

Library Number	RMK007
Library Name	Inborn Errors of Metabolism (IEM) Library - Small #1
Old Document Name	IEM (Small#1) Library (Andrew)
Library Purpose	CRISPR/Cas9 Knockout of select genes associated with Inborn Errors of Metabolism in mouse T cells. Genes were selected based off of results of <i>in vitro</i> screens
Location	Main Lab, '-20 Freezer, IEM (Small #1) box
Designer Name	Andrew Patterson
Designing Date	January 2020
Design Reference	Ferreira 2018, Genetics in Medicine; IEMBase
Usage Reference	n/a

Species	Mouse (<i>Mus musculus</i>)
Total Gene #	48
Total Target #	200
Gene Group	
1. Negative Controls	(Nontargeting controls from BRIE library)8
2. Positive Controls	n/a
3. IEM Genes	48
Target Number	
1. Negative Controls	8*1=8
2. Positive Controls	n/a
3. IEM Genes	48*4=192

Note: Design:

The complete IEM CRISPR Library was designed from genes associated with Inborn errors of metabolism as identified by IEMBase. Genes without mouse orthologs, mitochondrial DNA-encoded genes, genes encoding noncoding RNAs, and genes without guides in either the BRIE or Gecko libraries were excluded. Based on *in vitro* screens (See ARP.034 and ARP.037), 48 genes of interested were picked out for this library for further analysis *in vitro* and *in vivo*. Parameters for gene selection:

1. 25 genes from the top 50 depleted in ARP.037 (FDR <5%). Several of these could be counted as positive controls.
2. 15 genes that were neither significantly enriched nor depleted
3. 8 genes that trended toward enrichment
4. Genes within the same complex/pathway were limited to ensure a spread of targets
 - a. i.e. *ATP6AP1* but not *ATP6AP2*
 - b. i.e. *Alg1* but not *Alg2*

Number	Gene Name	sgRNA sequence
1	Mat2a	CCTGATGCTAAAGTGGCTTG
2	Mat2a	GTGCAATATATGCAAGATCG
3	Mat2a	ACCAAGGCAATGTACCATTG
4	Mat2a	ATTTACCACCTACAGCCAAG
5	Tfrc	CTACACGCTTACAATAGCCC
6	Tfrc	GAATACATACACTCCTCGTG
7	Tfrc	GGGCTCCTACTACAACATAA
8	Tfrc	AACCCTCGGGAGACTCCACT
9	Atp6ap2	TTAGCATATTAAGATCGCCA
10	Atp6ap2	TGAACTTGGGAAGCGTTATG
11	Atp6ap2	CCGGTGGAAATAGGTTACCCA
12	Atp6ap2	TGGACAGTGCAGCTACGTCT
13	Vcp	ACTGTCTTCACAGACTCATG
14	Vcp	TATAGGTCGCTTTGACAGAG
15	Vcp	CCAATCGCCTTAAAGAGCGC
16	Vcp	CTTCAGGAGTTGGTTCAGGT
17	Atp6v1a	TGACTGCTGATATCCGACAG
18	Atp6v1a	AGTCGGCCATCATACTGACG
19	Atp6v1a	ATGTTGCCCCACGTAACAG
20	Atp6v1a	CTTACGGGAAAAGGGCATCG
21	Cog4	GGAAACTCACCAACCCATCG
22	Cog4	GCTGTGTACGAACGACTCTG
23	Cog4	GCACAAGTAACGATGAATGT
24	Cog4	CAACAGAAAAAATTGAACCA
25	Nus1	GTGGTCGTAGACGCTAATGT
26	Nus1	TCCAGGTGCCGAAGCGAACG
27	Nus1	ACAGCACCTTCACTGCCGAA
28	Nus1	CCAGCGCAGCCGAGGATGGG
29	Gmppb	GTGGCTTCTCAACAAAACGG
30	Gmppb	GTGCCGATGAAACTGCACCA
31	Gmppb	TTCCCAGTTATGGCCAAGGA
32	Gmppb	GAGCACTCCGAAGCCATTGG
33	Ogt	TTTGAGCCCAAATCATGCGG
34	Ogt	AGCATTATCGACATGCCTTG
35	Ogt	ACAGTGCACTACTAGTCCCA
36	Ogt	GAAAGTTTGTACCATCATCC
37	Gfpt1	TGTGGCACAAGTTACCACGC
38	Gfpt1	AAGCTGCGGTCTTTCCCGTG
39	Gfpt1	GGAGAGAGGAGCCTTAACTG
40	Gfpt1	TCTGTTGTGAACACAATGAG
41	Slc7a5	GCCCTCCTCGCAGTACATCG
42	Slc7a5	ACCCCTACTTACGCACGCAG
43	Slc7a5	AGCGGCCTCTTCGCTACGG
44	Slc7a5	GTAGCAGAGTGCGCCACGA
45	Dhdds	GGATGTCGGGATGAGGAGAG

Number	Gene Name	sgRNA sequence
46	Dhdds	CTATGCCAAGAAGTGTCCAGG
47	Dhdds	CTTCAAACGTTCCAAGAGTG
48	Dhdds	GCAGCAGATGCAGATCACCC
49	Alg11	GGAAACCAGCAAATGCCCTG
50	Alg11	TTTCCTGGACTGATGATATG
51	Alg11	AGTGAACATAGCTTCCGACT
52	Alg11	TAAACCATATCCTCTCACTG
53	Pgm3	TACGGCCTCACATAACCCTG
54	Pgm3	AACTTCTTCAAGGTACCGCG
55	Pgm3	TACACCATGTAGTGCAACTG
56	Pgm3	CTGCTATGACATACCCTGTG
57	Ddost	GAACTCCCCGTAATAATGA
58	Ddost	CCCAGATAAACCAATCACCC
59	Ddost	AGGCAACTATGAACTAGCTG
60	Ddost	GGTCAGAAACATCATAGTTG
61	Rnf31	GATGGATTGAGTTTCCCCGA
62	Rnf31	GAACTATGAGTTGTTGGACG
63	Rnf31	CTACCTCAACACCCTATCCA
64	Rnf31	GGAGGAACCAAGGTGTTGTG
65	Ogdh	TTGGCCCACTCATAGATACG
66	Ogdh	GACTAGTTCGAACTATGTGG
67	Ogdh	GTAAGTGAAGACCTTGCA
68	Ogdh	AAAGCTGAACAGTTCTACTG
69	Slc35a2	TCACCCGCTGTAGTGGACCC
70	Slc35a2	CTGCTCTTCGCACAAAAGAG
71	Slc35a2	CTGCAAGGTATAGATGAGAG
72	Slc35a2	GGCCACTGGATCAGAACCCG
73	Pisd	CAAACCTTGCTAGTCACTGGG
74	Pisd	GGTCCCCAGAAAATGGCGTG
75	Pisd	GGGCCCTCGAGCCAATACAG
76	Pisd	CGTATGTGGCTTGCACTGTG
77	Umps	GAGCAGATAACTGTGCCAG
78	Umps	CCGCAGGTCGATGTAGACTG
79	Umps	AGAGCGTGCACACGGCGTGG
80	Umps	TCTGTCTGCCGATGTGTCCG
81	Gpx4	CGTGTGCATCGTCACCAACG
82	Gpx4	CATGCCCGATATGCTGAGTG
83	Gpx4	TGGTCTGGCAGGCACCATGG
84	Gpx4	TAAGCCAGCACTGCTGTGCG
85	Gale	ATCTTCACCGATGCGCCCAG
86	Gale	AGAACTTGGACTTGCCGTAG
87	Gale	TTAACTCTATAGTAGTCCAG
88	Gale	CTGGGGGTTCCCGTACACGG
89	Alg13	GATCTTGTCAATTAGCCACGC
90	Alg13	GTGAATGACTCAGTACGGAA

Number	Gene Name	sgRNA sequence
91	Alg13	GGTTGTAACCCAGACTCTCG
92	Alg13	TTTCGACGAGCTCGTCGCAC
93	Hcfc1	GGTACCCTTCACAACCAATG
94	Hcfc1	ACAGCAGTATGTGACTCCCG
95	Hcfc1	TGGAAGGGCTAGTTGCACAA
96	Hcfc1	CCCAAGGTTAGCCACAACAG
97	Slc25a22	GTGTCTTAGCCAGGTCGATG
98	Slc25a22	ATACATGCCGAAGTAGCCCT
99	Slc25a22	TGATTCAGGTTGGCAAACAG
100	Slc25a22	GACACCAGCTCTCTAAGGAT
101	Pten	CCTCCAATTCAGGACCCACG
102	Pten	TGTGCATATTTATTGCATCG
103	Pten	ACTATTCCAATGTTTCAGTGG
104	Pten	GGTTTGATAAGTTCTAGCTG
105	Asah1	GCAAGGTGTACGTTACCTAG
106	Asah1	TAACATTTATAACATACCGC
107	Asah1	AGTGATAAACCCCTACCCACT
108	Asah1	GAATATAAATAATAACACTT
109	Mmadhc	TCTGTGAGGCAGTCCCATTG
110	Mmadhc	GTGTGGCCTGATGAAACTAT
111	Mmadhc	TCACTAAAGAACAAAATCCT
112	Mmadhc	TATGTAAATGAGTTTCAGGT
113	Agps	GTACCAATGAGTGCAAAGCG
114	Agps	GTA AAAACCAAGCCACTAAGT
115	Agps	TCAGAGAAGGGATGTTTGAG
116	Agps	TCCCTGGAATTCAGCACCGT
117	Pex2	GTATGCTGTGTGCACCATTG
118	Pex2	TCCCAAAAGACGCTAAATGA
119	Pex2	GTTCTGGGGCTTGCAAAATA
120	Pex2	ATGAAAGCACTGAGTAAACT
121	Mtm1	AGGGAACCACCAAAGAGCA
122	Mtm1	TTACCACTCATACCGACAAG
123	Mtm1	ATGGGAGGCGCGACAAGTAG
124	Mtm1	TCTGACCGGTGCCATTCAAG
125	Esr2	TGGCGCTTGACTAGTAACA
126	Esr2	TTCGTGACGGCTCTCTACAT
127	Esr2	GAAGTAGGAATGGTCAAGTG
128	Esr2	CGGCTCACTAGCACATTGGG
129	Arsb	GGTGGGCAGACTAGGTCTGG
130	Arsb	GAATGTCTGCCGACACGCCG
131	Arsb	AGCACAGACGTATTTATGCA
132	Arsb	GCCAGCACGAAGACCACATG
133	Piga	TCTTCCACGCCAAGACAATG
134	Piga	ATGGGTGCAGGTCTATCGT
135	Piga	CAGACTGTGAAAGAGAGTCG

Number	Gene Name	sgRNA sequence
136	Piga	CCATGCTTATGGAAATCGAA
137	Coa5	CCGGTATTATGAGGACAAGC
138	Coa5	ATCCGCTACCTGGAGCACAC
139	Coa5	GCGGGCGTGAAGGAGGATCT
140	Coa5	GCCGGAGGGCGGCGCGTGTG
141	Adar	ACTCCAACAAGCCGCCTACG
142	Adar	AGAGGTAACCCCAGTAACAG
143	Adar	TTCTTGTAGGGTGAACACCG
144	Adar	TGTATCCAGGAATTCCCTAG
145	Pus1	CCTGCAAAGAGGGTCAAGGG
146	Pus1	CTTACCCAGAATCCGAATGT
147	Pus1	TACTCGGGCAAGGGCTACCA
148	Pus1	TCCAGGCCCTCACGTACGAA
149	Dse	GTCAAAGTATAAGCATGACC
150	Dse	CAGCACACAGAACATTGCCA
151	Dse	AGTTTCATACATATAGCCCG
152	Dse	TAATGAACGGCACACCATTG
153	Nr3c1	CATTATGGGGTGCTGACGTG
154	Nr3c1	AGCTTGCCTGGCAATAAACC
155	Nr3c1	AAAGCCGTTTCACTGTCCAT
156	Nr3c1	AAAACCTGGAATAGGTGCCAA
157	Ext2	TGTTTCGATGTCTACCGCTG
158	Ext2	CTGGAGGACTCAATGGAGTG
159	Ext2	TCCTGCAGAACATCCCACAG
160	Ext2	AGGGCAGTGTGTAATCTGG
161	Pigc	TGTA CTGACAGACTCCGTCA
162	Pigc	GAATAAAACATACCCAACCA
163	Pigc	TCCGGAAAAACATCTATGCC
164	Pigc	GGCCGACCTGAAGAGTACTC
165	Ehhadh	TTCATATGGATGCTTCACGG
166	Ehhadh	CCACATCATGAGGTTACTAG
167	Ehhadh	GTAAACCCATAGAACCCCGC
168	Ehhadh	TCACTATGGCTCTAACCGTA
169	Mogs	TCTAGGTCATTCTTCCCACG
170	Mogs	TCGGCAGCATATCCACGATG
171	Mogs	TGCCGAAATAGACGTGTGGG
172	Mogs	GAGGTCCTACTACCAGAGAT
173	Slc6a9	ATACCTCTGCTATCGCAACG
174	Slc6a9	GTAGTACATGATACCCGTGA
175	Slc6a9	ATGGTGGTGTCCACATACAT
176	Slc6a9	TGTGCTACCAGCGTCTACGC
177	Slc39a8	TCAGCTGCTGTAAGATCGCG
178	Slc39a8	AGGGGGTTAAAATCAATCCC
179	Slc39a8	CGTTAGGCTCAGTGACAGCG
180	Slc39a8	CGGCGCCAACCGGAGCCTGT

