

Library Number	RMK005
Library Name	Inborn Errors of Immunity (IEI) Library #3 - IEI3
Old Document Name	IEI Library (Andrew)
Library Purpose	CRISPR/Cas9 Knockout of genes associated with Inborn Errors of Immunity/Primary immune deficiencies in mouse T cells to look at effects on immunometabolism.
Location	Main Lab, '-20 Freezer, IEI box
Designer Name	Andrew Patterson
Designing Date	January 2019
Design Reference	2017 IUIS report on Primary Immune Deficiencies/IEI
Usage Reference	n/a
Species	Mouse (Mus musculus)
Total Gene #	312
Total Target #	1278
Gene Group	
1. Negative Controls	(Nontargeting controls from BRIE library)30
2. Positive Controls	n/a
3. IEI Genes	312
Target Number	
1. Negative Controls	30*1=30
2. Positive Controls	n/a
3. IEI Genes	312*4=1248

The Inborn Errors of Immunity Genes Library was designed from genes that cause IEI when mutated as identified by the IUIS in 2017 (DOI: 10.1007/s10875-017-0464-9). Genes without mouse orthologs, genes linked with causative Gain-of-Function (GOF) mutations, and genes without guides in the Brie or Gecko libraries were excluded. 30 NTCs (~2.3%) were added from the Brie library controls.

Note 2: This library does **not** include genes added to the IEI list by IUIS after 2017. See their 2022 publication for a more updated list.

While no genes were included specifically as positive controls, this library included several genes involved in TCR and IL-2 signaling that we would predict to be either enriched or depleted following certain stimulation protocols.

Number	Target Gene Symbol	sgRNA.Target.Sequence
1	Acp5	ATACCAGGGGATGTTGCGAA
2	Acp5	TCCACGTACAAACATAACTG
3	Acp5	TACCTGGAACCTCTTGTGCGC
4	Acp5	ACAGCCACAAATCTCAGGGT
5	Actb	AATGCCTGTGGTACGACCAG
6	Actb	ATGGAGGGGAATACAGCCCG
7	Actb	GGACTCCTATGTGGGTGACG
8	Actb	CAGCACAGGGTGCTCCTCAG
9	Ada	GTTGTGGATCTTGTGAACCA
10	Ada	ATTCATCGGACCGTCCACGC
11	Ada	CTTCATCTCCACAAACTCGT
12	Ada	GCTGCGCAACATTATCGGCA
13	Adam17	GGTGTGTGGCAACTCCAGGG
14	Adam17	ACACGTCGTGGGATAATGCA
15	Adam17	CATCGACGTACGGCACACAC
16	Adam17	GCCCCAATGAGGACCAAGG
17	Cfd	TCTCACGTGGGGACCCAACG
18	Cfd	CCCCGAGGCCGGATTCTGGG
19	Cfd	TTGACACTCTGAGTTGATGC
20	Cfd	CCCCTGAACCCTACAAGCGA
21	Aicda	GTAGGAACAACAATTCCACG
22	Aicda	TTCACAGAAGTAGAGGCGCG
23	Aicda	ACCAGGTGACGCGGTAACAC
24	Aicda	TGAGACCTACCTCTGCTACG
25	Aire	TGTGCCGTGTGCCACGACGG
26	Aire	CTCTCCAGGAATTCAGACCA
27	Aire	ACAGAACCTGTCCCAGCCTG
28	Aire	GGTAGAGATGAGCAGAAAGT
29	Ak2	TGAAGGCGACAATGGATGCA
30	Ak2	GGTAGGACCGGCCACTCTTG
31	Ak2	TCCGAACCGGAGATTCCGAA
32	Ak2	TCAGCCAGTTTGGGTGCCTG
33	Ap3b1	TGTGGCCAGTAAAAACATCG
34	Ap3b1	GCTGCCTAATAAATCGTGTG
35	Ap3b1	ATATGCTAACAAGATACGCT
36	Ap3b1	TTGGCACATCTCACCCAAGT
37	Ap3d1	CCAACGCAATGGTATCTGTG
38	Ap3d1	AGCACATCACCAACTTCGAG
39	Ap3d1	TCTTCACAGTAAAGTACCTG
40	Ap3d1	TGTCCTCATCGCTCTCCGTG
41	Xiap	TTTCAGACACCATATACCCG
42	Xiap	AGCACTAGCTAACTCTCTGG

Number	Target Gene Symbol	sgRNA.Target.Sequence
43	Xiap	CTTGGGAACAGCATGCGAAG
44	Xiap	ATGGACATCCTCAGTTAACA
45	Arpc1b	CACAATGCGGTTACTCTCAG
46	Arpc1b	CAATGAGAACAAGTTCGCCG
47	Arpc1b	CCAGTCCAGGCTGAGCACTG
48	Arpc1b	GAAGCGAGCACTCACGTGTA
49	Rab27a	TGGTTAAGCTACGAAACCTA
50	Rab27a	AGTGTACTGGTAGAGTACAC
51	Rab27a	AACCCAGATATAGTGCTGTG
52	Rab27a	CCTGAAATCAATGCCCACTG
53	Atm	TAAGTCATATAGGAAGCCGA
54	Atm	GAGTATAAATAACATCGCGA
55	Atm	AAGACTTGAACACCGGACAA
56	Atm	TGCAAGATACACATGAATCG
57	B2m	ATTTGGATTTCAATGTGAGG
58	B2m	ACTCACTCTGGATAGCATAAC
59	B2m	TGAGTATACTTGAATTTGAG
60	B2m	TCGGCTTCCCATTCTCCGGT
61	Bach2	TGGACAGACGAAAGATGACT
62	Bach2	AATTACGGACAGCCCCACGT
63	Bach2	CTCCTCGTATTCCTACGCAG
64	Bach2	TCTCTGTTCGGTATAACGAA
65	Bcl10	CTCCGGGTGGTACATGACAG
66	Bcl10	GATTCAGAAGATAACGGATG
67	Bcl10	ATAAACTGGAGCACCTCAA
68	Bcl10	CCTGGTGGAATCCATCCGCA
69	Blm	TTACCTGGAACATTTCAACG
70	Blm	GGTGGGTAAACATTCTCAG
71	Blm	CCTGCAAGTGGATTTAACGA
72	Blm	CCTTCACCGACTTACACCTG
73	Btk	AATCCGGTACAATAGTGACC
74	Btk	TATGAATATGACTTTGAACG
75	Btk	TGGAGGAGAGCAACCTACCG
76	Btk	AGATTTAGCAAACACAGACA
77	Serping1	GCTCTGAGATGCATTCACAT
78	Serping1	ACAATAACAAATGACACCAT
79	Serping1	AGAACTCATCAACACCTGGG
80	Serping1	GGACACAGGCAAAATCCTTG
81	C1qa	CACAGATGAAGCGACCCGTG
82	C1qa	CCCAATGACGCTTGGCAACG
83	C1qa	TTCAGCCACTGTCCATACTA
84	C1qa	AGGCAATCCAGGCAATATCA

Number	Target Gene Symbol	sgRNA.Target.Sequence
85	C1qb	AGGCACTCCAGGGATAAAGG
86	C1qb	TGACCTGGTTCGGTCGCAAG
87	C1qb	GAATCGCCTTTGGGACCGCG
88	C1qb	CAGGTGAACTTGCCGTTGCG
89	C1qc	GGGTGACTGTGAATACCGAC
90	C1qc	CTGTGGTCACCAACCCTCAG
91	C1qc	ATCATGCCCCGTCTTCCCAG
92	C1qc	GCTCCCCCGGAGGCCCTG
93	C2	GTTCTAGGAAAGTCCAACAT
94	C2	GTGTGATGTGAGCTAGACCT
95	C2	AGTCAATACCATATTTGAGG
96	C2	TTGGGGCGACAGTACCGCAC
97	Ciita	AGCTCGACTAAGGCTCCGGG
98	Ciita	AGGTCCTTGATTATATCGTG
99	Ciita	TCCAGTGCCTAATCTACCA
100	Ciita	AGCAGGCCAAGACTTACATG
101	C9	CTACAACGGACTCTGTGACC
102	C9	TTTCCATTAAACTGTCCGA
103	C9	ATTCTGCAGTCTATCGGTAT
104	C9	TTGAGAGGAGTGGTCCAAC
105	Hyou1	ACAGGCGGATAACCCTCATG
106	Hyou1	ACATCGTACTCACTTGCCCA
107	Hyou1	TGGAATTGATATCTTTCCGG
108	Hyou1	TGGCGTGCTCAGTTTAGACA
109	Casp8	GATTATGAAAGATCAAGCAC
110	Casp8	CTTCCTAGACTGCAACCGAG
111	Casp8	ATGATCAGACAGTATCCCCG
112	Casp8	CAAGAAGCAGGAGACCATCG
113	Ctla4	TGTGATGGTGAATATTCACA
114	Ctla4	GGACTGAGAGCTGTTGACAC
115	Ctla4	ACAGGTGACCCAACCTTCAG
116	Ctla4	TGCCACAAAGTATGGCGGT
117	Cd19	GAATGACTGACCCCGCCAGG
118	Cd19	AATGTCTCAGACCATATGGG
119	Cd19	GGCACCTATTATTGTCTCCG
120	Cd19	TTTAGCCCACACATACAGCT
121	Ms4a1	GTTACAGTACTGTGTAGATG
122	Ms4a1	TACCATACACTCAAACAGAT
123	Ms4a1	CAGTCGTAGATATCAACATA
124	Ms4a1	CCACACAAAGCTTCTTCATG
125	Cd3d	TTACACAGATATATCCCTCG
126	Cd3d	TCCATCTAGATGCATGACGC

Number	Target Gene Symbol	sgRNA.Target.Sequence
127	Cd3d	AAGAATAAAACACTCAACTT
128	Cd3d	GATACAAGTGACCGAATATG
129	Cd3e	AGGGCACGTCAACTCTACAC
130	Cd3e	TTCTCGGAAGTCGAGGACAG
131	Cd3e	TACTTGTACCTGAAAGCTCG
132	Cd3e	TCAGAAGCATGATAAGCACC
133	Cd3g	TGACACTGATACGTGCCTCG
134	Cd3g	TTCTGTAATACACTTGCAGG
135	Cd3g	AACTGCATTGAGCTAAACAT
136	Cd3g	GTACAAGTGGATGGCAGCCG
137	Cd247	GCTCGGGATCCAGAGATGGG
138	Cd247	GCTCAATCTAGGGCGAAGAG
139	Cd247	CTCCTGGGAACCGCACGTGG
140	Cd247	CATTGTATACGCCTTCTGG
141	Cd79a	GGAACCCTAATATCACATGG
142	Cd79a	CCTACTCACTGCGCACGCGG
143	Cd79a	CGAAGTAAACAAGAACCACA
144	Cd79a	AGGCGTATGACAAGAAGAGG
145	Cd81	GCAACCACAGAGCTACACCT
146	Cd81	GGGCTTCGTAAACAAAGACC
147	Cd81	ATCCATCACAGCTTGCTGAA
148	Cd81	GGCAAACAGGATCACAAGGC
149	Cd8a	TGGGTGAGTCGATTATCCTG
150	Cd8a	ATCCCACAACAAGATAACGT
151	Cd8a	GTGTTGGGGTCCGTTTCGCA
152	Cd8a	GGACGCCGAACCTTGGTCAGA
153	Cfh	ATTTACGCATAACTCCACCA
154	Cfh	CAAGTGTTCCGTATCCAGGG
155	Cfh	GAAATTGATTACCGTGAATG
156	Cfh	CATATTTCACTTCCACCA
157	Cfi	CTTGTGGATTACCTTCACAA
158	Cfi	TGTTATTACACAGGTTGCCG
159	Cfi	AAGGTCGACGCAGGCCACGT
160	Cfi	TGCCTGCATGTACATTGCCG
161	Cftr	GCCGTGTGACTGACATACGT
162	Cftr	TTCTAACTGAGACCTTACGC
163	Cftr	GTGGCGATCATGTTGCTGCG
164	Cftr	TATGGAGAGTAAATATCGT
165	Coro1a	TGACACGAACTCGCTTGTC
166	Coro1a	ACCAGGCGATGTCTAGCACA
167	Coro1a	AGAAGGGAAGATTCTAACCA
168	Coro1a	GCCACAGAGGTAGACAATGT

Number	Target Gene Symbol	sgRNA.Target.Sequence
169	Tpp1	TGAGTTTCATCGCTATGTAG
170	Tpp1	TTATGGTAGAAGGTTACCTG
171	Tpp1	AACCTGACAGCCAAAGATGT
172	Tpp1	GATCGAGGCCAGTCTAGATG
173	Copa	CTTGCGGTTACAGATCACAA
174	Copa	CTCTCTCTGACACATCACCT
175	Copa	CACCAGAAATATCCCAAACG
176	Copa	GAATGTCTAGGTACTIONCACACA
177	Cr2	ATGTTGACCAGTTTGTGCG
178	Cr2	CTATACATTGCACCCCTGAG
179	Cr2	AGACGGATTTCTATAAACCA
180	Cr2	ATGCAATGCTCATGGCACAT
181	Csf2ra	AGGACGCGGTGACGTCACGT
182	Csf2ra	CCTACTTGGTCGTGACCGGT
183	Csf2ra	CTAGCGTCACTAACCCAGAA
184	Csf2ra	TGACATCCAGCGTGACACCG
185	Csf2rb	TACACTTGAAGACTGACTG
186	Csf2rb	TGATGGAAAATCGTGTATAG
187	Csf2rb	GAAGAAATCGGACAGCTGGG
188	Csf2rb	TGGAGACTGTAGGCATCCTG
189	Csf3r	TCAGCTCTACAGAATTACAG
190	Csf3r	TGAGGCAGGATAGGTTTGAG
191	Csf3r	TGAGCTGCGTGGTGTGCAA
192	Csf3r	CTTTGCCACACAATCCGGGA
193	Ctsc	CTGCAAGATAACAACCTCCTG
194	Ctsc	GGCAGTAACTGATAGCTGTG
195	Ctsc	TCACAACCACAACCTTTGTGA
196	Ctsc	CTGTATTTTCATCAGTCATCG
197	Cyba	AGTAGAAGGATACATAGAGT
198	Cyba	AATGACTTACCATCGCTCCA
199	Cyba	GGACGTAGTAATTCCTGGTG
200	Cyba	CAGATAGATCACACTGGCAA
201	Cybb	CCTCTACCAAACCATTCGG
202	Cybb	TTTACCAGACGAATTGTACG
203	Cybb	ATTCTAACTTGGATACCTTG
204	Cybb	TTATACTCGAAAACCTCCTTG
205	Cd55	CTCTTATACGTATAGCCAGG
206	Cd55	CTGCTGTCCCCAACTGTACG
207	Cd55	TGTGACAGAACAGAAAGTAG
208	Cd55	CGAAAACAACCTCCACTCCC
209	Dnase1b3	TCTCGGGAGTTGTGTGCAAG
210	Dnase1b3	TCACACTCACTTGTAGACGA

Number	Target Gene Symbol	sgRNA.Target.Sequence
211	Dnase1l3	TTCATGGGTGATTTCAACGC
212	Dnase1l3	CACTACCATGACTATCAGGA
213	Dnase2a	TACACCGTCTTGCCAACCGT
214	Dnase2a	AGGCCAGGTGTATGCACCAG
215	Dnase2a	CGAAGCCCTGAGCTGCTATG
216	Dnase2a	GAAATTACCTGACCTAGAGA
217	Dnmt3b	TGGTAGCCGGAAACTCCACA
218	Dnmt3b	CAGCCTTCTGAATTACACGC
219	Dnmt3b	GGAGGGTATGGATACCACAC
220	Dnmt3b	CAGTAGGCTTGAAGCCACCG
221	Fadd	TAGATCGTGTGCGCGCAGCG
222	Fadd	AAGCTGGAGCGCGTGCAGAG
223	Fadd	TTCGTTTGCTCACGCGCTCG
224	Fadd	GCGCCTGGACGACTTCGAGG
225	Fas	CAGTTAAGAGTTCATACTCA
226	Fas	TATTTATATATCGAAAGTAC
227	Fas	CATTTGCATACTCACACGAC
228	Fas	GAGGACTGCAAATGAATGG
229	Fasl	AGGACCACAACACAAATCTG
230	Fasl	CTTCACTCCAGAGATCAGAG
231	Fasl	CCTCTGAAAAAAAAAGAGCCG
232	Fasl	GGAAGTGGCAGAACTCCGTG
233	Fcgr3	TGGTGACACTGATGTGCGAA
234	Fcgr3	ATGCACACTCTGGAAGCCAA
235	Fcgr3	TGGTGAAACTGGACCCCCCA
236	Fcgr3	TGCTGCTCCAGACCCCTCAG
237	Fpr1	AGAAGGTAATCATCGTACCC
238	Fpr1	TGGTGACAGTGTGTTTCATG
239	Fpr1	GGCAATGTAAAATGGCAAAG
240	Fpr1	GATGCAGAACACAAATACAG
241	G6pdx	AGAGGTGGAAACTGACAACG
242	G6pdx	TGCCCCGCTCACGACTCACAG
243	G6pdx	ATGACCCACAGTACCCCAT
244	G6pdx	AGAGATGGTCCAGAATCTCA
245	Slc37a4	CTACGTTGACCAGACCAACC
246	Slc37a4	TCTTTACTCCGAAGACCACG
247	Slc37a4	CACAACTTGCTGATGGCGT
248	Slc37a4	CAGAGCGATCTCATCCACCA
249	Gata2	CCTGGGCTGTGCAACAAGTG
250	Gata2	GGCCGGGAGTGTGTCAACTG
251	Gata2	ACAGCTGCTGCCTCCCGACG
252	Gata2	GGCACATAGGAGGGATAGGT

Number	Target Gene Symbol	sgRNA.Target.Sequence
253	Gfi1	CAAATGCATCAAATGCAGCA
254	Gfi1	CCCCGACTCTCAGCTTACCG
255	Gfi1	CTGCACGCGGACAAGAGCGT
256	Gfi1	CTACGGCGACTTCGCGCCTG
257	Ostm1	CATCAGCCGAAACATCGGGG
258	Ostm1	TTGCCTAACAAACAATGGTG
259	Ostm1	AGCGCTGCGCACCATACAGG
260	Ostm1	CAGAATGCAGATAGTTCTCA
261	Hc	GCAGATGACTCCCATTATCG
262	Hc	AGACAAACCTGTTTACACGC
263	Hc	ACCCTAAGGGAATTCGTGGT
264	Hc	GAACCTCCCATCAAATGTGA
265	Hells	TCTGCGGTACCGAATTTAG
266	Hells	ACGGTCATTAATAACTTACAG
267	Hells	GCTGTATCATGGAACCCGGG
268	Hells	ACAACACTTTCTCGCTTAGG
269	Foxn1	CCAGGTACTTACGTTCTGTG
270	Foxn1	GAACAGTACATATGTTGCAA
271	Foxn1	CACCTCACTATCCCTATCAG
272	Foxn1	CCACAGACAGCCCTTTGAG
273	Hmox1	TCGTGCTCGAATGAACACTC
274	Hmox1	TCAGGACCTGACCCCCTGAG
275	Hmox1	ACGCTTTACATAGTGCTGTG
276	Hmox1	TTCCTTGTACCATATCTACA
277	Irf8	AGTTTACCGAATTGTCCCCG
278	Irf8	TCGACAGCAGCATGTACCCG
279	Irf8	GCGTAACCTCGTCTTCCACG
280	Irf8	CAAGCAGGATTACAATCAGG
281	Ifnar2	CAAAGACGAAAATCTGACGA
282	Ifnar2	GCCATCGTCATAGTGCACAG
283	Ifnar2	TAACTGGATAATCCCTGAA
284	Ifnar2	ACTGTGGAATTACGATTATG
285	Ifngr1	TATGTGGAGCATAACCGGAG
286	Ifngr1	GGTATTCCCAGCATACGACA
287	Ifngr1	TTCAGGGTGAAATACGAGGA
288	Ifngr1	TATACCAATACGCAAATACC
289	Ifngr2	AGGGAACCTCACTTCCAAGT
290	Ifngr2	TGGACCTCCGAAAAACATCT
291	Ifngr2	TCCCTTTGATGTGTTCCACG
292	Ifngr2	TGATGAGCAGATTCTAACTT
293	Cd79b	TGACCTGGTTCCGAAAGCGA
294	Cd79b	TCCCCAGGATTCAGCACGT

Number	Target Gene Symbol	sgRNA.Target.Sequence
295	Cd79b	CATAATGTCACCGACAGCTG
296	Cd79b	CGAGGTTTGCAGCCAAAAAG
297	Igll1	CTGTTCCAGATCATCCCACG
298	Igll1	GCTCACCAAACACACTAGTG
299	Igll1	CCAAAGACATACCAAACCTG
300	Igll1	GGAGAACTTCACACTGCCTG
301	Ikbkb	TCACACATACCCCGTGACGG
302	Ikbkb	CAAGATCCATGTCCAACGTG
303	Ikbkb	ATGTGGCACCCCTCGGCAAAG
304	Ikbkb	GAAGCCAGTGATGCACTCGA
305	Ikbkg	AAGGATCGGCAAGCTTTAGA
306	Ikbkg	AGGCTGCCTTGCGAATGGAG
307	Ikbkg	TGGGTGAAGAATCTTCTCTG
308	Ikbkg	GCTCAGGTGACATCATTGCT
309	Il10	GCTAACCGACTCCTTAATGC
310	Il10	AACTGCACCCACTTCCCAGT
311	Il10	AAGGAGCATTGAATCCCT
312	Il10	ACTGGCATGAGGATCAGCAG
313	Il10ra	GCAGTGTTTACTTATCACGA
314	Il10ra	GTGGGGACAACACGGACAGT
315	Il10ra	GGTGAACGTTGTGAGATCAC
316	Il10ra	TCTGGCTTCAAACCACACAT
317	Il10rb	TGGCGGATGAACATTCCGGAG
318	Il10rb	ATTTCAAGAACATTCTACAG
319	Il10rb	CGGAGGACCTCAGAGTCGTA
320	Il10rb	AGAGAAGTCGCACTGAGTCG
321	Il12rb1	GTCGGTGAGGAACCAAACCG
322	Il12rb1	CCTCCGAACCATACCCACAC
323	Il12rb1	TGAGAAGACATCGTTCCCAG
324	Il12rb1	TCAAGGTGTCACAATCACAC
325	Il17ra	ACTGAAGTAGCAAACAACGT
326	Il17ra	ATGAGGCCATACCCCACAG
327	Il17ra	GAAGGTCTGGATCGTCTACT
328	Il17ra	GACCTGGAGATGTTTGAACC
329	Irak1	ACAGAAGGGCCAGCAAACCG
330	Irak1	TGGGCAAGAAGCCATAAACA
331	Irak1	GGTGCGTGAGGATGTGAACG
332	Irak1	CCCACCGAACTGGCACCAGT
333	Il1rn	TTCTCCAGAAAAGATAGACA
334	Il1rn	GTGTTCTTGGGCATCCACGG
335	Il1rn	CTGCCTCTGAATGAAACAGA
336	Il1rn	CTTGATATCATCTCCAGACT

Number	Target Gene Symbol	sgRNA.Target.Sequence
337	Il2ra	GTGTCTGTATGACCCACCCG
338	Il2ra	ATCTTGCAGATGCTAATAGC
339	Il2ra	GAGAGGTTTCCGAAGACTAA
340	Il2ra	GAATCTTCATGTTTCCAAGG
341	Il2rg	TTCCACAGATTGGGTATAG
342	Il2rg	GGAGCAACAGAGATCGAAGC
343	Il2rg	CCCGATTACCAAGATTCTGT
344	Il2rg	CATACCTATAGTGCAGCGTG
345	Il7r	GGGAGACTAGGCCATACGAC
346	Il7r	AGACCTAGAAGATGCAGACG
347	Il7r	CAGAACCCAAGAATCAAGGT
348	Il7r	CCTTTGAAGTAATCGTTATG
349	Itch	TCCCGCACATAGGCTATCTG
350	Itch	AAAACATAATTTACTCGTAG
351	Itch	GCCAAGCTCCCCTACCACCT
352	Itch	ACAACACTCGGATTACTCAG
353	Itgb2	GAGTATAGGCAAATCCCGTG
354	Itgb2	TTGGCTGGCGCAATGTCACG
355	Itgb2	ATCCTGAGTTCGACCAACGG
356	Itgb2	TGGAGTAGGAGAGATCCATG
357	Itk	CAGCCCCAAGCGCTACTACG
358	Itk	GTAAGCCTTCTCATACCCCG
359	Itk	TCAGGAACCTGAAGAAACCC
360	Itk	TTGCTCCAGACTGTGAGAGT
361	Jak1	CGATGCCATTTCGAATGACAG
362	Jak1	TGAATAAATCCATCAGACAG
363	Jak1	TCCGAACCGAATCATCACTG
364	Jak1	AAACATATAGTGTACCTCTA
365	Jak3	CAGACATCGGAACTGCATGG
366	Jak3	AGAAAAGTCCAATTTGATCG
367	Jak3	GGGCTTTGGAGCCACCACGT
368	Jak3	CACCACCGAGACCTTCCGTG
369	Rpsa	GAAGCGGCCAGCGATCGGAG
370	Rpsa	CTTACAGGGAGCTCACTCAG
371	Rpsa	GACGTCAGCAGGATTCTCGA
372	Rpsa	AGGGAAGTACTCCGCATGCG
373	Lck	AAGATCCGTAACCTAGACAA
374	Lck	GTAACAACGGACACACGA
375	Lck	CCGGGAAAGCGAAAGCACTG
376	Lck	GCTTTATGCAGTGGTCACCC
377	Lig1	GACCTCACTGACACCCCGAG
378	Lig1	GACAATTCAAGACACTCTTG

Number	Target Gene Symbol	sgRNA.Target.Sequence
379	Lig1	TCTTCTCATAGAATTTCCCA
380	Lig1	AGAGTGATTCTCCAGTGAAG
381	Psemb8	CCGGAGCTCGCACTTCCCCG
382	Psemb8	ACATGATGCTGCAGTACCGG
383	Psemb8	CTCGCCTTCAAGTTCCAGCA
384	Psemb8	AGGTTGTATTATCTTCGGAA
385	Blnk	CTATGCAGGTCGAAACAGTG
386	Blnk	AAGATAATCGATCCAGCCAG
387	Blnk	GTCTGTGACTAGACCCTCGG
388	Blnk	GATATTAAGAACAATGAAGG
389	Lyst	GGAGCCCTGAAAGATCGCGG
390	Lyst	GGGATGAGTCTTACCCACGT
391	Lyst	TAGGAAGTGGTGAACCACGT
392	Lyst	CATACCCCGAGTTTAAGCAA
393	Masp2	GGCCTGTGATATAGTCCACA
394	Masp2	CCTTTGCCACTGACGAGTCG
395	Masp2	CTGCGAGTATGACTTTGTCA
396	Masp2	TGTGGCAATAATGGTCACAA
397	Mcm4	TTGTTGACAAGGTTCAACCA
398	Mcm4	ACCCGGGTGGAGATAGATCG
399	Mcm4	GGTTATACCAACCTTTGACA
400	Mcm4	CTCAGGGTCTTTCATCACAT
401	Cd46	CTGTGAGCCAAATCATACAT
402	Cd46	TCCATAGCTTCAAATGGCCG
403	Cd46	GGCCTCAGCATAGACGCCCA
404	Cd46	ACAGTTGTGATCCTACCCCA
405	Msh6	AGTTTCGTGATACCAAACAG
406	Msh6	CATCAGTGACCGTCTAGATG
407	Msh6	TAAGTAAAGACACGGCTGAG
408	Msh6	GAGGCAAAGGATCTCAACGG
409	Msn	CGCTTGTTAATCCGAAGCCG
410	Msn	CCGGGCCAAGTTCTACCCAG
411	Msn	GAAGCAACTTATCTCCAGCC
412	Msn	CAGACTAAGAAGGCTCAGCA
413	Mvk	AGCGTCAATTTACCCAACAT
414	Mvk	GTGGTCGGAACCTTCCCCCG
415	Mvk	CAAGGTCCC GCGGAGTACCA
416	Mvk	TCTGAAGTCAATCAACAAGT
417	Myd88	GGTTCAAGAACAGCGATAGG
418	Myd88	AAGGAGCTGAAGTCGCGCAT
419	Myd88	CCTGTCCTCAGGACAAACGC
420	Myd88	GCATCCAACAACTGCGAGT

Number	Target Gene Symbol	sgRNA.Target.Sequence
421	Ncf1	TCTTCACGGGCAGTCCCATG
422	Ncf1	GATCCGGATCCCAACTACGC
423	Ncf1	GCTACGCACTGGCTGTCAGT
424	Ncf1	CGTTGCCCATCAAACCACCT
425	Ncf2	GCACAAAGCCAAACAATACG
426	Ncf2	TGGAATATCGGATTCTGGAG
427	Ncf2	TCTCACCTGTGGCTGCAGAG
428	Ncf2	TGAAGCAAATCCTCGAGTGG
429	Ncf4	AGAAGAAGATCCTGACGTCCG
430	Ncf4	CGTAGAACTGGCGATAGCGG
431	Ncf4	CGATCCATGATGGCCCCTTG
432	Ncf4	ACCTCGATGACAAAAACCTG
433	Nfkb1	TGTGAAGGCCCATCACACGG
434	Nfkb1	GGAGTCACGAAATCCAACGC
435	Nfkb1	TTTCGACTACGCAGTGACGG
436	Nfkb1	ATGACAGAGGCGTGTATTAG
437	Nfkb2	ACTGAGCGTGATAAATGACG
438	Nfkb2	CGGAACACAATGGCATACTG
439	Nfkb2	CCCACGCTGCTGGATCGGCA
440	Nfkb2	ACCCGGATAGCAGCCCATTG
441	Pepd	CACAAATCGGATCTCCAGCG
442	Pepd	CTGCTATGGTGTTCATCGATG
443	Pepd	GCCCTGCAACACGACAGCTG
444	Pepd	CTTGCTAATGCCCTCGAAGG
445	Cfp	GTTACACATTTGGTTCCGAG
446	Cfp	TATGAGCATAAGGCCTGCAG
447	Cfp	GATTATCACATACTCGTTGA
448	Cfp	CCTACTTGGGAGAGACATCA
449	Prf1	GTTTCGTGCCAGGTGTATGGA
450	Prf1	TGCCACAGGTAGGCGCTGTG
451	Prf1	TCAATAACGACTGGCGTGTG
452	Prf1	GGTAGGAGACTGCCTGAACG
453	Pik3r1	GAGCTTTATAAGGAGAGGGCG
454	Pik3r1	TCCATTAACCTTCAACTCTG
455	Pik3r1	TGGCTACAATGAAACCACTG
456	Pik3r1	CTGGAAATCTGAAAAGCACG
457	Prkcd	AGAAGGTGGCGATAAACTCG
458	Prkcd	TTATAAACCTTGAATCGGTG
459	Prkcd	AGCCCACCATGTATCCTGAG
460	Prkcd	CGATGATGTAGAGTGTACCA
461	Pms2	TCTCAGGAAACCATAAACTG
462	Pms2	GTAAGCTGCACTAATCAGCT

Number	Target Gene Symbol	sgRNA.Target.Sequence
463	Pms2	AGTTTCAGACAATGGATGTG
464	Pms2	ACTAAAGAGATCAAGTCTAG
465	Pnp	AGATGCTGTGTGATGATGCA
466	Pnp	TCAGTGCCTGGAAACAAATG
467	Pnp	TGTGGCCAGAACCCTCTCCG
468	Pnp	CCTCAAGTGGCAGTGATCTG
469	Pola1	CTAACGTTTACCATTTACAG
470	Pola1	AAGAAAGCAACTTACGCTGG
471	Pola1	AAAGAAAAAAGATCTACTG
472	Pola1	TGTACAGAACCATCAACATG
473	Pole	CATTATGGTCACCTACAATG
474	Pole	GATGCTGAGACCTACGTCGG
475	Pole	CATTGACCTCAGAATCCATG
476	Pole	AGGCTGGAAGGATCATAGCA
477	Pole2	GATCGAACGATCTGTCGTGG
478	Pole2	CCACAGTGGCTTATACACCG
479	Pole2	TCAAGCGCTTTAATACCTTG
480	Pole2	ATAGCGTTCAAGATACAGCT
481	Prkdc	AGAGCCAATTCAGTGACCCG
482	Prkdc	TGGCCCTTGTAAGTAGACGA
483	Prkdc	CATGCAGGGTAAGTAATCGT
484	Prkdc	ACAGAGGATGCTCAAAAATG
485	Psen1	TTTCAACCAGCATAACGAAGT
486	Psen1	TGCTACTGTAACGTAGTCCA
487	Psen1	CTGAGCCAATATCTAATGGG
488	Psen1	AGTCAGCTTCTATACCCGGA
489	Pstpip1	CTGGTTACAGTGCACCCACA
490	Pstpip1	TGTTTGTAGAAAGAGTGTAC
491	Pstpip1	ATTGGCACTCACACGCTCGA
492	Pstpip1	GTCGCTCTACAAGAAGACCA
493	Pten	CCTCCAATTCAGGACCCACG
494	Pten	TGTGCATATTTATTGCATCG
495	Pten	ACTATTCCAATGTTCAAGTGG
496	Pten	GGTTTGATAAGTTCTAGCTG
497	Ptprc	GTAGCAGAAATCTTATATCG
498	Ptprc	TTTCACAATGGAGTGTACGA
499	Ptprc	TTGTCAAGCTAAGGCGACAG
500	Ptprc	ACCACAACGAAGCAAACATG
501	Rac2	GAGAAGACACGTCTTGCCCA
502	Rac2	GCTGGACCTTCGCGATGACA
503	Rac2	AAGAAGCCACTCACACAGTG
504	Rac2	GGCACGGACATTCTCATAGG

Number	Target Gene Symbol	sgRNA.Target.Sequence
505	Rag1	ACACCAAAGCAGAGTCGTAG
506	Rag1	TGAAACGATTCCCACAGATG
507	Rag1	TCCCGCGCAAGATTGCAATG
508	Rag1	TGGGAAGTAGACCTGACTGT
509	Rag2	CATCAATATATCATTACGG
510	Rag2	ATTGACGTGGTGTATAGTCG
511	Rag2	TAACTTGTATAGAATAAGAG
512	Rag2	CATACCAGGAGACAATAAGC
513	Ranbp2	AAATTATTCTCGTCACAAAG
514	Ranbp2	TGCTAATGTAACTCCCACCA
515	Ranbp2	ATGTTGTTAAACTTAAGTCG
516	Ranbp2	ACATGCAATGCACCTAGAGA
517	Rasgrp1	ACGTACAGATATCCGTCGGA
518	Rasgrp1	TAAGAACTATGATCTCGACC
519	Rasgrp1	ACAGTTGGTTATTCCGACAC
520	Rasgrp1	TGACCTTATTGATCTCATGT
521	Relb	GTTCAAACGCCACCCTACG
522	Relb	TACACCCACATAGCCTCGTG
523	Relb	GCGGATTTGCCGAATCAACA
524	Relb	GCCTCCTATCGGGACCAGCA
525	Rfxank	GTTCTACTTACAGTCCAGGG
526	Rfxank	ATCAACAAACCGGATGAGCG
527	Rfxank	GCACTGTCACTTGCCAGTAT
528	Rfxank	AGTTCGCTTCTGCTAGACT
529	Rorc	CTTGAGTATAGTCCAGAACG
530	Rorc	GTCATCTGGGATCCACTACG
531	Rorc	TCTGGGGCACTGCAGAACT
532	Rorc	GACAAGCAGAGGCCTCGGGT
533	Sema3e	ACACGATCTACACCCGAGTG
534	Sema3e	TGTGCCAGCAAAGTAAACGG
535	Sema3e	AAGATAATTACCAACTAGCG
536	Sema3e	TGTGATACACACATACAGCA
537	Foxp3	CATACCTGATGCATGAAGTG
538	Foxp3	TCTACCCACAGGGATCAATG
539	Foxp3	AGGTCGGGACCTGCGAAGTG
540	Foxp3	GCAAGAGCTCTTGTCCATTG
541	Sh2d1a	AGAAGCTCTTACTCGCTACC
542	Sh2d1a	GATGCAGTGAAGTGTACCA
543	Sh2d1a	AACAGGTTCTTGGAGTGCCG
544	Sh2d1a	CACACAGGCAGTACACGCCA
545	Clpb	AGGACCGCGTCCGACGAGG
546	Clpb	GGAGAACGGCTGGTACGATG

Number	Target Gene Symbol	sgRNA.Target.Sequence
547	Clpb	CGTTGTCACCGGAGACCGCG
548	Clpb	CTCTCGAGTGACTAGGACTG
549	Stat1	GGATAGACGCCAGCCACTG
550	Stat1	TGTGATGTTAGATAAACAGA
551	Stat1	TTAATGACGAGCTCGTGGAG
552	Stat1	GAAAAGCAAGCGTAATCTCC
553	Stat3	CCAACAAATTAAGAACTGG
554	Stat3	CTGCTTCTCTGTCACTACGG
555	Stat3	GTTTACCACGAAAGTCAGGT
556	Stat3	CAAAGAGTCACATGCCACGT
557	Stat5b	CTGATTTCGAGTGATTACAG
558	Stat5b	TACAGCGAACCAGCTCCATG
559	Stat5b	GCGGTTGTCCCAGAGGACAG
560	Stat5b	AGTGGATCGAAAGCCAAGCC
561	Stim1	TGAGGATAAGCTTATCAGCG
562	Stim1	GAATACAGGAGCTAGCTCCG
563	Stim1	GAGCCGTCAAAAATATGCTG
564	Stim1	CAGCAGATCGAGATCCTCTG
565	Stxbp2	CGTGTAATAGTGGGGACACG
566	Stxbp2	CATCCATCCGATAACGCAAG
567	Stxbp2	TATTATAGGTACCTTCTCCG
568	Stxbp2	AAGGTTGTAGGTGCTATGTG
569	Tap1	ACTAATGGACTCGCACACGT
570	Tap1	GTCTCTAGCAAAGTCCACGC
571	Tap1	TGCCACATAACTGATAGCGA
572	Tap1	TGGACATGAGCCATATGTTG
573	Tap2	AGAAGCCACTCGGACTACTG
574	Tap2	TTACACGACCCGAATAGCGA
575	Tap2	GCTGTGGGGACTGCTAAAAG
576	Tap2	CATGCACACATACCTGATGG
577	Tapbp	TGGTGTTAGAGACACTCTGG
578	Tapbp	CTTTCCCAGCTGGACTCGAG
579	Tapbp	CGCCACTCCAGCCCAAAGGG
580	Tapbp	AGCCGTGAAGCCTTCTCAGG
581	Tbx1	ACATAGACAACATGGAATCG
582	Tbx1	CTTCCGGGATTGCGACCCGG
583	Tbx1	ACACTACCACCCGGACTCGC
584	Tbx1	GCGCACGGATCGTAGCGCGG
585	Tcf3	ATTATTGCTGGAGTGATCCG
586	Tcf3	GCTCCTAGGAACGTGGAAGG
587	Tcf3	GAAGAGCCGTACCTAGCAT
588	Tcf3	CTGCAAACCTGGGTTCCCCCG

Number	Target Gene Symbol	sgRNA.Target.Sequence
589	Tcn2	GAAGCGGCTCCATGACAGCG
590	Tcn2	TCTGAGACCACGAATCACCA
591	Tcn2	GAGACTAGCAATACCGCAGG
592	Tcn2	GAATATCTATAGCACCCAC
593	Tert	CCTCCAGCCTAACTTGACTG
594	Tert	CACAGAGGGCCAGATATCCG
595	Tert	TCAGCATGCTCAACTATGAG
596	Tert	AAGTCCTGCTCGGTCCCCG
597	Thbd	TACCTACAACACCCCGTTCCG
598	Thbd	GTGTGAGACAGGCTACCAGT
599	Thbd	CTGTGAAGTAAAACCTCACAG
600	Thbd	TCGCAGTTAGATCCGAAACA
601	Tnfaip3	GCAGCTTGTCAGTACATGTG
602	Tnfaip3	ATATCCATGAGTGATAGCTG
603	Tnfaip3	AGCCCCGAGGAAACCGCTGG
604	Tnfaip3	AGGACTTTGCTACGACACTC
605	Tnfrsf11a	ACCAGCACAACGGTCCCCTG
606	Tnfrsf11a	ACACTGAGGAGACCACCCAA
607	Tnfrsf11a	GTTTAAGCCAGTGTTTCACC
608	Tnfrsf11a	AGACGCAAGGAGACCTCTCG
609	Tnfrsf1a	AGTTGCAAGACATGTCCGAA
610	Tnfrsf1a	AGACCTAGCAAGATAACCAG
611	Tnfrsf1a	GATGGGGATACATCCATCAG
612	Tnfrsf1a	GGATCCCGTGCCTGTCAAAG
613	Cd40	ATTCGCCTGAGTCACATGGG
614	Cd40	GGGATGACAGACGGTATCAG
615	Cd40	AGTCAGACTAATGTCATCTG
616	Cd40	CTGCACCAGCAAGGATTGCG
617	Cd27	TCTCTCCAGACTACCACACC
618	Cd27	TGCTGCATACCTGTGCCATG
619	Cd27	AGACAAACACTACTGGACTG
620	Cd27	CTCAGGTACATTCTTTGTGA
621	Tnfsf11	GCCTCGATCGTGGTACCAAG
622	Tnfsf11	GACCCTCGTGTGGGACGCCG
623	Tnfsf11	GTTAAGCAACGGAAAATAA
624	Tnfsf11	AGATTTGCAGGACTCGACTC
625	Tnfsf12	GGCTGACCACGACCAGCAGG
626	Tnfsf12	GCCCAGGCTCAGCACCAGCG
627	Tnfsf12	CAACGCTGTCTGCCAGGTG
628	Tnfsf12	GGAAGTGAATCCCCAGACAG
629	Cd40lg	TATTTCAAACAGGTCTGAAG
630	Cd40lg	AAGCTAAAGAGATGCAACAA

Number	Target Gene Symbol	sgRNA.Target.Sequence
631	Cd40lg	TTATACCATGAAAAGCAACT
632	Cd40lg	TGAACTGTGAGGAGATGAGA
633	Cd70	TTGGGAAGGTCCTTCACACA
634	Cd70	AGCTGTAACCTCAGCTGTGTG
635	Cd70	AAGGACCCCACACTGCGCTG
636	Cd70	CATCTGCGTATCCATCAAGA
637	Traf3	GCTGGGGGCATTGACACACT
638	Traf3	CAGGTTACGTGCTGTACCG
639	Traf3	AGTGA CTGCACGTGGCCTCG
640	Traf3	GCTTTGAGATCGAGATTGAG
641	Trex1	TTTCCTCGAACCATTCCCTG
642	Trex1	ACACAGAAGGTACCATCTAG
643	Trex1	AGCTTGTCCACCACACGGGG
644	Trex1	GGAGCAGAGGAAAGTCATAG
645	Tfrc	CTACACGCTTACAATAGCCC
646	Tfrc	GAATACATACTCCTCGTG
647	Tfrc	GGGCTCCTACTACAACATAA
648	Tfrc	AACCCTCGGGAGACTCCACT
649	Tnfrsf4	GAGCCGCTGTGATCATACCA
650	Tnfrsf4	TCACACTTGGAGTTACAGCA
651	Tnfrsf4	TTCCAGATAAGGTACAACCTG
652	Tnfrsf4	GTAGACCAGGCACCCAACCT
653	Ung	ACGGACCTAATCAAGCTCAC
654	Ung	TTGTCAGGGTGGGCCCGACA
655	Ung	CCAACCCCGACTCTGACTCC
656	Ung	CCACAAGGTCTATCCGCCCC
657	Vps45	AAAGCTGATAACGAATCATG
658	Vps45	ACGAACTCTTTGAATTCCGG
659	Vps45	TGTCTCAAAGCACGTGACAG
660	Vps45	TTGTTTCCTTCGACCCACAA
661	Was	CAACTGATAAGAAACGCTCA
662	Was	CCACCAGCACCAATCAATGA
663	Was	TCACCTGTAGGCCATAAAGG
664	Was	GCAGGTGAACAACCTAGACC
665	Wdr1	GTAGCCAAGTATGCACCCAG
666	Wdr1	GGCCCTACCGACTAGCAACA
667	Wdr1	GTGTGCGATTCTCTCCTGAT
668	Wdr1	ATGGCTCCCAGAATAGATGT
669	Zap70	CAACGGCACGTACGCCATCG
670	Zap70	GAAGCGAGAGAATCTCCTCG
671	Zap70	TCGACAACCCCTACATCGTG
672	Zap70	CGCGCACCATAGCATCACGC

