAACACCGAGATGCTGCGCGTGTGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGCTGCGCGTGTGTCGG	
2616	Dhcr24	Dhcr24_2616	GGAAAGGACGAAACACCGGTCTGCCAGGATCAGCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTGCCAGGATCAGCTCGT	
2617	Atp13a2	Atp13a2_2617	GGAAAGGACGAAACACCGCGTCATCACAGGTACGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCATCACAGGTACGACCG	
2618	Atp13a2	Atp13a2_2618	GGAAAGGACGAAACACCGCCAGCTACATGACACCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCTACATGACACCCCGG	
2619	Atp13a2	Atp13a2_2619	GGAAAGGACGAAACACCGGGGACCCCGTGTGCTAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACCCCGTGTGCTAGCAG	
2620	Atp13a2	Atp13a2_2620	GGAAAGGACGAAACACCGTGTGGTAGTGACATGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGTAGTGACATGGCCAG	
2621	Ppa2	Ppa2_2621	GGAAAGGACGAAACACCGTGGTTGTGGAAATACCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTTGTGGAAATACCTCGG	
2622	Ppa2	Ppa2_2622	GGAAAGGACGAAACACCGCCGAACATCTTCCCTCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAACATCTTCCCTCACAA	
2623	Ppa2	Ppa2_2623	GGAAAGGACGAAACACCGTACAGGGACATGACGCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGGGACATGACGCGGCG	
2624	Ppa2	Ppa2_2624	GGAAAGGACGAAACACCGTAAGAGCACCGACTGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGAGCACCGACTGCTGTG	
2625	Ndufs7	Ndufs7_2625	GGAAAGGACGAAACACCGAAGCGGTCCATGTCATAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGGTCCATGTCATAGCG	
2626	Ndufs7	Ndufs7_2626	GGAAAGGACGAAACACCGCATCAGAGTGTAGCCACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCAGAGTGTAGCCACTGA	
2627	Ndufs7	Ndufs7_2627	GGAAAGGACGAAACACCGTGGCACGCTTACCAACAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCACGCTTACCAACAAGA	
2628	Ndufs7	Ndufs7_2628	GGAAAGGACGAAACACCGCCCGGCGTGCCCAGTTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCGGCGTGCCCAGTTGATG	
2629	Secisbp2	Secisbp2_2629	GGAAAGGACGAAACACCGAGTACGACTACAGCCAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACGACTACAGCCAAGCA	
2630	Secisbp2	Secisbp2_2630	GGAAAGGACGAAACACCGCTGTACAAATGGATAGTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTACAAATGGATAGTAGG	
2631	Secisbp2	Secisbp2_2631	GGAAAGGACGAAACACCGACCGTCAGGACTTCATAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGTCAGGACTTCATAACT	
2632	Secisbp2	Secisbp2_2632	GGAAAGGACGAAACACCGTGCCGAACAATATAACCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCGAACAATATAACCCAT	
2633	Oplah	Oplah_2633	GGAAAGGACGAAACACCGTGGTGCGGATTGTTCCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGCGGATTGTTCCTCGG	
2634	Oplah	Oplah_2634	GGAAAGGACGAAACACCGTGACTGTCATCACACCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTGTCATCACACCGGTG	
2635	Oplah	Oplah_2635	GGAAAGGACGAAACACCGCTGTGCTTCGTGAACCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGCTTCGTGAACCACAT	
2636	Oplah	Oplah_2636	GGAAAGGACGAAACACCGGCTCCAAAGTCACCAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCAAAGTCACCAGCACG	
2637	Lyrm7	Lyrm7_2637	GGAAAGGACGAAACACCGTCTTAACAGATGATGAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAACAGATGATGAAACT	
2638	Lyrm7	Lyrm7_2638	GGAAAGGACGAAACACCGAATGATAAGAGAGCATTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGATAAGAGAGCATTGGA	
2639	Lyrm7	Lyrm7_2639	GGAAAGGACGAAACACCGAGCTCTTTAAAACACTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCTTTAAAACACTGCAC	
2640	Lyrm7	Lyrm7_2640	GGAAAGGACGAAACACCGGATGAAACTAGGTTCTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAAACTAGGTTCTGATG	
2641	Ndufaf2	Ndufaf2_2641	GGAAAGGACGAAACACCGCAGGAGACATCCCAACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAGACATCCCAACCGAG	
2642	Ndufaf2	Ndufaf2_2642	GGAAAGGACGAAACACCGATTCTTACCTCCATAGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCTTACCTCCATAGTGGG	
2643	Ndufaf2	Ndufaf2_2643	GGAAAGGACGAAACACCGACGTGGGCACGGACCATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTGGGCACGGACCATCTG	
2644	Ndufaf2	Ndufaf2_2644	GGAAAGGACGAAACACCGTTGGAGCGCCTTGTCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGAGCGCCTTGTCCAGGG	
2645	Gns	Gns_2645	GGAAAGGACGAAACACCGCCAAAGTGTTGTTAACGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAAGTGTTGTTAACGACG	
2646	Gns	Gns_2646	GGAAAGGACGAAACACCGTGCTGGGAAGTATTTAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTGGGAAGTATTTAAACG	
2647	Gns	Gns_2647	GGAAAGGACGAAACACCGTCAGACAACGGCTACCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGACAACGGCTACCACAC	
2648	Gns	Gns_2648	GGAAAGGACGAAACACCGCAGAGGAACCTACCGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGGAACCTACCGTCCCG	
2649	Fastkd2	Fastkd2_2649	GGAAAGGACGAAACACCGATGTGAATGCGCTTCGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTGAATGCGCTTCGAGCA	
2650	Fastkd2	Fastkd2_2650	GGAAAGGACGAAACACCGTGAAAGAGGTATCTAACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAAGAGGTATCTAACAGA	
2651	Fastkd2	Fastkd2_2651	GGAAAGGACGAAACACCGTAGCATTAAGGCTGAACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCATTAAGGCTGAACAAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2652	Fastkd2	Fastkd2_2652	GGAAAGGACGAAACACCGATAAGCTTGTCCATCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAGCTTGTCCATCAAACC	
2653	Mff	Mff_2653	GGAAAGGACGAAACACCGGGATAAGCGACAAAATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATAAGCGACAAAATGCCA	
2654	Mff	Mff_2654	GGAAAGGACGAAACACCGGCAAGTCCCAGAGAGGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAGTCCCAGAGAGGATCG	
2655	Mff	Mff_2655	GGAAAGGACGAAACACCGAGGTATTAGTCAGCGAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTATTAGTCAGCGAATGA	
2656	Mff	Mff_2656	GGAAAGGACGAAACACCGTGTTCGCCAAAATGGACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCGCCAAAATGGACAGT	
2657	Ispd	Ispd_2657	GGAAAGGACGAAACACCGCGGCGGCCACGGTTCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGGCCACGGTTCCAGGG	
2658	Ispd	Ispd_2658	GGAAAGGACGAAACACCGTAAGCGCATCTCACTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGCGCATCTCACTAGCTG	
2659	Ispd	Ispd_2659	GGAAAGGACGAAACACCGTGGTCACTTAGACCACTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTCACTTAGACCACTCAC	
2660	Ispd	Ispd_2660	GGAAAGGACGAAACACCGTCTTAGCAGCTAAGGAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAGCAGCTAAGGAACAT	
2661	Cant1	Cant1_2661	GGAAAGGACGAAACACCGGGAGTGGGATAAAGACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTGGGATAAAGACCACG	
2662	Cant1	Cant1_2662	GGAAAGGACGAAACACCGCAGCACCCACAAAGGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCACCCACAAAGGACGTG	
2663	Cant1	Cant1_2663	GGAAAGGACGAAACACCGCCATCAGAAAGGATCACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCAGAAAGGATCACCCA	
2664	Cant1	Cant1_2664	GGAAAGGACGAAACACCGGGAGTGGACCACCACGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTGGACCACCACGACAG	
2665	Coa5	Coa5_2665	GGAAAGGACGAAACACCGCCGGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTATTATGAGGACAAGC	
2666	Coa5	Coa5_2666	GGAAAGGACGAAACACCGATCCGCTACCTGGAGCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCGCTACCTGGAGCACAC	
2667	Coa5	Coa5_2667	GGAAAGGACGAAACACCGGCGGGCGTGAAGGAGGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGGCGTGAAGGAGGATCT	
2668	Coa5	Coa5_2668	GGAAAGGACGAAACACCGGCCGGAGGGCGGCGCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCGGAGGGCGGCGCGTGTG	
2669	Abhd12	Abhd12_2669	GGAAAGGACGAAACACCGTGACTCAGTAGGAACACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTCAGTAGGAACACCAT	
2670	Abhd12	Abhd12_2670	GGAAAGGACGAAACACCGGATAATCCTGTGTATATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAATCCTGTGTATATTTG	
2671	Abhd12	Abhd12_2671	GGAAAGGACGAAACACCGGCCGCACAGCGCATCCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCGCACAGCGCATCCGACG	
2672	Abhd12	Abhd12_2672	GGAAAGGACGAAACACCGGCAGGTATAGTATGATGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGTATAGTATGATGGCA	
2673	Grhpr	Grhpr_2673	GGAAAGGACGAAACACCGTGGAGCCCATTATGGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGCCCATTATGGATGTG	
2674	Grhpr	Grhpr_2674	GGAAAGGACGAAACACCGTCCAGAGATTTCTTTACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGAGATTTCTTTACACG	
2675	Grhpr	Grhpr_2675	GGAAAGGACGAAACACCGCTTTGGATGAAATCAAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGGATGAAATCAAGAAG	
2676	Grhpr	Grhpr_2676	GGAAAGGACGAAACACCGAAGAAACTTCTGGATGCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAACTTCTGGATGCCGC	
2677	Cog2	Cog2_2677	GGAAAGGACGAAACACCGGACGGTGTGCCAACAAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACGGTGTGCCAACAAAGGT	
2678	Cog2	Cog2_2678	GGAAAGGACGAAACACCGTGCCACCATTGATAAGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCACCATTGATAAGACAC	
2679	Cog2	Cog2_2679	GGAAAGGACGAAACACCGTCTTCTCGTAACTGTCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCTCGTAACTGTCCCAA	
2680	Cog2	Cog2_2680	GGAAAGGACGAAACACCGGTGATGCCAGCTATACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGATGCCAGCTATACGCTG	
2681	Trmt5	Trmt5_2681	GGAAAGGACGAAACACCGAGAGGAAAATATGCTGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGAAAATATGCTGACCA	
2682	Trmt5	Trmt5_2682	GGAAAGGACGAAACACCGCAGCAGTAAGCATCCTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCAGTAAGCATCCTGTAG	
2683	Trmt5	Trmt5_2683	GGAAAGGACGAAACACCGATTCCTCGAACGTCAGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCTCGAACGTCAGAGGG	
2684	Trmt5	Trmt5_2684	GGAAAGGACGAAACACCGTTTCCTAAGTCTCGGCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCCTAAGTCTCGGCACCA	
2685	Lmf1	Lmf1_2685	GGAAAGGACGAAACACCGGATCTGCCCTACGTTGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCTGCCCTACGTTGACCA	
2686	Lmf1	Lmf1_2686	GGAAAGGACGAAACACCGCTTCAGAATCATGCTTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAGAATCATGCTTGGAG	
2687	Lmf1	Lmf1_2687	GGAAAGGACGAAACACCGGGTGGCATTCAATCAGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGCATTCAATCAGAACA	
2688	Lmf1	Lmf1_2688	GGAAAGGACGAAACACCGCCTATGCACCAACCATTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTATGCACCAACCATTATG	
2689	Cln6	Cln6_2689	GGAAAGGACGAAACACCGCCTGCACGAACGCGACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCACGAACGCGACACCG	
2690	Cln6	Cln6_2690	GGAAAGGACGAAACACCGCTGACATAGACTATAGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGACATAGACTATAGACCG	
2691	Cln6	Cln6_2691	GGAAAGGACGAAACACCGTGGATCGGGAATACCAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGATCGGGAATACCAGCTG	
2692	Cln6	Cln6_2692	GGAAAGGACGAAACACCGATAGTAGTACAACAGCTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGTAGTACAACAGCTCAA	
2693	Qrsl1	Qrsl1_2693	GGAAAGGACGAAACACCGACGTCCATTGAATTCACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTCCATTGAATTCACCAG	
2694	Qrsl1	Qrsl1_2694	GGAAAGGACGAAACACCGATCAGGGTGCCCTACTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAGGGTGCCCTACTCATG	
2695	Qrsl1	Qrsl1_2695	GGAAAGGACGAAACACCGTTACGCAAAGCAGGTGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACGCAAAGCAGGTGAACG	
2696	Qrsl1	Qrsl1_2696	GGAAAGGACGAAACACCGGCTGTGTATAGGAATCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGTATAGGAATCCCAA	
2697	Mfsd2a	Mfsd2a_2697	GGAAAGGACGAAACACCGTCAGGGACGGAAAGTTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGGACGGAAAGTTCACA	
2698	Mfsd2a	Mfsd2a_2698	GGAAAGGACGAAACACCGGCAGCCGGTCAACTGGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGCCGGTCAACTGGTACG	
2699	Mfsd2a	Mfsd2a_2699	GGAAAGGACGAAACACCGGAGGGACTTACTGTATGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGGACTTACTGTATGCCG	
2700	Mfsd2a	Mfsd2a_2700	GGAAAGGACGAAACACCGTCTCTACTTACCAGGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTACTTACCAGGGCATG	
2701	Alpi	Alpi_2701	GGAAAGGACGAAACACCGAAACTAAGGTATTACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTAAGGTATTACCCATG	
2702	Alpi	Alpi_2702	GGAAAGGACGAAACACCGAAGGCCAACTACAAGACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCCAACTACAAGACCAT	
2703	Alpi	Alpi_2703	GGAAAGGACGAAACACCGAGCCGGCACCTACGCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCGGCACCTACGCACACA	
2704	Alpi	Alpi_2704	GGAAAGGACGAAACACCGACAGTAACCAGTCTGGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTAACCAGTCTGGAACC	
2705	Slc10a7	Slc10a7_2705	GGAAAGGACGAAACACCGCCGTCGGTCGGAGTGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTCGGTCGGAGTGAACGG	
2706	Slc10a7	Slc10a7_2706	GGAAAGGACGAAACACCGGTTGAAGAATATCGTTGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGAAGAATATCGTTGCGA	
2707	Slc10a7	Slc10a7_2707	GGAAAGGACGAAACACCGGAAGAAGCCACCATTTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGAAGCCACCATTTGGTG	
2708	Slc10a7	Slc10a7_2708	GGAAAGGACGAAACACCGAACTGCCTTGGTTAAAATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTGCCTTGGTTAAAATCA	
2709	Nubpl	Nubpl_2709	GGAAAGGACGAAACACCGCCCAAAGCTCGGCACCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAAAGCTCGGCACCCCCG	
2710	Nubpl	Nubpl_2710	GGAAAGGACGAAACACCGGTGGAGACAATCACAGCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAGACAATCACAGCACC	

No.	*Oligo name	*Oligo name	*Sequence(5' to3')	nt#	Remarks	5'	guide sequence	3'
2711	Nubpl	Nubpl_2711	GGAAAGGACGAAACACCGTCAGCTGGACTATTTAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCTGGACTATTTAGTTG	
2712	Nubpl	Nubpl_2712	GGAAAGGACGAAACACCGACACCTTACAATACCTGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCTTACAATACCTGCGG	
2713	Timmdc1	Timmdc1_2713	GGAAAGGACGAAACACCGATCCGGATTCCAGGGAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCGGATTCCAGGGAACCG	
2714	Timmdc1	Timmdc1_2714	GGAAAGGACGAAACACCGGGAAATTGACTATATCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAATTGACTATATCTACA	
2715	Timmdc1	Timmdc1_2715	GGAAAGGACGAAACACCGATACCGGATGAAGCCCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCGGATGAAGCCCCTTG	
2716	Timmdc1	Timmdc1_2716	GGAAAGGACGAAACACCGCACCGGCAGCAAAGACTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGGCAGCAAAGACTCGG	
2717	Ndufaf6	Ndufaf6_2717	GGAAAGGACGAAACACCGAATTATGCTGAGAATACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTATGCTGAGAATACGCA	
2718	Ndufaf6	Ndufaf6_2718	GGAAAGGACGAAACACCGACACGTTCCCACGCATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACGTTCCCACGCATCCCG	
2719	Ndufaf6	Ndufaf6_2719	GGAAAGGACGAAACACCGAACATAACCTAACTAAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATAACCTAACTAAAAGG	
2720	Ndufaf6	Ndufaf6_2720	GGAAAGGACGAAACACCGGCAGTTCTGGAAAAAAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTTCTGGAAAAAAGCTG	
2721	Mrap	Mrap_2721	GGAAAGGACGAAACACCGGAGAAAGAGGAGCACCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAAAGAGGAGCACCACGA	
2722	Mrap	Mrap_2722	GGAAAGGACGAAACACCGGTCCATGAACATATTGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCATGAACATATTGGCTG	
2723	Mrap	Mrap_2723	GGAAAGGACGAAACACCGCAACCACAGGGCGATGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACCACAGGGCGATGACAA	
2724	Mrap	Mrap_2724	GGAAAGGACGAAACACCGGGTGAGCGGGACAGAGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAGCGGGACAGAGGCGT	
2725	Mtmr2	Mtmr2_2725	GGAAAGGACGAAACACCGTGCTCGGCCAAGTGTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCGGCCAAGTGTCAATG	
2726	Mtmr2	Mtmr2_2726	GGAAAGGACGAAACACCGGCCTTCTGTACTCTAGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTTCTGTACTCTAGAAGG	
2727	Mtmr2	Mtmr2_2727	GGAAAGGACGAAACACCGGTGGCATCCTTTAGGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCATCCTTTAGGTCACG	
2728	Mtmr2	Mtmr2_2728	GGAAAGGACGAAACACCGGTAATGATTCTCTCATAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAATGATTCTCTCATAACA	
2729	Agl	Agl_2729	GGAAAGGACGAAACACCGACTGGTCTACCGGTACGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGGTCTACCGGTACGGAG	
2730	Agl	Agl_2730	GGAAAGGACGAAACACCGAGAAATGGCCTTATCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAATGGCCTTATCCGCAG	
2731	Agl	Agl_2731	GGAAAGGACGAAACACCGTGGTCATCACTTAAGTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTCATCACTTAAGTACGC	
2732	Agl	Agl_2732	GGAAAGGACGAAACACCGAACAGACTGGTGGATGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGACTGGTGGATGCTCG	
2733	Vps33a	Vps33a_2733	GGAAAGGACGAAACACCGGCAAGAGGTTATCAAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAGAGGTTATCAAACACG	
2734	Vps33a	Vps33a_2734	GGAAAGGACGAAACACCGTAATTGCTGAGAATGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATTGCTGAGAATGTACTC	
2735	Vps33a	Vps33a_2735	GGAAAGGACGAAACACCGACACAACGCTAAGACAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACAACGCTAAGACAGTCG	
2736	Vps33a	Vps33a_2736	GGAAAGGACGAAACACCGGCCTGTACCACGCAGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGTACCACGCAGCCAAG	
2737	Mboat7	Mboat7_2737	GGAAAGGACGAAACACCGTGATCAGAGAATGCAAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATCAGAGAATGCAAACTG	
2738	Mboat7	Mboat7_2738	GGAAAGGACGAAACACCGATAGCAGTCGATGTTACGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGCAGTCGATGTTACGGA	
2739	Mboat7	Mboat7_2739	GGAAAGGACGAAACACCGAGCTATAGCTACTGTTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTATAGCTACTGTTACGT	
2740	Mboat7	Mboat7_2740	GGAAAGGACGAAACACCGGCCTGGATTGCGGCCGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTGGATTGCGGCCGAGTG	
2741	Mmab	Mmab_2741	GGAAAGGACGAAACACCGCAGTGCATGCTACAGGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGCATGCTACAGGACGT	
2742	Mmab	Mmab_2742	GGAAAGGACGAAACACCGATCAAGTATTTGAAGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAAGTATTTGAAGCCGTG	
2743	Mmab	Mmab_2743	GGAAAGGACGAAACACCGGAAGCTCTTCGGCAAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCTCTTCGGCAAACATG	
2744	Mmab	Mmab_2744	GGAAAGGACGAAACACCGTGTCCCCGTTTCCAGAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCCCGTTTCCAGAGCCG	
2745	Rdh12	Rdh12_2745	GGAAAGGACGAAACACCGGGAAAGGTTGACCACCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAAGGTTGACCACCCGTG	
2746	Rdh12	Rdh12_2746	GGAAAGGACGAAACACCGCAATTTCCGCACTAGCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATTTCCGCACTAGCACCT	
2747	Rdh12	Rdh12_2747	GGAAAGGACGAAACACCGTGCTAGGAAGCGTTCAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTAGGAAGCGTTCAGCAA	
2748	Rdh12	Rdh12_2748	GGAAAGGACGAAACACCGCCCAAAGATACTTACCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAAAGATACTTACCCAGG	
2749	Sbf1	Sbf1_2749	GGAAAGGACGAAACACCGATTGTGCCCTCATCTAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGTGCCCTCATCTAGCCG	
2750	Sbf1	Sbf1_2750	GGAAAGGACGAAACACCGAGAGCAGGGCTACACTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCAGGGCTACACTACAG	
2751	Sbf1	Sbf1_2751	GGAAAGGACGAAACACCGATTGTTGCTGATCTTGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGTTGCTGATCTTGACGG	
2752	Sbf1	Sbf1_2752	GGAAAGGACGAAACACCGTGTGTCGTGACAGGAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTCGTGACAGGAGACTG	
2753	Mccc2	Mccc2_2753	GGAAAGGACGAAACACCGTTACCAGTTATATGGCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCAGTTATATGGCGACG	
2754	Mccc2	Mccc2_2754	GGAAAGGACGAAACACCGGAGGAGCTTTGATGTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGAGCTTTGATGTCCGAG	
2755	Mccc2	Mccc2_2755	GGAAAGGACGAAACACCGTGACTGTGAAAAAGCACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTGTGAAAAAGCACGTG	
2756	Mccc2	Mccc2_2756	GGAAAGGACGAAACACCGGGTGGTCGTCCAAAGCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGTCGTCCAAAGCATAG	
2757	Cpt1c	Cpt1c_2757	GGAAAGGACGAAACACCGCCACTCGGACAGGAGTATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTCGGACAGGAGTATGT	
2758	Cpt1c	Cpt1c_2758	GGAAAGGACGAAACACCGTCATACTGGGCGGAACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATACTGGGCGGAACACAA	
2759	Cpt1c	Cpt1c_2759	GGAAAGGACGAAACACCGCATTTGCCAGCGCTGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTTGCCAGCGCTGTAGCG	
2760	Cpt1c	Cpt1c_2760	GGAAAGGACGAAACACCGTGGGAGAGTGAGTCCCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGAGAGTGAGTCCCTACA	
2761	Bola3	Bola3_2761	GGAAAGGACGAAACACCGGCGAATGTTTGCCTCTCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGAATGTTTGCCTCTCAGA	
2762	Bola3	Bola3_2762	GGAAAGGACGAAACACCGGCTGCGCACAGTGCCACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCGCACAGTGCCACAGA	
2763	Bola3	Bola3_2763	GGAAAGGACGAAACACCGCCCGCGCAGCAGAGGCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCGCGCAGCAGAGGCGCAG	
2764	Bola3	Bola3_2764	GGAAAGGACGAAACACCGGTATGAAATTAAAATCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATGAAATTAAAATCGAAT	
2765	Ak7	Ak7_2765	GGAAAGGACGAAACACCGTCTCCCTTAGGACGACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCCTTAGGACGACAACG	
2766	Ak7	Ak7_2766	GGAAAGGACGAAACACCGGGAGGCGATTGTCGCACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGCGATTGTCGCACCCA	
2767	Ak7	Ak7_2767	GGAAAGGACGAAACACCGCTCCAAACACGGGTAGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCAAACACGGGTAGTGCG	
2768	Ak7	Ak7_2768	GGAAAGGACGAAACACCGGGAGAACTTTAACATCCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGAACTTTAACATCCGCT	
2769	Slc25a12	Slc25a12_2769	GGAAAGGACGAAACACCGACCCGGATGCAAAACCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCGGATGCAAAACCAGCG	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
2770	Slc25a12	Slc25a12_2770	GGAAAGGACGAAACACCGATAGCACTTTAGCAGGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGCACTTTAGCAGGCACG	
2771	Slc25a12	Slc25a12_2771	GGAAAGGACGAAACACCGCTCTTGATAGGAGATCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTTGATAGGAGATCAACC	
2772	Slc25a12	Slc25a12_2772	GGAAAGGACGAAACACCGTCACTGGAAGTCTTACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACTGGAAGTCTTACCCTG	
2773	Pigt	Pigt_2773	GGAAAGGACGAAACACCGGATCCGAATCCCAACGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCCGAATCCCAACGCGTG	
2774	Pigt	Pigt_2774	GGAAAGGACGAAACACCGAAACAAGTCATAGACGGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACAAGTCATAGACGGCAT	
2775	Pigt	Pigt_2775	GGAAAGGACGAAACACCGGGTAACTGGTGTGGAACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAACTGGTGTGGAACAAG	
2776	Pigt	Pigt_2776	GGAAAGGACGAAACACCGTGAGAGTCCGGGAGAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAGTCCGGGAGAACATG	
2777	Mrps34	Mrps34_2777	GGAAAGGACGAAACACCGTGGGTACCAAACGCCAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGTACCAAACGCCAATCG	
2778	Mrps34	Mrps34_2778	GGAAAGGACGAAACACCGAGTCGGGCCTCACACGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGGGCCTCACACGCGTG	
2779	Mrps34	Mrps34_2779	GGAAAGGACGAAACACCGGCGGCTCTCGCGACGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGCTCTCGCGACGCACGT	
2780	Mrps34	Mrps34_2780	GGAAAGGACGAAACACCGACGCTGACCCGGCCGCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGCTGACCCGGCCGCACTC	
2781	Lrat	Lrat_2781	GGAAAGGACGAAACACCGGAAATCAGCTCTTTCGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAATCAGCTCTTTCGTCCG	
2782	Lrat	Lrat_2782	GGAAAGGACGAAACACCGTCCTAGTCAATCACCTAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTAGTCAATCACCTAGAC	
2783	Lrat	Lrat_2783	GGAAAGGACGAAACACCGCAAGGTGGCTAGCATCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGTGGCTAGCATCCGTG	
2784	Lrat	Lrat_2784	GGAAAGGACGAAACACCGTCTAATGCCTGACATCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAATGCCTGACATCCTGT	
2785	Lias	Lias_2785	GGAAAGGACGAAACACCGAGGTTGCCTTACCATGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTTGCCTTACCATGATCG	
2786	Lias	Lias_2786	GGAAAGGACGAAACACCGGCAGTCACCTCTGTAACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTCACCTCTGTAACTCG	
2787	Lias	Lias_2787	GGAAAGGACGAAACACCGATAAACTGAAAAATACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAACTGAAAAATACATTG	
2788	Lias	Lias_2788	GGAAAGGACGAAACACCGGGATTATGTTGTCCTGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATTATGTTGTCCTGACGT	
2789	Slc19a3	Slc19a3_2789	GGAAAGGACGAAACACCGCTGTCGGAGTATCACACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTCGGAGTATCACACTGG	
2790	Slc19a3	Slc19a3_2790	GGAAAGGACGAAACACCGTGCCAATTCAAAGAATCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCAATTCAAAGAATCTAG	
2791	Slc19a3	Slc19a3_2791	GGAAAGGACGAAACACCGACCAGAGGGACCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGAGGGACCAGTAAACA	
2792	Slc19a3	Slc19a3_2792	GGAAAGGACGAAACACCGACAACGTGTAGCATGATGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAACGTGTAGCATGATGAC	
2793	Ctns	Ctns_2793	GGAAAGGACGAAACACCGAGGCATCATTACTGTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCATCATTACTGTCGACG	
2794	Ctns	Ctns_2794	GGAAAGGACGAAACACCGTGGAGGGCCATGACACACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGGGCCATGACACACGC	
2795	Ctns	Ctns_2795	GGAAAGGACGAAACACCGTAACAGGTTATAGTGCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACAGGTTATAGTGCCTCG	
2796	Ctns	Ctns_2796	GGAAAGGACGAAACACCGCCCAAGGGTGATGTCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAAGGGTGATGTCGACGT	
2797	Elovl4	Elovl4_2797	GGAAAGGACGAAACACCGTTCATGGGATCATACAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCATGGGATCATACAACGC	
2798	Elovl4	Elovl4_2798	GGAAAGGACGAAACACCGACACCGTGGAGTTCTATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCGTGGAGTTCTATCGC	
2799	Elovl4	Elovl4_2799	GGAAAGGACGAAACACCGTGCAGTGGTGGTACACGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTGGTGGTACACGTGA	
2800	Elovl4	Elovl4_2800	GGAAAGGACGAAACACCGCGATACAAAATACCACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGATACAAAATACCACCACA	
2801	Hamp	Hamp_2801	GGAAAGGACGAAACACCGCACCTGTTGATGGAGATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCTGTTGATGGAGATAGG	
2802	Hamp	Hamp_2802	GGAAAGGACGAAACACCGAGATACCAATGCAGAAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATACCAATGCAGAAGAGA	
2803	Hamp	Hamp_2803	GGAAAGGACGAAACACCGAGAGCTGCAGCCTTTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTGCAGCCTTTGCACG	
2804	Hamp	Hamp_2804	GGAAAGGACGAAACACCGAGAAAGCAGGGCAGACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAGCAGGGCAGACATTG	
2805	Cox4i2	Cox4i2_2805	GGAAAGGACGAAACACCGGGGCGTAGCAGTCAACGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCGTAGCAGTCAACGTAG	
2806	Cox4i2	Cox4i2_2806	GGAAAGGACGAAACACCGCCAGCGCTCCTATCCCATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGCTCCTATCCCATGC	
2807	Cox4i2	Cox4i2_2807	GGAAAGGACGAAACACCGGGACAGGACTCAGAACTAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAGGACTCAGAACTAGA	
2808	Cox4i2	Cox4i2_2808	GGAAAGGACGAAACACCGCTTCTGCACAGAGCTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCTGCACAGAGCTCAGCG	
2809	Kars	Kars_2809	GGAAAGGACGAAACACCGCTCATCTTCTATGACCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCATCTTCTATGACCTGCG	
2810	Kars	Kars_2810	GGAAAGGACGAAACACCGGGAGCGTTGTGAAAGGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCGTTGTGAAAGGAGCA	
2811	Kars	Kars_2811	GGAAAGGACGAAACACCGTGTATGTGATGATCTTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTATGTGATGATCTTAGAG	
2812	Kars	Kars_2812	GGAAAGGACGAAACACCGTGTGGCTATTGACTACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCTATTGACTACCTTG	
2813	Acox2	Acox2_2813	GGAAAGGACGAAACACCGTAGGCCGAAGACGAGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCCGAAGACGAGACTGG	
2814	Acox2	Acox2_2814	GGAAAGGACGAAACACCGGATGAGCAGATTGCTAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAGCAGATTGCTAAATG	
2815	Acox2	Acox2_2815	GGAAAGGACGAAACACCGCTTGAGTGACCAGTGTCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGAGTGACCAGTGTCGGT	
2816	Acox2	Acox2_2816	GGAAAGGACGAAACACCGATGCCAAGATAATTGCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCCAAGATAATTGCTCTG	
2817	Echs1	Echs1_2817	GGAAAGGACGAAACACCGAGTCGGCAAATCGCTAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGGCAAATCGCTAGCAA	
2818	Echs1	Echs1_2818	GGAAAGGACGAAACACCGGACAGCCAGAAATCCTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAGCCAGAAATCCTCCTG	
2819	Echs1	Echs1_2819	GGAAAGGACGAAACACCGGATGACCGGTTTCTTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGACCGGTTTCTTGACCC	
2820	Echs1	Echs1_2820	GGAAAGGACGAAACACCGGTGCATTGAGTGCTTTGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCATTGAGTGCTTTGGGG	
2821	Amn	Amn_2821	GGAAAGGACGAAACACCGGCAGACGTTCTCGCGCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGACGTTCTCGCGCGACG	
2822	Amn	Amn_2822	GGAAAGGACGAAACACCGACAGACGCAGCCCGACGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGACGCAGCCCGACGCGT	
2823	Amn	Amn_2823	GGAAAGGACGAAACACCGCCAGAACCGGACCCCGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGAACCGGACCCCGTGCG	
2824	Amn	Amn_2824	GGAAAGGACGAAACACCGGCGCGATGGATCTTTCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCGATGGATCTTTCCGCG	
2825	Mrpl3	Mrpl3_2825	GGAAAGGACGAAACACCGGGAGACCAGTTGCTTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGACCAGTTGCTTAACAA	
2826	Mrpl3	Mrpl3_2826	GGAAAGGACGAAACACCGTGTGTTAAAATACACTCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTTAAAATACACTCCCA	
2827	Mrpl3	Mrpl3_2827	GGAAAGGACGAAACACCGCCCACCTTCTCTCTAAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACCTTCTCTCTAAGCCG	
2828	Mrpl3	Mrpl3_2828	GGAAAGGACGAAACACCGGAAAACCTTTACCAATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAACCTTTACCAATACTG	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
2829	Mcoln1	Mcoln1_2829	GGAAAGGACGAAACACCGGACATAGGCATACCGGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACATAGGCATACCGGCCCA	
2830	Mcoln1	Mcoln1_2830	GGAAAGGACGAAACACCGTTTGACAATAAAGCGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGACAATAAAGCGCACAG	
2831	Mcoln1	Mcoln1_2831	GGAAAGGACGAAACACCGATACCTTTGACATTGATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCTTTGACATTGATCCA	
2832	Mcoln1	Mcoln1_2832	GGAAAGGACGAAACACCGTGGCCCGGAACTTGTCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCCGGAACTTGTCACAT	
2833	Nans	Nans_2833	GGAAAGGACGAAACACCGTATGTGACGTTCCAACACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGTGACGTTCCAACACCT	
2834	Nans	Nans_2834	GGAAAGGACGAAACACCGTATACTTCGAAGCATTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATACTTCGAAGCATTCATG	
2835	Nans	Nans_2835	GGAAAGGACGAAACACCGTCGTGCCCGGAATACCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTGCCCGGAATACCCGAT	
2836	Nans	Nans_2836	GGAAAGGACGAAACACCGGAGATCACCATAGGACGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATCACCATAGGACGACC	
2837	Cnnm2	Cnnm2_2837	GGAAAGGACGAAACACCGACCGTCGTGGTAAATCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCGTCGTGGTAAATCCAGG	
2838	Cnnm2	Cnnm2_2838	GGAAAGGACGAAACACCGCGGCGATTGAGAATGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGATTGAGAATGATGTG	
2839	Cnnm2	Cnnm2_2839	GGAAAGGACGAAACACCGTGCTAACCGGATAAGAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTAACCGGATAAGAAGCG	
2840	Cnnm2	Cnnm2_2840	GGAAAGGACGAAACACCGCTGCTTCATGATAACCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCTTCATGATAACCGGCG	
2841	Srd5a2	Srd5a2_2841	GGAAAGGACGAAACACCGCCCAGCAGCACATTCCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAGCAGCACATTCCCCGG	
2842	Srd5a2	Srd5a2_2842	GGAAAGGACGAAACACCGACAGACATGCGGTTTAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGACATGCGGTTTAGCGT	
2843	Srd5a2	Srd5a2_2843	GGAAAGGACGAAACACCGCATCCCTACCGACACCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCCCTACCGACACCACAA	
2844	Srd5a2	Srd5a2_2844	GGAAAGGACGAAACACCGGGTATTCCGCGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTATTCCGCGCAATAAACC	
2845	Sfxn4	Sfxn4_2845	GGAAAGGACGAAACACCGTTAAGCCAAAAGTTATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAAGCCAAAAGTTATTCGG	
2846	Sfxn4	Sfxn4_2846	GGAAAGGACGAAACACCGAGCACATGAGACATACCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACATGAGACATACCACT	
2847	Sfxn4	Sfxn4_2847	GGAAAGGACGAAACACCGTGCAGTCAGGAACTCACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGTCAGGAACTCACCAT	
2848	Sfxn4	Sfxn4_2848	GGAAAGGACGAAACACCGCCATCGAGGAATTGAGGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCGAGGAATTGAGGTGA	
2849	Hadha	Hadha_2849	GGAAAGGACGAAACACCGACACTTTGTGCTTTACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTTTGTGCTTTACACCG	
2850	Hadha	Hadha_2850	GGAAAGGACGAAACACCGTATTAATTATGGCGTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTAATTATGGCGTCAAAG	
2851	Hadha	Hadha_2851	GGAAAGGACGAAACACCGTTAAAGACACCACAGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAAAGACACCACAGTGACG	
2852	Hadha	Hadha_2852	GGAAAGGACGAAACACCGAAGGACAATTGAATACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGACAATTGAATACCTAG	
2853	Cog8	Cog8_2853	GGAAAGGACGAAACACCGCTACAAGACGTTCATTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACAAGACGTTCATTCGCG	
2854	Cog8	Cog8_2854	GGAAAGGACGAAACACCGACACACGTGTCCATAAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACACGTGTCCATAAGCTG	
2855	Cog8	Cog8_2855	GGAAAGGACGAAACACCGTGGCGTGAGAAGCCCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCGTGAGAAGCCCGACGT	
2856	Cog8	Cog8_2856	GGAAAGGACGAAACACCGAGGTGGCTACCTGGATAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGGCTACCTGGATAACG	
2857	B3galnt2	B3galnt2_2857	GGAAAGGACGAAACACCGTAGTGGCTAAATTTCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTGGCTAAATTTCCAGTG	
2858	B3galnt2	B3galnt2_2858	GGAAAGGACGAAACACCGACACCTTCCATGAATTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCTTCCATGAATTCATG	
2859	B3galnt2	B3galnt2_2859	GGAAAGGACGAAACACCGACCCACCGTTGACTTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCACCGTTGACTTAATGT	
2860	B3galnt2	B3galnt2_2860	GGAAAGGACGAAACACCGGGAACAGTTCATCTTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACAGTTCATCTTACCAG	
2861	Kmo	Kmo_2861	GGAAAGGACGAAACACCGGCTGTCGAAATGCATTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTCGAAATGCATTCCGG	
2862	Kmo	Kmo_2862	GGAAAGGACGAAACACCGGATGTGTACGAAGCTAGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTGTACGAAGCTAGGGA	
2863	Kmo	Kmo_2863	GGAAAGGACGAAACACCGGACAATTCCACCTAAGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAATTCCACCTAAGAATG	
2864	Kmo	Kmo_2864	GGAAAGGACGAAACACCGTTGCCCAAAAAATGGGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCCCAAAAAATGGGACAA	
2865	D2hgdh	D2hgdh_2865	GGAAAGGACGAAACACCGGGCTCACAGAGCATACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTCACAGAGCATACTCCG	
2866	D2hgdh	D2hgdh_2866	GGAAAGGACGAAACACCGAGGCCTGGGTGGGCACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCTGGGTGGGCACACAA	
2867	D2hgdh	D2hgdh_2867	GGAAAGGACGAAACACCGGGATACTGAATGCATGCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATACTGAATGCATGCAGT	
2868	D2hgdh	D2hgdh_2868	GGAAAGGACGAAACACCGGACTGGCTGAAGACCGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTGGCTGAAGACCGTCCG	
2869	Lbr	Lbr_2869	GGAAAGGACGAAACACCGTTCAAGTGACCACTCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAAGTGACCACTCCACAG	
2870	Lbr	Lbr_2870	GGAAAGGACGAAACACCGGCGCCCTGGATTGATTGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCCTGGATTGATTGGAT	
2871	Lbr	Lbr_2871	GGAAAGGACGAAACACCGGAAGTAAGTACCAACACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTAAGTACCAACACAAG	
2872	Lbr	Lbr_2872	GGAAAGGACGAAACACCGGAGCTTGAACGAAAAACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCTTGAACGAAAAACCAG	
2873	Pomt1	Pomt1_2873	GGAAAGGACGAAACACCGTGTGAACAGAGAGTCCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGAACAGAGAGTCCAACC	
2874	Pomt1	Pomt1_2874	GGAAAGGACGAAACACCGATAGTCGGGTAAGTAGTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGTCGGGTAAGTAGTCCC	
2875	Pomt1	Pomt1_2875	GGAAAGGACGAAACACCGGGGGCACTCACGTGTTAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCACTCACGTGTTAAGG	
2876	Pomt1	Pomt1_2876	GGAAAGGACGAAACACCGGTCCACGCGTGGAATCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCACGCGTGGAATCTGAT	
2877	Dpyd	Dpyd_2877	GGAAAGGACGAAACACCGCTATAACCTTCCGTGGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATAACCTTCCGTGGCGAG	
2878	Dpyd	Dpyd_2878	GGAAAGGACGAAACACCGGAGGCACAGCTTATACTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCACAGCTTATACTCGC	
2879	Dpyd	Dpyd_2879	GGAAAGGACGAAACACCGTTTGTCCAGGGCCATACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTCCAGGGCCATACAAG	
2880	Dpyd	Dpyd_2880	GGAAAGGACGAAACACCGAGAGCTAAGAGTCATTTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTAAGAGTCATTTCAT	
2881	Ldlrap1	Ldlrap1_2881	GGAAAGGACGAAACACCGGCTCCACCAGCGTCATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCACCAGCGTCATACCA	
2882	Ldlrap1	Ldlrap1_2882	GGAAAGGACGAAACACCGTCGGTCAGGATGATCCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGTCAGGATGATCCCCCG	
2883	Ldlrap1	Ldlrap1_2883	GGAAAGGACGAAACACCGTGCAGACAAGATGCACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAGACAAGATGCACGACA	
2884	Ldlrap1	Ldlrap1_2884	GGAAAGGACGAAACACCGCAGAGAACTGGACGGACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGAACTGGACGGACACG	
2885	Pcsk9	Pcsk9_2885	GGAAAGGACGAAACACCGGCTGCCAGGAACCTACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCCAGGAACCTACATTG	
2886	Pcsk9	Pcsk9_2886	GGAAAGGACGAAACACCGTGGAGCGAATTATCCCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGCGAATTATCCCAGCA	
2887	Pcsk9	Pcsk9_2887	GGAAAGGACGAAACACCGAGGACCAGCCAGTTACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCAGCCAGTTACCTTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
2888	Pcsk9	Pcsk9_2888	GGAAAGGACGAAACACCGCATGCTTCATGTCACAGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCTTCATGTCACAGAGT	
2889	H6pd	H6pd_2889	GGAAAGGACGAAACACCGTAGGCGTAGTAATCAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCGTAGTAATCAGACAG	
2890	H6pd	H6pd_2890	GGAAAGGACGAAACACCGCTTGAAGGAGACCATAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGAAGGAGACCATAGATG	
2891	H6pd	H6pd_2891	GGAAAGGACGAAACACCGAGTTCCACGCCCATACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTCCACGCCCATACCCAG	
2892	H6pd	H6pd_2892	GGAAAGGACGAAACACCGATGTCTGCGTAGGCAAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTCTGCGTAGGCAAAGGG	
2893	Psph	Psph_2893	GGAAAGGACGAAACACCGTTCGTACATTTCAGACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGTACATTTCAGACACTG	
2894	Psph	Psph_2894	GGAAAGGACGAAACACCGCTTATGCCAGGAGTCAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTATGCCAGGAGTCAGATG	
2895	Psph	Psph_2895	GGAAAGGACGAAACACCGCCTGGACATTACGCTCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGACATTACGCTCCTGG	
2896	Psph	Psph_2896	GGAAAGGACGAAACACCGCAGCCTATTGGCAAACACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCTATTGGCAAACACAT	
2897	Acacb	Acacb_2897	GGAAAGGACGAAACACCGAGAACAACGATATCGACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACAACGATATCGACACG	
2898	Acacb	Acacb_2898	GGAAAGGACGAAACACCGCCAGTGTGCCGACCACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGTGTGCCGACCACATGG	
2899	Acacb	Acacb_2899	GGAAAGGACGAAACACCGGTGGCCGTACATGTCGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCCGTACATGTCGATGG	
2900	Acacb	Acacb_2900	GGAAAGGACGAAACACCGTTCATTACGGAACATCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCATTACGGAACATCTCGT	
2901	Eogt	Eogt_2901	GGAAAGGACGAAACACCGGTCGACATAGCTGCAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCGACATAGCTGCAAACGG	
2902	Eogt	Eogt_2902	GGAAAGGACGAAACACCGGAGGCTGGAGTAGTCATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCTGGAGTAGTCATACA	
2903	Eogt	Eogt_2903	GGAAAGGACGAAACACCGACATCAAGAGAAACCACGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATCAAGAGAAACCACGAC	
2904	Eogt	Eogt_2904	GGAAAGGACGAAACACCGAACAGCCCGTACCGCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGCCCGTACCGCATGCG	
2905	Hsd3b7	Hsd3b7_2905	GGAAAGGACGAAACACCGCCTTCACCATAAATGCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTCACCATAAATGCCCGT	
2906	Hsd3b7	Hsd3b7_2906	GGAAAGGACGAAACACCGTGCTTGGATGCACATACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTTGGATGCACATACTGG	
2907	Hsd3b7	Hsd3b7_2907	GGAAAGGACGAAACACCGATCCACAAAGTCAACGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCACAAAGTCAACGTGCA	
2908	Hsd3b7	Hsd3b7_2908	GGAAAGGACGAAACACCGATGTGGTCATCCATACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTGGTCATCCATACAGCT	
2909	Phkb	Phkb_2909	GGAAAGGACGAAACACCGTCGGCCATAAAGTGTATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGCCATAAAGTGTATGAG	
2910	Phkb	Phkb_2910	GGAAAGGACGAAACACCGAAGCGGTTTCCAAGTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGGTTTCCAAGTAACTG	
2911	Phkb	Phkb_2911	GGAAAGGACGAAACACCGCCGTGTTATAGATTATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGTGTTATAGATTATCTGG	
2912	Phkb	Phkb_2912	GGAAAGGACGAAACACCGAACGCAGGGTAACTGATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGCAGGGTAACTGATGCA	
2913	Cog4	Cog4_2913	GGAAAGGACGAAACACCGGGAAACTCACCAACCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAACTCACCAACCCATCG	
2914	Cog4	Cog4_2914	GGAAAGGACGAAACACCGGCTGTGTACGAACGACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTGTACGAACGACTCTG	
2915	Cog4	Cog4_2915	GGAAAGGACGAAACACCGGCACAAGTAACGATGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAAGTAACGATGAATGT	
2916	Cog4	Cog4_2916	GGAAAGGACGAAACACCGCAACAGAAAAAATTGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACAGAAAAAATTGAACCA	
2917	Lars2	Lars2_2917	GGAAAGGACGAAACACCGGGTTAGCCATGATAACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTAGCCATGATAACGATG	
2918	Lars2	Lars2_2918	GGAAAGGACGAAACACCGTCTTAATGAACCACTGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTAATGAACCACTGTCGG	
2919	Lars2	Lars2_2919	GGAAAGGACGAAACACCGCAAATGCATCCCACCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAATGCATCCCACCCCATG	
2920	Lars2	Lars2_2920	GGAAAGGACGAAACACCGCATCTATGGCATCTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTATGGCATCTCCCACG	
2921	Alg9	Alg9_2921	GGAAAGGACGAAACACCGATGAGCGGATGGCATACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAGCGGATGGCATACACG	
2922	Alg9	Alg9_2922	GGAAAGGACGAAACACCGATACAAAACAATGTTGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACAAAACAATGTTGAGAG	
2923	Alg9	Alg9_2923	GGAAAGGACGAAACACCGTCCCGTCATGGCGATCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCGTCATGGCGATCAGCG	
2924	Alg9	Alg9_2924	GGAAAGGACGAAACACCGTCAAGTGTCTGCTCTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAGTGTCTGCTCTCAGCG	
2925	Slc6a8	Slc6a8_2925	GGAAAGGACGAAACACCGGGAAGCGCCACACGTTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGCGCCACACGTTACCG	
2926	Slc6a8	Slc6a8_2926	GGAAAGGACGAAACACCGGCATCAGTGTGACAGCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATCAGTGTGACAGCCCGT	
2927	Slc6a8	Slc6a8_2927	GGAAAGGACGAAACACCGGCACAACGAGGACCACGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAACGAGGACCACGTAG	
2928	Slc6a8	Slc6a8_2928	GGAAAGGACGAAACACCGACTCGATGACAGGGGACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCGATGACAGGGGACCGG	
2929	Upb1	Upb1_2929	GGAAAGGACGAAACACCGTCTCGTGTACAAAAAGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCGTGTACAAAAAGCGAA	
2930	Upb1	Upb1_2930	GGAAAGGACGAAACACCGCTGTACATGAGCCAGTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTACATGAGCCAGTTGAG	
2931	Upb1	Upb1_2931	GGAAAGGACGAAACACCGGTAGAGAATTCGCTTCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGAGAATTCGCTTCACCT	
2932	Upb1	Upb1_2932	GGAAAGGACGAAACACCGACTGAAGGGATATGCCTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGAAGGGATATGCCTTCG	
2933	Fig4	Fig4_2933	GGAAAGGACGAAACACCGCTTGGTGGTAATCGACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGTGGTAATCGACGACA	
2934	Fig4	Fig4_2934	GGAAAGGACGAAACACCGAAATCCGAACAGAGTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCCGAACAGAGTCATTG	
2935	Fig4	Fig4_2935	GGAAAGGACGAAACACCGGAAGGATTAATTACACAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGATTAATTACACAGGG	
2936	Fig4	Fig4_2936	GGAAAGGACGAAACACCGCACAGGTGGAATGAACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGGTGGAATGAACTAGG	
2937	Pnpo	Pnpo_2937	GGAAAGGACGAAACACCGAATGCGCAAGAGTTACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGCGCAAGAGTTACCGCG	
2938	Pnpo	Pnpo_2938	GGAAAGGACGAAACACCGACTAACTACGAGAGCCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTAACTACGAGAGCCGGAA	
2939	Pnpo	Pnpo_2939	GGAAAGGACGAAACACCGGGTAGCCACACACATAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAGCCACACACATAGCAT	
2940	Pnpo	Pnpo_2940	GGAAAGGACGAAACACCGCTGAACAGCCTCGTCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAACAGCCTCGTCAAACC	
2941	Pex12	Pex12_2941	GGAAAGGACGAAACACCGTTTCATCAAACCACCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCATCAAACCACCGCCAG	
2942	Pex12	Pex12_2942	GGAAAGGACGAAACACCGTTATGGCTTAAAGCGGATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATGGCTTAAAGCGGATTG	
2943	Pex12	Pex12_2943	GGAAAGGACGAAACACCGGGAACATGGCAGATTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACATGGCAGATTTCCAG	
2944	Pex12	Pex12_2944	GGAAAGGACGAAACACCGGGCCATGTTAACAAAAGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCATGTTAACAAAAGGGT	
2945	Plin1	Plin1_2945	GGAAAGGACGAAACACCGACAGCCCTGCCCAACCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCCCTGCCCAACCCGAG	
2946	Plin1	Plin1_2946	GGAAAGGACGAAACACCGGTCATGGCTCTCATCCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATGGCTCTCATCCTGAG	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
2947	Plin1	Plin1_2947	GGAAAGGACGAAACACCGATACCTGACTCCTTGTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACCTGACTCCTTGTCTGG	
2948	Plin1	Plin1_2948	GGAAAGGACGAAACACCGGGTGTGTCGAGAAAGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTGTCGAGAAAGAGTGT	
2949	Gck	Gck_2949	GGAAAGGACGAAACACCGTTCTGGGGTGGAACGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGGGGTGGAACGCACGT	
2950	Gck	Gck_2950	GGAAAGGACGAAACACCGAAGGCACGAAGACATAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCACGAAGACATAGACA	
2951	Gck	Gck_2951	GGAAAGGACGAAACACCGCCATCCGGTCGTACTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCCGGTCGTACTCCAGG	
2952	Gck	Gck_2952	GGAAAGGACGAAACACCGCCAGATGTATTCCATCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGATGTATTCCATCCCCG	
2953	Synj1	Synj1_2953	GGAAAGGACGAAACACCGTATGTCAATCAAGGCAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGTCAATCAAGGCAACGA	
2954	Synj1	Synj1_2954	GGAAAGGACGAAACACCGGGGACAAGGTTCAATGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACAAGGTTCAATGTCCG	
2955	Synj1	Synj1_2955	GGAAAGGACGAAACACCGTAAAATATATGCAGGCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAAATATATGCAGGCACCG	
2956	Synj1	Synj1_2956	GGAAAGGACGAAACACCGGAAGAGCATCCGAATTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGAGCATCCGAATTGCAA	
2957	Cyp27a1	Cyp27a1_2957	GGAAAGGACGAAACACCGCTACACGGATGCCTTAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACACGGATGCCTTAAACG	
2958	Cyp27a1	Cyp27a1_2958	GGAAAGGACGAAACACCGAGACCAAGTATGGTCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCAAGTATGGTCCAATG	
2959	Cyp27a1	Cyp27a1_2959	GGAAAGGACGAAACACCGGAGGACGCGTCCATTTGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGACGCGTCCATTTGGGA	
2960	Cyp27a1	Cyp27a1_2960	GGAAAGGACGAAACACCGGGTCCTTCCACTGATCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCTTCCACTGATCCATG	
2961	Ndufb11	Ndufb11_2961	GGAAAGGACGAAACACCGTGTAATCGCCCCATCCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAATCGCCCCATCCGGTG	
2962	Ndufb11	Ndufb11_2962	GGAAAGGACGAAACACCGGGACGAAAACGTCTACGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACGAAAACGTCTACGCGA	
2963	Ndufb11	Ndufb11_2963	GGAAAGGACGAAACACCGTATTCCAGACGTCCACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTCCAGACGTCCACCACA	
2964	Ndufb11	Ndufb11_2964	GGAAAGGACGAAACACCGGTCGCTGCCTGTCAGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCGCTGCCTGTCAGCAGCG	
2965	Gldc	Gldc_2965	GGAAAGGACGAAACACCGCCACTGAAATCCATTTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTGAAATCCATTTCGTG	
2966	Gldc	Gldc_2966	GGAAAGGACGAAACACCGTTTACTCAACTACCAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTACTCAACTACCAGACCA	
2967	Gldc	Gldc_2967	GGAAAGGACGAAACACCGCTTGATCCAGGGATGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGATCCAGGGATGCCACA	
2968	Gldc	Gldc_2968	GGAAAGGACGAAACACCGAGGCCACAAACAGCTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCACAAACAGCTACCAG	
2969	Slc6a5	Slc6a5_2969	GGAAAGGACGAAACACCGGGGATGGTCACCGATAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGATGGTCACCGATAACAC	
2970	Slc6a5	Slc6a5_2970	GGAAAGGACGAAACACCGGTGTACGCATCACTGGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTACGCATCACTGGCGAA	
2971	Slc6a5	Slc6a5_2971	GGAAAGGACGAAACACCGGCTTACCGGTATGGTAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTACCGGTATGGTAGTGG	
2972	Slc6a5	Slc6a5_2972	GGAAAGGACGAAACACCGGAGGACGCGAACGTGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGACGCGAACGTGAGTGT	
2973	Aldh6a1	Aldh6a1_2973	GGAAAGGACGAAACACCGTAGATGTGTCTGCCCACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATGTGTCTGCCCACGCA	
2974	Aldh6a1	Aldh6a1_2974	GGAAAGGACGAAACACCGTAAGTTACTTACCACTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGTTACTTACCACTGATG	
2975	Aldh6a1	Aldh6a1_2975	GGAAAGGACGAAACACCGTTCAACAGCCATCCTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAACAGCCATCCTCGTAG	
2976	Aldh6a1	Aldh6a1_2976	GGAAAGGACGAAACACCGAATGTTCAGTGTTCCGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTTCAGTGTTCCGTCAG	
2977	Tecpr2	Tecpr2_2977	GGAAAGGACGAAACACCGAGCAGACATCCTGACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGACATCCTGACCCATG	
2978	Tecpr2	Tecpr2_2978	GGAAAGGACGAAACACCGGTGGCAAAGTCACCATCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCAAAGTCACCATCAAG	
2979	Tecpr2	Tecpr2_2979	GGAAAGGACGAAACACCGTCTCGCCTGAGAAACACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCGCCTGAGAAACACCTG	
2980	Tecpr2	Tecpr2_2980	GGAAAGGACGAAACACCGAGCAGATTGGATCCCAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAGATTGGATCCCAACCA	
2981	Nhlrc1	Nhlrc1_2981	GGAAAGGACGAAACACCGGCACGACGTGAAGTACCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACGACGTGAAGTACCCAC	
2982	Nhlrc1	Nhlrc1_2982	GGAAAGGACGAAACACCGACTGTGCCCCAAGACCGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTGCCCCAAGACCGGAC	
2983	Nhlrc1	Nhlrc1_2983	GGAAAGGACGAAACACCGGGAGATCACCCCTCACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGATCACCCCTCACAATG	
2984	Nhlrc1	Nhlrc1_2984	GGAAAGGACGAAACACCGTCCCTGAAGGGGTCCTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCTGAAGGGGTCCTTCGG	
2985	Tecr	Tecr_2985	GGAAAGGACGAAACACCGTACGTCCAGTCGGCATACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGTCCAGTCGGCATACGG	
2986	Tecr	Tecr_2986	GGAAAGGACGAAACACCGACTCTACTTCCGGGACCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCTACTTCCGGGACCTCG	
2987	Tecr	Tecr_2987	GGAAAGGACGAAACACCGTGTCTGGACCCACTTACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCTGGACCCACTTACTAG	
2988	Tecr	Tecr_2988	GGAAAGGACGAAACACCGACTTTGAAGATGTTTCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTTGAAGATGTTTCGCAA	
2989	Ppcs	Ppcs_2989	GGAAAGGACGAAACACCGATAGAAATCTGACACTGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGAAATCTGACACTGCCG	
2990	Ppcs	Ppcs_2990	GGAAAGGACGAAACACCGATGCAGATAATCCGCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCAGATAATCCGCCAAAG	
2991	Ppcs	Ppcs_2991	GGAAAGGACGAAACACCGAACTTCAGTAGCGGGCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTCAGTAGCGGGCGACG	
2992	Ppcs	Ppcs_2992	GGAAAGGACGAAACACCGGTTCTTGTACCGAGCGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCTTGTACCGAGCGCGCT	
2993	Uqcc3	Uqcc3_2993	GGAAAGGACGAAACACCGAGATGCCGGAAAGGGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGCCGGAAAGGGACTCG	
2994	Uqcc3	Uqcc3_2994	GGAAAGGACGAAACACCGGGACGAAGCAGTCAGGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACGAAGCAGTCAGGACCA	
2995	Uqcc3	Uqcc3_2995	GGAAAGGACGAAACACCGGGTGGCTCGTAAAGCACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGCTCGTAAAGCACTTG	
2996	Uqcc3	Uqcc3_2996	GGAAAGGACGAAACACCGGCAGTTGCAGTGCTAGGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTTGCAGTGCTAGGCGG	
2997	Psat1	Psat1_2997	GGAAAGGACGAAACACCGTGGAAGGAGTGCTGACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAGGAGTGCTGACTACG	
2998	Psat1	Psat1_2998	GGAAAGGACGAAACACCGTGCAAACGAGACTGTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCAAACGAGACTGTGCACG	
2999	Psat1	Psat1_2999	GGAAAGGACGAAACACCGCAATACAGAGAATCTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATACAGAGAATCTTGTGA	
3000	Psat1	Psat1_3000	GGAAAGGACGAAACACCGCTTTGTAGTCAAGGACTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGTAGTCAAGGACTGAT	
3001	Acaca	Acaca_3001	GGAAAGGACGAAACACCGGCCATTCATTATCACTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCATTCATTATCACTACGT	
3002	Acaca	Acaca_3002	GGAAAGGACGAAACACCGAATGCATGCGATCTATCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGCATGCGATCTATCCGT	
3003	Acaca	Acaca_3003	GGAAAGGACGAAACACCGTTGATTCATAGGTACCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGATTCATAGGTACCGAAG	
3004	Acaca	Acaca_3004	GGAAAGGACGAAACACCGAAGCCCTTCGAACATACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCCTTCGAACATACACC	
3005	Haao	Haao_3005	GGAAAGGACGAAACACCGTGGGTGCTAACTGCGTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGTGCTAACTGCGTGCCA	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
3006	Haao	Haao_3006	GGAAAGGACGAAACACCGAGAGGTTTGCCAACACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGTTTGCCAACACCATG	
3007	Haao	Haao_3007	GGAAAGGACGAAACACCGGCAAACCGGAGGCTGAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAAACCGGAGGCTGAAAGG	
3008	Haao	Haao_3008	GGAAAGGACGAAACACCGCGGGACGTGCCTATACGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGGACGTGCCTATACGGCA	
3009	Cth	Cth_3009	GGAAAGGACGAAACACCGTGCATGGATGAAGTGTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCATGGATGAAGTGTATGG	
3010	Cth	Cth_3010	GGAAAGGACGAAACACCGGCAATGGAATTCTCGTGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAATGGAATTCTCGTGCCG	
3011	Cth	Cth_3011	GGAAAGGACGAAACACCGTTCCAAAACCAAATTGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCAAAACCAAATTGCTAG	
3012	Cth	Cth_3012	GGAAAGGACGAAACACCGTTTGTGGACAATTTGTGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTGGACAATTTGTGCGC	
3013	Mthfs	Mthfs_3013	GGAAAGGACGAAACACCGTTGCTCTGGAATTGGTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCTCTGGAATTGGTACCG	
3014	Mthfs	Mthfs_3014	GGAAAGGACGAAACACCGCTTCTCGCACCTTCTGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCTCGCACCTTCTGCGTG	
3015	Mthfs	Mthfs_3015	GGAAAGGACGAAACACCGGATGAGGTCAAGTCCACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAGGTCAAGTCCACCTG	
3016	Mthfs	Mthfs_3016	GGAAAGGACGAAACACCGATCTTGCATGCTTAGAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTTGCATGCTTAGAAAGA	
3017	Grm6	Grm6_3017	GGAAAGGACGAAACACCGATTCTCATTGAACATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCTCATTGAACATCACTG	
3018	Grm6	Grm6_3018	GGAAAGGACGAAACACCGGGAGTCAGGAGGCACCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTCAGGAGGCACCACTC	
3019	Grm6	Grm6_3019	GGAAAGGACGAAACACCGCCGGTGTGCGACTAGGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTGTGCGACTAGGCGCG	
3020	Grm6	Grm6_3020	GGAAAGGACGAAACACCGGTGGTCAGGCGACCCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTCAGGCGACCCCCATG	
3021	Prkag2	Prkag2_3021	GGAAAGGACGAAACACCGGGGACGAGGAAGCATAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACGAGGAAGCATAGATG	
3022	Prkag2	Prkag2_3022	GGAAAGGACGAAACACCGAAGAACATAAGATTGAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAACATAAGATTGAAACG	
3023	Prkag2	Prkag2_3023	GGAAAGGACGAAACACCGCCACTGAAGCTCATCCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACTGAAGCTCATCCGGCG	
3024	Prkag2	Prkag2_3024	GGAAAGGACGAAACACCGGCGTTTATATGCGATTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTTTATATGCGATTCATG	
3025	Atic	Atic_3025	GGAAAGGACGAAACACCGAGACGACTGTCACTCGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGACTGTCACTCGAGCG	
3026	Atic	Atic_3026	GGAAAGGACGAAACACCGGAGATGTGTCTGAGCTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATGTGTCTGAGCTAACA	
3027	Atic	Atic_3027	GGAAAGGACGAAACACCGAATTGCTTCATCGTATTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTGCTTCATCGTATTGAG	
3028	Atic	Atic_3028	GGAAAGGACGAAACACCGTTCTTTCAAGCACGTCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTTCAAGCACGTCAGCC	
3029	Ogt	Ogt_3029	GGAAAGGACGAAACACCGTTTGAGCCCAAATCATGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGAGCCCAAATCATGCGG	
3030	Ogt	Ogt_3030	GGAAAGGACGAAACACCGAGCATTATCGACATGCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCATTATCGACATGCCTTG	
3031	Ogt	Ogt_3031	GGAAAGGACGAAACACCGACAGTGCACCACTAGTCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTGCACCACTAGTCCCA	
3032	Ogt	Ogt_3032	GGAAAGGACGAAACACCGGAAAGTTTGTACCATCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAAGTTTGTACCATCATCC	
3033	Mthfd1	Mthfd1_3033	GGAAAGGACGAAACACCGACACCAACGATAGATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCAACGATAGATTCCTG	
3034	Mthfd1	Mthfd1_3034	GGAAAGGACGAAACACCGCACTATGAATCCGTGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTATGAATCCGTGCACAG	
3035	Mthfd1	Mthfd1_3035	GGAAAGGACGAAACACCGGATTGCCGGAAGGCACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTGCCGGAAGGCACGCGG	
3036	Mthfd1	Mthfd1_3036	GGAAAGGACGAAACACCGGGTAGCGTCCAGTAAGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAGCGTCCAGTAAGAAAG	
3037	Zdhhc15	Zdhhc15_3037	GGAAAGGACGAAACACCGTGGAACTTAGAGCGAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAACTTAGAGCGAACACT	
3038	Zdhhc15	Zdhhc15_3038	GGAAAGGACGAAACACCGGAATCAAAAGGGCATACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATCAAAAGGGCATACCAT	
3039	Zdhhc15	Zdhhc15_3039	GGAAAGGACGAAACACCGGTGTACACAAGAACCGGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTACACAAGAACCGGGAG	
3040	Zdhhc15	Zdhhc15_3040	GGAAAGGACGAAACACCGAGACTGTTGTAGCAATGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACTGTTGTAGCAATGTAC	
3041	Atad3a	Atad3a_3041	GGAAAGGACGAAACACCGAAGCAGGAGGCCATACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCAGGAGGCCATACGGCG	
3042	Atad3a	Atad3a_3042	GGAAAGGACGAAACACCGTTACCTGATAGACTCCAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCTGATAGACTCCAAGA	
3043	Atad3a	Atad3a_3043	GGAAAGGACGAAACACCGTGCCACATCAACTCACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCACATCAACTCACACTG	
3044	Atad3a	Atad3a_3044	GGAAAGGACGAAACACCGGCTGTCGAGCGAGCTTATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTCGAGCGAGCTTATCC	
3045	B4gat1	B4gat1_3045	GGAAAGGACGAAACACCGCCGGGATTAATTATGCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGGATTAATTATGCACTA	
3046	B4gat1	B4gat1_3046	GGAAAGGACGAAACACCGGTAGACGCGATAATCGCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGACGCGATAATCGCCGC	
3047	B4gat1	B4gat1_3047	GGAAAGGACGAAACACCGTTTACCTGGTCTACGGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTACCTGGTCTACGGATCG	
3048	B4gat1	B4gat1_3048	GGAAAGGACGAAACACCGCGAGGGGCACACGAGGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGGGGCACACGAGGTGCA	
3049	Rars2	Rars2_3049	GGAAAGGACGAAACACCGAAACCTGGTGGCATAGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACCTGGTGGCATAGAGAG	
3050	Rars2	Rars2_3050	GGAAAGGACGAAACACCGTGTCACCCATTTCTAGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCACCCATTTCTAGTCGG	
3051	Rars2	Rars2_3051	GGAAAGGACGAAACACCGTCAGCTTAAGTGTGATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCTTAAGTGTGATACAG	
3052	Rars2	Rars2_3052	GGAAAGGACGAAACACCGATTATCTTGATAGGTCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTATCTTGATAGGTCTGCT	
3053	Slc30a9	Slc30a9_3053	GGAAAGGACGAAACACCGAAGGACTCGGTGTCATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGACTCGGTGTCATCGTG	
3054	Slc30a9	Slc30a9_3054	GGAAAGGACGAAACACCGACTGAGACCGCTCTGGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGAGACCGCTCTGGAACG	
3055	Slc30a9	Slc30a9_3055	GGAAAGGACGAAACACCGATTATCTGATACTTGTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTATCTGATACTTGTAACC	
3056	Slc30a9	Slc30a9_3056	GGAAAGGACGAAACACCGCTACGAATGTCCAGAAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACGAATGTCCAGAAAGGA	
3057	Mmadhc	Mmadhc_3057	GGAAAGGACGAAACACCGTCTGTGAGGCAGTCCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGTGAGGCAGTCCCATTG	
3058	Mmadhc	Mmadhc_3058	GGAAAGGACGAAACACCGGTGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTGGCCTGATGAAACTAT	
3059	Mmadhc	Mmadhc_3059	GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACTAAAGAACAAAATCCT	
3060	Mmadhc	Mmadhc_3060	GGAAAGGACGAAACACCGTATGTAAATGAGTTTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGTAAATGAGTTTCAGGT	
3061	Mmaa	Mmaa_3061	GGAAAGGACGAAACACCGCGACCTACTCGAAATGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACCTACTCGAAATGTGAG	
3062	Mmaa	Mmaa_3062	GGAAAGGACGAAACACCGAGGACAGAGAGCTTGCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACAGAGAGCTTGCCTAG	
3063	Mmaa	Mmaa_3063	GGAAAGGACGAAACACCGTCAGGCCCTCTCCTACCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGCCCTCTCCTACCAGT	
3064	Mmaa	Mmaa_3064	GGAAAGGACGAAACACCGACTTGAGTGAAGGAGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTGAGTGAAGGAGCCATG	

No.	*Oligo name	*Oligo name	*Sequence(5'to3')	nt#	Remarks	5'	guide sequence	3'
3065	Trip11	Trip11_3065	GGAAAGGACGAAACACCGTACTGATCATAAACGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTGATCATAAACGAACCA	
3066	Trip11	Trip11_3066	GGAAAGGACGAAACACCGTTATTGAGTCAAGAAAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATTGAGTCAAGAAAAGGT	
3067	Trip11	Trip11_3067	GGAAAGGACGAAACACCGATCCTGTGAGTAGGACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTGTGAGTAGGACGCGG	
3068	Trip11	Trip11_3068	GGAAAGGACGAAACACCGGAAGGAGAACCATGAACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGGAGAACCATGAACTGA	
3069	Acy1	Acy1_3069	GGAAAGGACGAAACACCGAATCTGACCAAGCTTGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCTGACCAAGCTTGAAGG	
3070	Acy1	Acy1_3070	GGAAAGGACGAAACACCGTGTATCCTCAATGAAGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTATCCTCAATGAAGCGTG	
3071	Acy1	Acy1_3071	GGAAAGGACGAAACACCGGACAGGTACCACATCTGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAGGTACCACATCTGTGT	
3072	Acy1	Acy1_3072	GGAAAGGACGAAACACCGAAAGACAGTAAAGGCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGACAGTAAAGGCATCCG	
3073	Cyb5a	Cyb5a_3073	GGAAAGGACGAAACACCGGTCCAAAACATACATCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCAAAACATACATCATCG	
3074	Cyb5a	Cyb5a_3074	GGAAAGGACGAAACACCGTCTGACCAAGTTTCTCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGACCAAGTTTCTCGAAG	
3075	Cyb5a	Cyb5a_3075	GGAAAGGACGAAACACCGCTTATGATGCAGGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTATGATGCAGGATCACCC	
3076	Cyb5a	Cyb5a_3076	GGAAAGGACGAAACACCGGTCCTAAGAGAGCAAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCTAAGAGAGCAAGCTGG	
3077	Ampd2	Ampd2_3077	GGAAAGGACGAAACACCGCACTGCCTACGACTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTGCCTACGACTTAAGTG	
3078	Ampd2	Ampd2_3078	GGAAAGGACGAAACACCGCAAATGCAAGGAGATCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAATGCAAGGAGATCGCTG	
3079	Ampd2	Ampd2_3079	GGAAAGGACGAAACACCGTCATAAGTTCGAGTCTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATAAGTTCGAGTCTCCAG	
3080	Ampd2	Ampd2_3080	GGAAAGGACGAAACACCGATATTGTAGAAGTCCCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATTGTAGAAGTCCCGGTG	
3081	Cyb5r3	Cyb5r3_3081	GGAAAGGACGAAACACCGGTCATCATCGCTCGACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCATCATCGCTCGACACAG	
3082	Cyb5r3	Cyb5r3_3082	GGAAAGGACGAAACACCGACTTCACCGTCCTGACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTCACCGTCCTGACAACG	
3083	Cyb5r3	Cyb5r3_3083	GGAAAGGACGAAACACCGGGAGACACCATTGAATTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGACACCATTGAATTCCG	
3084	Cyb5r3	Cyb5r3_3084	GGAAAGGACGAAACACCGAGGTCATCAGTCCTGACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTCATCAGTCCTGACACT	
3085	Blvra	Blvra_3085	GGAAAGGACGAAACACCGTCTGAAACAGACGAGAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGAAACAGACGAGAACTT	
3086	Blvra	Blvra_3086	GGAAAGGACGAAACACCGTAAGAGAAAGCTCCCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGAGAAAGCTCCCCAAAG	
3087	Blvra	Blvra_3087	GGAAAGGACGAAACACCGATGCCATGGGGTATTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCCATGGGGTATTCCACG	
3088	Blvra	Blvra_3088	GGAAAGGACGAAACACCGTATAGGCGACATCAACCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATAGGCGACATCAACCTCT	
3089	Pgm3	Pgm3_3089	GGAAAGGACGAAACACCGTACGGCCTCACATAACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACGGCCTCACATAACCCTG	
3090	Pgm3	Pgm3_3090	GGAAAGGACGAAACACCGAACTTCTTCAAGGTACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTCTTCAAGGTACCGCG	
3091	Pgm3	Pgm3_3091	GGAAAGGACGAAACACCGTACACCATGTAGTGCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACCATGTAGTGCAACTG	
3092	Pgm3	Pgm3_3092	GGAAAGGACGAAACACCGCTGCTATGACATACCCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCTATGACATACCCTGTG	
3093	Asl	Asl_3093	GGAAAGGACGAAACACCGCTCGTGTCAGCGCAACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGTGTCAGCGCAACAGCG	
3094	Asl	Asl_3094	GGAAAGGACGAAACACCGTGGTTCCAATGAGCACCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTTCCAATGAGCACCCGG	
3095	Asl	Asl_3095	GGAAAGGACGAAACACCGAGATGCAGCAGATACTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGCAGCAGATACTGCAA	
3096	Asl	Asl_3096	GGAAAGGACGAAACACCGGCTGCAGGGAAGCTACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCAGGGAAGCTACACAC	
3097	Gusb	Gusb_3097	GGAAAGGACGAAACACCGGTATCTTGGGTCCATCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATCTTGGGTCCATCGCCG	
3098	Gusb	Gusb_3098	GGAAAGGACGAAACACCGTGTTCGAATCCCGATAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTCGAATCCCGATAGGAA	
3099	Gusb	Gusb_3099	GGAAAGGACGAAACACCGGGAGCGCGCACCTCCCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCGCGCACCTCCCGTAG	
3100	Gusb	Gusb_3100	GGAAAGGACGAAACACCGGGTGTCAGTCTTGTAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTCAGTCTTGTAGACGA	
3101	Phka2	Phka2_3101	GGAAAGGACGAAACACCGGGGTCATAATGCAATCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCATAATGCAATCGGTG	
3102	Phka2	Phka2_3102	GGAAAGGACGAAACACCGACAGTAGACCGAGTTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTAGACCGAGTTCCACT	
3103	Phka2	Phka2_3103	GGAAAGGACGAAACACCGCACAGAAAGTATGTCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGAAAGTATGTCCCGAG	
3104	Phka2	Phka2_3104	GGAAAGGACGAAACACCGCAAACAAATTGGTATCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACAAATTGGTATCCCAG	
3105	Pygl	Pygl_3105	GGAAAGGACGAAACACCGAAACCAACGGGATTACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACCAACGGGATTACCCCG	
3106	Pygl	Pygl_3106	GGAAAGGACGAAACACCGGGGCGAAGTAGTAGTCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCGAAGTAGTAGTCGCGG	
3107	Pygl	Pygl_3107	GGAAAGGACGAAACACCGCTTACAAAATGCCTGCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACAAAATGCCTGCGATG	
3108	Pygl	Pygl_3108	GGAAAGGACGAAACACCGAGGAGGCAAACGGATCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGGCAAACGGATCAACA	
3109	Cyp11b1	Cyp11b1_3109	GGAAAGGACGAAACACCGTTGCTATCCCATCCACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCTATCCCATCCACCAAG	
3110	Cyp11b1	Cyp11b1_3110	GGAAAGGACGAAACACCGATAGTCCATAGAGAACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGTCCATAGAGAACTCCG	
3111	Cyp11b1	Cyp11b1_3111	GGAAAGGACGAAACACCGCAAAGAAAGTCATTACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGAAAGTCATTACCAAG	
3112	Cyp11b1	Cyp11b1_3112	GGAAAGGACGAAACACCGGGCTCAGATCACGGCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTCAGATCACGGCCAATG	
3113	Mpi	Mpi_3113	GGAAAGGACGAAACACCGTGGATGGGGACACACCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGATGGGGACACACCCCCG	
3114	Mpi	Mpi_3114	GGAAAGGACGAAACACCGCGAAACATCCGATATCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAACATCCGATATCACCT	
3115	Mpi	Mpi_3115	GGAAAGGACGAAACACCGAGGGTGTGCCTGGATAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGTGTGCCTGGATAGACA	
3116	Mpi	Mpi_3116	GGAAAGGACGAAACACCGCAGGTAGGCATGGGGTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGTAGGCATGGGGTACGT	
3117	Manba	Manba_3117	GGAAAGGACGAAACACCGGTCTGGTTCCCATGTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCTGGTTCCCATGTCCACG	
3118	Manba	Manba_3118	GGAAAGGACGAAACACCGAACCAACGGGATGAAAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCAACGGGATGAAAACCA	
3119	Manba	Manba_3119	GGAAAGGACGAAACACCGGTTCACGTCTTTGACTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCACGTCTTTGACTACGT	
3120	Manba	Manba_3120	GGAAAGGACGAAACACCGTTGAAGTAGAAACTCAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAAGTAGAAACTCAGACC	
3121	Fdps	Fdps_3121	GGAAAGGACGAAACACCGAGATACACTGAAAAGAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATACACTGAAAAGAGGTG	
3122	Fdps	Fdps_3122	GGAAAGGACGAAACACCGCCAACTCACCATGTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACTCACCATGTACATGG	
3123	Fdps	Fdps_3123	GGAAAGGACGAAACACCGACAGATCTGCTGGTATCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGATCTGCTGGTATCAGA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3124	Fdps	Fdps_3124	GGAAAGGACGAAACACCGTTGCCCGGCTCAAGGAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCCCGGCTCAAGGAGGTG	
3125	Cox6b1	Cox6b1_3125	GGAAAGGACGAAACACCGAAGGCAATGACGGCCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCAATGACGGCCAAGGG	
3126	Cox6b1	Cox6b1_3126	GGAAAGGACGAAACACCGAACTGTTGGCAGAACTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTGTTGGCAGAACTACCT	
3127	Cox6b1	Cox6b1_3127	GGAAAGGACGAAACACCGAGAACCAGACTAAGAACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACCAGACTAAGAACTGT	
3128	Cox6b1	Cox6b1_3128	GGAAAGGACGAAACACCGACGCCGGTACCACTCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGCCGGTACCACTCACACA	
3129	Qdpr	Qdpr_3129	GGAAAGGACGAAACACCGTGTCATCTTAACAACCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCATCTTAACAACCACGC	
3130	Qdpr	Qdpr_3130	GGAAAGGACGAAACACCGCTTACCAGGAGTCCCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACCAGGAGTCCCATCCA	
3131	Qdpr	Qdpr_3131	GGAAAGGACGAAACACCGGGTGGATGCAATTCTCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGGATGCAATTCTCTGTG	
3132	Qdpr	Qdpr_3132	GGAAAGGACGAAACACCGCACGCAGTGTTACCCAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACGCAGTGTTACCCAGTTG	
3133	Pigh	Pigh_3133	GGAAAGGACGAAACACCGCTTGTCCATCTCTATGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGTCCATCTCTATGAAGG	
3134	Pigh	Pigh_3134	GGAAAGGACGAAACACCGGGTCAATCTTCACAAAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCAATCTTCACAAAATGG	
3135	Pigh	Pigh_3135	GGAAAGGACGAAACACCGTGATGAAGATGGTGGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGAAGATGGTGGCAGAG	
3136	Pigh	Pigh_3136	GGAAAGGACGAAACACCGTGAGTAGTAGCGGCACCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGTAGTAGCGGCACCGCA	
3137	Acat1	Acat1_3137	GGAAAGGACGAAACACCGGTCCCATACGTAATGAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCCATACGTAATGAGCAG	
3138	Acat1	Acat1_3138	GGAAAGGACGAAACACCGAGTGCTATAAGAACTCCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGCTATAAGAACTCCCAT	
3139	Acat1	Acat1_3139	GGAAAGGACGAAACACCGAGGCAAGCAACACTGGGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCAAGCAACACTGGGCGC	
3140	Acat1	Acat1_3140	GGAAAGGACGAAACACCGGCCTCTCAAAGTCTTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTCTCAAAGTCTTATGTG	
3141	Acat2	Acat2_3141	GGAAAGGACGAAACACCGCAAACCTGATGCGTTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACCTGATGCGTTCGCTG	
3142	Acat2	Acat2_3142	GGAAAGGACGAAACACCGCTGAGAACAGGAGTCAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAGAACAGGAGTCAGGAT	
3143	Acat2	Acat2_3143	GGAAAGGACGAAACACCGTCCTACTCGACAAGCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTACTCGACAAGCCAGTG	
3144	Acat2	Acat2_3144	GGAAAGGACGAAACACCGTGCCTTTCACAACTACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCTTTCACAACTACCACA	
3145	Aldh7a1	Aldh7a1_3145	GGAAAGGACGAAACACCGGGGCTCCGCGAGGATAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTCCGCGAGGATAACGA	
3146	Aldh7a1	Aldh7a1_3146	GGAAAGGACGAAACACCGTGGTGGAGCAGATATCGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGGAGCAGATATCGGGT	
3147	Aldh7a1	Aldh7a1_3147	GGAAAGGACGAAACACCGACACTAACGAGGGACGTAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTAACGAGGGACGTAGT	
3148	Aldh7a1	Aldh7a1_3148	GGAAAGGACGAAACACCGTAGATTCCTGCCCCAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATTCCTGCCCCAAAACG	
3149	Nr3c2	Nr3c2_3149	GGAAAGGACGAAACACCGGATGATTGGGCTCTTAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGATTGGGCTCTTAACGA	
3150	Nr3c2	Nr3c2_3150	GGAAAGGACGAAACACCGCAAGGAACTTTCAGCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGGAACTTTCAGCCACGG	
3151	Nr3c2	Nr3c2_3151	GGAAAGGACGAAACACCGTCCACTAATGCATTGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACTAATGCATTGACAGG	
3152	Nr3c2	Nr3c2_3152	GGAAAGGACGAAACACCGGAATGGAAATGGGTTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATGGAAATGGGTTGACTG	
3153	Pcca	Pcca_3153	GGAAAGGACGAAACACCGCTGGACAATTATGTGATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGACAATTATGTGATCCG	
3154	Pcca	Pcca_3154	GGAAAGGACGAAACACCGCCTGGATTTCTATATGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGATTTCTATATGACGA	
3155	Pcca	Pcca_3155	GGAAAGGACGAAACACCGGTAAACCGAAAGACTTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAACCGAAAGACTTGTAG	
3156	Pcca	Pcca_3156	GGAAAGGACGAAACACCGTTAGGTTCACGTGAAAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAGGTTCACGTGAAAATGG	
3157	Etfb	Etfb_3157	GGAAAGGACGAAACACCGCATCCACGTGGAGATACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCCACGTGGAGATACCAG	
3158	Etfb	Etfb_3158	GGAAAGGACGAAACACCGCCTGAGAGGCGAATGTACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGAGAGGCGAATGTACCC	
3159	Etfb	Etfb_3159	GGAAAGGACGAAACACCGAAAGCCGGACAAGTCTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCCGGACAAGTCTGGAG	
3160	Etfb	Etfb_3160	GGAAAGGACGAAACACCGCATGGCCAGAGCAGTTCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGCCAGAGCAGTTCGGA	
3161	Etfa	Etfa_3161	GGAAAGGACGAAACACCGTGGCGTAGCAAAGGTTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCGTAGCAAAGGTTCTGG	
3162	Etfa	Etfa_3162	GGAAAGGACGAAACACCGTTTGTGAGAACTATCTATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTGAGAACTATCTATGC	
3163	Etfa	Etfa_3163	GGAAAGGACGAAACACCGGGTAGTGCTAGTTCAGAAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAGTGCTAGTTCAGAAAA	
3164	Etfa	Etfa_3164	GGAAAGGACGAAACACCGAGTTACACACACATCTGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTACACACACATCTGTGC	
3165	Hlcs	Hlcs_3165	GGAAAGGACGAAACACCGCAGCAATGTGAGAAGACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCAATGTGAGAAGACACG	
3166	Hlcs	Hlcs_3166	GGAAAGGACGAAACACCGACAGTACCATTGACTCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTACCATTGACTCGGTG	
3167	Hlcs	Hlcs_3167	GGAAAGGACGAAACACCGATGGCCTATCTTTCTCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCCTATCTTTCTCAGGG	
3168	Hlcs	Hlcs_3168	GGAAAGGACGAAACACCGCGGCGGCCTTGCAATCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGCGGCCTTGCAATCACCT	
3169	Cldn16	Cldn16_3169	GGAAAGGACGAAACACCGGGCCACGATCAAAAACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCACGATCAAAAACCCAG	
3170	Cldn16	Cldn16_3170	GGAAAGGACGAAACACCGGAACGCTGATGACTCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACGCTGATGACTCCCTGG	
3171	Cldn16	Cldn16_3171	GGAAAGGACGAAACACCGAGTACCTGCAATGAGTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTACCTGCAATGAGTAATG	
3172	Cldn16	Cldn16_3172	GGAAAGGACGAAACACCGTATATTGTGTAAAACGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATATTGTGTAAAACGAGAG	
3173	Slc13a3	Slc13a3_3173	GGAAAGGACGAAACACCGAGTTTCTTGCCAGTTCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTTCTTGCCAGTTCGGAA	
3174	Slc13a3	Slc13a3_3174	GGAAAGGACGAAACACCGTCCAGAGCCAGCCCACCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGAGCCAGCCCACCAGT	
3175	Slc13a3	Slc13a3_3175	GGAAAGGACGAAACACCGGGCTAAAGCGGTGATCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTAAAGCGGTGATCCAGG	
3176	Slc13a3	Slc13a3_3176	GGAAAGGACGAAACACCGCCACCGTACCTTGGGCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCGTACCTTGGGCGGCA	
3177	Ddhd1	Ddhd1_3177	GGAAAGGACGAAACACCGTCGTTGCGCTACTACAGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTTGCGCTACTACAGCGA	
3178	Ddhd1	Ddhd1_3178	GGAAAGGACGAAACACCGTCAAAGCTTACTCTTGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAAGCTTACTCTTGATGG	
3179	Ddhd1	Ddhd1_3179	GGAAAGGACGAAACACCGGATAAAATACCAGTAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAAAATACCAGTAATGCG	
3180	Ddhd1	Ddhd1_3180	GGAAAGGACGAAACACCGATAAGTGATTACACACCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAGTGATTACACACCCCA	
3181	Slc19a2	Slc19a2_3181	GGAAAGGACGAAACACCGGGAGTAGTAGGCGATTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTAGTAGGCGATTTCGG	
3182	Slc19a2	Slc19a2_3182	GGAAAGGACGAAACACCGGACTCAGCCTGATTGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTCAGCCTGATTGTGACG	

No.	*Oligo name	*Oligo name	*Sequence（5’ to3’）	nt#	Remarks	5'	guide sequence	3'
3183	Slc19a2	Slc19a2_3183	GGAAAGGACGAAACACCGCAAGTGGTGAACTACGCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTGGTGAACTACGCGCA	
3184	Slc19a2	Slc19a2_3184	GGAAAGGACGAAACACCGGCAGGAACCAGCACTCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGAACCAGCACTCGCGA	
3185	Slc2a9	Slc2a9_3185	GGAAAGGACGAAACACCGCGGAGAGGTTGTACCCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGAGAGGTTGTACCCGTAG	
3186	Slc2a9	Slc2a9_3186	GGAAAGGACGAAACACCGGCATGCCATCAGCAACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATGCCATCAGCAACGCTG	
3187	Slc2a9	Slc2a9_3187	GGAAAGGACGAAACACCGCCAACTATGTGGACTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACTATGTGGACTCAATG	
3188	Slc2a9	Slc2a9_3188	GGAAAGGACGAAACACCGTCTCAACGAGATCTCACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCAACGAGATCTCACCCA	
3189	B3galt6	B3galt6_3189	GGAAAGGACGAAACACCGGCGCGCCAGGTACAACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCGCCAGGTACAACAGAG	
3190	B3galt6	B3galt6_3190	GGAAAGGACGAAACACCGCCTGGTGGACCTACGCGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGGTGGACCTACGCGCAC	
3191	B3galt6	B3galt6_3191	GGAAAGGACGAAACACCGGTTCTCGTAGGCGTCGCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCTCGTAGGCGTCGCGCA	
3192	B3galt6	B3galt6_3192	GGAAAGGACGAAACACCGTGGCGGACCCGAGGACGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCGGACCCGAGGACGTGT	
3193	Mrps2	Mrps2_3193	GGAAAGGACGAAACACCGCTTGCGGTAGGCCACGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGCGGTAGGCCACGTGCG	
3194	Mrps2	Mrps2_3194	GGAAAGGACGAAACACCGCCTGTGCCAACTACCTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTGCCAACTACCTATGG	
3195	Mrps2	Mrps2_3195	GGAAAGGACGAAACACCGCACACCCGCTACTTCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACACCCGCTACTTCAAGGG	
3196	Mrps2	Mrps2_3196	GGAAAGGACGAAACACCGGCGTATCTAGGATCCTGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTATCTAGGATCCTGCTC	
3197	Pofut1	Pofut1_3197	GGAAAGGACGAAACACCGTGTTGGTATTCAATCCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGGTATTCAATCCATGG	
3198	Pofut1	Pofut1_3198	GGAAAGGACGAAACACCGGCGCCTCCTACAAAGAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCTCCTACAAAGAACAA	
3199	Pofut1	Pofut1_3199	GGAAAGGACGAAACACCGCCGGAGGCCTTACCCATGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGAGGCCTTACCCATGCA	
3200	Pofut1	Pofut1_3200	GGAAAGGACGAAACACCGAGCTCCAGAAGTACATGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCCAGAAGTACATGGTG	
3201	Slc2a10	Slc2a10_3201	GGAAAGGACGAAACACCGCAGCCCCGTGGCGACCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCCCGTGGCGACCAAGG	
3202	Slc2a10	Slc2a10_3202	GGAAAGGACGAAACACCGAGAGGCGTAATACAGCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGCGTAATACAGCACAT	
3203	Slc2a10	Slc2a10_3203	GGAAAGGACGAAACACCGTGTGCTGGTGTCCCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGCTGGTGTCCCTCTACG	
3204	Slc2a10	Slc2a10_3204	GGAAAGGACGAAACACCGAGCCAACAGATAAACGGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCAACAGATAAACGGCCC	
3205	Bbox1	Bbox1_3205	GGAAAGGACGAAACACCGGTGGTGAGATCATAAAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTGAGATCATAAAACTT	
3206	Bbox1	Bbox1_3206	GGAAAGGACGAAACACCGTACACAGAATGTCAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACAGAATGTCAGTACTG	
3207	Bbox1	Bbox1_3207	GGAAAGGACGAAACACCGGTTGAAGCTCACCTTACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGAAGCTCACCTTACCCC	
3208	Bbox1	Bbox1_3208	GGAAAGGACGAAACACCGCAAGATTGATGCCAACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGATTGATGCCAACAATG	
3209	Idh3b	Idh3b_3209	GGAAAGGACGAAACACCGTTCACCCTTATACTCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCACCCTTATACTCCATTG	
3210	Idh3b	Idh3b_3210	GGAAAGGACGAAACACCGTCGGCACAACAATCTAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGCACAACAATCTAGACC	
3211	Idh3b	Idh3b_3211	GGAAAGGACGAAACACCGACAGGCACAAGATGTGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGGCACAAGATGTGAGGG	
3212	Idh3b	Idh3b_3212	GGAAAGGACGAAACACCGTAAGGAGCATCATCTGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGGAGCATCATCTGAGCG	
3213	Rtn4ip1	Rtn4ip1_3213	GGAAAGGACGAAACACCGATATTTATCTATCACCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATTTATCTATCACCCAAG	
3214	Rtn4ip1	Rtn4ip1_3214	GGAAAGGACGAAACACCGTGAGGTCATTGATTACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGTCATTGATTACACGT	
3215	Rtn4ip1	Rtn4ip1_3215	GGAAAGGACGAAACACCGGCAGGTAATGAAAGCATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGTAATGAAAGCATGGG	
3216	Rtn4ip1	Rtn4ip1_3216	GGAAAGGACGAAACACCGGAGAGCCACATATGGCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAGCCACATATGGCAAAG	
3217	Mfn2	Mfn2_3217	GGAAAGGACGAAACACCGCCGAGGCAGACGCATCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAGGCAGACGCATCCCAG	
3218	Mfn2	Mfn2_3218	GGAAAGGACGAAACACCGGTGGTATGACCAATCCCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGTATGACCAATCCCAGA	
3219	Mfn2	Mfn2_3219	GGAAAGGACGAAACACCGATAAACCTTGAGGACAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAACCTTGAGGACAACTG	
3220	Mfn2	Mfn2_3220	GGAAAGGACGAAACACCGAGAACTGGACCCGGTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAACTGGACCCGGTTACCA	
3221	Sugct	Sugct_3221	GGAAAGGACGAAACACCGAAGATCTCCTAAATTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGATCTCCTAAATTCATCG	
3222	Sugct	Sugct_3222	GGAAAGGACGAAACACCGGGTGATGACACACGATCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGATGACACACGATCTTG	
3223	Sugct	Sugct_3223	GGAAAGGACGAAACACCGAGGAGTGAGAATCGTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGTGAGAATCGTCAAAG	
3224	Sugct	Sugct_3224	GGAAAGGACGAAACACCGAATCTAAGGATACCTACCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCTAAGGATACCTACCTC	
3225	Mvd	Mvd_3225	GGAAAGGACGAAACACCGCCCGCCGAGCCACTTCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCGCCGAGCCACTTCGGAG	
3226	Mvd	Mvd_3226	GGAAAGGACGAAACACCGCATCTGGCTGAATGGTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCTGGCTGAATGGTCGCG	
3227	Mvd	Mvd_3227	GGAAAGGACGAAACACCGCCACGTGCACCTTATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGTGCACCTTATAGCTG	
3228	Mvd	Mvd_3228	GGAAAGGACGAAACACCGTGTTGTGCCTGAGCGCATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTGCCTGAGCGCATGA	
3229	Sardh	Sardh_3229	GGAAAGGACGAAACACCGCCTTGACTACGACTACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGACTACGACTACTACG	
3230	Sardh	Sardh_3230	GGAAAGGACGAAACACCGCGTCGTCACTGAGCGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCGTCACTGAGCGCATCG	
3231	Sardh	Sardh_3231	GGAAAGGACGAAACACCGAACCGAGTAGTTCTTGGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCGAGTAGTTCTTGGCAT	
3232	Sardh	Sardh_3232	GGAAAGGACGAAACACCGCGGTGACTGGCATCCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTGACTGGCATCCGTGTG	
3233	Klf11	Klf11_3233	GGAAAGGACGAAACACCGCAGTGTGATCCGTCACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGTGATCCGTCACACCG	
3234	Klf11	Klf11_3234	GGAAAGGACGAAACACCGAGCTCACGGAGCCGTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTCACGGAGCCGTCAACA	
3235	Klf11	Klf11_3235	GGAAAGGACGAAACACCGACCAGCATCACAGTTCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGCATCACAGTTCCCTG	
3236	Klf11	Klf11_3236	GGAAAGGACGAAACACCGCCTTGCTTGCACAAGTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTGCTTGCACAAGTCCGG	
3237	Tmem199	Tmem199_3237	GGAAAGGACGAAACACCGTAGCCAATGAGGAGTATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCCAATGAGGAGTATAAG	
3238	Tmem199	Tmem199_3238	GGAAAGGACGAAACACCGCGGAATGAAACCAGGCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGAATGAAACCAGGCGCCG	
3239	Tmem199	Tmem199_3239	GGAAAGGACGAAACACCGTTTCTGTTACATACCCGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCTGTTACATACCCGGGG	
3240	Tmem199	Tmem199_3240	GGAAAGGACGAAACACCGTGCTCTGGGAAAGAAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTCTGGGAAAGAAACACG	
3241	Alg11	Alg11_3241	GGAAAGGACGAAACACCGGGAAACCAGCAAATGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAACCAGCAAATGCCCTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3242	Alg11	Alg11_3242	GGAAAGGACGAAACACCGTTTCCTGGACTGATGATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCCTGGACTGATGATATG	
3243	Alg11	Alg11_3243	GGAAAGGACGAAACACCGAGTGAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGAACATAGCTTCCGACT	
3244	Alg11	Alg11_3244	GGAAAGGACGAAACACCGTAAACCATATCCTCTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAACCATATCCTCTCACTG	
3245	Alg1	Alg1_3245	GGAAAGGACGAAACACCGGTGAAGTTGACAGATCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAAGTTGACAGATCTGCG	
3246	Alg1	Alg1_3246	GGAAAGGACGAAACACCGTCTGGAAAGGAGAGTACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGAAAGGAGAGTACGTG	
3247	Alg1	Alg1_3247	GGAAAGGACGAAACACCGTGTGACCAATGCTATGCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGACCAATGCTATGCGGG	
3248	Alg1	Alg1_3248	GGAAAGGACGAAACACCGTGAGAGGGATTGTCAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGAGGGATTGTCAGAGCG	
3249	Alg3	Alg3_3249	GGAAAGGACGAAACACCGAAGAAGGAATAGCAATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAGGAATAGCAATCCCG	
3250	Alg3	Alg3_3250	GGAAAGGACGAAACACCGGGAAAAGAAACTGACGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAAAGAAACTGACGACCA	
3251	Alg3	Alg3_3251	GGAAAGGACGAAACACCGGCCACCAGCAATGTGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCACCAGCAATGTGTAGCG	
3252	Alg3	Alg3_3252	GGAAAGGACGAAACACCGATTGATGAAACCCTCCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGATGAAACCCTCCACCT	
3253	Slc25a38	Slc25a38_3253	GGAAAGGACGAAACACCGTCCAGGGACACATCTCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCAGGGACACATCTCACAA	
3254	Slc25a38	Slc25a38_3254	GGAAAGGACGAAACACCGCTGAGAAGGGGGCATCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAGAAGGGGGCATCACGG	
3255	Slc25a38	Slc25a38_3255	GGAAAGGACGAAACACCGAGAGGAAAGCCTTAATCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGAAAGCCTTAATCACT	
3256	Slc25a38	Slc25a38_3256	GGAAAGGACGAAACACCGAGTGATCAAGACACGCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGATCAAGACACGCTATG	
3257	Akr1d1	Akr1d1_3257	GGAAAGGACGAAACACCGTTGTCTGGGTGAAATACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTCTGGGTGAAATACGGG	
3258	Akr1d1	Akr1d1_3258	GGAAAGGACGAAACACCGTGAAGACAGCTATTGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGACAGCTATTGATGAG	
3259	Akr1d1	Akr1d1_3259	GGAAAGGACGAAACACCGAACAAATCTGTGTGCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAAATCTGTGTGCCACGT	
3260	Akr1d1	Akr1d1_3260	GGAAAGGACGAAACACCGGGGCTGGGAGGACCATTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCTGGGAGGACCATTGAT	
3261	Zdhhc9	Zdhhc9_3261	GGAAAGGACGAAACACCGTGGAAATTCTTAATACGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAATTCTTAATACGAGG	
3262	Zdhhc9	Zdhhc9_3262	GGAAAGGACGAAACACCGGTGCTCGAGGAATCACTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCTCGAGGAATCACTCCA	
3263	Zdhhc9	Zdhhc9_3263	GGAAAGGACGAAACACCGAGAAGAGTGTACATGTCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAGAGTGTACATGTCCCC	
3264	Zdhhc9	Zdhhc9_3264	GGAAAGGACGAAACACCGAAGAGCATAGCGGCAAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGCATAGCGGCAAACAC	
3265	Pycr1	Pycr1_3265	GGAAAGGACGAAACACCGCCGGGGTGTTAGTCATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGGGTGTTAGTCATACAT	
3266	Pycr1	Pycr1_3266	GGAAAGGACGAAACACCGTTGGGGCGAACATTGAGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGGGCGAACATTGAGGAC	
3267	Pycr1	Pycr1_3267	GGAAAGGACGAAACACCGCACAGGTACTCACGCTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGGTACTCACGCTCAGG	
3268	Pycr1	Pycr1_3268	GGAAAGGACGAAACACCGGGAGGGCCGAGACCGTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGGCCGAGACCGTAGCT	
3269	Dhtkd1	Dhtkd1_3269	GGAAAGGACGAAACACCGCTGATGTTCCGTAAAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGATGTTCCGTAAAATGCG	
3270	Dhtkd1	Dhtkd1_3270	GGAAAGGACGAAACACCGGCCACGGTGAAGAGATACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCACGGTGAAGAGATACGG	
3271	Dhtkd1	Dhtkd1_3271	GGAAAGGACGAAACACCGTCTTCTTTAGGAAAGCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCTTTAGGAAAGCTCGT	
3272	Dhtkd1	Dhtkd1_3272	GGAAAGGACGAAACACCGGATGGGGACTACTCCCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGGGACTACTCCCCGAA	
3273	Mtrr	Mtrr_3273	GGAAAGGACGAAACACCGGATGAAGCGGTTGTAATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGAAGCGGTTGTAATCAG	
3274	Mtrr	Mtrr_3274	GGAAAGGACGAAACACCGGGTGAGCAAAATAGTCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGAGCAAAATAGTCCGTG	
3275	Mtrr	Mtrr_3275	GGAAAGGACGAAACACCGGAACAAAATGAGACAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACAAAATGAGACAAACAG	
3276	Mtrr	Mtrr_3276	GGAAAGGACGAAACACCGCTCGACCGTACTCATGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGACCGTACTCATGTGCA	
3277	Sepsecs	Sepsecs_3277	GGAAAGGACGAAACACCGGAGGACGTCTAAGGACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGACGTCTAAGGACGGCG	
3278	Sepsecs	Sepsecs_3278	GGAAAGGACGAAACACCGTAAGCGTTGTTGACTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGCGTTGTTGACTACATG	
3279	Sepsecs	Sepsecs_3279	GGAAAGGACGAAACACCGCAGGACTTCTGGTCTATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGACTTCTGGTCTATCCG	
3280	Sepsecs	Sepsecs_3280	GGAAAGGACGAAACACCGCACCGGATCGTCCAATTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGGATCGTCCAATTCCG	
3281	Cln5	Cln5_3281	GGAAAGGACGAAACACCGGACAAAATTCGAACAGTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAAAATTCGAACAGTCGT	
3282	Cln5	Cln5_3282	GGAAAGGACGAAACACCGCCAGCGTTGCCCAGACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGTTGCCCAGACGTCG	
3283	Cln5	Cln5_3283	GGAAAGGACGAAACACCGGCCCCTTGGTTACACCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCCTTGGTTACACCAGAA	
3284	Cln5	Cln5_3284	GGAAAGGACGAAACACCGATATTTAAATTCCCAAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATTTAAATTCCCAAATCG	
3285	Suox	Suox_3285	GGAAAGGACGAAACACCGAGGGGGACATGCTATCTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGGACATGCTATCTTCG	
3286	Suox	Suox_3286	GGAAAGGACGAAACACCGTCCTCTTTAGAGTACATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTCTTTAGAGTACATCCG	
3287	Suox	Suox_3287	GGAAAGGACGAAACACCGAAACTTATGCAAATCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTTATGCAAATCATCCA	
3288	Suox	Suox_3288	GGAAAGGACGAAACACCGCAGTCCTTCAAAACAGACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTCCTTCAAAACAGACAT	
3289	Pde12	Pde12_3289	GGAAAGGACGAAACACCGAGCTGTCGGAGAACACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGTCGGAGAACACCGCG	
3290	Pde12	Pde12_3290	GGAAAGGACGAAACACCGAGCTTGGATCGAGACCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTTGGATCGAGACCGGTG	
3291	Pde12	Pde12_3291	GGAAAGGACGAAACACCGTCTTGGTGTACAGATGTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTGGTGTACAGATGTCGA	
3292	Pde12	Pde12_3292	GGAAAGGACGAAACACCGAAGAACCGAGCCCACTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAACCGAGCCCACTCGAG	
3293	Zfyve26	Zfyve26_3293	GGAAAGGACGAAACACCGGAAGTCCTCACCTATCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTCCTCACCTATCGCCG	
3294	Zfyve26	Zfyve26_3294	GGAAAGGACGAAACACCGCCTTCCCGAGGACTATGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTTCCCGAGGACTATGCCG	
3295	Zfyve26	Zfyve26_3295	GGAAAGGACGAAACACCGCTGAATCCTGATGGTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAATCCTGATGGTATGCG	
3296	Zfyve26	Zfyve26_3296	GGAAAGGACGAAACACCGGGCCCTGGACATACTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCCTGGACATACTAACTG	
3297	Aldh4a1	Aldh4a1_3297	GGAAAGGACGAAACACCGGTTCAACGCAAAGTTCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCAACGCAAAGTTCGCCG	
3298	Aldh4a1	Aldh4a1_3298	GGAAAGGACGAAACACCGCGCTCGGCATTCGAGTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCTCGGCATTCGAGTACGG	
3299	Aldh4a1	Aldh4a1_3299	GGAAAGGACGAAACACCGCAACTGGTACTGTATATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACTGGTACTGTATATCGG	
3300	Aldh4a1	Aldh4a1_3300	GGAAAGGACGAAACACCGACCTTTATGACAGGGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTTATGACAGGGCAACG	

No.	*Oligo name	*Oligo name	*Sequence(5’ to3’)	nt#	Remarks	5'	guide sequence	3'
3301	Mars2	Mars2_3301	GGAAAGGACGAAACACCGACTCGCAGACCATCTACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCGCAGACCATCTACGTG	
3302	Mars2	Mars2_3302	GGAAAGGACGAAACACCGGAGTGGACATAGATGCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTGGACATAGATGCGATG	
3303	Mars2	Mars2_3303	GGAAAGGACGAAACACCGTCGATCGCACAGCTCGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGATCGCACAGCTCGATCG	
3304	Mars2	Mars2_3304	GGAAAGGACGAAACACCGTGTCCCGTGTCTCTCGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCCGTGTCTCTCGAGAG	
3305	Dse	Dse_3305	GGAAAGGACGAAACACCGGTCAAAGTATAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCAAAGTATAAGCATGACC	
3306	Dse	Dse_3306	GGAAAGGACGAAACACCGCAGCACACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCACACAGAACATTGCCA	
3307	Dse	Dse_3307	GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTTCATACATATAGCCCG	
3308	Dse	Dse_3308	GGAAAGGACGAAACACCGTAATGAACGGCACACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATGAACGGCACACCATTG	
3309	Kctd7	Kctd7_3309	GGAAAGGACGAAACACCGCGGTACTTCATCGATCGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGTACTTCATCGATCGAGA	
3310	Kctd7	Kctd7_3310	GGAAAGGACGAAACACCGCCGCAGAGTAGACAAGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCAGAGTAGACAAGCGCG	
3311	Kctd7	Kctd7_3311	GGAAAGGACGAAACACCGGTAATGCCGCCCGCTGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAATGCCGCCCGCTGAACA	
3312	Kctd7	Kctd7_3312	GGAAAGGACGAAACACCGGAGAACATGCAGCCACTGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAACATGCAGCCACTGAA	
3313	Slc39a14	Slc39a14_3313	GGAAAGGACGAAACACCGGAGCGAGCGATCTCAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCGAGCGATCTCAGATCG	
3314	Slc39a14	Slc39a14_3314	GGAAAGGACGAAACACCGGTAGAGGGTTCCAATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGAGGGTTCCAATCGCCA	
3315	Slc39a14	Slc39a14_3315	GGAAAGGACGAAACACCGTAAAATGGTTATGCCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAAATGGTTATGCCCGTGA	
3316	Slc39a14	Slc39a14_3316	GGAAAGGACGAAACACCGGTGACCGAGAAGCTACAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCGAGAAGCTACAGAA	
3317	Slc18a2	Slc18a2_3317	GGAAAGGACGAAACACCGCGAGCCATACGTACCTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGCCATACGTACCTACGA	
3318	Slc18a2	Slc18a2_3318	GGAAAGGACGAAACACCGCCATCTGCTTTGCAAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCTGCTTTGCAAACATG	
3319	Slc18a2	Slc18a2_3319	GGAAAGGACGAAACACCGGTACATACCTAAGACCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACATACCTAAGACCCCCA	
3320	Slc18a2	Slc18a2_3320	GGAAAGGACGAAACACCGATGCAGAATCCAGCAAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCAGAATCCAGCAAACAT	
3321	Gnptg	Gnptg_3321	GGAAAGGACGAAACACCGGGCCTACCTAACAAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTACCTAACAAAGAGTG	
3322	Gnptg	Gnptg_3322	GGAAAGGACGAAACACCGCTGTGGAAAGATCAACCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGGAAAGATCAACCGAC	
3323	Gnptg	Gnptg_3323	GGAAAGGACGAAACACCGTTACCCAAGGATCCCGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACCCAAGGATCCCGCTGT	
3324	Gnptg	Gnptg_3324	GGAAAGGACGAAACACCGACAATACCTTCAAGGGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAATACCTTCAAGGGCATG	
3325	Aldh5a1	Aldh5a1_3325	GGAAAGGACGAAACACCGCCTCTGCCAAAGATAAGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCTGCCAAAGATAAGCGA	
3326	Aldh5a1	Aldh5a1_3326	GGAAAGGACGAAACACCGACTGTCAAAGACAATGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTCAAAGACAATGAATG	
3327	Aldh5a1	Aldh5a1_3327	GGAAAGGACGAAACACCGACACCAATGGATCGGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCAATGGATCGGTACAC	
3328	Aldh5a1	Aldh5a1_3328	GGAAAGGACGAAACACCGAGACACACCCTATTCCGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACACACCCTATTCCGCCC	
3329	Spg11	Spg11_3329	GGAAAGGACGAAACACCGTCCCCGGAAACACAACGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCCGGAAACACAACGCGT	
3330	Spg11	Spg11_3330	GGAAAGGACGAAACACCGATTCCCGGGGATGTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCCGGGGATGTCCCACG	
3331	Spg11	Spg11_3331	GGAAAGGACGAAACACCGTCATTCCGCTCAACGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATTCCGCTCAACGACTGG	
3332	Spg11	Spg11_3332	GGAAAGGACGAAACACCGAGAGCTACAAATCCCGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTACAAATCCCGTGCA	
3333	Pomgnt2	Pomgnt2_3333	GGAAAGGACGAAACACCGAAAGCCGTATTGGTACCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCCGTATTGGTACCAGG	
3334	Pomgnt2	Pomgnt2_3334	GGAAAGGACGAAACACCGTCAACCACGGTAGCCCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAACCACGGTAGCCCCGCG	
3335	Pomgnt2	Pomgnt2_3335	GGAAAGGACGAAACACCGGTGGCTCTGCTACTCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCTCTGCTACTCCAATG	
3336	Pomgnt2	Pomgnt2_3336	GGAAAGGACGAAACACCGAGACGTGCATGAGGTTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACGTGCATGAGGTTATCG	
3337	Micu1	Micu1_3337	GGAAAGGACGAAACACCGATGGGATCTCCACTAGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGATCTCCACTAGACCG	
3338	Micu1	Micu1_3338	GGAAAGGACGAAACACCGTTCTTGCTGTTAACGCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTTGCTGTTAACGCATGG	
3339	Micu1	Micu1_3339	GGAAAGGACGAAACACCGTTGAAAGTAATCAACGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAAAGTAATCAACGAACC	
3340	Micu1	Micu1_3340	GGAAAGGACGAAACACCGCCGAACATAAGCCAGACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAACATAAGCCAGACTTG	
3341	Iba57	Iba57_3341	GGAAAGGACGAAACACCGCAGACTCCCAGAGTGTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGACTCCCAGAGTGTACGG	
3342	Iba57	Iba57_3342	GGAAAGGACGAAACACCGGAAGATCACAGACTCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGATCACAGACTCCCTCG	
3343	Iba57	Iba57_3343	GGAAAGGACGAAACACCGACGGGCTAGGCAGTGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGGCTAGGCAGTGACTCG	
3344	Iba57	Iba57_3344	GGAAAGGACGAAACACCGACCCCCGGACTGCACGTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCCCGGACTGCACGTATG	
3345	Ptrh2	Ptrh2_3345	GGAAAGGACGAAACACCGCTCAAAGAGTGGGAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAAAGAGTGGGAGTACTG	
3346	Ptrh2	Ptrh2_3346	GGAAAGGACGAAACACCGACTGACCTTAAAATGGGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGACCTTAAAATGGGGAA	
3347	Ptrh2	Ptrh2_3347	GGAAAGGACGAAACACCGCCCCCAGAACTCAACAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCCCAGAACTCAACAAGTG	
3348	Ptrh2	Ptrh2_3348	GGAAAGGACGAAACACCGGTTGCTTGTGGCATGTGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCTTGTGGCATGTGCCT	
3349	Xylt2	Xylt2_3349	GGAAAGGACGAAACACCGGTATACAGATGACCCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATACAGATGACCCCCTCG	
3350	Xylt2	Xylt2_3350	GGAAAGGACGAAACACCGGTGCCACTGACTATCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCACTGACTATCCAACG	
3351	Xylt2	Xylt2_3351	GGAAAGGACGAAACACCGTGTAGGCGATGCGTACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAGGCGATGCGTACTGGA	
3352	Xylt2	Xylt2_3352	GGAAAGGACGAAACACCGGGACGTCGCTGAGTCCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACGTCGCTGAGTCCGCCA	
3353	Nags	Nags_3353	GGAAAGGACGAAACACCGGGATGAACTAAGGCACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATGAACTAAGGCACAACG	
3354	Nags	Nags_3354	GGAAAGGACGAAACACCGCAGCTACGGTGGCATCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCTACGGTGGCATCGTCG	
3355	Nags	Nags_3355	GGAAAGGACGAAACACCGGACAGCCAGAAGGTGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAGCCAGAAGGTGCCGTG	
3356	Nags	Nags_3356	GGAAAGGACGAAACACCGGCTAGCGGCTGTAATGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTAGCGGCTGTAATGACTG	
3357	Mgat2	Mgat2_3357	GGAAAGGACGAAACACCGGAAGTTCAACTGGTACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTTCAACTGGTACACCA	
3358	Mgat2	Mgat2_3358	GGAAAGGACGAAACACCGTGTAATGGCCGAAGGAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAATGGCCGAAGGAGTCA	
3359	Mgat2	Mgat2_3359	GGAAAGGACGAAACACCGAAAAGTCTGGGGCTAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGTCTGGGGCTAAGTAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3360	Mgat2	Mgat2_3360	GGAAAGGACGAAACACCGCTGGACGCGGAGCCCGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGACGCGGAGCCCGTACG	
3361	L2hgdh	L2hgdh_3361	GGAAAGGACGAAACACCGCGGACGCCGGTCCACTTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGGACGCCGGTCCACTTGCG	
3362	L2hgdh	L2hgdh_3362	GGAAAGGACGAAACACCGAACAGCGGTGTCATACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGCGGTGTCATACACAG	
3363	L2hgdh	L2hgdh_3363	GGAAAGGACGAAACACCGGCTATTGATTGTCCATACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTATTGATTGTCCATACAC	
3364	L2hgdh	L2hgdh_3364	GGAAAGGACGAAACACCGGACCGTATTTCAGAGTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCGTATTTCAGAGTTGAG	
3365	Coq6	Coq6_3365	GGAAAGGACGAAACACCGAGACACCGTGTACGACGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACACCGTGTACGACGTGG	
3366	Coq6	Coq6_3366	GGAAAGGACGAAACACCGGGCCTTGATAATGTTCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCTTGATAATGTTCGACA	
3367	Coq6	Coq6_3367	GGAAAGGACGAAACACCGCTAGGGTAATATGGACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGGGTAATATGGACCCAA	
3368	Coq6	Coq6_3368	GGAAAGGACGAAACACCGGTGTGATGTGGACCAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTGATGTGGACCAGACCA	
3369	Pomt2	Pomt2_3369	GGAAAGGACGAAACACCGTGGACAGATCCAGTACGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGACAGATCCAGTACGGTG	
3370	Pomt2	Pomt2_3370	GGAAAGGACGAAACACCGGTAGTCCTTATGCAAATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGTCCTTATGCAAATAGG	
3371	Pomt2	Pomt2_3371	GGAAAGGACGAAACACCGCCTGCACAGTCACTATCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCACAGTCACTATCATG	
3372	Pomt2	Pomt2_3372	GGAAAGGACGAAACACCGTCTTTATCATCGTGCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTATCATCGTGCAAGTG	
3373	B4galt7	B4galt7_3373	GGAAAGGACGAAACACCGCACTACAAGACCTATGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTACAAGACCTATGTGGG	
3374	B4galt7	B4galt7_3374	GGAAAGGACGAAACACCGCTACATCGCCATGCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACATCGCCATGCACGATG	
3375	B4galt7	B4galt7_3375	GGAAAGGACGAAACACCGGGAAGATGGAGCATTTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGATGGAGCATTTCCGG	
3376	B4galt7	B4galt7_3376	GGAAAGGACGAAACACCGTCGGGCAGCACTCATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGGGCAGCACTCATCAATG	
3377	Alg12	Alg12_3377	GGAAAGGACGAAACACCGGTACCAAAGAAGACTGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACCAAAGAAGACTGACGG	
3378	Alg12	Alg12_3378	GGAAAGGACGAAACACCGAAGCGAGAGCACATAAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGAGAGCACATAAACCA	
3379	Alg12	Alg12_3379	GGAAAGGACGAAACACCGTGTAGGGACATATAACCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAGGGACATATAACCAGG	
3380	Alg12	Alg12_3380	GGAAAGGACGAAACACCGCTGAACAAAAGTTCCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAACAAAAGTTCCAACTG	
3381	Poglut1	Poglut1_3381	GGAAAGGACGAAACACCGATGATATCATGTATCCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATATCATGTATCCTGCG	
3382	Poglut1	Poglut1_3382	GGAAAGGACGAAACACCGATTTCTTGACCAAATTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTCTTGACCAAATTAACA	
3383	Poglut1	Poglut1_3383	GGAAAGGACGAAACACCGGGACCCCAGAGGATACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACCCCAGAGGATACCTGG	
3384	Poglut1	Poglut1_3384	GGAAAGGACGAAACACCGGAGGACCTGACTCCTTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGACCTGACTCCTTTCCG	
3385	Aars2	Aars2_3385	GGAAAGGACGAAACACCGAGGACGCCATAACGACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACGCCATAACGACCTGG	
3386	Aars2	Aars2_3386	GGAAAGGACGAAACACCGCTACACTCTTCACCCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACACTCTTCACCCCAACG	
3387	Aars2	Aars2_3387	GGAAAGGACGAAACACCGGATAGACACAGCGTACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAGACACAGCGTACCGAG	
3388	Aars2	Aars2_3388	GGAAAGGACGAAACACCGGAGGCTACCTTGTCCGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGCTACCTTGTCCGTACA	
3389	Pex6	Pex6_3389	GGAAAGGACGAAACACCGTGTAACTCTCGAGCAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAACTCTCGAGCAAACGG	
3390	Pex6	Pex6_3390	GGAAAGGACGAAACACCGAGGAAATGCCGTCTGCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAAATGCCGTCTGCACAT	
3391	Pex6	Pex6_3391	GGAAAGGACGAAACACCGGCACGGGGAGGGTCTCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACGGGGAGGGTCTCCCCG	
3392	Pex6	Pex6_3392	GGAAAGGACGAAACACCGAGCACACAGCTCATTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCACACAGCTCATTTACCA	
3393	Ndufs8	Ndufs8_3393	GGAAAGGACGAAACACCGATGTGGACAGAACTCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTGGACAGAACTCATCCG	
3394	Ndufs8	Ndufs8_3394	GGAAAGGACGAAACACCGTCAGTGGGCCCTTCTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTGGGCCCTTCTCAAAG	
3395	Ndufs8	Ndufs8_3395	GGAAAGGACGAAACACCGAAGCCTTCATAGCAGCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCTTCATAGCAGCGCAG	
3396	Ndufs8	Ndufs8_3396	GGAAAGGACGAAACACCGCCGAGCTGCATTGTCAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGAGCTGCATTGTCAGTTG	
3397	Trpm6	Trpm6_3397	GGAAAGGACGAAACACCGAGAGTGCATACAGTTTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTGCATACAGTTTAGCG	
3398	Trpm6	Trpm6_3398	GGAAAGGACGAAACACCGTGTCAACAGTTATGGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCAACAGTTATGGCCGAG	
3399	Trpm6	Trpm6_3399	GGAAAGGACGAAACACCGAGGTCATGATGTAGCGATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTCATGATGTAGCGATAG	
3400	Trpm6	Trpm6_3400	GGAAAGGACGAAACACCGTATTCTATAGCTCGAGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATTCTATAGCTCGAGAGAA	
3401	Cox15	Cox15_3401	GGAAAGGACGAAACACCGAGAAAGGGTTGGCTCAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAAGGGTTGGCTCAACCG	
3402	Cox15	Cox15_3402	GGAAAGGACGAAACACCGAGGCGGTACTGACTGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCGGTACTGACTGACCCG	
3403	Cox15	Cox15_3403	GGAAAGGACGAAACACCGGGTACATGGAATACTCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTACATGGAATACTCACAC	
3404	Cox15	Cox15_3404	GGAAAGGACGAAACACCGTAGGGTGGCGTCCAGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGGTGGCGTCCAGAACAC	
3405	Lct	Lct_3405	GGAAAGGACGAAACACCGTGAGTTGTTCGATAGCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGTTGTTCGATAGCTATG	
3406	Lct	Lct_3406	GGAAAGGACGAAACACCGTCAGCCTATCAAATCGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCCTATCAAATCGAAGG	
3407	Lct	Lct_3407	GGAAAGGACGAAACACCGCTCCCGTGGATACGCCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCCGTGGATACGCCCCAG	
3408	Lct	Lct_3408	GGAAAGGACGAAACACCGCTTAAACTTGTACATCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTAAACTTGTACATCAACG	
3409	Dars2	Dars2_3409	GGAAAGGACGAAACACCGGTTGCTCGGACCAACACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCTCGGACCAACACATG	
3410	Dars2	Dars2_3410	GGAAAGGACGAAACACCGTCTTCTAAGAAAATGCCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCTAAGAAAATGCCGAC	
3411	Dars2	Dars2_3411	GGAAAGGACGAAACACCGTAGACAGCCAGAGTTCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGACAGCCAGAGTTCACTC	
3412	Dars2	Dars2_3412	GGAAAGGACGAAACACCGAAAGCAATATGTGTTCATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGCAATATGTGTTCATGA	
3413	Ndufs2	Ndufs2_3413	GGAAAGGACGAAACACCGGCGGCGTATATCCGACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGCGTATATCCGACCTGG	
3414	Ndufs2	Ndufs2_3414	GGAAAGGACGAAACACCGTAGCACTCACCATTCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCACTCACCATTCCAAGG	
3415	Ndufs2	Ndufs2_3415	GGAAAGGACGAAACACCGCCTCGGGCACAGTGGATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTCGGGCACAGTGGATCCG	
3416	Ndufs2	Ndufs2_3416	GGAAAGGACGAAACACCGCACATCGGGCTCCTGCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACATCGGGCTCCTGCACCG	
3417	Slc30a10	Slc30a10_3417	GGAAAGGACGAAACACCGCCATGACAACAGTCAAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATGACAACAGTCAAACTG	
3418	Slc30a10	Slc30a10_3418	GGAAAGGACGAAACACCGAGCCGTGATGACCACAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCGTGATGACCACAACCA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3419	Slc30a10	Slc30a10_3419	GGAAAGGACGAAACACCGGCACAGCAGTGACTCTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAGCAGTGACTCTCCGG	
3420	Slc30a10	Slc30a10_3420	GGAAAGGACGAAACACCGTGCTGCAGATGGTCCCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTGCAGATGGTCCCCAAG	
3421	Hhat	Hhat_3421	GGAAAGGACGAAACACCGCTGAGCCACGCAGAACGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGAGCCACGCAGAACGCGA	
3422	Hhat	Hhat_3422	GGAAAGGACGAAACACCGGCACAGACCCTGGATTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACAGACCCTGGATTGTCA	
3423	Hhat	Hhat_3423	GGAAAGGACGAAACACCGGACGGGATAATAGAAGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACGGGATAATAGAAGACGT	
3424	Hhat	Hhat_3424	GGAAAGGACGAAACACCGAGAGGGCATGCATGTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGGCATGCATGTACATG	
3425	Hibch	Hibch_3425	GGAAAGGACGAAACACCGAGTCCATGGTCAATTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCCATGGTCAATTCCGAG	
3426	Hibch	Hibch_3426	GGAAAGGACGAAACACCGCAGATGTTGCAGAATAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATGTTGCAGAATAACGC	
3427	Hibch	Hibch_3427	GGAAAGGACGAAACACCGCCTGCAACATCCTCAGCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCAACATCCTCAGCTGA	
3428	Hibch	Hibch_3428	GGAAAGGACGAAACACCGCTATTGCAGACCTTTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATTGCAGACCTTTAGCTG	
3429	Ndufs1	Ndufs1_3429	GGAAAGGACGAAACACCGAATGGATCTCTGATAAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGGATCTCTGATAAAACC	
3430	Ndufs1	Ndufs1_3430	GGAAAGGACGAAACACCGTGTCCTATTTGTGACCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCTATTTGTGACCAGGG	
3431	Ndufs1	Ndufs1_3431	GGAAAGGACGAAACACCGTAGAGGTTAGGGCCCCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAGGTTAGGGCCCCTACA	
3432	Ndufs1	Ndufs1_3432	GGAAAGGACGAAACACCGTGATGGTCAGTCTGTCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGGTCAGTCTGTCATGG	
3433	Cps1	Cps1_3433	GGAAAGGACGAAACACCGTGAGCCTCACAATTTCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCCTCACAATTTCGTCG	
3434	Cps1	Cps1_3434	GGAAAGGACGAAACACCGATGCAGACCGAATCATCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCAGACCGAATCATCACA	
3435	Cps1	Cps1_3435	GGAAAGGACGAAACACCGTACAGTATTCCATGGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGTATTCCATGGAAGTG	
3436	Cps1	Cps1_3436	GGAAAGGACGAAACACCGGTTGGTGGCATCTCGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGTGGCATCTCGTGTCG	
3437	Man1b1	Man1b1_3437	GGAAAGGACGAAACACCGGAGCACCATTCGCATCTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCACCATTCGCATCTTAG	
3438	Man1b1	Man1b1_3438	GGAAAGGACGAAACACCGGGTTACCAAAAGTTTGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTACCAAAAGTTTGCTTG	
3439	Man1b1	Man1b1_3439	GGAAAGGACGAAACACCGGTGGACTTCAGACAGCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGACTTCAGACAGCACGG	
3440	Man1b1	Man1b1_3440	GGAAAGGACGAAACACCGATGTTCATCAACACGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTCATCAACACGAACAG	
3441	Coq4	Coq4_3441	GGAAAGGACGAAACACCGTCATCGTCCACAAAGCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATCGTCCACAAAGCGTGT	
3442	Coq4	Coq4_3442	GGAAAGGACGAAACACCGGCGTACGGGGCCGAAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTACGGGGCCGAAGACTG	
3443	Coq4	Coq4_3443	GGAAAGGACGAAACACCGCCAGGAAGCGAAGATACTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGAAGCGAAGATACTCA	
3444	Coq4	Coq4_3444	GGAAAGGACGAAACACCGCTCTACAACCCCTATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTACAACCCCTATCGCCA	
3445	Dolk	Dolk_3445	GGAAAGGACGAAACACCGGGACCGATACTCCTGGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACCGATACTCCTGGTGCG	
3446	Dolk	Dolk_3446	GGAAAGGACGAAACACCGCAGTGTAGGCGAGGTGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGTAGGCGAGGTGATCG	
3447	Dolk	Dolk_3447	GGAAAGGACGAAACACCGAAAGTATTTCCACTTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTATTTCCACTTCATTG	
3448	Dolk	Dolk_3448	GGAAAGGACGAAACACCGCCAGCAAAGACCAATAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCAAAGACCAATAGGCA	
3449	Agps	Agps_3449	GGAAAGGACGAAACACCGGTACCAATGAGTGCAAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACCAATGAGTGCAAAGCG	
3450	Agps	Agps_3450	GGAAAGGACGAAACACCGGTAAAACCAAGCCACTAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAAACCAAGCCACTAAGT	
3451	Agps	Agps_3451	GGAAAGGACGAAACACCGTCAGAGAAGGGATGTTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGAGAAGGGATGTTTGAG	
3452	Agps	Agps_3452	GGAAAGGACGAAACACCGTCCCTGGAATTCAGCACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCCTGGAATTCAGCACCGT	
3453	Slc35c1	Slc35c1_3453	GGAAAGGACGAAACACCGAGGGCACCCCTACGTACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCACCCCTACGTACTTG	
3454	Slc35c1	Slc35c1_3454	GGAAAGGACGAAACACCGAGGTTAGGCGCCAGATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTTAGGCGCCAGATACTG	
3455	Slc35c1	Slc35c1_3455	GGAAAGGACGAAACACCGCTCACCAATGATGACGCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCAATGATGACGCCGC	
3456	Slc35c1	Slc35c1_3456	GGAAAGGACGAAACACCGGCAGTGAGGTCACCAGGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTGAGGTCACCAGGCAT	
3457	Acad9	Acad9_3457	GGAAAGGACGAAACACCGTCTGCCCAAACTGTCGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGCCCAAACTGTCGTCTG	
3458	Acad9	Acad9_3458	GGAAAGGACGAAACACCGATTTCCCGACTGCTCTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTCCCGACTGCTCTATCG	
3459	Acad9	Acad9_3459	GGAAAGGACGAAACACCGGGACTCTCGAAAAATTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACTCTCGAAAAATTGACC	
3460	Acad9	Acad9_3460	GGAAAGGACGAAACACCGGAGCATACATCGTGTTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCATACATCGTGTTGGAG	
3461	Gatb	Gatb_3461	GGAAAGGACGAAACACCGGTTCATTTGATTATAAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCATTTGATTATAAGCTG	
3462	Gatb	Gatb_3462	GGAAAGGACGAAACACCGGTGACCTCAGGTCGTCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACCTCAGGTCGTCATGG	
3463	Gatb	Gatb_3463	GGAAAGGACGAAACACCGCTTCCCTAGATAGATACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCCCTAGATAGATACAGT	
3464	Gatb	Gatb_3464	GGAAAGGACGAAACACCGAATATATCTGTACATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATATATCTGTACATCACCC	
3465	Msto1	Msto1_3465	GGAAAGGACGAAACACCGCTGTTCTGTACAAGACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTTCTGTACAAGACGTCG	
3466	Msto1	Msto1_3466	GGAAAGGACGAAACACCGGGACAGACTACACTTCTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACAGACTACACTTCTATG	
3467	Msto1	Msto1_3467	GGAAAGGACGAAACACCGGGGCGGGGAGTCCTAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCGGGGAGTCCTAACCTG	
3468	Msto1	Msto1_3468	GGAAAGGACGAAACACCGAGCCCCCATACCCATCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCCCATACCCATCATGG	
3469	Ampd1	Ampd1_3469	GGAAAGGACGAAACACCGAATGACAAATACAATCCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGACAAATACAATCCCGT	
3470	Ampd1	Ampd1_3470	GGAAAGGACGAAACACCGCAAAGCACGACTCACCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGCACGACTCACCCCCG	
3471	Ampd1	Ampd1_3471	GGAAAGGACGAAACACCGCGAGATCTCCCCCTTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGATCTCCCCCTTCGACG	
3472	Ampd1	Ampd1_3472	GGAAAGGACGAAACACCGATGGATGTGAGTATCCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGATGTGAGTATCCACCT	
3473	Slc25a24	Slc25a24_3473	GGAAAGGACGAAACACCGATGAGAAAAAATCAGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAGAAAAAATCAGGACAG	
3474	Slc25a24	Slc25a24_3474	GGAAAGGACGAAACACCGAGAGACTGGACAATTTCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGACTGGACAATTTCAGA	
3475	Slc25a24	Slc25a24_3475	GGAAAGGACGAAACACCGAAGAAGTTGCTTACCGAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAGTTGCTTACCGAGGA	
3476	Slc25a24	Slc25a24_3476	GGAAAGGACGAAACACCGATCTTTGTTGACATCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTTTGTTGACATCGCCAG	
3477	Slc35a3	Slc35a3_3477	GGAAAGGACGAAACACCGGCTGTAGAAGACAGATAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTAGAAGACAGATAACG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3478	Slc35a3	Slc35a3_3478	GGAAAGGACGAAACACCGTGAAGCTCGCTATCCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGCTCGCTATCCCGTCA	
3479	Slc35a3	Slc35a3_3479	GGAAAGGACGAAACACCGTCCTGCCATCAGAATTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGCCATCAGAATTACTA	
3480	Slc35a3	Slc35a3_3480	GGAAAGGACGAAACACCGCAAACTGTGAGCCTGTTGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACTGTGAGCCTGTTGAA	
3481	Gba2	Gba2_3481	GGAAAGGACGAAACACCGCTCACCTCAAGCCCATACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCTCAAGCCCATACCG	
3482	Gba2	Gba2_3482	GGAAAGGACGAAACACCGCGTCATCCCTCATGACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTCATCCCTCATGACATTG	
3483	Gba2	Gba2_3483	GGAAAGGACGAAACACCGACCAAGCTACTGCAATTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAAGCTACTGCAATTCAG	
3484	Gba2	Gba2_3484	GGAAAGGACGAAACACCGCATCGTATGTGTTGTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCGTATGTGTTGTACATG	
3485	Aldob	Aldob_3485	GGAAAGGACGAAACACCGTATCCACAGTTGGACCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCCACAGTTGGACCAAGG	
3486	Aldob	Aldob_3486	GGAAAGGACGAAACACCGAATTCCATTAGCCAGAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTCCATTAGCCAGAGCAT	
3487	Aldob	Aldob_3487	GGAAAGGACGAAACACCGCCGCCTGCAAAGGATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCCTGCAAAGGATAAAGG	
3488	Aldob	Aldob_3488	GGAAAGGACGAAACACCGGGTCCCTATTGTTGAGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCCTATTGTTGAGCCAG	
3489	Pigv	Pigv_3489	GGAAAGGACGAAACACCGGAGGGCAAAAGGCATCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGGCAAAAGGCATCTGCG	
3490	Pigv	Pigv_3490	GGAAAGGACGAAACACCGGTAGGCACGATACTGAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGGCACGATACTGAAAGA	
3491	Pigv	Pigv_3491	GGAAAGGACGAAACACCGTTCCTGTTTATCGCTGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCTGTTTATCGCTGAGCA	
3492	Pigv	Pigv_3492	GGAAAGGACGAAACACCGCAGGAGAAAATGCACCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGAGAAAATGCACCCCCA	
3493	Slc30a2	Slc30a2_3493	GGAAAGGACGAAACACCGCTGGTCGGGAAGACACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTCGGGAAGACACCCAG	
3494	Slc30a2	Slc30a2_3494	GGAAAGGACGAAACACCGTGGAGATTATGAGATCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGATTATGAGATCAAAG	
3495	Slc30a2	Slc30a2_3495	GGAAAGGACGAAACACCGAGGCCACATAGAGTTTGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCACATAGAGTTTGCGT	
3496	Slc30a2	Slc30a2_3496	GGAAAGGACGAAACACCGGATGGAAAGCACGGACAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGAAAGCACGGACAACA	
3497	Hadhb	Hadhb_3497	GGAAAGGACGAAACACCGATATACAAGTCTTACCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATACAAGTCTTACCTCAG	
3498	Hadhb	Hadhb_3498	GGAAAGGACGAAACACCGCTGACAGCAGAAATGGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGACAGCAGAAATGGAATG	
3499	Hadhb	Hadhb_3499	GGAAAGGACGAAACACCGGCATCGGACCAATATTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATCGGACCAATATTCCAA	
3500	Hadhb	Hadhb_3500	GGAAAGGACGAAACACCGTCAAACCAAGCCATGACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAAACCAAGCCATGACCAC	
3501	Slc26a1	Slc26a1_3501	GGAAAGGACGAAACACCGACAGGCCAACATATGTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGGCCAACATATGTGATG	
3502	Slc26a1	Slc26a1_3502	GGAAAGGACGAAACACCGCCAGCCGGAGGATACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCCGGAGGATACCCATG	
3503	Slc26a1	Slc26a1_3503	GGAAAGGACGAAACACCGTACCAGACCCTAAGATAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCAGACCCTAAGATAATG	
3504	Slc26a1	Slc26a1_3504	GGAAAGGACGAAACACCGGCCCACATTAACATGGCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCACATTAACATGGCGGG	
3505	Ap5z1	Ap5z1_3505	GGAAAGGACGAAACACCGTGCGTCCAGTACCTTCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGTCCAGTACCTTCCATG	
3506	Ap5z1	Ap5z1_3506	GGAAAGGACGAAACACCGTAGGTCCACACAGACTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGTCCACACAGACTCCGT	
3507	Ap5z1	Ap5z1_3507	GGAAAGGACGAAACACCGATAGCCCGGTCCCATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGCCCGGTCCCATCACTG	
3508	Ap5z1	Ap5z1_3508	GGAAAGGACGAAACACCGGGCCGCAGACAGCACAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCGCAGACAGCACAGACA	
3509	Mat2a	Mat2a_3509	GGAAAGGACGAAACACCGCCTGATGCTAAAGTGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGATGCTAAAGTGGCTTG	
3510	Mat2a	Mat2a_3510	GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCAATATATGCAAGATCG	
3511	Mat2a	Mat2a_3511	GGAAAGGACGAAACACCGACCAAGGCAATGTACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAAGGCAATGTACCATTG	
3512	Mat2a	Mat2a_3512	GGAAAGGACGAAACACCGATTTACCACCTACAGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTACCACCTACAGCCAAG	
3513	Cyp26b1	Cyp26b1_3513	GGAAAGGACGAAACACCGACTGCTGGGTCCCAACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCTGGGTCCCAACACGG	
3514	Cyp26b1	Cyp26b1_3514	GGAAAGGACGAAACACCGGCACCGGTCACACGAATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCACCGGTCACACGAATCAG	
3515	Cyp26b1	Cyp26b1_3515	GGAAAGGACGAAACACCGACTGCTGGTATACCTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCTGGTATACCTCAAAG	
3516	Cyp26b1	Cyp26b1_3516	GGAAAGGACGAAACACCGGGCCATCAATGTATATCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCATCAATGTATATCAGG	
3517	Slc6a1	Slc6a1_3517	GGAAAGGACGAAACACCGCACCAACATGACCAGCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCAACATGACCAGCGCCG	
3518	Slc6a1	Slc6a1_3518	GGAAAGGACGAAACACCGGCAGAAATACACGAGCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGAAATACACGAGCACCC	
3519	Slc6a1	Slc6a1_3519	GGAAAGGACGAAACACCGTACCTCTGTGGGAAAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTCTGTGGGAAAAACGG	
3520	Slc6a1	Slc6a1_3520	GGAAAGGACGAAACACCGTCCATGTGTCCCGGTCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCATGTGTCCCGGTCAGGG	
3521	Gys2	Gys2_3521	GGAAAGGACGAAACACCGGCATAAGAGTAACGTCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATAAGAGTAACGTCACCG	
3522	Gys2	Gys2_3522	GGAAAGGACGAAACACCGGTGGATGCGATGAATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGATGCGATGAATAAACA	
3523	Gys2	Gys2_3523	GGAAAGGACGAAACACCGGAGATAACGCCCAAGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATAACGCCCAAGCAGTG	
3524	Gys2	Gys2_3524	GGAAAGGACGAAACACCGAAAACGACAGCCGATGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACGACAGCCGATGAGTG	
3525	Pgap2	Pgap2_3525	GGAAAGGACGAAACACCGAAACGCCACACGTAGCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGCCACACGTAGCGTTG	
3526	Pgap2	Pgap2_3526	GGAAAGGACGAAACACCGCATTAACTTCAGTCTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTAACTTCAGTCTCAATG	
3527	Pgap2	Pgap2_3527	GGAAAGGACGAAACACCGGTAGTGGTTCCAATAGGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAGTGGTTCCAATAGGCGA	
3528	Pgap2	Pgap2_3528	GGAAAGGACGAAACACCGGACAACATCTACACACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAACATCTACACACTGTG	
3529	Xylt1	Xylt1_3529	GGAAAGGACGAAACACCGCCTGTACGGGAACTATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGTACGGGAACTATCCTG	
3530	Xylt1	Xylt1_3530	GGAAAGGACGAAACACCGCATGCGCTGTAGCTGTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCGCTGTAGCTGTCGAG	
3531	Xylt1	Xylt1_3531	GGAAAGGACGAAACACCGGTGCCAGTACAAGCATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCAGTACAAGCATATCG	
3532	Xylt1	Xylt1_3532	GGAAAGGACGAAACACCGGATGCCCAGGACAAACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCCCAGGACAAACGACA	
3533	Cog7	Cog7_3533	GGAAAGGACGAAACACCGGTGCTATCAGACATTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCTATCAGACATTACCAG	
3534	Cog7	Cog7_3534	GGAAAGGACGAAACACCGTGAACGATGCTACGATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAACGATGCTACGATCTGG	
3535	Cog7	Cog7_3535	GGAAAGGACGAAACACCGGTGGCACACACAAACCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCACACACAAACCCAGT	
3536	Cog7	Cog7_3536	GGAAAGGACGAAACACCGGGTGCTGGTAGAGATTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGCTGGTAGAGATTGACC	

No.	*Oligo name	*Oligo name	*Sequence（5’to3’）	nt#	Remarks	5'	guide sequence	3'
3537	Tufm	Tufm_3537	GGAAAGGACGAAACACCGGAGGAAACTCCAGTCATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGAAACTCCAGTCATCGT	
3538	Tufm	Tufm_3538	GGAAAGGACGAAACACCGCCGGTAGTTCTAGCCGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGGTAGTTCTAGCCGAGGG	
3539	Tufm	Tufm_3539	GGAAAGGACGAAACACCGGTGACAGGTACATTAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGACAGGTACATTAGAGCG	
3540	Tufm	Tufm_3540	GGAAAGGACGAAACACCGTCCACCCAGAATATGATCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACCCAGAATATGATCAC	
3541	Csgalnact1	Csgalnact1_3541	GGAAAGGACGAAACACCGTTATTGTGCCCCTAGCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTATTGTGCCCCTAGCGAGG	
3542	Csgalnact1	Csgalnact1_3542	GGAAAGGACGAAACACCGCAGGGATTTACCGAACCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGATTTACCGAACCGAA	
3543	Csgalnact1	Csgalnact1_3543	GGAAAGGACGAAACACCGAGGGCTGTTTAGACTCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCTGTTTAGACTCTCCA	
3544	Csgalnact1	Csgalnact1_3544	GGAAAGGACGAAACACCGCTTGACACCGGCATGTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGACACCGGCATGTACCT	
3545	Tat	Tat_3545	GGAAAGGACGAAACACCGATGTTCGCGTCAATATTGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTCGCGTCAATATTGGC	
3546	Tat	Tat_3546	GGAAAGGACGAAACACCGGGCAAGCTTACCGATAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAAGCTTACCGATAGATG	
3547	Tat	Tat_3547	GGAAAGGACGAAACACCGAACAACCCGTCCAATCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAACCCGTCCAATCCCTG	
3548	Tat	Tat_3548	GGAAAGGACGAAACACCGTGAGCTGTGTCTAGCCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCTGTGTCTAGCCGTGT	
3549	Slc38a8	Slc38a8_3549	GGAAAGGACGAAACACCGTCACGGTGCAATACTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACGGTGCAATACTACCTG	
3550	Slc38a8	Slc38a8_3550	GGAAAGGACGAAACACCGATTTCCCGAAGTGCTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTCCCGAAGTGCTGACAG	
3551	Slc38a8	Slc38a8_3551	GGAAAGGACGAAACACCGGCTGGTCCCCGATCACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGTCCCCGATCACTCTG	
3552	Slc38a8	Slc38a8_3552	GGAAAGGACGAAACACCGTCTTTGGTCTTCCTGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTGGTCTTCCTGATCAG	
3553	Spg7	Spg7_3553	GGAAAGGACGAAACACCGTTCCAAATGCAGTCAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCAAATGCAGTCAGACTG	
3554	Spg7	Spg7_3554	GGAAAGGACGAAACACCGGAACTCCCTCAGTACAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTCCCTCAGTACAAGTG	
3555	Spg7	Spg7_3555	GGAAAGGACGAAACACCGATCAATGTACACTATGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCAATGTACACTATGCAAG	
3556	Spg7	Spg7_3556	GGAAAGGACGAAACACCGGGATTCCCGTGTCCTACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATTCCCGTGTCCTACAAG	
3557	Foxred1	Foxred1_3557	GGAAAGGACGAAACACCGACTCCTTCTACGTTTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTCCTTCTACGTTTATCCA	
3558	Foxred1	Foxred1_3558	GGAAAGGACGAAACACCGCCCAATGAAGACCCCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAATGAAGACCCCAACTG	
3559	Foxred1	Foxred1_3559	GGAAAGGACGAAACACCGTGGAGCAGGACCACACGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGCAGGACCACACGGTG	
3560	Foxred1	Foxred1_3560	GGAAAGGACGAAACACCGTTGAACTGAAGTTCCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAACTGAAGTTCCACAGG	
3561	Sc5d	Sc5d_3561	GGAAAGGACGAAACACCGCGTATGTATATCCAGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTATGTATATCCAGCCACG	
3562	Sc5d	Sc5d_3562	GGAAAGGACGAAACACCGCATGACTTGCAAACGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGACTTGCAAACGGCGTG	
3563	Sc5d	Sc5d_3563	GGAAAGGACGAAACACCGATAGACAAAATAATAGCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGACAAAATAATAGCTGA	
3564	Sc5d	Sc5d_3564	GGAAAGGACGAAACACCGAAGTAGACCACCTTGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTAGACCACCTTGTGCAG	
3565	Dlat	Dlat_3565	GGAAAGGACGAAACACCGACTACCGCAACGGACCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTACCGCAACGGACCGCAG	
3566	Dlat	Dlat_3566	GGAAAGGACGAAACACCGCAGGCTCTCAAACCCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGCTCTCAAACCCAACAG	
3567	Dlat	Dlat_3567	GGAAAGGACGAAACACCGCGACAAGGCCACCATAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACAAGGCCACCATAGGTG	
3568	Dlat	Dlat_3568	GGAAAGGACGAAACACCGTTCAGAACCACACCTACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAGAACCACACCTACCGG	
3569	Slc17a5	Slc17a5_3569	GGAAAGGACGAAACACCGTCGTCACCCAGATTCCCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTCACCCAGATTCCCGGT	
3570	Slc17a5	Slc17a5_3570	GGAAAGGACGAAACACCGTAGAACGTCTAAGGAGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAACGTCTAAGGAGTGTG	
3571	Slc17a5	Slc17a5_3571	GGAAAGGACGAAACACCGGATCGTTATCTTACCCGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCGTTATCTTACCCGCAT	
3572	Slc17a5	Slc17a5_3572	GGAAAGGACGAAACACCGGCTGGCCGCAGACTTAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGCCGCAGACTTAGGCG	
3573	Glyctk	Glyctk_3573	GGAAAGGACGAAACACCGGGTGTGATCAGCGTACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTGATCAGCGTACCCAA	
3574	Glyctk	Glyctk_3574	GGAAAGGACGAAACACCGGCGGGAAAACCTCTACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGGGAAAACCTCTACCTAG	
3575	Glyctk	Glyctk_3575	GGAAAGGACGAAACACCGCTGTGCTCAACACCATGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGCTCAACACCATGGCA	
3576	Glyctk	Glyctk_3576	GGAAAGGACGAAACACCGAGTGATTGCCAGTGGCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGATTGCCAGTGGCCCTA	
3577	Phgdh	Phgdh_3577	GGAAAGGACGAAACACCGCCACACTGAGAGCCTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACACTGAGAGCCTACCTG	
3578	Phgdh	Phgdh_3578	GGAAAGGACGAAACACCGCTCACTTCTGACCAGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACTTCTGACCAGACTGT	
3579	Phgdh	Phgdh_3579	GGAAAGGACGAAACACCGTAGTAGCAGACCGGACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTAGCAGACCGGACAATG	
3580	Phgdh	Phgdh_3580	GGAAAGGACGAAACACCGCTGCGATTTCCTCCCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCGATTTCCTCCCCACAG	
3581	Slc13a5	Slc13a5_3581	GGAAAGGACGAAACACCGGATAGCCGCCAATACAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATAGCCGCCAATACAGCTG	
3582	Slc13a5	Slc13a5_3582	GGAAAGGACGAAACACCGGGGTCCCGTCCCGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGTCCCGTCCCGGTCAAGG	
3583	Slc13a5	Slc13a5_3583	GGAAAGGACGAAACACCGAGTCCAGAACCTTCAAAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCCAGAACCTTCAAAAGT	
3584	Slc13a5	Slc13a5_3584	GGAAAGGACGAAACACCGAAGAAGGTGTGTTTACCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAGGTGTGTTTACCGTG	
3585	Apob	Apob_3585	GGAAAGGACGAAACACCGGCTGGTAGTGACATCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGTAGTGACATCAACAG	
3586	Apob	Apob_3586	GGAAAGGACGAAACACCGAGTCTCACCTGTTAACTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCTCACCTGTTAACTGCG	
3587	Apob	Apob_3587	GGAAAGGACGAAACACCGATGTTGCATGAGTATGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTTGCATGAGTATGCCAA	
3588	Apob	Apob_3588	GGAAAGGACGAAACACCGGAATGGAATCATGCCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATGGAATCATGCCCATTG	
3589	Cog5	Cog5_3589	GGAAAGGACGAAACACCGGGAGACTGTTACCAGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGACTGTTACCAGTGTCG	
3590	Cog5	Cog5_3590	GGAAAGGACGAAACACCGGGAGGATTACGTCCTCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGATTACGTCCTCCCGG	
3591	Cog5	Cog5_3591	GGAAAGGACGAAACACCGCAACTAGCAAAACTTGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACTAGCAAAACTTGCCCA	
3592	Cog5	Cog5_3592	GGAAAGGACGAAACACCGTTTCACAGCATATAACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCACAGCATATAACTGGA	
3593	Mtr	Mtr_3593	GGAAAGGACGAAACACCGTCAGGTGCTCGATATCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGTGCTCGATATCAACA	
3594	Mtr	Mtr_3594	GGAAAGGACGAAACACCGGGGGTCCGAATGAGACACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGTCCGAATGAGACACGC	
3595	Mtr	Mtr_3595	GGAAAGGACGAAACACCGTGTGGATAGCATCATACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGATAGCATCATACACA	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3596	Mtr	Mtr_3596	GGAAAGGACGAAACACCGCTTCAAAAACACTAGCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAAAAACACTAGCAGGG	
3597	A4galt	A4galt_3597	GGAAAGGACGAAACACCGTCTTCCTAGAGACATCGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCCTAGAGACATCGGAC	
3598	A4galt	A4galt_3598	GGAAAGGACGAAACACCGGCTGATGAAAGGGCTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGATGAAAGGGCTGCCTA	
3599	A4galt	A4galt_3599	GGAAAGGACGAAACACCGTCAGGGGCACCCCCAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGGGCACCCCCAGACAG	
3600	A4galt	A4galt_3600	GGAAAGGACGAAACACCGACTGTTTGAGGACACACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTTTGAGGACACACCAC	
3601	Pgap1	Pgap1_3601	GGAAAGGACGAAACACCGATAGACAACAATATGCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAGACAACAATATGCGACA	
3602	Pgap1	Pgap1_3602	GGAAAGGACGAAACACCGATATGTAACTTACCACACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATGTAACTTACCACACGA	
3603	Pgap1	Pgap1_3603	GGAAAGGACGAAACACCGAGAATTTGCTCCTACAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAATTTGCTCCTACAAGTG	
3604	Pgap1	Pgap1_3604	GGAAAGGACGAAACACCGGTCGTCAGACTGTCAGTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCGTCAGACTGTCAGTATG	
3605	Impad1	Impad1_3605	GGAAAGGACGAAACACCGATTCCTGTGTAGCATCAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTCCTGTGTAGCATCAAGT	
3606	Impad1	Impad1_3606	GGAAAGGACGAAACACCGTCCTTCACGAGAAGTCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTTCACGAGAAGTCCAAG	
3607	Impad1	Impad1_3607	GGAAAGGACGAAACACCGCTCCCACTAGATAAATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCCACTAGATAAATACTG	
3608	Impad1	Impad1_3608	GGAAAGGACGAAACACCGGCTTGGGCAATGGTAGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTGGGCAATGGTAGATGG	
3609	Gabbr2	Gabbr2_3609	GGAAAGGACGAAACACCGCCTGCGACTCTACGACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGCGACTCTACGACACCG	
3610	Gabbr2	Gabbr2_3610	GGAAAGGACGAAACACCGCATGGAAGGCTACATCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGGAAGGCTACATCGGAG	
3611	Gabbr2	Gabbr2_3611	GGAAAGGACGAAACACCGGCTGACAGGATGCTATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGACAGGATGCTATACAG	
3612	Gabbr2	Gabbr2_3612	GGAAAGGACGAAACACCGCTTATCCGCAAGAACAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTATCCGCAAGAACAGGCG	
3613	Slc35d1	Slc35d1_3613	GGAAAGGACGAAACACCGGGCGCCGGCCGAAACGCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGCCGGCCGAAACGCTAA	
3614	Slc35d1	Slc35d1_3614	GGAAAGGACGAAACACCGTGTGTGTGGAGGATTTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTGTGGAGGATTTCGCG	
3615	Slc35d1	Slc35d1_3615	GGAAAGGACGAAACACCGACTGTATTTGCAATGATCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTATTTGCAATGATCAT	
3616	Slc35d1	Slc35d1_3616	GGAAAGGACGAAACACCGTGGTTCCCAAAATATAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTTCCCAAAATATAGTAG	
3617	Cldn19	Cldn19_3617	GGAAAGGACGAAACACCGCCACACGGCTCTTGGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACACGGCTCTTGGCAGTG	
3618	Cldn19	Cldn19_3618	GGAAAGGACGAAACACCGCTGGGCACTCACCTGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGCACTCACCTGCCAAG	
3619	Cldn19	Cldn19_3619	GGAAAGGACGAAACACCGTGCTGACTGGATATGACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTGACTGGATATGACCTG	
3620	Cldn19	Cldn19_3620	GGAAAGGACGAAACACCGACATCCACAGCCCTTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACATCCACAGCCCTTCGTAG	
3621	Slc45a1	Slc45a1_3621	GGAAAGGACGAAACACCGGAGTACCGGAGTCACGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTACCGGAGTCACGTACG	
3622	Slc45a1	Slc45a1_3622	GGAAAGGACGAAACACCGAGGAGTACTCACCCGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGTACTCACCCGCCATG	
3623	Slc45a1	Slc45a1_3623	GGAAAGGACGAAACACCGGGAGTGACCGATGTACCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTGACCGATGTACCTCA	
3624	Slc45a1	Slc45a1_3624	GGAAAGGACGAAACACCGCCACCCCGCACACTGTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACCCCGCACACTGTCAGG	
3625	Ppm1k	Ppm1k_3625	GGAAAGGACGAAACACCGCAGGTGGGCATAACTCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGTGGGCATAACTCGCGA	
3626	Ppm1k	Ppm1k_3626	GGAAAGGACGAAACACCGGCAGAATTGGCTCATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGAATTGGCTCATCAATG	
3627	Ppm1k	Ppm1k_3627	GGAAAGGACGAAACACCGCTAGGATCAAGAAATTCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGGATCAAGAAATTCGGT	
3628	Ppm1k	Ppm1k_3628	GGAAAGGACGAAACACCGAAAATTAGCCTGGAGAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAATTAGCCTGGAGAACGT	
3629	Uroc1	Uroc1_3629	GGAAAGGACGAAACACCGTGTCACAACCCGTTCAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCACAACCCGTTCAATGG	
3630	Uroc1	Uroc1_3630	GGAAAGGACGAAACACCGTCTGCCCCAGCATTGAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGCCCCAGCATTGAGATG	
3631	Uroc1	Uroc1_3631	GGAAAGGACGAAACACCGGGGAATCGTCCATGGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAATCGTCCATGGCACAG	
3632	Uroc1	Uroc1_3632	GGAAAGGACGAAACACCGCACCCCAATGCATCCAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCCCAATGCATCCAACGA	
3633	Fkrp	Fkrp_3633	GGAAAGGACGAAACACCGGCTGGACTTGACCTTCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGGACTTGACCTTCGCCG	
3634	Fkrp	Fkrp_3634	GGAAAGGACGAAACACCGCCAATGGCAGAAGTCCGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAATGGCAGAAGTCCGGCG	
3635	Fkrp	Fkrp_3635	GGAAAGGACGAAACACCGCCATCCAAAGCGTCGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATCCAAAGCGTCGCAGCG	
3636	Fkrp	Fkrp_3636	GGAAAGGACGAAACACCGCACAAACTCGGTGGCTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAAACTCGGTGGCTACGT	
3637	Nars2	Nars2_3637	GGAAAGGACGAAACACCGTCACATCCAACGACTGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACATCCAACGACTGTGAG	
3638	Nars2	Nars2_3638	GGAAAGGACGAAACACCGGGAACTCTTCAAGGCGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACTCTTCAAGGCGACCA	
3639	Nars2	Nars2_3639	GGAAAGGACGAAACACCGCTCAGGGTCCAGGACGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCAGGGTCCAGGACGCGAG	
3640	Nars2	Nars2_3640	GGAAAGGACGAAACACCGTCAGTCCAAGAGGCAAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTCCAAGAGGCAAAATG	
3641	Cyp2r1	Cyp2r1_3641	GGAAAGGACGAAACACCGTAGGCATCAACAAAATGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCATCAACAAAATGGTG	
3642	Cyp2r1	Cyp2r1_3642	GGAAAGGACGAAACACCGGCAGAGCCGGGTGTATGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGAGCCGGGTGTATGGCG	
3643	Cyp2r1	Cyp2r1_3643	GGAAAGGACGAAACACCGGATGCTATTGAAACATACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCTATTGAAACATACAA	
3644	Cyp2r1	Cyp2r1_3644	GGAAAGGACGAAACACCGAAAGGTAAGATGCCAATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGGTAAGATGCCAATCCA	
3645	Snx14	Snx14_3645	GGAAAGGACGAAACACCGAGCTGTGCTGCCTAATTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCTGTGCTGCCTAATTACG	
3646	Snx14	Snx14_3646	GGAAAGGACGAAACACCGCTTCAAGAGTTATTTCCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAAGAGTTATTTCCGCA	
3647	Snx14	Snx14_3647	GGAAAGGACGAAACACCGGACAGATGCAAAAAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACAGATGCAAAAAACCGTA	
3648	Snx14	Snx14_3648	GGAAAGGACGAAACACCGTCAACATCGATACAAAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAACATCGATACAAAACAC	
3649	Slc36a2	Slc36a2_3649	GGAAAGGACGAAACACCGTGACTAGGATGTGCATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTAGGATGTGCATACAG	
3650	Slc36a2	Slc36a2_3650	GGAAAGGACGAAACACCGGGTAGTTCTGACGCCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAGTTCTGACGCCCACCA	
3651	Slc36a2	Slc36a2_3651	GGAAAGGACGAAACACCGAGCAAAGTACCTCCCCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAAAGTACCTCCCCCAGT	
3652	Slc36a2	Slc36a2_3652	GGAAAGGACGAAACACCGAGCCCCGATAGCAATGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCCGATAGCAATGTACA	
3653	Fktn	Fktn_3653	GGAAAGGACGAAACACCGGAGTCTATTCCATCTAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTCTATTCCATCTAGCCG	
3654	Fktn	Fktn_3654	GGAAAGGACGAAACACCGCACTCGATAAATCTGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTCGATAAATCTGGAGTG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3655	Fktn	Fktn_3655	GGAAAGGACGAAACACCGGACTCAAAGGACACATGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTCAAAGGACACATGGAT	
3656	Fktn	Fktn_3656	GGAAAGGACGAAACACCGTAATTGATTCCAGAATCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAATTGATTCCAGAATCCAT	
3657	Atpaf2	Atpaf2_3657	GGAAAGGACGAAACACCGACAATGAATTAGCTACAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAATGAATTAGCTACAGGG	
3658	Atpaf2	Atpaf2_3658	GGAAAGGACGAAACACCGAATGGGATCCCGTCATAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGGGATCCCGTCATAGAG	
3659	Atpaf2	Atpaf2_3659	GGAAAGGACGAAACACCGCTATGTCCCGCCAACAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTATGTCCCGCCAACAGGTG	
3660	Atpaf2	Atpaf2_3660	GGAAAGGACGAAACACCGTGGCCCCGGCCATACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCCCCGGCCATACTGAGA	
3661	Slc5a2	Slc5a2_3661	GGAAAGGACGAAACACCGATGATTTATACTGTGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATTTATACTGTGACAGG	
3662	Slc5a2	Slc5a2_3662	GGAAAGGACGAAACACCGCTGGCACAAAAAGCCATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGCACAAAAAGCCATCCG	
3663	Slc5a2	Slc5a2_3663	GGAAAGGACGAAACACCGGGTCTCTTCGACAAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCTCTTCGACAAATACCT	
3664	Slc5a2	Slc5a2_3664	GGAAAGGACGAAACACCGATTGGTTCTGAACATAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTGGTTCTGAACATAGACT	
3665	Acsf3	Acsf3_3665	GGAAAGGACGAAACACCGCACAGCGGCTAGGTTACGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACAGCGGCTAGGTTACGGT	
3666	Acsf3	Acsf3_3666	GGAAAGGACGAAACACCGCATGAATACGGTAATCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGAATACGGTAATCTGTG	
3667	Acsf3	Acsf3_3667	GGAAAGGACGAAACACCGGGCCCACTGTGCTACAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCCCACTGTGCTACAACGT	
3668	Acsf3	Acsf3_3668	GGAAAGGACGAAACACCGATATGGCCATCACACCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATGGCCATCACACCTACA	
3669	Gphn	Gphn_3669	GGAAAGGACGAAACACCGGCTTTGTCCATAGACGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTTGTCCATAGACGTCAG	
3670	Gphn	Gphn_3670	GGAAAGGACGAAACACCGTGAAGGAGTAGTGCTAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGGAGTAGTGCTAAGGG	
3671	Gphn	Gphn_3671	GGAAAGGACGAAACACCGACCACGAGATGTCACTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCACGAGATGTCACTCCAG	
3672	Gphn	Gphn_3672	GGAAAGGACGAAACACCGATCGGCCATGACATTAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCGGCCATGACATTAAGAG	
3673	Sptlc1	Sptlc1_3673	GGAAAGGACGAAACACCGAATGTGCCATAGAACCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATGTGCCATAGAACCCTCG	
3674	Sptlc1	Sptlc1_3674	GGAAAGGACGAAACACCGCCCTCCAACCCACAACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTCCAACCCACAACATCG	
3675	Sptlc1	Sptlc1_3675	GGAAAGGACGAAACACCGTCCTGCGTACTCTAAGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGCGTACTCTAAGAGAG	
3676	Sptlc1	Sptlc1_3676	GGAAAGGACGAAACACCGTTTGTCGTAGAATCCTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTCGTAGAATCCTCGCA	
3677	Rnf31	Rnf31_3677	GGAAAGGACGAAACACCGGATGGATTGAGTTTCCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGATTGAGTTTCCCCGA	
3678	Rnf31	Rnf31_3678	GGAAAGGACGAAACACCGGAACTATGAGTTGTTGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAACTATGAGTTGTTGGACG	
3679	Rnf31	Rnf31_3679	GGAAAGGACGAAACACCGCTACCTCAACACCCTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACCTCAACACCCTATCCA	
3680	Rnf31	Rnf31_3680	GGAAAGGACGAAACACCGGGAGGAACCAAGGTGTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGGAACCAAGGTGTTGTG	
3681	Abat	Abat_3681	GGAAAGGACGAAACACCGGAGCAGAGGTAACTACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCAGAGGTAACTACCTAG	
3682	Abat	Abat_3682	GGAAAGGACGAAACACCGGCTCCAGGAGTCCTTGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCAGGAGTCCTTGATGT	
3683	Abat	Abat_3683	GGAAAGGACGAAACACCGTTTCGGCAGAGTAAGGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCGGCAGAGTAAGGAACG	
3684	Abat	Abat_3684	GGAAAGGACGAAACACCGAACGGTGGCTGGAATCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGTGGCTGGAATCATCG	
3685	Ahcy	Ahcy_3685	GGAAAGGACGAAACACCGGCGCACCTGACAGAAGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCACCTGACAGAAGCTGT	
3686	Ahcy	Ahcy_3686	GGAAAGGACGAAACACCGTGTCAACGATTCTGTCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCAACGATTCTGTCACCA	
3687	Ahcy	Ahcy_3687	GGAAAGGACGAAACACCGTGACCCTATCATACCCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACCCTATCATACCCTCCA	
3688	Ahcy	Ahcy_3688	GGAAAGGACGAAACACCGTGTGATGATTGCGGGCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGATGATTGCGGGCAAGG	
3689	Fbxl4	Fbxl4_3689	GGAAAGGACGAAACACCGAGTTGTGCTGCATGGTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGTGCTGCATGGTACGA	
3690	Fbxl4	Fbxl4_3690	GGAAAGGACGAAACACCGTTGAGGTGGATATATTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGAGGTGGATATATTGCAG	
3691	Fbxl4	Fbxl4_3691	GGAAAGGACGAAACACCGACAGTATGTCCTATACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGTATGTCCTATACCATG	
3692	Fbxl4	Fbxl4_3692	GGAAAGGACGAAACACCGAGTGGCTGCAGGATAACTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGGCTGCAGGATAACTCA	
3693	Vcp	Vcp_3693	GGAAAGGACGAAACACCGACTGTCTTCACAGACTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGTCTTCACAGACTCATG	
3694	Vcp	Vcp_3694	GGAAAGGACGAAACACCGTATAGGTCGCTTTGACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATAGGTCGCTTTGACAGAG	
3695	Vcp	Vcp_3695	GGAAAGGACGAAACACCGCCAATCGCCTTAAAGAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAATCGCCTTAAAGAGCGC	
3696	Vcp	Vcp_3696	GGAAAGGACGAAACACCGCTTCAGGAGTTGGTTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAGGAGTTGGTTCAGGT	
3697	Chsy1	Chsy1_3697	GGAAAGGACGAAACACCGGGTGTAAGGTGATCGCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTGTAAGGTGATCGCTCGG	
3698	Chsy1	Chsy1_3698	GGAAAGGACGAAACACCGGCGTGTGAACCCCATGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTGTGAACCCCATGTACG	
3699	Chsy1	Chsy1_3699	GGAAAGGACGAAACACCGAAGAGAAAGTTCCTGTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAGAAAGTTCCTGTCGCG	
3700	Chsy1	Chsy1_3700	GGAAAGGACGAAACACCGCAAGTACGAGTGGTTTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAGTACGAGTGGTTTATGA	
3701	Gcdh	Gcdh_3701	GGAAAGGACGAAACACCGGATGATCATACCGGTAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGATCATACCGGTAGCCG	
3702	Gcdh	Gcdh_3702	GGAAAGGACGAAACACCGCAGGATCACCAACTCCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGATCACCAACTCCCCTG	
3703	Gcdh	Gcdh_3703	GGAAAGGACGAAACACCGGGTCCTTCCAGTCAAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCTTCCAGTCAAACACG	
3704	Gcdh	Gcdh_3704	GGAAAGGACGAAACACCGCTCCTGGCAGTAGTTACGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCTGGCAGTAGTTACGGA	
3705	Clpx	Clpx_3705	GGAAAGGACGAAACACCGAAGAATTCTCGAAAACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAATTCTCGAAAACTACG	
3706	Clpx	Clpx_3706	GGAAAGGACGAAACACCGTGGTGATTTGTGTACACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGATTTGTGTACACACG	
3707	Clpx	Clpx_3707	GGAAAGGACGAAACACCGTCTCTTATAATGATTATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTTATAATGATTATACA	
3708	Clpx	Clpx_3708	GGAAAGGACGAAACACCGTGTTATTTACCTGACCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTATTTACCTGACCCAGT	
3709	Pigs	Pigs_3709	GGAAAGGACGAAACACCGACCATAATGCCACCCCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCATAATGCCACCCCAGCG	
3710	Pigs	Pigs_3710	GGAAAGGACGAAACACCGGGGCGACCTGGACTATGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCGACCTGGACTATGCGA	
3711	Pigs	Pigs_3711	GGAAAGGACGAAACACCGGATCTCTCGCTCATGCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATCTCTCGCTCATGCACAA	
3712	Pigs	Pigs_3712	GGAAAGGACGAAACACCGCTACCTAAGCTGGACTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACCTAAGCTGGACTTGAG	
3713	Flad1	Flad1_3713	GGAAAGGACGAAACACCGACAAACTCGCGGAGTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAAACTCGCGGAGTCAGGT	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3714	Flad1	Flad1_3714	GGAAAGGACGAAACACCGTCACTCACGTCCTCACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACTCACGTCCTCACCGCG	
3715	Flad1	Flad1_3715	GGAAAGGACGAAACACCGGCTAAGCCTACGCCCAAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTAAGCCTACGCCCAAAGT	
3716	Flad1	Flad1_3716	GGAAAGGACGAAACACCGGAAGCTGATTCTAGACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGCTGATTCTAGACTCCG	
3717	Pik3r5	Pik3r5_3717	GGAAAGGACGAAACACCGCCACAGGAATCTCCTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACAGGAATCTCCTACCAG	
3718	Pik3r5	Pik3r5_3718	GGAAAGGACGAAACACCGCGAGAGGCCTGAGACAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGAGGCCTGAGACAAAGG	
3719	Pik3r5	Pik3r5_3719	GGAAAGGACGAAACACCGTGTACTTACACAGAGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACTTACACAGAGGACAG	
3720	Pik3r5	Pik3r5_3720	GGAAAGGACGAAACACCGGCTGAGCGGGACAGTCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGAGCGGGACAGTCCAAG	
3721	Alg6	Alg6_3721	GGAAAGGACGAAACACCGTTTGCTCATTTACGTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGCTCATTTACGTACCCG	
3722	Alg6	Alg6_3722	GGAAAGGACGAAACACCGTCTCATAGCCTCGTGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCATAGCCTCGTGATGTG	
3723	Alg6	Alg6_3723	GGAAAGGACGAAACACCGTAGTCGATAAGAATAAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGTCGATAAGAATAAGACC	
3724	Alg6	Alg6_3724	GGAAAGGACGAAACACCGGCTTCATAATCACCAAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCATAATCACCAAACAT	
3725	Ocrl	Ocrl_3725	GGAAAGGACGAAACACCGTTTCGAATCATATTTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCGAATCATATTTGTACG	
3726	Ocrl	Ocrl_3726	GGAAAGGACGAAACACCGCCAATGCAGTAAATATCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAATGCAGTAAATATCAGG	
3727	Ocrl	Ocrl_3727	GGAAAGGACGAAACACCGATTTACCCCAATATGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTTACCCCAATATGGAACA	
3728	Ocrl	Ocrl_3728	GGAAAGGACGAAACACCGACGTGGAAGAGTTCGAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTGGAAGAGTTCGAACGA	
3729	Pgap3	Pgap3_3729	GGAAAGGACGAAACACCGCATGCAGGTATGGTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCAGGTATGGTACATGG	
3730	Pgap3	Pgap3_3730	GGAAAGGACGAAACACCGAGTCGCGGTACACGGGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCGCGGTACACGGGCTCG	
3731	Pgap3	Pgap3_3731	GGAAAGGACGAAACACCGACTGCAAGTATGAGTGTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGCAAGTATGAGTGTATG	
3732	Pgap3	Pgap3_3732	GGAAAGGACGAAACACCGGGGACTACAGCACCCGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGACTACAGCACCCGTCTG	
3733	Trappc11	Trappc11_3733	GGAAAGGACGAAACACCGGCAGGCCGGGACTTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGCCGGGACTTACATCG	
3734	Trappc11	Trappc11_3734	GGAAAGGACGAAACACCGAGAGCTTGGAAAACCTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGCTTGGAAAACCTAATG	
3735	Trappc11	Trappc11_3735	GGAAAGGACGAAACACCGCGAGTGGTACATCCCTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAGTGGTACATCCCTAAAG	
3736	Trappc11	Trappc11_3736	GGAAAGGACGAAACACCGAGAGGAGTACTACTATGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGAGTACTACTATGCAA	
3737	Gfm2	Gfm2_3737	GGAAAGGACGAAACACCGGGATACACAAGATCATTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATACACAAGATCATTGGG	
3738	Gfm2	Gfm2_3738	GGAAAGGACGAAACACCGACCAGCAGAGGCGTCAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCAGCAGAGGCGTCAAACA	
3739	Gfm2	Gfm2_3739	GGAAAGGACGAAACACCGGGAGCATGGAAAGAAGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGCATGGAAAGAAGAGAG	
3740	Gfm2	Gfm2_3740	GGAAAGGACGAAACACCGCCAATTACCTGTAAAATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAATTACCTGTAAAATCAG	
3741	Pisd	Pisd_3741	GGAAAGGACGAAACACCGCAAACTTGCTAGTCACTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACTTGCTAGTCACTGGG	
3742	Pisd	Pisd_3742	GGAAAGGACGAAACACCGGGTCCCCAGAAAATGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCCCCAGAAAATGGCGTG	
3743	Pisd	Pisd_3743	GGAAAGGACGAAACACCGGGGCCCTCGAGCCAATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGCCCTCGAGCCAATACAG	
3744	Pisd	Pisd_3744	GGAAAGGACGAAACACCGCGTATGTGGCTTGCACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTATGTGGCTTGCACTGTG	
3745	Rfx6	Rfx6_3745	GGAAAGGACGAAACACCGTGAGCATAAAGAATGCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCATAAAGAATGCACCG	
3746	Rfx6	Rfx6_3746	GGAAAGGACGAAACACCGGGACATAGGATGTCTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGACATAGGATGTCTCCACG	
3747	Rfx6	Rfx6_3747	GGAAAGGACGAAACACCGGGTAAGATTATGCATCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTAAGATTATGCATCACGC	
3748	Rfx6	Rfx6_3748	GGAAAGGACGAAACACCGTCAGAAATGCAGTTAAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGAAATGCAGTTAAACAA	
3749	Serac1	Serac1_3749	GGAAAGGACGAAACACCGAGCCATAGTAAAGCATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCATAGTAAAGCATTCGG	
3750	Serac1	Serac1_3750	GGAAAGGACGAAACACCGAACCTGGACCGAGAAACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTGGACCGAGAAACTGT	
3751	Serac1	Serac1_3751	GGAAAGGACGAAACACCGCACCCTGCTATAGTCCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCCTGCTATAGTCCACTC	
3752	Serac1	Serac1_3752	GGAAAGGACGAAACACCGGAGCAGCATTTAAAACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCAGCATTTAAAACCTGG	
3753	Dna2	Dna2_3753	GGAAAGGACGAAACACCGACACGATGCGAAGGATACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACGATGCGAAGGATACGG	
3754	Dna2	Dna2_3754	GGAAAGGACGAAACACCGGCCCTTCAGTCCAAACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCTTCAGTCCAAACCTAG	
3755	Dna2	Dna2_3755	GGAAAGGACGAAACACCGTGCCTTGCCACAGATAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCTTGCCACAGATAATCG	
3756	Dna2	Dna2_3756	GGAAAGGACGAAACACCGCAGGCGTTAACCAGATACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGCGTTAACCAGATACTC	
3757	Pigl	Pigl_3757	GGAAAGGACGAAACACCGCTTGTCAATAATCATTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGTCAATAATCATTACAC	
3758	Pigl	Pigl_3758	GGAAAGGACGAAACACCGTTGATTGTAGTAGTTTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGATTGTAGTAGTTTCCTG	
3759	Pigl	Pigl_3759	GGAAAGGACGAAACACCGGTTCCGCTGAGTTCCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCCGCTGAGTTCCAAACC	
3760	Pigl	Pigl_3760	GGAAAGGACGAAACACCGGCGTGCCAAGCCTAGCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGTGCCAAGCCTAGCATGG	
3761	Rft1	Rft1_3761	GGAAAGGACGAAACACCGAGGACCAAAATATACCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACCAAAATATACCCAGT	
3762	Rft1	Rft1_3762	GGAAAGGACGAAACACCGGAATAATCTTGGCTCCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAATAATCTTGGCTCCCTTG	
3763	Rft1	Rft1_3763	GGAAAGGACGAAACACCGGGTTCTTGCTGAGAGCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTCTTGCTGAGAGCATGT	
3764	Rft1	Rft1_3764	GGAAAGGACGAAACACCGGGCAAAGCCAAAAACAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCAAAGCCAAAAACAGTCA	
3765	Slc5a6	Slc5a6_3765	GGAAAGGACGAAACACCGCTTACTTAATCCCAGAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACTTAATCCCAGAGATG	
3766	Slc5a6	Slc5a6_3766	GGAAAGGACGAAACACCGCAAACATGACCAGACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAACATGACCAGACCAATG	
3767	Slc5a6	Slc5a6_3767	GGAAAGGACGAAACACCGGCAGTTCACCAACGGTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGTTCACCAACGGTATGG	
3768	Slc5a6	Slc5a6_3768	GGAAAGGACGAAACACCGATCCTATAGGTGATATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCCTATAGGTGATATACAT	
3769	Gmppb	Gmppb_3769	GGAAAGGACGAAACACCGGTGGCTTCTCAACAAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCTTCTCAACAAAACGG	
3770	Gmppb	Gmppb_3770	GGAAAGGACGAAACACCGGTGCCGATGAAACTGCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCGATGAAACTGCACCA	
3771	Gmppb	Gmppb_3771	GGAAAGGACGAAACACCGTTCCCAGTTATGGCCAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCCCAGTTATGGCCAAGGA	
3772	Gmppb	Gmppb_3772	GGAAAGGACGAAACACCGGAGCACTCCGAAGCCATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGCACTCCGAAGCCATTGG	

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3773	Cndp1	Cndp1_3773	GGAAAGGACGAAACACCGCACTCACTTATGGAACCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTCACTTATGGAACCCGG	
3774	Cndp1	Cndp1_3774	GGAAAGGACGAAACACCGAGTCAGCCATTGGTTCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCAGCCATTGGTTCGTTG	
3775	Cndp1	Cndp1_3775	GGAAAGGACGAAACACCGCAGCTCAGAAGGACGACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCTCAGAAGGACGACGGG	
3776	Cndp1	Cndp1_3776	GGAAAGGACGAAACACCGAGCCGGTTCCATCGCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCGGTTCCATCGCCCTGG	
3777	Fa2h	Fa2h_3777	GGAAAGGACGAAACACCGTTCGTGCGGCATCATCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGTGCGGCATCATCCGGG	
3778	Fa2h	Fa2h_3778	GGAAAGGACGAAACACCGTCTTGAGCCACAGTTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTGAGCCACAGTTCAAAG	
3779	Fa2h	Fa2h_3779	GGAAAGGACGAAACACCGCTACTACCGAACCCTCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACTACCGAACCCTCACCC	
3780	Fa2h	Fa2h_3780	GGAAAGGACGAAACACCGGTGGATGACGTATTCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGATGACGTATTCCACAA	
3781	Gars	Gars_3781	GGAAAGGACGAAACACCGAGTCAGCAAATTTGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCAGCAAATTTGTCTACG	
3782	Gars	Gars_3782	GGAAAGGACGAAACACCGGAGATATTCCAACCTTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGATATTCCAACCTTCGTG	
3783	Gars	Gars_3783	GGAAAGGACGAAACACCGTAAGTTAAAAGGTACCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGTTAAAAGGTACCGGAG	
3784	Gars	Gars_3784	GGAAAGGACGAAACACCGCCAACAGTGAGTACCTGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACAGTGAGTACCTGACT	
3785	Lyrm4	Lyrm4_3785	GGAAAGGACGAAACACCGACAGATCTAAAACTTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGATCTAAAACTTGTGCG	
3786	Lyrm4	Lyrm4_3786	GGAAAGGACGAAACACCGCCAGGGCTTGAATTTCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGGGCTTGAATTTCTACA	
3787	Lyrm4	Lyrm4_3787	GGAAAGGACGAAACACCGTCATTAGAATGTATGCTGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATTAGAATGTATGCTGTC	
3788	Lyrm4	Lyrm4_3788	GGAAAGGACGAAACACCGCCCGGGTCACCTGTAATTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCGGGTCACCTGTAATTGT	
3789	Iars2	Iars2_3789	GGAAAGGACGAAACACCGCCAAACTAAAACGCTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAACTAAAACGCTAACAG	
3790	Iars2	Iars2_3790	GGAAAGGACGAAACACCGAAATCGGCGTTTGTCCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATCGGCGTTTGTCCGCTG	
3791	Iars2	Iars2_3791	GGAAAGGACGAAACACCGAGGCGGCAGATACCGTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCGGCAGATACCGTGACA	
3792	Iars2	Iars2_3792	GGAAAGGACGAAACACCGAATCGATTCCATATGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATCGATTCCATATGATGAG	
3793	Pdp1	Pdp1_3793	GGAAAGGACGAAACACCGGAGGTCAACACCATCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGTCAACACCATCTACAT	
3794	Pdp1	Pdp1_3794	GGAAAGGACGAAACACCGGTGTACCTCAGACGATTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTACCTCAGACGATTCTG	
3795	Pdp1	Pdp1_3795	GGAAAGGACGAAACACCGACTGGAACACCCAAAAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGGAACACCCAAAAAATG	
3796	Pdp1	Pdp1_3796	GGAAAGGACGAAACACCGTGCTTGTGCCACTGAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTTGTGCCACTGAAGGAT	
3797	B3glct	B3glct_3797	GGAAAGGACGAAACACCGTGAGGCAGAGTAGTCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGGCAGAGTAGTCTACCG	
3798	B3glct	B3glct_3798	GGAAAGGACGAAACACCGTGGAACGTGGTGACGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAACGTGGTGACGCAGCG	
3799	B3glct	B3glct_3799	GGAAAGGACGAAACACCGCATACAGCAAGAATTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACAGCAAGAATTCAGCG	
3800	B3glct	B3glct_3800	GGAAAGGACGAAACACCGTGCCAAAAGATTAAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCAAAAGATTAAAGAGTG	
3801	Alg8	Alg8_3801	GGAAAGGACGAAACACCGTTGTCCGCGTTACTTCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTCCGCGTTACTTCCCTG	
3802	Alg8	Alg8_3802	GGAAAGGACGAAACACCGACAGCCTCCCAATATCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCCTCCCAATATCTCAG	
3803	Alg8	Alg8_3803	GGAAAGGACGAAACACCGCCGCAGCAGATAGACACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGCAGCAGATAGACACCAT	
3804	Alg8	Alg8_3804	GGAAAGGACGAAACACCGAGTTTGGAGCCCAGTAGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTTGGAGCCCAGTAGGCA	
3805	Rrm2b	Rrm2b_3805	GGAAAGGACGAAACACCGGAGAATGTACAAGCAAGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGAATGTACAAGCAAGCAC	
3806	Rrm2b	Rrm2b_3806	GGAAAGGACGAAACACCGTTGGAAAGATGACGAACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGAAAGATGACGAACCGT	
3807	Rrm2b	Rrm2b_3807	GGAAAGGACGAAACACCGGGAGATAAAATACTTCTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGATAAAATACTTCTCGT	
3808	Rrm2b	Rrm2b_3808	GGAAAGGACGAAACACCGTCTCCTAGGGGAAAGAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCTAGGGGAAAGAGTGG	
3809	Gatc	Gatc_3809	GGAAAGGACGAAACACCGCAGATGCTCGATTACCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGATGCTCGATTACCGCGG	
3810	Gatc	Gatc_3810	GGAAAGGACGAAACACCGGCCCCTAGAGTCGGTACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCCTAGAGTCGGTACTGG	
3811	Gatc	Gatc_3811	GGAAAGGACGAAACACCGCAAAGCGAATCCACAGGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAAAGCGAATCCACAGGGAA	
3812	Gatc	Gatc_3812	GGAAAGGACGAAACACCGGGCGTGCAGCTGATCCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGTGCAGCTGATCCGCAA	
3813	Ugt1a1	Ugt1a1_3813	GGAAAGGACGAAACACCGAGACAAACTCTTGGGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACAAACTCTTGGGCACGT	
3814	Ugt1a1	Ugt1a1_3814	GGAAAGGACGAAACACCGCAGTGGCAAGTGACCCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTGGCAAGTGACCCATAG	
3815	Ugt1a1	Ugt1a1_3815	GGAAAGGACGAAACACCGACTTTGTGAAAGATTACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTTTGTGAAAGATTACCCC	
3816	Ugt1a1	Ugt1a1_3816	GGAAAGGACGAAACACCGACACTAACAGCCTCCCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACTAACAGCCTCCCAGCG	
3817	Opa3	Opa3_3817	GGAAAGGACGAAACACCGATGCGCATAATGGGTTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCGCATAATGGGTTTCCG	
3818	Opa3	Opa3_3818	GGAAAGGACGAAACACCGAGGTCTTGAAGAACTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTCTTGAAGAACTCGCTG	
3819	Opa3	Opa3_3819	GGAAAGGACGAAACACCGTCCTTGATACGGTTGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTTGATACGGTTGGCCAG	
3820	Opa3	Opa3_3820	GGAAAGGACGAAACACCGTCAGCAGCGCAATAAGGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCAGCGCAATAAGGAGG	
3821	Ndufs6	Ndufs6_3821	GGAAAGGACGAAACACCGGGGGTTCAAGTGTCGCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGTTCAAGTGTCGCCGAG	
3822	Ndufs6	Ndufs6_3822	GGAAAGGACGAAACACCGCGAAACCCCGTGCAGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAACCCCGTGCAGCCCTG	
3823	Ndufs6	Ndufs6_3823	GGAAAGGACGAAACACCGTGGGGAGAGTCAACAGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGGAGAGTCAACAGCCGG	
3824	Ndufs6	Ndufs6_3824	GGAAAGGACGAAACACCGTGATGAAAAAGACTACAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATGAAAAAGACTACAGGA	
3825	Gnptab	Gnptab_3825	GGAAAGGACGAAACACCGTGTTTGCAATGGACGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTTGCAATGGACGCGTGG	
3826	Gnptab	Gnptab_3826	GGAAAGGACGAAACACCGTCTGCCCATGCCAATCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGCCCATGCCAATCGACG	
3827	Gnptab	Gnptab_3827	GGAAAGGACGAAACACCGAGGAGTGAAATATTTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGTGAAATATTTACCCG	
3828	Gnptab	Gnptab_3828	GGAAAGGACGAAACACCGCATGCTGGACCGTTTAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCTGGACCGTTTAAGGG	
3829	Pnpla1	Pnpla1_3829	GGAAAGGACGAAACACCGTTTGTACGATGTGCTACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTACGATGTGCTACCGG	
3830	Pnpla1	Pnpla1_3830	GGAAAGGACGAAACACCGCTGCAGAGATACATCGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCAGAGATACATCGACGG	
3831	Pnpla1	Pnpla1_3831	GGAAAGGACGAAACACCGGGTTTCCGAGTACCGATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTTCCGAGTACCGATCCA	

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3832	Pnpla1	Pnpla1_3832	GGAAAGGACGAAACACCGAAATGTTCAAACTCCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGTTCAAACTCCAAACC	
3833	Pigg	Pigg_3833	GGAAAGGACGAAACACCGAGGTGGATAAAAATGTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGTGGATAAAAATGTCACA	
3834	Pigg	Pigg_3834	GGAAAGGACGAAACACCGACCCCAGCGTCACTCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCCAGCGTCACTCCCATG	
3835	Pigg	Pigg_3835	GGAAAGGACGAAACACCGAAAGTACTCAGGCATTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGTACTCAGGCATTACCT	
3836	Pigg	Pigg_3836	GGAAAGGACGAAACACCGGATTCGAGGCATAGTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATTCGAGGCATAGTAACTG	
3837	Amt	Amt_3837	GGAAAGGACGAAACACCGAAATGGTGGCGTTTGCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAATGGTGGCGTTTGCAGGG	
3838	Amt	Amt_3838	GGAAAGGACGAAACACCGTTGTAAGCAATACTTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGTAAGCAATACTTCTGAG	
3839	Amt	Amt_3839	GGAAAGGACGAAACACCGTGCGGAACTAAGGCCTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGGAACTAAGGCCTAACC	
3840	Amt	Amt_3840	GGAAAGGACGAAACACCGTGTAACACCTGTGTTGCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTAACACCTGTGTTGCCGT	
3841	Cers3	Cers3_3841	GGAAAGGACGAAACACCGTATCATGAATAAACATCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCATGAATAAACATCACG	
3842	Cers3	Cers3_3842	GGAAAGGACGAAACACCGGTTTAGAAAATGGTTCTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTAGAAAATGGTTCTGGT	
3843	Cers3	Cers3_3843	GGAAAGGACGAAACACCGACACCTCTAGCAAATGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACACCTCTAGCAAATGCACT	
3844	Cers3	Cers3_3844	GGAAAGGACGAAACACCGATGGGCATATGACCTCTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGGCATATGACCTCTGGG	
3845	Cyp26c1	Cyp26c1_3845	GGAAAGGACGAAACACCGCCCTTGGACGTACCGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCTTGGACGTACCGTTCAG	
3846	Cyp26c1	Cyp26c1_3846	GGAAAGGACGAAACACCGGTCACACACACTACTTGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCACACACACTACTTGGCG	
3847	Cyp26c1	Cyp26c1_3847	GGAAAGGACGAAACACCGGTGCGCCGCCCAACGACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCGCCGCCCAACGACCGG	
3848	Cyp26c1	Cyp26c1_3848	GGAAAGGACGAAACACCGCTGTCCCGTAGCGCTCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTCCCGTAGCGCTCGCGG	
3849	Lipt1	Lipt1_3849	GGAAAGGACGAAACACCGGGTTGATGTTACCCATGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTTGATGTTACCCATGTCG	
3850	Lipt1	Lipt1_3850	GGAAAGGACGAAACACCGCTGTAAAATGAGCCCATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTAAAATGAGCCCATGTG	
3851	Lipt1	Lipt1_3851	GGAAAGGACGAAACACCGTGAAGTTCTGATGAGTGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGTTCTGATGAGTGCGG	
3852	Lipt1	Lipt1_3852	GGAAAGGACGAAACACCGAGTCCGGCCGATCTTTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTCCGGCCGATCTTTGATG	
3853	Gpx4	Gpx4_3853	GGAAAGGACGAAACACCGCGTGTGCATCGTCACCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGTGCATCGTCACCAACG	
3854	Gpx4	Gpx4_3854	GGAAAGGACGAAACACCGCATGCCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCCCGATATGCTGAGTG	
3855	Gpx4	Gpx4_3855	GGAAAGGACGAAACACCGTGGTCTGGCAGGCACCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTCTGGCAGGCACCATGG	
3856	Gpx4	Gpx4_3856	GGAAAGGACGAAACACCGTAAGCCAGCACTGCTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAGCCAGCACTGCTGTGCG	
3857	Vps13b	Vps13b_3857	GGAAAGGACGAAACACCGTGTCCATACTACCCAAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCCATACTACCCAAATCG	
3858	Vps13b	Vps13b_3858	GGAAAGGACGAAACACCGTAAACACTGCAATACAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAAACACTGCAATACAAGCG	
3859	Vps13b	Vps13b_3859	GGAAAGGACGAAACACCGGAAACCTCTTCCCGATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACCTCTTCCCGATACAG	
3860	Vps13b	Vps13b_3860	GGAAAGGACGAAACACCGTGGCAGTAGTCCATGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGCAGTAGTCCATGTACTG	
3861	Pex10	Pex10_3861	GGAAAGGACGAAACACCGCAGAAGGACGAGTACTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAAGGACGAGTACTACCT	
3862	Pex10	Pex10_3862	GGAAAGGACGAAACACCGACCTGGCCAAGAGACTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTGGCCAAGAGACTAGCA	
3863	Pex10	Pex10_3863	GGAAAGGACGAAACACCGGTACGTTGGGATCATCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTACGTTGGGATCATCCAAG	
3864	Pex10	Pex10_3864	GGAAAGGACGAAACACCGTGGAGGACGCAGCCGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAGGACGCAGCCGATCAG	
3865	Sco2	Sco2_3865	GGAAAGGACGAAACACCGTTCAGCCTACTAGACCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAGCCTACTAGACCACAA	
3866	Sco2	Sco2_3866	GGAAAGGACGAAACACCGCTGTTCCTTCTCAGCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTTCCTTCTCAGCCCTCG	
3867	Sco2	Sco2_3867	GGAAAGGACGAAACACCGGCTCATCGGGGCAAATATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCATCGGGGCAAATATCA	
3868	Sco2	Sco2_3868	GGAAAGGACGAAACACCGGCATAGAAATTCCCGACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATAGAAATTCCCGACACT	
3869	Epg5	Epg5_3869	GGAAAGGACGAAACACCGACAGCCGACTCGTTGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCCGACTCGTTGTAACA	
3870	Epg5	Epg5_3870	GGAAAGGACGAAACACCGTCGAGCCAGAAGAACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGAGCCAGAAGAACCAATG	
3871	Epg5	Epg5_3871	GGAAAGGACGAAACACCGTGGGTACCATACCCATATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGTACCATACCCATATTG	
3872	Epg5	Epg5_3872	GGAAAGGACGAAACACCGGAAACGCTGTCTTACACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAACGCTGTCTTACACAAG	
3873	Pet100	Pet100_3873	GGAAAGGACGAAACACCGGGAGATCCAGAACATAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGATCCAGAACATAACCA	
3874	Pet100	Pet100_3874	GGAAAGGACGAAACACCGCTGTGGCCAAGAGAGAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGTGGCCAAGAGAGAAGGA	
3875	Pet100	Pet100_3875	GGAAAGGACGAAACACCGCTTTGATACCCACCTTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTTGATACCCACCTTACGC	
3876	Pet100	Pet100_3876	GGAAAGGACGAAACACCGGGATCTCCAATCAGGCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATCTCCAATCAGGCTGAG	
3877	Nt5c3	Nt5c3_3877	GGAAAGGACGAAACACCGAGAGTAGAAGAAATTATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGTAGAAGAAATTATCTG	
3878	Nt5c3	Nt5c3_3878	GGAAAGGACGAAACACCGCTCACCACTCTACCATGTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCACTCTACCATGTAA	
3879	Nt5c3	Nt5c3_3879	GGAAAGGACGAAACACCGCCAGCAGAAAATATGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCAGAAAATATGAACAC	
3880	Nt5c3	Nt5c3_3880	GGAAAGGACGAAACACCGTCTCACTTACTATGACACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCACTTACTATGACACGT	
3881	Hprt	Hprt_3881	GGAAAGGACGAAACACCGCTAGAATGATCAGTCAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAGAATGATCAGTCAACGG	
3882	Hprt	Hprt_3882	GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATACCTAATCATTATGCCG	
3883	Hprt	Hprt_3883	GGAAAGGACGAAACACCGAACAAATCTAGGTCATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAAATCTAGGTCATAACC	
3884	Hprt	Hprt_3884	GGAAAGGACGAAACACCGAGCCCCCCTTGAGCACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCCCCCCTTGAGCACACAG	
3885	Rnaset2a	Rnaset2a_3885	GGAAAGGACGAAACACCGCTCACCTTGCATACTGTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCTTGCATACTGTTGG	
3886	Rnaset2a	Rnaset2a_3886	GGAAAGGACGAAACACCGAAACATGAGTGGGTTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACATGAGTGGGTTAAACA	
3887	Rnaset2a	Rnaset2a_3887	GGAAAGGACGAAACACCGAGAAGACCGGTGAATCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAAGACCGGTGAATCACAT	
3888	Rnaset2a	Rnaset2a_3888	GGAAAGGACGAAACACCGCAGAAGATTGTAACCAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAAGATTGTAACCAGTCC	
3889	Oas1a	Oas1a_3889	GGAAAGGACGAAACACCGGGGAGGTACATTCCTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAGGTACATTCCTCGATG	
3890	Oas1a	Oas1a_3890	GGAAAGGACGAAACACCGGTTGGTACCAGTGCTTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGGTACCAGTGCTTGACC	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3891	Oas1a	Oas1a_3891	GGAAAGGACGAAACACCGAAAGACAGTGAGCAACTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGACAGTGAGCAACTCTA	
3892	Oas1a	Oas1a_3892	GGAAAGGACGAAACACCGGAGGATCAGTTAAACCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGGATCAGTTAAACCGACG	
3893	Car5a	Car5a_3893	GGAAAGGACGAAACACCGATTACAAGAAAGCCTCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATTACAAGAAAGCCTCCGTG	
3894	Car5a	Car5a_3894	GGAAAGGACGAAACACCGGACACTGGGCCAGTCCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACACTGGGCCAGTCCAGAG	
3895	Car5a	Car5a_3895	GGAAAGGACGAAACACCGGGAGTTTGACGATTCCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAGTTTGACGATTCCTGTG	
3896	Car5a	Car5a_3896	GGAAAGGACGAAACACCGAGTGTTTACGAACCTCAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTTTACGAACCTCAGCT	
3901	Apoa1bp	Apoa1bp_3901	GGAAAGGACGAAACACCGTGTGGCCCCGGAAATAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGGCCCCGGAAATAACGG	
3902	Apoa1bp	Apoa1bp_3902	GGAAAGGACGAAACACCGTAACGAGTATCAGTTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACGAGTATCAGTTCAGCG	
3903	Apoa1bp	Apoa1bp_3903	GGAAAGGACGAAACACCGCTCTTGGACATAGACGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTTGGACATAGACGTGGG	
3904	Apoa1bp	Apoa1bp_3904	GGAAAGGACGAAACACCGGAGTCACTAGCCCAGTGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTCACTAGCCCAGTGAAG	
3905	Carkd	Carkd_3905	GGAAAGGACGAAACACCGTAGGCCAGGTCCCACGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGGCCAGGTCCCACGACAA	
3906	Carkd	Carkd_3906	GGAAAGGACGAAACACCGCTGACGTCGAAGAAGCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGACGTCGAAGAAGCACAA	
3907	Carkd	Carkd_3907	GGAAAGGACGAAACACCGCATTCTCACCCCCAACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTCTCACCCCCAACCACG	
3908	Carkd	Carkd_3908	GGAAAGGACGAAACACCGCCATACAGCACATGCGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCATACAGCACATGCGACAA	
3909	Ppat	Ppat_3909	GGAAAGGACGAAACACCGACCTTGGAATCGGACATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCTTGGAATCGGACATACG	
3910	Ppat	Ppat_3910	GGAAAGGACGAAACACCGATAAGACGCCCGATGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAAGACGCCCGATGCAGAG	
3911	Ppat	Ppat_3911	GGAAAGGACGAAACACCGTGATCACTCTGGGACTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGATCACTCTGGGACTCGTG	
3912	Ppat	Ppat_3912	GGAAAGGACGAAACACCGAGGGGTGTATGCGAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGTGTATGCGAGTAACT	
3913	Prosc	Prosc_3913	GGAAAGGACGAAACACCGTATGCTGGAAACCGTAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATGCTGGAAACCGTAGACT	
3914	Prosc	Prosc_3914	GGAAAGGACGAAACACCGATGGTCCAGATTAACACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGTCCAGATTAACACCAG	
3915	Prosc	Prosc_3915	GGAAAGGACGAAACACCGAGACCCACGAACTCCAGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACCCACGAACTCCAGGCT	
3916	Prosc	Prosc_3916	GGAAAGGACGAAACACCGTTGCTGACCGCAACGAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCTGACCGCAACGAGCCG	
3917	Ftl1	Ftl1_3917	GGAAAGGACGAAACACCGGCTGCTCACCAGAGAGAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGCTCACCAGAGAGAGGT	
3918	Ftl1	Ftl1_3918	GGAAAGGACGAAACACCGTTGGCCGAGGAGAAGCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGCCGAGGAGAAGCGCGA	
3919	Ftl1	Ftl1_3919	GGAAAGGACGAAACACCGGAGTTTCAGAACGATCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGTTTCAGAACGATCGCGG	
3920	Ftl1	Ftl1_3920	GGAAAGGACGAAACACCGTCGTCAGAATTATTCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCGTCAGAATTATTCCACCG	
3921	Sis	Sis_3921	GGAAAGGACGAAACACCGTCAGTCACGAATGACAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGTCACGAATGACAACAG	
3922	Sis	Sis_3922	GGAAAGGACGAAACACCGAATTTACCGGGAGTAAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTTACCGGGAGTAAAAGG	
3923	Sis	Sis_3923	GGAAAGGACGAAACACCGGGGAAGTAAAGTGTAGCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGAAGTAAAGTGTAGCGGA	
3924	Sis	Sis_3924	GGAAAGGACGAAACACCGGTAATACGGATGGAATCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAATACGGATGGAATCCAT	
3925	G6pdx	G6pdx_3925	GGAAAGGACGAAACACCGAGAGGTGGAAACTGACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGGTGGAAACTGACAACG	
3926	G6pdx	G6pdx_3926	GGAAAGGACGAAACACCGTGCCCGCTCACGACTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCCCGCTCACGACTCACAG	
3927	G6pdx	G6pdx_3927	GGAAAGGACGAAACACCGATGACCCCACAGTACCCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGACCCCACAGTACCCCAT	
3928	G6pdx	G6pdx_3928	GGAAAGGACGAAACACCGAGAGATGGTCCAGAATCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGAGATGGTCCAGAATCTCA	
3929	Ins1	Ins1_3929	GGAAAGGACGAAACACCGTAGAGAGCCTCTACCAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAGAGCCTCTACCAGGTG	
3930	Ins1	Ins1_3930	GGAAAGGACGAAACACCGCTGGGAGCCCAAACCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGAGCCCAAACCCACCC	
3931	Ins1	Ins1_3931	GGAAAGGACGAAACACCGACCCAAGTCCCGCCGTGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACCCAAGTCCCGCCGTGAAG	
3932	Ins1	Ins1_3932	GGAAAGGACGAAACACCGGTGGAACAACTGGAGCTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGAACAACTGGAGCTGGG	
3933	Gyg	Gyg_3933	GGAAAGGACGAAACACCGAACAGCACAGGACTACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGCACAGGACTACTAGG	
3934	Gyg	Gyg_3934	GGAAAGGACGAAACACCGCTTACGCTTTAAATGCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACGCTTTAAATGCCGGG	
3935	Gyg	Gyg_3935	GGAAAGGACGAAACACCGCTGGTTATACGTTTCAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTTATACGTTTCAATGG	
3936	Gyg	Gyg_3936	GGAAAGGACGAAACACCGCACTAAAATATGTATTCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACTAAAATATGTATTCAGT	
3937	Pcx	Pcx_3937	GGAAAGGACGAAACACCGAGGCTGCCATCTCATACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCTGCCATCTCATACACG	
3938	Pcx	Pcx_3938	GGAAAGGACGAAACACCGACGAGCAGAGAGTCATAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGAGCAGAGAGTCATAGTG	
3939	Pcx	Pcx_3939	GGAAAGGACGAAACACCGGCGCATGGCAACGTCGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCATGGCAACGTCGAACG	
3940	Pcx	Pcx_3940	GGAAAGGACGAAACACCGGACTGGGGCTCACATTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACTGGGGCTCACATTGACA	
3941	Fh1	Fh1_3941	GGAAAGGACGAAACACCGAATTGGGCGAACTCACACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATTGGGCGAACTCACACGC	
3942	Fh1	Fh1_3942	GGAAAGGACGAAACACCGCAGAGCTTCAAACTTATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGAGCTTCAAACTTATTCG	
3943	Fh1	Fh1_3943	GGAAAGGACGAAACACCGGCGACGTTCGGAGCACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGACGTTCGGAGCACACCG	
3944	Fh1	Fh1_3944	GGAAAGGACGAAACACCGCTCGTAGATTCTTGGCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGTAGATTCTTGGCATGG	
3945	Atp5a1	Atp5a1_3945	GGAAAGGACGAAACACCGTGGTCAGAAGCGGTCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTCAGAAGCGGTCCACTG	
3946	Atp5a1	Atp5a1_3946	GGAAAGGACGAAACACCGGCTCCCGCACAGAGATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTCCCGCACAGAGATTCGG	
3947	Atp5a1	Atp5a1_3947	GGAAAGGACGAAACACCGACTGGGCGTGTGTTAAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTGGGCGTGTGTTAAGCAT	
3948	Atp5a1	Atp5a1_3948	GGAAAGGACGAAACACCGCCAACAGCTCCTCGCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAACAGCTCCTCGCCAACG	
3949	Atp5d	Atp5d_3949	GGAAAGGACGAAACACCGTCAGGCGCGTACATACGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGGCGCGTACATACGCCG	
3950	Atp5d	Atp5d_3950	GGAAAGGACGAAACACCGGTGAGTTCGTACCTGCGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGAGTTCGTACCTGCGTCG	
3951	Atp5d	Atp5d_3951	GGAAAGGACGAAACACCGCCAAAGGCTCCAGTCAGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAAGGCTCCAGTCAGCGT	
3952	Atp5d	Atp5d_3952	GGAAAGGACGAAACACCGCTCACCAAAGTACTTAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCACCAAAGTACTTAGTCG	
3953	Atp5e	Atp5e_3953	GGAAAGGACGAAACACCGGAGACACCATGGTGGCGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAGACACCATGGTGGCGTAC	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
3954	Atp5e	Atp5e_3954	GGAAAGGACGAAACACCGGTGGCGTACTGGCGACAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGGCGTACTGGCGACAGGC	
3955	Atp5e	Atp5e_3955	GGAAAGGACGAAACACCGAGATCTGTGCAAAAGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATCTGTGCAAAAGCAGTG	
3956	Atp5e	Atp5e_3956	GGAAAGGACGAAACACCGCTGGGAAAACCGGATGTAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGGAAAACCGGATGTAGC	
3957	Usmg5	Usmg5_3957	GGAAAGGACGAAACACCGTTACATTCATTCTACCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTACATTCATTCTACCTGTG	
3958	Usmg5	Usmg5_3958	GGAAAGGACGAAACACCGTGTGTCCTGGCCACATATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTGTCCTGGCCACATATGG	
3959	Usmg5	Usmg5_3959	GGAAAGGACGAAACACCGATGGCTGGTGCAGAAAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGGCTGGTGCAGAAAGTGA	
3960	Usmg5	Usmg5_3960	GGAAAGGACGAAACACCGGATGGCCAATTCCAGTTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGGCCAATTCCAGTTCAC	
3961	Peo1	Peo1_3961	GGAAAGGACGAAACACCGCATGTGCACGTAAATACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGTGCACGTAAATACTGG	
3962	Peo1	Peo1_3962	GGAAAGGACGAAACACCGCTAACCAGAACACAATCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAACCAGAACACAATCCGA	
3963	Peo1	Peo1_3963	GGAAAGGACGAAACACCGACGTGGCCTGAAGCTACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTGGCCTGAAGCTACTAG	
3964	Peo1	Peo1_3964	GGAAAGGACGAAACACCGAGGGCGGTACGAAGAATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGCGGTACGAAGAATACG	
3965	2810006K23Rik	2810006K23Rik_3965	GGAAAGGACGAAACACCGTCCTGATCAGTGGTAGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCTGATCAGTGGTAGAGGG	
3966	2810006K23Rik	2810006K23Rik_3966	GGAAAGGACGAAACACCGGTGCCACCAAACAAGATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGCCACCAAACAAGATCTG	
3967	2810006K23Rik	2810006K23Rik_3967	GGAAAGGACGAAACACCGCGTGAAAGGACATGGCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGTGAAAGGACATGGCCCAG	
3968	2810006K23Rik	2810006K23Rik_3968	GGAAAGGACGAAACACCGTACCTTGACCACAATGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTTGACCACAATGCCGG	
3969	Timm8a1	Timm8a1_3969	GGAAAGGACGAAACACCGTTCTGAACAGGAGAAGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCTGAACAGGAGAAGTGCA	
3970	Timm8a1	Timm8a1_3970	GGAAAGGACGAAACACCGTCAGCCCGACTGTCCAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCCCGACTGTCCAACTT	
3971	Timm8a1	Timm8a1_3971	GGAAAGGACGAAACACCGGCCCAGAGCCGAGCCCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCAGAGCCGAGCCCGAAG	
3972	Timm8a1	Timm8a1_3972	GGAAAGGACGAAACACCGGTTGCAGCATTTCATCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTGCAGCATTTCATCGAGG	
3973	Park2	Park2_3973	GGAAAGGACGAAACACCGCCAAACAGATCACGTGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAAACAGATCACGTGACGG	
3974	Park2	Park2_3974	GGAAAGGACGAAACACCGTACACATAGTACAGAGACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACACATAGTACAGAGACCA	
3975	Park2	Park2_3975	GGAAAGGACGAAACACCGAAGTGGTTGCTAAGCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTGGTTGCTAAGCGACAG	
3976	Park2	Park2_3976	GGAAAGGACGAAACACCGTTAATTCCAAACCGGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTAATTCCAAACCGGATGAG	
3977	2410015M20Rik	2410015M20Rik_3977	GGAAAGGACGAAACACCGGGGGCCTAGTGACAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGCCTAGTGACAAGAGTG	
3978	2410015M20Rik	2410015M20Rik_3978	GGAAAGGACGAAACACCGTGGAAATTTAATCTTTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGAAATTTAATCTTTGGAG	
3979	2410015M20Rik	2410015M20Rik_3979	GGAAAGGACGAAACACCGCTCGAGTGTGGTCGCTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGAGTGTGGTCGCTAATG	
3980	2410015M20Rik	2410015M20Rik_3980	GGAAAGGACGAAACACCGCAATATGTGTGCCAGCAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATATGTGTGCCAGCAGAC	
3981	Clk1	Clk1_3981	GGAAAGGACGAAACACCGTTCGCAGCACCATTCACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCGCAGCACCATTCACACG	
3982	Clk1	Clk1_3982	GGAAAGGACGAAACACCGATACTTACAAAGTACTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACTTACAAAGTACTATGG	
3983	Clk1	Clk1_3983	GGAAAGGACGAAACACCGACTACATGGGCTACGAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTACATGGGCTACGAGCCA	
3984	Clk1	Clk1_3984	GGAAAGGACGAAACACCGCTGATATGATCCATTCGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGATATGATCCATTCGAAA	
3985	Adck3	Adck3_3985	GGAAAGGACGAAACACCGAGTTCAGTTCTCAACACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTCAGTTCTCAACACCAC	
3986	Adck3	Adck3_3986	GGAAAGGACGAAACACCGCATGCCACTGAAACAGATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATGCCACTGAAACAGATGA	
3987	Adck3	Adck3_3987	GGAAAGGACGAAACACCGCCAGCGAAGATCCTTCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCAGCGAAGATCCTTCCACC	
3988	Adck3	Adck3_3988	GGAAAGGACGAAACACCGCATTGTGAGTACACTGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGTGAGTACACTGTGCA	
3989	Adck4	Adck4_3989	GGAAAGGACGAAACACCGGACCTTATGTACAGTCCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCTTATGTACAGTCCGGG	
3990	Adck4	Adck4_3990	GGAAAGGACGAAACACCGACTAAGAAGTCCTTGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACTAAGAAGTCCTTGCCAGG	
3991	Adck4	Adck4_3991	GGAAAGGACGAAACACCGATGAGTGTGGGCCTGCCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAGTGTGGGCCTGCCAGA	
3992	Adck4	Adck4_3992	GGAAAGGACGAAACACCGGCTAAAGGATGGGACTGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTAAAGGATGGGACTGAGG	
3993	Gyk	Gyk_3993	GGAAAGGACGAAACACCGTCCATCTAGAGTTTAACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCATCTAGAGTTTAACAGG	
3994	Gyk	Gyk_3994	GGAAAGGACGAAACACCGGACCTTGTCCCAGACTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GACCTTGTCCCAGACTACTG	
3995	Gyk	Gyk_3995	GGAAAGGACGAAACACCGTACAGCACCAGCTATAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACAGCACCAGCTATAGCCA	
3996	Gyk	Gyk_3996	GGAAAGGACGAAACACCGCTACCTATAGGTATGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACCTATAGGTATGGAACA	
3997	Ept1	Ept1_3997	GGAAAGGACGAAACACCGCAATTCCAGCACCCCGTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAATTCCAGCACCCCGTTAG	
3998	Ept1	Ept1_3998	GGAAAGGACGAAACACCGGTGTACTCCATCTTTGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTGTACTCCATCTTTGGACG	
3999	Ept1	Ept1_3999	GGAAAGGACGAAACACCGTGACTGGGTTTGGATTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACTGGGTTTGGATTGTCG	
4000	Ept1	Ept1_4000	GGAAAGGACGAAACACCGGGTCGAAGTATGTCAGGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCGAAGTATGTCAGGAGT	
4001	Cyp4f39	Cyp4f39_4001	GGAAAGGACGAAACACCGGGGGAAAGAATTATCTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGGAAAGAATTATCTGACG	
4002	Cyp4f39	Cyp4f39_4002	GGAAAGGACGAAACACCGCTTCAGGACTTACCTAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTCAGGACTTACCTAACCA	
4003	Cyp4f39	Cyp4f39_4003	GGAAAGGACGAAACACCGTCAGCTTGCGACAGGTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCAGCTTGCGACAGGTAATG	
4004	Cyp4f39	Cyp4f39_4004	GGAAAGGACGAAACACCGTGTACTACCTCACAGCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACTACCTCACAGCCGAT	
4005	Cyp21a1	Cyp21a1_4005	GGAAAGGACGAAACACCGGCTTACCTTGCATCCCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTACCTTGCATCCCCAAG	
4006	Cyp21a1	Cyp21a1_4006	GGAAAGGACGAAACACCGTACCATTTAGCATATGGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCATTTAGCATATGGGGT	
4007	Cyp21a1	Cyp21a1_4007	GGAAAGGACGAAACACCGAGGAGATGATACTACAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAGATGATACTACAAGTG	
4008	Cyp21a1	Cyp21a1_4008	GGAAAGGACGAAACACCGATGATTGACTACATGCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGATTGACTACATGCTCCA	
4009	Akr1c21	Akr1c21_4009	GGAAAGGACGAAACACCGAGGACTAACCAAGTCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGACTAACCAAGTCCATTG	
4010	Akr1c21	Akr1c21_4010	GGAAAGGACGAAACACCGGTATCTCATTCATTACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTATCTCATTCATTACCCAA	
4011	Akr1c21	Akr1c21_4011	GGAAAGGACGAAACACCGAGATGATTCTGAATAAGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATGATTCTGAATAAGCCT	
4012	Akr1c21	Akr1c21_4012	GGAAAGGACGAAACACCGTACTGAAGATCATGTAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACTGAAGATCATGTAGGAG	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
4013	Rab7	Rab7_4013	GGAAAGGACGAAACACCGGGAAGTTCTCGGGATCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAAGTTCTCGGGATCCCGG	
4014	Rab7	Rab7_4014	GGAAAGGACGAAACACCGACGGTTCCAGTCTCTTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGGTTCCAGTCTCTTGGTG	
4015	Rab7	Rab7_4015	GGAAAGGACGAAACACCGCGACAGACTTGTTACCATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGACAGACTTGTTACCATGC	
4016	Rab7	Rab7_4016	GGAAAGGACGAAACACCGCACATACTGGTTCATGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACATACTGGTTCATGAGAG	
4017	Tmem5	Tmem5_4017	GGAAAGGACGAAACACCGTGCATAAATTAACCACTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCATAAATTAACCACTGGG	
4018	Tmem5	Tmem5_4018	GGAAAGGACGAAACACCGGCGCCCGAAGAAGACGTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCCCGAAGAAGACGTGGT	
4019	Tmem5	Tmem5_4019	GGAAAGGACGAAACACCGATGTCTGCACCATTAATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGTCTGCACCATTAATCCA	
4020	Tmem5	Tmem5_4020	GGAAAGGACGAAACACCGTCTTTACAGTGACTTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTTACAGTGACTTACCAA	
4021	Large	Large_4021	GGAAAGGACGAAACACCGGATGTGTCTGATTTAAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGTGTCTGATTTAAAGGT	
4022	Large	Large_4022	GGAAAGGACGAAACACCGCAGCAATAGAATCAGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCAATAGAATCAGCAATG	
4023	Large	Large_4023	GGAAAGGACGAAACACCGGCAGGTAACAGCTCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGGTAACAGCTCTGAGTG	
4024	Large	Large_4024	GGAAAGGACGAAACACCGACAGCAGAGAGGGAACTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACAGCAGAGAGGGAACTCAT	
4025	Chst5	Chst5_4025	GGAAAGGACGAAACACCGGTAAGCCTCTGTGCGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGCCTCTGTGCGCAACG	
4026	Chst5	Chst5_4026	GGAAAGGACGAAACACCGGCGAAGGCTTCGCAGACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGAAGGCTTCGCAGACCGG	
4027	Chst5	Chst5_4027	GGAAAGGACGAAACACCGCAGCCATGTGCGCATCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGCCATGTGCGCATCGCAG	
4028	Chst5	Chst5_4028	GGAAAGGACGAAACACCGTGAGCGGATCAGGTCACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGCGGATCAGGTCACGCA	
4029	Hykk	Hykk_4029	GGAAAGGACGAAACACCGCTCCGTATGCCGAACTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGTATGCCGAACTAAAG	
4030	Hykk	Hykk_4030	GGAAAGGACGAAACACCGCCTGAGCCAAAGTCGAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGAGCCAAAGTCGAAACC	
4031	Hykk	Hykk_4031	GGAAAGGACGAAACACCGCCCAGGAAGACCAATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCAGGAAGACCAATAGCTG	
4032	Hykk	Hykk_4032	GGAAAGGACGAAACACCGTTTCGTGTTCACATTGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTCGTGTTCACATTGCAAG	
4033	Fdx1l	Fdx1l_4033	GGAAAGGACGAAACACCGCGCCCGGGTCCTGTTACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCCCGGGTCCTGTTACGGG	
4034	Fdx1l	Fdx1l_4034	GGAAAGGACGAAACACCGGTTTGTCCCCAGGGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTTGTCCCCAGGGTCAACG	
4035	Fdx1l	Fdx1l_4035	GGAAAGGACGAAACACCGCTGGCAAGCGGATCCCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGCAAGCGGATCCCGGTG	
4036	Fdx1l	Fdx1l_4036	GGAAAGGACGAAACACCGTCTAGGACGTTCGGGACTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTAGGACGTTCGGGACTAC	
4037	Zfp143	Zfp143_4037	GGAAAGGACGAAACACCGGCATTTCGGTGCAAATACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCATTTCGGTGCAAATACGA	
4038	Zfp143	Zfp143_4038	GGAAAGGACGAAACACCGCTAATTATAAAAACCATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAATTATAAAAACCATGTG	
4039	Zfp143	Zfp143_4039	GGAAAGGACGAAACACCGCCTGACGGAGGCAGTAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTGACGGAGGCAGTAACCG	
4040	Zfp143	Zfp143_4040	GGAAAGGACGAAACACCGAGTGTGAGCATTCAGGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGTGAGCATTCAGGCTGT	
4041	Cyp51	Cyp51_4041	GGAAAGGACGAAACACCGGCTGTCAAAAGAACCAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTGTCAAAAGAACCAGCTG	
4042	Cyp51	Cyp51_4042	GGAAAGGACGAAACACCGATGCAGAAGAAGTCTACGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCAGAAGAAGTCTACGGT	
4043	Cyp51	Cyp51_4043	GGAAAGGACGAAACACCGTAGAAGTCAACTCAACGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGAAGTCAACTCAACGAGA	
4044	Cyp51	Cyp51_4044	GGAAAGGACGAAACACCGAGGAACATACTGCTTAAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGAACATACTGCTTAAAGT	
4045	Pigyl	Pigyl_4045	GGAAAGGACGAAACACCGGGGATGAGGACGGTCATGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGGATGAGGACGGTCATGGT	
4046	Pigyl	Pigyl_4046	GGAAAGGACGAAACACCGAGGCCTGCCAGCGAGACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGCCTGCCAGCGAGACCAG	
4047	Pigyl	Pigyl_4047	GGAAAGGACGAAACACCGTGGGAAGCCTTCCTCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGGAAGCCTTCCTCCACGG	
4048	Pigyl	Pigyl_4048	GGAAAGGACGAAACACCGCCACGGAGGCGGAGTAGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACGGAGGCGGAGTAGAGC	
4053	Fmo3	Fmo3_4053	GGAAAGGACGAAACACCGGATGCTACAATGATTTGTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GATGCTACAATGATTTGTTC	
4054	Fmo3	Fmo3_4054	GGAAAGGACGAAACACCGTTCACAGGACCATATAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCACAGGACCATATAGAAG	
4055	Fmo3	Fmo3_4055	GGAAAGGACGAAACACCGTGTCACAGCCTGAGTTCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTCACAGCCTGAGTTCCCC	
4056	Fmo3	Fmo3_4056	GGAAAGGACGAAACACCGCTTGGGTGATGAGTCGAGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTGGGTGATGAGTCGAGTC	
4057	Bckdhb	Bckdhb_4057	GGAAAGGACGAAACACCGGCCAAGTATCGCTACCGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAAGTATCGCTACCGCTC	
4058	Bckdhb	Bckdhb_4058	GGAAAGGACGAAACACCGCTCGTAAACCAACAGTGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCGTAAACCAACAGTGCAT	
4059	Bckdhb	Bckdhb_4059	GGAAAGGACGAAACACCGCCACACAACCCCACGGGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACACAACCCCACGGGGCC	
4060	Bckdhb	Bckdhb_4060	GGAAAGGACGAAACACCGCACCGGTGCTACAGCTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCGGTGCTACAGCTATTG	
4061	Agxt2	Agxt2_4061	GGAAAGGACGAAACACCGCATCACCATGGCCAGGTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATCACCATGGCCAGGTCGT	
4062	Agxt2	Agxt2_4062	GGAAAGGACGAAACACCGTAGCAAAGGCTTCCGGAAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGCAAAGGCTTCCGGAAAT	
4063	Agxt2	Agxt2_4063	GGAAAGGACGAAACACCGAGACAGAACTTGTATGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGACAGAACTTGTATGCCAC	
4064	Agxt2	Agxt2_4064	GGAAAGGACGAAACACCGAAAAACAGATAGACCGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAACAGATAGACCGCCTG	
4065	Nnt	Nnt_4065	GGAAAGGACGAAACACCGACGAACGCTTCGTACTCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGAACGCTTCGTACTCACC	
4066	Nnt	Nnt_4066	GGAAAGGACGAAACACCGGTTATACATACCTTCGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTATACATACCTTCGCAGG	
4067	Nnt	Nnt_4067	GGAAAGGACGAAACACCGTTCAATGTTGTCGTGGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAATGTTGTCGTGGAATC	
4068	Nnt	Nnt_4068	GGAAAGGACGAAACACCGGCTTCGTGAGCGCCTAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCGTGAGCGCCTAACGT	
4069	Slc25a3	Slc25a3_4069	GGAAAGGACGAAACACCGTGCGGCACTTTACTAAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCGGCACTTTACTAAGTCC	
4070	Slc25a3	Slc25a3_4070	GGAAAGGACGAAACACCGTTCAACAGTACGTTCAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAACAGTACGTTCAAAGC	
4071	Slc25a3	Slc25a3_4071	GGAAAGGACGAAACACCGGCCTTATATAGCAACATACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTTATATAGCAACATACT	
4072	Slc25a3	Slc25a3_4072	GGAAAGGACGAAACACCGGCCCCGAAGTGAATGTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCCGAAGTGAATGTACAA	
4073	Ndufv1	Ndufv1_4073	GGAAAGGACGAAACACCGGCCGCCTATATCTACATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCGCCTATATCTACATCCG	
4074	Ndufv1	Ndufv1_4074	GGAAAGGACGAAACACCGTGTACCAGTCACCCCGTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTACCAGTCACCCCGTCTC	
4075	Ndufv1	Ndufv1_4075	GGAAAGGACGAAACACCGGCCAATCAGACCTGCTTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCAATCAGACCTGCTTCAT	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
4076	Ndufv1	Ndufv1_4076	GGAAAGGACGAAACACCGCCCACAGGTAGCTATCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCACAGGTAGCTATCCGAG	
4077	Ndufa12	Ndufa12_4077	GGAAAGGACGAAACACCGCTTAAAGGGCAAATGATATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTAAAGGGCAAATGATATA	
4078	Ndufa12	Ndufa12_4078	GGAAAGGACGAAACACCGCTGGTGGGAGAAGACAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTGGGAGAAGACAAATA	
4079	Ndufa12	Ndufa12_4079	GGAAAGGACGAAACACCGTGGTGTAGATGACCCATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGGTGTAGATGACCCATCGG	
4080	Ndufa12	Ndufa12_4080	GGAAAGGACGAAACACCGCCTACCTGAAGAAAACCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTACCTGAAGAAAACCCGT	
4081	Ndufa12	Ndufa12_4081	GGAAAGGACGAAACACCGTCCACCCTTAGAGATTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCACCCTTAGAGATTGTTG	
4082	Ndufa12	Ndufa12_4082	GGAAAGGACGAAACACCGAGCAATTCCCCGCTGCCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGCAATTCCCCGCTGCCTCA	
4083	Ndufa12	Ndufa12_4083	GGAAAGGACGAAACACCGCATACAGGTGGGATCTCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATACAGGTGGGATCTCATC	
4084	Ndufa12	Ndufa12_4084	GGAAAGGACGAAACACCGATCTGCGGAAATCGCGTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATCTGCGGAAATCGCGTGTT	
4085	Bcs1l	Bcs1l_4085	GGAAAGGACGAAACACCGTTGGTTATCCGCGCCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGTTATCCGCGCCGACGT	
4086	Bcs1l	Bcs1l_4086	GGAAAGGACGAAACACCGACGTCGGCGCGGATAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ACGTCGGCGCGGATAACCAA	
4087	Bcs1l	Bcs1l_4087	GGAAAGGACGAAACACCGTACCTTCTTTATGGGCCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TACCTTCTTTATGGGCCCCC	
4088	Bcs1l	Bcs1l_4088	GGAAAGGACGAAACACCGAAGAAGGTAGCCACGTCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGAAGGTAGCCACGTCTGT	
4089	Tymp	Tymp_4089	GGAAAGGACGAAACACCGCACCAGGTGCCAATGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CACCAGGTGCCAATGATCAG	
4090	Tymp	Tymp_4090	GGAAAGGACGAAACACCGATACTTAGGGGCCATGCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATACTTAGGGGCCATGCTAA	
4091	Tymp	Tymp_4091	GGAAAGGACGAAACACCGTTCAGGTCACCTGTAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAGGTCACCTGTAATGAG	
4092	Tymp	Tymp_4092	GGAAAGGACGAAACACCGTCACATCTCGTGCAGCATACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCACATCTCGTGCAGCATAC	
4093	Sacs	Sacs_4093	GGAAAGGACGAAACACCGTTTGTAAACCTTCAATCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTTGTAAACCTTCAATCAAA	
4094	Sacs	Sacs_4094	GGAAAGGACGAAACACCGTCTCCAATCTTGATCCAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCCAATCTTGATCCAATC	
4095	Sacs	Sacs_4095	GGAAAGGACGAAACACCGATATAAAAATTTAACCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATATAAAAATTTAACCTCTG	
4096	Sacs	Sacs_4096	GGAAAGGACGAAACACCGGTCCGCGTGACCGTGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTCCGCGTGACCGTGCTCCG	
4097	Tmlhe	Tmlhe_4097	GGAAAGGACGAAACACCGAGTTGTTGCACCAACAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTGTTGCACCAACAAAGC	
4098	Tmlhe	Tmlhe_4098	GGAAAGGACGAAACACCGTATCTAGTCACATGACCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TATCTAGTCACATGACCATC	
4099	Tmlhe	Tmlhe_4099	GGAAAGGACGAAACACCGATGCCGGTCTAGAGCTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGCCGGTCTAGAGCTAGCT	
4100	Tmlhe	Tmlhe_4100	GGAAAGGACGAAACACCGCTCCGTAATTTGATGAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCCGTAATTTGATGAAGAG	
4101	Sbf2	Sbf2_4101	GGAAAGGACGAAACACCGTGTTGGCTGTTTCCGCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGGCTGTTTCCGCTCTC	
4102	Sbf2	Sbf2_4102	GGAAAGGACGAAACACCGGGATGACACGCCTTTCCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGATGACACGCCTTTCCCAC	
4103	Sbf2	Sbf2_4103	GGAAAGGACGAAACACCGCTTACCAATTCAATTCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTTACCAATTCAATTCCCTG	
4104	Sbf2	Sbf2_4104	GGAAAGGACGAAACACCGCTAATCTGGATACCAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTAATCTGGATACCAACACC	
4105	Pikfyve	Pikfyve_4105	GGAAAGGACGAAACACCGCTGGCATCCAATATTGCTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGCATCCAATATTGCTTC	
4106	Pikfyve	Pikfyve_4106	GGAAAGGACGAAACACCGTGTTGTAATCAAGAAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGTTGTAATCAAGAAATCCC	
4107	Pikfyve	Pikfyve_4107	GGAAAGGACGAAACACCGGGCTGGTTCTGCTTTCCTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCTGGTTCTGCTTTCCTTC	
4108	Pikfyve	Pikfyve_4108	GGAAAGGACGAAACACCGCGAAGCTGAACAGCTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGAAGCTGAACAGCTGTACG	
4109	Plcg2	Plcg2_4109	GGAAAGGACGAAACACCGTTGCCAAACTGAGCGTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGCCAAACTGAGCGTGCTG	
4110	Plcg2	Plcg2_4110	GGAAAGGACGAAACACCGCGCTCACTTTGAAGTTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCTCACTTTGAAGTTGACC	
4111	Plcg2	Plcg2_4111	GGAAAGGACGAAACACCGTAGATCAAACCCGAAGAAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAGATCAAACCCGAAGAAAC	
4112	Plcg2	Plcg2_4112	GGAAAGGACGAAACACCGAGATAAAGGAAATCCGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGATAAAGGAAATCCGTCCG	
4113	ApoE	ApoE_4113	GGAAAGGACGAAACACCGGCCTCTGCGCGATCGCGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTCTGCGCGATCGCGCCC	
4114	ApoE	ApoE_4114	GGAAAGGACGAAACACCGCCGACTCGGAGCCGACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCGACTCGGAGCCGACATGG	
4115	ApoE	ApoE_4115	GGAAAGGACGAAACACCGCTACACAGGATGCCTAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACACAGGATGCCTAGCCG	
4116	ApoE	ApoE_4116	GGAAAGGACGAAACACCGGCTTCTGGGATTACCTGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCTTCTGGGATTACCTGCGC	
4117	Fdft1	Fdft1_4117	GGAAAGGACGAAACACCGAACCTTGTCCCAGTCCTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTTGTCCCAGTCCTGTT	
4118	Fdft1	Fdft1_4118	GGAAAGGACGAAACACCGCTCTCAGTGAACCGCCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTCTCAGTGAACCGCCACTC	
4119	Fdft1	Fdft1_4119	GGAAAGGACGAAACACCGCTGCCATCCCACACCCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGCCATCCCACACCCCATC	
4120	Fdft1	Fdft1_4120	GGAAAGGACGAAACACCGCAGTACTGCCACTACGTTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGTACTGCCACTACGTTGC	
4121	Abcd1	Abcd1_4121	GGAAAGGACGAAACACCGTCATCCTGCTTGAGCGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCATCCTGCTTGAGCGCCTA	
4122	Abcd1	Abcd1_4122	GGAAAGGACGAAACACCGGTTCCAGCATGACATACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTTCCAGCATGACATACCAT	
4123	Abcd1	Abcd1_4123	GGAAAGGACGAAACACCGCAGGGTGTACGAGATGTTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGTGTACGAGATGTTCC	
4124	Abcd1	Abcd1_4124	GGAAAGGACGAAACACCGTCTCTCTACAGGCCAAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTCTCTACAGGCCAAGTTG	
4125	Pex26	Pex26_4125	GGAAAGGACGAAACACCGGCGCTCTGCGGCCTTCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCGCTCTGCGGCCTTCAGCG	
4126	Pex26	Pex26_4126	GGAAAGGACGAAACACCGTCTGGATCCGGCGGAAGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTGGATCCGGCGGAAGAGC	
4127	Pex26	Pex26_4127	GGAAAGGACGAAACACCGCTGGTAGTACCGGAGGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTGGTAGTACCGGAGGACCC	
4128	Pex26	Pex26_4128	GGAAAGGACGAAACACCGGGTCAAACCGTAGAATCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGTCAAACCGTAGAATCAAG	
4129	Tusc3	Tusc3_4129	GGAAAGGACGAAACACCGAAAAGCAGATGAATAACGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAAGCAGATGAATAACGCC	
4130	Tusc3	Tusc3_4130	GGAAAGGACGAAACACCGCATTCTGAAGATCGAGCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTCTGAAGATCGAGCGCC	
4131	Tusc3	Tusc3_4131	GGAAAGGACGAAACACCGTAACGAAGAATATCAAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TAACGAAGAATATCAAATCC	
4132	Tusc3	Tusc3_4132	GGAAAGGACGAAACACCGCGCTCGATCTTCAGAATGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CGCTCGATCTTCAGAATGAA	
4133	Pigo	Pigo_4133	GGAAAGGACGAAACACCGCAGGGGACTCATAGAACGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAGGGGACTCATAGAACGCC	
4134	Pigo	Pigo_4134	GGAAAGGACGAAACACCGTCCGGGGAAGAGGTCTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCCGGGGAAGAGGTCTCTCC	

No.	*Oligo name	*Oligo name	*Sequence(5’to3’)	nt#	Remarks	5'	guide sequence	3'
4135	Pigo	Pigo_4135	GGAAAGGACGAAACACCGCCCATCCCGTTTGGGAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCCATCCCGTTTGGGAACAC	
4136	Pigo	Pigo_4136	GGAAAGGACGAAACACCGCCACAGTGGACGGCGGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCACAGTGGACGGCGGTTCG	
4137	Atp6v0a2	Atp6v0a2_4137	GGAAAGGACGAAACACCGTGAAGAGCTCGAACGAATACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAAGAGCTCGAACGAATAC	
4138	Atp6v0a2	Atp6v0a2_4138	GGAAAGGACGAAACACCGCAACAGAGAGTCGTTCTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CAACAGAGAGTCGTTCTCTA	
4139	Atp6v0a2	Atp6v0a2_4139	GGAAAGGACGAAACACCGCTACAGCTGCATGCAGCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CTACAGCTGCATGCAGCGGC	
4140	Atp6v0a2	Atp6v0a2_4140	GGAAAGGACGAAACACCGTCTTCGTGACCCTCAGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TCTTCGTGACCCTCAGCATG	
4141	Cers1	Cers1_4141	GGAAAGGACGAAACACCGGCAGACGACACCGCTTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCAGACGACACCGCTTGGCC	
4142	Cers1	Cers1_4142	GGAAAGGACGAAACACCGTGACGTCAGCGATGTGCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGACGTCAGCGATGTGCAGC	
4143	Cers1	Cers1_4143	GGAAAGGACGAAACACCGATGAACTCACCGGAAGGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATGAACTCACCGGAAGGCGT	
4144	Cers1	Cers1_4144	GGAAAGGACGAAACACCGGTAAGCGCAGTAGCTCCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GTAAGCGCAGTAGCTCCAAC	
4145	Cers2	Cers2_4145	GGAAAGGACGAAACACCGTTGGGAGGGATATCCCATACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTGGGAGGGATATCCCATAC	
4146	Cers2	Cers2_4146	GGAAAGGACGAAACACCGGGCGGAACCAGCGTTCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGCGGAACCAGCGTTCTACC	
4147	Cers2	Cers2_4147	GGAAAGGACGAAACACCGCATTGGGAGGTGCCCGCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CATTGGGAGGTGCCCGCAGT	
4148	Cers2	Cers2_4148	GGAAAGGACGAAACACCGGCCCACTCTGCCGTGACAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCCACTCTGCCGTGACAAA	
4149	Ears2	Ears2_4149	GGAAAGGACGAAACACCGTGCTATCCGCTTCCGTCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGCTATCCGCTTCCGTCTAG	
4150	Ears2	Ears2_4150	GGAAAGGACGAAACACCGAGGGGCAGATGAGCAAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGGGGCAGATGAGCAAATCG	
4151	Ears2	Ears2_4151	GGAAAGGACGAAACACCGTTCAGAAGCTCCAGCCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TTCAGAAGCTCCAGCCGCTG	
4152	Ears2	Ears2_4152	GGAAAGGACGAAACACCGAGTGGCAGGTGATCCGCGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTGGCAGGTGATCCGCGTC	
4153	Hars2	Hars2_4153	GGAAAGGACGAAACACCGGGAACCTTGATGACAAAATTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GGAACCTTGATGACAAAATT	
4154	Hars2	Hars2_4154	GGAAAGGACGAAACACCGGCCTCCAGACCTTTCCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GCCTCCAGACCTTTCCAACT	
4155	Hars2	Hars2_4155	GGAAAGGACGAAACACCGGAAGTTGTCTTCATACTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			GAAGTTGTCTTCATACTTCT	
4156	Hars2	Hars2_4156	GGAAAGGACGAAACACCGAACAGCTGATAATCTTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACAGCTGATAATCTTATCG	
4157	Stat2	Stat2_4157	GGAAAGGACGAAACACCGAGTTCTTGGTGAGATCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AGTTCTTGGTGAGATCCATC	
4158	Stat2	Stat2_4158	GGAAAGGACGAAACACCGATAACTTGCGAAAATTCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			ATAACTTGCGAAAATTCAGC	
4159	Stat2	Stat2_4159	GGAAAGGACGAAACACCGCCTACTTAGACCTTTCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			CCTACTTAGACCTTTCCCAA	
4160	Stat2	Stat2_4160	GGAAAGGACGAAACACCGTGAGATTGAAAATCGAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			TGAGATTGAAAATCGAATCC	
4161	BRDN0000737505	BRDN0000737505_4161	GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73		NTCs	AAAAAGTCCGCGATTACGTC	
4162	BRDN0000737693	BRDN0000737693_4162	GGAAAGGACGAAACACCGAAAACGGCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACGGCTCGATCGGTGAT	
4163	BRDN0000737637	BRDN0000737637_4163	GGAAAGGACGAAACACCGAAAACGTAATTATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAACGTAATTATACCGAGC	
4164	BRDN0000738185	BRDN0000738185_4164	GGAAAGGACGAAACACCGAAAATTGCACCTTCCCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAATTGCACCTTCCCGGCC	
4165	BRDN0000737801	BRDN0000737801_4165	GGAAAGGACGAAACACCGAAACCCCCGCGCGGAGCGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACCCCCGCGCGGAGCGTC	
4166	BRDN0000737467	BRDN0000737467_4166	GGAAAGGACGAAACACCGAAACCTAGCGTAGATTCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACCTAGCGTAGATTCGGC	
4167	BRDN0000737848	BRDN0000737848_4167	GGAAAGGACGAAACACCGAAACGAGGCTGTTCGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACGAGGCTGTTCGTACAC	
4168	BRDN0000737609	BRDN0000737609_4168	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTCATACGTAGCGAATC	
4169	BRDN0000737434	BRDN0000737434_4169	GGAAAGGACGAAACACCGAAACTCCCGTGTCAACCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAACTCCCGTGTCAACCGAT	
4170	BRDN0000738254	BRDN0000738254_4170	GGAAAGGACGAAACACCGAAAGACGTGCATTCAGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAAGACGTGCATTCAGCGAG	
4171	BRDN0000737777	BRDN0000737777_4171	GGAAAGGACGAAACACCGAACATGTTAAGTCGCGTTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACATGTTAAGTCGCGTTAT	
4172	BRDN0000737611	BRDN0000737611_4172	GGAAAGGACGAAACACCGAACCAGCATTTGACCGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCAGCATTTGACCGCGCT	
4173	BRDN0000737528	BRDN0000737528_4173	GGAAAGGACGAAACACCGAACCCCGGCTGTCATCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCCCGGCTGTCATCGCCG	
4174	BRDN0000738228	BRDN0000738228_4174	GGAAAGGACGAAACACCGAACCCGCCGGAACAATCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCCGCCGGAACAATCAGC	
4175	BRDN0000737727	BRDN0000737727_4175	GGAAAGGACGAAACACCGAACCGGCTGCGCGTTTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCGGCTGCGCGTTTGCAA	
4176	BRDN0000737483	BRDN0000737483_4176	GGAAAGGACGAAACACCGAACCGTACTGCGAGGAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCGTACTGCGAGGAGCAT	
4177	BRDN0000737872	BRDN0000737872_4177	GGAAAGGACGAAACACCGAACCTCGTCTCATGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACCTCGTCTCATGTACGAA	
4178	BRDN0000737516	BRDN0000737516_4178	GGAAAGGACGAAACACCGAACGCCCCGGATTTCGTTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGCCCCGGATTTCGTTGA	
4179	BRDN0000737844	BRDN0000737844_4179	GGAAAGGACGAAACACCGAACGGCTGCGCCCGCGGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGCTGCGCCCGCGGCAA	
4180	BRDN0000737412	BRDN0000737412_4180	GGAAAGGACGAAACACCGAACGGGCGCAATACCCTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGGCGCAATACCCTTTT	
4181	BRDN0000737631	BRDN0000737631_4181	GGAAAGGACGAAACACCGAACGGTAGCGTACCCGTGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGTAGCGTACCCGTGAA	
4182	BRDN0000737750	BRDN0000737750_4182	GGAAAGGACGAAACACCGAACGGTCAAATCCGTGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGGTCAAATCCGTGAGGG	
4183	BRDN0000737875	BRDN0000737875_4183	GGAAAGGACGAAACACCGAACGTCACCAACCTCGATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGTCACCAACCTCGATCC	
4184	BRDN0000738229	BRDN0000738229_4184	GGAAAGGACGAAACACCGAACGTTATAGCTTCGTCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACGTTATAGCTTCGTCTCT	
4185	BRDN0000737806	BRDN0000737806_4185	GGAAAGGACGAAACACCGAACTAACTCACTACGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTAACTCACTACGCACGA	
4186	BRDN0000738366	BRDN0000738366_4186	GGAAAGGACGAAACACCGAACTCCTCATCGTACGCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTCCTCATCGTACGCTAA	
4187	BRDN0000737593	BRDN0000737593_4187	GGAAAGGACGAAACACCGAACTCGCGTGGGAAGTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTCGCGTGGGAAGTCCGG	
4188	BRDN0000738128	BRDN0000738128_4188	GGAAAGGACGAAACACCGAACTTATACGTAATCTGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AACTTATACGTAATCTGATC	
4189	BRDN0000738307	BRDN0000738307_4189	GGAAAGGACGAAACACCGAAGACTCCTACGTATCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGACTCCTACGTATCGAGC	
4190	BRDN0000737391	BRDN0000737391_4190	GGAAAGGACGAAACACCGAAGCACAAGAACGGTCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCACAAGAACGGTCCGCC	
4191	BRDN0000737912	BRDN0000737912_4191	GGAAAGGACGAAACACCGAAGCAGCGACTACTCGACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCAGCGACTACTCGACGC	
4192	BRDN0000738101	BRDN0000738101_4192	GGAAAGGACGAAACACCGAAGCCTAACGGAGCTCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCTAACGGAGCTCGCGG	
4193	BRDN0000738296	BRDN0000738296_4193	GGAAAGGACGAAACACCGAAGCCTACTTCACCGGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCCTACTTCACCGGTCGG	

No.	*Oligo name	*Oligo name	*Sequence（5’ to3’ ）	nt#	Remarks	5'	guide sequence	3'
4194	BRDN0000738095	BRDN0000738095_4194	GGAAAGGACGAAACACCGAAGCGAGCCGCAGACCGTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGAGCCGCAGACCGTTT	
4195	BRDN0000737714	BRDN0000737714_4195	GGAAAGGACGAAACACCGAAGCGTACCCCACTCGTTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGTACCCCACTCGTTAA	
4196	BRDN0000738016	BRDN0000738016_4196	GGAAAGGACGAAACACCGAAGCGTGAGATTCACCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGCGTGAGATTCACCGCCG	
4197	BRDN0000737416	BRDN0000737416_4197	GGAAAGGACGAAACACCGAAGGCCTTAACACGTCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCCTTAACACGTCGACC	
4198	BRDN0000737993	BRDN0000737993_4198	GGAAAGGACGAAACACCGAAGGCGTAAACGAGTACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGCGTAAACGAGTACACG	
4199	BRDN0000738351	BRDN0000738351_4199	GGAAAGGACGAAACACCGAAGGGTAAGTACAGTATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGGGTAAGTACAGTATCGT	
4200	BRDN0000738301	BRDN0000738301_4200	GGAAAGGACGAAACACCGAAGTCCCCTTCGGGAACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCCCCTTCGGGAACTCC	
4201	BRDN0000737395	BRDN0000737395_4201	GGAAAGGACGAAACACCGAAGTCTATGCGGGGCTCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AAGTCTATGCGGGGCTCGTA	
4202	BRDN0000737589	BRDN0000737589_4202	GGAAAGGACGAAACACCGAATAAGCCTACCCGGCGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC	73			AATAAGCCTACCCGGCGAGA	