Number	Gene Name	sgRNA sequence
181	Mmaa	CGACCTACTCGAAATGTGAG
182	Mmaa	AGGACAGAGAGCTTGCCTAG
183	Mmaa	TCAGGCCCTCTCCTACCAGT
184	Mmaa	ACTTGAGTGAAGGAGCCATG
185	Lipe	GAGTATGTCACGCTACACAA
186	Lipe	CACTTAGAGAGTACGCTCAG
187	Lipe	TGCGGTTAGAAGCCACATAG
188	Lipe	AGAGCGGATATGCCTTGCAG
189	Hprt	CTAGAATGATCAGTCAACGG
190	Hprt	TATACCTAATCATTATGCCG
191	Hprt	AACAAATCTAGGTCATAACC
192	Hprt	AGCCCCCCTTGAGCACACAG
193	BRDN0000737505	AAAAAGTCCGCGATTACGTC
194	BRDN0000737693	AAAACGGCTCGATCGGTGAT
195	BRDN0000737637	AAAACGTAATTATACCGAGC
196	BRDN0000738185	AAAATTGCACCTTCCCGGCC
197	BRDN0000737801	AAACCCCGCGCGGAGCGTC
198	BRDN0000737467	AAACCTAGCGTAGATTCCGGC
199	BRDN0000737848	AAACGAGGCTGTTCGTACAC
200	BRDN0000737609	AAACTCATACGTAGCGAATC

Original Doc Name: IEM (Small#1) Library (Andrew)

Oligo Name	sgRNA sequence	Gene Name
Mat2a_1	CCTGATGCTAAAGTGGCTTG	Mat2a
Mat2a_2	GTGCAATATATGCAAGATCG	Mat2a
Mat2a_3	ACCAAGGCAATGTACCATTG	Mat2a
Mat2a_4	ATTTACCACCTACAGCCAAG	Mat2a
Tfrc_5	CTACACGCTTACAATAGCCC	Tfrc
Tfrc_6	GAATACATACACTCCTCGTG	Tfrc
Tfrc_7	GGGCTCCTACTACAACATAA	Tfrc
Tfrc_8	AACCCTCGGGAGACTCCACT	Tfrc
Atp6ap2_9	TTAGCATATTAAGATCGCCA	Atp6ap2
Atp6ap2_10	TGAACTTGGGAAGCGTTATG	Atp6ap2
Atp6ap2_11	CCGGTGGAAATAGGTTACCCA	Atp6ap2
Atp6ap2_12	TGGACAGTGCAGCTACGTCT	Atp6ap2
Vcp_13	ACTGTCTTCACAGACTCATG	Vcp
Vcp_14	TATAGGTCGCTTTGACAGAG	Vcp
Vcp_15	CCAATCGCCTTAAAGAGCGC	Vcp
Vcp_16	CTTCAGGAGTTGGTTCAGGT	Vcp
Atp6v1a_17	TGACTGCTGATATCCGACAG	Atp6v1a
Atp6v1a_18	AGTCGGCCATCATACTGACG	Atp6v1a
Atp6v1a_19	ATGTTGCCCCACGTAACAG	Atp6v1a
Atp6v1a_20	CTTACGGGAAAAGGGCATCG	Atp6v1a
Cog4_21	GGAAACTCACCAACCCATCG	Cog4
Cog4_22	GCTGTGTACGAACGACTCTG	Cog4
Cog4_23	GCACAAGTAACGATGAATGT	Cog4
Cog4_24	CAACAGAAAAAATTGAACCA	Cog4
Nus1_25	GTGGTCGTAGACGCTAATGT	Nus1
Nus1_26	TCCAGGTGCCGAAGCGAACG	Nus1
Nus1_27	ACAGCACCTTCACTGCCGAA	Nus1
Nus1_28	CCAGCGCAGCCGAGGATGGG	Nus1
Gmppb_29	GTGGCTTCTCAACAAAACGG	Gmppb
Gmppb_30	GTGCCGATGAAACTGCACCA	Gmppb
Gmppb_31	TTCCCAGTTATGGCCAAGGA	Gmppb
Gmppb_32	GAGCACTCCGAAGCCATTGG	Gmppb
Ogt_33	TTTGAGCCCAAATCATGCGG	Ogt
Ogt_34	AGCATTATCGACATGCCTTG	Ogt
Ogt_35	ACAGTGCACCACTAGTCCCA	Ogt
Ogt_36	GAAAGTTTGTACCATCATCC	Ogt
Gfpt1_37	TGTGGCACAAAGTTACCACGC	Gfpt1
Gfpt1_38	AAGCTGCGGTCTTTCCCGTG	Gfpt1
Gfpt1_39	GGAGAGAGGAGCCTTAACTG	Gfpt1
Gfpt1_40	TCTGTTGTGAACACAATGAG	Gfpt1
Slc7a5_41	GCCCTCCTCGCAGTACATCG	Slc7a5
Slc7a5_42	ACCCCTACTTACGCACGCAG	Slc7a5
Slc7a5_43	AGCGGCCTCTTCGCCTACGG	Slc7a5

Oligo Name	sgRNA sequence	Gene Name
Slc7a5_44	GTAGCAGAGTGCGCCACGA	Slc7a5
Dhdds_45	GGATGTCGGGATGAGGAGAG	Dhdds
Dhdds_46	CTATGCCAAGAAGTGTCCAGG	Dhdds
Dhdds_47	CTTCAAACGTTCCAAGAGTG	Dhdds
Dhdds_48	GCAGCAGATGCAGATCACCC	Dhdds
Alg11_49	GGAAACCAGCAAATGCCCTG	Alg11
Alg11_50	TTTCCTGGACTGATGATATG	Alg11
Alg11_51	AGTGAACATAGCTTCCGACT	Alg11
Alg11_52	TAAACCATATCCTCTCACTG	Alg11
Pgm3_53	TACGGCCTCACATAACCCTG	Pgm3
Pgm3_54	AACTTCTTCAAGGTACCGCG	Pgm3
Pgm3_55	TACACCATGTAGTGCAACTG	Pgm3
Pgm3_56	CTGCTATGACATACCCTGTG	Pgm3
Ddost_57	GAACTCCCCGTAATAATGA	Ddost
Ddost_58	CCCAGATAAACCAATCACCC	Ddost
Ddost_59	AGGCAACTATGAACTAGCTG	Ddost
Ddost_60	GGTCAGAAACATCATAGTTG	Ddost
Rnf31_61	GATGGATTGAGTTTCCCGA	Rnf31
Rnf31_62	GAACTATGAGTTGTTGGACG	Rnf31
Rnf31_63	CTACCTCAACACCCTATCCA	Rnf31
Rnf31_64	GGAGGAACCAAGGTGTTGTG	Rnf31
Ogdh_65	TTGGCCCACTCATAGATACG	Ogdh
Ogdh_66	GACTAGTTCGAACTATGTGG	Ogdh
Ogdh_67	GTAAGTGGAAGACCTTGTC	Ogdh
Ogdh_68	AAAGCTGAACAGTTCTACTG	Ogdh
Slc35a2_69	TCACCCGCTGTAGTGGACCC	Slc35a2
Slc35a2_70	CTGCTCTTCGCACAAAAGAG	Slc35a2
Slc35a2_71	CTGCAAGGTATAGATGAGAG	Slc35a2
Slc35a2_72	GGCCACTGGATCAGAACCCG	Slc35a2
Pisd_73	CAAACCTGCTAGTCACTGGG	Pisd
Pisd_74	GGTCCCCAGAAAATGGCGTG	Pisd
Pisd_75	GGGCCCTCGAGCCAATACAG	Pisd
Pisd_76	CGTATGTGGCTTGCACTGTG	Pisd
Umps_77	GAGCAGATAACTGTGCCAG	Umps
Umps_78	CCGCAGGTCGATGTAGACTG	Umps
Umps_79	AGAGCGTGACACGGCGTGG	Umps
Umps_80	TCTGTCTGCCGATGTGTCGG	Umps
Gpx4_81	CGTGTGCATCGTCACCAACG	Gpx4
Gpx4_82	CATGCCCGATATGCTGAGTG	Gpx4
Gpx4_83	TGGTCTGGCAGGCACCATGG	Gpx4
Gpx4_84	TAAGCCAGCACTGCTGTGCG	Gpx4
Gale_85	ATCTTCACCGATGCGCCAG	Gale
Gale_86	AGAACTTGGACTTGCCGTAG	Gale
Gale_87	TTAACTCTATAGTAGTCCAG	Gale

Oligo Name	sgRNA sequence	Gene Name
Gale_88	CTGGGGGTTCCCGTACACGG	Gale
Alg13_89	GATCTTGTTCATTAGCCACGC	Alg13
Alg13_90	GTGAATGACTCAGTACGGAA	Alg13
Alg13_91	GGTTGTAACCCAGACTCTCG	Alg13
Alg13_92	TTTCGACGAGCTCGTCGCAC	Alg13
Hcfc1_93	GGTACCCTTCACAACCAATG	Hcfc1
Hcfc1_94	ACAGCAGTATGTGACTCCCG	Hcfc1
Hcfc1_95	TGGAAGGGCTAGTTGCACAA	Hcfc1
Hcfc1_96	CCCAAGGTTAGCCACAACAG	Hcfc1
Slc25a22_97	GTGTCTTAGCCAGGTCGATG	Slc25a22
Slc25a22_98	ATACATGCCGAAGTAGCCCT	Slc25a22
Slc25a22_99	TGATTCAGGTTGGCAAACAG	Slc25a22
Slc25a22_100	GACACCAGCTCTCTAAGGAT	Slc25a22
Pten_101	CCTCCAATTCAGGACCCACG	Pten
Pten_102	TGTGCATATTTATTGCATCG	Pten
Pten_103	ACTATTCCAATGTTCAAGTGG	Pten
Pten_104	GGTTTGATAAGTTCTAGCTG	Pten
Asah1_105	GCAAGGTGTACGTTACCTAG	Asah1
Asah1_106	TAACATTTATAACATACCGC	Asah1
Asah1_107	AGTGATAAACCCCTACCCACT	Asah1
Asah1_108	GAATATAAATAATAACAATT	Asah1
Mmadhc_109	TCTGTGAGGCAGTCCCATTG	Mmadhc
Mmadhc_110	GTGTGGCCTGATGAAACTAT	Mmadhc
Mmadhc_111	TCACTAAAGAACAAAATCCT	Mmadhc
Mmadhc_112	TATGTAAATGAGTTTCAGGT	Mmadhc
Agps_113	GTACCAATGAGTGCAAAGCG	Agps
Agps_114	GTAACCAAGCCACTAAGT	Agps
Agps_115	TCAGAGAAGGGATGTTTGAG	Agps
Agps_116	TCCCTGGAATTCAGCACCGT	Agps
Pex2_117	GTATGCTGTGTGCACCATTG	Pex2
Pex2_118	TCCCAAAGACGCTAAATGA	Pex2
Pex2_119	GTTCTGGGGCTTGCAAATA	Pex2
Pex2_120	ATGAAAGCACTGAGTAAACT	Pex2
Mtm1_121	AGGGAACCACCAAAGAGCA	Mtm1
Mtm1_122	TTACCACTCATACCGACAAG	Mtm1
Mtm1_123	ATGGGAGGCGCGACAAGTAG	Mtm1
Mtm1_124	TCTGACCGGTGCCATTCAAG	Mtm1
Esr2_125	TGGCGCTTGACTAGTAACA	Esr2
Esr2_126	TTCGTGACGGCTCTCTACAT	Esr2
Esr2_127	GAAGTAGGAATGGTCAAGTG	Esr2
Esr2_128	CGGCTCACTAGCACATTGGG	Esr2
Arsb_129	GGTGGGCAGACTAGGTCTGG	Arsb
Arsb_130	GAATGTCTGCCGACACGCCG	Arsb
Arsb_131	AGCACAGACGTATTTATGCA	Arsb

Oligo Name	sgRNA sequence	Gene Name
Arsb_132	GCCAGCACGAAGACCACATG	Arsb
Piga_133	TCTTCCACGCCAAGACAATG	Piga
Piga_134	ATGGGTGCAGGTCCTATCGT	Piga
Piga_135	CAGACTGTGAAAGAGAGTCG	Piga
Piga_136	CCATGCTTATGGAAATCGAA	Piga
Coa5_137	CCGGTATTATGAGGACAAGC	Coa5
Coa5_138	ATCCGCTACCTGGAGCACAC	Coa5
Coa5_139	GCGGGCGTGAAGGAGGATCT	Coa5
Coa5_140	GCCGGAGGGCGGGCGCTGTG	Coa5
Adar_141	ACTCCAACAAGCCGCCTACG	Adar
Adar_142	AGAGGTAACCCCAGTAACAG	Adar
Adar_143	TTCTTGTAGGGTGAACACCG	Adar
Adar_144	TGTATCCAGGAATTCCCTAG	Adar
Pus1_145	CCTGCAAAGAGGGTCAAGGG	Pus1
Pus1_146	CTTACCCAGAATCCGAATGT	Pus1
Pus1_147	TACTCGGGCAAGGGCTACCA	Pus1
Pus1_148	TCCAGGCCCTCACGTACGAA	Pus1
Dse_149	GTCAAAGTATAAGCATGACC	Dse
Dse_150	CAGCACACAGAACATTGCCA	Dse
Dse_151	AGTTTCATACATATAGCCCG	Dse
Dse_152	TAATGAACGGCACACCATTG	Dse
Nr3c1_153	CATTATGGGGTGCTGACGTG	Nr3c1
Nr3c1_154	AGCTTGCCCTGGCAATAAACC	Nr3c1
Nr3c1_155	AAAGCCGTTTCACTGTCCAT	Nr3c1
Nr3c1_156	AAAACCTGGAATAGGTGCCAA	Nr3c1
Ext2_157	TGTTTCGATGTCTACCGCTG	Ext2
Ext2_158	CTGGAGGACTCAATGGAGTG	Ext2
Ext2_159	TCCTGCAGAACATCCCACAG	Ext2
Ext2_160	AGGGCAGTGTTGTAATCTGG	Ext2
Pigc_161	TGTA CTGACAGACTCCGTCA	Pigc
Pigc_162	GAATAAAACATACCCAACCA	Pigc
Pigc_163	TCCGGAAAAACATCTATGCC	Pigc
Pigc_164	GGCCGACCTGAAGAGTACTC	Pigc
Ehhadh_165	TTCATATGGATGCTTCACGG	Ehhadh
Ehhadh_166	CCACATCATGAGGTTACTAG	Ehhadh
Ehhadh_167	GTA AACCCATAGAACCCCGC	Ehhadh
Ehhadh_168	TCACTATGGCTCTAACCGTA	Ehhadh
Mogs_169	TCTAGGTCATTCTTCCCACG	Mogs
Mogs_170	TCGGCAGCATATCCACGATG	Mogs
Mogs_171	TGCCGAAATAGACGTGTGGG	Mogs
Mogs_172	GAGGTCCTACTACCAGAGAT	Mogs
Slc6a9_173	ATACCTCTGCTATCGCAACG	Slc6a9
Slc6a9_174	GTAGTACATGATACCCGTGA	Slc6a9
Slc6a9_175	ATGGTGGTGTCCACATACAT	Slc6a9