Number	Target Gene Symbol	sgRNA.Target.Sequence
673	Ikzf1	GATGGCCTGGTCCATCACGT
674	Ikzf1	GTTGGTAAGCCTCACAAATG
675	Ikzf1	CAGAACTCCAAGAGTGATCG
676	Ikzf1	AGAAACTAACCACAACGAGA
677	Hax1	CAGAACTATTCTCACCTCCG
678	Hax1	AATTCACACACCAGGAGAGT
679	Hax1	CTGAAACCGAATTCCTCTGG
680	Hax1	GCTCCAGATTGGGGGTCGCA
681	Sh3bp2	TCAGCAAGAAGCACCGAACA
682	Sh3bp2	GAGGTGAACGAGTGGGCACG
683	Sh3bp2	ACCTGGAGCCTGATTCCCCG
684	Sh3bp2	TGGGTACATTGCTCATTGGG
685	Srp54a	CTTATAGAGAAGTTGAAGCA
686	Srp54a	AAAGCGTGGACACCGACTAA
687	Srp54a	TATGTGATGGATGCATCCAT
688	Srp54a	AAACTCGACGGTCATGCGAA
689	Rbck1	TGCTTCATACCAGCCTGACG
690	Rbck1	AGTACGCCCGGATATGACAG
691	Rbck1	TGCATTACACGGCATTCCGG
692	Rbck1	ACCCGAGGTCTCCCCAACAC
693	Usp18	CATCATGAACACTTGAAGCA
694	Usp18	ACAGCTCTCGCAGCACATGT
695	Usp18	TGTACAGCCCACGCAAATCA
696	Usp18	CAGGCACTGAACGAGCTCCG
697	Cln7	GGAAAGACGAATCAACCACA
698	Cln7	ATAGCTGCAGGGATTTACA
699	Cln7	AATCGGACAGATGAACAACG
700	Cln7	ACTCTGCCTTCGTACTIONG
701	Tcirg1	ACACAAGTGCCTCATCGCGG
702	Tcirg1	TCTCCCGAAAGCTGGCAATG
703	Tcirg1	CAGCCACACTCCAACCTGAG
704	Tcirg1	CGCTACAGGGAAGTTAACCC
705	Nbn	TATTCTACATCAACAACGC
706	Nbn	TGGAGAAAGCTGATAGCTCG
707	Nbn	ATAGCTGGTTCATCAATGGG
708	Nbn	GAGAATTACTIONGTAATCCGCA
709	Tinf2	CAAAGGCGTGCCATAAAGAG
710	Tinf2	CCGGTAGCAAACCAAGCCGG
711	Tinf2	CCAAAGGGGCCAGATTAAG
712	Tinf2	AGTGCTCTACGCGGCGACGG
713	Elane	CCGGCCACCAACAATCTCTG
714	Elane	CTCACAGGCCGTTACACAG

Number	Target Gene Symbol	sgRNA.Target.Sequence
715	Elane	GAACGACATTGTGATTATCC
716	Elane	ATGACCTCCACGCCTCTGCA
717	Cfhr1	TTGCCTTCTTAGATCCAACA
718	Cfhr1	TGCATATACTGGTAACGACA
719	Cfhr1	ACTGGTGGAAATGCATTTGG
720	Cfhr1	AGAAGGTGACATTGTACAAG
721	Ctps	ATTGGCCATTAACCACAAGC
722	Ctps	ATACCAGTACGTCATTAACA
723	Ctps	GCCCACAAGAGCGATCGAGC
724	Ctps	TTAATACCCGTAGACGAAGA
725	Slc46a1	AGAGCTAACATCTGCCACAG
726	Slc46a1	GGGCAATGGATCGATGATGG
727	Slc46a1	TGGACCAGAAGAGTCCCACC
728	Slc46a1	GAACTGTGGGAACCAAAGCG
729	Nhp2	GCAGAAGCAGATTCGTCGCG
730	Nhp2	CCATCTTCCAGTTCTGTGCG
731	Nhp2	AGGAGATACATTGCCGATTG
732	Nhp2	GGCCGCTCCCGAAGAGTCCG
733	Map3k14	GCAAAGCCC GAAAAAACGT
734	Map3k14	CGTGGTTTAGACATTGCAAG
735	Map3k14	CCCCGAACTGAGGACAACG
736	Map3k14	TGGGCCAGTTGGCTTAGATG
737	Rfx5	ACATAATGACCGTTCTCGAG
738	Rfx5	ATGGGTGTGATAAGTGATCG
739	Rfx5	AGAGCGTCTATGATGCCTAT
740	Rfx5	TCTACCTTCAGCTCCCATCG
741	Irf7	CTTGCGCCAAGACAATTCAG
742	Irf7	GGCAGGTAACTCCACTAGG
743	Irf7	TGTGCGGCCCTTGTACATGA
744	Irf7	GGAGCAAGACCGTGTTTACG
745	Irf3	CCAGTGGTGCCTACACCCCG
746	Irf3	AGAAACAATAGCCAGATCTG
747	Irf3	GGCTGGACGAGAGCCGAACG
748	Irf3	CTGGCGGCCTCGGTAGAAGG
749	Icos	TGGTCTTGGTGAGTTCGCAG
750	Icos	TATGCAAATATCCTCCACTA
751	Icos	GCAGAAGTAATAGCTTCCCT
752	Icos	AAATGAAAACATCCTATGAT
753	Smarcal1	CTCCAGGTGAAGCGCACAG
754	Smarcal1	TTTGGGTTATAAATCCAGCG
755	Smarcal1	TCATTGCAGATATCAAGACC
756	Smarcal1	GCTTGGCATCCACTCCGGAA

Number	Target Gene Symbol	sgRNA.Target.Sequence
757	Atp6ap1	GAGGATTTACAGCATACGG
758	Atp6ap1	GATATGACCCTCATGTGTGT
759	Atp6ap1	TAGCTAGATCCACATGCAAG
760	Atp6ap1	GTGTCATTGTAACACAGG
761	Unc93b1	CTGGGAACGCTACTACACGC
762	Unc93b1	CCGCAGTTGGACGAACTCGT
763	Unc93b1	AGGTGAAGTATGGCAACATG
764	Unc93b1	GCACACGCGAAGCTCAACTG
765	Nfat5	TCAGCCATTTACGTACACTC
766	Nfat5	AGTATCCGGTTAAAAGTGAG
767	Nfat5	GCCGTGGGGGTAAGTAACAG
768	Nfat5	AAGACCAACTTCTATAACAG
769	Il1f5	GTCATCCTGGGCGTTCAAGG
770	Il1f5	AACATCATGGAGCTCTACCT
771	Il1f5	AGGGCCAATTCTGAAACTTG
772	Il1f5	TGTTGTCCCAAATCGGGCAC
773	Mefv	TCTGATAACCTACTACGGGG
774	Mefv	AAGGAGGGTACCTTCACAAG
775	Mefv	ACCAAAGGAAGGATCAGAG
776	Mefv	TCTGAATGGAAGGACTACGG
777	Extl3	GCCCAAGCCTCGCGTCACAG
778	Extl3	TCAGACATAGCATGGACAAG
779	Extl3	CCACACAGTGCCCACTCAGT
780	Extl3	ATTGCGGAGGTATTTAGGTG
781	Tyk2	GTGTGGTTACGGCGACAGAG
782	Tyk2	TAGACCCCGCATGATGACG
783	Tyk2	CTTCCAGGACATTTCCCACG
784	Tyk2	ATCCACATCGCACACAAAGT
785	Samhd1	ATCCTTACATTATGTCGATG
786	Samhd1	GCTTGATATAGCGAAGTCGC
787	Samhd1	CTTGGGCTGCCATCGCAGCG
788	Samhd1	TTAGGATCTTACCTAGGTCG
789	Adar	ACTCCAACAAGCCGCCTACG
790	Adar	AGAGGTAACCCAGTAACAG
791	Adar	TTCTTGTAGGGTGAACACCG
792	Adar	TGTATCCAGGAATTCCTAG
793	Tbk1	TGCCGTTTAGACCCTTCGAG
794	Tbk1	CTTCTCGCTACAACACATGA
795	Tbk1	CAACATCATGCGCGTCATAG
796	Tbk1	CGGGAACAACCTCAATACCGT
797	Mogs	TCTAGGTCATTCTTCCCACG
798	Mogs	TCGGCAGCATATCCACGATG

Number	Target Gene Symbol	sgRNA.Target.Sequence
799	Mogs	TGCCGAAATAGACGTGTGGG
800	Mogs	GAGGTCCTACTACCAGAGAT
801	Tnfrsf13b	GTACTIONGACCATCTCCTGG
802	Tnfrsf13b	GAAGTCAGGTCAGACAACCT
803	Tnfrsf13b	GTGGCTCTCCTCTACGCCTG
804	Tnfrsf13b	ATCAGTACTGGGACTCCTCA
805	Bcl11b	GTTGTGCAAATGTAGCTGGA
806	Bcl11b	CTGAGAGCCCCTCGTCTGAG
807	Bcl11b	GCGGGAAGTTCATCTGACAC
808	Bcl11b	CAGAGGTGAAGTAATCACGG
809	Stk4	AATACACCGAGATATCAAGG
810	Stk4	TATCTGATATCATTCGGCTA
811	Stk4	TGCTGATATCCATCCAATGA
812	Stk4	TTCAGGAGCCATCCAAAACG
813	Ncstn	CCAGCAGAACCATGTAAGGG
814	Ncstn	GTGCTATCAAGATCACAACC
815	Ncstn	AGGGACAGAACTCACCCGTG
816	Ncstn	GGTGACTCACCGATTGTGGA
817	Il21r	GCACGTGTACCATATATGTG
818	Il21r	AGGACGCTATGATATCTCCT
819	Il21r	GCCACCTCACACAGCATAG
820	Il21r	GGGCTGGAAGAACTCTCAG
821	Il21	GGTGACGAAGTCTAATCAGG
822	Il21	GAAAATCTATGAAAATGACT
823	Il21	AAACTCAAGCCATCAAACCC
824	Il21	GACATTCATCATTGACCTCG
825	Lpin2	GGATACTCACGTTTCTAATG
826	Lpin2	GGTTATATATCCGGATCACG
827	Lpin2	TGCAGGTCACCAAAGAGAA
828	Lpin2	AACCTGGATCCGTGTCCTG
829	Nop10	CGATCGCGTTTATACGCTGA
830	Nop10	CAATATTACCTCAACGAGCA
831	Nop10	GGAGAACCGAGCAGGATGGG
832	Nop10	GAGCAGAAATTTGACCCTAT
833	Psenen	CGAGAATGATCACCCAGAAG
834	Psenen	CCGGAAGTACTATCTTGGTA
835	Psenen	CTTGGAGCGGGTATCCAATG
836	Psenen	ATGTTGACTAACCAAAGAAA
837	Ndn12	CACGTATTGCAGGCGCTCGG
838	Ndn12	CAACACCATCACCGAGACTG
839	Ndn12	AGAAGAAGATCCCGATCAAG
840	Ndn12	CCCTGTCGGCCCCGACCGTG

Number	Target Gene Symbol	sgRNA.Target.Sequence
841	Sbds	CCAGATCCGACTGACCAATG
842	Sbds	CCTTCATGGCTCTCTCGATG
843	Sbds	ACTGAAATCTGCAAGCAGGT
844	Sbds	TAGGGATATCGCCACCATTG
845	Taz	TTTGGAGAAGCTTAACCATG
846	Taz	GGTCATCCATGCAAGACTGG
847	Taz	AGCAGCTCACCTCGACACAC
848	Taz	TATGAGCTCATTGAGAACCG
849	Cdca7	TCTACTGGTCGGATTATATG
850	Cdca7	GCTGTCACAACTGTCATCGG
851	Cdca7	TGTGGCTACCAGAAGGAACC
852	Cdca7	GTCGTCCAGAGAACAAGCCA
853	Magt1	TGTGTGTGCGATCGCAGCGG
854	Magt1	CAGCTGAGCAGATTGCCCGG
855	Magt1	TTATGCTGGACCCCTAATGT
856	Magt1	GTGGAGCTTTAACAAGACGA
857	Rnaseh2b	CTCCTAGGTCAACCAAACCTG
858	Rnaseh2b	TCAGCCCTTGGACCAAGTCG
859	Rnaseh2b	CAGCCTTTAGGAGATAGTGA
860	Rnaseh2b	TGGCCAGCTTTACGAACAGG
861	Jagn1	GCACTACCAGATGAGGTACG
862	Jagn1	GTACCTCATCTGGTAGTGCA
863	Jagn1	AGTGCATGGCGACGCGCTCC
864	Jagn1	CCGTCGGTGCCGGCCGCTCG
865	Ino80	GGGTTGCGGAATATCCTCAC
866	Ino80	AGAAAATGAATTGTCTGACA
867	Ino80	TGCCCATCAATGCATGAAGG
868	Ino80	GTGACGTGGAGATTCTTCAG
869	Rnaseh2c	CGTGAAGAAGCGATCTACCG
870	Rnaseh2c	CGGCTGACTAGAACGTCGCA
871	Rnaseh2c	AGGGTTTGCGGGATTTCGTGA
872	Rnaseh2c	ACCGTCTGCATCGTGGCGGA
873	G6pc3	TAGGCCGACTGCCAATAGGA
874	G6pc3	TTCCCGGGCTAGAGAATATG
875	G6pc3	GGGGCTCATTAGCCAGCCAA
876	G6pc3	TAAAGAGAGTCCAATACATG
877	Ctc1	CTGGTCTGAATAACCCGCTG
878	Ctc1	CTTGATAGATGAGATCCTCCA
879	Ctc1	AATTGCAAGTAACCAAGACC
880	Ctc1	CTTGGA ACTATGGGGTACAC
881	Gins1	CCGGCGCGCGGTGTAACCTCG
882	Gins1	TGCTTCGGATTAGAGCACTC

Number	Target Gene Symbol	sgRNA.Target.Sequence
883	Gins1	GTTGTTGTTACAGACGGAG
884	Gins1	AGTCTCTTGCTACTTACATG
885	C8g	TGGGACTCACAGCTTTCGGA
886	C8g	CTGGGGAGCTGCGTGCAATG
887	C8g	CCTCACCTTGAACAAGAAG
888	C8g	CTGAGCACTGAAATTGACCT
889	Rnaseh2a	TGTCACACGATACAGCTGCG
890	Rnaseh2a	GTAACAGATGGCGTAGACCA
891	Rnaseh2a	AGACCTTGACAGAGAACGAG
892	Rnaseh2a	GGCTCCTTGAGACACACAGC
893	Trnt1	CATGAATTAAGAATAGCAGG
894	Trnt1	ATTCGCATGATCAACAACAA
895	Trnt1	AACCTGTTCTCACCTATGTG
896	Trnt1	GGCAGAATTGTGACAGACC
897	Rnf168	GGTGTGCCCCAGTTAACTGG
898	Rnf168	CCCGGGCCACAGTTATGTGT
899	Rnf168	AGCATGGGTTACAGAGCGTG
900	Rnf168	AATCTCTGGACAAGAATCAA
901	Unc13d	AATCTGGTACAGGACGTCAT
902	Unc13d	ACAGAGACCTACCCAGACCG
903	Unc13d	TGGCTGGCTGAAACCAGCGG
904	Unc13d	GCAGCCCTGTGTCCCGACGT
905	Nbas	AACAAAACAGCATATTCGTG
906	Nbas	ATAGCAGTATTTATTCCATG
907	Nbas	ATTGATTGATGTCAATTGGT
908	Nbas	TTTGCCGAATGACATGACAT
909	Slc29a3	AATGATGGCCATGCACGCGA
910	Slc29a3	GGGAAACTGCGCAGAACCCG
911	Slc29a3	CAAGGAAGACTGCTGCCATG
912	Slc29a3	ACCAGAAAACACTCGAACTG
913	Ifih1	TGTGGGTTTGACATAGCGCG
914	Ifih1	CGTAGACGACATATTACCAG
915	Ifih1	TGGGTTCCAAAATCTGACAT
916	Ifih1	GATTGATGCATATAGCCACC
917	Snx10	GCAGAGCCATCTGAACTCCG
918	Snx10	CATGTCGACCAACGCCGCCA
919	Snx10	AAACATCTTGTGTACGAAGA
920	Snx10	AAAGCAAGAGTGCATTCTGC
921	Tnfrsf13c	CAGACTCACTAGACCCACCA
922	Tnfrsf13c	GACACGCAGTTTCTCACCAG
923	Tnfrsf13c	CTCCGCGCTGAGACCCGACG
924	Tnfrsf13c	GCACTCGGTCTGATTGCACT

Number	Target Gene Symbol	sgRNA.Target.Sequence
925	Spink5	CGGGAAAGTGACCCAATCCG
926	Spink5	AGGGAGAGTGACCCTGTACG
927	Spink5	CGAGAAAATGACCCTGTGCG
928	Spink5	TGGAAGACTTGGATGTACAC
929	Tmem173	GAAGGCCAAACATCCAACCTG
930	Tmem173	TATCTCGGAATCGAATGTTG
931	Tmem173	AGTATGACCAGGCCAGCCCG
932	Tmem173	CAGTAGTCCAAGTTCGTGCG
933	Parn	AAAACGGTCTCAAGCCAATG
934	Parn	GGTCATACTTAAAAGCACAA
935	Parn	AAGACATATAGTTATCAGCA
936	Parn	CCAACCTACCGAATTAGCAA
937	Stx11	TCGAACACTATGTCCTCCCG
938	Stx11	AGCCATGTACGAGTACAACC
939	Stx11	CATGTCGGGCGAGCAGATTG
940	Stx11	AGCTGCTTCTGATAGACGTG
941	Rhoh	GGTACTGATGTGCTACTCTG
942	Rhoh	CCCACGGTGTACGAGAATAC
943	Rhoh	ACAACCAGCACCGGGGTACA
944	Rhoh	CAGGGGCCGGATACTTCTGA
945	Dock8	ACTTCCGGTTTTCGACACCG
946	Dock8	CCGGAACACGTAGTGCACGT
947	Dock8	AGCACGTTTAAGGGATGACG
948	Dock8	TAGCGAAGTTCAGTCGCTGG
949	Ercc6l2	CTGTTACAGACCAACTCACG
950	Ercc6l2	CGTACCAAGACTCTTATCAA
951	Ercc6l2	GGTACTTGCGAGATTACCAA
952	Ercc6l2	AAGGATGAATTGGATACCTG
953	Dnajc21	TAGGTACGATAACCACCGAG
954	Dnajc21	CTCCAGAGCGACTATGACA
955	Dnajc21	TAAACGAGATAAGAGAGTGC
956	Dnajc21	TGGATCAGATGAAAACGAAG
957	Lrba	GACCGTCCCAATGAACTCAG
958	Lrba	GTGTGGCGAGTGGACGAAGA
959	Lrba	ATAGTTACCATGTACCACTG
960	Lrba	CAGATGCAGTAGACCAACAA
961	Lamtor2	GTTCCCGTTCCTATCATAACG
962	Lamtor2	GCTGGCCTACTCCGGTTATG
963	Lamtor2	CCACCCTCGTAATGGCTACA
964	Lamtor2	CACAGATGCCCGGGTCACTG
965	Smarcd2	GAGATAATGCGGGAACTGCG
966	Smarcd2	GCATCGGATGCCCAACACAC

Number	Target Gene Symbol	sgRNA.Target.Sequence
967	Smarcd2	CCCAACACACTCACTCGCTG
968	Smarcd2	CGGAGCAGCTGTGCCAAATG
969	C230052I12Rik	CTAGCCACAATATGTCCTAG
970	C230052I12Rik	TGAGGCAGGATGCTTCCGAC
971	C230052I12Rik	CAGTAAACTTCTGGACTGCT
972	C230052I12Rik	TATGATCCCTTGAAGATGTG
973	Usb1	ACACGGTATGTAGATGTGGG
974	Usb1	TCCTCGATCCTCACCAACGG
975	Usb1	GGTACAAACATCTGAGCTCG
976	Usb1	GACGACAGTGCAAAGCATGG
977	Traf3ip2	GTCCTGCAGGTAACACGAGG
978	Traf3ip2	GTAGTACTGACAGTTCCATG
979	Traf3ip2	CCTGCGAGCTAAAGTCCTGG
980	Traf3ip2	CCAAAGCATTAGGTAAACTT
981	Ticam1	AAGATGCCATCGATCACTCG
982	Ticam1	TCTGGAACGCTAATTTCTGTG
983	Ticam1	GATATCAAGGGGGACCCAG
984	Ticam1	CTTCACACCATGGAACCCAT
985	Fermt3	GGAGGTGCATGACCTGACAA
986	Fermt3	CTGTCACACTCCGAGTCACG
987	Fermt3	GGGCTACCGCCAGTACTGGG
988	Fermt3	CTCACCCACATCCCCGCTCA
989	Mthfd1	ACACCAACGATAGATTCTCTG
990	Mthfd1	CACTATGAATCCGTGCACAG
991	Mthfd1	GATTGCCGGAAGGCACGCGG
992	Mthfd1	GGTAGCGTCCAGTAAGAAAG
993	Obfc1	GACGCAGTTTATAACCCAG
994	Obfc1	CAACGGGCATCCAATAAGGC
995	Obfc1	GGAGATATCATCCGAGTCCG
996	Obfc1	TCGCAGTGCTCAGAATAGCT
997	Card11	GCAGCATAACTGTGTTTCATG
998	Card11	ACTATGGAGTCATTTCCCGG
999	Card11	CACACACTTCTGATGAACG
1000	Card11	GCGACCTCCAACCTCGAGGTG
1001	Sp110	AAATGACCTGGAAATGGCCA
1002	Sp110	GGTCAAATTCCAAAGAAGA
1003	Sp110	TCCTGAATGCAGCCAAGGAG
1004	Sp110	AGCTCAAGGCAGTGAGCAGG
1005	Orai1	GATCGGCCAGAGTTACTCCG
1006	Orai1	TGGCGATGCATGCGCTCGTG
1007	Orai1	AAGACGATGAGCAACCCTGG
1008	Orai1	AATCCGGAGCTTCCCGTGAG

Number	Target Gene Symbol	sgRNA.Target.Sequence
1009	Pgm3	TACGGCCTCACATAACCCTG
1010	Pgm3	AACTTCTTCAAGGTACCGCG
1011	Pgm3	TACACCATGTAGTGCAACTG
1012	Pgm3	CTGCTATGACATACCCTGTG
1013	C7	CATACTGATCGATTAACCGT
1014	C7	ATCAACACCAAAAAGTTTCGG
1015	C7	CAATCCTGCAAACCTGAACG
1016	C7	GTGTCTCCACAACAATAGCG
1017	C8b	AAAGACGCCATGGAGCAAGG
1018	C8b	ATTGTGTGACTTGTCCGACA
1019	C8b	TTGACTGTGAGCTATCCACC
1020	C8b	CAAGGACAGAGCGCGCGTGG
1021	Cebpe	CAGTACCAAGTGGCACACTG
1022	Cebpe	GCAGGTAGTGAGGAAACGAG
1023	Cebpe	CAGACTCGATGTAGGCGGAG
1024	Cebpe	CTTACCTTGAGGACACGCAA
1025	Tirap	CTGTCTGTGAACCATCATAG
1026	Tirap	CGAAACAATGGCGCCACCCG
1027	Tirap	TGCAGCTCGAGGGTGAGCTA
1028	Tirap	CAAGTAGGAGACCAGCTCCT
1029	Dclre1b	TGCTAGACAAACCCACCGTG
1030	Dclre1b	TCCACTGAAGCATGGCAGAG
1031	Dclre1b	AGAGAAACATGACAGAACCA
1032	Dclre1b	TGAATGGTCAGAGTACGGGA
1033	Tlr3	CTTAGATGAAATCCCAGTCG
1034	Tlr3	GTTGTAGGAAAGATCGAGCT
1035	Tlr3	GAATGGTCAAGTTACGAAGA
1036	Tlr3	ATCTACAAAGTTGGGAACGG
1037	Card14	CCACAGCCGCATGAAACGTG
1038	Card14	TGTTCTACCTTAGAGACTCG
1039	Card14	CACTCTGGAGAATACAACGC
1040	Card14	AGAACTAAATCGGCTTAAGG
1041	Rfxap	TCCAAGACCTGCACGTACGA
1042	Rfxap	GCACCGCAACAAGATGTACA
1043	Rfxap	CTGGACACATCGGACCCGGC
1044	Rfxap	GTCACCGGAGGGGCCGTCCG
1045	Il17rc	CTGTGGAACGATGACAACAT
1046	Il17rc	AGCAATACTTACCCCAGAGG
1047	Il17rc	GGAGCCACAAGATTTCCAGT
1048	Il17rc	ATCTAGCTGCCATACCCCTG
1049	Wipf1	GGAACAGAATGCCTCCCCCG
1050	Wipf1	CCGTGAGTCTGCACAACCG

Number	Target Gene Symbol	sgRNA.Target.Sequence
1051	Wipf1	GGGGCTTGTCCATCCAAGGCT
1052	Wipf1	GCTGAGGTCCACCGCCAACA
1053	Wrap53	GGTCATTACCACTTACTAGG
1054	Wrap53	AGAAACGAATCTCCCCGAGT
1055	Wrap53	GAAGAGTTGGGAACCATCCG
1056	Wrap53	GACACAACCAAGCTAGCCAC
1057	Tmc6	GGAGTCATGTCGCTCCAGAG
1058	Tmc6	TTTCCAAGGTCGCAGCCGTG
1059	Tmc6	GACCAGAAAACGTAGGCACG
1060	Tmc6	TACCGGGTTGGCAGTACCAA
1061	Tmc8	GGAGCTCTCTACGAGATTGG
1062	Tmc8	CAACGCTTGC GACTACCAGG
1063	Tmc8	CTTCTACGGTGCCTACCGAG
1064	Tmc8	CATCCGCACAGGCGTCCGGG
1065	Ttc37	ACAAACAGATCACTTCTAGT
1066	Ttc37	CGCCTGTGTT CAGACAGGCG
1067	Ttc37	TGACGTGTGTAAGAACTCG
1068	Ttc37	GAGGCGTACTTAAGCAGAGG
1069	Mkl1	AGACAGTTCCTCCTTCGACG
1070	Mkl1	GTGATGAGAATTCCACACCT
1071	Mkl1	CTGCCCCCAAGCCTAGCCAA
1072	Mkl1	GTCAGGATGCACATTCTGGA
1073	Ttc7	TGGGATCGATGACATATCCG
1074	Ttc7	TCCAAGACCAATTACTACCG
1075	Ttc7	GCAACACACCTGTCGGACGA
1076	Ttc7	CTGCCCCAAAGACAACATAG
1077	Dclre1c	TTTATTCACCAACCTAAGCG
1078	Dclre1c	CAGGGAAACATACACGACTT
1079	Dclre1c	GCATCAAGCCATCTACCATG
1080	Dclre1c	TCAACTAAAGATATCTGCGT
1081	Slc35c1	AGGGCACCCCTACGTACTTG
1082	Slc35c1	AGGTTAGGCGCCAGATACTG
1083	Slc35c1	CTCACCAATGATGACGCCGC
1084	Slc35c1	GCAGTGAGGTCACCAGGCAT
1085	C8a	TCCTGCTATAGGTACTACTG
1086	C8a	GGAGATTGAAGTATCCGCCA
1087	C8a	CATTGTACACAGTTTCACAC
1088	C8a	CTTGCCTTAGACAAGGTGTG
1089	Rltpr	GCCTGACTTACCATGAAGGG
1090	Rltpr	CAACCAAGTAGACTCTACTT
1091	Rltpr	AGACCACCCTGGATACCACA
1092	Rltpr	ACATGCGCCTGTCAATCACT

Number	Target Gene Symbol	sgRNA.Target.Sequence
1093	Malt1	GTCCTATGCCTCACTACCAG
1094	Malt1	ATATGAGATGTGTAACGCTG
1095	Malt1	CCACTGGCTAAATTCAAAG
1096	Malt1	AGCTTGGACCGCGCTCCGGA
1097	Dkc1	TTTACTGCAGCAATAAGTGG
1098	Dkc1	TCTCTACCCGAAGTATTCGT
1099	Dkc1	TACGCATAGTGTCGAATGT
1100	Dkc1	ATGATGTACTIONCGATGCTCAG
1101	Ap1s3	CCCACTCCCTGACAAGGAG
1102	Ap1s3	TCCAGACCGTCCTCTCTCGT
1103	Ap1s3	TCAGTCGACAAGGGAAGCTG
1104	Ap1s3	TAATATCCAGCTCACAGACC
1105	Il17f	GACTTACTTGTAATCCCATG
1106	Il17f	TGGGAAGTGCCTCCCCTGG
1107	Il17f	AGCGGTTCTGGAATTCACGT
1108	Il17f	GGCCTCAGCGATCTCTGAG
1109	Nod2	CCGACCCATCGTAAGTACTG
1110	Nod2	AGATGCCGACACCATACTGG
1111	Nod2	GCAGAGTCTGGACTGACGTG
1112	Nod2	GTTGTAGAGTCTCCTCACAA
1113	Irak4	GTAGCTATCAAAAAGCCGTC
1114	Irak4	CTGTGTGAACAACACCATCG
1115	Irak4	TGTAAGCATACTAAGCAC
1116	Irak4	CAAGGTGCAAGGTTGCTCAG
1117	Zbtb24	GGAAATCGAAGTTACCCGTG
1118	Zbtb24	TGAGAAATACTCGCTACTGG
1119	Zbtb24	ACACGTCCATAAACTTTCCGG
1120	Zbtb24	GATCCTCTGAAACGGAAACG
1121	Rnf31	GATGGATTGAGTTTCCCCGA
1122	Rnf31	GAACATGAGTTGTTGGACG
1123	Rnf31	CTACCTCAACACCCTATCCA
1124	Rnf31	GGAGGAACCAAGGTGTTGTG
1125	Rtel1	ACACGGGGATCCATGCGTGG
1126	Rtel1	TATGCCGACATACCGGTAGG
1127	Rtel1	GTTGTCATACACCTTAAGGT
1128	Rtel1	GAGGCGTCACCAAACCTGGA
1129	Irf2bp2	CGCACGCGTGCTGAAGTCGG
1130	Irf2bp2	GCGGCAGAACCGTTGACCAG
1131	Irf2bp2	TCTCGATGACGAACTCCACG
1132	Irf2bp2	GGCCGACAGCTTATCCAGCG
1133	Gimap5	GTCACCAGTAACAACACATG
1134	Gimap5	AGCTAGATTCTTGTACACAG

Number	Target Gene Symbol	sgRNA.Target.Sequence
1135	Gimap5	ACTGGAATGCTGGTCGTCGG
1136	Gimap5	CTGAAGATGCCATGGCTGTG
1137	Lig4	TTAGACGTCCTAATTGTGGG
1138	Lig4	GCAACTCAACTGCATCATTG
1139	Lig4	GAACGCATTGTGAATAAATG
1140	Lig4	CATCCGTGCGAGCTCCACTG
1141	Chd7	GACATGCCCATAAACGAACG
1142	Chd7	AAACGGTTTAAGTCAAACA
1143	Chd7	CCTACCGGAATGATTTAGCA
1144	Chd7	TCGATGACCACACAGCGCCA
1145	Ccbe1	GACCTACCGAGAGGAACCCG
1146	Ccbe1	CAGCAGTGCACGGATAACTT
1147	Ccbe1	ACAGAGAGTGGTATTGCTGG
1148	Ccbe1	GAACTGGGCAAGTATGTCAA
1149	Fat4	GACATCGTGGACGATCGAGG
1150	Fat4	CAGTTATCTCATCACTACCG
1151	Fat4	GGGATGTCGAAAGAGTACAC
1152	Fat4	ATTAGATCCTATGTCCGCGT
1153	Card9	GATGTACAAGGACCGTATCG
1154	Card9	GTGACTTTCCGGTATAACTG
1155	Card9	TAGATAGGGTGTGATCCGGG
1156	Card9	CCAACCTGGTCATCCGCAAG
1157	Plekhm1	TGACTTGTAGGAGAGTTCGA
1158	Plekhm1	TGATGAGGAACGCACCTGTG
1159	Plekhm1	GCTGGTAGCTAGGCTATGGA
1160	Plekhm1	ACTCACCGGACTCGTAGGAG
1161	Kmt2d	AAATGGCTGTTGATCCCATG
1162	Kmt2d	G TTCACCATTAATAACCCCA
1163	Kmt2d	TCGGGCCGGACTAACATCCG
1164	Kmt2d	TGGGGATGGACAGCCCGACG
1165	Otulin	GGAACTTCACAGCTTCGTAG
1166	Otulin	TGATAACTACTGTGCACTGA
1167	Otulin	AACAGAACCCAGGTTAAGTG
1168	Otulin	AGTATACCTGGATCAAGCAG
1169	Cfhr2	TTGTCCCCTTAGACTCAACA
1170	Cfhr2	GAATGGAGACTCTACATACT
1171	Cfhr2	ACTTATTCCTATAGACACT
1172	Cfhr2	ATACCATTTAGAATATAAGG
1173	Nlrp1b	CTAAATGACCTGTGTGACGA
1174	Nlrp1b	AGATGCTAAAGAGCACCCTA
1175	Nlrp1b	AGAAGATCATTCTTATGTG
1176	Nlrp1b	CTGTAAGCAAGGGTTAGCAG

Number	Target Gene Symbol	sgRNA.Target.Sequence
1177	Vps13b	TGTCCATACTACCCAAATCG
1178	Vps13b	TAAACACTGCAATACAAGCG
1179	Vps13b	GAAACCTCTTCCCGATACAG
1180	Vps13b	TGGCAGTAGTCCATGTACTG
1181	Isg15	GTCCGTGACTAACTCCATGA
1182	Isg15	CAGCAGCACAGTGATGCTAG
1183	Isg15	GCATCCTGGTGAGGAACGAA
1184	Isg15	TGGAAAGGGTAAGACCGTCC
1185	Epg5	ACAGCCGACTCGTTGTAACA
1186	Epg5	TCGAGCCAGAAGAACCAATG
1187	Epg5	TGGGTACCATACCCATATTG
1188	Epg5	GAAACGCTGTCTTACACAAG
1189	C1ra	TTTGCCAGAATGATGGCACA
1190	C1ra	TGTGCAGGTATATATCCCTG
1191	C1ra	CCACACAGACTTCTCCAATG
1192	C1ra	TGGTTGTCTCCAAGTCACTG
1193	C1s2	AATTCCTCATGTCATCATGG
1194	C1s2	TTCTCTTAGATAATCTCAGG
1195	C1s2	TCTTTCAAAGTCTAATG
1196	C1s2	AACACACAGTTAAACTGTCA
1197	C4b	GCACAAGATGCCTCTTAGTG
1198	C4b	CAGGCACAGCCCCTCAACTG
1199	C4b	GTAAGCCACAAAGTAGAACG
1200	C4b	TGAAACAAAGGACCATGCTG
1201	Cd59b	TATTATGAGCCGATTAGACG
1202	Cd59b	ATGCTACAAGTGTGTTAGACC
1203	Cd59b	GGCAAGTGTATCAACAGTGT
1204	Cd59b	TTGATACACTTGCCTTCCTG
1205	Lat	ACTCACGAGGTGGCTTGATG
1206	Lat	GCATCCGATGGGAACCCCA
1207	Lat	ATACTCACGGGATGGGGAGC
1208	Lat	CTCTGTGGAAGTGCTGTCAT
1209	Nhej1	CCCTATGCATAGAGCTCGGC
1210	Nhej1	ACCAGCCGAGCTCTATGCAT
1211	Nhej1	GGCTGGTTATCAGTTCCTCG
1212	Nhej1	TCACCAACAGCACACGCCTC
1213	Dock2	AAGAAGTGACAACCACGCTC
1214	Dock2	CAGCATCTCACGCTACAGAT
1215	Dock2	GTGACAGTTTATGCTTTATG
1216	Dock2	TACATCCTTTATCCATCTCA
1217	Mysm1	ATCACTATCTTGATTCAACG
1218	Mysm1	AAAATTCTGGGTTAATCAAA

Number	Target Gene Symbol	sgRNA.Target.Sequence
1219	Mysm1	TATCATTGAGAAAATGCTGT
1220	Mysm1	TTATCTAATAAATCACTTCC
1221	Kdm6a	TTGGATAATCTTCCAATAAG
1222	Kdm6a	TAGCATTATCTGCATACCAG
1223	Kdm6a	GAAACCTCACGAACCCGAAA
1224	Kdm6a	CGCCAGGATGAAGGCCCTGC
1225	Top2	CACACCAAGCAGTCATATAC
1226	Top2	ATTGATATCATTGATACAAC
1227	Top2	ATAGGCCAATAAACTAATCA
1228	Top2	TGGTTATGACTTCTATCCAA
1229	Il12b	CCTGCCATTGAACTGGCGT
1230	Il12b	CCATGAGCACGTGAACCGTC
1231	Il12b	CATGTCACTGCCCGAGAGTC
1232	Il12b	GACTGGACTCCCGATGCCCC
1233	Stat2	TGAGATTGAAAATCGAATCC
1234	Stat2	TCCACAACGCTTCGGGGGC
1235	Stat2	CTGAGCTGTAGTGGTCCCAC
1236	Stat2	AGTTCTTGGTGAGATCCATC
1237	C3	GATGACGACTGTCTTGCCCA
1238	C3	ACAAAGGCAAGATGCCGTGT
1239	C3	GAGCGAAGAGACCATCGTAC
1240	C3	GACAGTCGTCATCCTCATTG
1241	C6	TAGTAGTGAACGATTACTAT
1242	C6	CGATAAGCTTTGTATCAAGC
1243	C6	TGAAACACGGTATGGATTAC
1244	C6	GGTTGCCCCCAAACGACT
1245	Cfb	TTCGAGTCTGCACGGGGTAT
1246	Cfb	AATACGCTGCCACGACCGC
1247	Cfb	GCTGGATACTGTCCAATCC
1248	Cfb	AGCCACGCAGGACAAGTCCC
1249	BRDN0000737505	AAAAAGTCCGCGATTACGTC
1250	BRDN0000737693	AAAACGGCTCGATCGGTGAT
1251	BRDN0000737637	AAAACGTAATTATACCGAGC
1252	BRDN0000738185	AAAATTGCACCTTCCCGGCC
1253	BRDN0000737801	AAACCCCGCGCGGAGCGTC
1254	BRDN0000737467	AAACCTAGCGTAGATTCGGC
1255	BRDN0000737848	AAACGAGGCTGTTTCGTACAC
1256	BRDN0000737609	AAACTCATACGTAGCGAATC
1257	BRDN0000737434	AAACTCCCGTGTCAACCGAT
1258	BRDN0000738254	AAAGACGTGCATTACGCGAG
1259	BRDN0000737777	AACATGTTAAGTCGCGTTAT
1260	BRDN0000737611	AACCAGCATTTGACCGCGCT

Number	Target Gene Symbol	sgRNA.Target.Sequence
1261	BRDN0000737528	AACCCCGGCTGTCATCGCCG
1262	BRDN0000738228	AACCCGCCGGAACAATCAGC
1263	BRDN0000737727	AACCGGCTGCGCGTTTGCAA
1264	BRDN0000737483	AACCGTACTGCGAGGAGCAT
1265	BRDN0000737872	AACCTCGTCTCATGTACGAA
1266	BRDN0000737516	AACGCCCCGGATTTTCGTTGA
1267	BRDN0000737844	AACGGCTGCGCCCGCGGCAA
1268	BRDN0000737412	AACGGGCGCAATACCCTTTT
1269	BRDN0000737631	AACGGTAGCGTACCCGTGAA
1270	BRDN0000737750	AACGGTCAAATCCGTGAGGG
1271	BRDN0000737875	AACGTCACCAACCTCGATCC
1272	BRDN0000738229	AACGTTATAGCTTCGTCTCT
1273	BRDN0000737806	AACTAACTCACTACGCACGA
1274	BRDN0000738366	AACTCCTCATCGTACGCTAA
1275	BRDN0000737593	AACTCGCGTGGGAAGTCCGG
1276	BRDN0000738128	AACTTATACGTAATCTGATC
1277	BRDN0000738307	AAGACTCCTACGTATCGAGC
1278	BRDN0000737391	AAGCAAGAACGGTCCGCC

Target Gene Symbol	sgRNA.Target.Sequence
Acp5	ATACCAGGGGATGTTGCGAA
Acp5	TCCACGTACAAACATAACTG
Acp5	TACCTGGAACCTCTTGTCGC
Acp5	ACAGCCACAAATCTCAGGGT
Actb	AATGCCTGTGGTACGACCAG
Actb	ATGGAGGGGAATACAGCCCG
Actb	GGACTCCTATGTGGGTGACG
Actb	CAGCACAGGGTGCTCCTCAG
Ada	GTTGTGGATCTTGTGAACCA
Ada	ATTCATCGGACCGTCCACGC
Ada	CTTCATCTCCACAAACTCGT
Ada	GCTGCGCAACATTATCGGCA
Adam17	GGTGTGTGGCAACTCCAGGG
Adam17	ACACGTCGTGGGATAATGCA
Adam17	CATCGACGTACGGCACACAC
Adam17	GCCCCAAATGAGGACCAAGG
Cfd	TCTCACGTGGGGACCCAACG
Cfd	CCCCGAGGCCGGATTCTGGG
Cfd	TTGACACTCTGAGTTGATGC
Cfd	CCCCTGAACCCTACAAGCGA
Aicda	GTAGGAACAACAATTCCACG
Aicda	TTCACAGAAGTAGAGGCGCG
Aicda	ACCAGGTGACGCGGTAACAC
Aicda	TGAGACCTACCTCTGCTACG
Aire	TGTGCCGTGTGCCACGACGG
Aire	CTCTCCAGGAATTCAGACCA
Aire	ACAGAACCTGTCCCAGCCTG
Aire	GGTAGAGATGAGCAGAAAGT
Ak2	TGAAGGCGACAATGGATGCA
Ak2	GGTAGGACCGGCACTCTTG
Ak2	TCCGAACCGGAGATTCCGAA
Ak2	TCAGCCAGTTTGGGTGCCTG
Ap3b1	TGTGGCCAGTAAAAACATCG
Ap3b1	GCTGCCTAATAAATCGTGTG
Ap3b1	ATATGCTAACAAGATACGCT
Ap3b1	TTGGCACATCTCACCCAAGT
Ap3d1	CCAACGCAATGGTATCTGTG
Ap3d1	AGCACATCACCAACTTCGAG
Ap3d1	TCTTCACAGTAAAGTACCTG
Ap3d1	TGTCCTCATCGCTCTCCGTG
Xiap	TTTCAGACACCATATACCCG
Xiap	AGCACTAGCTAACTCTCTGG
Xiap	CTTGGGAACAGCATGCGAAG
Xiap	ATGGACATCCTCAGTTAACA
Arpc1b	CACAATGCGGTTACTCTCAG

Target Gene Symbol	sgRNA.Target.Sequence
Arpc1b	CAATGAGAACAAGTTCGCCG
Arpc1b	CCAGTCCAGGCTGAGCACTG
Arpc1b	GAAGCGAGCACTCACGTGTA
Rab27a	TGGTTAAGCTACGAAACCTA
Rab27a	AGTGTACTGGTAGAGTACAC
Rab27a	AACCCAGATATAGTGCTGTG
Rab27a	CCTGAAATCAATGCCCACTG
Atm	TAAGTCATATAGGAAGCCGA
Atm	GAGTATAAATAACATCGCGA
Atm	AAGACTTGAACACCCGGACAA
Atm	TGCAAGATACACATGAATCG
B2m	ATTTGGATTTCAATGTGAGG
B2m	ACTCACTCTGGATAGCATAAC
B2m	TGAGTATACTTGAATTTGAG
B2m	TCGGCTTCCCATTCTCCGGT
Bach2	TGGACAGACGAAAGATGACT
Bach2	AATTACGGACAGCCCCACGT
Bach2	CTCCTCGTATTCTCTACGCAG
Bach2	TCTCTGTTCCGGTATAACGAA
Bcl10	CTCCGGGTGGTACATGACAG
Bcl10	GATTCAGAAGATAACGGATG
Bcl10	ATAAACTGGAGCACCTCAA
Bcl10	CCTGGTGGAAATCCATCCGCA
Blm	TTACCTGGAACATTTCAACG
Blm	GGTGGGTAACATTCCTCAG
Blm	CCTGCAAGTGGATTTAACGA
Blm	CCTTCACCGACTTACACCTG
Btk	AATCCGGTACAATAGTGACC
Btk	TATGAATATGACTTTGAACG
Btk	TGGAGGAGAGCAACCTACCG
Btk	AGATTTAGCAAACACAGACA
Serping1	GCTCTGAGATGCATTCACAT
Serping1	ACAATAACAAATGACACCAT
Serping1	AGAACTCATCAACACCTGGG
Serping1	GGACACAGGCAAATCCTTG
C1qa	CACAGATGAAGCGACCCGTG
C1qa	CCCAATGACGCTTGCAACG
C1qa	TTCAGCCACTGTCCATACTA
C1qa	AGGCAATCCAGGCAATATCA
C1qb	AGGCACTCCAGGGATAAAGG
C1qb	TGACCTGGTTCGGTCGCAAG
C1qb	GAATCGCCTTTGGGACCGCG
C1qb	CAGGTGAACTTGCCGTTGCG
C1qc	GGGTGACTGTGAATACCGAC
C1qc	CTGTGGTCACCAACCCTCAG

Target Gene Symbol	sgRNA.Target.Sequence
C1qc	ATCATGCCCGTCCTCCCAG
C1qc	GCTCCCCGGAGCCCCCTG
C2	GTTCTAGGAAAGTCCAACAT
C2	GTGTGATGTGAGCTAGACCT
C2	AGTCAATACCATATTTGAGG
C2	TTGGGGCGACAGTACCGCAC
Ciita	AGCTCGACTAAGGCTCCGGG
Ciita	AGGTCCTTGATTATATCGTG
Ciita	TCCAGTGCCTAATCTACCA
Ciita	AGCAGGCCAAGACTTACATG
C9	CTACAACGGACTCTGTGACC
C9	TTTCCCATTAAACTGTCCGA
C9	ATTCTGCAGTCTATCGGTAT
C9	TTGAGAGGAGTGGTCCAAC
Hyou1	ACAGGCGGATAACCCTCATG
Hyou1	ACATCGTACTCACTTGCCCA
Hyou1	TGGAATTGATATCTTTCCGG
Hyou1	TGGCGTGCTCAGTTTAGACA
Casp8	GATTATGAAAGATCAAGCAC
Casp8	CTTCCTAGACTGCAACCGAG
Casp8	ATGATCAGACAGTATCCCCG
Casp8	CAAGAAGCAGGAGACCATCG
Ctla4	TGTGATGGTGAATATTCACA
Ctla4	GGACTGAGAGCTGTTGACAC
Ctla4	ACAGGTGACCCAACCTTCAG
Ctla4	TGCCACAAAGTATGGCGGT
Cd19	GAATGACTGACCCCGCCAGG
Cd19	AATGTCTCAGACCATATGGG
Cd19	GGCACCTATTATTGTCTCCG
Cd19	TTAGCCCACACATACAGCT
Ms4a1	GTTACAGTACTGTGTAGATG
Ms4a1	TACCATACACTCAAACAGAT
Ms4a1	CAGTCGTAGATATCAACATA
Ms4a1	CCACACAAAGCTTCTTCATG
Cd3d	TTACACAGATATATCCCTCG
Cd3d	TCCATCTAGATGCATGACGC
Cd3d	AAGAATAAAACACTCAACTT
Cd3d	GATACAAGTGACCGAATATG
Cd3e	AGGGCACGTCAACTCTACAC
Cd3e	TTCTCGGAAGTCGAGGACAG
Cd3e	TACTTGTACCTGAAAGCTCG
Cd3e	TCAGAAGCATGATAAGCACC
Cd3g	TGACACTGATACGTGCCTCG
Cd3g	TTCTGTAATACACTTGCAGG
Cd3g	AACTGCATTGAGCTAAACAT

Target Gene Symbol	sgRNA.Target.Sequence
Cd3g	GTACAAGTGGATGGCAGCCG
Cd247	GCTCGGGATCCAGAGATGGG
Cd247	GCTCAATCTAGGGCGAAGAG
Cd247	CTCCTGGGAACCGCACGTGG
Cd247	CATTGTATACGCCTTCCTGG
Cd79a	GGAACCCTAATATCACATGG
Cd79a	CCTACTCACTGCGCACGCGG
Cd79a	CGAAGTAAACAAGAACCACA
Cd79a	AGGCGTATGACAAGAAGAGG
Cd81	GCAACCACAGAGCTACACCT
Cd81	GGGCTTCGTAAACAAAGACC
Cd81	ATCCATCACAGCTTGCTGAA
Cd81	GGCAAACAGGATCACAAGGC
Cd8a	TGGGTGAGTCGATTATCCTG
Cd8a	ATCCCACAACAAGATAACGT
Cd8a	GTGTTGGGGTCCGTTTCGCA
Cd8a	GGACGCCGAACCTTGGTCAGA
Cfh	ATTTACGCATAACTCCACCA
Cfh	CAAGTGTTCCGGTATCCAGGG
Cfh	GAAATTGATTACCGTGAATG
Cfh	CATATTCACCACTTCACCA
Cfi	CTTGTGGATTACCTTCACAA
Cfi	TGTTATTACACAGGTTGCCG
Cfi	AAGGTCGACGCAGGCCACGT
Cfi	TGCCTGCATGTACATTGCCG
Cftr	GCCGTGTGACTGACATACGT
Cftr	TTCTAACTGAGACCTTACGC
Cftr	GTGGCGATCATGTTGCTGCG
Cftr	TATGGAGAGTAAAATATCGT
Coro1a	TGACACGAACTCGCTTGTC
Coro1a	ACCAGGCGATGTCTAGCACA
Coro1a	AGAAGGGAAGATTCTAACCA
Coro1a	GCCACAGAGGTAGACAATGT
Tpp1	TGAGTTTCATCGCTATGTAG
Tpp1	TTATGGTAGAAGGTTACCTG
Tpp1	AACCTGACAGCCAAAGATGT
Tpp1	GATCGAGGCCAGTCTAGATG
Copa	CTTGCGGTTACAGATCACAA
Copa	CTCTCTGACACATCACCT
Copa	CACCAGAAATATCCCAAACG
Copa	GAATGTCTAGGTACTIONCAC
Cr2	ATGTTGACCAGTTTGTGCG
Cr2	CTATACATTGCACCCCTGAG
Cr2	AGACGGATTTCTATAAACCA
Cr2	ATGCAATGCTCATGGCACAT

Target Gene Symbol	sgRNA.Target.Sequence
Csf2ra	AGGACGCGGTGACGTCACGT
Csf2ra	CCTACTTGGTCGTGACCGGT
Csf2ra	CTAGCGTCACTAACCCAGAA
Csf2ra	TGACATCCAGCGTGACACCG
Csf2rb	TACACTTGGAAAGACTGACTG
Csf2rb	TGATGGAAAATCGTGTATAG
Csf2rb	GAAGAAATCGGACAGCTGGG
Csf2rb	TGGAGACTGTAGGCATCCTG
Csf3r	TCAGCTCTACAGAATTACAG
Csf3r	TGAGGCAGGATAGGTTTGAG
Csf3r	TGAGCTGCGTGGTGTTGCAA
Csf3r	CTTTGCCACACAATCCGGGA
Ctsc	CTGCAAGATACAACCTCCTG
Ctsc	GGCAGTAACTGATAGCTGTG
Ctsc	TCACAACCACAACCTTTGTGA
Ctsc	CTGTATTTTCATCAGTCATCG
Cyba	AGTAGAAGGATACATAGAGT
Cyba	AATGACTTACCATCGCTCCA
Cyba	GGACGTAGTAATTCCTGGTG
Cyba	CAGATAGATCACACTGGCAA
Cybb	CCTCTACCAAACCATTCCGG
Cybb	TTTACCAGACGAATTGTACG
Cybb	ATTCTAACTTGGATACCTTG
Cybb	TTATACTCGAAAACCTCTTG
Cd55	CTCTTATACGTATAGCCAGG
Cd55	CTGCTGTCCCCAACTGTACG
Cd55	TGTGACAGAACAGAAAGTAG
Cd55	CGAAAACAACCTCCACTCCC
Dnase1l3	TCTCGGGAGTTGTGTGCAAG
Dnase1l3	TCACACTCACTTGTAGACGA
Dnase1l3	TTCATGGGTGATTTCAACGC
Dnase1l3	CACTACCATGACTATCAGGA
Dnase2a	TACACCGTCTTGCCAACCGT
Dnase2a	AGGCCAGGTGTATGCACCAG
Dnase2a	CGAAGCCCTGAGCTGCTATG
Dnase2a	GAAATTACCTGACCTAGAGA
Dnmt3b	TGGTAGCCGGAAACTCCACA
Dnmt3b	CAGCCTTCTGAATTACACGC
Dnmt3b	GGAGGGTATGGATACCACAC
Dnmt3b	CAGTAGGCTTGAAGCCACCG
Fadd	TAGATCGTGTGCGCGCAGCG
Fadd	AAGCTGGAGCGCGTGCAGAG
Fadd	TTCGTTTGCTCACGCGCTCG
Fadd	GCGCCTGGACGACTTCGAGG
Fas	CAGTTAAGAGTTCATACTCA

Target Gene Symbol	sgRNA.Target.Sequence
Fas	TATTTATATATCGAAAGTAC
Fas	CATTTGCATACTCACACGAC
Fas	GAGGACTGCAAAATGAATGG
Fasl	AGGACCACAACACAAATCTG
Fasl	CTTCACTCCAGAGATCAGAG
Fasl	CCTCTGAAAAAAAAGAGCCG
Fasl	GGAAGTGGCAGAACTCCGTG
Fcgr3	TGGTGACACTGATGTGCGAA
Fcgr3	ATGCACACTCTGGAAGCCAA
Fcgr3	TGGTGAAACTGGACCCCCCA
Fcgr3	TGCTGCTCCAGACCCCTCAG
Fpr1	AGAAGGTAATCATCGTACCC
Fpr1	TGGTGACAGTGTGTTTCATG
Fpr1	GGCAATGTAAATGGCAAAG
Fpr1	GATGCAGAACACAAATACAG
G6pdx	AGAGGTGGAACTGACAACG
G6pdx	TGCCCGCTCACGACTCACAG
G6pdx	ATGACCCACAGTACCCCAT
G6pdx	AGAGATGGTCCAGAATCTCA
Slc37a4	CTACGTTGACCAGACCAACC
Slc37a4	TCTTTACTCCGAAGACCACG
Slc37a4	CACAACTTGCTGATGGCGT
Slc37a4	CAGAGCGATCTCATCCACCA
Gata2	CCTGGGCTGTGCAACAAGTG
Gata2	GGCCGGGAGTGTGCAACTG
Gata2	ACAGCTGCTGCCTCCCGACG
Gata2	GGCACATAGGAGGGATAGGT
Gfi1	CAAATGCATCAAATGCAGCA
Gfi1	CCCCGACTCTCAGCTTACCG
Gfi1	CTGCACGCGGACAAGAGCGT
Gfi1	CTACGGCGACTTCGCGCCTG
Ostm1	CATCAGCCGAAACATCGGGG
Ostm1	TTGCCTAACAACAATGGTG
Ostm1	AGCGCTGCGCACCATACAGG
Ostm1	CAGAATGCAGATAGTTCTCA
Hc	GCAGATGACTCCCATTATCG
Hc	AGACAAACCTGTTTACACGC
Hc	ACCCTAAGGGAATTCGTGGT
Hc	GAACCTCCCATCAAATGTGA
Hells	TCTGCGGTACCGAATTTAG
Hells	ACGGTCATTAATACTTACAG
Hells	GCTGTATCATGGAACCCGGG
Hells	ACAACACTTCTCGCTTAGG
Foxn1	CCAGGTACTTACGTTCTGTG
Foxn1	GAACAGTACATATGTTGCAA

Target Gene Symbol	sgRNA.Target.Sequence
Foxn1	CACCTCACTATCCCTATCAG
Foxn1	CCACAGACAGCCCTTTCGAG
Hmox1	TCGTGCTCGAATGAACACTC
Hmox1	TCAGGACCTGACCCCTGAG
Hmox1	ACGCTTTACATAGTGCTGTG
Hmox1	TTCCTTGTACCATATCTACA
Irf8	AGTTTACCGAATTGTCCCG
Irf8	TCGACAGCAGCATGTACCCG
Irf8	GCGTAACCTCGTCTTCCACG
Irf8	CAAGCAGGATTACAATCAGG
Ifnar2	CAAAGACGAAAATCTGACGA
Ifnar2	GCCATCGTCATAGTGCACAG
Ifnar2	TAACCTGGATAATCCCTGAA
Ifnar2	ACTGTGGAATTACGATTATG
Ifngr1	TATGTGGAGCATAACCGGAG
Ifngr1	GGTATTCCCAGCATACGACA
Ifngr1	TTCAGGGTGAAATACGAGGA
Ifngr1	TATACCAATACGCAAATACC
Ifngr2	AGGGAACCTCACTTCCAAGT
Ifngr2	TGGACCTCCGAAAAACATCT
Ifngr2	TCCCTTTGATGTGTTCCACG
Ifngr2	TGATGAGCAGATTCTAACTT
Cd79b	TGACCTGGTTCGAAAGCGA
Cd79b	TCCCCAGGATTCAGCACGT
Cd79b	CATAATGTCACCGACAGCTG
Cd79b	CGAGGTTTGCAGCCAAAAAG
Igll1	CTGTTCCAGATCATCCCACG
Igll1	GCTCACCAAACACACTAGTG
Igll1	CCAAAGACATACCAAACTG
Igll1	GGAGAACTTCACACTGCCTG
Ikbkb	TCACACATACCCCGTGACGG
Ikbkb	CAAGATCCATGTCCAACGTG
Ikbkb	ATGTGGCACCCCTCGCAAAG
Ikbkb	GAAGCCAGTGATGCACTCGA
Ikbkg	AAGGATCGGCAAGCTTTAGA
Ikbkg	AGGCTGCCTTGCGAATGGAG
Ikbkg	TGGGTGAAGAATCTTCTCTG
Ikbkg	GCTCAGGTGACATCATTGCT
Il10	GCTAACCGACTCCTTAATGC
Il10	AACTGCACCCACTTCCCAGT
Il10	AAGGAGCATTGGAATTCCCT
Il10	ACTGGCATGAGGATCAGCAG
Il10ra	GCAGTGTTTACTTATCACGA
Il10ra	GTGGGGACAACACGGACAGT
Il10ra	GGTGAACGTTGTGAGATCAC

Target Gene Symbol	sgRNA.Target.Sequence
Il10ra	TCTGGCTTCAAACCACACAT
Il10rb	TGGCGGATGAACATTCGGAG
Il10rb	ATTTCAAGAACATTCTACAG
Il10rb	CGGAGGACCTCAGAGTCGTA
Il10rb	AGAGAAGTCGCACTGAGTCG
Il12rb1	GTCGGTGAGGAACCAAACCG
Il12rb1	CCTCCGAACCATACCCACAC
Il12rb1	TGAGAAGACATCGTTCCCAG
Il12rb1	TCAAGGTGTCACAATCACAC
Il17ra	ACTGAAGTAGCAAACAACGT
Il17ra	ATGAGGCCATACACCCACAG
Il17ra	GAAGGTCTGGATCGTCTACT
Il17ra	GACCTGGAGATGTTTGAACC
Irak1	ACAGAAGGGCCAGCAAAACG
Irak1	TGGGCAAGAAGCCATAAACA
Irak1	GGTGCCTGAGGATGTGAACG
Irak1	CCCACCGAACTGGCACCAGT
Il1rn	TTCTCCAGAAAAGATAGACA
Il1rn	GTGTTCTTGGGCATCCACGG
Il1rn	CTGCCTCTGAATGAAACAGA
Il1rn	CTTGATATCATCTCCAGACT
Il2ra	GTGTCTGTATGACCCACCCG
Il2ra	ATCTTGACAGATGCTAATAGC
Il2ra	GAGAGGTTTCCGAAGACTAA
Il2ra	GAATCTTCATGTTTCCAAGG
Il2rg	TTCCACAGATTGGGTTATAG
Il2rg	GGAGCAACAGAGATCGAAGC
Il2rg	CCCGATTACCAAGATTCTGT
Il2rg	CATACCTATAGTGCAGCGTG
Il7r	GGGAGACTAGGCCATACGAC
Il7r	AGACCTAGAAGATGCAGACG
Il7r	CAGAACCCAAGAATCAAGGT
Il7r	CCTTTGAAGTAATCGTTATG
Itch	TCCCGCACATAGGCTATCTG
Itch	AAAACATAATTTACTCGTAG
Itch	GCCAAGCTCCCCTACCACCT
Itch	ACAACACTCGGATTACTIONCAG
Itgb2	GAGTATAGGCAAATCCCGTG
Itgb2	TTGGCTGGCGCAATGTCACG
Itgb2	ATCCTGAGTTCGACCAACGG
Itgb2	TGGAGTAGGAGAGATCCATG
Itk	CAGCCCCAAGCGCTACTACG
Itk	GTAAGCCTTCTCATACCCCG
Itk	TCAGGAACCTGAAGAAACCC
Itk	TTGCTCCAGACTGTGAGAGT

Target Gene Symbol	sgRNA.Target.Sequence
Jak1	CGATGCCATTCTGAATGACAG
Jak1	TGAATAAATCCATCAGACAG
Jak1	TCCGAACCGAATCATCACTG
Jak1	AAACATATAGTGACCTCTA
Jak3	CAGACATCGGAACTGCATGG
Jak3	AGAAAAGTCCAATTTGATCG
Jak3	GGGCTTTGGAGCCACCACGT
Jak3	CACCACCGAGACCTTCCGTG
Rpsa	GAAGCGGCCAGCGATCGGAG
Rpsa	CTTACAGGGAGCTCACTCAG
Rpsa	GACGTCAGCAGGATTCTCGA
Rpsa	AGGGAAGTACTCCGCATGCG
Lck	AAGATCCGTAACCTAGACAA
Lck	GTACTACAACGGACACACGA
Lck	CCGGGAAAGCGAAAGCACTG
Lck	GCTTTATGCAGTGGTCACCC
Lig1	GACCTCACTGACACCCCGAG
Lig1	GACAATTCAAGACACTCTTG
Lig1	TCTTTCATAGAATTTCCCA
Lig1	AGAGTGATTCTCCAGTGAAG
Psmb8	CCGGAGCTCGCACTTCCCCG
Psmb8	ACATGATGCTGCAGTACCGG
Psmb8	CTCGCCTTCAAGTTCCAGCA
Psmb8	AGGTTGTATTATCTTCGGAA
Blnk	CTATGCAGGTCGAAACAGTG
Blnk	AAGATAATCGATCCAGCCAG
Blnk	GTCTGTGACTAGACCCTCGG
Blnk	GATATTAAGAACAATGAAGG
Lyst	GGAGCCCTGAAAGATCGCGG
Lyst	GGGATGAGTCTTACCCACGT
Lyst	TAGGAAGTGGTGAACCACGT
Lyst	CATACCCCGAGTTTAAGCAA
Masp2	GGCCTGTGATATAGTCCACA
Masp2	CCTTTGCCACTGACGAGTCG
Masp2	CTGCGAGTATGACTTTGTCA
Masp2	TGTGGCAATAATGGTCACAA
Mcm4	TTGTTGACAAGGTTCAACCA
Mcm4	ACCCGGGTGGAGATAGATCG
Mcm4	GGTTATACCAACCTTTGACA
Mcm4	CTCAGGGTCTTTTCATCACAT
Cd46	CTGTGAGCCAAATCATAACAT
Cd46	TCCATAGCTTCAAATGGCCG
Cd46	GGCCTCAGCATAGACGCCCA
Cd46	ACAGTTGTGATCCTACCCCA
Msh6	AGTTTCGTGATACCAAACAG

Target Gene Symbol	sgRNA.Target.Sequence
Msh6	CATCAGTGACCGTCTAGATG
Msh6	TAAGTAAAGACACGGCTGAG
Msh6	GAGGCAAAGGATCTCAACGG
Msn	CGCTTGTTAATCCGAAGCCG
Msn	CCGGGCCAAGTTCTACCCAG
Msn	GAAGCAACTTATCTCCAGCC
Msn	CAGACTAAGAAGGCTCAGCA
Mvk	AGCGTCAATTTACCCAACAT
Mvk	GTGGTCGGAACTCCCCCG
Mvk	CAAGGTCCCGCGGAGTACCA
Mvk	TCTGAAGTCAATCAACAAGT
Myd88	GGTTCAAGAACAGCGATAGG
Myd88	AAGGAGCTGAAGTCGCGCAT
Myd88	CCTGTCCTCAGGACAAACGC
Myd88	GCATCCAACAAACTGCGAGT
Ncf1	TCTTACGGGCAGTCCCATG
Ncf1	GATCCGGATCCCAACTACGC
Ncf1	GCTACGCACTGGCTGTCAGT
Ncf1	CGTTGCCCATCAAACCACCT
Ncf2	GCACAAAGCCAAACAATACG
Ncf2	TGGAATATCGGATTCTGGAG
Ncf2	TCTCACCTGTGGCTGCAGAG
Ncf2	TGAAGCAAATCCTCGAGTGG
Ncf4	AGAAGAAGATCCTGACGTCG
Ncf4	CGTAGAACTGGCGATAGCGG
Ncf4	CGATCCATGATGGCCCCTTG
Ncf4	ACCTCGATGACAAAAACCTG
Nfkb1	TGTGAAGGCCCATCACACGG
Nfkb1	GGAGTACGAAATCCAACGC
Nfkb1	TTTCGACTACGCAGTGACGG
Nfkb1	ATGACAGAGGCGTGTATTAG
Nfkb2	ACTGAGCGTGATAAATGACG
Nfkb2	CGGAACACAATGGCATACTG
Nfkb2	CCCACGCTGCTGGATCGGCA
Nfkb2	ACCCGGATAGCAGCCCATTG
Pepd	CACAAATCGGATCTCCAGCG
Pepd	CTGCTATGGTGCATCGATG
Pepd	GCCCTGCAACACGACAGCTG
Pepd	CTTGCTAATGCCCTCGAAGG
Cfp	GTTACACATTTGGTTCCGAG
Cfp	TATGAGCATAAGGCCTGCAG
Cfp	GATTATCACATACTCGTTGA
Cfp	CCTACTTGGGAGAGACATCA
Prf1	GTTTCGTGCCAGGTGTATGGA
Prf1	TGCCACAGGTAGGCGCTGTG

Target Gene Symbol	sgRNA.Target.Sequence
Prf1	TCAATAACGACTGGCGTGTG
Prf1	GGTAGGAGACTGCCTGAACG
Pik3r1	GAGCTTTATAAGGAGAGGCG
Pik3r1	TCCATTAACCTTCAACTCTG
Pik3r1	TGGCTACAATGAAACCACTG
Pik3r1	CTGGAAATCTGAAAAGCACG
Prkcd	AGAAGGTGGCGATAAACTCG
Prkcd	TTATAAACCTTGAATCGGTG
Prkcd	AGCCCACCATGTATCCTGAG
Prkcd	CGATGATGTAGAGTGTACCA
Pms2	TCTCAGGAAACCATAAACTG
Pms2	GTAAGCTGCACTAATCAGCT
Pms2	AGTTTCAGACAATGGATGTG
Pms2	ACTAAAGAGATCAAGTCTAG
Pnp	AGATGCTGTGTGATGATGCA
Pnp	TCAGTGCCTGGAAACAAATG
Pnp	TGTGGCCAGAACCCTCTCCG
Pnp	CCTCAAGTGGCAGTGATCTG
Pola1	CTAACGTTTACCATTTCACG
Pola1	AAGAAAGCAACTTACGCTGG
Pola1	AAAGAAAAAAGATCTACTG
Pola1	TGTACAGAACCATCAACATG
Pole	CATTATGGTCACCTACAATG
Pole	GATGCTGAGACCTACGTCCG
Pole	CATTGACCTCAGAATCCATG
Pole	AGGCTGGAAGGATCATAGCA
Pole2	GATCGAACGATCTGTCTGG
Pole2	CCACAGTGGCTTATACACCG
Pole2	TCAAGCGCTTTAATACCTTG
Pole2	ATAGCGTTCAAGATACAGCT
Prkdc	AGAGCCAATTCAGTGACCCG
Prkdc	TGGCCCTTGTAAGTAGACGA
Prkdc	CATGCAGGGTAAGTAATCGT
Prkdc	ACAGAGGATGCTCAAAAATG
Psen1	TTTCAACCAGCATACGAAGT
Psen1	TGCTACTGTAACGTAGTCCA
Psen1	CTGAGCCAATATCTAATGGG
Psen1	AGTCAGCTTCTATACCCGGA
Pstpip1	CTGGTTACAGTGACCCACA
Pstpip1	TGTTTGTAGAAAGAGTGTAC
Pstpip1	ATTGGCACTCACACGCTCGA
Pstpip1	GTCGCTCTACAAGAAGACCA
Pten	CCTCCAATTCAGGACCCACG
Pten	TGTGCATATTTATTGCATCG
Pten	ACTATTCCAATGTTTCAGTGG

Target Gene Symbol	sgRNA.Target.Sequence
Pten	GGTTTGATAAGTTCTAGCTG
Ptprc	GTAGCAGAAATCTTATATCG
Ptprc	TTTCAATGGAGGTACGA
Ptprc	TTGTCAAGCTAAGGCGACAG
Ptprc	ACCACAACGAAGCAAACATG
Rac2	GAGAAGACACGTCTTGCCCA
Rac2	GCTGGACCTTCGCGATGACA
Rac2	AAGAAGCCACTCACACAGTG
Rac2	GGCACGGACATTCTCATAGG
Rag1	ACACCAAAGCAGAGTCGTAG
Rag1	TGAAACGATTCCCACAGATG
Rag1	TCCCGCGCAAGATTGCAATG
Rag1	TGGGAAGTAGACCTGACTGT
Rag2	CATCAATATATCATTACGG
Rag2	ATTGACGTGGTGTATAGTCG
Rag2	TAACCTGTATAGAATAAGAG
Rag2	CATACCAGGAGACAATAAGC
Ranbp2	AAATTATTCTCGTCACAAAG
Ranbp2	TGCTAATGTAACCTCCACCA
Ranbp2	ATGTTGTTAAACTTAAGTCG
Ranbp2	ACATGCAATGCACCTAGAGA
Rasgrp1	ACGTACAGATATCCGTCGGA
Rasgrp1	TAAGAACTATGATCTCGACC
Rasgrp1	ACAGTTGGTTATTCCGACAC
Rasgrp1	TGACCTTATTGATCTCATGT
Relb	GTTCAAACGCCACCCTACG
Relb	TACACCCACATAGCCTCGTG
Relb	GCGGATTTGCCGAATCAACA
Relb	GCCTCCTATCGGGACCAGCA
Rfxank	GTTCTACTTACAGTCCAGGG
Rfxank	ATCAACAAACCGGATGAGCG
Rfxank	GCACTGTCACTTGCCAGTAT
Rfxank	AGTTCGCTTCCTGCTAGACT
Rorc	CTTGAGTATAGTCCAGAACG
Rorc	GTCATCTGGGATCCACTACG
Rorc	TCTGGGGCACTGCAGAAACT
Rorc	GACAAGCAGAGGCCTCGGGT
Sema3e	ACACGATCTACACCCGAGTG
Sema3e	TGTGCCAGCAAAGTAAACGG
Sema3e	AAGATAATTACCAACTAGCG
Sema3e	TGTGATACACACATACAGCA
Foxp3	CATACCTGATGCATGAAGTG
Foxp3	TCTACCCACAGGGATCAATG
Foxp3	AGGTCGGGACCTGCGAAGTG
Foxp3	GCAAGAGCTCTTGCCATTG

Target Gene Symbol	sgRNA.Target.Sequence
Sh2d1a	AGAAGCTCTTACTCGCTACC
Sh2d1a	GATGCAGTGACTGTGTACCA
Sh2d1a	AACAGGTTCTTGGAGTGCCG
Sh2d1a	CACACAGGCAGTACACGCCA
Clpb	AGGACCGCGTTCCGACGAGG
Clpb	GGAGAACGGCTGGTACGATG
Clpb	CGTTGTCACCGGAGACCGCG
Clpb	CTCTCGAGTGACTAGGACTG
Stat1	GGATAGACGCCAGCCACTG
Stat1	TGTGATGTTAGATAAACAGA
Stat1	TTAATGACGAGCTCGTGGAG
Stat1	GAAAAGCAAGCGTAATCTCC
Stat3	CCAACAAATTAAGAACTGG
Stat3	CTGCTTCTCTGCTACTACGG
Stat3	GTTTACCACGAAAGTCAGGT
Stat3	CAAAGAGTCACATGCCACGT
Stat5b	CTGATTGCGAGTGATTACAG
Stat5b	TACAGCGAACCAGCTCCATG
Stat5b	GCGGTTGTCCCAGAGGACAG
Stat5b	AGTGGATCGAAAGCCAAGCC
Stim1	TGAGGATAAGCTTATCAGCG
Stim1	GAATACAGGAGCTAGCTCCG
Stim1	GAGCCGTCAAAAATATGCTG
Stim1	CAGCAGATCGAGATCCTCTG
Stxbp2	CGTGTAAATAGTGGGGACACG
Stxbp2	CATCCATCCGATACCGCAAG
Stxbp2	TATTATAGGTACCTTCTCCG
Stxbp2	AAGGTTGTAGGTGCTATGTG
Tap1	ACTAATGGACTCGCACACGT
Tap1	GTCTCTAGCAAAGTCCACGC
Tap1	TGCCACATAACTGATAGCGA
Tap1	TGGACATGAGCCATATGTTG
Tap2	AGAAGCCACTCGGACTACTG
Tap2	TTACACGACCCGAATAGCGA
Tap2	GCTGTGGGGACTGCTAAAAG
Tap2	CATGCACACATACCTGATGG
Tapbp	TGGTGTTAGAGACACTCTGG
Tapbp	CTTCCCAGCTGGACTCGAG
Tapbp	CGCCACTCCAGCCCAAAGGG
Tapbp	AGCCGTGAAGCCTTCTCAGG
Tbx1	ACATAGACAACATGGAATCG
Tbx1	CTTCCGGGATTGCGACCCGG
Tbx1	ACACTACCACCCGGACTCGC
Tbx1	GCGCACGGATCGTAGCGCGG
Tcf3	ATTATTGCTGGAGTGATCCG

Target Gene Symbol	sgRNA.Target.Sequence
Tcf3	GCTCCTAGGAACGTGGAAGG
Tcf3	GAAGAGCCGTACCTAGCAT
Tcf3	CTGCAAACCTGGGTTCCCCCG
Tcn2	GAAGCGGCTCCATGACAGCG
Tcn2	TCTGAGACCACGAATCACCA
Tcn2	GAGACTAGCAATACCGCAGG
Tcn2	GAATATCTATAGCACCCCAC
Tert	CCTCCAGCCTAACTTGACTG
Tert	CACAGAGGGCCAGATATCCG
Tert	TCAGCATGCTCAACTATGAG
Tert	AAGTCCTGCTCGGTCCCCCG
Thbd	TACCTACAACACCCCGTTCCG
Thbd	GTGTGAGACAGGCTACCACT
Thbd	CTGTGAAGTAAACTCACAG
Thbd	TCGCAGTTAGATCCGAAACA
Tnfaip3	GCAGCTTGTCAGTACATGTG
Tnfaip3	ATATCCATGAGTGATAGCTG
Tnfaip3	AGCCCCGAGGAAACCGCTGG
Tnfaip3	AGGACTTTGCTACGACTC
Tnfrsf11a	ACCAGCACAACGGTCCCCTG
Tnfrsf11a	ACACTGAGGAGACCACCCAA
Tnfrsf11a	GTTTAAGCCAGTGTTTCACC
Tnfrsf11a	AGACGCAAGGAGACCTCTCG
Tnfrsf1a	AGTTGCAAGACATGTCGGAA
Tnfrsf1a	AGACCTAGCAAGATAACCAG
Tnfrsf1a	GATGGGGATACATCCATCAG
Tnfrsf1a	GGATCCCGTGCCTGTCAAAG
Cd40	ATTCGCCTGAGTCACATGGG
Cd40	GGGATGACAGACGGTATCAG
Cd40	AGTCAGACTAATGTCATCTG
Cd40	CTGCACCAGCAAGGATTGCG
Cd27	TCTCTCCAGACTACCACACC
Cd27	TGCTGCATACCTGTGCCATG
Cd27	AGACAAACACTACTGGACTG
Cd27	CTCAGGTACATTCTTTGTGA
Tnfsf11	GCCTCGATCGTGGTACCAAG
Tnfsf11	GACCCTCGTGTGGGACGCCG
Tnfsf11	GTTAAGCAACGGAAAATAA
Tnfsf11	AGATTTGCAGGACTCGACTC
Tnfsf12	GGCTGACCACGACCAGCAGG
Tnfsf12	GCCCAGGCTCAGCACCAGCG
Tnfsf12	CAACGCTGTCTGCCAGGTG
Tnfsf12	GGAAGTGAATCCCCAGACAG
Cd40lg	TATTTCAAACAGGTCTGAAG
Cd40lg	AAGCTAAAGAGATGCAACAA

Target Gene Symbol	sgRNA.Target.Sequence
Cd40lg	TTATACCATGAAAAGCAACT
Cd40lg	TGAACTGTGAGGAGATGAGA
Cd70	TTGGGAAGGTCCTTCACACA
Cd70	AGCTGTAACCTCAGCTGTGTG
Cd70	AAGGACCCACACTGCGCTG
Cd70	CATCTGCGTATCCATCAAGA
Traf3	GCTGGGGGCATTGACACACT
Traf3	CAGGTTACGTGCTGTACCG
Traf3	AGTGACTGCACGTGGCCTCG
Traf3	GCTTTGAGATCGAGATTGAG
Trex1	TTTCCTCGAACCATTCCCTG
Trex1	ACACAGAAGGTACCATCTAG
Trex1	AGCTTGTCCACCACACGGGG
Trex1	GGAGCAGAGGAAAGTCATAG
Tfr3	CTACACGCTTACAATAGCCC
Tfr3	GAATACATACACTCCTCGTG
Tfr3	GGGCTCCTACTACAACATAA
Tfr3	AACCCTCGGGAGACTCCACT
Tnfrsf4	GAGCCGCTGTGATCATACCA
Tnfrsf4	TCACACTTGGAGTTACAGCA
Tnfrsf4	TTCCAGATAAGGTACAACCTG
Tnfrsf4	GTAGACCAGGCACCCAACCT
Ung	ACGGACCTAATCAAGCTCAC
Ung	TTGTCAGGGTGGGCCCCGACA
Ung	CCAACCCCGACTCTGACTCC
Ung	CCACAAGGTCTATCCGCCCC
Vps45	AAAGCTGATAACGAATCATG
Vps45	ACGAACTCTTTGAATTCCGG
Vps45	TGTCTCAAAGCACGTGACAG
Vps45	TTGTTTCCTTCGACCCACAA
Was	CAACTGATAAGAAACGCTCA
Was	CCACCAGCACCAATCAATGA
Was	TCACCTGTAGGCCATAAAGG
Was	GCAGGTGAACAACCTAGACC
Wdr1	GTAGCCAAGTATGCACCCAG
Wdr1	GGCCCTACCGACTAGCAACA
Wdr1	GTGTGCGATTCTCTCCTGAT
Wdr1	ATGGCTCCCAGAATAGATGT
Zap70	CAACGGCACGTACGCCATCG
Zap70	GAAGCGAGAGAATCTCCTCG
Zap70	TCGACAACCCCTACATCGTG
Zap70	CGCGCACCATAGCATCACGC
Ikzf1	GATGGCCTGGTCCATCACGT
Ikzf1	GTTGGTAAGCCTCACAAATG
Ikzf1	CAGAACTCCAAGAGTGATCG

Target Gene Symbol	sgRNA.Target.Sequence
Ikzf1	AGAAACTAACCACAACGAGA
Hax1	CAGAACTATTCTCACCTCCG
Hax1	AATTCACACACCAGGAGAGT
Hax1	CTGAAACCGAATTCCTCTGG
Hax1	GCTCCAGATTGGGGGTCGCA
Sh3bp2	TCAGCAAGAAGCACCGAACA
Sh3bp2	GAGGTGAACGAGTGGGCACG
Sh3bp2	ACCTGGAGCCTGATTCCCCG
Sh3bp2	TGGGTACATTGCTCATTGGG
Srp54a	CTTATAGAGAAGTTGAAGCA
Srp54a	AAAGCGTGGACACCGACTAA
Srp54a	TATGTGATGGATGCATCCAT
Srp54a	AAACTCGACGGTCATGCGAA
Rbck1	TGCTTCATACCAGCCTGACG
Rbck1	AGTACGCCCCGGATATGACAG
Rbck1	TGCATTCACACGGCATTCCG
Rbck1	ACCCGAGGTCTCCCCAACAC
Usp18	CATCATGAACACTTGAAGCA
Usp18	ACAGCTCTCGCAGCACATGT
Usp18	TGTACAGCCCACGCAAATCA
Usp18	CAGGCACTGAACGAGCTCCG
Clcn7	GGAAAGACGAATCAACCACA
Clcn7	ATAGCTGCAGGGATTCACA
Clcn7	AATCGGACAGATGAACAACG
Clcn7	ACTCTGCCTTCGTA CTCTG
Tcirg1	ACACAAGTGCCTCATCGCGG
Tcirg1	TCTCCCGAAAGCTGGCAATG
Tcirg1	CAGCCCACTCCAACCTGAG
Tcirg1	CGCTACAGGGAAGTTAACCC
Nbn	TATTCCTACATCAACAACGC
Nbn	TGGAGAAAGCTGATAGCTCG
Nbn	ATAGCTGGTTCATCAATGGG
Nbn	GAGAATTACTGTAATCCGCA
Tinf2	CAAAGGCGTGCCATAAAGAG
Tinf2	CCGGTAGCAAACCAAGCCGG
Tinf2	CCAAAGGGGCCAGATTAAG
Tinf2	AGTGCTCTACGCGGCGACGG
Elane	CCGGCCACCAACAATCTCTG
Elane	CTCACAGGCCGTTACACAG
Elane	GAACGACATTGTGATTATCC
Elane	ATGACCTCCACGCCTCTGCA
Cfhr1	TTGCCTTCTTAGATCCAACA
Cfhr1	TGCATATACTGGTAACGACA
Cfhr1	ACTGGTGGAAATGCATTTGG
Cfhr1	AGAAGGTGACATTGTACAAG

Target Gene Symbol	sgRNA.Target.Sequence
Ctps	ATTGGCCATTAACCACAAGC
Ctps	ATACCAGTACGTCATTAACA
Ctps	GCCCACAAGAGCGATCGAGC
Ctps	TTAATACCCGTAGACGAAGA
Slc46a1	AGAGCTAACATCTGCCACAG
Slc46a1	GGGCAATGGATCGATGATGG
Slc46a1	TGGACCAGAAGAGTCCCACC
Slc46a1	GAACTGTGGGAACCAAAGCG
Nhp2	GCAGAAGCAGATTCGTGCGG
Nhp2	CCATCTCCAGTTCTGTGCG
Nhp2	AGGAGATACATTGCCGATTG
Nhp2	GGCCGCTCCCGAAGAGTCCG
Map3k14	GCAAAGCCCGAAAAAACGT
Map3k14	CGTGGTTTAGACATTGCAAG
Map3k14	CCCCGAACTGAGGACAACG
Map3k14	TGGGCCAGTTGGCTTAGATG
Rfx5	ACATAATGACCGTTCTCGAG
Rfx5	ATGGGTGTGATAAGTGATCG
Rfx5	AGAGCGTCTATGATGCCTAT
Rfx5	TCTACCTCAGCTCCCATCG
Irf7	CTTGCGCCAAGACAATTCAG
Irf7	GGCAGGTTAACTCCACTAGG
Irf7	TGTGCGGCCCTTGACATGA
Irf7	GGAGCAAGACCGTGTTTACG
Irf3	CCAGTGGTGCCTACACCCCG
Irf3	AGAAACAATAGCCAGATCTG
Irf3	GGCTGGACGAGAGCCGAACG
Irf3	CTGGCGGCCTCGGTAGAAGG
Icos	TGGTCTTGGTGAGTTGCGAG
Icos	TATGCAAATATCCTCCACTA
Icos	GCAGAAGTAATAGCTTCCCT
Icos	AAATGAAAACATCCTATGAT
Smarcal1	CTCCCAGGTGAAGCGCACAG
Smarcal1	TTTGGGTTATAAATCCAGCG
Smarcal1	TCATTGCAGATATCAAGACC
Smarcal1	GCTTGGCATCCACTCCGGAA
Atp6ap1	GAGGATTTACAGCATAACGG
Atp6ap1	GATATGACCCTCATGTGTGT
Atp6ap1	TAGCTAGATCCACATGCAAG
Atp6ap1	GTGTCATTGTAACCTCACAGG
Unc93b1	CTGGGAACGCTACTACACGC
Unc93b1	CCGCAGTTGGACGAACTCGT
Unc93b1	AGGTGAAGTATGGCAACATG
Unc93b1	GCACACGCGAAGCTCAACTG
Nfat5	TCAGCCATTTACGTACACTC

Target Gene Symbol	sgRNA.Target.Sequence
Nfat5	AGTATCCGGTTAAAAGTGAG
Nfat5	GCCGTGGGGGTAAGTAACAG
Nfat5	AAGACCAACTTCTATAACAG
Il1f5	GTCATCCTGGGCGTTCAAGG
Il1f5	AACATCATGGAGCTCTACCT
Il1f5	AGGGCCAATTCTGAAACTTG
Il1f5	TGTTGTCCCAAATCGGGCAC
Mefv	TCTGATAACCTACTACGGGG
Mefv	AAGGAGGGTACCTTCACAAG
Mefv	ACCAAAGGAAGGATCAGAG
Mefv	TCTGAATGGAAGGACTACGG
Extl3	GCCCAAGCCTCGCGTCACAG
Extl3	TCAGACATAGCATGGACAAG
Extl3	CCACACAGTGCCCACTCAGT
Extl3	ATTGCGGAGGTATTTAGGTG
Tyk2	GTGTGGTTACGGCGACAGAG
Tyk2	TAGACCCCGCATGATGACG
Tyk2	CTTCCAGGACATTTCCACG
Tyk2	ATCCACATCGCACACAAAGT
Samhd1	ATCCTTACATTATGTCGATG
Samhd1	GCTTGATATAGCGAAGTCGC
Samhd1	CTTGGGCTGCCATCGCAGCG
Samhd1	TTAGGATCTTACCTAGGTCG
Adar	ACTCCAACAAGCCGCTACG
Adar	AGAGGTAACCCAGTAACAG
Adar	TTCTTGTAGGGTGAACACCG
Adar	TGTATCCAGGAATTCCTAG
Tbk1	TGCCGTTTAGACCCTTCGAG
Tbk1	CTTCTCGCTACAACACATGA
Tbk1	CAACATCATGCGCGTCATAG
Tbk1	CGGGAACAACCTCAATACCGT
Mogs	TCTAGGTCATTCTTCCACG
Mogs	TCGGCAGCATATCCACGATG
Mogs	TGCCGAAATAGACGTGTGGG
Mogs	GAGGTCCTACTACCAGAGAT
Tnfrsf13b	GTACTIONGACCATCTCCTGG
Tnfrsf13b	GAAGTCAGGTCAGACAACCTC
Tnfrsf13b	GTGGCTCTCCTCTACGCCTG
Tnfrsf13b	ATCAGTACTGGGACTCCTCA
Bcl11b	GTTGTGCAAATGTAGCTGGA
Bcl11b	CTGAGAGCCCCTCGTCTGAG
Bcl11b	GCGGGAAGTTCATCTGACAC
Bcl11b	CAGAGGTGAAGTAATCACGG
Stk4	AATACACCGAGATATCAAGG
Stk4	TATCTGATATCATTTCGGCTA