Oligo Name	sgRNA sequence	Gene Name
Slc6a9_176	TGTGCTACCAGCGTCTACGC	Slc6a9
Slc39a8_177	TCAGCTGCTGTAAGATCGCG	Slc39a8
Slc39a8_178	AGGGGGTTAAAATCAATCCC	Slc39a8
Slc39a8_179	CGTTAGGCTCAGTGACAGCG	Slc39a8
Slc39a8_180	CGGCGCCAACCGGAGCCTGT	Slc39a8
Mmaa_181	CGACCTACTCGAAATGTGAG	Mmaa
Mmaa_182	AGGACAGAGAGCTTGCCTAG	Mmaa
Mmaa_183	TCAGGCCCTCTCCTACCAGT	Mmaa
Mmaa_184	ACTTGAGTGAAGGAGCCATG	Mmaa
Lipe_185	GAGTATGTCACGCTACACAA	Lipe
Lipe_186	CACTTAGAGAGTACGCTCAG	Lipe
Lipe_187	TGCGGTTAGAAGCCACATAG	Lipe
Lipe_188	AGAGCGGATATGCCTTGCGAG	Lipe
Hprt_189	CTAGAATGATCAGTCAACGG	Hprt
Hprt_190	TATACCTAATCATTATGCCG	Hprt
Hprt_191	AACAAATCTAGGTCATAACC	Hprt
Hprt_192	AGCCCCCCTTGAGCACACAG	Hprt
BRDN0000737505	AAAAAGTCCGCGATTACGTC	NTC
BRDN0000737693	AAAACGGCTCGATCGGTGAT	NTC
BRDN0000737637	AAAACGTAATTATACCGAGC	NTC
BRDN0000738185	AAAATTGCACCTTCCCGGCC	NTC
BRDN0000737801	AAACCCCGCGCGGAGCGTC	NTC
BRDN0000737467	AAACCTAGCGTAGATTCCGGC	NTC
BRDN0000737848	AAACGAGGCTGTTCGTACAC	NTC
BRDN0000737609	AAACTCATACGTAGCGAATC	NTC

Original Doc Name: IEM (Small#1) Library (Andrew)

Genes from IEM (all) screen

Depleted (25) Enriched (8) Neither (15)

Mat2a	Pten	Arsb
Tfrc	Asah1	Piga
Atp6ap2	Mmadhc	Coa5
Vcp	Agps	Adar
Atp6v1a	Pex2	Pus1
Cog4	Mtm1	Dse
Nus1	Hprt (Hgppt)	Nr3c1
Gmppb	<u>Esr2</u>	Ext2
Ogt		Pigc
Gfpt1		Ehhadh
Slc7a5		Mogs
Dhdds		Slc6a9
Alg11		Mmaa
Pgm3		Slc39a8
Ddost		<u>Lipe</u>
Rnf31		
Ogdh		
Slc35a2		
Pisd		
Umps		
Gpx4		
Gale		
Alg13		
Hcfc1		
<u>Slc25a22</u>		

Oligo Name	Oligo Sequence	5'	3'
Mat2a_1	GGAAAGGACGAAACACCCGCTGATGCTAAAGTGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCCGGTCAATATATGCAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCCGCAAGGCAATGTACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCCGATTTTACCACCTACAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCCGCTACACGCTTACAATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCCGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCCGACCCCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_9	GGAAAGGACGAAACACCCGTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10	GGAAAGGACGAAACACCCGTGAECTTGGGAAGCGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11	GGAAAGGACGAAACACCCGGTGGAAATAGTTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12	GGAAAGGACGAAACACCCGTGGACAGTGCAGCTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13	GGAAAGGACGAAACACCCGCTGCTTCCACAGACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14	GGAAAGGACGAAACACCCGTATAGTTCGCTTTGACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15	GGAAAGGACGAAACACCCGCAATCGCCTTAAAGAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16	GGAAAGGACGAAACACCCGCTTCCAGGTTGGTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17	GGAAAGGACGAAACACCCGTGACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_18	GGAAAGGACGAAACACCCGAGTCGGCCATCATCTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_19	GGAAAGGACGAAACACCCGATGTTGCCCCACGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_20	GGAAAGGACGAAACACCCGCTACGGGAAAAGGGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_21	GGAAAGGACGAAACACCCGGAAACTCACCACCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_22	GGAAAGGACGAAACACCCGGCTGTGACGAACGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_23	GGAAAGGACGAAACACCCGGCACAAGTACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_24	GGAAAGGACGAAACACCCGCAACAGAAAAATGAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_25	GGAAAGGACGAAACACCCGGTGGTCTGAGACGCTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_26	GGAAAGGACGAAACACCCGTCAGGTCGCAAGCGAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_27	GGAAAGGACGAAACACCCGCTTCCAGCAGCACCCTTCACTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCCGACGCGCAGCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCCGTTGCTTCAACAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCCGTCGCGATGAACTGCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCCGTTCCAGTTATGGCCAAGGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCCGAGCCTCCGGAAGCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCCGTTTGGCCCAATATCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCCGACCTTATCGACATCGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCCGACAGTGCACCACTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCCGGAAGTTTGTACCATCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCCGTGGCACAAGTACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCCGAAGTGCGGTCTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCCGGAGAGAGGAGCCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCCGCTGTTGTGAACCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCCGCTCCTCGCAGTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCCGACTTACGACGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCCGAGCGGCCCTTCTCGCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCCGTCAGCAGAGTGCGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCCGGATGTGGGATGAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCCGATGTCGAAGAAGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCCGTTCAACCTTCAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCCGACGAGATGACATCACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49	GGAAAGGACGAAACACCCGGAAACAGCAAAATGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCCGTTCTGGACTGATGATATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCCGAGTGAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCCGTAACCATATCCTCTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53	GGAAAGGACGAAACACCCGTACCGGCTCACATAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54	GGAAAGGACGAAACACCCGAACTTCTCAAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55	GGAAAGGACGAAACACCCGTACACCATGTAGTCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56	GGAAAGGACGAAACACCCGCTGCTATGACATACCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57	GGAAAGGACGAAACACCCGAACTCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58	GGAAAGGACGAAACACCCGTCAGTAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59	GGAAAGGACGAAACACCCGAGCACTATGAACATAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60	GGAAAGGACGAAACACCCGGTCAAGAACATCATAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61	GGAAAGGACGAAACACCCGATGGATTGAGTTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62	GGAAAGGACGAAACACCCGAACTATGAGTTGTTGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63	GGAAAGGACGAAACACCCGCTACCTCAACCCCTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64	GGAAAGGACGAAACACCCGGAGGAACCAAGGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65	GGAAAGGACGAAACACCCGTCACCTATAGATACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66	GGAAAGGACGAAACACCCGACTGTTCAACTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67	GGAAAGGACGAAACACCCGTAAGTGGAGACCTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68	GGAAAGGACGAAACACCCGAAAGCTGAACAGTTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69	GGAAAGGACGAAACACCCGTCAGTGGAGCCTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70	GGAAAGGACGAAACACCCGCTGCTTCTCGCACAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71	GGAAAGGACGAAACACCCGTGCAAGGATATAGTAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72	GGAAAGGACGAAACACCCGCTGATGATCAGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73	GGAAAGGACGAAACACCCGAACTTGTAGTCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74	GGAAAGGACGAAACACCCGGTCCCGAAAAATGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75	GGAAAGGACGAAACACCCGGGCCCTCGAGCCAATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76	GGAAAGGACGAAACACCCGCTATGTGGCTTGACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77	GGAAAGGACGAAACACCCGGAGCAGATAACTGTCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78	GGAAAGGACGAAACACCCGCGCAGGTTCGATGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_79	GGAAAGGACGAAACACCCGAGCGTGCACACCGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_80	GGAAAGGACGAAACACCCGCTGCTGCTGCCGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_81	GGAAAGGACGAAACACCCGCTGTGTCATCGTACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_82	GGAAAGGACGAAACACCCGATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_83	GGAAAGGACGAAACACCCGTGGTCTGGCAGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_84	GGAAAGGACGAAACACCCGTAAGCCAGCACTGCTGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_85	GGAAAGGACGAAACACCCGATCTTACCAGTGCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_86	GGAAAGGACGAAACACCCGAACTGGACTTGCCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC	GGAAAGGACGAAACACCCG	GTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Gale_87	GGAAAGGACGAAACACCGTTAACTCTATAGTAGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_88	GGAAAGGACGAAACACCGCTGGGGGTTCCCGTACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_89	GGAAAGGACGAAACACCGGATCTTGTCATTAGCCACCGCTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_90	GGAAAGGACGAAACACCGGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_91	GGAAAGGACGAAACACCGGGTGTAAACCCAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_92	GGAAAGGACGAAACACCGTTTCGACGAGCTCGTCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_93	GGAAAGGACGAAACACCGGTACCCCTTCAACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_94	GGAAAGGACGAAACACCGACAGCAGTATGTACTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_95	GGAAAGGACGAAACACCGTGAAGGGCTAGTTGCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_96	GGAAAGGACGAAACACCGCCAAAGTTAGCCACAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_97	GGAAAGGACGAAACACCGGTGTCTTAGCCAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_98	GGAAAGGACGAAACACCGATACATGCCCAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_99	GGAAAGGACGAAACACCGTGATCAGTTGGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_100	GGAAAGGACGAAACACCGGACACCGCTCTCTAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_101	GGAAAGGACGAAACACCGCTCCAATTAGCCAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_102	GGAAAGGACGAAACACCGTGTGCATATTTATTCGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_103	GGAAAGGACGAAACACCGACTATTCCTAATGTTTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_104	GGAAAGGACGAAACACCGGTTTTGATAAGTTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_105	GGAAAGGACGAAACACCGGCAAGGTGTACGTTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_106	GGAAAGGACGAAACACCGTAAACATTTATAACATACCGCTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_107	GGAAAGGACGAAACACCGAGTGATAAACCCCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_108	GGAAAGGACGAAACACCGGAATATAAATAAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_109	GGAAAGGACGAAACACCGTCTGTGAGGCAGTCCCTATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_110	GGAAAGGACGAAACACCGGTGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_111	GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_112	GGAAAGGACGAAACACCGTATGTAATGAGTTTCCAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_113	GGAAAGGACGAAACACCGGTACCAATGAGTGCAAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_114	GGAAAGGACGAAACACCGGTAAACCCAAAGCCACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_115	GGAAAGGACGAAACACCGTCAGAGAAGGATGTTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_116	GGAAAGGACGAAACACCGTCCCTGGAAATTCAGCACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_117	GGAAAGGACGAAACACCGGTATGCTGTGTGCACCTATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_118	GGAAAGGACGAAACACCGTCCCAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_119	GGAAAGGACGAAACACCGTCTGGGGCTGCAAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_120	GGAAAGGACGAAACACCGTGAAGCACTGAGTAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_121	GGAAAGGACGAAACACCGAGGGAAACCCAAAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_122	GGAAAGGACGAAACACCGTTACACTCATACCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_123	GGAAAGGACGAAACACCGATGGGAGGCGGACAAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_124	GGAAAGGACGAAACACCGTCTGACCGGTCATCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_125	GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_126	GGAAAGGACGAAACACCGTTCGTGACGGCTCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_127	GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_128	GGAAAGGACGAAACACCGCGCTCACTAGCACATTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_129	GGAAAGGACGAAACACCGGTGGCAGACTAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_130	GGAAAGGACGAAACACCGGAATGTCTGCCGACACGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_131	GGAAAGGACGAAACACCGAGCAGACGACGATTTATGCAATTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_132	GGAAAGGACGAAACACCGCCAGCAGCAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_133	GGAAAGGACGAAACACCGTCTCCACGCCAAGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_134	GGAAAGGACGAAACACCGTGGGTGCGAGTCTCTATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_135	GGAAAGGACGAAACACCGCAGACTGTGAAAGAGAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_136	GGAAAGGACGAAACACCGCTATGCTTTATGGAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_137	GGAAAGGACGAAACACCGCGGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_138	GGAAAGGACGAAACACCGTACCGCTACCTGGAGCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_139	GGAAAGGACGAAACACCGCGGCGGTGAAGGAGGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_140	GGAAAGGACGAAACACCGCGGAGGCGGCGCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_141	GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_142	GGAAAGGACGAAACACCGGAGGTAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_143	GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_144	GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_145	GGAAAGGACGAAACACCGCTCGCAAAAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_146	GGAAAGGACGAAACACCGTACCCAGAATCCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_147	GGAAAGGACGAAACACCGTACTCGGCAAGGCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_148	GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_149	GGAAAGGACGAAACACCGTCAAAAGTATAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_150	GGAAAGGACGAAACACCGCAGCACACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_151	GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_152	GGAAAGGACGAAACACCGTAATGAACGGCACACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_153	GGAAAGGACGAAACACCGCATTATGGGGTGTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_154	GGAAAGGACGAAACACCGAGCTTGCTGGCAATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_155	GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_156	GGAAAGGACGAAACACCGAAACTGGAATAGGTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_157	GGAAAGGACGAAACACCGTGTTCGATGTCTACCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_158	GGAAAGGACGAAACACCGTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_159	GGAAAGGACGAAACACCGTCTGCAGAACATCCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_160	GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_161	GGAAAGGACGAAACACCGTACTGACAGACTCCGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_162	GGAAAGGACGAAACACCGGAATAAAACATACCCAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_163	GGAAAGGACGAAACACCGTCCGGAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_164	GGAAAGGACGAAACACCGGCCGACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_165	GGAAAGGACGAAACACCGTTCATATGATGCTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_166	GGAAAGGACGAAACACCGCCACATCATGAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_167	GGAAAGGACGAAACACCGTAAACCCATAGAACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_168	GGAAAGGACGAAACACCGTCACTATGGCTCTAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_169	GGAAAGGACGAAACACCGTCTAGTCTTCTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_170	GGAAAGGACGAAACACCGTCCGCGCAGCATATCCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_171	GGAAAGGACGAAACACCGTCCGAAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_172	GGAAAGGACGAAACACCGGAGTCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_173	GGAAAGGACGAAACACCGTATCTGCTATCGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Slc6a9_174 GGAAAGGACGAAACACCGGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_175 GGAAAGGACGAAACACCGATGGTGGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_176 GGAAAGGACGAAACACCGTCTACCAGCGTCTACCGCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_177 GGAAAGGACGAAACACCGTCACTGCTGTAAAGATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_178 GGAAAGGACGAAACACCGAGGGGGTTAAAAATCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_179 GGAAAGGACGAAACACCGCTTAGCTCAGTGACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_180 GGAAAGGACGAAACACCGCGGCCAACCCGGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_181 GGAAAGGACGAAACACCGGACCTACTCGAAATGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_182 GGAAAGGACGAAACACCGGAGACAGAGAGCTTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_183 GGAAAGGACGAAACACCGTCAAGCCCTCTCCTACCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_184 GGAAAGGACGAAACACCGACTTGTAGTGAAGGACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_185 GGAAAGGACGAAACACCGGAGTATGTACGCTACACAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_186 GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_187 GGAAAGGACGAAACACCGTGGGTTGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_188 GGAAAGGACGAAACACCGAGAGCGGATAGCCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_189 GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_190 GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_191 GGAAAGGACGAAACACCGAACAAATCTAGGTCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_192 GGAAAGGACGAAACACCGAGCCCTCTTGCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737505 GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737693 GGAAAGGACGAAACACCGAAAAACCGCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737637 GGAAAGGACGAAACACCGAAAAACGTAATATACCGAGCCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000738185 GGAAAGGACGAAACACCGAAAAATTCACCTTCCCGGCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737801 GGAAAGGACGAAACACCGAAAAACCGCGCGGAGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737467 GGAAAGGACGAAACACCGAAAAACCTAGCTAGATTCGCGCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737848 GGAAAGGACGAAACACCGAAAAACGAGGCTGTTCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737609 GGAAAGGACGAAACACCGAAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_1 GGAAAGGACGAAACACCGCTGATGCTAAAGTGGCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_2 GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_3 GGAAAGGACGAAACACCGGACCAAGGCAATGACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_4 GGAAAGGACGAAACACCGTTTTACCACTACAGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_5 GGAAAGGACGAAACACCGTACACGCTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_6 GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_7 GGAAAGGACGAAACACCGGGGCTCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_8 GGAAAGGACGAAACACCGAACCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_9 GGAAAGGACGAAACACCGTGTAGCATTTAAGATCCCGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_10 GGAAAGGACGAAACACCGTGAACCTTGGGAAGCGTTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_11 GGAAAGGACGAAACACCGCGGTGGAATAGGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_12 GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_13 GGAAAGGACGAAACACCGACTGTCTTCCAGACTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_14 GGAAAGGACGAAACACCGTATAGTTCGCTTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_15 GGAAAGGACGAAACACCGCCCAATCGCCTTAAAGAGCGCTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_16 GGAAAGGACGAAACACCGCTTCAGGAGTGGTTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_17 GGAAAGGACGAAACACCGTGACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_18 GGAAAGGACGAAACACCGATCGGCCATCATCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_19 GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_20 GGAAAGGACGAAACACCGCTTACGGAAAAAGGCAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_21 GGAAAGGACGAAACACCGGAAACTCACCACCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_22 GGAAAGGACGAAACACCGGCTGTGACGAACGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_23 GGAAAGGACGAAACACCGGCAAGTAAACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_24 GGAAAGGACGAAACACCGCAACAGAAAAATGAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_25 GGAAAGGACGAAACACCGGTGGTCTGAGACGCTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_26 GGAAAGGACGAAACACCGTCCAGTCCGAGCGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_27 GGAAAGGACGAAACACCGACAGCACCTTCACTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_28 GGAAAGGACGAAACACCGCCAGCGCAGCGCAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_29 GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_30 GGAAAGGACGAAACACCGTGGCGATGAACTGCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_31 GGAAAGGACGAAACACCGTCCCGATTAAGCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_32 GGAAAGGACGAAACACCGGAGCACTCCGAGCCATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_33 GGAAAGGACGAAACACCGTGGAGCCAAATCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_34 GGAAAGGACGAAACACCGAGCATTTACGACATGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_35 GGAAAGGACGAAACACCGGACAGTGCACCACTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_36 GGAAAGGACGAAACACCGGAAAGTTTTGACCATCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gfpt1_37 GGAAAGGACGAAACACCGTGGCACAAGTTACCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gfpt1_38 GGAAAGGACGAAACACCGAAGCTGCGGCTTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gfpt1_39 GGAAAGGACGAAACACCGGAGAGGAGGCGCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gfpt1_40 GGAAAGGACGAAACACCGTCTGTTGTGAACACAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc7a5_41 GGAAAGGACGAAACACCGGCCCTCTCGCAGTACATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc7a5_42 GGAAAGGACGAAACACCGACCCCTACTTACGACGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc7a5_43 GGAAAGGACGAAACACCGAGCGGCTCTTCCGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc7a5_44 GGAAAGGACGAAACACCGTAGCAGAGTGCGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dhdds_45 GGAAAGGACGAAACACCGGATGTGGGATGAGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dhdds_46 GGAAAGGACGAAACACCGCTATGCCAAGAAGTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dhdds_47 GGAAAGGACGAAACACCGCTTCAAACGTTCCAAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dhdds_48 GGAAAGGACGAAACACCGGACGAGATGCAGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg11_49 GGAAAGGACGAAACACCGGAAACAGCAAAATGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg11_50 GGAAAGGACGAAACACCGTCTTCCGACTGATGATATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg11_51 GGAAAGGACGAAACACCGTGAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg11_52 GGAAAGGACGAAACACCGTAAACCATCTCTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pgm3_53 GGAAAGGACGAAACACCGTACCGGCTCACATAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pgm3_54 GGAAAGGACGAAACACCGACTTCTTCAAGGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pgm3_55 GGAAAGGACGAAACACCGTACACCATGTAGTCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pgm3_56 GGAAAGGACGAAACACCGTGTATGACATACCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ddost_57 GGAAAGGACGAAACACCGGAACTCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ddost_58 GGAAAGGACGAAACACCGCCAGATAAACCAATACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ddost_59 GGAAAGGACGAAACACCGGCAACTATGAACCTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ddost_60 GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Pus1_148 GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAAGTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_149 GGAAAGGACGAAACACCGGTCAAAGTATAAGCATGACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_150 GGAAAGGACGAAACACCGCAGCACACGAACATTGCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_151 GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_152 GGAAAGGACGAAACACCGTAATGAACGGCACACCATTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_153 GGAAAGGACGAAACACCGCATTATGGGGTGTGACGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_154 GGAAAGGACGAAACACCGAGCTTGCTGGCAATAAACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_155 GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_156 GGAAAGGACGAAACACCGGAACTGGAATAGTGCCAAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGTCTACCGCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_158 GGAAAGGACGAAACACCGCTGGAGGACTCAATGGAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_159 GGAAAGGACGAAACACCGTCTGCAGAACATCCCACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_160 GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_162 GGAAAGGACGAAACACCGGAATAAACACATACCCAACCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_163 GGAAAGGACGAAACACCGTCCGGAACATCTATGCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_164 GGAAAGGACGAAACACCGGGCCGACCTGAAGAGTACTCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTTCCGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ehhadh_166 GGAAAGGACGAAACACCGCCACATCATGAGGTTACTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ehhadh_167 GGAAAGGACGAAACACCGTAAACCCATAGAACCCCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ehhadh_168 GGAAAGGACGAAACACCGTCACTATGGCTCAACCGTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mogs_169 GGAAAGGACGAAACACCGTCTAGGTCATCTTCCACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mogs_170 GGAAAGGACGAAACACCGTCCGCGCAGCATATCCACGATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mogs_171 GGAAAGGACGAAACACCGTCCGAAATAGACGTGTGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mogs_172 GGAAAGGACGAAACACCGGAGTCTACTACCAGAGATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_173 GGAAAGGACGAAACACCGATACCTCTGCTATCGCAACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_174 GGAAAGGACGAAACACCGGTAGTACATGATACCCGTTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_175 GGAAAGGACGAAACACCGTGGTGGTTCACATACATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc6a9_176 GGAAAGGACGAAACACCGTGTGTACCAGCGTCTACGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_177 GGAAAGGACGAAACACCGTCACTGTGTAAGTACGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_178 GGAAAGGACGAAACACCGGGGTTAAAAATCAATCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_179 GGAAAGGACGAAACACCGCTTAGGCTCAGTGACAGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc39a8_180 GGAAAGGACGAAACACCGCGGCCAACCCGAGCGCTGTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_181 GGAAAGGACGAAACACCGGACCTACTCGAATGTGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_182 GGAAAGGACGAAACACCGAGGACAGAGAGCTTGCCTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_183 GGAAAGGACGAAACACCGTCCGCTCTCTACCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmaa_184 GGAAAGGACGAAACACCGACTTGAGTGAAGGAGCCATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_185 GGAAAGGACGAAACACCGGAGTATGTACAGCTACCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_186 GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_187 GGAAAGGACGAAACACCGTCCGTTTGAAGCCACATAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Lipe_188 GGAAAGGACGAAACACCGGAGCGGATGCTTGCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_189 GGAAAGGACGAAACACCGTAGAATGATCAGTCAACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_190 GGAAAGGACGAAACACCGTATACCTAATCATTTATGCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_191 GGAAAGGACGAAACACCGAACAAATCTAGGTCATAACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hprt_192 GGAAAGGACGAAACACCGAGCCCTTGAGCACACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737505 GGAAAGGACGAAACACCGAAAGTCCGCGATTACGTCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737693 GGAAAGGACGAAACACCGCCGCTCGATCGGTGATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737637 GGAAAGGACGAAACACCGAAACGTAAATATACCAGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000738185 GGAAAGGACGAAACACCGAAATTTGCACCTTCCGCGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737801 GGAAAGGACGAAACACCGAAACCCCGCGGAGCGTCTTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737467 GGAAAGGACGAAACACCGAAACCTAGCGTAGATTCCGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737848 GGAAAGGACGAAACACCGAAACGAGGCTGTTCTGACACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

BRDN0000737609 GGAAAGGACGAAACACCGAATCTATACGTAGCGAATCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_1 GGAAAGGACGAAACACCGCTGATGCTAAAGTGGCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_2 GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_3 GGAAAGGACGAAACACCGACCAAGGCAATGACCATTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mat2a_4 GGAAAGGACGAAACACCGATTTACCACCTACAGCCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_5 GGAAAGGACGAAACACCGTACACGCTTACAATAGCCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_6 GGAAAGGACGAAACACCGGAAATACATACACTCCTCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_7 GGAAAGGACGAAACACCGGGCTCTACTACACATAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Tfrc_8 GGAAAGGACGAAACACCGAACCTCGGGAGACTCCACTTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_9 GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_10 GGAAAGGACGAAACACCGTGAACCTGGGAAGCGTTATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_11 GGAAAGGACGAAACACCGCGTGAATAGTTACCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6ap2_12 GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_13 GGAAAGGACGAAACACCGACTGTCTTCCACAGACTCATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_14 GGAAAGGACGAAACACCGTATAGTTCGTTTTGACAGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_15 GGAAAGGACGAAACACCGCAATCGCCTTAAAGAGCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Vcp_16 GGAAAGGACGAAACACCGCTTCAGGAGTTGGTTCAAGTGTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_17 GGAAAGGACGAAACACCGTGACTGCTGATATCCGACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_18 GGAAAGGACGAAACACCGAGTCCGCCATCATACTGACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_19 GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Atp6v1a_20 GGAAAGGACGAAACACCGTTACGGAAGGCAATCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_21 GGAAAGGACGAAACACCGGAAACTACCAACCCATCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_22 GGAAAGGACGAAACACCGGCTGTGTCGAACGACTCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_23 GGAAAGGACGAAACACCGGCACAAGTAACGATGAATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Cog4_24 GGAAAGGACGAAACACCGCAACGAAAAATGAACCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_25 GGAAAGGACGAAACACCGTGGTCTGACAGCTAATGTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_26 GGAAAGGACGAAACACCGTCCAGGTGCCGAGCGAACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_27 GGAAAGGACGAAACACCGCACGACCTTCACTGCCGAAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nus1_28 GGAAAGGACGAAACACCGTCCGATGAACTGCACCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_29 GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_30 GGAAAGGACGAAACACCGTGCCGATGAACTGCACCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_31 GGAAAGGACGAAACACCGTCCAGTTATGGCCAGGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gmppb_32 GGAAAGGACGAAACACCGGACCTCCGAAGCCATTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_33 GGAAAGGACGAAACACCGTTGACCCAAATCATGCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ogt_34 GGAAAGGACGAAACACCGACATTTATCGACATGCCCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Ogt_35 GGAAAGGACGAAACACCGACAGTGCACCAGTCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ogt_36 GGAAAGGACGAAACACCGGAAAGTTTTGACCATCATCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gfpt1_37 GGAAAGGACGAAACACCGTGTGGCACAAAGTTACCAACCGCTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gfpt1_38 GGAAAGGACGAAACACCGAGCTGCGGTCTTCCCGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gfpt1_39 GGAAAGGACGAAACACCGGGAGAGAGGAGCCCTTAAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gfpt1_40 GGAAAGGACGAAACACCGTCTGTGTGAACCAATAGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc7a5_41 GGAAAGGACGAAACACCGGCCCTCCTCGCAGTACATCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc7a5_42 GGAAAGGACGAAACACCGCCCTACTTACGCACGCAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc7a5_43 GGAAAGGACGAAACACCGGACCGCCCTCTTCGCCTACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc7a5_44 GGAAAGGACGAAACACCGGTAGCAGAGTGCGCCACGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Dhdds_45 GGAAAGGACGAAACACCGGGATGTCGGGATGAGGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Dhdds_46 GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Dhdds_47 GGAAAGGACGAAACACCGCTTCAAACGTTCCAAGAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Dhdds_48 GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg11_49 GGAAAGGACGAAACACCGGAAACCAGCAATGCCCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg11_50 GGAAAGGACGAAACACCGTCTTCCGGACTGATGATATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg11_51 GGAAAGGACGAAACACCGGATGAACTAGCTTCCGACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg11_52 GGAAAGGACGAAACACCGTAAACCATCTCTCACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pgm3_53 GGAAAGGACGAAACACCGTACCGCCCTCACATAACCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pgm3_54 GGAAAGGACGAAACACCGTCTTCAAGTACCAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pgm3_55 GGAAAGGACGAAACACCGTACACCATGAGTGAACCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pgm3_56 GGAAAGGACGAAACACCGTGTATGACATACCCCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ddost_57 GGAAAGGACGAAACACCGGAACTCCCGTACTTAAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ddost_58 GGAAAGGACGAAACACCGCCAGATAAACCACTACCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ddost_59 GGAAAGGACGAAACACCGGCAACTATGAACTAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ddost_60 GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Rnf31_61 GGAAAGGACGAAACACCGGATGGATTGAGTTTCCCGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Rnf31_62 GGAAAGGACGAAACACCGGAACTATGAGTTGTGGACGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Rnf31_63 GGAAAGGACGAAACACCGTACCTCAACCCCTATCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Rnf31_64 GGAAAGGACGAAACACCGGGAGGAAACCAAGGTGTTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ogdh_65 GGAAAGGACGAAACACCGTGTGCCCACTCATAGATACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ogdh_66 GGAAAGGACGAAACACCGGACTAGTTCGAACTATGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ogdh_67 GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Ogdh_68 GGAAAGGACGAAACACCGAACTGAAACAGTTCTACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc35a2_69 GGAAAGGACGAAACACCGTCAACCGCTGTAGTGGACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc35a2_70 GGAAAGGACGAAACACCGCTCTTCCGACAAAAGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc35a2_71 GGAAAGGACGAAACACCGTGCAGGATAGATGAGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc35a2_72 GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pisd_73 GGAAAGGACGAAACACCGCAACTTGCTAGTCACTGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pisd_74 GGAAAGGACGAAACACCGGTCCCGAGAAAATGGCGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pisd_75 GGAAAGGACGAAACACCGGGCCCTCGAGCCAATACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pisd_76 GGAAAGGACGAAACACCGCCTATGTGCTTGCACCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Umps_77 GGAAAGGACGAAACACCGGACAGATAACTGTCCGACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Umps_78 GGAAAGGACGAAACACCGCCGCAAGTTCGATGTAGACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Umps_79 GGAAAGGACGAAACACCGGAGCGTGCACACCGCGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Umps_80 GGAAAGGACGAAACACCGTCTGTGCGGATGTGTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gpx4_81 GGAAAGGACGAAACACCGGTGTGTCATGTCACCAACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gpx4_82 GGAAAGGACGAAACACCGGATGCCCGATATGCTGAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gpx4_83 GGAAAGGACGAAACACCGTGTGTCGACGACCACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gpx4_84 GGAAAGGACGAAACACCGTGAAGCCAGCACTGCTGTCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gale_85 GGAAAGGACGAAACACCGATCTTCCCGATGCGCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gale_86 GGAAAGGACGAAACACCGGAACTTGGACTTCCCGTAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gale_87 GGAAAGGACGAAACACCGTAACTCTATAGTAGTCCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Gale_88 GGAAAGGACGAAACACCGTGGGGTCCCGTACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg13_89 GGAAAGGACGAAACACCGGATCTTGTCTATGACCACGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg13_90 GGAAAGGACGAAACACCGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg13_91 GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Alg13_92 GGAAAGGACGAAACACCGTTCGACGAGCTCGTCCGACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Hcfc1_93 GGAAAGGACGAAACACCGGTACCCCTTCAACCACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Hcfc1_94 GGAAAGGACGAAACACCGCAGCAGTATGTACTCCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Hcfc1_95 GGAAAGGACGAAACACCGTGGAGGGCTAGTTCACAAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Hcfc1_96 GGAAAGGACGAAACACCGCCCAAGTTAGCCACAACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc25a22_97 GGAAAGGACGAAACACCGGTGCTTATGCCAGGTCGATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc25a22_98 GGAAAGGACGAAACACCGTATACATGCCGAAGTAGCCCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc25a22_99 GGAAAGGACGAAACACCGTGATTCAGTTGGCAACACGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Slc25a22_100 GGAAAGGACGAAACACCGGACACAGCTCTTCAAGGATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pten_101 GGAAAGGACGAAACACCGCTCAATTACAGACCCACGCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pten_102 GGAAAGGACGAAACACCGTGTGCATATTTATGTCATCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pten_103 GGAAAGGACGAAACACCGACTATTCCAATGTTCACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pten_104 GGAAAGGACGAAACACCGGTTTTGATAAGTTCTAGCTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Asah1_105 GGAAAGGACGAAACACCGCAAGGTGACGTTACCTAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Asah1_106 GGAAAGGACGAAACACCGTAACTTTATAACATACCCGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Asah1_107 GGAAAGGACGAAACACCGAGTGTATAAACCTACCCACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Asah1_108 GGAAAGGACGAAACACCGGAAATAATAAATAACACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Mmadhc_109 GGAAAGGACGAAACACCGTCTGTGAGGCAGTCCCAATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Mmadhc_110 GGAAAGGACGAAACACCGTGTGGCCTGATGAACTATGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTTCAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Agps_113 GGAAAGGACGAAACACCGTACCAATGAGTGAACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Agps_114 GGAAAGGACGAAACACCGTAAACCAAGCCACTAAGTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Agps_115 GGAAAGGACGAAACACCGTCAAGAGGAGGATGTTGAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Agps_116 GGAAAGGACGAAACACCGTCCCTGGAATTCAGCACCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pex2_117 GGAAAGGACGAAACACCGTATGTGTGTCACCAATTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pex2_118 GGAAAGGACGAAACACCGTCCCAAAAGACGCTAAATGAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pex2_119 GGAAAGGACGAAACACCGTCTCGGGCTTCAAAAATAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Pex2_120 GGAAAGGACGAAACACCGTAAAGCACTGATAACTGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Mtm1_121 GGAAAGGACGAAACACCGGAAACCACAAAAGAGCAGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGC

Oligo Name	Oligo Sequence
Mtm1_122	GGAAAGGACGAAACACCGTTACCCTCATACCGACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_123	GGAAAGGACGAAACACCGGATGGGAGGCGCGCAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_124	GGAAAGGACGAAACACCGTGCACCGTGCATTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_125	GGAAAGGACGAAACACCGTGGCGCTGGACTAGTAAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_126	GGAAAGGACGAAACACCGTTCGTGACGGCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_127	GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_128	GGAAAGGACGAAACACCGCGGCTCACTAGCACATTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_129	GGAAAGGACGAAACACCGGGTGGGCAGACTAGGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_130	GGAAAGGACGAAACACCGGAATGTCTGCCGACACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_131	GGAAAGGACGAAACACCGAGCACAGCGTATTTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_132	GGAAAGGACGAAACACCGGCCAGCACGAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_133	GGAAAGGACGAAACACCGTCTCCACGCCAAGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_134	GGAAAGGACGAAACACCGATGGGTGCAGGTCCTATCGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_135	GGAAAGGACGAAACACCGCAGACTGTGAAGAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_136	GGAAAGGACGAAACACCGCCATGCTTATGGAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_137	GGAAAGGACGAAACACCGCGGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_138	GGAAAGGACGAAACACCGTCCGCTACCTGGACACAGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_139	GGAAAGGACGAAACACCGCGGGCGTGAAGGAGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_140	GGAAAGGACGAAACACCGGCGGAGGGCGGCGGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_141	GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_142	GGAAAGGACGAAACACCGAGAGGTAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_143	GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_144	GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_145	GGAAAGGACGAAACACCGCTGCAAAAGAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_146	GGAAAGGACGAAACACCGCTTACCAGAATCCGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_147	GGAAAGGACGAAACACCGTACTCGGGCAAGGGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_148	GGAAAGGACGAAACACCGTCCAGGCCCTCAGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_149	GGAAAGGACGAAACACCGTCAAAAGTAAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_150	GGAAAGGACGAAACACCGCAGCACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_151	GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_152	GGAAAGGACGAAACACCGTAAATGAACGGCACACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_153	GGAAAGGACGAAACACCGCATTTATGGGGTGTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_154	GGAAAGGACGAAACACCGAGCTTGCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_155	GGAAAGGACGAAACACCGTCAAAAGCCGTTTTCACTGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_156	GGAAAGGACGAAACACCGAAAATGGAATAGTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_157	GGAAAGGACGAAACACCGTGTTCGATGCTACCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_158	GGAAAGGACGAAACACCGTGGAGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_159	GGAAAGGACGAAACACCGTCTCGCAGAACATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_160	GGAAAGGACGAAACACCGGAGGCGAGTGTGTAATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_161	GGAAAGGACGAAACACCGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_162	GGAAAGGACGAAACACCGGAATAAAACATACCCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_163	GGAAAGGACGAAACACCGTCCGGAATAAAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_164	GGAAAGGACGAAACACCGGCGGACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_165	GGAAAGGACGAAACACCGTTCATATGGATGCTTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_166	GGAAAGGACGAAACACCGCCACACATCATGAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_167	GGAAAGGACGAAACACCGTAAACCCATAGAACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_168	GGAAAGGACGAAACACCGTCTACTATGGCTTAAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_169	GGAAAGGACGAAACACCGTCTAGGTCATTCTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_170	GGAAAGGACGAAACACCGTCCGCGCATATCCACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_171	GGAAAGGACGAAACACCGTCCGAAATAGACGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_172	GGAAAGGACGAAACACCGGAGTCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_173	GGAAAGGACGAAACACCGATACCTCTGCTATCGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_174	GGAAAGGACGAAACACCGTGTAGTACATGATACCCGTTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_175	GGAAAGGACGAAACACCGATGGTGGTTCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_176	GGAAAGGACGAAACACCGTGTCTACACGCTCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_177	GGAAAGGACGAAACACCGTCACTGCTGTAAAGTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_178	GGAAAGGACGAAACACCGAGGGGTTAAAAATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_179	GGAAAGGACGAAACACCGGTTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_180	GGAAAGGACGAAACACCGCGCCCAACCGGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_181	GGAAAGGACGAAACACCGGACCTACTCGAAATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_182	GGAAAGGACGAAACACCGGACGAGAGCTTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_183	GGAAAGGACGAAACACCGTCAAGGCTCTCTACCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_184	GGAAAGGACGAAACACCGACTTGAGTGAAGGAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_185	GGAAAGGACGAAACACCGGAGTATGTACACGCTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_186	GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_187	GGAAAGGACGAAACACCGTCCGTTGAAGGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_188	GGAAAGGACGAAACACCGAGAGCGGATATGCCTTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_189	GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_190	GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_191	GGAAAGGACGAAACACCGGAACAATCTAGGTCTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_192	GGAAAGGACGAAACACCGAGCCCTTGAAGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737505	GGAAAGGACGAAACACCGAAAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737693	GGAAAGGACGAAACACCGGAAACCGGCTCGATCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737637	GGAAAGGACGAAACACCGAAAACGTAATATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000738185	GGAAAGGACGAAACACCGAAAATTTGCACCTTCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737801	GGAAAGGACGAAACACCGAAAACCCCGCGCGGAGCGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737467	GGAAAGGACGAAACACCGAAAACCTAGCGTAGATTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737848	GGAAAGGACGAAACACCGGAAACCGGAGGCTGTTGCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737609	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_1	GGAAAGGACGAAACACCGCTGATGCTAAAGTGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCGACCAAGGCAATGTACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCGATTTTACCACCTACAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCGTACACGTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCGGAATACATACACTCCTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCGAACCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

5'

3'

Oligo Name

Oligo Sequence

5'

3'