Target Gene Symbol	sgRNA.Target.Sequence
Stk4	TGCTGATATCCATCCAATGA
Stk4	TTCAGGAGCCATCCAAAACG
Ncstn	CCAGCAGAACCATGTAAGGG
Ncstn	GTGCTATCAAGATCACAACC
Ncstn	AGGGACAGAACTCACCCGTG
Ncstn	GGTGACTCACCGATTGTGGA
Il21r	GCACGTGTACCATATATGTG
Il21r	AGGACGCTATGATATCTCT
Il21r	GCCACCTCACCACAGCATAG
Il21r	GGGCTGGAAGAACTCTCAG
Il21	GGTGACGAAGTCTAATCAGG
Il21	GAAAATCTATGAAAATGACT
Il21	AAACTCAAGCCATCAAACCC
Il21	GACATTCATCATTGACCTCG
Lpin2	GGATACTCACGTTTCTAATG
Lpin2	GGTTATATATCCGGATCACG
Lpin2	TGCAGGTCACCAAAAGAGAA
Lpin2	AACCTGGATCCGTGTCCTG
Nop10	CGATCGCGTTTATACGCTGA
Nop10	CAATATTACCTCAACGAGCA
Nop10	GGAGAACCGAGCAGGATGGG
Nop10	GAGCAGAAATTTGACCCTAT
Psenen	CGAGAATGATCACCCAGAAG
Psenen	CCGGAAGTACTATCTTGGTA
Psenen	CTTGGAGCGGGTATCCAATG
Psenen	ATGTTGACTAACCAAAGAAA
Ndn12	CACGTATTGCAGGCGCTCGG
Ndn12	CAACACCATCACCGAGACTG
Ndn12	AGAAGAAGATCCCGATCAAG
Ndn12	CCCTGTCGGCCCCGACCGTG
Sbds	CCAGATCCGACTGACCAATG
Sbds	CCTTCATGGCTCTCTCGATG
Sbds	ACTGAAATCTGCAAGCAGGT
Sbds	TAGGGATATCGCCACCATTG
Taz	TTTGGAGAAGCTTAACCATG
Taz	GGTCATCCATGCAAGACTGG
Taz	AGCAGCTCACCTCGACACAC
Taz	TATGAGCTCATTGAGAACCG
Cdca7	TCTACTGGTCGGATTATATG
Cdca7	GCTGTCACAACTGTCATCGG
Cdca7	TGTGGCTACCAGAAGGAACC
Cdca7	GTCGTCCAGAGAACAAGCCA
Magt1	TGTGTGTGCGATCGCAGCGG
Magt1	CAGCTGAGCAGATTGCCCGG
Magt1	TTATGCTGGACCCCTAATGT

Target Gene Symbol	sgRNA.Target.Sequence
Magt1	GTGGAGCTTTAACAAGACGA
Rnaseh2b	CTCCTAGGTCAACCAAAGT
Rnaseh2b	TCAGCCCTTGGACCAAGTCG
Rnaseh2b	CAGCCTTTAGGAGATAGTGA
Rnaseh2b	TGGCCAGCTTTACGAACAGG
Jagn1	GCACTACCAGATGAGGTACG
Jagn1	GTACCTCATCTGGTAGTGCA
Jagn1	AGTGCATGGCGACGCGCTCC
Jagn1	CCGTCGGTGCCGCCGCTCG
Ino80	GGGTTGCGGAATATCCTCAC
Ino80	AGAAAATGAATTGTCTGACA
Ino80	TGCCCATCAATGCATGAAGG
Ino80	GTGACGTGGAGATTCTTCAG
Rnaseh2c	CGTGAAGAAGCGATCTACCG
Rnaseh2c	CGGCTGACTAGAACGTGCGCA
Rnaseh2c	AGGGTTTGCGGGATTCGTGA
Rnaseh2c	ACCGTCTGCATCGTGGCGGA
G6pc3	TAGGCCGACTGCCAATAGGA
G6pc3	TTCCCGGGCTAGAGAATATG
G6pc3	GGGGCTCATTAGCCAGCCAA
G6pc3	TAAAGAGAGTCCAATACATG
Ctc1	CTGGTCTGAATAACCCGCTG
Ctc1	CTTGTAGATGAGATCCTCCA
Ctc1	AATTGCAAGTAACCAAGACC
Ctc1	CTTGGAATATGGGGTACAC
Gins1	CCGGCGCGCGGTGTAAGTCCG
Gins1	TGCTTCGGATTAGAGCACTC
Gins1	GTTGTTGTTACAGACGGAG
Gins1	AGTCTCTTGCTACTTACATG
C8g	TGGGACTCACAGCTTTCGGA
C8g	CTGGGGAGCTGCGTGCAATG
C8g	CCTCACCTTGAACAAGAAG
C8g	CTGAGCACTGAAATTGACCT
Rnaseh2a	TGTCACACGATACAGCTGCG
Rnaseh2a	GTAACAGATGGCGTAGACCA
Rnaseh2a	AGACCTTGACAGAGAACGAG
Rnaseh2a	GGCTCCTTGAGACACACAGC
Trnt1	CATGAATTAAGAATAGCAGG
Trnt1	ATTGCGATGATCAACAACAA
Trnt1	AACCTGTTCTCACCTATGTG
Trnt1	GGCAGAATTGTCGACAGACC
Rnf168	GGTGTGCCCCAGTAACTGG
Rnf168	CCCGGGCCACAGTTATGTGT
Rnf168	AGCATGGGTTACAGAGCGTG
Rnf168	AATCTCTGGACAAGAATCAA

Target Gene Symbol	sgRNA.Target.Sequence
Unc13d	AATCTGGTACAGGACGTCAT
Unc13d	ACAGAGACCTACCCAGACCG
Unc13d	TGGCTGGCTGAAACCAGCGG
Unc13d	GCAGCCCTGTGTCCCGACGT
Nbas	AACAAAACAGCATATTCGTG
Nbas	ATAGCAGTATTTATTCCATG
Nbas	ATTGATTGATGTCAATTGGT
Nbas	TTTGCCGAATGACATGACAT
Slc29a3	AATGATGGCCATGCACGCGA
Slc29a3	GGGAAACTGCGCAGAACCCG
Slc29a3	CAAGGAAGACTGCTGCCATG
Slc29a3	ACCAGAAAACACTCGAACTG
Ifih1	TGTGGGTTTGACATAGCGCG
Ifih1	CGTAGACGACATATTACCAG
Ifih1	TGGGTTCCAAAATCTGACAT
Ifih1	GATTGATGCATATAGCCACC
Snx10	GCAGAGCCATCTGAACTCCG
Snx10	CATGTGACCAACGCCGCCA
Snx10	AAACATCTTGTGTACGAAGA
Snx10	AAAGCAAGAGTGCATTCTGC
Tnfrsf13c	CAGACTCACTAGACCCACCA
Tnfrsf13c	GACACGCGATTTCTCACCAG
Tnfrsf13c	CTCCGCGCTGAGACCCGACG
Tnfrsf13c	GCACTCGGTCTGATTGCACT
Spink5	CGGGAAAGTGACCCAATCCG
Spink5	AGGGAGAGTGACCCTGTACG
Spink5	CGAGAAAATGACCCTGTGCG
Spink5	TGGAAGACTTGGATGTACAC
Tmem173	GAAGGCCAAACATCCAATG
Tmem173	TATCTCGGAATCGAATGTTG
Tmem173	AGTATGACCAGGCCAGCCCG
Tmem173	CAGTAGTCCAAGTTCGTGCG
Parn	AAAACGGTCTCAAGCCAATG
Parn	GGTCATACTTAAAAGCACAA
Parn	AAGACATATAGTTATCAGCA
Parn	CCAACCTACCCGAATTAGCAA
Stx11	TCGAACACTATGTCCTCCCG
Stx11	AGCCATGTACGAGTACAACC
Stx11	CATGTGCGGGCAGCAGATTG
Stx11	AGCTGCTTCTGATAGACGTG
Rhoh	GGTACTGATGTGCTACTCTG
Rhoh	CCCACGGTGTACGAGAATAC
Rhoh	ACAACCAGCACCGGGGTACA
Rhoh	CAGGGGCCGGATACTTCTGA
Dock8	ACTTCCGGTTTGCGACACCG

Target Gene Symbol	sgRNA.Target.Sequence
Dock8	CCGGAACACGTAGTGACG
Dock8	AGCACGTTTAAGGGATGACG
Dock8	TAGCGAAGTTCAGTCGCTGG
Ercc6l2	CTGTTACAGACCAACTCACG
Ercc6l2	CGTACCAAGACTCTTATCAA
Ercc6l2	GGTACTTGCGAGATTACCAA
Ercc6l2	AAGGATGAATTGGATACCTG
Dnajc21	TAGGTACGATAACCACCGAG
Dnajc21	CTCCCAGAGCGACTATGACA
Dnajc21	TAAACGAGATAAGAGAGTGC
Dnajc21	TGGATCAGATGAAAACGAAG
Lrba	GACCGTCCAATGAACTCAG
Lrba	GTGTGGCGAGTGGACGAAGA
Lrba	ATAGTTACCATGTACCACTG
Lrba	CAGATGCAGTAGACCAACAA
Lamtor2	GTTCCCGTTCCTATCATACG
Lamtor2	GCTGGCCTACTCCGTTATG
Lamtor2	CCACCCTCGTAATGGCTACA
Lamtor2	CACAGATGCCCGGGTCACTG
Smarcd2	GAGATAATGCGGGAAGTGG
Smarcd2	GCATCGGATGCCACACAC
Smarcd2	CCCAACACACTCACTCGCTG
Smarcd2	CGGAGCAGCTGTGCCAAATG
C230052I12Rik	CTAGCCACAATATGTCCTAG
C230052I12Rik	TGAGGCAGGATGCTTCCGAC
C230052I12Rik	CAGTAACTTCTGGACTGCT
C230052I12Rik	TATGATCCCTGAAGATGTG
Usb1	ACACGGTATGTAGATGTGGG
Usb1	TCCTCGATCCTACCAACGG
Usb1	GGTACAAACATCTGAGCTCG
Usb1	GACGACAGTGCAAAGCATGG
Traf3ip2	GTCCTGCAGGTAACACGAGG
Traf3ip2	GTAGTACTGACAGTTCCATG
Traf3ip2	CCTGCGAGCTAAAGTCCTGG
Traf3ip2	CCAAAGCATTAGGTAACTT
Ticam1	AAGATGCCATCGATCACTCG
Ticam1	TCTGGAACGCTAATTTCTGTG
Ticam1	GATATCAAGGGGGACCCAG
Ticam1	CTTACACCATGGAACCCAT
Fermt3	GGAGGTGCATGACCTGACAA
Fermt3	CTGTCACACTCCGAGTCACG
Fermt3	GGGCTACCGCCAGTACTGGG
Fermt3	CTCACCACATCCCCGCTCA
Mthfd1	ACACCAACGATAGATTCTG
Mthfd1	CACTATGAATCCGTGCACAG

Target Gene Symbol	sgRNA.Target.Sequence
Mthfd1	GATTGCCGGAAGGCACGCGG
Mthfd1	GGTAGCGTCCAGTAAGAAAG
Obfc1	GACGCAGTTTATAACCCCAG
Obfc1	CAACGGGCATCCAATAAGGC
Obfc1	GGAGATATCATCCGAGTCCG
Obfc1	TCGCAGTGCTCAGAATAGCT
Card11	GCAGCATAACTGTGTTTCATG
Card11	ACTATGGAGTCATTTCCCGG
Card11	CACACACTTCTGATGAACG
Card11	GCGACCTCCAACCTCGAGGTG
Sp110	AAATGACCTGGAAATGGCCA
Sp110	GGTCAAATTCCAAAAGAAGA
Sp110	TCCTGAATGCAGCCAAGGAG
Sp110	AGCTCAAGGCAGTGAGCAGG
Orai1	GATCGGCCAGAGTTACTCCG
Orai1	TGGCGATGCATGCGCTCGTG
Orai1	AAGACGATGAGCAACCCTGG
Orai1	AATCCGGAGCTTCCCGTGAG
Pgm3	TACGGCCTCACATAACCCTG
Pgm3	AACTTCTCAAGGTACCGCG
Pgm3	TACACCATGTAGTGCAACTG
Pgm3	CTGCTATGACATACCCTGTG
C7	CATACTGATCGATTAACCGT
C7	ATCAACACCAAAGTTTCGG
C7	CAATCCTGCAAACCTGAACG
C7	GTGTCTCCACAACAATAGCG
C8b	AAAGACGCCATGGAGCAAGG
C8b	ATTGTGTGACTTGTCCGACA
C8b	TTGACTGTGAGCTATCCACC
C8b	CAAGGACAGAGCGCGCTGG
Cebpe	CAGTACCAAGTGGCACACTG
Cebpe	GCAGGTAGTGAGGAAACGAG
Cebpe	CAGACTCGATGTAGCGGAG
Cebpe	CTTACCTTGAGGACACGCAA
Tirap	CTGTCTGTGAACCATCATAG
Tirap	CGAAACAATGGCGCCACCCG
Tirap	TGCAGCTCGAGGTTGAGCTA
Tirap	CAAGTAGGAGACCAGCTCCT
Dclre1b	TGCTAGACAAACCCACCGTG
Dclre1b	TCCACTGAAGCATGGCAGAG
Dclre1b	AGAGAAACATGACAGAACCA
Dclre1b	TGAATGGTCAGAGTACGGGA
Tlr3	CTTAGATGAAATCCCAGTCG
Tlr3	GTTGTAGGAAAGATCGAGCT
Tlr3	GAATGGTCAAGTTACGAAGA

Target Gene Symbol	sgRNA.Target.Sequence
Tlr3	ATCTACAAAGTTGGGAACGG
Card14	CCACAGCCGCATGAAACGTG
Card14	TGTTCTACCTTAGAGACTCG
Card14	CACTCTGGAGAATACAACGC
Card14	AGAACTAAATCGGCTTAAGG
Rfxap	TCCAAGACCTGCACGTACGA
Rfxap	GCACCGCAACAAGATGTACA
Rfxap	CTGGACACATCGGACCCGGC
Rfxap	GTCACCGGAGGGGCCGTCCG
Il17rc	CTGTGGAACGATGACAACAT
Il17rc	AGCAATACTTACCCCAGAGG
Il17rc	GGAGCCACAAGATTTCCAGT
Il17rc	ATCTAGCTGCCATACCCCTG
Wipf1	GGAACAGAATGCCTCCCCCG
Wipf1	CCGTCGAGTCTGCACAACCG
Wipf1	GGGGCTTGTCATCCAAGGCT
Wipf1	GCTGAGGTCCACCGCCAACA
Wrap53	GGTCATTACCACTTACTAGG
Wrap53	AGAAACGAATCTCCCCGAGT
Wrap53	GAAGAGTTGGGAACCATCCG
Wrap53	GACACAACCAAGCTAGCCAC
Tmc6	GGAGTCATGTCGCTCCAGAG
Tmc6	TTTCCAAGGTCGCAGCCGTG
Tmc6	GACCAGAAAACGTAGGCACG
Tmc6	TACCGGGTTGGCAGTACCAA
Tmc8	GGAGCTCTCTACGAGATTGG
Tmc8	CAACGCTTGCGACTACCAGG
Tmc8	CTTCTACGGTGCCTACCGAG
Tmc8	CATCCGCACAGGCGTCCGGG
Ttc37	ACAAACAGATCACTTCTAGT
Ttc37	CGCCTGTGTTTCAGACAGGCG
Ttc37	TGACGTGTGTAAGAAACTCG
Ttc37	GAGGCGTACTTAAGCAGAGG
Mkl1	AGACAGTTCCTCCTTCGACG
Mkl1	GTGATGAGAATTCCACACCT
Mkl1	CTGCCCCCAAGCCTAGCCAA
Mkl1	GTCAGGATGCACATTCTGGA
Ttc7	TGGGATCGATGACATATCCG
Ttc7	TCCAAGACCAATTACTACCG
Ttc7	GCAACACACCTGTCGGACGA
Ttc7	CTGCCCCAAAGACAACATAG
Dclre1c	TTTATTCACCAACCTAAGCG
Dclre1c	CAGGGAAACATACACGACTT
Dclre1c	GCATCAAGCCATCTACCATG
Dclre1c	TCAACTAAAGATATCTGCGT

Target Gene Symbol	sgRNA.Target.Sequence
Slc35c1	AGGGCACCCCTACGTA CTTG
Slc35c1	AGGTTAGGCGCCAGATACTG
Slc35c1	CTCACCAATGATGACGCCG
Slc35c1	GCAGTGAGGTCACCAGGCAT
C8a	TCCTGCTATAGGTA CTACTG
C8a	GGAGATTGAAGTATCCGCCA
C8a	CATTGTACACAGTTTCACAC
C8a	CTTGCCTTAGACAAGGTGTG
Rltpr	GCCTGACTTACCATGAAGGG
Rltpr	CAACCAAGTAGACTCTACTT
Rltpr	AGACCACCCTGGATAACCACA
Rltpr	ACATGCGCCTGTCAATCACT
Malt1	GTCCTATGCCTCACTACCAG
Malt1	ATATGAGATGTGTAACGCTG
Malt1	CCACTGGCTAAATTCAAAAG
Malt1	AGCTTGGACCGCGCTCCGGA
Dkc1	TTTACTGCAGCAATAAGTGG
Dkc1	TCTCTACCCGAAGTATTCGT
Dkc1	TACGCATAGTGTCCGAATGT
Dkc1	ATGATGTA CTGATGCTCAG
Ap1s3	CCACACTCCCTGACAAGGAG
Ap1s3	TCCAGACCGTCCTCTCTCGT
Ap1s3	TCAGTCGACAAGGGAAGCTG
Ap1s3	TAATATCCAGCTCACAGACC
Il17f	GACTTACTTGTAAATCCCATG
Il17f	TGGGAACTGTCTCCCCTGG
Il17f	AGCGTTCTGGAATTCACGT
Il17f	GGGCCTCAGCGATCTCTGAG
Nod2	CCGACCCATCGTAAGTACTG
Nod2	AGATGCCGACACCATACTGG
Nod2	GCAGAGTCTGGACTGACGTG
Nod2	GTTGTAGAGTCTCCTCACAA
Irak4	GTAGCTATCAAAAAGCCGTC
Irak4	CTGTGTGAACAACACCATCG
Irak4	TGTAAGCATACACTAAGCAC
Irak4	CAAGGTGCAAGGTTGCTCAG
Zbtb24	GGAAATCGAAGTTACCCGTG
Zbtb24	TGAGAAATACTCGCTACTGG
Zbtb24	ACACGTCCATAAACTTTCCGG
Zbtb24	GATCCTCTGAAACGGAAACG
Rnf31	GATGGATTGAGTTTCCCCGA
Rnf31	GAACATGAGTTGTTGGACG
Rnf31	CTACCTCAACACCCTATCCA
Rnf31	GGAGGAACCAAGGTGTTGTG
Rtel1	ACACGGGGATCCATGCGTGG

Target Gene Symbol	sgRNA.Target.Sequence
Rtel1	TATGCCGACATACCGGTAGG
Rtel1	GTTGTCATACACCTTAAGGT
Rtel1	GAGGCGTCACCAAACCTGGA
Irf2bp2	CGCACGCGTGCTGAAGTCGG
Irf2bp2	GCGGCAGAACCGTTGACCAG
Irf2bp2	TCTCGATGACGAACTCCACG
Irf2bp2	GGCCGACAGCTTATCCAGCG
Gimap5	GTCACCAGTAACAACACATG
Gimap5	AGCTAGATTCTTGTACACAG
Gimap5	ACTGGAATGCTGGTCGTCGG
Gimap5	CTGAAGATGCCATGGCTGTG
Lig4	TTAGACGTCCTAATTGTGGG
Lig4	GCAACTCAACTGCATCATTG
Lig4	GAACGCATTGTGAATAAATG
Lig4	CATCCGTGCGAGCTCCACTG
Chd7	GACATGCCATAAACGAACG
Chd7	AAACGGTTTAAGTCAAAACA
Chd7	CCTACCGAATGATTTAGCA
Chd7	TCGATGACCACACAGCGCCA
Ccbe1	GACCTACCGAGAGGAACCCG
Ccbe1	CAGCAGTGACGGATAACTT
Ccbe1	ACAGAGAGTGGTATTGCTGG
Ccbe1	GAACTGGGCAAGTATGTCAA
Fat4	GACATCGTGGACGATCGAGG
Fat4	CAGTTATCTCATCACTACCG
Fat4	GGGATGTCGAAAGAGTACAC
Fat4	ATTAGATCCTATGTCCGCGT
Card9	GATGTACAAGGACCGTATCG
Card9	GTGACTTTCCGGTATAACTG
Card9	TAGATAGGGTGTGATCCGGG
Card9	CCAACCTGGTCATCCGCAAG
Plekhm1	TGACTTGTAGGAGAGTTCGA
Plekhm1	TGATGAGGAACGCACCTGTG
Plekhm1	GCTGGTAGCTAGGCTATGGA
Plekhm1	ACTCACCGGACTCGTAGGAG
Kmt2d	AAATGGCTGTTGATCCCATG
Kmt2d	GTTACACATTAATACCCCA
Kmt2d	TCGGGCCGGACTAACATCCG
Kmt2d	TGGGGATGGACAGCCCGACG
Otulin	GGAACTTCACAGCTTCGTAG
Otulin	TGATAACTACTGTGCACTGA
Otulin	AACAGAACCCAGGTTAAGTG
Otulin	AGTATACCTGGATCAAGCAG
Cfhr2	TTGTCCCCTTAGACTCAACA
Cfhr2	GAATGGAGACTCTACATACT

Target Gene Symbol	sgRNA.Target.Sequence
Cfhr2	ACTTATTTCTATAGACT
Cfhr2	ATACCATTTAGAATATAAGG
Nlrp1b	CTAAATGACCTGTGTGACGA
Nlrp1b	AGATGCTAAAGAGCACCCCTA
Nlrp1b	AGAAGATCATTCTTATGTG
Nlrp1b	CTGTAAGCAAGGGTTAGCAG
Vps13b	TGTCCATACTACCCAAATCG
Vps13b	TAAACACTGCAATACAAGCG
Vps13b	GAAACCTCTCCCGATACAG
Vps13b	TGGCAGTAGTCCATGACTG
Isg15	GTCCGTGACTAACTCCATGA
Isg15	CAGCAGCACAGTGATGCTAG
Isg15	GCATCCTGGTGAGGAACGAA
Isg15	TGGAAAGGGTAAGACCGTCC
Epg5	ACAGCCGACTCGTTGTAACA
Epg5	TCGAGCCAGAAGAACCAATG
Epg5	TGGGTACCATACCCATATTG
Epg5	GAAACGCTGTCTTACACAAG
C1ra	TTTGCCAGAATGATGGCACA
C1ra	TGTGCAGGTATATATCCCTG
C1ra	CCACACAGACTTCTCCAATG
C1ra	TGGTTGTCTCCAAGTCACTG
C1s2	AATTCCTCATGTCATCATGG
C1s2	TTCTCTTAGATAATCTCAGG
C1s2	TCTTTCAAAGTATCTAATG
C1s2	AACACACAGTTAACTGTCA
C4b	GCACAAGATGCCTCTTAGTG
C4b	CAGGCACAGCCCCTCAACTG
C4b	GTAAGCCACAAAGTAGAACG
C4b	TGAAACAAAGGACCATGCTG
Cd59b	TATTATGAGCCGATTAGACG
Cd59b	ATGCTACAAGTGTGTTAGACC
Cd59b	GGCAAGTGTATCAACAGTGT
Cd59b	TTGATACACTTGCCTTCCTG
Lat	ACTCACGAGGTGGCTTGATG
Lat	GCATCCGATGGGAACCCCA
Lat	ATACTCACGGGATGGGGAGC
Lat	CTCTGTGGAAGTGCTGTCAT
Nhej1	CCCTATGCATAGAGCTCGGC
Nhej1	ACCAGCCGAGCTCTATGCAT
Nhej1	GGCTGGTTATCAGTTCCTCG
Nhej1	TCACCAACAGCACACGCCTC
Dock2	AAGAAGTGACAACCACGCTC
Dock2	CAGCATCTCACGCTACAGAT
Dock2	GTGACAGTTTATGCTTTATG

Gecko Library v2

Target Gene Symbol	sgRNA.Target.Sequence
Dock2	TACATCCTTTATCCATCTCA
Mysm1	ATCACTATCTTGATTCAACG
Mysm1	AAAATTCTGGGTTAATCAAA
Mysm1	TATCATTGAGAAAATGCTGT
Mysm1	TTATCTAATAAATCACTTCC
Kdm6a	TTGGATAATCTTCCAATAAG
Kdm6a	TAGCATTATCTGCATACCAG
Kdm6a	GAAACCTCACGAACCCGAAA
Kdm6a	CGCCAGGATGAAGGCCCTGC
Tpp2	CACACCAAGCAGTCATATAC
Tpp2	ATTGATATCATTGATACAAC
Tpp2	ATAGGCCAATAAACTAATCA
Tpp2	TGGTTATGACTTCTATCCAA
Il12b	CCTGCCCATTGAACTGGCGT
Il12b	CCATGAGCACGTGAACCGTC
Il12b	CATGTCACTGCCCAGAGATC
Il12b	GACTGGACTCCCGATGCCCC
Stat2	TGAGATTGAAAATCGAATCC
Stat2	TCCACAACCTGCTTCGGGGGC
Stat2	CTGAGCTGTAGTGGTCCCAC
Stat2	AGTTCTTGGTGAGATCCATC
C3	GATGACGACTGTCTTGCCCA
C3	ACAAAGGCAAGATGCCGTGT
C3	GAGCGAAGAGACCATCGTAC
C3	GACAGTCGTCATCCTCATTG
C6	TAGTAGTGAACGATTACTAT
C6	CGATAAGCTTTGTATCAAGC
C6	TGAAACACGGTATGGATTAC
C6	GGTTGCCCCCAAACCTGACT
Cfb	TTCGAGTCTGCACGGGGTAT
Cfb	AATACGCTGCCACGACCGC
Cfb	GCTGGATACTGTCCCAATCC
Cfb	AGCCACGCAGGACAAGTCCC
BRDN0000737505	AAAAAGTCCGCGATTACGTC
BRDN0000737693	AAAACGGCTCGATCGGTGAT
BRDN0000737637	AAAACGTAATTATACCGAGC
BRDN0000738185	AAAATTGCACCTTCCCGGCC
BRDN0000737801	AAACCCCGCGCGGAGCGTC
BRDN0000737467	AAACCTAGCGTAGATTCCGGC
BRDN0000737848	AAACGAGGCTGTTTCGTACAC
BRDN0000737609	AAACTCATACGTAGCGAATC
BRDN0000737434	AAACTCCCGTGTCAACCGAT
BRDN0000738254	AAAGACGTGCATTACGCGAG
BRDN0000737777	AACATGTTAAGTCGCGTTAT
BRDN0000737611	AACCAGCATTTGACCGCGCT

NTCs

Target Gene Symbol	sgRNA.Target.Sequence
BRDN0000737528	AACCCCGGCTGTCATCGCCG
BRDN0000738228	AACCCGCCGGAACAATCAGC
BRDN0000737727	AACCGGCTGCGCGTTTGCAA
BRDN0000737483	AACCGTACTGCGAGGAGCAT
BRDN0000737872	AACCTCGTCTCATGTACGAA
BRDN0000737516	AACGCCCCGGATTTGTTGA
BRDN0000737844	AACGGCTGCGCCCGCGGCAA
BRDN0000737412	AACGGGCGCAATACCCTTTT
BRDN0000737631	AACGGTAGCGTACCCGTGAA
BRDN0000737750	AACGGTCAAATCCGTGAGGG
BRDN0000737875	AACGTCACCAACCTCGATCC
BRDN0000738229	AACGTTATAGCTTCGTCTCT
BRDN0000737806	AACTAACTCACTACGCACGA
BRDN0000738366	AACTCCTCATCGTACGCTAA
BRDN0000737593	AACTCGCGTGGGAAGTCCGG
BRDN0000738128	AACTTATACGTAATCTGATC
BRDN0000738307	AAGACTCCTACGTATCGAGC
BRDN0000737391	AAGCACAAGAACGGTCCGCC