Atp6ap2_9 GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10 GGAAAGGACGAAACACCGTGAACCTGGGAAAGCGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11 GGAAAGGACGAAACACCGCGGTTGGAATAGGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12 GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13 GGAAAGGACGAAACACCGACTGTCTTCACAGACTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14 GGAAAGGACGAAACACCGTATAGGTCGCTTTGACAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15 GGAAAGGACGAAACACCGCAATCGCCTTAAAGAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16 GGAAAGGACGAAACACCGCTTCAGGAGTTGGTTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17 GGAAAGGACGAAACACCGTACTGCTGATATCCGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_18 GGAAAGGACGAAACACCGAGTCGGCCATCACTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_19 GGAAAGGACGAAACACCGATGTGCCCCACGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_20 GGAAAGGACGAAACACCGCTTACGGGAAAAGGCGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_21 GGAAAGGACGAAACACCGGAAACTCACCACCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_22 GGAAAGGACGAAACACCGGCTGTGTCGAACGACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_23 GGAAAGGACGAAACACCGGCACAAGTAACGATGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_24 GGAAAGGACGAAACACCGCAACGAAAAATGAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_25 GGAAAGGACGAAACACCGTGGTCTGACGACGCTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_26 GGAAAGGACGAAACACCGTCCAGGTGCCGAAGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_27 GGAAAGGACGAAACACCGACAGCACCTTCACTGCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28 GGAAAGGACGAAACACCGCAGCCGACGCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29 GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30 GGAAAGGACGAAACACCGTGGCCGATGAACTGCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31 GGAAAGGACGAAACACCGTCCCGATTATGGCCAAAGGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32 GGAAAGGACGAAACACCGGAGCCTCCGAAAGCATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33 GGAAAGGACGAAACACCGTGTGAGCCAAATATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34 GGAAAGGACGAAACACCGAGCATTATCGACATGCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35 GGAAAGGACGAAACACCGCAGTGCACCACTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36 GGAAAGGACGAAACACCGGAAAGTTTTGACCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37 GGAAAGGACGAAACACCGTGTGGCACAAGTTACCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38 GGAAAGGACGAAACACCGAAGCTGCGGCTTTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39 GGAAAGGACGAAACACCGGAGAGAGAGGACCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40 GGAAAGGACGAAACACCGTCTGTGTGAACCAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41 GGAAAGGACGAAACACCGGCCCTCTCGCAGTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42 GGAAAGGACGAAACACCGGACCCCTACTTACGCAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43 GGAAAGGACGAAACACCGAGCGGCCCTTCTCGCCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44 GGAAAGGACGAAACACCGTGTAGCAGAGTGCGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45 GGAAAGGACGAAACACCGGATGTGCGGATGAGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46 GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47 GGAAAGGACGAAACACCGTCTCAAACGTTCCAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48 GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49 GGAAAGGACGAAACACCGGAAACAGCAATGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50 GGAAAGGACGAAACACCGTCTTCTGGACTGATGATATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51 GGAAAGGACGAAACACCGAGTGAACATAGTCTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52 GGAAAGGACGAAACACCGTAACCATATCCTCTCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53 GGAAAGGACGAAACACCGTACCGGCTCACATAACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54 GGAAAGGACGAAACACCGAATCTTCAAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55 GGAAAGGACGAAACACCGTACACCATGTAGTGAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56 GGAAAGGACGAAACACCGTCTGATGACATACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57 GGAAAGGACGAAACACCGGAACCTCCCGTACTTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58 GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59 GGAAAGGACGAAACACCGAGGCAACTATGAACACTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60 GGAAAGGACGAAACACCGGTCAGAAACATCATAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61 GGAAAGGACGAAACACCGGATGGATTGAGTTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62 GGAAAGGACGAAACACCGAATATGAGTGTGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63 GGAAAGGACGAAACACCGTCACTCAACACCTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64 GGAAAGGACGAAACACCGGAGGAACCAAGGTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65 GGAAAGGACGAAACACCGTGGCCACTCATAGATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66 GGAAAGGACGAAACACCGACTAGTTCGAACATGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67 GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68 GGAAAGGACGAAACACCGAAGCTGAACAGTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69 GGAAAGGACGAAACACCGTCAACCCGCTGTAGTGGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70 GGAAAGGACGAAACACCGCTGCTCTTCCGCAAAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71 GGAAAGGACGAAACACCGTGCAGGATATAGATGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72 GGAAAGGACGAAACACCGGCCACTGATCAGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73 GGAAAGGACGAAACACCGCAAACTTGCTAGTCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74 GGAAAGGACGAAACACCGGTTCCCGAAAATGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75 GGAAAGGACGAAACACCGGGCCCTCGAGCCAATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76 GGAAAGGACGAAACACCGGTATGTGGCTTGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77 GGAAAGGACGAAACACCGAGCAGATAACTGTCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78 GGAAAGGACGAAACACCGCCGAGTTCGATGTAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_79 GGAAAGGACGAAACACCGAGAGCTGCACACGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_80 GGAAAGGACGAAACACCGTCTGTCTGCCGATGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_81 GGAAAGGACGAAACACCGCGTGTGATCGTCCACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_82 GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_83 GGAAAGGACGAAACACCGTGGTCTGGCAGCACCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_84 GGAAAGGACGAAACACCGTAAGCCAGCAGTGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_85 GGAAAGGACGAAACACCGATCTTACCAGTGCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_86 GGAAAGGACGAAACACCGGAACCTGGACTTCCGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_87 GGAAAGGACGAAACACCGTAACTCTATAGTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_88 GGAAAGGACGAAACACCGTGGGGTTCCTGACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_89 GGAAAGGACGAAACACCGGATCTGTCTATGACCCAGCCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_90 GGAAAGGACGAAACACCGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_91 GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_92 GGAAAGGACGAAACACCGTTCGACGAGCTGTCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_93 GGAAAGGACGAAACACCGGATCCCTTCAACCAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_94 GGAAAGGACGAAACACCGACAGCAGTATGTACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_95 GGAAAGGACGAAACACCGTGGAAAGGCTAGTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Hfc1_96 GGAAAGGACGAAACACCGCCCAAGGTTAGCCACAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc25a22_97 GGAAAGGACGAAACACCGGTGTCTTAGCCAGGTCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc25a22_98 GGAAAGGACGAAACACCGATACATGCCAAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc25a22_99 GGAAAGGACGAAACACCGTGATTCAGGTTGGCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc25a22_100 GGAAAGGACGAAACACCGGACACAGCTCTTAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pten_101 GGAAAGGACGAAACACCGCCTCCAATTCAGGACCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pten_102 GGAAAGGACGAAACACCGTGTGCATATTTATTGTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pten_103 GGAAAGGACGAAACACCGACTATTCGAATGTTCAAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pten_104 GGAAAGGACGAAACACCGGTTTTGATAAGTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Asah1_105 GGAAAGGACGAAACACCGGCAAGGTGTACGTTACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Asah1_106 GGAAAGGACGAAACACCGTAACTTTATAACATACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Asah1_107 GGAAAGGACGAAACACCGGTGATAAACCCCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Asah1_108 GGAAAGGACGAAACACCGGAATAAAATAAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmadhc_109 GGAAAGGACGAAACACCGTCTGTGAGGCAGTCCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmadhc_110 GGAAAGGACGAAACACCGGTGTGGCCTGATGAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTTCAGGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Agps_113 GGAAAGGACGAAACACCGGTACCAATGAGTGCACAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Agps_114 GGAAAGGACGAAACACCGGTAACCAAGCCACTAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Agps_115 GGAAAGGACGAAACACCGTCAGAGAAAGGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Agps_116 GGAAAGGACGAAACACCGTCCCTGGAATTCAGCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pex2_117 GGAAAGGACGAAACACCGGTATGCTGTGTGCACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pex2_118 GGAAAGGACGAAACACCGTCCCAAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pex2_119 GGAAAGGACGAAACACCGTCTCGGGGCTTGCAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pex2_120 GGAAAGGACGAAACACCGTGAAGCAGTGAAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mtm1_121 GGAAAGGACGAAACACCGAGGGAACCAAAAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mtm1_122 GGAAAGGACGAAACACCGTATCCACTCATACCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mtm1_123 GGAAAGGACGAAACACCGTGGGAGGCGGACAAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mtm1_124 GGAAAGGACGAAACACCGTCTGACCGTGCCTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Esr2_125 GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Esr2_126 GGAAAGGACGAAACACCGTCTGTGACGGCTCTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Esr2_127 GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Esr2_128 GGAAAGGACGAAACACCGCGGCTCACTAGCACATTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Arsh_129 GGAAAGGACGAAACACCGGTGGCAGACTAGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Arsh_130 GGAAAGGACGAAACACCGGAATGTCTGCCGACACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Arsh_131 GGAAAGGACGAAACACCGGACACAGCAGTATTTATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Arsh_132 GGAAAGGACGAAACACCGGCCAGCACGAAAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Piga_133 GGAAAGGACGAAACACCGTCTCCACGCCAAGCAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Piga_134 GGAAAGGACGAAACACCGATGGGTGCAAGTCTATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Piga_135 GGAAAGGACGAAACACCGCAGACTGTGAAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Piga_136 GGAAAGGACGAAACACCGCATGCTTATGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Coa5_137 GGAAAGGACGAAACACCGCGGTATTATGAGGACAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Coa5_138 GGAAAGGACGAAACACCGATCCGCTACCTGGACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Coa5_139 GGAAAGGACGAAACACCGGCGGGCGTGAAGGAGGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Coa5_140 GGAAAGGACGAAACACCGGTGGGAGGCGCGCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Adar_141 GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Adar_142 GGAAAGGACGAAACACCGAGAGTAAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Adar_143 GGAAAGGACGAAACACCGTCTTTGAGGGTGAACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Adar_144 GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pus1_145 GGAAAGGACGAAACACCGCTCGCAAGAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pus1_146 GGAAAGGACGAAACACCGCTTACCAGAAATCCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pus1_147 GGAAAGGACGAAACACCGTACTCGGGCAAGGGCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pus1_148 GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Dse_149 GGAAAGGACGAAACACCGTCAAAGTATAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Dse_150 GGAAAGGACGAAACACCGCAGCACAGCAACATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Dse_151 GGAAAGGACGAAACACCGGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Dse_152 GGAAAGGACGAAACACCGTAATGAACGGCACACCAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Nr3c1_153 GGAAAGGACGAAACACCGCATTATGGGGTGTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Nr3c1_154 GGAAAGGACGAAACACCGAGCTTGCCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Nr3c1_155 GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Nr3c1_156 GGAAAGGACGAAACACCGAAACTGGAATAGTGGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGCTACCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ext2_158 GGAAAGGACGAAACACCGTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ext2_159 GGAAAGGACGAAACACCGTCTGCAGAACATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ext2_160 GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pigc_162 GGAAAGGACGAAACACCGGAATAAAACATACCCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pigc_163 GGAAAGGACGAAACACCGTCCGAAAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Pigc_164 GGAAAGGACGAAACACCGGCGGACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ehhadh_166 GGAAAGGACGAAACACCGCCACATCATGAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ehhadh_167 GGAAAGGACGAAACACCGGTAACCCATAGAACCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Ehhadh_168 GGAAAGGACGAAACACCGTCACTATGGCTCAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mogs_169 GGAAAGGACGAAACACCGTCTAGGTCATTTCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mogs_170 GGAAAGGACGAAACACCGTCCGAGCATATCCACAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mogs_171 GGAAAGGACGAAACACCGTGCCGAAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mogs_172 GGAAAGGACGAAACACCGGAGGTCCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc6a9_173 GGAAAGGACGAAACACCGTATCCCTGCTATCGCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc6a9_174 GGAAAGGACGAAACACCGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc6a9_175 GGAAAGGACGAAACACCGTGTGTGTCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc6a9_176 GGAAAGGACGAAACACCGTGTCTACCAGCTCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc39a8_177 GGAAAGGACGAAACACCGTCACTGTAAGTATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc39a8_178 GGAAAGGACGAAACACCGAGGGGTTAAAAATCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc39a8_179 GGAAAGGACGAAACACCGTCTAGCTCAGTGCACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Slc39a8_180 GGAAAGGACGAAACACCGCGGCCAACCCGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmaa_181 GGAAAGGACGAAACACCGCACTACTGCAAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC
Mmaa_182 GGAAAGGACGAAACACCGGACGAGAGCTGCGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGCC

Oligo Name	Oligo Sequence
Mmaa_183	GGAAAGGACGAAACACCGTACGGCCCTCTCCTACCGTGTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_184	GGAAAGGACGAAACACCGACTTGTAGTGAAGGAGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_185	GGAAAGGACGAAACACCGGGATATGTCACGCTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_186	GGAAAGGACGAAACACCGCCTTAGAGAGTACGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_187	GGAAAGGACGAAACACCGTGGCTTGAAGGCCACATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_188	GGAAAGGACGAAACACCGAGCGGATATGCCTTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_189	GGAAAGGACGAAACACCGCTAGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_190	GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_191	GGAAAGGACGAAACACCGAACAATCTAGGTCATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_192	GGAAAGGACGAAACACCGAGCCCTTGTAGCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737505	GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737693	GGAAAGGACGAAACACCGAAAAACCGGCTCGATCGGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737637	GGAAAGGACGAAACACCGAAAAACGTAATTATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000738185	GGAAAGGACGAAACACCGAAAAATGACCTTCCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737801	GGAAAGGACGAAACACCGAAAAACCGCGCGGAGCGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737467	GGAAAGGACGAAACACCGAAAAACCTAGCGTAGATTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737848	GGAAAGGACGAAACACCGAAAAACGAGGCTGTTCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737609	GGAAAGGACGAAACACCGAAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_1	GGAAAGGACGAAACACCGCCTGATGCTAAAGTGGCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCGACCAAGGCAATGTACCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCGATTTCACCTACAGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCGCTACACGTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCGAACCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_9	GGAAAGGACGAAACACCGTTAGCATATTAAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10	GGAAAGGACGAAACACCGTGAACCTGGGAAGCGTTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11	GGAAAGGACGAAACACCGCGGTGGAATAGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12	GGAAAGGACGAAACACCGTGGACGTCGACCTACGTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13	GGAAAGGACGAAACACCGACTGCTTCCACAGACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14	GGAAAGGACGAAACACCGTATAGTTCGCTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15	GGAAAGGACGAAACACCGCAATCGCCTTAAAGAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16	GGAAAGGACGAAACACCGTTCAGGAGTTGGTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17	GGAAAGGACGAAACACCGTACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_18	GGAAAGGACGAAACACCGAGTCGGCCATCATCTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_19	GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_20	GGAAAGGACGAAACACCGCTTACGGGAAAAGGGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_21	GGAAAGGACGAAACACCGGAACTCACCACCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_22	GGAAAGGACGAAACACCGCTGTGTACGACGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_23	GGAAAGGACGAAACACCGGCACAGTAACGATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_24	GGAAAGGACGAAACACCGCAACAGAAAAAATTGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_25	GGAAAGGACGAAACACCGTGGTCTGAGCGCTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_26	GGAAAGGACGAAACACCGTCCAGGTGCCGAAGCGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_27	GGAAAGGACGAAACACCGGACCGCAGCACCCTTCACTGCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCGCCAGCGCAGCCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCGGTGGCTTCTCAACAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCGGTGCCGATGAAACTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCGTCCCGATTTAGGCCAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCGGACCACTCCGAAGCCATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCGTTTTAGGCCAAATCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCGAGCATTTATCGCATGCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCGGACAGTGCACCTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCGAAAGTTGTACCATCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCGTGGCACAAGTTACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCGAAGCTGCGGCTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCGGAGAGAGGAGCCCTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCGTCTGTTGTGAACCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCGGCCCTCCTCGCAGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCGACCCCTACTTACGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCGGACCGCCTCTTCCCTACGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCGGTACGAGAGTGCGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCGGATGTCGGGATGAGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCGCTTCAACCTTCCAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49	GGAAAGGACGAAACACCGGAAACCAAGCAATGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCGTTCCTGGACTGATGATATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCGAGTGAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCGTAAACCATATCCTCTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53	GGAAAGGACGAAACACCGTACGGCCTCACATAACCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54	GGAAAGGACGAAACACCGAACTCTTCAAGGTACCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55	GGAAAGGACGAAACACCGTACACCATGTAGTCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56	GGAAAGGACGAAACACCGCTGCTATGACATCCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57	GGAAAGGACGAAACACCGGACTTCAACTTAAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58	GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59	GGAAAGGACGAAACACCGAGGCAACTATGAACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60	GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61	GGAAAGGACGAAACACCGGATGGATTGAGTTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62	GGAAAGGACGAAACACCGGAATATGAGTTGTTGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63	GGAAAGGACGAAACACCGCTACCTCAACACCCCTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64	GGAAAGGACGAAACACCGGAGGAACCAAGGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65	GGAAAGGACGAAACACCGTGGCCACTCATAGATACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66	GGAAAGGACGAAACACCGGACTAGTTGAACTATGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67	GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68	GGAAAGGACGAAACACCGAAGCTGAACAGTTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69	GGAAAGGACGAAACACCGCTACCCGCTGTAGTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