No.	Target Gene	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
Example row, don't delete	Target Gene Symbol	example 1	AATATTTAAGGCTGCCTTAACGTGATCCCACTTGCTGAATTTTACCTCCTGACTCCA	###		GGAAGGACGAAACACCG		GTTTAGAGCTAGAATAGCAAGTTAAAAATAAG
1	Acp5	Acp5_1	GGAAGGACGAAACACCGATACCAGGGGATGTTGCGAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ATACCAGGGGATGTTGCGAA	
2	Acp5	Acp5_2	GGAAGGACGAAACACCGTCCACGTACAACATAACTGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TCCACGTACAACATAACTG	
3	Acp5	Acp5_3	GGAAGGACGAAACACCGTACCTGGAACCTCTGTGCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TACCTGGAACCTCTGTGCG	
4	Acp5	Acp5_4	GGAAGGACGAAACACCGACAGCCACAATCTCAGGGTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ACAGCCACAATCTCAGGGT	
5	Actb	Actb_5	GGAAGGACGAAACACCGAATGCCTGTGGTACGACCAGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			AATGCCTGTGGTACGACCAG	
6	Actb	Actb_6	GGAAGGACGAAACACCGATGCAGGGGAAATACAGCCCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ATGGAGGGAAATACAGCCCG	
7	Actb	Actb_7	GGAAGGACGAAACACCGGACTCCTATGTGGTGCAGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GGACTCCTATGTGGGTGACG	
8	Actb	Actb_8	GGAAGGACGAAACACCGCAGCACAGGGTCTCCTCAGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CAGCACAGGGTCTCCTCAG	
9	Ada	Ada_9	GGAAGGACGAAACACCGGTTGTGGATCTGTGAACCAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GTTGTGGATCTTGTGAACCA	
10	Ada	Ada_10	GGAAGGACGAAACACCGATTTCATCGACCGTCCACCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ATTCATCGGACCGTCCACGC	
11	Ada	Ada_11	GGAAGGACGAAACACCGCTTCATCTCCACAACCTCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CTTCATCTCCACAACCTCGT	
12	Ada	Ada_12	GGAAGGACGAAACACCGGCTGCGCAACATTATCGGCAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GCTGCGCAACATTATCGGCA	
13	Adam17	Adam17_13	GGAAGGACGAAACACCGGTTGTGGCAACTCCAGGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GGTGTGTGGCAACTCCAGGG	
14	Adam17	Adam17_14	GGAAGGACGAAACACCGCTGGGATGATGCAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ACACGCTGTGGGTAATGCA	
15	Adam17	Adam17_15	GGAAGGACGAAACACCGCATCGAGCTACGGCACACGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CATCGAGCTACGGCACACAC	
16	Adam17	Adam17_16	GGAAGGACGAAACACCGCCCAAAATGAGGACCAAGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GCCCAAAATGAGGACCAAGG	
17	Cfd	Cfd_17	GGAAGGACGAAACACCGTCTCACGTGGGACCAACCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TCTCACGTGGGACCAACCG	
18	Cfd	Cfd_18	GGAAGGACGAAACACCGCCCGGCGGATTCTGGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CCCGGAGGCGGATTCTGGG	
19	Cfd	Cfd_19	GGAAGGACGAAACACCGTTGACACTCTGAGTTGATGCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TTGACTCTGAGTTGATGCG	
20	Cfd	Cfd_20	GGAAGGACGAAACACCGCCCTGAACCTACAAGCGAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CCCTGAACCTACAAGCGA	
21	Aicda	Aicda_21	GGAAGGACGAAACACCGTAGGAACAACAATCCACGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GTAGGAACAACAATCCACG	
22	Aicda	Aicda_22	GGAAGGACGAAACACCGTTCACAGAAGTAGAGGCGCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TTACAGAAGTAGAGGCGCG	
23	Aicda	Aicda_23	GGAAGGACGAAACACCGACAGGTGACCGGTTAACACGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ACCAGGTGACCGGTTAACAC	
24	Aicda	Aicda_24	GGAAGGACGAAACACCGTGAGACCTACCTCTGCTACGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGAGACTACCTCTGCTACG	
25	Aire	Aire_25	GGAAGGACGAAACACCGTGTGCCGTGTGCCACGACGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGTGCCGTGTGCCACGACGG	
26	Aire	Aire_26	GGAAGGACGAAACACCGTCTCCAGGAATTGACACCAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CTCTCCAGGAATTCAGACCA	
27	Aire	Aire_27	GGAAGGACGAAACACCGACAGAACTGTCCAGCGTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ACAGAACCTGTCCCGACTG	
28	Aire	Aire_28	GGAAGGACGAAACACCGGTAGAGATGAGCAGAAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GGTAGAGATGAGCAGAAAGT	
29	Ak2	Ak2_29	GGAAGGACGAAACACCGTGAAGCGCAATGATGCAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGAAGCGCAATGGATGCA	
30	Ak2	Ak2_30	GGAAGGACGAAACACCGTAGGACCGGCACTTTGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GGTAGGACCGGCACTTTG	
31	Ak2	Ak2_31	GGAAGGACGAAACACCGTCCGAACCGGAGATTCCGAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TCCGAACCGGAGATCCGAA	
32	Ak2	Ak2_32	GGAAGGACGAAACACCGTACGACGTTTTGGGTGCTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TCAGCAGTTTTGGTGCCTG	
33	Ap3b1	Ap3b1_33	GGAAGGACGAAACACCGTGTGCCAGTAAAAACATCGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGTGCCAGTAAAAACATCG	
34	Ap3b1	Ap3b1_34	GGAAGGACGAAACACCGGCTGCCTAATAAATCGTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GCTGCCTAATAAATCGTGTG	
35	Ap3b1	Ap3b1_35	GGAAGGACGAAACACCGATGCTAACAAGATACGCTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ATATGCTAACAAGATACGCT	
36	Ap3b1	Ap3b1_36	GGAAGGACGAAACACCGTTGGCAGTCTCACCAGTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TTGGCAGTCTCACCAGT	
37	Ap3d1	Ap3d1_37	GGAAGGACGAAACACCGCAACGCAATGATCTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CCAACGCAATGGATCTGTG	
38	Ap3d1	Ap3d1_38	GGAAGGACGAAACACCGAGCAGTACCAACTTCGAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			AGCAGTACCAACTTCGAG	
39	Ap3d1	Ap3d1_39	GGAAGGACGAAACACCGTCTTACAGTAAAGTACCTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TCTTACAGTAAAGTACCTG	
40	Ap3d1	Ap3d1_40	GGAAGGACGAAACACCGTGTCTCATCGCTCTCCGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGTCTCATCGCTCTCCGTG	
41	Xiap	Xiap_41	GGAAGGACGAAACACCGTTTCAGACCAATATACCGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TTTCAGACCAATATACCGG	
42	Xiap	Xiap_42	GGAAGGACGAAACACCGAGCAGTAACTCTCGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			AGCACTAGTAACTCTCGG	
43	Xiap	Xiap_43	GGAAGGACGAAACACCGCTTGGAAACAGCATGCGAAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CTTGGAAACAGCATGCGAAG	
44	Xiap	Xiap_44	GGAAGGACGAAACACCGATGGACATCCTCAGTTAACAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			ATGGACATCCTCAGTTAAC	
45	Arpc1b	Arpc1b_45	GGAAGGACGAAACACCGCACAAATGCGGTTACTCTCAGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CACAATGCGTTACTCTCAG	
46	Arpc1b	Arpc1b_46	GGAAGGACGAAACACCGCAATGAGAACAAGTTCGCGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CAATGAGAACAAGTTCGCGG	
47	Arpc1b	Arpc1b_47	GGAAGGACGAAACACCGTCCAGGCTGAGCACTGGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			CCAGTCCAGGCTGAGCACTG	
48	Arpc1b	Arpc1b_48	GGAAGGACGAAACACCGGAGCGAGCACTCACGTGTAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			GAAGCGAGCACTCACGTGTA	
49	Rab27a	Rab27a_49	GGAAGGACGAAACACCGTGGTTAAGTACGAAACCTAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			TGTTAAGTACGAAACCTA	
50	Rab27a	Rab27a_50	GGAAGGACGAAACACCGAGTGTACTGGTAGAGTACAGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			AGTGTACTGGTAGAGTACAC	
51	Rab27a	Rab27a_51	GGAAGGACGAAACACCGAACCCAGATATAGTGTGTGTTTTAGAGCTAGAATAGCAAGTTAAAAATAAG	73			AACCCAGATATAGTGTGTG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
52	Rab27a	Rab27a_52	GGAAAGGACGAAACACCCGCTGAAATCAATGCCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTGAAATCAATGCCCACTG	
53	Atm	Atm_53	GGAAAGGACGAAACACCCGTAAGTCATATAGGAAGCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TAAGTCATATAGGAAGCCGA	
54	Atm	Atm_54	GGAAAGGACGAAACACCCGAGTATAAATAACATCCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGTATAAATAACATCCGCGA	
55	Atm	Atm_55	GGAAAGGACGAAACACCCGAAAGCTTGAACACCCGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAGACTTGAACACCCGGACAA	
56	Atm	Atm_56	GGAAAGGACGAAACACCCGTGCAAGATACACATGAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCAAGATACACATGAATCG	
57	B2m	B2m_57	GGAAAGGACGAAACACCCGATTTGGATTTCAATGTGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATTTGGATTTCAATGTGAGG	
58	B2m	B2m_58	GGAAAGGACGAAACACCCGACTCACTCTGGATAGCATACTTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTCACTCTGGATAGCATACT	
59	B2m	B2m_59	GGAAAGGACGAAACACCCGTGAGTATACTTGAATTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGAGTATACTTGAATTTGAG	
60	B2m	B2m_60	GGAAAGGACGAAACACCCGCTCGGCTTCCATCTCCGGTGTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGGCTTCCATCTCCGGT	
61	Bach2	Bach2_61	GGAAAGGACGAAACACCCGTGGACAGACGAAAGATGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGACAGACGAAAGATGACT	
62	Bach2	Bach2_62	GGAAAGGACGAAACACCCGATTTACGGACAGCCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AATTACGGACAGCCCACTG	
63	Bach2	Bach2_63	GGAAAGGACGAAACACCCGCTCCTCGTATTCCTACGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTCCTCGTATTCCTACGCA	
64	Bach2	Bach2_64	GGAAAGGACGAAACACCCGTCTGTTCCGTTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTCTGTTCCGTTAACAAG	
65	Bcl10	Bcl10_65	GGAAAGGACGAAACACCCGCTCCGGTGGTACATGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTCCGGTGGTACATGACAG	
66	Bcl10	Bcl10_66	GGAAAGGACGAAACACCCGATTCAGAAGATAACCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATTAGAAGATAACCGATG	
67	Bcl10	Bcl10_67	GGAAAGGACGAAACACCCGATAAACTGGAGCACCTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATAAACTGGAGCACCTCAA	
68	Bcl10	Bcl10_68	GGAAAGGACGAAACACCCGCTGGTGAATCCATCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTGGTGAATCCATCCGCA	
69	Blm	Blm_69	GGAAAGGACGAAACACCCGTACCTGGAACATTTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTACCTGGAACATTTCAACG	
70	Blm	Blm_70	GGAAAGGACGAAACACCCGGTGGGTAACATTTCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTGGGTAACATTTCTCAG	
71	Blm	Blm_71	GGAAAGGACGAAACACCCGCTGCAAGTGGATTTAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTGCAAGTGGATTTAACGA	
72	Blm	Blm_72	GGAAAGGACGAAACACCCGCTTACCGACTACACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTTACCGACTTACACCTG	
73	Btk	Btk_73	GGAAAGGACGAAACACCCGATCCGGTACAATAGTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AATCCGGTACAATAGTGACC	
74	Btk	Btk_74	GGAAAGGACGAAACACCCGTATGAATATGACTTTGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATGAATATGACTTTGAACG	
75	Btk	Btk_75	GGAAAGGACGAAACACCCGTGGAGGAGACCACTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGAGGAGAGCAACCTACCG	
76	Btk	Btk_76	GGAAAGGACGAAACACCCGAGATTTAGCAACACAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGATTTAGCAACACAGACA	
77	Serping1	Serping1_77	GGAAAGGACGAAACACCCGCTCTGAGATGCATTCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCTCTGAGATGCATTCACAT	
78	Serping1	Serping1_78	GGAAAGGACGAAACACCCGACAATAACAAATGACACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACAATAACAAATGACACCAT	
79	Serping1	Serping1_79	GGAAAGGACGAAACACCCGAGAATCATCAACACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAATCATCAACACCTGGG	
80	Serping1	Serping1_80	GGAAAGGACGAAACACCCGGACAGGCAAAATCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGACACAGGCAAAATCCTTG	
81	C1qa	C1qa_81	GGAAAGGACGAAACACCCGACAGATGAAGCGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CACAGATGAAGCGACCCGTG	
82	C1qa	C1qa_82	GGAAAGGACGAAACACCCGCCAATGACGCTTGGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCCAATGACGCTTGGCAACG	
83	C1qa	C1qa_83	GGAAAGGACGAAACACCCGTTGAGCCTACTCCATACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGAGCCTACTCCATACTA	
84	C1qa	C1qa_84	GGAAAGGACGAAACACCCGAGCAATCCAGGCAATATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGGCAATCCAGGCAATATCA	
85	C1qb	C1qb_85	GGAAAGGACGAAACACCCGAGCCTCCAGGGATAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGGCACTCCAGGGATAAAGG	
86	C1qb	C1qb_86	GGAAAGGACGAAACACCCGTGACCTGGTTCGGTCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGACCTGGTTCGGTCGAAG	
87	C1qb	C1qb_87	GGAAAGGACGAAACACCCGATTCGCCTTTGGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAATCGCCTTTGGACCCGG	
88	C1qb	C1qb_88	GGAAAGGACGAAACACCCGAGTGAATTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGGTGAATTCGCGTTGCG	
89	C1qc	C1qc_89	GGAAAGGACGAAACACCCGGTGAATGACTGTGAATACGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGGTGACTGTGAATTCGAC	
90	C1qc	C1qc_90	GGAAAGGACGAAACACCCGTGTGGTCCCAACCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGTGGTCCCAACCTCAG	
91	C1qc	C1qc_91	GGAAAGGACGAAACACCCGATCATGCCCGCTCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATCATGCCCGCTCTCCAG	
92	C1qc	C1qc_92	GGAAAGGACGAAACACCCGCTCCCGGAGGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCTCCCGGAGGCCCTCG	
93	C2	C2_93	GGAAAGGACGAAACACCCGTTCTAGGAAAGTCCAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTCTAGGAAAGTCCAACAT	
94	C2	C2_94	GGAAAGGACGAAACACCCGTGTGATGTGAGCTAGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGTGATGTGAGCTAGACCT	
95	C2	C2_95	GGAAAGGACGAAACACCCGAGTCAATACCATAATTTGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGTCAATACCATAATTTGAGG	
96	C2	C2_96	GGAAAGGACGAAACACCCGTTGGGGCAGTACCGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGGGGCAGTACCGCAC	
97	Ciita	Ciita_97	GGAAAGGACGAAACACCCGAGCTCAGTAAGGCTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGCTCAGTAAGGCTCCGGG	
98	Ciita	Ciita_98	GGAAAGGACGAAACACCCGAGTCTTGATTATATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGGTCTTGATTATATCGTG	
99	Ciita	Ciita_99	GGAAAGGACGAAACACCCGTCCAGTGTCTAATCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCCAGTGTCTAATCTACCA	
100	Ciita	Ciita_100	GGAAAGGACGAAACACCCGAGCAGGCCAAGACTTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGCAGGCCAAGACTTACATG	
101	C9	C9_101	GGAAAGGACGAAACACCCGCTACAACGACTCTGTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTACAACGACTCTGTGACC	
102	C9	C9_102	GGAAAGGACGAAACACCCGTTCCCATTAACCTGTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTTCCCATTAACCTGTCCGA	
103	C9	C9_103	GGAAAGGACGAAACACCCGATCTGCAGTCTATCCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATCTGCAGTCTATCCGAT	
104	C9	C9_104	GGAAAGGACGAAACACCCGTTGAGAGGAGTGGTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGAGAGGAGTGGTCCAAGT	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
105	Hyou1	Hyou1_105	GGAAAGGACGAAACACCCGACAGCGGATAACCCCTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGGCGGATAACCCCTCATG	
106	Hyou1	Hyou1_106	GGAAAGGACGAAACACCCGACATCGTACTCACTTGCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACATCGTACTCACTTGCCCA	
107	Hyou1	Hyou1_107	GGAAAGGACGAAACACCCGTGGAATTGATATCTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGAATTGATATCTTCCGG	
108	Hyou1	Hyou1_108	GGAAAGGACGAAACACCCGTGGCGTGCTCAGTTTACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGCGTGTCTCAGTTTAGACA	
109	Casp8	Casp8_109	GGAAAGGACGAAACACCCGATTATGAAAGATCAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATTATGAAAGATCAAGCAC	
110	Casp8	Casp8_110	GGAAAGGACGAAACACCCGCTTCTAGACTGCAACCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTTCTAGACTGCAACCCGAG	
111	Casp8	Casp8_111	GGAAAGGACGAAACACCCGATGATCAGACAGTATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATGATCAGACAGTATCCCGG	
112	Casp8	Casp8_112	GGAAAGGACGAAACACCCGCAAGAAGCAGGAGACCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAAGAAGCAGGAGACCATCG	
113	Ctla4	Ctla4_113	GGAAAGGACGAAACACCCGTGTGATGGTGAATATTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGTGATGGTGAATTCACA	
114	Ctla4	Ctla4_114	GGAAAGGACGAAACACCCGGACTGAGAGCTGTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGACTGAGAGCTGTGACAC	
115	Ctla4	Ctla4_115	GGAAAGGACGAAACACCCGACAGGTGACCAACCTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGGTGACCAACCTTCAG	
116	Ctla4	Ctla4_116	GGAAAGGACGAAACACCCGTGCCACAAAGTATGGCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCCACAAAGTATGGCGGT	
117	Cd19	Cd19_117	GGAAAGGACGAAACACCCGGAATGACTGACCCGCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAATGACTGACCCGCGCAGG	
118	Cd19	Cd19_118	GGAAAGGACGAAACACCCGAATGTCTCAGACCATATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AATGTCTCAGACCATATGGG	
119	Cd19	Cd19_119	GGAAAGGACGAAACACCCGGCACCTATTATTGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCACCTATTATTGCTCCG	
120	Cd19	Cd19_120	GGAAAGGACGAAACACCCGTTAGCCACACATACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTTAGCCACACATACAGCT	
121	Ms4a1	Ms4a1_121	GGAAAGGACGAAACACCCGTTACACTGCTGTAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTACAGTCTGTGATGATG	
122	Ms4a1	Ms4a1_122	GGAAAGGACGAAACACCCGTACCATACACTCAACAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TACCATACACTCAACAGAT	
123	Ms4a1	Ms4a1_123	GGAAAGGACGAAACACCCGAGTCGTAGATATCAACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGTCGTAGATATCAACATA	
124	Ms4a1	Ms4a1_124	GGAAAGGACGAAACACCCGCCACACAAAGCTTCTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCACACAAAGCTTCTCATG	
125	Cd3d	Cd3d_125	GGAAAGGACGAAACACCCGTTACACAGATATATCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTACACAGATATCCCTCG	
126	Cd3d	Cd3d_126	GGAAAGGACGAAACACCCGTCCATCTAGATGCATGACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCATCTAGATGCATGACGC	
127	Cd3d	Cd3d_127	GGAAAGGACGAAACACCCGAAGAATAAAACACTCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAGAATAAAACACTCAACT	
128	Cd3d	Cd3d_128	GGAAAGGACGAAACACCCGATACAAGTGACCGAATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATACAAGTGACCGAATATG	
129	Cd3e	Cd3e_129	GGAAAGGACGAAACACCCGAGGCGAGTCAACTCTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGGCGAGTCAACTCTACAC	
130	Cd3e	Cd3e_130	GGAAAGGACGAAACACCCGTTCTCGGAAGTCGAGGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTCTCGGAAGTCGAGGACAG	
131	Cd3e	Cd3e_131	GGAAAGGACGAAACACCCGTACTGTACCTGAAAGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TACTGTACCTGAAAGCTCG	
132	Cd3e	Cd3e_132	GGAAAGGACGAAACACCCGTCAGAAGCATGATAAGCACCCTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCAGAAGCATGATAAGCACC	
133	Cd3g	Cd3g_133	GGAAAGGACGAAACACCCGTGACACTGATACGTCGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGACACTGATACGTGCTCG	
134	Cd3g	Cd3g_134	GGAAAGGACGAAACACCCGTTCTGTAATACACTTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTCTGTAATACACTTGACGG	
135	Cd3g	Cd3g_135	GGAAAGGACGAAACACCCGAAGTGCATTAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AACTGCATTGAGCTAAACAT	
136	Cd3g	Cd3g_136	GGAAAGGACGAAACACCCGTACAAGTGGATGGCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTACAAGTGGATGGCAGCCG	
137	Cd247	Cd247_137	GGAAAGGACGAAACACCCGCTCGGATCCAGAGATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCTCGGGATCCAGAGATGGG	
138	Cd247	Cd247_138	GGAAAGGACGAAACACCCGCTCAACTCTAGGGCGAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCTCAATCTAGGGCGAAGAG	
139	Cd247	Cd247_139	GGAAAGGACGAAACACCCGCTCCTGGGAACCGCACGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTCCTGGGAACCGCACGTGG	
140	Cd247	Cd247_140	GGAAAGGACGAAACACCCGATTTGATACGCTTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATTGTATACGCTTCTGG	
141	Cd79a	Cd79a_141	GGAAAGGACGAAACACCCGGAACCTAATATCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAACCTAATATCACATGG	
142	Cd79a	Cd79a_142	GGAAAGGACGAAACACCCGCTCACTCACTCGCACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCTACTCACTGCGCACGCGG	
143	Cd79a	Cd79a_143	GGAAAGGACGAAACACCCGGAAGTAAACAAGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGAAGTAAACAAGAACCACA	
144	Cd79a	Cd79a_144	GGAAAGGACGAAACACCCGAGCGTATGACAAGAAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGGCGTATGACAAGAAGAGG	
145	Cd81	Cd81_145	GGAAAGGACGAAACACCCGCAACCCACAGAGCTACACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAACCACAGAGCTACACCT	
146	Cd81	Cd81_146	GGAAAGGACGAAACACCCGGGCTCTGTAACAAGAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGGCTCTGTAACAAGAGACC	
147	Cd81	Cd81_147	GGAAAGGACGAAACACCCGATCCATCACAGCTTGTGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATCCATCACAGCTTGTCTGAA	
148	Cd81	Cd81_148	GGAAAGGACGAAACACCCGGGCAACAGGATCAACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCAACAGGATCAACAGGC	
149	Cd8a	Cd8a_149	GGAAAGGACGAAACACCCGTGGGTGAGTGCATTATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGGTGAGTGCATTATCTCTG	
150	Cd8a	Cd8a_150	GGAAAGGACGAAACACCCGATCCACAAACAGATAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATCCACAAACAGATAACCTG	
151	Cd8a	Cd8a_151	GGAAAGGACGAAACACCCGTTGGGGTCCGTTTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTGTTGGGGTCCGTTCCGCA	
152	Cd8a	Cd8a_152	GGAAAGGACGAAACACCCGGGACGCGCAACTTGGTCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGACGCGCAACTTGGTCAGA	
153	Cfh	Cfh_153	GGAAAGGACGAAACACCCGATTTACGCATAAATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATTTACGCATAAATCCACCA	
154	Cfh	Cfh_154	GGAAAGGACGAAACACCCGCAAGTGTTCGGTATCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAAGTGTTCGGTATCCAGGG	
155	Cfh	Cfh_155	GGAAAGGACGAAACACCCGAAATGATTACCGTGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAATGATTACCGTGAATG	
156	Cfh	Cfh_156	GGAAAGGACGAAACACCCGATATTTACCACCTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATATTTACCACCTTACCACA	
157	Cfi	Cfi_157	GGAAAGGACGAAACACCCGTTGTGGATTACCTTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTTGTGGATTACCTTACAAA	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
158	Cfi	Cfi_158	GGAAAGGACGAAACACCGTGTATTACACAGGTTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGTTATTACACAGGTTGCCG	
159	Cfi	Cfi_159	GGAAAGGACGAAACACCGAAGGTCGACGACGAGCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AAGGTCGACGACGAGCCACGT	
160	Cfi	Cfi_160	GGAAAGGACGAAACACCGTGCTGCATGTACATTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGCTGCATGTACATTGCCG	
161	Cftr	Cftr_161	GGAAAGGACGAAACACCGGCCGTGTGACTGACATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCCGTGTGACTGACATACGT	
162	Cftr	Cftr_162	GGAAAGGACGAAACACCGTTCTAAGTGAGACCTTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCTAACTGAGACCTTACCG	
163	Cftr	Cftr_163	GGAAAGGACGAAACACCGTGCGCATCATGTTGCTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GTGGCGCATGTTGCTGCCG	
164	Cftr	Cftr_164	GGAAAGGACGAAACACCGTATGGAGAGTAAATATCGTGTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TATGGAGAGTAAATATCGT	
165	Coro1a	Coro1a_165	GGAAAGGACGAAACACCGTGACACGAACCTCGTTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGACACGAACCTCGTTGTC	
166	Coro1a	Coro1a_166	GGAAAGGACGAAACACCGACCGGATGTCTAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ACCAGGCGATGTCTAGCACA	
167	Coro1a	Coro1a_167	GGAAAGGACGAAACACCGAGAAGGGAAGATTCTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGAAGGGAAGATTCTAACCA	
168	Coro1a	Coro1a_168	GGAAAGGACGAAACACCGGCCACAGAGGTAGACAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCCACAGAGGTAGACAATGT	
169	Tpp1	Tpp1_169	GGAAAGGACGAAACACCGTGAGTTTTCATCGCTATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGAGTTTTCATCGCTATGTAG	
170	Tpp1	Tpp1_170	GGAAAGGACGAAACACCGTTATGGTAGAAGGTTACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TTATGGTAGAAGGTTACCTG	
171	Tpp1	Tpp1_171	GGAAAGGACGAAACACCGAACCTGACAGCCAAAGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACCTGACAGCCAAAGATGT	
172	Tpp1	Tpp1_172	GGAAAGGACGAAACACCGGATCGAGGCCAGTCTAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GATCGAGGCCAGTCTAGATG	
173	Copa	Copa_173	GGAAAGGACGAAACACCGCTTGCAGTTACAGATCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTTGCAGTTACAGATCACA	
174	Copa	Copa_174	GGAAAGGACGAAACACCGTCTCTGACACATCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTCTCTGACACATCACCT	
175	Copa	Copa_175	GGAAAGGACGAAACACCGCACCAGAAATATCCAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CACCAGAAATATCCAAACG	
176	Copa	Copa_176	GGAAAGGACGAAACACCGGAATGTCTAGGTACTCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GAATGTCTAGGTACTCCACA	
177	Cr2	Cr2_177	GGAAAGGACGAAACACCGATGTTGACCAGTTTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ATGTTGACCAGTTTGTGCG	
178	Cr2	Cr2_178	GGAAAGGACGAAACACCGTATACATTGCACCCCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTATACATTGCACCCCTGAG	
179	Cr2	Cr2_179	GGAAAGGACGAAACACCGAGACGGATTCTATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGACGGATTTCTATAAACCA	
180	Cr2	Cr2_180	GGAAAGGACGAAACACCGATGCAATGTCTATGGCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ATGCAATGCTCATGGCACAT	
181	Csf2ra	Csf2ra_181	GGAAAGGACGAAACACCGAGGACGCGGTGACGTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGGACGCGGTGACGTCACGT	
182	Csf2ra	Csf2ra_182	GGAAAGGACGAAACACCGCTACTTGGTCTGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CCTACTTGGTCTGACCGGT	
183	Csf2ra	Csf2ra_183	GGAAAGGACGAAACACCGTAGCGTCACTAACCAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTAGCGTCACTAACCAGAA	
184	Csf2ra	Csf2ra_184	GGAAAGGACGAAACACCGTGACATCCAGCGTGACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGACATCCAGCGTGACACCG	
185	Csf2rb	Csf2rb_185	GGAAAGGACGAAACACCGTACTTGGAAAGACTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TACACTTGGAAAGACTGACTG	
186	Csf2rb	Csf2rb_186	GGAAAGGACGAAACACCGTGATGGAAAATCGTGATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGATGGAAAATCGTGATAG	
187	Csf2rb	Csf2rb_187	GGAAAGGACGAAACACCGGAAGAAAATCGGACAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GAAGAAAATCGGACAGCTGGG	
188	Csf2rb	Csf2rb_188	GGAAAGGACGAAACACCGTGGAGACTGTAGGCATCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGGAGACTGTAGGCATCTCG	
189	Csf3r	Csf3r_189	GGAAAGGACGAAACACCGTCACTACAGAATTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCAGCTTACAGAATTACAG	
190	Csf3r	Csf3r_190	GGAAAGGACGAAACACCGTGAGGCAGGATAGGTTTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGAGGACGATAGGTTTTGAG	
191	Csf3r	Csf3r_191	GGAAAGGACGAAACACCGTGAGCTGCGTGGTGTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGAGCTGCGTGGTGTGCAA	
192	Csf3r	Csf3r_192	GGAAAGGACGAAACACCGCTTGGCCACACAATCCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTTGGCCACACAATCCGGGA	
193	Ctsc	Ctsc_193	GGAAAGGACGAAACACCGCTGCAAGATACAACCTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTGCAAGATACAACCTCCTG	
194	Ctsc	Ctsc_194	GGAAAGGACGAAACACCGGCGAGTAACTGATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCCAGTAACTGATAGCTGTG	
195	Ctsc	Ctsc_195	GGAAAGGACGAAACACCGTCAACACCAACTTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCACAACCAACTTTGTGA	
196	Ctsc	Ctsc_196	GGAAAGGACGAAACACCGCTGATTTTCATCAGTCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTGATTTTCATCAGTCATCG	
197	Cyba	Cyba_197	GGAAAGGACGAAACACCGAGTAGAAGGATACATAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGTAGAAGGATACATAGAGT	
198	Cyba	Cyba_198	GGAAAGGACGAAACACCGAATGACTTACCATCGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AATGACTTACCATCGTCCA	
199	Cyba	Cyba_199	GGAAAGGACGAAACACCGGACGTAGTAATTCCTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGACGTAGTAATTCCTGGTG	
200	Cyba	Cyba_200	GGAAAGGACGAAACACCGCAGATAGATCACACTGGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CAGATAGATCACACTGGCAA	
201	Cybb	Cybb_201	GGAAAGGACGAAACACCGCTTACCAAAACCAATTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CCTTACCAAAACCAATTCGG	
202	Cybb	Cybb_202	GGAAAGGACGAAACACCGTTTACCAGACGAATTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TTTACCAGACGAATTGTACG	
203	Cybb	Cybb_203	GGAAAGGACGAAACACCGATTCTAAGCTGGATACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ATTCTAAGCTGGATACCTTGA	
204	Cybb	Cybb_204	GGAAAGGACGAAACACCGTTATACTCGAAAACCTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TTATACTCGAAAACCTCCTG	
205	Cd55	Cd55_205	GGAAAGGACGAAACACCGCTTATACGTATAGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTCTTATACGTATAGCCAGG	
206	Cd55	Cd55_206	GGAAAGGACGAAACACCGTCTGTCGCCAACTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTGCTGTGCCAACTGTACG	
207	Cd55	Cd55_207	GGAAAGGACGAAACACCGTGTGACAGAACAGAAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGTGACAGAACAGAAAGTAG	
208	Cd55	Cd55_208	GGAAAGGACGAAACACCGGAAAAACCTCCACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGAAAAACCTCCACTCCC	
209	Dnase113	Dnase113_209	GGAAAGGACGAAACACCGTCTCGGGAGTTGTGTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCTCGGGAGTTGTGTGCAAG	
210	Dnase113	Dnase113_210	GGAAAGGACGAAACACCGTCACTACTCTGTAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCACACTACTGTAGACGA	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
264	Hc	Hc_264	GGAAAGGACGAAACACCCGGAACCTCCCATCAAATGTGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GAACCTCCCATCAAATGTGA	
265	Hells	Hells_265	GGAAAGGACGAAACACCCGCTGCGGTACCGAATTTACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCTGCGGTACCGAATTTACAG	
266	Hells	Hells_266	GGAAAGGACGAAACACCCGACGGTCATTAACCTTACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACGGTCATTAACCTTACAG	
267	Hells	Hells_267	GGAAAGGACGAAACACCCGCTGTATCATGGAAACCCGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCTGTATCATGGAACCCGGG	
268	Hells	Hells_268	GGAAAGGACGAAACACCCGACAACTACTTCTCGTTAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACAACCTACTTCTCGTTAGG	
269	Foxn1	Foxn1_269	GGAAAGGACGAAACACCCGACAGTACTTACGTTCTGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCAGTACTTACGTTCTGTG	
270	Foxn1	Foxn1_270	GGAAAGGACGAAACACCCGAAACAGTACATATGTTGCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GAACAGTACATATGTTGCAA	
271	Foxn1	Foxn1_271	GGAAAGGACGAAACACCCGACCTCACTATCCCTATCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CACCTCACTATCCCTATCAG	
272	Foxn1	Foxn1_272	GGAAAGGACGAAACACCCGCCACAGCAGCCCTTTCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCACAGACAGCCCTTTCGAG	
273	Hmox1	Hmox1_273	GGAAAGGACGAAACACCCGCTGTGCTGCAATGAACACTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCGTGCTGCAATGAACACTC	
274	Hmox1	Hmox1_274	GGAAAGGACGAAACACCCGTCAGGACCTGACCCCTGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCAGGACCTGACCCCTGAG	
275	Hmox1	Hmox1_275	GGAAAGGACGAAACACCCGACGCTTACATAGTGTGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACGCTTACATAGTGTGTG	
276	Hmox1	Hmox1_276	GGAAAGGACGAAACACCCGTTCCCTGTACCATATCTACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTCTGTACCATATCTACA	
277	Irf8	Irf8_277	GGAAAGGACGAAACACCCGAGTTTACCGAATTTGCCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGTTTACCGAATTTGCCCG	
278	Irf8	Irf8_278	GGAAAGGACGAAACACCCGTCGACAGCAGCATGTACCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCGACAGCAGCATGTACCCG	
279	Irf8	Irf8_279	GGAAAGGACGAAACACCCGCGTAACTCTGCTTCCACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CGGTAACCTCGTCTCCAG	
280	Irf8	Irf8_280	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
281	Irf8	Irf8_281	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
282	Irf8	Irf8_282	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
283	Irf8	Irf8_283	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
284	Irf8	Irf8_284	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
285	Irf8	Irf8_285	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
286	Irf8	Irf8_286	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
287	Irf8	Irf8_287	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
288	Irf8	Irf8_288	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
289	Irf8	Irf8_289	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
290	Irf8	Irf8_290	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
291	Irf8	Irf8_291	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
292	Irf8	Irf8_292	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
293	Cd79b	Cd79b_293	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
294	Cd79b	Cd79b_294	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
295	Cd79b	Cd79b_295	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
296	Cd79b	Cd79b_296	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
297	Igll1	Igll1_297	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
298	Igll1	Igll1_298	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
299	Igll1	Igll1_299	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
300	Igll1	Igll1_300	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
301	Ikbkb	Ikbkb_301	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
302	Ikbkb	Ikbkb_302	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
303	Ikbkb	Ikbkb_303	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
304	Ikbkb	Ikbkb_304	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
305	Ikbkg	Ikbkg_305	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
306	Ikbkg	Ikbkg_306	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
307	Ikbkg	Ikbkg_307	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
308	Ikbkg	Ikbkg_308	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
309	Il10	Il10_309	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
310	Il10	Il10_310	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
311	Il10	Il10_311	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
312	Il10	Il10_312	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
313	Il10ra	Il10ra_313	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
314	Il10ra	Il10ra_314	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
315	Il10ra	Il10ra_315	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	
316	Il10ra	Il10ra_316	GGAAAGGACGAAACACCCGCAAGCAGGATTACAATCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAAGCAGGATTACAATCAGG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
317	Il10rb	Il10rb_317	GGAAAGGACGAAACACCCGTGGCGGATGAACATTTCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGCGGATGAACATTTCGGAG	
318	Il10rb	Il10rb_318	GGAAAGGACGAAACACCCGATTTCAAGAACCTTACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATTTCAAGAACATTCTACAG	
319	Il10rb	Il10rb_319	GGAAAGGACGAAACACCCGGAGGACCTCAGAGTCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGGAGGACCTCAGAGTCGTA	
320	Il10rb	Il10rb_320	GGAAAGGACGAAACACCCGAGAGAAGTGCCTGAGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAGAAGTGCCTGAGTTCG	
321	Il12rb1	Il12rb1_321	GGAAAGGACGAAACACCCGTCGGTGAGGAAACCAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTCCGTTGAGGAAACCAACCCG	
322	Il12rb1	Il12rb1_322	GGAAAGGACGAAACACCCCTCCGAACCATACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTCCGAACCATACCCACAC	
323	Il12rb1	Il12rb1_323	GGAAAGGACGAAACACCCGTGAGAAACATCGTCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGAGAAGACATCGTCCAG	
324	Il12rb1	Il12rb1_324	GGAAAGGACGAAACACCCGTCAAGGTGTCAATCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCAAGGTGTCAATCACAC	
325	Il17ra	Il17ra_325	GGAAAGGACGAAACACCCGCTGAAGTAGCAACCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACTGAAGTAGCAACCAACCGT	
326	Il17ra	Il17ra_326	GGAAAGGACGAAACACCCGATGAGGCCATACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATGAGGCCATACCCACAG	
327	Il17ra	Il17ra_327	GGAAAGGACGAAACACCCGGAAGTCTGGATCGTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAGGTCTGGATCGTCTACT	
328	Il17ra	Il17ra_328	GGAAAGGACGAAACACCCGACCTGGAGATGTTGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GACCTGGAGATGTTGAACC	
329	Irak1	Irak1_329	GGAAAGGACGAAACACCCGACAGAAAGGCCAACAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGAAGGCCAGCAACAACCG	
330	Irak1	Irak1_330	GGAAAGGACGAAACACCCGTGGCAAGAAGCCATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGGCAAGAAGCCATAAACA	
331	Irak1	Irak1_331	GGAAAGGACGAAACACCCGGTGCCTGAGGATGTGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGTGCCTGAGGATGTGAACG	
332	Irak1	Irak1_332	GGAAAGGACGAAACACCCGCCACCACTGGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCCACCGAAGTGGCAGCAGT	
333	Il1rn	Il1rn_333	GGAAAGGACGAAACACCCGTTCTCCAGAAAGATAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTCCTCAGAAAGATAGACA	
334	Il1rn	Il1rn_334	GGAAAGGACGAAACACCCGTTCTTGGGCATCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTGTTCTTGGGCATCCACGG	
335	Il1rn	Il1rn_335	GGAAAGGACGAAACACCCGCTGCTGTAATGAAACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGCCTGTAATGAAACAGA	
336	Il1rn	Il1rn_336	GGAAAGGACGAAACACCCGTTGATATCATCTCCAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTTGATATCATCTCCAGACT	
337	Il2ra	Il2ra_337	GGAAAGGACGAAACACCCGTCTGTATGACCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTGTCTGTATGACCCACCCG	
338	Il2ra	Il2ra_338	GGAAAGGACGAAACACCCGATCTTGAGATGCTAATAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATCTTGAGATGCTAATAGC	
339	Il2ra	Il2ra_339	GGAAAGGACGAAACACCCGAGAGGTTCCGAAGACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGAGGTTCCGAAGACTAA	
340	Il2ra	Il2ra_340	GGAAAGGACGAAACACCCGAAATCTTCAATGTTTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAATCTTCAATGTTTCAAGG	
341	Il2rg	Il2rg_341	GGAAAGGACGAAACACCCGTTCCAGAGATTGGGTTATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTCACAGATTGGGTTATAG	
342	Il2rg	Il2rg_342	GGAAAGGACGAAACACCCGGAGCAACAGAGATCGAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAGCAACAGAGATCGAAGC	
343	Il2rg	Il2rg_343	GGAAAGGACGAAACACCCGCCGATTACCAAGATCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCGATTACCAAGATTCTGT	
344	Il2rg	Il2rg_344	GGAAAGGACGAAACACCCGCATACCTATAGTCGACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATACCTATAGTCAGCGTGT	
345	Il7r	Il7r_345	GGAAAGGACGAAACACCCGGAGACTAGGCCATACGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGGAGACTAGGCCATACGAC	
346	Il7r	Il7r_346	GGAAAGGACGAAACACCCGAGACTAGAAGATGCAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGACCTAGAAGATGCAGACG	
347	Il7r	Il7r_347	GGAAAGGACGAAACACCCGAGAACCCAAGAATCAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGAACCAGAATCAAGGT	
348	Il7r	Il7r_348	GGAAAGGACGAAACACCCGCTTTGAAGTAACTGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCTTTGAAGTAACTGTTATG	
349	Itch	Itch_349	GGAAAGGACGAAACACCCGACATAGGCTATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCCGACATAGGCTACTCTG	
350	Itch	Itch_350	GGAAAGGACGAAACACCCGAAACATAATTTACTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAAAATAATTTACTCGTAG	
351	Itch	Itch_351	GGAAAGGACGAAACACCCGCCAAGCTCCCTACACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCCAAGCTCCCTACCACCT	
352	Itch	Itch_352	GGAAAGGACGAAACACCCGACAACACTCGGATTACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAACACTCGGATTACTCAG	
353	Itgb2	Itgb2_353	GGAAAGGACGAAACACCCGAGTATAGGCAAAATCCGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGTATAGGCAAAATCCCGT	
354	Itgb2	Itgb2_354	GGAAAGGACGAAACACCCGTTGGCTGGCCGAATGTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTGGCTGGCCGAATGTACCG	
355	Itgb2	Itgb2_355	GGAAAGGACGAAACACCCGATCTGAGTTCGACCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATCCTGAGTTCGACCAACGG	
356	Itgb2	Itgb2_356	GGAAAGGACGAAACACCCGTGAGTAGGAGAGATCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGAGTAGGAGAGATCCATG	
357	Itk	Itk_357	GGAAAGGACGAAACACCCGAGCCCAAGCGCTACTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGCCCAAGCGCTACTACG	
358	Itk	Itk_358	GGAAAGGACGAAACACCCGTAAGCCTTCTATACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTAAAGCCTTCTATACCCG	
359	Itk	Itk_359	GGAAAGGACGAAACACCCGTGAGAACCTGAAGAAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCAGGAACCTGAAGAAACCC	
360	Itk	Itk_360	GGAAAGGACGAAACACCCGTTGCTCCAGACTGTGAGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTGCTCCAGACTGTGAGAGT	
361	Jak1	Jak1_361	GGAAAGGACGAAACACCCGATGCCATTGCAATGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGATGCCATTGCAATGACAG	
362	Jak1	Jak1_362	GGAAAGGACGAAACACCCGTAATAAAATCCATCAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGAATAAATCCATCAGACAG	
363	Jak1	Jak1_363	GGAAAGGACGAAACACCCGTCGAAACCAATCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCGAACCAATCATCACTG	
364	Jak1	Jak1_364	GGAAAGGACGAAACACCCGAAACATATAGTGTACCTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAACATATAGTGTACCTCTA	
365	Jak3	Jak3_365	GGAAAGGACGAAACACCCGAGACATCGGAAGTGCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGACATCGGAAGTGCATGG	
366	Jak3	Jak3_366	GGAAAGGACGAAACACCCGAGAAAGTCCAATTTGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAAAGTCCAATTTGATCG	
367	Jak3	Jak3_367	GGAAAGGACGAAACACCCGGGCTTTGGAGCCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGGCTTTGGAGCCACACGTT	
368	Jak3	Jak3_368	GGAAAGGACGAAACACCCGACCCAGGAGACCTTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACCAGGAGACCTTCCGTG	
369	Rpsa	Rpsa_369	GGAAAGGACGAAACACCCGGAAGCGCCAGCGATCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAGCGCCAGCGATCGGAG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
370	Rpsa	Rpsa_370	GGAAAGGACGAAACACCCGCTTACAGGGAGCTCACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTTACAGGGAGCTCACTCAG	
371	Rpsa	Rpsa_371	GGAAAGGACGAAACACCCGACGTCAGCAGGATTCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GACGTCAGCAGGATTCTCGA	
372	Rpsa	Rpsa_372	GGAAAGGACGAAACACCCGAGGGAAGTACTCCGCATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AGGGAAGTACTCCGCATGCG	
373	Lck	Lck_373	GGAAAGGACGAAACACCCGAAGATCCGTAACTAGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AAGATCCGTAACTAGACAA	
374	Lck	Lck_374	GGAAAGGACGAAACACCCGTACTACAACCGACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GTACTACAACCGACACCA	
375	Lck	Lck_375	GGAAAGGACGAAACACCCCGGAAAGCGAAAGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CCGGGAAAGCGAAAGCACTG	
376	Lck	Lck_376	GGAAAGGACGAAACACCCGCTTATGCACTGGTCAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GCTTTATGCACTGGTCAACC	
377	Lig1	Lig1_377	GGAAAGGACGAAACACCCGACCTCACTGACACCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GACCTCACTGACACCCGAG	
378	Lig1	Lig1_378	GGAAAGGACGAAACACCCGACAATTCAAGCACTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GACAATTCAGCACTCTTG	
379	Lig1	Lig1_379	GGAAAGGACGAAACACCCGCTTCTCATAGAAATTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TCTTCTCATAGAAATTCACA	
380	Lig1	Lig1_380	GGAAAGGACGAAACACCCGAGAGTGATTCCTCAGTGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AGAGTGATTCCTCAGTGAAG	
381	Psmb8	Psmb8_381	GGAAAGGACGAAACACCCCGGAGCTCGCACTTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CCGAGCTCGCACTTCCCGG	
382	Psmb8	Psmb8_382	GGAAAGGACGAAACACCCGATGATGCTGACACCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			ACATGATGCTCGACACCCG	
383	Psmb8	Psmb8_383	GGAAAGGACGAAACACCCGCTCGCTTCAAGTTCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTCGCTTCAAGTTCAGCA	
384	Psmb8	Psmb8_384	GGAAAGGACGAAACACCCGAGTTGATATCTTCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AGTTGATATCTTCGGA	
385	Blnk	Blnk_385	GGAAAGGACGAAACACCCGATGCAAGTTCGAAACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTATGCAAGTTCGAAACAGT	
386	Blnk	Blnk_386	GGAAAGGACGAAACACCCGATGATGCTGACACCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AAGATAATCGATCCAGCCAG	
387	Blnk	Blnk_387	GGAAAGGACGAAACACCCGCTGCTGACTAGACCCCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GTCTGTGACTAGACCCCTCGG	
388	Blnk	Blnk_388	GGAAAGGACGAAACACCCGATATTAGAAACAATGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GATATTAAGAAACAATGAAGG	
389	Lyst	Lyst_389	GGAAAGGACGAAACACCCGGAGCCCTGAAAGATCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGAGCCCTGAAAGATCGCGG	
390	Lyst	Lyst_390	GGAAAGGACGAAACACCCGGGATGAGTCTTACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGGATGAGTCTTACCACCG	
391	Lyst	Lyst_391	GGAAAGGACGAAACACCCGTAGGAAGTGGTGAACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TAGGAAGTGGTGAACCACGT	
392	Lyst	Lyst_392	GGAAAGGACGAAACACCCGCATACCCGAGTTTAAAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CATACCCGAGTTTAAAGCAA	
393	Masp2	Masp2_393	GGAAAGGACGAAACACCCGGCCTGTGATATAGTCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGCCTGTGATATAGTCCACA	
394	Masp2	Masp2_394	GGAAAGGACGAAACACCCGCTTGGCAGCTGACGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CCTTTGCCACTGACGACTCG	
395	Masp2	Masp2_395	GGAAAGGACGAAACACCCGCTGCGAGTATGACTTTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTGCGAGTATGACTTTGTCA	
396	Masp2	Masp2_396	GGAAAGGACGAAACACCCGTGGGCAATAATGGTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TGTGGCAATAATGGTCACAA	
397	Mcm4	Mcm4_397	GGAAAGGACGAAACACCCGTTGTGACAAGGTTCAACCACTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TTGTTGACAAGGTTCAACCA	
398	Mcm4	Mcm4_398	GGAAAGGACGAAACACCCGAGGTTGGAGATAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			ACCCGGTGGAGATAGATCG	
399	Mcm4	Mcm4_399	GGAAAGGACGAAACACCCGGTTATACCACTTTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGTTATACCACTTTGACA	
400	Mcm4	Mcm4_400	GGAAAGGACGAAACACCCGCTCAGGCTTTCATCACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTCAGGCTTTCATCACAT	
401	Cd46	Cd46_401	GGAAAGGACGAAACACCCGCTGTGAGCCAAATCATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CTGTGAGCCAAATCATACAT	
402	Cd46	Cd46_402	GGAAAGGACGAAACACCCGTTCAATGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TCCATAGCTTCAAGTGCCCG	
403	Cd46	Cd46_403	GGAAAGGACGAAACACCCGGCCTCAGCATAGACGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGCCTCAGCATAGACGCCCA	
404	Cd46	Cd46_404	GGAAAGGACGAAACACCCGACAGTTGTGATCCTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			ACAGTTGTGATCCTACCCCA	
405	Msh6	Msh6_405	GGAAAGGACGAAACACCCGATTCGTGATACCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AGTTTCGTGATACCAACAG	
406	Msh6	Msh6_406	GGAAAGGACGAAACACCCGATCAGTGACCGTCTAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CATCAGTGACCGTCTAGATG	
407	Msh6	Msh6_407	GGAAAGGACGAAACACCCGTAAGTAAAGACACCGCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TAAGTAAAGACACCGCTGAG	
408	Msh6	Msh6_408	GGAAAGGACGAAACACCCGAGGCAAAGATCTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GAGGCAAAGGATCTCAACGG	
409	Msn	Msn_409	GGAAAGGACGAAACACCCGCTGTTAATCCGGAAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CGCTTGTTAATCCGGAAGCCG	
410	Msn	Msn_410	GGAAAGGACGAAACACCCGGCCAGTTCTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CCGGCCAGTTCTACCCAG	
411	Msn	Msn_411	GGAAAGGACGAAACACCCGGAAGCACTTCTCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GAAGCACTTCTCCAGCCG	
412	Msn	Msn_412	GGAAAGGACGAAACACCCGAGACTAAGAAGGCTCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CAGACTAAGAAGGCTCAGCA	
413	Mvk	Mvk_413	GGAAAGGACGAAACACCCGAGCGTCAATTTACCAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AGCGTCAATTTACCAACAT	
414	Mvk	Mvk_414	GGAAAGGACGAAACACCCGTTGTCGGAACCTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GTGGTCGGAACCTCCCGCG	
415	Mvk	Mvk_415	GGAAAGGACGAAACACCCGAGGTCCTCCGCGAGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CAAGTCCCGCGAGTACCA	
416	Mvk	Mvk_416	GGAAAGGACGAAACACCCGCTGTAAGTCAATCAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TCTGAAGTCAATCAACAAGT	
417	Myd88	Myd88_417	GGAAAGGACGAAACACCCGGTCAAGAACAGCGATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GGTTCAAGAACAGCGATAGG	
418	Myd88	Myd88_418	GGAAAGGACGAAACACCCGAGGAGCTGAAGTCGCGCATTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			AAGGAGCTGAAGTCGCGCAT	
419	Myd88	Myd88_419	GGAAAGGACGAAACACCCGCTGTCTCAGGACAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			CCTGTCTCAGGACAACCG	
420	Myd88	Myd88_420	GGAAAGGACGAAACACCCGCATCCAACAACTGCGAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GCATCCAACAACTGCGAGT	
421	Ncf1	Ncf1_421	GGAAAGGACGAAACACCCGCTTCCACGGCAGTCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			TCTCACGGGAGTCCCATG	
422	Ncf1	Ncf1_422	GGAAAGGACGAAACACCCGATCCGGATCCCACTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAC	73			GATCCGGATCCCACTACCG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
423	Ncf1	Ncf1_423	GGAAAGGACGAAACACCCGGCTACGCACTGGCTGTGAGTGTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCTACGCACTGGCTGTGAGT	
424	Ncf1	Ncf1_424	GGAAAGGACGAAACACCCGCTGCCATCAAACCACCTGTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGTTGCCATCAAACCACCT	
425	Ncf2	Ncf2_425	GGAAAGGACGAAACACCCGCAAAAGCCAACAATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCACAAAGCCTAAACATACG	
426	Ncf2	Ncf2_426	GGAAAGGACGAAACACCCGTGGAATATCGGATTCGGAGTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGAATATCGGATTCGGAG	
427	Ncf2	Ncf2_427	GGAAAGGACGAAACACCCGTCTCACCTGTGGCTGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTCACCTGTGGCTGCAGAG	
428	Ncf2	Ncf2_428	GGAAAGGACGAAACACCCGTGAAGCAAATCCTCGAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGAAGCAAATCCTCGAGTGG	
429	Ncf4	Ncf4_429	GGAAAGGACGAAACACCCGAGAAGAAGATCCTGACGTCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAAGAAGATCCTGACGTCG	
430	Ncf4	Ncf4_430	GGAAAGGACGAAACACCCGCTAGAAGTGGCGATAGCGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGTAGAAGTGGCGATAGCGG	
431	Ncf4	Ncf4_431	GGAAAGGACGAAACACCCGATCCATGATGGCCCTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGATCCATGATGGCCCTTG	
432	Ncf4	Ncf4_432	GGAAAGGACGAAACACCCGACCTCGATGACAAAAACCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACCTCGATGACAAAAACCTG	
433	Nfkb1	Nfkb1_433	GGAAAGGACGAAACACCCGTGTGAAGGCCCATCACACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTGAAGGCCCATCACACGG	
434	Nfkb1	Nfkb1_434	GGAAAGGACGAAACACCCGGAGTCAAGAAATCAACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGAGTCAAGAAATCAACCG	
435	Nfkb1	Nfkb1_435	GGAAAGGACGAAACACCCGTTTCCGACTACGAGTGCAGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTTGCAGTGCAGTGCAGCG	
436	Nfkb1	Nfkb1_436	GGAAAGGACGAAACACCCGATGACAGAGCGGTGATTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATGACAGAGCGGTGATTAG	
437	Nfkb2	Nfkb2_437	GGAAAGGACGAAACACCCGACTGAGCGTGTAAATGACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTGAGCGTGTAAATGACG	
438	Nfkb2	Nfkb2_438	GGAAAGGACGAAACACCCGGAACCAATGGCATACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGGAACCAATGGCATACTG	
439	Nfkb2	Nfkb2_439	GGAAAGGACGAAACACCCGCTGCTGATCGGATCGGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCACGCTGCGGATCGGCA	
440	Nfkb2	Nfkb2_440	GGAAAGGACGAAACACCCGACCCGATAGCAGCCATTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACCCGGATAGCAGCCATTG	
441	Pepd	Pepd_441	GGAAAGGACGAAACACCCGCACAAATCGGATCTCCAGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CACAAATCGGATCTCCAGCG	
442	Pepd	Pepd_442	GGAAAGGACGAAACACCCGCTGCTATGGTGTATCGATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGCTATGGTGTATCGATG	
443	Pepd	Pepd_443	GGAAAGGACGAAACACCCGCTTCAACACGACAGCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCCCTGCAACACGACAGCTG	
444	Pepd	Pepd_444	GGAAAGGACGAAACACCCGCTTCTAATGCCTCGAAGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTTGCTAATGCCTCGAAGG	
445	Cfp	Cfp_445	GGAAAGGACGAAACACCCGTTACACATTTGGTCCGAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTACACATTTGGTCCGAG	
446	Cfp	Cfp_446	GGAAAGGACGAAACACCCGTATGAGCATAAGGCCTGCAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATGAGCATAAGGCCTGCAG	
447	Cfp	Cfp_447	GGAAAGGACGAAACACCCGATTACACATACTCGTTGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATTATCACATACTCGTTGA	
448	Cfp	Cfp_448	GGAAAGGACGAAACACCCGCTACTGGGAGAGACATCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTACTGGGAGAGACATCA	
449	Prf1	Prf1_449	GGAAAGGACGAAACACCCGTTCCGTCAGGTTGATGGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTCGTGCCAGGTGATGGGA	
450	Prf1	Prf1_450	GGAAAGGACGAAACACCCGTGCCACAGTAGGCGCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCCACAGGTAGGCGCTGTG	
451	Prf1	Prf1_451	GGAAAGGACGAAACACCCGTCATAAAGACTGGCGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCAATAACGACTGGCGTGTG	
452	Prf1	Prf1_452	GGAAAGGACGAAACACCCGGTAGGAGACTGCCTGAACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTAGGAGACTGCCTGAACG	
453	Pik3r1	Pik3r1_453	GGAAAGGACGAAACACCCGAGCTTTATAAGGAGAGGCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGCTTTATAAGGAGAGGCG	
454	Pik3r1	Pik3r1_454	GGAAAGGACGAAACACCCGTCCATTAACCTCAACTCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCCATTAACCTCAACTCTG	
455	Pik3r1	Pik3r1_455	GGAAAGGACGAAACACCCGTGCTACAATGAAACCACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGTACAATGAAACCACTG	
456	Pik3r1	Pik3r1_456	GGAAAGGACGAAACACCCGTGGAATCTGAAAAGCACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGGAATCTGAAAAGCACG	
457	Prkcd	Prkcd_457	GGAAAGGACGAAACACCCGAGAAGGTGGCGATAAACTCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAAGTGGCGATAAACTCG	
458	Prkcd	Prkcd_458	GGAAAGGACGAAACACCCGTTATAAACCTTGAATCGGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTATAAACCTTGAATCGGTG	
459	Prkcd	Prkcd_459	GGAAAGGACGAAACACCCGAGCCCACTGATCCTGAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGCCCACTGATCCTGAG	
460	Prkcd	Prkcd_460	GGAAAGGACGAAACACCCGATGATGAGAGTGATCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGATGATGAGAGTGATCCA	
461	Pms2	Pms2_461	GGAAAGGACGAAACACCCGTCTCAGGAAACATAAACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTCAGGAAACATAAACTG	
462	Pms2	Pms2_462	GGAAAGGACGAAACACCCGTAAGCTGCACTAATCAGCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAAGCTGCACTAATCAGCT	
463	Pms2	Pms2_463	GGAAAGGACGAAACACCCGATTTAGAGCAATGGATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGTTTACAGCAATGGATGTG	
464	Pms2	Pms2_464	GGAAAGGACGAAACACCCGACTAAAGAGATCAAGTCTAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTAAGAGATCAAGTCTAG	
465	Pnp	Pnp_465	GGAAAGGACGAAACACCCGATGCTGTGTGATGATGCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGATGCTGTGTGATGATGCA	
466	Pnp	Pnp_466	GGAAAGGACGAAACACCCGTGAGTGGCTGGAACCAATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCAGTGGCTGGAACCAATG	
467	Pnp	Pnp_467	GGAAAGGACGAAACACCCGTGTGGCCAGAACCTCTCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTGGCCAGAACCTCTCCG	
468	Pnp	Pnp_468	GGAAAGGACGAAACACCCGCTCAAGTGGCAGTGTCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTCAAGTGGCAGTGTCTG	
469	Pola1	Pola1_469	GGAAAGGACGAAACACCCGTAACGTTTACCATTTACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTAACGTTTACCATTTACCG	
470	Pola1	Pola1_470	GGAAAGGACGAAACACCCGAAAGAAAGCAACTACGCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAGAAAGCAACTACGCTGG	
471	Pola1	Pola1_471	GGAAAGGACGAAACACCCGAAAGAAAAAAGATCTACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAAGAAAAAAGATCTACTG	
472	Pola1	Pola1_472	GGAAAGGACGAAACACCCGTACAGAACCATCAACATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTACAGAACCATCAACATG	
473	Pole	Pole_473	GGAAAGGACGAAACACCCGATTATGGTCACTCAATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CATTATGGTCACTCAATG	
474	Pole	Pole_474	GGAAAGGACGAAACACCCGATGCTGAGACCTACGTCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATGCTGAGACCTACGTCGG	
475	Pole	Pole_475	GGAAAGGACGAAACACCCGATTGACCTCAGAATCCATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CATTGACCTCAGAATCCATG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
476	Pole	Pole_476	GGAAAGGACGAAACACCCGAGGCTGGAAGGATCATAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGGCTGGAAGGATCATAGCA	
477	Pole2	Pole2_477	GGAAAGGACGAAACACCCGGATCGAACGATCTGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATCGAACGATCTGCTGG	
478	Pole2	Pole2_478	GGAAAGGACGAAACACCCGCCAGTGGCTTATACACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCACAGTGGCTTATACACCC	
479	Pole2	Pole2_479	GGAAAGGACGAAACACCCGCTCAAGCGCTTAACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCAAGCGCTTAACTCTTG	
480	Pole2	Pole2_480	GGAAAGGACGAAACACCCGATAGCGTTCAAGATACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATAGCGTTCAAGATACAGCT	
481	Prkdc	Prkdc_481	GGAAAGGACGAAACACCCGAGACCAATTCAGTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAGCCAATTCAGTGACCCG	
482	Prkdc	Prkdc_482	GGAAAGGACGAAACACCCGTGGCCCTTGAAGTAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGCCCTTGAAGTAGACGA	
483	Prkdc	Prkdc_483	GGAAAGGACGAAACACCCGATGCAGGGTAAGTAACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATGCAGGGTAAGTAACTCGT	
484	Prkdc	Prkdc_484	GGAAAGGACGAAACACCCGACAGAGGATGCTCAAAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGAGGATGCTCAAAAATG	
485	Psen1	Psen1_485	GGAAAGGACGAAACACCCGTTCAACCAGCATACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTTCAACCAGCATACGAAGT	
486	Psen1	Psen1_486	GGAAAGGACGAAACACCCGTGCTACTGTAACTGATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCTACTGTAACGTAGTCCA	
487	Psen1	Psen1_487	GGAAAGGACGAAACACCCGCTGAGCCAATATCTAATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGAGCCAATATCTAATGGG	
488	Psen1	Psen1_488	GGAAAGGACGAAACACCCGAGTCACTTCTATACCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTCAGTCTATACCCGGA	
489	Pstpip1	Pstpip1_489	GGAAAGGACGAAACACCCGCTGGTTACAGTGCACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGGTTACAGTGCACCCACA	
490	Pstpip1	Pstpip1_490	GGAAAGGACGAAACACCCGTGTTGTAGAAAGAGTGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGTTGTAGAAAGAGTGTAC	
491	Pstpip1	Pstpip1_491	GGAAAGGACGAAACACCCGATTGGCACTCACAGCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATTGGCACTCACAGCTCGA	
492	Pstpip1	Pstpip1_492	GGAAAGGACGAAACACCCGCTCGCTTCAAGAAGACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTCCGCTTCAAGAAGACCA	
493	Pten	Pten_493	GGAAAGGACGAAACACCCCTCCAATTCAGGACCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCTCCAATTCAGGACCCACG	
494	Pten	Pten_494	GGAAAGGACGAAACACCCGTGTCATATTTATGTCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGTGCATATTTATGTCATCG	
495	Pten	Pten_495	GGAAAGGACGAAACACCCGACTATTCGAATGTTCAAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACTATTCGAATGTTCAAGTGG	
496	Pten	Pten_496	GGAAAGGACGAAACACCCGGTTGATAAGTTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGTTTGATAAGTTCAAGCTG	
497	Ptprc	Ptprc_497	GGAAAGGACGAAACACCCGTAGCAGAAATCTTATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTAGCAGAAATCTTATATCG	
498	Ptprc	Ptprc_498	GGAAAGGACGAAACACCCGTTTCACAATGGAGTGTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTTCACAATGGAGTGTACGA	
499	Ptprc	Ptprc_499	GGAAAGGACGAAACACCCGTTGCAAGCTAAGCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTGTCAGCTAAGCGCAGAG	
500	Ptprc	Ptprc_500	GGAAAGGACGAAACACCCGACCAACAGCAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACCACAACGAAAGCAACATG	
501	Rac2	Rac2_501	GGAAAGGACGAAACACCCGAGAAAGACAGCTTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGAAGACAGCTTCCGCGCA	
502	Rac2	Rac2_502	GGAAAGGACGAAACACCCGCTGGACCTTCGCGATGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCTGGACCTTCGCGATGACA	
503	Rac2	Rac2_503	GGAAAGGACGAAACACCCGAAAGCCACTCACACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAGAAGCCACTCACACAGTG	
504	Rac2	Rac2_504	GGAAAGGACGAAACACCCGACCGACACTTCTCATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCACGGCAATTCATATAGG	
505	Rag1	Rag1_505	GGAAAGGACGAAACACCCGACCAAAAGCAGAGTCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACACCAAAGCAGAGTCTAGT	
506	Rag1	Rag1_506	GGAAAGGACGAAACACCCGTGAAACGATTTCCACAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGAAACGATTTCCACAGATG	
507	Rag1	Rag1_507	GGAAAGGACGAAACACCCGTCGCGCAAGATTGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCCGCAGAGATTGCAATG	
508	Rag1	Rag1_508	GGAAAGGACGAAACACCCGTGGGAAGTAGACCTGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGGAAGTAGACCTGACTGT	
509	Rag2	Rag2_509	GGAAAGGACGAAACACCCGATCATATATCATTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATCAATATATCATTACCGG	
510	Rag2	Rag2_510	GGAAAGGACGAAACACCCGATTGACGTGGTGTATAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATTGACGTGGTGTATAGTCG	
511	Rag2	Rag2_511	GGAAAGGACGAAACACCCGTAACCTGTATAGAATAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TAACTGTATAGAATAAGAG	
512	Rag2	Rag2_512	GGAAAGGACGAAACACCCGATACCAGGAGACAATAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATACCAGGAGACAATAAGC	
513	Ranbp2	Ranbp2_513	GGAAAGGACGAAACACCCGAAATTTCTCTGTCACAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAATATTTCTGTCACAAAG	
514	Ranbp2	Ranbp2_514	GGAAAGGACGAAACACCCGTGTAATGTAACTCCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCTAATGTAACTCCCACCA	
515	Ranbp2	Ranbp2_515	GGAAAGGACGAAACACCCGATGTTGTTAACTTAAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATGTTGTTAACTTAAGTCG	
516	Ranbp2	Ranbp2_516	GGAAAGGACGAAACACCCGACATGCAATGCACCTAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACATGCAATGCACCTAGAGA	
517	Rasgrp1	Rasgrp1_517	GGAAAGGACGAAACACCCGACTACAGATATCCGTCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACGTACAGATATCCGTCGGA	
518	Rasgrp1	Rasgrp1_518	GGAAAGGACGAAACACCCGTAAGAACTATGATCTCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TAAGAACTATGATCTCGACC	
519	Rasgrp1	Rasgrp1_519	GGAAAGGACGAAACACCCGACAGTTGGTTATCCGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGTTGGTTATCCGACAC	
520	Rasgrp1	Rasgrp1_520	GGAAAGGACGAAACACCCGTGACCTTATTGATCTCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGACCTTATTGATCTCATGT	
521	Relb	Relb_521	GGAAAGGACGAAACACCCGTTCAAAACGCCACCCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTCAAAACGCCACCCTACG	
522	Relb	Relb_522	GGAAAGGACGAAACACCCGTACACCCACATAGCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TACACCCACATAGCCTCGTG	
523	Relb	Relb_523	GGAAAGGACGAAACACCCGCGGATTCGCCAATCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCGGATTTGCCAATCAACA	
524	Relb	Relb_524	GGAAAGGACGAAACACCCGCTCTATCCGGACCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCCTCTATCCGGACCAGCA	
525	Rfxank	Rfxank_525	GGAAAGGACGAAACACCCGTTCAACTTACAGTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTCTACTTACAGTCCAGGG	
526	Rfxank	Rfxank_526	GGAAAGGACGAAACACCCGATCAACAAACCCGGATGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATCAACAAACCCGGATGAGCG	
527	Rfxank	Rfxank_527	GGAAAGGACGAAACACCCGCACTGTCACTTGCAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAGTGCAGTGCAGAT	
528	Rfxank	Rfxank_528	GGAAAGGACGAAACACCCAGTTCGCTTCTGCTAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTTCGCTTCTGCTAGACT	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
529	Rorc	Rorc_529	GGAAAGGACGAAACACCGCTTGTAGTATAGTCCAGAACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CTTGAGTATAGTCCAGAACG	
530	Rorc	Rorc_530	GGAAAGGACGAAACACCGTCTATCTGGGATCCACTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GTCATCTGGGATCCACTACG	
531	Rorc	Rorc_531	GGAAAGGACGAAACACCGCTCTGGGGCACTGCAGAAAAGTGTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TCTGGGGCACTGCAGAAAAGT	
532	Rorc	Rorc_532	GGAAAGGACGAAACACCGGACAAGCAGAGGCTCGGGTGTGTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GACAAGCAGAGGCTCGGGT	
533	Sema3e	Sema3e_533	GGAAAGGACGAAACACCGACACGATCTACACCCGAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			ACACGATCTACACCCGAGTG	
534	Sema3e	Sema3e_534	GGAAAGGACGAAACACCGTGTGCCAGCAAAGTAAACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGTGCCAGCAAAGTAAACGG	
535	Sema3e	Sema3e_535	GGAAAGGACGAAACACCGAAGATAATTACCACTAGCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AAGATAATTACCACTAGCG	
536	Sema3e	Sema3e_536	GGAAAGGACGAAACACCGTGTATACACACATACAGCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGTGATACACACATACAGCA	
537	Foxp3	Foxp3_537	GGAAAGGACGAAACACCGCATACCTGATGCATGAAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CATACCTGATGCATGAAGTG	
538	Foxp3	Foxp3_538	GGAAAGGACGAAACACCGTCTACCCACAGGGATCAATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TCTACCCACAGGGATCAATG	
539	Foxp3	Foxp3_539	GGAAAGGACGAAACACCGAGTCCGGACCTGCGAAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGGTCGGGACCTGCGAAGTG	
540	Foxp3	Foxp3_540	GGAAAGGACGAAACACCGGCAAGAGCTCTGTCCATTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GCAAGAGCTCTGTCCATTG	
541	Sh2d1a	Sh2d1a_541	GGAAAGGACGAAACACCGAGAAGCTTACTCTGCTACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGAAGCTCTACTCTGCTACC	
542	Sh2d1a	Sh2d1a_542	GGAAAGGACGAAACACCGGATGCAGTACTGTGTACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GATGCAGTACTGTGTACCA	
543	Sh2d1a	Sh2d1a_543	GGAAAGGACGAAACACCGAACAGGTTCTTGGAGTCCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AACAGGTTCTTGGAGTGCCG	
544	Sh2d1a	Sh2d1a_544	GGAAAGGACGAAACACCGCACACAGGCAGTACACGCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CACACAGGCAGTACAGGCCA	
545	Clpb	Clpb_545	GGAAAGGACGAAACACCGAGAGCCGTTCCGACAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGGACCGGCTCCGACGAGG	
546	Clpb	Clpb_546	GGAAAGGACGAAACACCGGAGAACCAGGCTGGTACGATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GGAGAACCAGGCTGGTACGATG	
547	Clpb	Clpb_547	GGAAAGGACGAAACACCGCGTTGTACCCGAGACCCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CGTTGTACCCGAGACCCGG	
548	Clpb	Clpb_548	GGAAAGGACGAAACACCGCTCTCGAGTACTAGGACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CTCTCGAGTACTAGGACTG	
549	Stat1	Stat1_549	GGAAAGGACGAAACACCGGATAGAGCCAGCCAGCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GGATAGAGCCAGCCAGCAGT	
550	Stat1	Stat1_550	GGAAAGGACGAAACACCGTGTGATGTTAGATAAACAGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGTGATGTTAGATAAACAGA	
551	Stat1	Stat1_551	GGAAAGGACGAAACACCGTAAATGACGAGCTCGTGGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TAAATGACGAGCTCGTGGAG	
552	Stat1	Stat1_552	GGAAAGGACGAAACACCGGAAAGCAAGCGTAATCTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GAAAAGCAAGCGTAATCTCC	
553	Stat3	Stat3_553	GGAAAGGACGAAACACCGCAACAAATTAAGAACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CCAACAAATTAAGAACTGG	
554	Stat3	Stat3_554	GGAAAGGACGAAACACCGTCTCTCTGTCACTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CTGCTCTCTGTCACTACGG	
555	Stat3	Stat3_555	GGAAAGGACGAAACACCGTTTTACCACGAAAGTCAAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GTTTACCACGAAAGTCAAGT	
556	Stat3	Stat3_556	GGAAAGGACGAAACACCGCAAAGAGTACATGCCACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CAAAGAGTACATGCCACGT	
557	Stat5b	Stat5b_557	GGAAAGGACGAAACACCGTGAATTCGACAGTATTACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CTGATTTCGAGTGATTACAG	
558	Stat5b	Stat5b_558	GGAAAGGACGAAACACCGTACAGCGAACAGCTCCATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TACAGCGAACAGCTCCATG	
559	Stat5b	Stat5b_559	GGAAAGGACGAAACACCGGGCGTTGCCAGAGGACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GGCGTTGCCAGAGGACAG	
560	Stat5b	Stat5b_560	GGAAAGGACGAAACACCGAGTGGATCGAAAGCCAAAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGTGGATCGAAAGCCAAAGC	
561	Stim1	Stim1_561	GGAAAGGACGAAACACCGTGAAGGATAAGCTTATCAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGAGGATAAGCTTATCAGCG	
562	Stim1	Stim1_562	GGAAAGGACGAAACACCGGAATACAGGAGTACTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GAATACAGGAGTACTCCG	
563	Stim1	Stim1_563	GGAAAGGACGAAACACCGAGCCGCTAAAAATATGCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GAGCCGCTAAAAATATGCTG	
564	Stim1	Stim1_564	GGAAAGGACGAAACACCGCAGCAGATCGAGATCCTCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CAGCAGATCGAGATCCTCTG	
565	Stxbp2	Stxbp2_565	GGAAAGGACGAAACACCGTGAATAGTGGGACACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CGTGAATAGTGGGACACCG	
566	Stxbp2	Stxbp2_566	GGAAAGGACGAAACACCGCATCCGATCCGATACCCGCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CATCCATCCGATACCCGCAAG	
567	Stxbp2	Stxbp2_567	GGAAAGGACGAAACACCGTATTATAGGTACTTCTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TATTATAGGTACTTCTCCG	
568	Stxbp2	Stxbp2_568	GGAAAGGACGAAACACCGAAGGTTGTAGGTGCTATGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AAGGTTGTAGGTGCTATGTG	
569	Tap1	Tap1_569	GGAAAGGACGAAACACCGACTAATGGACTCGCACACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			ACTAATGGACTCGCACAGT	
570	Tap1	Tap1_570	GGAAAGGACGAAACACCGTCTCTAGCAAAGTCCACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GCTCTAGCAAAGTCCACCG	
571	Tap1	Tap1_571	GGAAAGGACGAAACACCGTGCCACATAACTGATAGCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGCCACATAACTGATAGCGA	
572	Tap1	Tap1_572	GGAAAGGACGAAACACCGTGGACATGAGCCATATGTTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGGACATGAGCCATATGTTG	
573	Tap2	Tap2_573	GGAAAGGACGAAACACCGAGAAGCCACTCGGACTACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGAAGCCACTCGGACTACTG	
574	Tap2	Tap2_574	GGAAAGGACGAAACACCGTTACACGACCCGAATAGCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TTACACGACCCGAATAGCGA	
575	Tap2	Tap2_575	GGAAAGGACGAAACACCGCTGTGGGACTGCTAAAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			GCTGTGGGACTGCTAAAAG	
576	Tap2	Tap2_576	GGAAAGGACGAAACACCGCATGCACACATACCTGATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CATGCACACATACCTGATGG	
577	Tapbp	Tapbp_577	GGAAAGGACGAAACACCGTGGTGTAGAGACACTCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			TGGTGTAGAGACACTCTGG	
578	Tapbp	Tapbp_578	GGAAAGGACGAAACACCGCTTCCAGCTGGACTCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CTTCCAGCTGGACTCGAG	
579	Tapbp	Tapbp_579	GGAAAGGACGAAACACCGCCACTCCAGCCAAAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			CGCCACTCCAGCCAAAGGG	
580	Tapbp	Tapbp_580	GGAAAGGACGAAACACCGAGCCGTGAAGCCTTCTCAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			AGCCGTGAAGCCTTCTCAGG	
581	Tbx1	Tbx1_581	GGAAAGGACGAAACACCGACATAGACAACATGGAATCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAC	73			ACATAGACAACATGGAATCG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
582	Tbx1	Tbx1_582	GGAAAGGACGAAACACCCGCTCCGGGATTGCGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			CTTCCGGGATTGCGACCCGG	
583	Tbx1	Tbx1_583	GGAAAGGACGAAACACCCGACTACCACCCGGACTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACACTACCACCCGGACTCGC	
584	Tbx1	Tbx1_584	GGAAAGGACGAAACACCCGCGCAGCGATCTAGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCGCAGCGATCGTAGCGCGG	
585	Tcf3	Tcf3_585	GGAAAGGACGAAACACCCGATTATTGCTGGAGTGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATTATTGCTGGAGTGATCCG	
586	Tcf3	Tcf3_586	GGAAAGGACGAAACACCCGCTCTAGGAACGTGGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCTCTAGGAACGTGGAAGG	
587	Tcf3	Tcf3_587	GGAAAGGACGAAACACCCGGAAGAGCCGTCACCTAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAGAGCCGTCACCTAGCAT	
588	Tcf3	Tcf3_588	GGAAAGGACGAAACACCCGCTGCAAACCTGGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGCAAACCTGGGTTCCCGC	
589	Tcn2	Tcn2_589	GGAAAGGACGAAACACCCGGAAGCGGCTCCATGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAGCGGCTCCATGACAGCG	
590	Tcn2	Tcn2_590	GGAAAGGACGAAACACCCGCTGAGACCAGCAATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCTGAGACCAGCAATACCA	
591	Tcn2	Tcn2_591	GGAAAGGACGAAACACCCGAGACTAGCAATACCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGACTAGCAATACCCGAGG	
592	Tcn2	Tcn2_592	GGAAAGGACGAAACACCCGGAATATCTATAGCACCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAATATCTATAGCACCCAC	
593	Tert	Tert_593	GGAAAGGACGAAACACCCCTCCAGCCTAAGTCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCTCCAGCCTAAGTCTGACTG	
594	Tert	Tert_594	GGAAAGGACGAAACACCCGCTCAGAGCCAGATATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACAGAGGCCAGATATCCG	
595	Tert	Tert_595	GGAAAGGACGAAACACCCGTCAGCATGCTCAACTATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCAGCATGCTCAACTATGAG	
596	Tert	Tert_596	GGAAAGGACGAAACACCCGAAGTCCTGCTCGGTCGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAGTCTGCTCGTCCCGC	
597	Thbd	Thbd_597	GGAAAGGACGAAACACCCGTACTACAACCCCGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TACACAACCCCGTTCG	
598	Thbd	Thbd_598	GGAAAGGACGAAACACCCGTGTGAGCAGGCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTGTGAGACAGGCTACCACT	
599	Thbd	Thbd_599	GGAAAGGACGAAACACCCGCTGGAAGTAAACTCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGTGAAGTAAACTCACAG	
600	Thbd	Thbd_600	GGAAAGGACGAAACACCCGTCGAGTTAGATCCGAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCGAGTTAGATCCGAAACA	
601	Tnfaip3	Tnfaip3_601	GGAAAGGACGAAACACCCGCGAGCTTGTAGTACATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAGCTTGTAGTACATGTG	
602	Tnfaip3	Tnfaip3_602	GGAAAGGACGAAACACCCGATATCCATGAGTGATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATATCCATGAGTGATAGCTG	
603	Tnfaip3	Tnfaip3_603	GGAAAGGACGAAACACCCGAGCCCCGAGGAAACCCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGCCCCGAGGAAACCCGCTGG	
604	Tnfaip3	Tnfaip3_604	GGAAAGGACGAAACACCCGAGGACTTGTCTACGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGGACTTGTCTACGACTCTG	
605	Tnfrs11a	Tnfrs11a_605	GGAAAGGACGAAACACCCGACCAACCGTCCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACCAGCAACCGTCCCTCG	
606	Tnfrs11a	Tnfrs11a_606	GGAAAGGACGAAACACCCGACTGAGGAGACCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACACTGAGGAGACCACCA	
607	Tnfrs11a	Tnfrs11a_607	GGAAAGGACGAAACACCCGTTAAGCCAGTGTTCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTAAGCCAGTGTTCACC	
608	Tnfrs11a	Tnfrs11a_608	GGAAAGGACGAAACACCCGAGACGCAAGGAGACCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGACGCAAGGAGACCTCTCG	
609	Tnfrs1a	Tnfrs1a_609	GGAAAGGACGAAACACCCGAGTTGCAAGACATGTCCGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTTGCAAGCATGTCCGAA	
610	Tnfrs1a	Tnfrs1a_610	GGAAAGGACGAAACACCCGAGACTAGCAAGATAACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGACCTAGCAAGATAACCCAG	
611	Tnfrs1a	Tnfrs1a_611	GGAAAGGACGAAACACCCGATGCGGATATCCATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATGGGATACATCCATCAG	
612	Tnfrs1a	Tnfrs1a_612	GGAAAGGACGAAACACCCGGATCCCGTGCCTGTCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGATCCCGTGCCTGCAAAG	
613	Cd40	Cd40_613	GGAAAGGACGAAACACCCGATTCGCTGAGTCACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATTCCGCTGAGTCACATGGG	
614	Cd40	Cd40_614	GGAAAGGACGAAACACCCGGGATGACAGACGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGGATGACAGACGTTATCAG	
615	Cd40	Cd40_615	GGAAAGGACGAAACACCCGAGTCAGACTAATGTCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTCAGACTAATGTCATCTG	
616	Cd40	Cd40_616	GGAAAGGACGAAACACCCGCTGCACAGCAAGGATTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGCACAGCAAGGATTGCG	
617	Cd27	Cd27_617	GGAAAGGACGAAACACCCGCTCTCCAGACTACCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCTCTCAGACTACCACACC	
618	Cd27	Cd27_618	GGAAAGGACGAAACACCCGCTGCATACCTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCTGCATACCTGTGCCACT	
619	Cd27	Cd27_619	GGAAAGGACGAAACACCCGAGACCAACACTACTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGACAAACACTACTGGAAGT	
620	Cd27	Cd27_620	GGAAAGGACGAAACACCCGCTCAGGTACATCTTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTCAGGTACATCTTTGTGA	
621	Tnfsf11	Tnfsf11_621	GGAAAGGACGAAACACCCGCTCGATCGTGGTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCCTCGATCGTGGTACCAAG	
622	Tnfsf11	Tnfsf11_622	GGAAAGGACGAAACACCCGACCTCGTGTGGGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GACCTCGTGTGGGACGCCG	
623	Tnfsf11	Tnfsf11_623	GGAAAGGACGAAACACCCGTTAAGCAACCGGAAACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTAAGCAACCGGAAACTAA	
624	Tnfsf11	Tnfsf11_624	GGAAAGGACGAAACACCCGAGATTTGACAGGACTCGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGATTTGACAGGACTCGACTC	
625	Tnfsf12	Tnfsf12_625	GGAAAGGACGAAACACCCGGCTGACCACGACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCTGACCACGACCAAGG	
626	Tnfsf12	Tnfsf12_626	GGAAAGGACGAAACACCCGCCCAGGCTCAGCACCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCCCAGGCTCAGCACCAGCG	
627	Tnfsf12	Tnfsf12_627	GGAAAGGACGAAACACCCGCAACCGTCTGCTGCCAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACCGTCTGCCAGGTTG	
628	Tnfsf12	Tnfsf12_628	GGAAAGGACGAAACACCCGGAAGTGAATCCCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAAGTGAATCCCGACAG	
629	Cd40lg	Cd40lg_629	GGAAAGGACGAAACACCCGATTTCAAACAGGTCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TATTTCAAACAGGTCGAAG	
630	Cd40lg	Cd40lg_630	GGAAAGGACGAAACACCCGAGCTAAAGAGATGCAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAGCTAAAGAGATGCAACAA	
631	Cd40lg	Cd40lg_631	GGAAAGGACGAAACACCCGTTATACCGTGAACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTATACCGTGAACGCAACT	
632	Cd40lg	Cd40lg_632	GGAAAGGACGAAACACCCGTAAGTGTGAGGAGATGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGAAGTGTGAGGAGATGAGA	
633	Cd70	Cd70_633	GGAAAGGACGAAACACCCGTTGGGAAGTCTTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTGGGAAGTCTTACACA	
634	Cd70	Cd70_634	GGAAAGGACGAAACACCCGAGCTGTAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGCTGTAAGTGTGTTTTAG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
635	Cd70	Cd70_635	GGAAAGGACGAAACACCCGAAGGACCCACACTGCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			AAGGACCCCACTGCGCTG	
636	Cd70	Cd70_636	GGAAAGGACGAAACACCCGCATCTCGTATCCATCAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CATCTGCGTATCCATCAAGA	
637	Traf3	Traf3_637	GGAAAGGACGAAACACCCGCTGGGGCATTGACACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			GCTGGGGGCATTGACACACT	
638	Traf3	Traf3_638	GGAAAGGACGAAACACCCGAGTTCACGTGCTGTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGGTTACGTGCTGTACCG	
639	Traf3	Traf3_639	GGAAAGGACGAAACACCCAGTGAACGCTGACGTCACGTGCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			AGTGACTGCAGTGGCCG	
640	Traf3	Traf3_640	GGAAAGGACGAAACACCCGCTTTGAGATCGAGATTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			GCTTTGAGATCGAGATTGAG	
641	Trex1	Trex1_641	GGAAAGGACGAAACACCCGTTTCCTCGAACCATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTTCCTCGAACCATTCCTG	
642	Trex1	Trex1_642	GGAAAGGACGAAACACCCGACAGAAAGTACCATCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			ACACAGAAGTACCATCTAG	
643	Trex1	Trex1_643	GGAAAGGACGAAACACCCGAGCTTCCACCACACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			AGCTTGCACACACGGGG	
644	Trex1	Trex1_644	GGAAAGGACGAAACACCCGGAGCAGAGGAAAGTATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			GGAGCAGAGGAAAGTATAG	
645	Tfrc	Tfrc_645	GGAAAGGACGAAACACCCGCTACACGCTTACAATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTACACGCTTACAATAGCCC	
646	Tfrc	Tfrc_646	GGAAAGGACGAAACACCCGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAATACATACACTCCTCGT	
647	Tfrc	Tfrc_647	GGAAAGGACGAAACACCCGGGCTCCTACTACACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGGCTCCTACTACAACATAA	
648	Tfrc	Tfrc_648	GGAAAGGACGAAACACCCGAACCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AACCTCGGGAGACTCCACT	
649	Tnfrsf4	Tnfrsf4_649	GGAAAGGACGAAACACCCGAGCCGCTGTGATCATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGCCGCTGTGATCATACCA	
650	Tnfrsf4	Tnfrsf4_650	GGAAAGGACGAAACACCCGTCACACTGGAGTTACAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCACACTTGGAGTTACAGCA	
651	Tnfrsf4	Tnfrsf4_651	GGAAAGGACGAAACACCCGTTCCAGTAAAGTACAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTCCAGATAAGGTACAACCTG	
652	Tnfrsf4	Tnfrsf4_652	GGAAAGGACGAAACACCCGTAGACCAGGCCAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAGACCAGGCCAACCT	
653	Ung	Ung_653	GGAAAGGACGAAACACCCGACGACCTAATCAAGCTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACGGACCTAATCAAGCTCAC	
654	Ung	Ung_654	GGAAAGGACGAAACACCCGTTGTCAGGGTGGCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAC	73			TTGTCAGGGTGGCCGACAG	
655	Ung	Ung_655	GGAAAGGACGAAACACCCGCAACCCGACTCTGACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCAACCCGACTCTGAATCC	
656	Ung	Ung_656	GGAAAGGACGAAACACCCGCAACAAGTCTATCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCACAAGTCTATCCGCC	
657	Vps45	Vps45_657	GGAAAGGACGAAACACCCGAAAGCTGATAACGAATCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAAGCTGATAACGAATCATG	
658	Vps45	Vps45_658	GGAAAGGACGAAACACCCGCAACTCTTTGAATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACGAACTCTTTGAATCCGG	
659	Vps45	Vps45_659	GGAAAGGACGAAACACCCGTCTCAAAGCAGTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCTCAAAGCAGTGCACAG	
660	Vps45	Vps45_660	GGAAAGGACGAAACACCCGTTGTTTCCTTCGACCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGTTTCCTTCGACCCACA	
661	Was	Was_661	GGAAAGGACGAAACACCCGCACTGATAAGAAACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAACTGATAAGAAACGCTCA	
662	Was	Was_662	GGAAAGGACGAAACACCCGCCACAGCAACATCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCACCAGCAACATCAATGA	
663	Was	Was_663	GGAAAGGACGAAACACCCGTACCTGTAGGCCATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCACCTGTAGGCCATAAAGG	
664	Was	Was_664	GGAAAGGACGAAACACCCGACAGTGAACAACCTAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCAGTGAACAACCTAGACC	
665	Wdr1	Wdr1_665	GGAAAGGACGAAACACCCGTAGCCAGATGACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAGCCAAGTATGACCCAG	
666	Wdr1	Wdr1_666	GGAAAGGACGAAACACCCGGCCCTACCGACTAGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGCCCTACCGACTAGCAACA	
667	Wdr1	Wdr1_667	GGAAAGGACGAAACACCCGTGCGGATTTCTCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGTGCGATTTCTCTGAT	
668	Wdr1	Wdr1_668	GGAAAGGACGAAACACCCGATGGCTCCAGATAAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATGGTCCAGAAATAGATGT	
669	Zap70	Zap70_669	GGAAAGGACGAAACACCCGACCGACGTCACGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAACGGCAGTACGCCATCG	
670	Zap70	Zap70_670	GGAAAGGACGAAACACCCGAAAGCAGAGAAATCTCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAAGCGAGAAATCTCCTCG	
671	Zap70	Zap70_671	GGAAAGGACGAAACACCCGTCGACAACCCCTACATCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGACAACCCCTACATCGTG	
672	Zap70	Zap70_672	GGAAAGGACGAAACACCCGCGCACCATAGCATCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGGCACCATAGCATCACGC	
673	Ikzf1	Ikzf1_673	GGAAAGGACGAAACACCCGATGCGCTGGTCCATCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATGGCTGGTCCATCACGT	
674	Ikzf1	Ikzf1_674	GGAAAGGACGAAACACCCGTTGGTAAGCCTCACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTGGTAAGCCTCACAATG	
675	Ikzf1	Ikzf1_675	GGAAAGGACGAAACACCCGAGAATCCAAGAGTGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGAACTCCAAGTGTATCG	
676	Ikzf1	Ikzf1_676	GGAAAGGACGAAACACCCGAGAAACTAACCAACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAAACTAACCAACAGAGA	
677	Hax1	Hax1_677	GGAAAGGACGAAACACCCGAGAATCTTCTCACCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGAATCTTCTCACCTCCG	
678	Hax1	Hax1_678	GGAAAGGACGAAACACCCGAATTCACACACCGAGAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AATTCACACACCGAGAGT	
679	Hax1	Hax1_679	GGAAAGGACGAAACACCCGCTGAAACCGAATCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGAAACCGAATCTCTG	
680	Hax1	Hax1_680	GGAAAGGACGAAACACCCGCTCGCATTTGGGGTTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCTCCAGATTGGGGTCCGA	
681	Sh3bp2	Sh3bp2_681	GGAAAGGACGAAACACCCGTAGCAAGAAGCACCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCAGCAAGAAGCACCAGACA	
682	Sh3bp2	Sh3bp2_682	GGAAAGGACGAAACACCCGAGGTGAACGAGTGGGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGGTGAACGAGTGGGCACG	
683	Sh3bp2	Sh3bp2_683	GGAAAGGACGAAACACCCGACCTGGAGCCTGATCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACCTGGAGCCTGATCCCCG	
684	Sh3bp2	Sh3bp2_684	GGAAAGGACGAAACACCCGTGGTCACTTGTCTATTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGGTACATTGCTATTGGG	
685	Srp54a	Srp54a_685	GGAAAGGACGAAACACCCGTTATAGAGAAGTTGAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTTATAGAGAAGTTGAAGCA	
686	Srp54a	Srp54a_686	GGAAAGGACGAAACACCCGAAAGCGTGGACACCGACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAAGCGTGGACACCGACTAA	
687	Srp54a	Srp54a_687	GGAAAGGACGAAACACCCGTATGTGATGGATGCATCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATGTGATGGATGCATCCAT	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
688	Srp54a	Srp54a_688	GGAAAGGACGAAACACCGAAACTCGACGGTCATGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAACTCGACGGTCATGCGAA	
689	Rbck1	Rbck1_689	GGAAAGGACGAAACACCGTGCTTCATACCAGCCTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCTTCATACCAGCCTGACG	
690	Rbck1	Rbck1_690	GGAAAGGACGAAACACCGAGTACGCCGGATATGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTACGCCGGGATAGACAG	
691	Rbck1	Rbck1_691	GGAAAGGACGAAACACCGTGCATTCACACGGCATTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCATTACACGGCATTCCGG	
692	Rbck1	Rbck1_692	GGAAAGGACGAAACACCGACCGGAGTCTCCCAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACCCGAGGTCTCCCAACAG	
693	Usp18	Usp18_693	GGAAAGGACGAAACACCGCATCATGAACACTTGAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CATCATGAACACTTGAAGCA	
694	Usp18	Usp18_694	GGAAAGGACGAAACACCGACAGCTCTCGCAGCAGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACAGCTCTCGCAGCAGATGT	
695	Usp18	Usp18_695	GGAAAGGACGAAACACCGTGTACAGCCACGCAATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGTACAGCCACGCAATCA	
696	Usp18	Usp18_696	GGAAAGGACGAAACACCGCAGGCACTGAACGAGCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGGCACTGAACGAGCTCCG	
697	Clcn7	Clcn7_697	GGAAAGGACGAAACACCGGAAAGACGAATCAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAAAGACGAATCAACCACA	
698	Clcn7	Clcn7_698	GGAAAGGACGAAACACCGTAGCTGACAGGGATTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATAGCTGACAGGGATTCACA	
699	Clcn7	Clcn7_699	GGAAAGGACGAAACACCGAATCGGACAGATGAACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AATCGGACAGATGAACAACG	
700	Clcn7	Clcn7_700	GGAAAGGACGAAACACCGACTCGCTCTGACTCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACTCTGCCTCTGTACTGTG	
701	Tcirg1	Tcirg1_701	GGAAAGGACGAAACACCGACACAAGTGCCTCATCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACACAAGTGCCTCATCGCGG	
702	Tcirg1	Tcirg1_702	GGAAAGGACGAAACACCGTCTCCCGAAAGCTGGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCTCCCGAAAGCTGGCAATG	
703	Tcirg1	Tcirg1_703	GGAAAGGACGAAACACCGCAGCCACACTCCAACCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGCCACACTCCAACCTGAG	
704	Tcirg1	Tcirg1_704	GGAAAGGACGAAACACCGCGCTACAGGGAGTTAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGCTACAGGGAGTTAAACCC	
705	Nbn	Nbn_705	GGAAAGGACGAAACACCGTATTCTCATCATCAACAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TATTCTCATCAACAACGCG	
706	Nbn	Nbn_706	GGAAAGGACGAAACACCGTGGAGAAAGTGATAGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGAGAAAGCTGATAGCTCG	
707	Nbn	Nbn_707	GGAAAGGACGAAACACCGTAGCTGGTTTCATCAATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATAGCTGGTTTCATCAATGG	
708	Nbn	Nbn_708	GGAAAGGACGAAACACCGGAGAAATTAAGTAACTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGAATTAAGTAACTCGCA	
709	Tinf2	Tinf2_709	GGAAAGGACGAAACACCGCAAAGCGTGCCATAAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAAAGCGTGCCATAAAGAG	
710	Tinf2	Tinf2_710	GGAAAGGACGAAACACCGCCGGTAGCAAAACCAAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCGGTAGCAAAACCAAGCCGG	
711	Tinf2	Tinf2_711	GGAAAGGACGAAACACCGCCAAAGGGCCAGATTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCAAAGGGCCAGATTAAGG	
712	Tinf2	Tinf2_712	GGAAAGGACGAAACACCGGACTTCTACCGCGGACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGTGTCTTACGCGGCGACGG	
713	Elane	Elane_713	GGAAAGGACGAAACACCGCCGCCACCAACAATCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCGGCCACCAACAATCTCTG	
714	Elane	Elane_714	GGAAAGGACGAAACACCGTCCACAGGCGTTTACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTCACAGGCGTTTACACAG	
715	Elane	Elane_715	GGAAAGGACGAAACACCGGAACGACATTTGATTATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAACGACATTTGATTATCC	
716	Elane	Elane_716	GGAAAGGACGAAACACCGTAGACTGACCTCCAGCCTCTGCGATTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATGACCTCCAGCCTTCGCA	
717	Cfhr1	Cfhr1_717	GGAAAGGACGAAACACCGTTCCTTCTAGATCCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTGCCTTCTAGATCCAACA	
718	Cfhr1	Cfhr1_718	GGAAAGGACGAAACACCGTGCATATACTGGTAAACGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGCATATACTGGTAAACGACA	
719	Cfhr1	Cfhr1_719	GGAAAGGACGAAACACCGACTGGTGAATGCATTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACTGGTGAATGCATTTGG	
720	Cfhr1	Cfhr1_720	GGAAAGGACGAAACACCGAGAGTGACATTTGACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAAGGTGACATTTGACAAG	
721	Ctps	Ctps_721	GGAAAGGACGAAACACCGATTGGCCATTAACCACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATTGGCATTAAACCACAAGC	
722	Ctps	Ctps_722	GGAAAGGACGAAACACCGATACCAAGTACGCTAATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATACCAGTACGCTAATACA	
723	Ctps	Ctps_723	GGAAAGGACGAAACACCGGCCACAAGAGCGATCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCCCAAGAGCGATCGAGC	
724	Ctps	Ctps_724	GGAAAGGACGAAACACCGTTAATACCCGTAGACGAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TTAATACCCGTAGACGAAGA	
725	Slc46a1	Slc46a1_725	GGAAAGGACGAAACACCGAGACTAACATCTGCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAGCTAACATCTGCCACAG	
726	Slc46a1	Slc46a1_726	GGAAAGGACGAAACACCGGGCAATGGATCGATGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCAATGGATCGATGATGG	
727	Slc46a1	Slc46a1_727	GGAAAGGACGAAACACCGTGGACAGAAGAGTCCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGACCAGAAGAGTCCCACC	
728	Slc46a1	Slc46a1_728	GGAAAGGACGAAACACCGGAAGTGGGAACCAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAAGTGGGAACCAAGCG	
729	Nhp2	Nhp2_729	GGAAAGGACGAAACACCGCAGAACGAGGATTCGTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAGAAGCAGATTCGTCGCG	
730	Nhp2	Nhp2_730	GGAAAGGACGAAACACCGCCATCTTCCAGTCTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCATCTTCCAGTCTGTGCG	
731	Nhp2	Nhp2_731	GGAAAGGACGAAACACCGAGGAGATACATTGCCGATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGGAGATACATTTGCCGATTG	
732	Nhp2	Nhp2_732	GGAAAGGACGAAACACCGGGCCGCTCCCGAAGAGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGCCGCTCCCGAAGAGTCCG	
733	Map3k14	Map3k14_733	GGAAAGGACGAAACACCGAAGCCGCAAAAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAAGGCCGCAAAAAACCGT	
734	Map3k14	Map3k14_734	GGAAAGGACGAAACACCGCTGGTTTTAGACATTGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGTGGTTTTAGACATTGCAAG	
735	Map3k14	Map3k14_735	GGAAAGGACGAAACACCGCCCGAACTGAGGACAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCCCGAAACTGAGGACAACG	
736	Map3k14	Map3k14_736	GGAAAGGACGAAACACCGTGGGCCAGTTGGCTTAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGGCCAGTTGGCTTAGATG	
737	Rfx5	Rfx5_737	GGAAAGGACGAAACACCGACATAATGACCGTTCTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACATAATGACGTTCTCGAG	
738	Rfx5	Rfx5_738	GGAAAGGACGAAACACCGATGGGTGTGATAAGTGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATGGGTGTGATAAGTGATCG	
739	Rfx5	Rfx5_739	GGAAAGGACGAAACACCGAGAGCGCTATGATGCCTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGAGCGTCTATGATGCCTAT	
740	Rfx5	Rfx5_740	GGAAAGGACGAAACACCGTCTACCTCAGCTCCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCTACCTCAGCTCCCATCG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
741		lrf7_741	GGAAAGGACGAAACACCGCTTGCGCCAAGACAATTCAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTTGCCCAAGACAATTCAG	
742		lrf7_742	GGAAAGGACGAAACACCGGGCAGGTTAACTCCACTAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGCAGGTTAACTCCACTAGG	
743		lrf7_743	GGAAAGGACGAAACACCGTGTGCGGCCCTTGTACATGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTGCGGCCCTTGTACATGA	
744		lrf7_744	GGAAAGGACGAAACACCGGGAGCAAGACCGTGTTCACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGAGCAAGACCGTGTTCACG	
745		lrf3_745	GGAAAGGACGAAACACCGCCAGTCCAGTCCACCCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCAGTGGTCCCTACCCCGC	
746		lrf3_746	GGAAAGGACGAAACACCGAGAAACAATAGCCAGATCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGAAACAATAGCCAGATCTG	
747		lrf3_747	GGAAAGGACGAAACACCGGGCTGGACGAGAGCCGAAACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGCTGGACGAGAGCCGAAACG	
748		lrf3_748	GGAAAGGACGAAACACCGCTGGCGCCCTCGGTAGAAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGCGGCCCTCGGTAGAAGG	
749		lcos_749	GGAAAGGACGAAACACCGTGGTCTTGGTGAGTTCGACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGGTCTTGGTGAGTTCGACG	
750		lcos_750	GGAAAGGACGAAACACCGTATGCAAAATCTCCCTCACTAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TATGCAAAATCTCCCTCACTA	
751		lcos_751	GGAAAGGACGAAACACCGCGAGAAGTAATAGCTTCCCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCAGAAGTAATAGCTTCCCT	
752		lcos_752	GGAAAGGACGAAACACCGAAATGAAAACATCTATGATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAATGAAAACATCTATGAT	
753		Smarcal1_753	GGAAAGGACGAAACACCGTCCAGGTGAAAGCGCACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTCCAGGTGAAGCGCACAG	
754		Smarcal1_754	GGAAAGGACGAAACACCGTTTGGGTTATAAATCCAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTTGGGTTATAAATCCAGCG	
755		Smarcal1_755	GGAAAGGACGAAACACCGTCATTGCAGATATCAAGACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCATTGCAGATATCAAGACC	
756		Smarcal1_756	GGAAAGGACGAAACACCGCTGGCATCCACTCCGGAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCTTGGCATCCACTCCGGAA	
757		Atp6ap1_757	GGAAAGGACGAAACACCGTCCAGGATTTACAGCATACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GAGGATTTACAGCATACCG	
758		Atp6ap1_758	GGAAAGGACGAAACACCGGATATGACCTCATGTGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GATATGACCTCATGTGTGT	
759		Atp6ap1_759	GGAAAGGACGAAACACCGTAGCTAGATCCACATGCAAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAGTAGATCCACATGCAAG	
760		Atp6ap1_760	GGAAAGGACGAAACACCGGTGCTATTGTAACCTACAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTGCTATTGTAACCTACAGG	
761		Unc93b1_761	GGAAAGGACGAAACACCGTCCGAAACCTACTACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGGGAACGCTACTACACCG	
762		Unc93b1_762	GGAAAGGACGAAACACCGCCGAGTTGGACGAAGCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCGAGTTGGACGAAGCTG	
763		Unc93b1_763	GGAAAGGACGAAACACCGAGGTGAAGTATGGCAACATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGGTGAAGTATGGCAACATG	
764		Unc93b1_764	GGAAAGGACGAAACACCGGCACACGCAAGCTCAACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCACACGCAAGCTCAACTG	
765		Nfat5_765	GGAAAGGACGAAACACCGTCAGGCATTTACGTACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCAGCCATTTACGTACTG	
766		Nfat5_766	GGAAAGGACGAAACACCGAGTATCCGGTTAAAAGTGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGTATCCGGTTAAAAGTGAG	
767		Nfat5_767	GGAAAGGACGAAACACCGCCGTTGGGGTAAAGTAACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCCGTGGGGTAAAGTAACAG	
768		Nfat5_768	GGAAAGGACGAAACACCGAAGACCACTCTATAACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAGACCACTTATAACAG	
769		Il1f5_769	GGAAAGGACGAAACACCGTCACTCTGGGGTCAAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTATCCTGGGGTCAAGG	
770		Il1f5_770	GGAAAGGACGAAACACCGAACATCATGGAGCTCTACCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACATCATGGAGCTCTACCT	
771		Il1f5_771	GGAAAGGACGAAACACCGAGGCGCAATTTGAAACTTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGGGCAATTTGAAACTTGG	
772		Il1f5_772	GGAAAGGACGAAACACCGTGTGTTCCCAAACTCGGCACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTTGTTCCCAAACTCGGGC	
773		Mefv_773	GGAAAGGACGAAACACCGTCTGATAACCTACTACGGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCTGATAACCTACTACGGGG	
774		Mefv_774	GGAAAGGACGAAACACCGAAGGGTACCTTCAACAAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAGGAGGTTACCTTCAAG	
775		Mefv_775	GGAAAGGACGAAACACCGACAAAAGGAGGATCAGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACCAAAGGAGGATCAGAG	
776		Mefv_776	GGAAAGGACGAAACACCGTCTGAATGGAAGGACTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCTGAATGGAAGGACTACGG	
777		Extl3_777	GGAAAGGACGAAACACCGGCCCAAGCTCGCGTCAACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCCCAAGCTCGGTCAACG	
778		Extl3_778	GGAAAGGACGAAACACCGTCAGACATAGCATGGACAAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCAGACATAGCGAAGTCCG	
779		Extl3_779	GGAAAGGACGAAACACCGCCACACAGTCCCACTCAGTGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCACAGTGCCCACTCAGT	
780		Extl3_780	GGAAAGGACGAAACACCGATTGCGGAGGATTTAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATTGCGGAGGATTTAGGTTG	
781		Tyk2_781	GGAAAGGACGAAACACCGTGTGTTACGCGCAGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTGTTGTTACGCGCAGAG	
782		Tyk2_782	GGAAAGGACGAAACACCGTAGACCCCGCATGATACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAGACCCCGCATGATGACG	
783		Tyk2_783	GGAAAGGACGAAACACCGTCCAGGACATTTCCACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTTCCAGGACATTTCCACG	
784		Tyk2_784	GGAAAGGACGAAACACCGATCCACATCGCACAAAAGTGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATCCACATCGCACAAAAGT	
785		Samhd1_785	GGAAAGGACGAAACACCGATCCTTACATATGTCGATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATCCTTACATATGTCGATG	
786		Samhd1_786	GGAAAGGACGAAACACCGCTTGATATAGCGAAGTCCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCTTGATATAGCGAAGTCCG	
787		Samhd1_787	GGAAAGGACGAAACACCGCTGGGCTGCCATCGACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTTGGGCTGCCATCGACGG	
788		Samhd1_788	GGAAAGGACGAAACACCGTTAGGATCTTACCTAGGTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTAGGATCTTACCTAGGTCG	
789		Adar_789	GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACTCCAACAAGCCGCTACG	
790		Adar_790	GGAAAGGACGAAACACCGAGAGGTAAACCCAGTAAACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGAGGTAACCCAGTAAACAG	
791		Adar_791	GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTCTGTAGGGTGAACACCG	
792		Adar_792	GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTATCCAGGAATTCCTAG	
793		Tbk1_793	GGAAAGGACGAAACACCGTGCCTTTAGACCCCTCGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGCCGTTAGACCCCTCGAG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
794	Tbk1	Tbk1_794	GGAAAGGACGAAACACCCGCTTCTCGCTACAACACATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTTCTCGCTACAACACATGA	
795	Tbk1	Tbk1_795	GGAAAGGACGAAACACCCGCAACATCATGCGCGTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAACATCATGCGCGTCATAG	
796	Tbk1	Tbk1_796	GGAAAGGACGAAACACCCGCGGAAACCACTCAATACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGGGAACAACCTCAATACCGT	
797	Mogs	Mogs_797	GGAAAGGACGAAACACCCGCTAGGTCATCTTCCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTAGGTCATTCTTCCCACG	
798	Mogs	Mogs_798	GGAAAGGACGAAACACCCGTCGGCAGCATATCCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGGCAGCATATCCAGATG	
799	Mogs	Mogs_799	GGAAAGGACGAAACACCCGTGCCGAAATAGACGTGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCCGAAATAGACGTGTGGG	
800	Mogs	Mogs_800	GGAAAGGACGAAACACCCGAGGTCCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGGTCCTACTACCAGAGAT	
801	Tnfrs13b	Tnfrs13b_801	GGAAAGGACGAAACACCCGTTACTACGACCATCTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAACGACCATCTCTCTGG	
802	Tnfrs13b	Tnfrs13b_802	GGAAAGGACGAAACACCCGGAAGTCAGTCCAGCAACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAAGTCAGGTCAGACAACCT	
803	Tnfrs13b	Tnfrs13b_803	GGAAAGGACGAAACACCCGTGGCTCTCTCTACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGGCTCTCTCTACGCTG	
804	Tnfrs13b	Tnfrs13b_804	GGAAAGGACGAAACACCCGATCAGTACTGGGACTCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATCAGTACTGGGACTCTCA	
805	Bcl11b	Bcl11b_805	GGAAAGGACGAAACACCCGTTGTGCAAAATGTAGCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTGTGCAAAATGTAGCTGGA	
806	Bcl11b	Bcl11b_806	GGAAAGGACGAAACACCCGTCGAGCCGCTCGTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGAGAGCCCGTCTGCTGAG	
807	Bcl11b	Bcl11b_807	GGAAAGGACGAAACACCCGCGGGAAGTTCATCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCGGGAAGTTCATCTGACAC	
808	Bcl11b	Bcl11b_808	GGAAAGGACGAAACACCCGAGAGGTGAAGTAATCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGAGGTGAAGTAATCACGG	
809	Stk4	Stk4_809	GGAAAGGACGAAACACCCGAAATACACCAGATATCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AATACACCAGATATCAAGG	
810	Stk4	Stk4_810	GGAAAGGACGAAACACCCGTATCTGATATCATTCCGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATCTGATATCATTCCGGCTA	
811	Stk4	Stk4_811	GGAAAGGACGAAACACCCGTGCTGATATCCATCCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCTGATATCCATCCAATGA	
812	Stk4	Stk4_812	GGAAAGGACGAAACACCCGTTCCAGGAGCCATCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTCAGGAGCCATCAAACCG	
813	Ncstn	Ncstn_813	GGAAAGGACGAAACACCCGACGAGAACCATGTAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCAGCAGAACCATGTAAGGG	
814	Ncstn	Ncstn_814	GGAAAGGACGAAACACCCGTGCTATCAAGATCAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGCTATCAAGTCAACAACC	
815	Ncstn	Ncstn_815	GGAAAGGACGAAACACCCGAGGACGAGAACCACCCGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGGGACAGAACCACCCGTG	
816	Ncstn	Ncstn_816	GGAAAGGACGAAACACCCGGTACTCACCATTGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTGACTCACCATTGTGGGA	
817	Il21r	Il21r_817	GGAAAGGACGAAACACCCGACGTTACTACATATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCACGTACTACATATGTG	
818	Il21r	Il21r_818	GGAAAGGACGAAACACCCGATGATATCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGGACGCTATGATATCTCT	
819	Il21r	Il21r_819	GGAAAGGACGAAACACCCGCCACCTCACACAGCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCCACCTCACACAGCATAG	
820	Il21r	Il21r_820	GGAAAGGACGAAACACCCGGGCTGGAAGAACTCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGGCTGGAAGAACTCTCAG	
821	Il21	Il21_821	GGAAAGGACGAAACACCCGGTGACGAAGTCTAATCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTGACGAAGTCTAATCAGG	
822	Il21	Il21_822	GGAAAGGACGAAACACCCGATAATCTATGAAATGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAAATCTATGAAATGACT	
823	Il21	Il21_823	GGAAAGGACGAAACACCCGAACTCAAGCCATCAAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAACTCAAGCCATCAAACCC	
824	Il21	Il21_824	GGAAAGGACGAAACACCCGACATTCATCATTGACCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GACATTCATCATTGACCTCG	
825	Lpin2	Lpin2_825	GGAAAGGACGAAACACCCGGATACTCAGTCTTCTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGATACTCAGTCTTCTAATG	
826	Lpin2	Lpin2_826	GGAAAGGACGAAACACCCGTTATATATCCGGATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTTATATATCCGGATCAGG	
827	Lpin2	Lpin2_827	GGAAAGGACGAAACACCCGTGCAGGTCACAAAAGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGCAGGTCAAAAAGAGAA	
828	Lpin2	Lpin2_828	GGAAAGGACGAAACACCCGACCTGGATCCGTGCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AACCTGGATCCGTGCTACTG	
829	Nop10	Nop10_829	GGAAAGGACGAAACACCCGATCGCGTTTTATACGCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGATCGGTTTTATACGCTGA	
830	Nop10	Nop10_830	GGAAAGGACGAAACACCCGCAATATACCTCAACGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAATATACCTCAACGACGA	
831	Nop10	Nop10_831	GGAAAGGACGAAACACCCGGAGCAGGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGAGAACCAGCAGGATGGG	
832	Nop10	Nop10_832	GGAAAGGACGAAACACCCGAGCAGAAATTTGACCCTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGCAGAAATTTGACCCTAT	
833	Psenen	Psenen_833	GGAAAGGACGAAACACCCGAGAAATGATCACCAGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGAGAATGATCACCAGAAAG	
834	Psenen	Psenen_834	GGAAAGGACGAAACACCCGGAAGTACTATCTTGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCGGAAGTACTATCTTGGTA	
835	Psenen	Psenen_835	GGAAAGGACGAAACACCCGTTGGAGCGGGTATCCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTTGGAGCGGGTATCCAAATG	
836	Psenen	Psenen_836	GGAAAGGACGAAACACCCGATGTTGACTAACCAAGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATGTTGACTAACCAAGAAAG	
837	Ndn12	Ndn12_837	GGAAAGGACGAAACACCCGACGTATGTCAGGCGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CACGTATGTCAGGCGCTCGG	
838	Ndn12	Ndn12_838	GGAAAGGACGAAACACCCGCAACCATCACCAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAACCATCACCAGACTG	
839	Ndn12	Ndn12_839	GGAAAGGACGAAACACCCGAGAAATCTCCGATCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAAGAGATCCCGATCAAG	
840	Ndn12	Ndn12_840	GGAAAGGACGAAACACCCCTGTCGGCCCCGACCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCCTGTCGGCCCCGACCGTG	
841	Sbds	Sbds_841	GGAAAGGACGAAACACCCGACGATCCGACTGACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCAGATCCGACTGACCAATG	
842	Sbds	Sbds_842	GGAAAGGACGAAACACCCCTTCATGGCTCTCTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTTCATGGCTCTCTCGATG	
843	Sbds	Sbds_843	GGAAAGGACGAAACACCCGACTGAAATCTGCAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTGAAATCTGCAAGCAGGT	
844	Sbds	Sbds_844	GGAAAGGACGAAACACCCGTAGGGATATCGCCACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TAGGGATATCGCCACCATTG	
845	Taz	Taz_845	GGAAAGGACGAAACACCCGTTGGAGAAGCTTAACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGGAGAAGCTTAACCATG	
846	Taz	Taz_846	GGAAAGGACGAAACACCCGGTCATCCATGCAAGACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGTCATCCATGCAAGACTGG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
847	Taz	Taz_847	GGAAAGGACGAAACACCGAGCAGCTCACCTCGACACACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGCAGCTCACCTCGACACAC	
848	Taz	Taz_848	GGAAAGGACGAAACACCGTATGAGCTCATTGAGAACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TATGAGCTCATTGAGAACCG	
849	Cdca7	Cdca7_849	GGAAAGGACGAAACACCGCTACTGGTGGGATTATATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCTACTGGTGGGATTATATG	
850	Cdca7	Cdca7_850	GGAAAGGACGAAACACCGGCTGTCAAACTGTCATCGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCTGTCAAACTGTCATCGG	
851	Cdca7	Cdca7_851	GGAAAGGACGAAACACCGGTGCTGCCAGGAAACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTGGCTACCAAGGAAAC	
852	Cdca7	Cdca7_852	GGAAAGGACGAAACACCGTCTGTCAGAGAAACAGCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTCGTCCAGAGAAACAGCCA	
853	Magt1	Magt1_853	GGAAAGGACGAAACACCGTGTGTGCGATCGCAGCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTGTGCGATCGCAGCGG	
854	Magt1	Magt1_854	GGAAAGGACGAAACACCGCAGCTGAGCAGATTGCCCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAGCTGAGCAGATTGCCCGG	
855	Magt1	Magt1_855	GGAAAGGACGAAACACCGTTATGCTGGACCCCTAATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTATGCTGGACCCCTAATGT	
856	Magt1	Magt1_856	GGAAAGGACGAAACACCGTGGAGCTTTAACAGACGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTGGAGCTTTAACAGACGA	
857	Rnaseh2b	Rnaseh2b_857	GGAAAGGACGAAACACCGCTCCTAGTCAACCAAACCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTCCTAGTCAACCAAACCTG	
858	Rnaseh2b	Rnaseh2b_858	GGAAAGGACGAAACACCGTCAGCCCTTGGACCAAGTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCAGCCCTTGGACCAAGTCG	
859	Rnaseh2b	Rnaseh2b_859	GGAAAGGACGAAACACCGTATGGAGATAGTGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CAGCCTTAGGAGATAGTA	
860	Rnaseh2b	Rnaseh2b_860	GGAAAGGACGAAACACCGTGGCCAGCTTTACGAAACAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGGCCAGCTTTACGAACAGG	
861	Jagn1	Jagn1_861	GGAAAGGACGAAACACCGGCACCTACAGATGAGGTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCACTACAGATGAGGTACG	
862	Jagn1	Jagn1_862	GGAAAGGACGAAACACCGTACTCTATCTGTAGTGCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTACCTCATCTGGTAGTGCA	
863	Jagn1	Jagn1_863	GGAAAGGACGAAACACCGAGTGCCTGCGCAGCGCTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGTGCATGGCAGCGCTCC	
864	Jagn1	Jagn1_864	GGAAAGGACGAAACACCGCCGTCGGTCCCGCCGCTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCGTCGGTCCCGCCGCTCG	
865	Ino80	Ino80_865	GGAAAGGACGAAACACCGGGTTCGGAATATCCTCACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGGTTGCGGAATATCCTCAC	
866	Ino80	Ino80_866	GGAAAGGACGAAACACCGAGAAAATGAATTGTCTGACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGAAAATGAATTGTCTGACA	
867	Ino80	Ino80_867	GGAAAGGACGAAACACCGTCCCATCAATGCATGAAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGCCATCAATGCATGAAGG	
868	Ino80	Ino80_868	GGAAAGGACGAAACACCGGTGACGTGGAGATTCTCAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTGACGTGGAGATTCTCAG	
869	Rnaseh2c	Rnaseh2c_869	GGAAAGGACGAAACACCGCGTGAAGAAAGCGATCTACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CGTGAAGAAAGCGATCACCG	
870	Rnaseh2c	Rnaseh2c_870	GGAAAGGACGAAACACCGCGGCTGACTAGAACCTGCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CGGCTGACTAGAACCTGCGA	
871	Rnaseh2c	Rnaseh2c_871	GGAAAGGACGAAACACCGAGGGTTCGCGGATTCTGTAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGGGTTGCGGGATTCTGTGA	
872	Rnaseh2c	Rnaseh2c_872	GGAAAGGACGAAACACCGACCGTCTGTCATCGTGGCGGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACCGTCTGCATCGTGGCGGA	
873	G6pc3	G6pc3_873	GGAAAGGACGAAACACCGTAGGCCGACTGCCAATAGGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAGGCCGACTGCCAATAGGA	
874	G6pc3	G6pc3_874	GGAAAGGACGAAACACCGTTCGCGGGCTAGAGAATATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTCCCGGGCTAGAGAATATG	
875	G6pc3	G6pc3_875	GGAAAGGACGAAACACCGGCTCATTAGCCACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGGGCTCATTAGCCAGCCAA	
876	G6pc3	G6pc3_876	GGAAAGGACGAAACACCGTAAAGAGATCCAATACATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAAAGAGAGTCCAATACATG	
877	Ctc1	Ctc1_877	GGAAAGGACGAAACACCGTGGTGAATAACCCGCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGGTGAATAACCCGCTG	
878	Ctc1	Ctc1_878	GGAAAGGACGAAACACCGCTGTAGATGAGATCCTCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTTGTAGATGAGATCCTCCA	
879	Ctc1	Ctc1_879	GGAAAGGACGAAACACCGAATTGCAAGTAACCAAGACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AATTGCAAGTAACCAAGACC	
880	Ctc1	Ctc1_880	GGAAAGGACGAAACACCGCTTGGACTATGGGGTACACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTTGGAACTATGGGGTACAC	
881	Gins1	Gins1_881	GGAAAGGACGAAACACCGCCGCGCGGTGTAACCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCGGCGCGGTGTAACCTCG	
882	Gins1	Gins1_882	GGAAAGGACGAAACACCGTGCTCGGATTAGAGCACTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGCTTCGGATTAGAGCACTC	
883	Gins1	Gins1_883	GGAAAGGACGAAACACCGTGTGTTGTTACAGACGGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTTGTTGTTACAGACGGAG	
884	Gins1	Gins1_884	GGAAAGGACGAAACACCGTCTTGTACTTACATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGTCTCTTGCTACTTACATG	
885	C8g	C8g_885	GGAAAGGACGAAACACCGTGGGACTCACAGCTTTCGGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGGACTCACAGCTTTCGGA	
886	C8g	C8g_886	GGAAAGGACGAAACACCGCTGGGGAGCTGCGTGCAATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGGGGAGCTGCGTGAATG	
887	C8g	C8g_887	GGAAAGGACGAAACACCGCTCACCTTGAACAAGAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCTCACCTTGAACAAGAAG	
888	C8g	C8g_888	GGAAAGGACGAAACACCGCTGAGCACTGAAATGACCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGAGCACTGAAATGACCT	
889	Rnaseh2a	Rnaseh2a_889	GGAAAGGACGAAACACCGTGTACACGATACAGCTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTACACGATACAGCTGCG	
890	Rnaseh2a	Rnaseh2a_890	GGAAAGGACGAAACACCGTAAACAGATGGCGTAGACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GTAAACAGATGGCGTAGACCA	
891	Rnaseh2a	Rnaseh2a_891	GGAAAGGACGAAACACCGAGACCTTGACAGAGAACGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGACCTTGACAGAGAACGAG	
892	Rnaseh2a	Rnaseh2a_892	GGAAAGGACGAAACACCGGCTCTTGAGACACACAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGCTCCTTGAGACACACAGC	
893	Trnt1	Trnt1_893	GGAAAGGACGAAACACCGCATGAATTAAGAATAGCAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CATGAATTAAGAATAGCAGG	
894	Trnt1	Trnt1_894	GGAAAGGACGAAACACCGATTGCGATGATCAACAACAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATTGCGATGATCAACAACA	
895	Trnt1	Trnt1_895	GGAAAGGACGAAACACCGAACCTGTTCTCACCTATGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACCTGTTCTCACCTATGTG	
896	Trnt1	Trnt1_896	GGAAAGGACGAAACACCGGAGCAATTGTCGACAGACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGCAAGATTGTCGACAGACC	
897	Rnf168	Rnf168_897	GGAAAGGACGAAACACCGGTGTGCCAGTTAACTGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGTGTGCCAGTTAACTGG	
898	Rnf168	Rnf168_898	GGAAAGGACGAAACACCGCCCGGGCCACAGTTATGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCCGGGCCACAGTTATGTGT	
899	Rnf168	Rnf168_899	GGAAAGGACGAAACACCGAGCATGGTTACAGAGCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGCATGGTTACAGAGCGTG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
900	Rnf168	Rnf168_900	GGAAAGGACGAAACACCGAATCTCTGGACAAGAATCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AATCTCTGGACAAGAATCAA	
901	Unc13d	Unc13d_901	GGAAAGGACGAAACACCGAATCTGGTACAGGACGTCATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AATCTGGTACAGGACGTCAT	
902	Unc13d	Unc13d_902	GGAAAGGACGAAACACCGACAGAGACCTACCCAGACCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ACAGAGACCTACCCAGACCG	
903	Unc13d	Unc13d_903	GGAAAGGACGAAACACCGTGGCTGGTGAACCCAGCGGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TGGCTGGCTGAAACAGCGG	
904	Unc13d	Unc13d_904	GGAAAGGACGAAACACCGGACCCGCTGTGCCGACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GCAGCCGTGTGCCGACAT	
905	Nbas	Nbas_905	GGAAAGGACGAAACACCGAACAAACAGCATATTCGTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AACAAAACAGCATATTCGTG	
906	Nbas	Nbas_906	GGAAAGGACGAAACACCGATAGCAGTATTTATCCATGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ATAGCAGTATTTATCCATG	
907	Nbas	Nbas_907	GGAAAGGACGAAACACCGATTGATGTGCAATTTGGTGTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ATTGATTGATGTCAATTGGT	
908	Nbas	Nbas_908	GGAAAGGACGAAACACCGTTGCGGAATGACATGACATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TTTGCCGAATGACATGACAT	
909	Slc29a3	Slc29a3_909	GGAAAGGACGAAACACCGAATGATGCCATGCACGCGAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AATGATGGCCATGCACGCGA	
910	Slc29a3	Slc29a3_910	GGAAAGGACGAAACACCGGGGAACTGCGCAGAACCCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GGGAAACTGCGCAGAACCCG	
911	Slc29a3	Slc29a3_911	GGAAAGGACGAAACACCGCAAGGAACTGCTGCCATGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CAAGGAACTGCTGCCATG	
912	Slc29a3	Slc29a3_912	GGAAAGGACGAAACACCGACCAAAAACACTCGAACTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ACCAGAAAACACTCGAACTG	
913	Ifih1	Ifih1_913	GGAAAGGACGAAACACCGTGTGGTTTTGACATAGCGCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TGTGGTTTTGACATAGCGCG	
914	Ifih1	Ifih1_914	GGAAAGGACGAAACACCGCTAGACGACATATACCAGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CGTAGACGACATATACCAG	
915	Ifih1	Ifih1_915	GGAAAGGACGAAACACCGTGGTTCCAAAATCTGACATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TGGTTCCAAAATCTGACAT	
916	Ifih1	Ifih1_916	GGAAAGGACGAAACACCGGATTGATGTCATATAGCCACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GATTGATGTCATATAGCCACC	
917	Snx10	Snx10_917	GGAAAGGACGAAACACCGCAGAGCCATCTGAATCCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GCAGAGCCATCTGAATCCG	
918	Snx10	Snx10_918	GGAAAGGACGAAACACCGCATGTGCGACCAACCGCCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CATGTGCGACCAACCGCCCA	
919	Snx10	Snx10_919	GGAAAGGACGAAACACCGAAACATCTTGTGTACGAAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AAACATCTTGTGTACGAAGA	
920	Snx10	Snx10_920	GGAAAGGACGAAACACCGAAAGAGTGCATTTCTGCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AAAGCAAGAGTGCATTTCTG	
921	Tnfrsf13c	Tnfrsf13c_921	GGAAAGGACGAAACACCGCAGACTCACTAGACCCACCACTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CAGACTCACTAGACCCACCA	
922	Tnfrsf13c	Tnfrsf13c_922	GGAAAGGACGAAACACCGGACACGCGAGTTTCTCACCAGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GACACGAGTTTCTCACCAG	
923	Tnfrsf13c	Tnfrsf13c_923	GGAAAGGACGAAACACCGCTCCGCGTGAGACCCGACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CTCCGCGTGAGACCCGCG	
924	Tnfrsf13c	Tnfrsf13c_924	GGAAAGGACGAAACACCGCACTCGAGTTGATGCACTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GCATCTCGGTTGATTCGACT	
925	Spink5	Spink5_925	GGAAAGGACGAAACACCGCGGAAAGTACCCAATCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CGGAAAGTACCCAATCCG	
926	Spink5	Spink5_926	GGAAAGGACGAAACACCGAGGAGAGTACCTGTACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AGGGAGAGTACCTGTATCG	
927	Spink5	Spink5_927	GGAAAGGACGAAACACCGCGAGAAAATGACCTGTGCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CGAGAAAATGACCTGTGCG	
928	Spink5	Spink5_928	GGAAAGGACGAAACACCGTGGAGACTTGGATGTACACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TGGAAGACTTGGATGTACAC	
929	Tmem173	Tmem173_929	GGAAAGGACGAAACACCGGAAGCCAAACATCCAATCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GAAGGCCAAACATCCAATG	
930	Tmem173	Tmem173_930	GGAAAGGACGAAACACCGTATCTCGGAATCGAATTTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TATCTCGGAATCGAATTTG	
931	Tmem173	Tmem173_931	GGAAAGGACGAAACACCGAGTATGACCAAGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AGTATGACCAAGCCAGCCG	
932	Tmem173	Tmem173_932	GGAAAGGACGAAACACCGCAGTAGTCCAAGTTCTGTCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CAGTAGTCCAAGTTCTGCG	
933	Parn	Parn_933	GGAAAGGACGAAACACCGAAAACCGTCTCAAGCCAAATGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AAAACGGTCTCAAGCCAAATG	
934	Parn	Parn_934	GGAAAGGACGAAACACCGGTCATACTAAAAGCACAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GGTCATACTAAAAGCACA	
935	Parn	Parn_935	GGAAAGGACGAAACACCGAAGACATATAGTTATCAGCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AAGACATATAGTTATCAGCA	
936	Parn	Parn_936	GGAAAGGACGAAACACCGCAACTCACCGAATAGCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CCAACCTCACCGAATAGCAA	
937	Stx11	Stx11_937	GGAAAGGACGAAACACCGTCAACACTATGCTCTCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TCGAACACTATGCTCTCCG	
938	Stx11	Stx11_938	GGAAAGGACGAAACACCGAGCCATGTACGAGTACAACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AGCCATGTACGAGTACAACC	
939	Stx11	Stx11_939	GGAAAGGACGAAACACCGCATGTGCGGCGAGCAGATTTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CATGTGCGGCGAGCAGATTG	
940	Stx11	Stx11_940	GGAAAGGACGAAACACCGAGTCTTCTGATAGACGTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AGCTGCTCTGATAGACGTTG	
941	Rhoh	Rhoh_941	GGAAAGGACGAAACACCGGTACTGTGCTACTCTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GGTACTGATGTGCTACTCTG	
942	Rhoh	Rhoh_942	GGAAAGGACGAAACACCGCCACGGTGTACGAGAATACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CCCACGGTGTACGAGAATAC	
943	Rhoh	Rhoh_943	GGAAAGGACGAAACACCGACAACACGACCCGGGTACAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ACAACGACACCCGGGTACA	
944	Rhoh	Rhoh_944	GGAAAGGACGAAACACCGCAGGGCCGGATACTTCTGAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CAGGGCCGGATACTTCTGA	
945	Dock8	Dock8_945	GGAAAGGACGAAACACCGTTCGTTTTGCGACACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			ACTCCGTTTTGCGACACCG	
946	Dock8	Dock8_946	GGAAAGGACGAAACACCGCCGAACAGTAGTGCACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CCGGAACAGTAGTGCACGT	
947	Dock8	Dock8_947	GGAAAGGACGAAACACCGAGCACGTTTTAAGGGATGACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AGCAGTTTTAAGGGATGACG	
948	Dock8	Dock8_948	GGAAAGGACGAAACACCGTAGCGAAGTTCACTGCTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			TAGCGAAGTTCACTGCTGG	
949	Ercc612	Ercc612_949	GGAAAGGACGAAACACCGCTGTACAGACCAACTCACGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CTGTACAGACCAACTCACG	
950	Ercc612	Ercc612_950	GGAAAGGACGAAACACCGCTACCAAGACTCTTATCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			CGTACCAAGACTCTTATCAA	
951	Ercc612	Ercc612_951	GGAAAGGACGAAACACCGGTACTTGCAGATTACCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			GGTACTTGCAGATTACCAA	
952	Ercc612	Ercc612_952	GGAAAGGACGAAACACCGAAGGATGAATGGATACCTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAAC	73			AAGGATGAATGGATACCTG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
953	Dnajc21	Dnajc21_953	GGAAAGGACGAAACACCGTAGGTACGATAACACCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TAGGTACGATAACCCCGAG	
954	Dnajc21	Dnajc21_954	GGAAAGGACGAAACACCGCTCCAGAGCGACTATGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTCCAGAGCGACTATGACA	
955	Dnajc21	Dnajc21_955	GGAAAGGACGAAACACCGTAAACGAGATAAGAGAGTGCCTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TAAACGAGATAAGAGAGTGC	
956	Dnajc21	Dnajc21_956	GGAAAGGACGAAACACCGTGGATCAGATGAAAACGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGGATCAGATGAAAACGAG	
957	Lrba	Lrba_957	GGAAAGGACGAAACACCGGACCTCAATGAACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GACCGTCCCAATGAACTAG	
958	Lrba	Lrba_958	GGAAAGGACGAAACACCGGTGTGGCGAGTGGACGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTGTGGCGAGTGGACGAAGA	
959	Lrba	Lrba_959	GGAAAGGACGAAACACCGATAGTTACCATGTACCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ATAGTTACCATGTACCACTG	
960	Lrba	Lrba_960	GGAAAGGACGAAACACCGCAGATGCAGTAGACCAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGATGCAGTAGACCAACAA	
961	Lamtor2	Lamtor2_961	GGAAAGGACGAAACACCGTTCCTATCATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTTCCGTTCTATCATACG	
962	Lamtor2	Lamtor2_962	GGAAAGGACGAAACACCGGTGCCTACTCCGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCTGGCCTACTCCGTTATG	
963	Lamtor2	Lamtor2_963	GGAAAGGACGAAACACCGCCACCTCGTAATGGCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCACCTCGTAATGGCTACA	
964	Lamtor2	Lamtor2_964	GGAAAGGACGAAACACCGCACAGATGCCCGGCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACAGATGCCCGGCTACTG	
965	Smarcd2	Smarcd2_965	GGAAAGGACGAAACACCGGAGATAATCGGGAACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GAGATAATGCGGGAATGCG	
966	Smarcd2	Smarcd2_966	GGAAAGGACGAAACACCGCATCGGATGCCACCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCATCGGATGCCACCACAC	
967	Smarcd2	Smarcd2_967	GGAAAGGACGAAACACCGCCCAACCACTCACTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCCAACCACTCACTCGCTG	
968	Smarcd2	Smarcd2_968	GGAAAGGACGAAACACCGCGGAGCAGCTGTGCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CGGAGCAGCTGTGCCAATG	
969	C230052i12Rik	C230052i12Rik_969	GGAAAGGACGAAACACCGTACGACCAATAATGCTCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTAGCCCAATAATGCTCTAG	
970	C230052i12Rik	C230052i12Rik_970	GGAAAGGACGAAACACCGTAGGCGAGGATGCTCCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TGAGGCGAGGATGCTCCGAC	
971	C230052i12Rik	C230052i12Rik_971	GGAAAGGACGAAACACCGCAGTAAACTCTGGACTGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CAGTAAACTCTGGACTGCT	
972	C230052i12Rik	C230052i12Rik_972	GGAAAGGACGAAACACCGTATGATCCCTTGAAGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TATGATCCCTTGAAGATGTG	
973	Usb1	Usb1_973	GGAAAGGACGAAACACCGCAGCTATGTAGATGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACACGGTATGTAGATGTGGG	
974	Usb1	Usb1_974	GGAAAGGACGAAACACCGTCTCGATCCTCACCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCTCGATCCTCACCAACGG	
975	Usb1	Usb1_975	GGAAAGGACGAAACACCGGTACAACATCTGAGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGTACAACATCTGAGCTCG	
976	Usb1	Usb1_976	GGAAAGGACGAAACACCGGACGACAGTGAAGCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GACGACAGTGAAGCATGG	
977	Traf3ip2	Traf3ip2_977	GGAAAGGACGAAACACCGTCTCAGGTAACACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTCTGCGAGTAAACGAGG	
978	Traf3ip2	Traf3ip2_978	GGAAAGGACGAAACACCGGTAGTACTGACAGTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GTAGTACTGACAGTTCATG	
979	Traf3ip2	Traf3ip2_979	GGAAAGGACGAAACACCGCTGCGAGCTAAAGTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCTGCGAGCTAAAGTCTCGG	
980	Traf3ip2	Traf3ip2_980	GGAAAGGACGAAACACCGCCAAGCATTAGGTAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CCAAAGCATTAGGTAACCTG	
981	Ticam1	Ticam1_981	GGAAAGGACGAAACACCGAAGATGCCATCGATCACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAGATGCCATCGATCACTG	
982	Ticam1	Ticam1_982	GGAAAGGACGAAACACCGTCTGGAACGCTAATTTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCTGGAACGCTAATTTCTGTG	
983	Ticam1	Ticam1_983	GGAAAGGACGAAACACCGGATACAAGGGGACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATATCAAGGGGACCCAG	
984	Ticam1	Ticam1_984	GGAAAGGACGAAACACCGCTCACACCATGGAACCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTTCACCATGGAACCCAT	
985	Fermt3	Fermt3_985	GGAAAGGACGAAACACCGGTGCATGACCTGACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAGGTGCATGACCTGACAA	
986	Fermt3	Fermt3_986	GGAAAGGACGAAACACCGCTGCACACTCCGAGTCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTGTCACTCCGAGTCCAG	
987	Fermt3	Fermt3_987	GGAAAGGACGAAACACCGGGCTACCCAGTACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGGCTACGCCAGTACTGGG	
988	Fermt3	Fermt3_988	GGAAAGGACGAAACACCGCTCACCCATCCCGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CTCACCCATCCCGCTCA	
989	Mthfd1	Mthfd1_989	GGAAAGGACGAAACACCGACCAACAGATAGATTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACACCAAGTATGATTCTCTG	
990	Mthfd1	Mthfd1_990	GGAAAGGACGAAACACCGTCAATCGTGACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACTATGAATCCGTCACAG	
991	Mthfd1	Mthfd1_991	GGAAAGGACGAAACACCGGATTGCCGGAAGGCACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATTGCCGGAAGGCACGCGG	
992	Mthfd1	Mthfd1_992	GGAAAGGACGAAACACCGGTAGCGTCCAGTAAGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGTAGCGTCCAGTAAGAAAG	
993	Obfc1	Obfc1_993	GGAAAGGACGAAACACCGGACGCGAGTTTTAATCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GACGAGTTTTAATCCCAAG	
994	Obfc1	Obfc1_994	GGAAAGGACGAAACACCGCAACCGGCATCCAATAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACCGGCATCCAATAAGGC	
995	Obfc1	Obfc1_995	GGAAAGGACGAAACACCGGAGATATCATCCGAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGAGATATCATCCGAGTCCG	
996	Obfc1	Obfc1_996	GGAAAGGACGAAACACCGTCCAGTGCTCAGAAATAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCGAGTCTCAGAAATAGCT	
997	Card11	Card11_997	GGAAAGGACGAAACACCGCAGCATAACTGTGTTTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCAGCATAACTGTGTTTCATG	
998	Card11	Card11_998	GGAAAGGACGAAACACCGACTATGGAGTCATTTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			ACTATGGAGTCATTTCCCGG	
999	Card11	Card11_999	GGAAAGGACGAAACACCGCACACTCTCTGATGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			CACACTCTCTGATGAACG	
1000	Card11	Card11_1000	GGAAAGGACGAAACACCGGCGACTCCAACCTCGAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GCGACCTCCAACCTCGAGGTG	
1001	Sp110	Sp110_1001	GGAAAGGACGAAACACCGAAATGACCTGGAATGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AAATGACCTGGAATGGCCA	
1002	Sp110	Sp110_1002	GGAAAGGACGAAACACCGGTCAAATTCCAAAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GGTCAAATTCCAAAGAGAGA	
1003	Sp110	Sp110_1003	GGAAAGGACGAAACACCGTCTGAATGCAGCCAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			TCCTGAATGCAGCCAAGGAG	
1004	Sp110	Sp110_1004	GGAAAGGACGAAACACCGAGCTCAAGGCAGTGAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			AGCTCAAGGCAGTGAGCAGG	
1005	Orai1	Orai1_1005	GGAAAGGACGAAACACCGGATCGGCCAGGTTACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAA	73			GATCGGCCAGGTTACTCCG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1006	Orai1	Orai1_1006	GGAAAGGACGAAACACCGTGCCGATGCATGCGCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGGCGATGCATGCGCTCGTG	
1007	Orai1	Orai1_1007	GGAAAGGACGAAACACCGAAGACGATGAGCAACCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AAGACGATGAGCAACCTGG	
1008	Orai1	Orai1_1008	GGAAAGGACGAAACACCGAATCCGGAGCTCCCGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AATCCGGAGCTCCCGTGAG	
1009	Pgm3	Pgm3_1009	GGAAAGGACGAAACACCGTACGCCTCACATAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TACGGCCTCACATAACCTGG	
1010	Pgm3	Pgm3_1010	GGAAAGGACGAAACACCGAAGTCTCAAGGTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AACTTCTTCAAGGTACCGCG	
1011	Pgm3	Pgm3_1011	GGAAAGGACGAAACACCGTACACCATGTAGTCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TACCCATGTAGTCAACTG	
1012	Pgm3	Pgm3_1012	GGAAAGGACGAAACACCGCTGCTATGACATACCCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGCTATGACATACCCTGTG	
1013	C7	C7_1013	GGAAAGGACGAAACACCGCATACTGATCGATTAACCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CATACTGATCGATTAACCTG	
1014	C7	C7_1014	GGAAAGGACGAAACACCGATCAACACCAAAGTTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATCAACACCAAAGTTTCGG	
1015	C7	C7_1015	GGAAAGGACGAAACACCGCAATCTCTGCAACCTGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAATCTGCAACCTGAACG	
1016	C7	C7_1016	GGAAAGGACGAAACACCGGTCTCCACCAATAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTGCTCCACCAATAGCGC	
1017	C8b	C8b_1017	GGAAAGGACGAAACACCGAAGACGCCATGGAGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AAAGACGCCATGGAGCAAG	
1018	C8b	C8b_1018	GGAAAGGACGAAACACCGATTGTGACTTGTCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATTGTGTGACTTCCGACA	
1019	C8b	C8b_1019	GGAAAGGACGAAACACCGTTGACTGTGAGCTATCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TTGACTGTGAGCTATCCACC	
1020	C8b	C8b_1020	GGAAAGGACGAAACACCGCAAGGACAGAGCGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAAGGACAGAGCGCGTGG	
1021	Cebpe	Cebpe_1021	GGAAAGGACGAAACACCGCAGTACCAAGTGGCACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAGTACCAAGTGGCACACTG	
1022	Cebpe	Cebpe_1022	GGAAAGGACGAAACACCGTAGTGTGAGGAAACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCAGGTAGTGGAAACGAG	
1023	Cebpe	Cebpe_1023	GGAAAGGACGAAACACCGCAGACTCGATGTAGGCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAGACTCGATGTAGGCGGAG	
1024	Cebpe	Cebpe_1024	GGAAAGGACGAAACACCGCTTACCTTGAGGACACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTTACCTTGAGGACACGCAA	
1025	Tirap	Tirap_1025	GGAAAGGACGAAACACCGCTGTCTGTGAACCATCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGTCTGTGAACCATCATAG	
1026	Tirap	Tirap_1026	GGAAAGGACGAAACACCGCGAAACAATGGCGCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CGAAACAATGGCGCCACCG	
1027	Tirap	Tirap_1027	GGAAAGGACGAAACACCGTGCAGCTCGAGGGTGTAGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGCAGCTCGAGGGTGTAGCTA	
1028	Tirap	Tirap_1028	GGAAAGGACGAAACACCGCAAGTAGGAGACGAGCTCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAAGTAGGAGACGAGCTCCT	
1029	Dclre1b	Dclre1b_1029	GGAAAGGACGAAACACCGTGTAGACAAACCCACCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGCTAGACAAACCCACCGTG	
1030	Dclre1b	Dclre1b_1030	GGAAAGGACGAAACACCGTCCACTGAAGCATGGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCCACTGAAGCATGGCAGAG	
1031	Dclre1b	Dclre1b_1031	GGAAAGGACGAAACACCGAGAGAAACATGACAGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGAGAAACATGACAGAACCA	
1032	Dclre1b	Dclre1b_1032	GGAAAGGACGAAACACCGTGAATGGTCAAGTACGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGAATGGTCAAGTACGGGA	
1033	Tlr3	Tlr3_1033	GGAAAGGACGAAACACCGCTTAGATGAAATCCAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTTAGATGAAATCCAGTCCG	
1034	Tlr3	Tlr3_1034	GGAAAGGACGAAACACCGTGTAGGAAAGATCGAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTTGTAGGAAAGATCGAGCT	
1035	Tlr3	Tlr3_1035	GGAAAGGACGAAACACCGAATGGTCAAGTTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GAATGGTCAAGTTACGAAGA	
1036	Tlr3	Tlr3_1036	GGAAAGGACGAAACACCGATCTACAAAGTTGGGAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATCTACAAAGTTGGGAACGG	
1037	Card14	Card14_1037	GGAAAGGACGAAACACCGCCACGCGCATGAAACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CCACGCGCATGAAACGTG	
1038	Card14	Card14_1038	GGAAAGGACGAAACACCGTCTTACTTAGAGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGTTCTACTTAGAGACTCG	
1039	Card14	Card14_1039	GGAAAGGACGAAACACCGCACTTGGAGAATACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CACTCGGAGAATACAAACGC	
1040	Card14	Card14_1040	GGAAAGGACGAAACACCGAGAATAAATCGGCTTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGAACTAAATCGGCTTAAGG	
1041	Rfxap	Rfxap_1041	GGAAAGGACGAAACACCGTCCAAGACCTGCAGTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCCAAGACCTGCAGTACGA	
1042	Rfxap	Rfxap_1042	GGAAAGGACGAAACACCGCACCAACAGATGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCACCGCAACAGATGTACA	
1043	Rfxap	Rfxap_1043	GGAAAGGACGAAACACCGTGGACACATCGGACCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGACACATCGAACCCGCG	
1044	Rfxap	Rfxap_1044	GGAAAGGACGAAACACCGTCAACGGAGGGCGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTCACCGAGGGCGCTCCG	
1045	Il17rc	Il17rc_1045	GGAAAGGACGAAACACCGCTGTGGAACGATGACAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGTGGAACGATGACAACAT	
1046	Il17rc	Il17rc_1046	GGAAAGGACGAAACACCGAGCAATACTTACCCAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGCAATACTTACCCAGAGG	
1047	Il17rc	Il17rc_1047	GGAAAGGACGAAACACCGGAGCCACAAGATTTCCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGAGCCACAAGATTTCCAGT	
1048	Il17rc	Il17rc_1048	GGAAAGGACGAAACACCGATCTAGCTGCCATACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATCTAGCTGCCATACCCTG	
1049	Wipf1	Wipf1_1049	GGAAAGGACGAAACACCGGGAACGAATGCCTCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGAAACGAATGCCTCCCCG	
1050	Wipf1	Wipf1_1050	GGAAAGGACGAAACACCGCGTTCGAGTCTGCACAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CCGTGAGTCTGCACAACCG	
1051	Wipf1	Wipf1_1051	GGAAAGGACGAAACACCGGGCTTGTCTCAAGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGGGCTTGTCTCAAGGCTG	
1052	Wipf1	Wipf1_1052	GGAAAGGACGAAACACCGGTGAGTCCACCGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCTGAGTCCACCGCAACA	
1053	Wrap53	Wrap53_1053	GGAAAGGACGAAACACCGGTCATTACCCTACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGTCATTACCCTACTAGG	
1054	Wrap53	Wrap53_1054	GGAAAGGACGAAACACCGAGAAACGAATCTCCCCGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGAAACGAATCTCCCCGAGT	
1055	Wrap53	Wrap53_1055	GGAAAGGACGAAACACCGGAAGAGTTGGGAACCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GAAGAGTTGGGAACCATCCG	
1056	Wrap53	Wrap53_1056	GGAAAGGACGAAACACCGGACACAACCAAGCTAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GACACAACCAAGCTAGCCAC	
1057	Tmc6	Tmc6_1057	GGAAAGGACGAAACACCGGAGTCAATGCTCCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGAGTCAATGCTCCAGAG	
1058	Tmc6	Tmc6_1058	GGAAAGGACGAAACACCGTTTCCAAGTGCAGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TTTCCAAGTGCAGCGCTG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1059	Tmc6	Tmc6_1059	GGAAAGGACGAAACACCGGACCGAAGAACTAGGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GACCAGAAAACGTAGGCACG	
1060	Tmc6	Tmc6_1060	GGAAAGGACGAAACACCGTACCCTGCGGTTGGCAGTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TACCGGTTGGCAGTACCAA	
1061	Tmc8	Tmc8_1061	GGAAAGGACGAAACACCGGAGCTCTACGAGATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGAGCTCTACGAGATTGG	
1062	Tmc8	Tmc8_1062	GGAAAGGACGAAACACCGCAACGCTTGCAGTACCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAACGCTTGCAGTACCAGG	
1063	Tmc8	Tmc8_1063	GGAAAGGACGAAACACCGCTTCTACGGTGCCTACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTTCTACGGTGCAGTACCAG	
1064	Tmc8	Tmc8_1064	GGAAAGGACGAAACACCGCATCCGCACAGGCGTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CATCCGCACAGGCGTCCGGG	
1065	Ttc37	Ttc37_1065	GGAAAGGACGAAACACCGCAAAACAGATCACTTCTAGTGTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ACAAACAGATCACTTCTAGT	
1066	Ttc37	Ttc37_1066	GGAAAGGACGAAACACCGCGCTGTGTTCAGACAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CGCCTGTGTTCAGACAGGCG	
1067	Ttc37	Ttc37_1067	GGAAAGGACGAAACACCGTGACGTGTGAAGAACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGACGTGTGAAGAACTCG	
1068	Ttc37	Ttc37_1068	GGAAAGGACGAAACACCGGAGGCGTACTTAAGCAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GAGGCGTACTTAAGCAGAGG	
1069	Mkl1	Mkl1_1069	GGAAAGGACGAAACACCGAGACAGTCTCTCCTCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGACAGTCTCCTCCTCGACG	
1070	Mkl1	Mkl1_1070	GGAAAGGACGAAACACCGGTGATGAGAATCCACACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTGATGAGAATCCACACT	
1071	Mkl1	Mkl1_1071	GGAAAGGACGAAACACCGCTGCCCAAGCTAGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGCCCAAGCTAGCCAA	
1072	Mkl1	Mkl1_1072	GGAAAGGACGAAACACCGTCCAGGATGCACATCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTCAGGATGCACATCTGGA	
1073	Ttc7	Ttc7_1073	GGAAAGGACGAAACACCGTGGGATCGATGACATATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGGGATCGATGACATATCCG	
1074	Ttc7	Ttc7_1074	GGAAAGGACGAAACACCGTCCAAAGCAATTAACCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCAAAGCAATTAACCTACCG	
1075	Ttc7	Ttc7_1075	GGAAAGGACGAAACACCGTCCAAAGCAATTAACCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCAACACACTGTCGCCACGA	
1076	Ttc7	Ttc7_1076	GGAAAGGACGAAACACCGTCCCAAGCAACATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTGCCCAAGCAACATAG	
1077	Dclre1c	Dclre1c_1077	GGAAAGGACGAAACACCGTTTATTCACCAACCTAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TTTATTCACCAACCTAAGCGG	
1078	Dclre1c	Dclre1c_1078	GGAAAGGACGAAACACCGCAGGAAACATACACGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAGGAAACATACACGACTT	
1079	Dclre1c	Dclre1c_1079	GGAAAGGACGAAACACCGCATCAAGCCATCTACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCATCAAGCCATCTGCTATG	
1080	Dclre1c	Dclre1c_1080	GGAAAGGACGAAACACCGTCAACTAAAGATATCTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCAACTAAAGATATCTGCGT	
1081	Slc35c1	Slc35c1_1081	GGAAAGGACGAAACACCGAGGCGCCCTACGTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGGGCACCCTACGTAAGTT	
1082	Slc35c1	Slc35c1_1082	GGAAAGGACGAAACACCGAGGTTAGGCGCCAGATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGGTTAGGCGCCAGATACTG	
1083	Slc35c1	Slc35c1_1083	GGAAAGGACGAAACACCGCATCAAGCCATCTACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTCACAATGATGACGCCCGC	
1084	Slc35c1	Slc35c1_1084	GGAAAGGACGAAACACCGCAGTGAGGTCACCAGGCGATTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCAGTGAGGTCACCAGGCGAT	
1085	C8a	C8a_1085	GGAAAGGACGAAACACCGTCTGTGCTATAGTACTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCTGCTATAGTACTACTG	
1086	C8a	C8a_1086	GGAAAGGACGAAACACCGGGAGATTGAAGTATCCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGAGATTGAAGTATCCGCCCA	
1087	C8a	C8a_1087	GGAAAGGACGAAACACCGCATTGTACACAGTTTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CATTGTACACAGTTTACAC	
1088	C8a	C8a_1088	GGAAAGGACGAAACACCGCTTGCCTTAGACAAGGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CTTGCTTAGACAAGGTTGG	
1089	Rltpr	Rltpr_1089	GGAAAGGACGAAACACCGCCTGACTTACCATGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCCTGACTTACCATGAAGGG	
1090	Rltpr	Rltpr_1090	GGAAAGGACGAAACACCGCAACCAAGTAGACTTACTTGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CAACCAAGTAGACTTACTT	
1091	Rltpr	Rltpr_1091	GGAAAGGACGAAACACCGAGCCAGCTGGATACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGACCACCTGGATCCACA	
1092	Rltpr	Rltpr_1092	GGAAAGGACGAAACACCGCATGACCTGTCAATCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ACATGCGCTGTCAATCACT	
1093	Malt1	Malt1_1093	GGAAAGGACGAAACACCGTCTATGCTCACTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GTCCTATGCTCACTACCAG	
1094	Malt1	Malt1_1094	GGAAAGGACGAAACACCGATATGAGATGTGTAACGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATATGAGATGTGTAACGCTG	
1095	Malt1	Malt1_1095	GGAAAGGACGAAACACCGCACTGGCTAAATCAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CCACTGGCTAAATCAAAAG	
1096	Malt1	Malt1_1096	GGAAAGGACGAAACACCGAGCTTGGACCGCTCCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGCTTGGACCGCTCCGGGA	
1097	Dkc1	Dkc1_1097	GGAAAGGACGAAACACCGTTACTGCAGCAATAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TTTACTGCAGCAATAAGTGG	
1098	Dkc1	Dkc1_1098	GGAAAGGACGAAACACCGTCTTACCCGAAGTATTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCTTACCCGAAGTATTCGT	
1099	Dkc1	Dkc1_1099	GGAAAGGACGAAACACCGTACGCATAGTGTCCGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TACGCATAGTGTCCGAATGT	
1100	Dkc1	Dkc1_1100	GGAAAGGACGAAACACCGATGATGTACTCGATGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			ATGATGTACTCGATGCTCAG	
1101	Ap1s3	Ap1s3_1101	GGAAAGGACGAAACACCGCCACTCCCTGACAAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CCACTCCCTGACAAGGAG	
1102	Ap1s3	Ap1s3_1102	GGAAAGGACGAAACACCGTCCAGACCGTCTCTCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCCAGACCGTCTCTCTCGT	
1103	Ap1s3	Ap1s3_1103	GGAAAGGACGAAACACCGTCACTGCAGCAAGGAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TCAGTGCAGCAAGGAAAGCTG	
1104	Ap1s3	Ap1s3_1104	GGAAAGGACGAAACACCGTAATATGCTACAGCTCACAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TAATATCCAGCTCACAGCC	
1105	Il17f	Il17f_1105	GGAAAGGACGAAACACCGGACTTACTGTAAATCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GACTTACTGTAAATCCCATG	
1106	Il17f	Il17f_1106	GGAAAGGACGAAACACCGTGGAACTGTCTCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			TGGGAATGTCTCCCTGGG	
1107	Il17f	Il17f_1107	GGAAAGGACGAAACACCGAGCGGTTCTGGAATTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGCGGTTCTGGAATTCACGT	
1108	Il17f	Il17f_1108	GGAAAGGACGAAACACCGGGCTCAGCGATCTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GGGCTCAGCGATCTCTGAG	
1109	Nod2	Nod2_1109	GGAAAGGACGAAACACCGCCAGCCATCGTAAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			CCGACCCATCGTAAGTACTG	
1110	Nod2	Nod2_1110	GGAAAGGACGAAACACCGAGATGCCGACACCTACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AGATGCCGACACCTACTGG	
1111	Nod2	Nod2_1111	GGAAAGGACGAAACACCGCAGAGTCTGGACTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			GCAGAGTCTGGACTGACGTG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1112	Nod2	Nod2_1112	GGAAAGGACGAAACACCCGGTTGTAGAGTCTCCTCACAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTGTAGAGTCTCCTCACAA	
1113	Irak4	Irak4_1113	GGAAAGGACGAAACACCCGTAGCTATCAAAAAGCCGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAGCTATCAAAAAGCCGTC	
1114	Irak4	Irak4_1114	GGAAAGGACGAAACACCCGCTGTGTGAACAACACCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGTGTGAACAACACCATCG	
1115	Irak4	Irak4_1115	GGAAAGGACGAAACACCCGTGAAGCATACACTAAGCAGCTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTAAGCATACACTAAGCAC	
1116	Irak4	Irak4_1116	GGAAAGGACGAAACACCCGCAAGGTGCAAGTTGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAAGGTGCAAGGTTGCTCAG	
1117	Zbtb24	Zbtb24_1117	GGAAAGGACGAAACACCCGGAATCGAAGTTACCCGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGAAATCGAAGTTACCCGTG	
1118	Zbtb24	Zbtb24_1118	GGAAAGGACGAAACACCCGTGAGAAATACTCGCTACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGAGAAATACTCGCTACTGG	
1119	Zbtb24	Zbtb24_1119	GGAAAGGACGAAACACCCGACACGCTCCATAAACTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACACGCTCCATAAACTTCCGG	
1120	Zbtb24	Zbtb24_1120	GGAAAGGACGAAACACCCGATCCTCTGAAACGGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATCCTCTGAAACGGAACCG	
1121	Rnf31	Rnf31_1121	GGAAAGGACGAAACACCCGGATGGATTGAGTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATGGATTGAGTTTCCCGGA	
1122	Rnf31	Rnf31_1122	GGAAAGGACGAAACACCCGAACTATGAGTTGTTGGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAACTATGAGTTGTTGGACG	
1123	Rnf31	Rnf31_1123	GGAAAGGACGAAACACCCGCTACCTCAACACCCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTACCTCAACACCCATCCCA	
1124	Rnf31	Rnf31_1124	GGAAAGGACGAAACACCCGGAGGACCAAGGTGTTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGAGGAACCAAGGTTGTGTG	
1125	Rtel1	Rtel1_1125	GGAAAGGACGAAACACCCGACACGGGATCCATGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACACGGGATCCATGCGTGG	
1126	Rtel1	Rtel1_1126	GGAAAGGACGAAACACCCGTATGCCGCATACCCGGTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATGCCGCATACCCGGTAGG	
1127	Rtel1	Rtel1_1127	GGAAAGGACGAAACACCCGTTGTCATACACCTAAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTGTCATACACCTAAGGT	
1128	Rtel1	Rtel1_1128	GGAAAGGACGAAACACCCGAGCGCTCCCAACCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAGGCGTCCCAACCTGGGA	
1129	Irf2bp2	Irf2bp2_1129	GGAAAGGACGAAACACCCGCGCAGCGTGTGAAGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGCAGCGTGTGAAGTCCGG	
1130	Irf2bp2	Irf2bp2_1130	GGAAAGGACGAAACACCCGCGCAGAACCTTGACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CGGCGAGAACCTTGACCAAG	
1131	Irf2bp2	Irf2bp2_1131	GGAAAGGACGAAACACCCGTCTCGATGACGAACCTCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTCGATGACGAACCTCCAG	
1132	Irf2bp2	Irf2bp2_1132	GGAAAGGACGAAACACCCGGGACGAGCTATCCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGCCGACAGCTTTACAGCGG	
1133	Gimap5	Gimap5_1133	GGAAAGGACGAAACACCCGTCACCAAGTAACAACACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTCACCAAGTAACAACATG	
1134	Gimap5	Gimap5_1134	GGAAAGGACGAAACACCCGAGCTAGATTCTTGTACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGCTAGATTCTTGTACACAG	
1135	Gimap5	Gimap5_1135	GGAAAGGACGAAACACCCGACTGGAATGCTGGTCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTGGAATGCTGGTCTCGG	
1136	Gimap5	Gimap5_1136	GGAAAGGACGAAACACCCGTAAGATGCCATGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGAAGATGCCATGGCTGTG	
1137	Lig4	Lig4_1137	GGAAAGGACGAAACACCCGTTAGAGCTCTAATTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTAGAGCTCTAATTGTGGG	
1138	Lig4	Lig4_1138	GGAAAGGACGAAACACCCGCAACTCAACTGCATCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCAACTCAACTGCATCATTG	
1139	Lig4	Lig4_1139	GGAAAGGACGAAACACCCGAAACGCAATTGTGAATAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAACGCAATTGTGAATAAATG	
1140	Lig4	Lig4_1140	GGAAAGGACGAAACACCCGATCCGTCGAGCTCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CATCCGTCGAGCTCCACTG	
1141	Chd7	Chd7_1141	GGAAAGGACGAAACACCCGACATGCCATAAACGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GACATGCCATAAACGAACCG	
1142	Chd7	Chd7_1142	GGAAAGGACGAAACACCCGAAACCGTTTTAAGTCAAAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAACGGTTTTAAGTCAAAAAC	
1143	Chd7	Chd7_1143	GGAAAGGACGAAACACCCGCTACCGGAATGATTTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCTACCGGAATGATTTAGCA	
1144	Chd7	Chd7_1144	GGAAAGGACGAAACACCCGTGATGACACACAGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGATGACACACAGGCCCA	
1145	Ccbe1	Ccbe1_1145	GGAAAGGACGAAACACCCGACCTACCGAGAGGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GACCTACCGAGAGGAACCCG	
1146	Ccbe1	Ccbe1_1146	GGAAAGGACGAAACACCCGACGAGTGCACGGATAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGCAGTGCACGGATAACTT	
1147	Ccbe1	Ccbe1_1147	GGAAAGGACGAAACACCCGACAGAGAGTGGTATTGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACAGAGAGTGGTATTGCTGG	
1148	Ccbe1	Ccbe1_1148	GGAAAGGACGAAACACCCGAACTGGCAAGTATGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAACTGGCAAGTATGTCAA	
1149	Fat4	Fat4_1149	GGAAAGGACGAAACACCCGACATCGTGGACGATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GACATCGTGGACGATCGAGG	
1150	Fat4	Fat4_1150	GGAAAGGACGAAACACCCGATTTATCTCATCACTACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGTTATCTCATCACTACCG	
1151	Fat4	Fat4_1151	GGAAAGGACGAAACACCCGGGATGTCGAAAGAGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGGATGTCGAAAGAGTACAC	
1152	Fat4	Fat4_1152	GGAAAGGACGAAACACCCGATAGATCCTATGTCGCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATTAGATCCTATGTCGCGT	
1153	Card9	Card9_1153	GGAAAGGACGAAACACCCGATGTAACAAGGACCGTATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GATGTAACAAGGACCGTATCG	
1154	Card9	Card9_1154	GGAAAGGACGAAACACCCGTGACTTTCCGGTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGACTTTCCGGTAACTG	
1155	Card9	Card9_1155	GGAAAGGACGAAACACCCGTAGATAGGTTGTGATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TAGATAGGTTGTGATCCGGG	
1156	Card9	Card9_1156	GGAAAGGACGAAACACCCGCAACTGGTATCCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCAACCTGGTATCCGCAAG	
1157	Plekhm1	Plekhm1_1157	GGAAAGGACGAAACACCCGACTGATGAGGAGTTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGACTTGTAGGAGAGTTCCA	
1158	Plekhm1	Plekhm1_1158	GGAAAGGACGAAACACCCGTGATGAGGAACCGACCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGATGAGGAACCGACCTGTG	
1159	Plekhm1	Plekhm1_1159	GGAAAGGACGAAACACCCGCTGGTAGCTAGGCTATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCTGGTAGCTAGGCTATGGA	
1160	Plekhm1	Plekhm1_1160	GGAAAGGACGAAACACCCGACTCACCGACTCGTAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTCACCGACTCGTAGGAG	
1161	Kmt2d	Kmt2d_1161	GGAAAGGACGAAACACCCGAAATGGCTGTTGATCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAATGGCTGTTGATCCCATG	
1162	Kmt2d	Kmt2d_1162	GGAAAGGACGAAACACCCGTTCCACCTAATACCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTTCCACCTAATACCCCA	
1163	Kmt2d	Kmt2d_1163	GGAAAGGACGAAACACCCGTCGGGCGGACTAACATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGGGCGGACTAACATCCG	
1164	Kmt2d	Kmt2d_1164	GGAAAGGACGAAACACCCGTGGGATGGACAGCCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGGATGGACAGCCGACG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1165	Otulin	Otulin_1165	GGAAAGGACGAAACACCCGGAACTTCACAGCTTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGAACTTACAGCTTCGTAG	
1166	Otulin	Otulin_1166	GGAAAGGACGAAACACCCGTGATACTACTGTGCACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGATAACTACTGTGCACTGA	
1167	Otulin	Otulin_1167	GGAAAGGACGAAACACCCGAAACAGAACCCAGGTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AACAGAACCCAGGTTAAGTG	
1168	Otulin	Otulin_1168	GGAAAGGACGAAACACCCGAGTATACCTGGATCAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGTATACCTGGATCAAGCAG	
1169	Cfhr2	Cfhr2_1169	GGAAAGGACGAAACACCCGTGTCCCTAGACTCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGCCCTTAGACTCAACA	
1170	Cfhr2	Cfhr2_1170	GGAAAGGACGAAACACCCGAAATGGAGACTCTACATACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAATGGAGACTCTACATACT	
1171	Cfhr2	Cfhr2_1171	GGAAAGGACGAAACACCCGACTTATTTCTATAGACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACTTATTTCTATAGACACT	
1172	Cfhr2	Cfhr2_1172	GGAAAGGACGAAACACCCGATACCATTTAGAAATATAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATACCATTTAGAAATATAAGG	
1173	Nlrp1b	Nlrp1b_1173	GGAAAGGACGAAACACCCGTAATGACCTGTGTGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTAAATGACCTGTGCGACGA	
1174	Nlrp1b	Nlrp1b_1174	GGAAAGGACGAAACACCCGAGATGCTAAAGAGCACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGATGCTAAAGAGCACCTTA	
1175	Nlrp1b	Nlrp1b_1175	GGAAAGGACGAAACACCCGAGAAGATCATTCTTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AGAAGATCATTCTTATGTG	
1176	Nlrp1b	Nlrp1b_1176	GGAAAGGACGAAACACCCGCTGAAGCAAGGGTTAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTGTAAGCAAGGGTTAGCAG	
1177	Vps13b	Vps13b_1177	GGAAAGGACGAAACACCCGTCCCTACTCCCAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTCATACTACCCAAATCG	
1178	Vps13b	Vps13b_1178	GGAAAGGACGAAACACCCGTAACACTGCAATACAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TAAACTGCAATACAAGCG	
1179	Vps13b	Vps13b_1179	GGAAAGGACGAAACACCCGAAACCTCTTCCCGATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAAACCTCTCCCGATACAG	
1180	Vps13b	Vps13b_1180	GGAAAGGACGAAACACCCGTGGCAGTAGTCCATGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGCAGTAGTCCATGACTG	
1181	Isg15	Isg15_1181	GGAAAGGACGAAACACCCGTCCGTAACCTAACTCAATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTCCGTGACTAACTGATGA	
1182	Isg15	Isg15_1182	GGAAAGGACGAAACACCCGACGACGACAGTGTGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGCAGCAGTGTGCTAG	
1183	Isg15	Isg15_1183	GGAAAGGACGAAACACCCGCATCTGTTGAGGAAACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCATCTGGTGAGGAAACGAA	
1184	Isg15	Isg15_1184	GGAAAGGACGAAACACCCGTGAAAGGGTAAGACCCGCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGAAAGGGTAAGACCCGCTCC	
1185	Epg5	Epg5_1185	GGAAAGGACGAAACACCCGACGCGACTCGTTGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACAGCCGACTCGTTGTAACA	
1186	Epg5	Epg5_1186	GGAAAGGACGAAACACCCGTCGAGCCAGAAGAACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCGAGCCAGAAGAACCAATG	
1187	Epg5	Epg5_1187	GGAAAGGACGAAACACCCGTGGTACCATACCCATATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGGTACCATACCCATATG	
1188	Epg5	Epg5_1188	GGAAAGGACGAAACACCCGAAACGCTGTTTACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GAAACGCTGTCTTACACAAG	
1189	C1ra	C1ra_1189	GGAAAGGACGAAACACCCGTTTCCGAGAATGATGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTTGCCAGAATGATGGCACA	
1190	C1ra	C1ra_1190	GGAAAGGACGAAACACCCGTGTGCAGGTATATATCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGTGCAGGTATATATCCCTG	
1191	C1ra	C1ra_1191	GGAAAGGACGAAACACCCGCCACACAGACTTCTCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCACACAGACTTCTCCAATG	
1192	C1ra	C1ra_1192	GGAAAGGACGAAACACCCGTGGTTGTCTCCAAGTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGGTTGTCTCCAAGTCACTG	
1193	C1s2	C1s2_1193	GGAAAGGACGAAACACCCGATCTCATGTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AATTCCTCATGTCTCATG	
1194	C1s2	C1s2_1194	GGAAAGGACGAAACACCCGTTCTCTAGATAATCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTCTCTAGATAATCTCAGG	
1195	C1s2	C1s2_1195	GGAAAGGACGAAACACCCGTTTCAAACCTGATCTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCTTCAAACCTGATCTAATG	
1196	C1s2	C1s2_1196	GGAAAGGACGAAACACCCGAAACACACAGTTAAACTGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AACACACAGTTAAACTGTCA	
1197	C4b	C4b_1197	GGAAAGGACGAAACACCCGCAAGATGCCTCTTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCACAAGATGCCTCTTAGTG	
1198	C4b	C4b_1198	GGAAAGGACGAAACACCCGACGACAGCCCTCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGGCACAGCCCTCAACTG	
1199	C4b	C4b_1199	GGAAAGGACGAAACACCCGTAAGCCACAAAGTGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTAAGCCACAAAGTGAACCG	
1200	C4b	C4b_1200	GGAAAGGACGAAACACCCGTGAAACAAAGGACCATGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TGAAACAAAGGACCATGCTG	
1201	Cd59b	Cd59b_1201	GGAAAGGACGAAACACCCGTAATATGAGCCGATTAGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TATTATGAGCCGATTAGACG	
1202	Cd59b	Cd59b_1202	GGAAAGGACGAAACACCCGATCTCAACTGTTAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATGCTACAACGTTTTAGACC	
1203	Cd59b	Cd59b_1203	GGAAAGGACGAAACACCCGGCAAGTGTATCAACAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGCAAGTGTATCAACAGTGT	
1204	Cd59b	Cd59b_1204	GGAAAGGACGAAACACCCGTTGATACACTTGCCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TTGATACACTTGCCTCTCGT	
1205	Lat	Lat_1205	GGAAAGGACGAAACACCCGACTCAGAGGTGGCTTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73	Gecko Library v2		ACTCAGAGGTGGCTTGTAGT	
1206	Lat	Lat_1206	GGAAAGGACGAAACACCCGCATCCGATGGGAAACCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GCATCCGATGGGAAACCCCA	
1207	Lat	Lat_1207	GGAAAGGACGAAACACCCGATACTCAGGGATGGGGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATACTCAGGGATGGGGAGC	
1208	Lat	Lat_1208	GGAAAGGACGAAACACCCGCTGTGGAAGTGCTGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CTCTGTGGAAGTGCTGTCAT	
1209	Nhej1	Nhej1_1209	GGAAAGGACGAAACACCCCTATGCATAGAGCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CCCTATGCATAGAGCTCGGC	
1210	Nhej1	Nhej1_1210	GGAAAGGACGAAACACCCGACCTCACTATGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ACCAGCCGAGCTCTTAGCAT	
1211	Nhej1	Nhej1_1211	GGAAAGGACGAAACACCCGGCTGGTTATCAGTTCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GGCTGGTTATCAGTTCCTCG	
1212	Nhej1	Nhej1_1212	GGAAAGGACGAAACACCCGTACCAACAGCACAGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TCACCAACAGCACAGCCTC	
1213	Dock2	Dock2_1213	GGAAAGGACGAAACACCCGAAAGTGAACACACGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			AAGAAGTGAACACACGCTC	
1214	Dock2	Dock2_1214	GGAAAGGACGAAACACCCGACGATCTCAGCTACAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			CAGCATCTCAGCTACAGAT	
1215	Dock2	Dock2_1215	GGAAAGGACGAAACACCCGTGACAGTTTTATGCTTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			GTGACAGTTTTATGCTTTATG	
1216	Dock2	Dock2_1216	GGAAAGGACGAAACACCCGTACATCCTTTATCCATCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			TACATCCTTTATCCATCTCA	
1217	Mysm1	Mysm1_1217	GGAAAGGACGAAACACCCGATCACTATCTTGATTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAG	73			ATCACTATCTTGATTCAACG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1218	Mysm1	Mysm1_1218	GGAAAGGACGAAACACCGAAAATCTGGGTTAATCAAAGTTTGTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAAAATCTGGGTTAATCAAAA	
1219	Mysm1	Mysm1_1219	GGAAAGGACGAAACACCGTATCATTGAGAAAATGCTGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TATCATTGAGAAAATGCTGT	
1220	Mysm1	Mysm1_1220	GGAAAGGACGAAACACCGTTATCTAATAAATCACTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTATCTAATAAATCACTTCC	
1221	Kdm6a	Kdm6a_1221	GGAAAGGACGAAACACCGTTGGATAATCTTCCAATAAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTGGATAATCTTCCAATAAG	
1222	Kdm6a	Kdm6a_1222	GGAAAGGACGAAACACCGTAGCATTATCTGCATACCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAGCATTATCTGCATACCAAG	
1223	Kdm6a	Kdm6a_1223	GGAAAGGACGAAACACCGGAAACCTCACGAACCCGAAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GAAACCTCACGAACCCGAAA	
1224	Kdm6a	Kdm6a_1224	GGAAAGGACGAAACACCGCGCCAGGATGAAGGCCCTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CGCCAGGATGAAGGCCCTGC	
1225	Thpp2	Thpp2_1225	GGAAAGGACGAAACACCGCACACCAAGCAGTCATATACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CACACCAAGCAGTCATATAC	
1226	Thpp2	Thpp2_1226	GGAAAGGACGAAACACCGATTGATATCATTGATACAACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATTGATATCATTGATACAAC	
1227	Thpp2	Thpp2_1227	GGAAAGGACGAAACACCGATAGGCCAATAAACTAATCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ATAGGCCAATAAACTAATCA	
1228	Thpp2	Thpp2_1228	GGAAAGGACGAAACACCGTGTATGACTTCTATCCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGTTATGACTTCTATCCAA	
1229	Il12b	Il12b_1229	GGAAAGGACGAAACACCGCTGCCATTGAACTGGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCTGCCATTGAACTGGCGT	
1230	Il12b	Il12b_1230	GGAAAGGACGAAACACCGCCATGAGCAGTGAACCGTGTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CCATGAGCAGTGAACCGT	
1231	Il12b	Il12b_1231	GGAAAGGACGAAACACCGCATGTCACTGCCGAGAGTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CATGTCACTGCCGAGAGTC	
1232	Il12b	Il12b_1232	GGAAAGGACGAAACACCGGACTGGAATCCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GACTGGACTCCCGATCCCC	
1233	Stat2	Stat2_1233	GGAAAGGACGAAACACCGTGAGATTGAAAATCGAATCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGAGATTGAAAATCGAATCC	
1234	Stat2	Stat2_1234	GGAAAGGACGAAACACCGTCCCAATCGCTCGGGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TCCCAACTCGCTCGGGGGC	
1235	Stat2	Stat2_1235	GGAAAGGACGAAACACCGCTGAGCTGTAGTGGTCCACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CTGAGCTGTAGTGGTCCAC	
1236	Stat2	Stat2_1236	GGAAAGGACGAAACACCGAGTCTTGGTGAGATCCATCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGTCTTGGTGAGATCCATC	
1237	C3	C3_1237	GGAAAGGACGAAACACCGGATGACGACTGCTTGGCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GATGACGACTGCTTGGCCCA	
1238	C3	C3_1238	GGAAAGGACGAAACACCGCAAAAGGCAAGATGCGGTGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			ACAAGGCAAGATGCGGTGT	
1239	C3	C3_1239	GGAAAGGACGAAACACCGGAGCGAAGAGACCATCGTACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GAGCGAAGAGACCATCGTAC	
1240	C3	C3_1240	GGAAAGGACGAAACACCGGACAGTCGTCATCCTCATTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GACAGTCGTCATCCTCATTG	
1241	C6	C6_1241	GGAAAGGACGAAACACCGTAGTAGTGAACGATTACTATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TAGTAGTGAACGATTACTAT	
1242	C6	C6_1242	GGAAAGGACGAAACACCGCGATAAGCTTTGATCAAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			CGATAAGCTTTGATCAAGC	
1243	C6	C6_1243	GGAAAGGACGAAACACCGTGAACACGGTATGATTACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TGAACACGGTATGATTAC	
1244	C6	C6_1244	GGAAAGGACGAAACACCGGTTGCCCCCAAACCTGACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GGTTGCCCCCAAACCTGACT	
1245	Cfb	Cfb_1245	GGAAAGGACGAAACACCGTTCGATCTGCACGGGTATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			TTGAGTCTGCACGGGTAT	
1246	Cfb	Cfb_1246	GGAAAGGACGAAACACCGAATACCGTCCACGACCGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AATACGCTGCCACGACCGC	
1247	Cfb	Cfb_1247	GGAAAGGACGAAACACCGCTGGATACGTCCCAATCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			GCTGGATACGTCCCAATCC	
1248	Cfb	Cfb_1248	GGAAAGGACGAAACACCGAGCCACGAGGACAAGTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AGCCAGCAGGACAAGTCCC	
1253	BRDN0000737505	BRDN0000737505_1253	GGAAAGGACGAAACACCGAAAAGTCCGCGATTACGTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73	NTCs		AAAAAGTCCGCGATTACGTC	
1254	BRDN0000737693	BRDN0000737693_1254	GGAAAGGACGAAACACCGCAAAACCGCTCGATCGGTGATTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAAAAGGCTCGATCGGTGAT	
1255	BRDN0000737637	BRDN0000737637_1255	GGAAAGGACGAAACACCGAAAACGTAATATACCGAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAAAAGTAAATATACCGAGC	
1256	BRDN0000738185	BRDN0000738185_1256	GGAAAGGACGAAACACCGAAAATGCACTTCCCGGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAAAATGCACTTCCCGGCC	
1257	BRDN0000737801	BRDN0000737801_1257	GGAAAGGACGAAACACCGAAAACCCCGCGCGGAGCGTCTTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACCCCGCGCGGAGCGTC	
1258	BRDN0000737467	BRDN0000737467_1258	GGAAAGGACGAAACACCGAAAACCTAGCGTAGATTGCGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACTAGCGTAGATTCCGC	
1259	BRDN0000737848	BRDN0000737848_1259	GGAAAGGACGAAACACCGAAAACCGAGGCTGTTTCTACACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACGAGCGTGTCTGTAAC	
1260	BRDN0000737609	BRDN0000737609_1260	GGAAAGGACGAAACACCGAAAACCTATACGTACGGAATCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACTATACGTACGGAATC	
1261	BRDN0000737434	BRDN0000737434_1261	GGAAAGGACGAAACACCGAAAACCTCCGCTGCAACCGATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACTCCGCTGCAACCGAT	
1262	BRDN0000738254	BRDN0000738254_1262	GGAAAGGACGAAACACCGAAAAGCGTCACTCAGCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAAGCGTGCATTACGCGAG	
1263	BRDN0000737777	BRDN0000737777_1263	GGAAAGGACGAAACACCGAAAACCGTAAAGTCCGCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACATGTTAAGTCCGCTTAT	
1264	BRDN0000737611	BRDN0000737611_1264	GGAAAGGACGAAACACCGAACCGCATTTGACCGCGCTTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGACATTTGACCGCGCT	
1265	BRDN0000737528	BRDN0000737528_1265	GGAAAGGACGAAACACCGAACCCCGGCTGTCATCGCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACCCGCTGTCATCGCGC	
1266	BRDN0000738228	BRDN0000738228_1266	GGAAAGGACGAAACACCGAACCCCGGGAACAATCAGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACCCGCGGAACAATCAGC	
1267	BRDN0000737727	BRDN0000737727_1267	GGAAAGGACGAAACACCGAACCGCTGCGCGTTTTGCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AAACCGCTGCGCGTTTTGCAA	
1268	BRDN0000737483	BRDN0000737483_1268	GGAAAGGACGAAACACCGAACCGTACTGCGAGGAGCATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACCGTACTGCGAGGAGCAT	
1269	BRDN0000737872	BRDN0000737872_1269	GGAAAGGACGAAACACCGAACCTCGTCTCATGTACGAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACCTCGTCTCATGTACGAA	
1270	BRDN0000737516	BRDN0000737516_1270	GGAAAGGACGAAACACCGAACCCCGGATTTTCGTTGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGCCCCGATTTTCGTTGA	
1271	BRDN0000737844	BRDN0000737844_1271	GGAAAGGACGAAACACCGAACCGCTGCGCGCGGCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGCGTGCAGCGCGGCAAA	
1272	BRDN0000737412	BRDN0000737412_1272	GGAAAGGACGAAACACCGAACCGGCGCAATACCCCTTTTGTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGCGCGCAATACCCCTTTT	
1273	BRDN0000737631	BRDN0000737631_1273	GGAAAGGACGAAACACCGAACCGTAGCGTACCGTGAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGCTAGCGTACCGTGAA	
1274	BRDN0000737750	BRDN0000737750_1274	GGAAAGGACGAAACACCGAACCGTCAATCCGTGAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAATAAG	73			AACGTTCAATCCGTGAGGG	

No.		*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	sgRNA.Target.Sequence	3'
1275	BRDN0000737875	BRDN0000737875_127	GGAAAGGACGAAACACCGAACGTACCAACCTCGATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACGTCACCAACCTCGATCC	
1276	BRDN0000738229	BRDN0000738229_127	GGAAAGGACGAAACACCGAACGTTATAGCTTCGTCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACGTTATAGCTTCGTCTCT	
1277	BRDN0000737806	BRDN0000737806_127	GGAAAGGACGAAACACCGAACTAACTCACTACGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACTAACTCACTACGCACGA	
1278	BRDN0000738366	BRDN0000738366_127	GGAAAGGACGAAACACCGAACTCCTCATCGTACGCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACTCCTCATCGTACGCTAA	
1279	BRDN0000737593	BRDN0000737593_127	GGAAAGGACGAAACACCGAACTCGCGTGGGAAAGTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AACTCGCGTGGGAAAGTCCGG	
1280	BRDN0000738128	BRDN0000738128_128	GGAAAGGACGAAACACCGAACTTATACGTAATCTGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AACTTATACGTAATCTGATC	
1281	BRDN0000738307	BRDN0000738307_128	GGAAAGGACGAAACACCGAAGACTCCTACGTATCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AAGACTCCTACGTATCGAGC	
1282	BRDN0000737391	BRDN0000737391_128	GGAAAGGACGAAACACCGAAGCACAGAACGGTCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA	73			AAGCACAGAACGGTCCGCC	