5'

3'

Oligo Name

Oligo Sequence

5'

3'

Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGCTACCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_158 GGAAAGGACGAAACACCGCTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_159 GGAAAGGACGAAACACCGCTGCCAGAACATCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_160 GGAAAGGACGAAACACCGAGGCGTGTGTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_162 GGAAAGGACGAAACACCGGAAATAAACATACCCACAGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_163 GGAAAGGACGAAACACCGTCCGGAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_164 GGAAAGGACGAAACACCGGGCCGACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_166 GGAAAGGACGAAACACCGCCACATCATGAGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_167 GGAAAGGACGAAACACCGGTAAACCCATAGAACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_168 GGAAAGGACGAAACACCGTCACTATGGCTTAACCGTATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_169 GGAAAGGACGAAACACCGTCTAGTCTATTCTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_170 GGAAAGGACGAAACACCGTCCGCGCATATCCACGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_171 GGAAAGGACGAAACACCGTCCGGAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_172 GGAAAGGACGAAACACCGGAGTCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_173 GGAAAGGACGAAACACCGTACCTACTCTGCTATCGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_174 GGAAAGGACGAAACACCGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_175 GGAAAGGACGAAACACCGATGGTGGTGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_176 GGAAAGGACGAAACACCGTGTCTACCAGCGTCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_177 GGAAAGGACGAAACACCGTCACTGCTGTAAGATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_178 GGAAAGGACGAAACACCGAGGGGTTAAATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_179 GGAAAGGACGAAACACCGTGTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_180 GGAAAGGACGAAACACCGCGGCCAACCCGAGCGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_181 GGAAAGGACGAAACACCGCCACTACTGAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_182 GGAAAGGACGAAACACCGAGGACGAGAGCTTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_183 GGAAAGGACGAAACACCGTCAAGCCCTCTCCTACCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_184 GGAAAGGACGAAACACCGTGTAGTGAGGAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_185 GGAAAGGACGAAACACCGGAGTATGTCACGCTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_186 GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_187 GGAAAGGACGAAACACCGTCCGTTAGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_188 GGAAAGGACGAAACACCGAGGCGGATAGCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_189 GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_190 GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_191 GGAAAGGACGAAACACCGAACAAATCTAGTGCATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_192 GGAAAGGACGAAACACCGAGCCCTTGAGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737505 GGAAAGGACGAAACACCGGAAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737693 GGAAAGGACGAAACACCGGAAACCGGCTGCATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737637 GGAAAGGACGAAACACCGTAAACCGTAATATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000738185 GGAAAGGACGAAACACCGAAATTCACCTTCCGCGCCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737801 GGAAAGGACGAAACACCGAAACCCCGCGGAGCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737467 GGAAAGGACGAAACACCGTAAACACCACTAGCTAGATTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737848 GGAAAGGACGAAACACCGAAACGAGGCTTTCGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737609 GGAAAGGACGAAACACCGAACTCATACGTAGCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mat2a_1 GGAAAGGACGAAACACCGTGTACTGCTAAAGTGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mat2a_2 GGAAAGGACGAAACACCGTGCATATATGCAAGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mat2a_3 GGAAAGGACGAAACACCGCAAGGCAATGTACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mat2a_4 GGAAAGGACGAAACACCGATTTTACCACCTACAGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Tfrc_5 GGAAAGGACGAAACACCGTACACGTTCAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Tfrc_6 GGAAAGGACGAAACACCGGAATACATACACTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Tfrc_7 GGAAAGGACGAAACACCGGGCTCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Tfrc_8 GGAAAGGACGAAACACCGAACCTCGGAGACTCCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6ap2_9 GGAAAGGACGAAACACCGTATAGCATATTAAGATCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6ap2_10 GGAAAGGACGAAACACCGTGAACCTGGAGCGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6ap2_11 GGAAAGGACGAAACACCGCGTGGAAATAGTTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6ap2_12 GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Vcp_13 GGAAAGGACGAAACACCGACTCTTCCAGACTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Vcp_14 GGAAAGGACGAAACACCGTATAGTTCGCTTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Vcp_15 GGAAAGGACGAAACACCGCAATCCGCTTAAAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Vcp_16 GGAAAGGACGAAACACCGTTCAGGAGTTGGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6v1a_17 GGAAAGGACGAAACACCGTACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6v1a_18 GGAAAGGACGAAACACCGTGGCCATCATACTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6v1a_19 GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Atp6v1a_20 GGAAAGGACGAAACACCGTTCAGGAAAGGGCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Cog4_21 GGAAAGGACGAAACACCGGAACTACCAACCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Cog4_22 GGAAAGGACGAAACACCGGCTGTACGAAAGCACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Cog4_23 GGAAAGGACGAAACACCGGACCAAGTAACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Cog4_24 GGAAAGGACGAAACACCGAACAGAAAATGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nus1_25 GGAAAGGACGAAACACCGTGTCTGAGACGCTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nus1_26 GGAAAGGACGAAACACCGTCCAGGTGCCAGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nus1_27 GGAAAGGACGAAACACCGACAGCACCTTCACTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nus1_28 GGAAAGGACGAAACACCGCCAGCGCAGCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gmppb_29 GGAAAGGACGAAACACCGTGGCTTCTCAACAAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gmppb_30 GGAAAGGACGAAACACCGTGCAGTGAACAGTGCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gmppb_31 GGAAAGGACGAAACACCGTTCAGGATTTAGGCAAGGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gmppb_32 GGAAAGGACGAAACACCGGAGCACTCCGAAGCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ogt_33 GGAAAGGACGAAACACCGTGTGAGCCAAATCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ogt_34 GGAAAGGACGAAACACCGGACATTCGACATGCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ogt_35 GGAAAGGACGAAACACCGACAGTGCACCAGTCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ogt_36 GGAAAGGACGAAACACCGGAAAGTTTTGACATCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gfpt1_37 GGAAAGGACGAAACACCGTGTGGCACAAGTTACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gfpt1_38 GGAAAGGACGAAACACCGAAGTGCAGTCTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gfpt1_39 GGAAAGGACGAAACACCGGAGAGGAGGAGCGCTTAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Gfpt1_40 GGAAAGGACGAAACACCGTCTGTTGAACCAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc7a5_41 GGAAAGGACGAAACACCGCCCTCTCGCAGTACATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc7a5_42 GGAAAGGACGAAACACCGCCCTACTTACGCAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc7a5_43 GGAAAGGACGAAACACCGAGCGGCTTTCGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Slc7a5_44 GGAAAGGACGAAACACCGGTAGCAGAGTGGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45 GGAAAGGACGAAACACCGGGATGTCGGGATGAGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46 GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47 GGAAAGGACGAAACACCGCTTCAACAGTTCACAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48 GGAAAGGACGAAACACCGGGCAGCAGATGCAGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49 GGAAAGGACGAAACACCGGAAACAGCAATGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50 GGAAAGGACGAAACACCGTTTCTGGACTGATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51 GGAAAGGACGAAACACCGAGTGAACATAGCTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52 GGAAAGGACGAAACACCGTAAACCATATCCTCTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53 GGAAAGGACGAAACACCGTACGGCTCACATAACCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54 GGAAAGGACGAAACACCGAACCTTTCAGAGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55 GGAAAGGACGAAACACCGTACACCATGTAGTGCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56 GGAAAGGACGAAACACCGTGTCTATGACATACCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57 GGAAAGGACGAAACACCGGAACCTCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58 GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59 GGAAAGGACGAAACACCGAGGCAACTATGAACCTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60 GGAAAGGACGAAACACCGGGTCCAGAACATCATAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61 GGAAAGGACGAAACACCGGATGATTGAGTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62 GGAAAGGACGAAACACCGGAACCTATGAGTTGTGGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63 GGAAAGGACGAAACACCGTACCTACCAACCCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64 GGAAAGGACGAAACACCGGAGGAAACCAAGGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65 GGAAAGGACGAAACACCGTGGCCACTCATAGATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66 GGAAAGGACGAAACACCGGACTAGTTGCAACTATGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67 GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68 GGAAAGGACGAAACACCGAACTGCAACAGTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69 GGAAAGGACGAAACACCGTACCCCGTGTAGTGGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70 GGAAAGGACGAAACACCGTGTCTTCCGCAAAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71 GGAAAGGACGAAACACCGTGCAGAGTATAGATGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72 GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73 GGAAAGGACGAAACACCGCAAACTGTAGTCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74 GGAAAGGACGAAACACCGGTCGCCAGAAAATGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75 GGAAAGGACGAAACACCGGGCCCTCGAGCCAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76 GGAAAGGACGAAACACCGGTATGTGGCTGCACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77 GGAAAGGACGAAACACCGGAGCAGATAACTGTCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78 GGAAAGGACGAAACACCGCGCAGGTGATGATGAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_79 GGAAAGGACGAAACACCGAGCGTGCACACGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_80 GGAAAGGACGAAACACCGTCTGTCTGCGGATGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_81 GGAAAGGACGAAACACCGCGTGTGATCCTGACCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_82 GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_83 GGAAAGGACGAAACACCGTGGTCTGGCAGGCACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_84 GGAAAGGACGAAACACCGTAAAGCCAGCACTGCTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_85 GGAAAGGACGAAACACCGATCTTCCCGATGCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_86 GGAAAGGACGAAACACCGAAGCTTGGACTTCCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_87 GGAAAGGACGAAACACCGTAACTCATAGTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_88 GGAAAGGACGAAACACCGTGGGGTTCCTGACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_89 GGAAAGGACGAAACACCGATCTTGTCAATAGCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_90 GGAAAGGACGAAACACCGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_91 GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_92 GGAAAGGACGAAACACCGTTCGACGAGCTGCTGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_93 GGAAAGGACGAAACACCGGTCACCCCTTCAACCAAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_94 GGAAAGGACGAAACACCGCAGCAGTATGTGACTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_95 GGAAAGGACGAAACACCGTGGAAAGGGTATGTCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_96 GGAAAGGACGAAACACCGCCAAAGTTAGCCACAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_97 GGAAAGGACGAAACACCGGTGTCTTAGCCAGTCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_98 GGAAAGGACGAAACACCGATACATGCCGAAAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_99 GGAAAGGACGAAACACCGTATTGATCAGTTGGCAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_100 GGAAAGGACGAAACACCGGACACAGCTCTCTAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_101 GGAAAGGACGAAACACCGCCTCAATTCAGGACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_102 GGAAAGGACGAAACACCGTGTGCATATTTGATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_103 GGAAAGGACGAAACACCGACTATCCCAATGTTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_104 GGAAAGGACGAAACACCGGTTTTGATAAGTTTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_105 GGAAAGGACGAAACACCGGCAAGGTGTACGTTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_106 GGAAAGGACGAAACACCGTAACTTTAATACATACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_107 GGAAAGGACGAAACACCGAGTGAATAAACCTACCCAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_108 GGAAAGGACGAAACACCGGAATAATAAATAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_109 GGAAAGGACGAAACACCGTCTGTGAGGCACTCCATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_110 GGAAAGGACGAAACACCGTGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_113 GGAAAGGACGAAACACCGTACCAATGAGTGCAAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_114 GGAAAGGACGAAACACCGTAAACCAAGCCACTAAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_115 GGAAAGGACGAAACACCGTCCAGAGAGGATGTTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_116 GGAAAGGACGAAACACCGTCCCTGGAATTCAGCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_117 GGAAAGGACGAAACACCGTATGCTGTGACCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_118 GGAAAGGACGAAACACCGTCCCAAAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_119 GGAAAGGACGAAACACCGTCTGGGGCTGCAAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_120 GGAAAGGACGAAACACCGTGAAGAAGCACTGAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_121 GGAAAGGACGAAACACCGGGAACCCAGGGAACCAAAAAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_122 GGAAAGGACGAAACACCGTACCCTCATACCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_123 GGAAAGGACGAAACACCGTGGGAGGCGCAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_124 GGAAAGGACGAAACACCGTCTGACCGGTGCCATTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_125 GGAAAGGACGAAACACCGTGGCCTTGGACTAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_126 GGAAAGGACGAAACACCGTCTGACCGCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_127 GGAAAGGACGAAACACCGGAAGTGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_128 GGAAAGGACGAAACACCGGCTCACTAGCAGTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsh_129 GGAAAGGACGAAACACCGGTGGCAGACTAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsh_130 GGAAAGGACGAAACACCGAATGTTCTGCCGACACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name	Oligo Sequence
Arsb_131	GGAAAGGACGAAACACCGAGCAGACGATTTATGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arsb_132	GGAAAGGACGAAACACCGGCCAGCAGCAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_133	GGAAAGGACGAAACACCGTCTCCACGCCAAGACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_134	GGAAAGGACGAAACACCGATGGGTGCAGGCTCTATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_135	GGAAAGGACGAAACACCGCAGACTGTGAAAGAGAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_136	GGAAAGGACGAAACACCGCATGCTTATGGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_137	GGAAAGGACGAAACACCGCCGGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_138	GGAAAGGACGAAACACCGATCCGCTACCTGGAGCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_139	GGAAAGGACGAAACACCGGCCGGCGTGAAGGAGGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_140	GGAAAGGACGAAACACCGCCGGAGGGCGGCCGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_141	GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_142	GGAAAGGACGAAACACCGAGAGGTAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_143	GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Adar_144	GGAAAGGACGAAACACCGTGTATCCAGGAATTCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_145	GGAAAGGACGAAACACCGCTGCAAGAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_146	GGAAAGGACGAAACACCGTACCAGAAATCCGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_147	GGAAAGGACGAAACACCGTACTCGGGCAAGGGCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pus1_148	GGAAAGGACGAAACACCGTCCAGGCCCTCAGCTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_149	GGAAAGGACGAAACACCGGTCAAAGTAAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_150	GGAAAGGACGAAACACCGCAGCACACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_151	GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dse_152	GGAAAGGACGAAACACCGTAAAGCCGACACCACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_153	GGAAAGGACGAAACACCGCATTTGGGGTGTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_154	GGAAAGGACGAAACACCGAGCTTGCCGTGGCAATAAACCCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_155	GGAAAGGACGAAACACCGAAGCCGTTTTCACTGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nr3c1_156	GGAAAGGACGAAACACCGAAACTGGAATAGTGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_157	GGAAAGGACGAAACACCGTGTTCGATGTCTACCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_158	GGAAAGGACGAAACACCGCTGGAGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_159	GGAAAGGACGAAACACCGTCTCGAACAATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ext2_160	GGAAAGGACGAAACACCGGAGGGCAGTGTGTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_161	GGAAAGGACGAAACACCGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_162	GGAAAGGACGAAACACCGGAATAAAACATACCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_163	GGAAAGGACGAAACACCGTCCGAAAAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pigc_164	GGAAAGGACGAAACACCGGCCGCCCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_165	GGAAAGGACGAAACACCGTTCATATGGATGCTTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_166	GGAAAGGACGAAACACCGCCACATCATAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_167	GGAAAGGACGAAACACCGGTAAACCCATAGAACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_168	GGAAAGGACGAAACACCGTCACTATGGCTTAAACCGTATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_169	GGAAAGGACGAAACACCGTCTAGTCTTCTTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_170	GGAAAGGACGAAACACCGTCCGACATATCCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_171	GGAAAGGACGAAACACCGTCCGAAATAGACGTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_172	GGAAAGGACGAAACACCGTGGAGTCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_173	GGAAAGGACGAAACACCGTACTCTGCTATCGCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_174	GGAAAGGACGAAACACCGGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_175	GGAAAGGACGAAACACCGTGGTGGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_176	GGAAAGGACGAAACACCGTGTCTACCAGGCTTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_177	GGAAAGGACGAAACACCGTCACTGCTGTAAGATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_178	GGAAAGGACGAAACACCGGAGGGGTTAAAAATCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_179	GGAAAGGACGAAACACCGGTTTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_180	GGAAAGGACGAAACACCGCCGCCAACCAGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_181	GGAAAGGACGAAACACCGCAGCTACTCGAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_182	GGAAAGGACGAAACACCGAGGACAGAGCTTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_183	GGAAAGGACGAAACACCGTCCAGGCCCTCTCTACCAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_184	GGAAAGGACGAAACACCGACTTGAGTGAAGGACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_185	GGAAAGGACGAAACACCGGAGTATGTCACGCTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_186	GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_187	GGAAAGGACGAAACACCGTGGGTTAGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_188	GGAAAGGACGAAACACCGGAGCGGATATGCCTTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_189	GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_190	GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_191	GGAAAGGACGAAACACCGAACAATCATAGTCTAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_192	GGAAAGGACGAAACACCGAGCCCTTCTGAGCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737505	GGAAAGGACGAAACACCGAAAAATCCCGGATTACGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737693	GGAAAGGACGAAACACCGAAAAACCGGCTCGATCGGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737637	GGAAAGGACGAAACACCGAAAAACGTAATTATACCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000738185	GGAAAGGACGAAACACCGAAAAATGCACTTCCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737801	GGAAAGGACGAAACACCGAAAAACCCCGCGCGGAGCGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737467	GGAAAGGACGAAACACCGAAAACTAGCGTAGTTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737848	GGAAAGGACGAAACACCGAAAAACGAGGCTGTTCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737609	GGAAAGGACGAAACACCGAAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_1	GGAAAGGACGAAACACCGCCTGATGCTAAAGTGGCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCGGTGCAATATAGCAAGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCGCAAGCAATGATCCATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCGATTTACCACCTACAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCGCTACACGCTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCGGGCTCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCGAACCCCTCGGAGACTCCAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_9	GGAAAGGACGAAACACCGTAGCATATTAAGATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10	GGAAAGGACGAAACACCGTGAATCGGAAAGCGTTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11	GGAAAGGACGAAACACCGCGTGGAAATAGGTTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12	GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13	GGAAAGGACGAAACACCGACTGCTTCCACAGACTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14	GGAAAGGACGAAACACCGTATAGTTCGCTTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15	GGAAAGGACGAAACACCGCAATCGCCTTAAAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16	GGAAAGGACGAAACACCGCTTCCAGGTTGGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17	GGAAAGGACGAAACACCGTACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