IL2RG
JAK3
IL7R
PTPRC
CD3D
CD3E
CD247
CORO1A
LAT
RAG1
RAG2
DCLRE1C
PRKDC
NHEJ1
LIG4
AK2
ADA
DOCK2
CD40LG
CD40
ICOS
CD3G
CD8A
ZAP70
TAP1
TAP2
TAPBP
B2M
CIITA
RFXANK
RFX5
RFXAP
DOCK8
RHOH
STK4
LCK
MALT1
BCL10
BCL11B
IL21
IL21R
TNFRSF4
IKBKB
MAP3K14
RELB
MSN
TFRC

WAS
WIPF1
ARPC1B
ATM
Nbn
BLM
DNMT3B
ZBTB24
CDCA7
HELLS
PMS2
RNF168
MCM4
POLE
POLE2
LIG1
Ndn2
ERCC6L2
GINS1
TBX1
CHD7
SEMA3E
FOXN1
SMARCAL1
MYSM1
EXTL3
STAT3
SPINK5
PGM3
CARD11
DKC1
NHP2
NOP10
RTEL1
TERT
TINF2
TPP1
DCLRE1B
PARN
WRAP53
Obfc1
CTC1
TCN2
SLC46A1
MTHFD1
IKBKG
ORAI1

STIM1
PNP
TTC7
SP110
EPG5
RBCK1
RNF31
CCBE1
FAT4
STAT5B
KMT2D
KDM6A
BTK
IGLL1
CD79A
CD79B
BLNK
PIK3R1
TCF3
PTEN
CD19
CD81
MS4A1
CR2
TNFRSF13B
TNFRSF13C
TNFSF12
MOGS
TRNT1
TTC37
NFKB1
NFKB2
IKZF1
IRF2BP2
ATP6AP1
AICDA
UNG
INO80
MSH6
PRF1
UNC13D
STX11
STXBP2
C230052I12Rik
LYST
RAB27A
AP3B1

AP3D1
FOXP3
IL2RA
CTLA4
LRBA
BACH2
AIRE
ITCH
TPP2
PEPD
DNASE1L3
FAS
FASL
CASP8
FADD
IL10
IL10RA
IL10RB
NFAT5
SH2D1A
XIAP
CD27
CTPS
RASGRP1
CD70
RLTPR
ITK
MAGT1
PRKCD
ELANE
GFI1
HAX1
G6PC3
VPS45
Slc37a4
LAMTOR2
TAZ
VPS13B
USB1
JAGN1
CLPB
CSF3R
SMARCD2
HYOU1
ITGB2
SLC35C1
FERMT3

RAC2
ACTB
FPR1
CTSC
CEBPE
SBDS
WDR1
CFTR
DNAJC21
SRP54a
MKL1
CYBB
CYBA
NCF1
NCF2
NCF4
G6pdx
GATA2
CSF2RB
CSF2RA
IL12RB1
IL12B
IFNGR1
IFNGR2
STAT1
IRF8
TYK2
ISG15
RORC
JAK1
TMC6
TMC8
STAT2
IRF7
IFNAR2
FCGR3
IFIH1
TLR3
UNC93B1
TRAF3
TICAM1
TBK1
IRF3
CARD9
IL17RA
IL17RC
IL17F

TRAF3IP2
IRAK4
MYD88
IRAK1
TIRAP
RPSA
<i>HMOX1</i>
NBAS
RANBP2
CLCN7
SNX10
OSTM1
PLEKHM1
TCIRG1
TNFRSF11A
TNFSF11
NCSTN
PSEN1
PSENE1
<i>TREX1</i>
<i>RNASEH2B</i>
<i>RNASEH2C</i>
<i>RNASEH2A</i>
<i>SAMHD1</i>
<i>ADAR</i>
<i>ACP5</i>
<i>TMEM173</i>
<i>POLA1</i>
<i>USP18</i>
<i>PSMB8</i>
<i>DNASE2a</i>
<i>MEFV</i>
<i>MVK</i>
<i>NLRP1b</i>
<i>TNFRSF1A</i>
<i>PSTPIP1</i>
<i>NOD2</i>
<i>ADAM17</i>
<i>LPIN2</i>
<i>IL1RN</i>
<i>Il1f5</i>
SLC29A3
<i>CARD14</i>
<i>SH3BP2</i>
<i>COPA</i>
<i>OTULIN</i>
<i>TNFAIP3</i>

<i>AP1S3</i>
<i>C1QA</i>
<i>C1QB</i>
<i>C1QC</i>
<i>C1R</i>
<i>C1S</i>
<i>C4A</i>
<i>C2</i>
<i>C3</i>
<i>Hc</i>
<i>C6</i>
<i>C7</i>
<i>C8A</i>
<i>C8G</i>
<i>C8B</i>
<i>C9</i>
<i>MASP2</i>
<i>SERPING1</i>
<i>CFB</i>
<i>CFD</i>
<i>CFP</i>
<i>CFI</i>
<i>CFH</i>
<i>CFHR1</i>
<i>CFHR2</i>
<i>THBD</i>
<i>CD46</i>
<i>CD59</i>
<i>CD55</i>
<i>GIMAP5</i>

x	
1 LAT	
2 NHEJ1	1700029B21Rik cernunno: XLF
3 DOCK2	
4 MYSM1	C130067A03Ri C530050H10Rik
7 KDM6A	Utx
8 TPP2	TppII
9 IL12B	
10 STAT2	
11 C1R	C1ra/C1rb
12 C1S	C1s1/C1s2
13 C4A	C4b
14 C3	
15 C6	
16 CFB	
17 CD59	CD59b/CD59a

Green: Found under other names in Brie Library
Others: Taken from Gecko Library