5'

3'

Oligo Name

Oligo Sequence

5'

3'

Atp6v1a_18	GGAAAGGACGAAACACCGAGTCGGCCATCATCTGACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Atp6v1a_19	GGAAAGGACGAAACACCGGATGTTGCCCCACGTAACAGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Atp6v1a_20	GGAAAGGACGAAACACCGTTACGGGAAAAGGCGATCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Cog4_21	GGAAAGGACGAAACACCGGAAACTACCAACCCATCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Cog4_22	GGAAAGGACGAAACACCGGCTGTGTCAAGACGACTCTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Cog4_23	GGAAAGGACGAAACACCGGCACCAAGTAAACGATGAATGTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Cog4_24	GGAAAGGACGAAACACCGCAACAGAAAATGAACCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Nus1_25	GGAAAGGACGAAACACCGTGTGTAGACGCTAATGTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Nus1_26	GGAAAGGACGAAACACCGTCCAGGTGCCGAAAGCGAACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Nus1_27	GGAAAGGACGAAACACCGACAGCACCTTCACTGCCAAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCGCCAGCCAGCCGAGGATGGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCGTGCAGTAAACTGCACCAAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCGTCCAGTTATGGCCAAAGGATTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCGGAGCCTCCGAAAGCCATTGGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCGTGTGAGCCAAATCATGCGGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCGGATCATTCGACATGCCTTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCGACAGTGCACCACTAGTCCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCGGAAAGTTTACCATCATCCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCGTGTGGCACAAGTTACCAACGCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCGAAGCTGCGGTCTTCCCGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCGGAGAGAGGAGCCCTAAGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCGTCTGTTGTGAACCAATAGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCGGCCCTCTCGCAGTACATCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCGGCTACTTACGCACGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCGAGCGGCTCTTCCGCTACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCGGTAGCAGATGCCGCCACGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCGGATGTCGGGATGAGGAGAGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCGCTATGCCAAGAGTGTGAGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCGCTTCAACCTTCCAAAGAGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCGGACGATGCAGATCACCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg11_49	GGAAAGGACGAAACACCGGAAACAGCAATGCCCTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCGTTCCTGGACTGATGATGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCGATGAACATAGCTCCGACTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCGTAACCATATCCTCTCACTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pgm3_53	GGAAAGGACGAAACACCGTACGGCCCTCACATAACCCTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pgm3_54	GGAAAGGACGAAACACCGAATCTTCAAGGTACCGCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pgm3_55	GGAAAGGACGAAACACCGTACACCATGATGCAACTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pgm3_56	GGAAAGGACGAAACACCGTGTCTATGACATACCCTGTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ddost_57	GGAAAGGACGAAACACCGGAATCCTCCGCTACTTAATGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ddost_58	GGAAAGGACGAAACACCGCCAGATAAACCAATCACCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ddost_59	GGAAAGGACGAAACACCGGCAACTATGAACATAGCTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ddost_60	GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Rnf31_61	GGAAAGGACGAAACACCGGATGGATTGAGTTCCCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Rnf31_62	GGAAAGGACGAAACACCGGAACCTATGAGTTGTTGGACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Rnf31_63	GGAAAGGACGAAACACCGCTACCTCAACACCTATCCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Rnf31_64	GGAAAGGACGAAACACCGGAGGAAACCAAGTGTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogdh_65	GGAAAGGACGAAACACCGTGTGGCCCACTCATAGATACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogdh_66	GGAAAGGACGAAACACCGGACTAGTTCGAACATGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogdh_67	GGAAAGGACGAAACACCGGTAAGTGGAAAGACCTTGTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Ogdh_68	GGAAAGGACGAAACACCGAAGCTGAACAGTCTACTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc35a2_69	GGAAAGGACGAAACACCGTCAACCGCTGTAGTGGACCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc35a2_70	GGAAAGGACGAAACACCGCTGCTCTTCCGACAAAAGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc35a2_71	GGAAAGGACGAAACACCGTGAAGTATAGATGAGAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc35a2_72	GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pisd_73	GGAAAGGACGAAACACCGCAACTTGTACTGCTGCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pisd_74	GGAAAGGACGAAACACCGGTCGCCAGAAAATGGCGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pisd_75	GGAAAGGACGAAACACCGGGGCCCTCGAGCCAATACAGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pisd_76	GGAAAGGACGAAACACCGCTATGTGGCTTGAACATGTTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Umps_77	GGAAAGGACGAAACACCGGAGCAGATAACTGTGCCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Umps_78	GGAAAGGACGAAACACCGCCGAGTGTAGACTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Umps_79	GGAAAGGACGAAACACCGGAGCGGTGCACACGCGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Umps_80	GGAAAGGACGAAACACCGTCTGTCTGCCAGATGTGCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gpx4_81	GGAAAGGACGAAACACCGGTTGTCATCGTACCAACGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gpx4_82	GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gpx4_83	GGAAAGGACGAAACACCGTGGTCTGGCAGCCACTATGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gpx4_84	GGAAAGGACGAAACACCGTAAGCCAGCACTGCTGTGCGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gale_85	GGAAAGGACGAAACACCGATCTTCCAGCATGCCGCCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gale_86	GGAAAGGACGAAACACCGAGAACTGGACTTGGCTAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gale_87	GGAAAGGACGAAACACCGTAACTCTATAGTAGTCCAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Gale_88	GGAAAGGACGAAACACCGTGGGGTCCCGTACACGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg13_89	GGAAAGGACGAAACACCGGATCTTGTCTATGACACGCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg13_90	GGAAAGGACGAAACACCGGTTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg13_91	GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Alg13_92	GGAAAGGACGAAACACCGTTCGACGAGCTGTGTCGCAAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Hcfc1_93	GGAAAGGACGAAACACCGGTACCCTTCAACAACATGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Hcfc1_94	GGAAAGGACGAAACACCGACAGCAGTATGTACTCCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Hcfc1_95	GGAAAGGACGAAACACCGTGAAGGGCTAGTTGCACAAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Hcfc1_96	GGAAAGGACGAAACACCGCCAAAGTTAGCCACAACAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc25a22_97	GGAAAGGACGAAACACCGTGTCTTATGCCAGTCTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc25a22_98	GGAAAGGACGAAACACCGTATACATGCCGAAGTAGCCCTGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc25a22_99	GGAAAGGACGAAACACCGTGATTCAGTTGGCAAAACAGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Slc25a22_100	GGAAAGGACGAAACACCGGACACAGCTCTCAAGGATGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pten_101	GGAAAGGACGAAACACCGCTCAATTCAGGACCCAGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pten_102	GGAAAGGACGAAACACCGTGTGCATATTTATGTCATCGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pten_103	GGAAAGGACGAAACACCGACTATCCAAATGTCAGTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC
Pten_104	GGAAAGGACGAAACACCGGTTGATAAGTCTAGCTGGTTTTAGAGCTAGAAAAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Asah1_105 GGAAAGGACGAAACACCGGCAAGGTGACGTTACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Asah1_106 GGAAAGGACGAAACACCGTAAACATTTAATACATACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Asah1_107 GGAAAGGACGAAACACCGGTGATAAAACCCCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Asah1_108 GGAAAGGACGAAACACCGGAATATAAATAAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmadhc_109 GGAAAGGACGAAACACCGTCTGTGAGGCAGTCCCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmadhc_110 GGAAAGGACGAAACACCGGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Agps_113 GGAAAGGACGAAACACCGGTACCAATGAGTGCAAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Agps_114 GGAAAGGACGAAACACCGTAAACCAAGCCACTAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Agps_115 GGAAAGGACGAAACACCGTCCAGAGAGGGATGTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Agps_116 GGAAAGGACGAAACACCGTCCCTGGAAATTCAGCACCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_117 GGAAAGGACGAAACACCGGTATGCTGTGTGACCAATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_118 GGAAAGGACGAAACACCGTCCCAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_119 GGAAAGGACGAAACACCGTCTGGGGCTGCAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_120 GGAAAGGACGAAACACCGTGAAGCACTGAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_121 GGAAAGGACGAAACACCGGAGGAAACCCAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_122 GGAAAGGACGAAACACCGTACCCTCATACCGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_123 GGAAAGGACGAAACACCGATGGGAGGCGCACAAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_124 GGAAAGGACGAAACACCGTCCGCTGACCGGTGCCATTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_125 GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_126 GGAAAGGACGAAACACCGTCTGTCGACGGCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_127 GGAAAGGACGAAACACCGGAAGTGAATGTTAGGTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_128 GGAAAGGACGAAACACCGCGGCTCACTAGCACATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_129 GGAAAGGACGAAACACCGGTTGGCAGACTAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_130 GGAAAGGACGAAACACCGGAATGTCTGCCGACACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_131 GGAAAGGACGAAACACCGGACGACAGACTATTTAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_132 GGAAAGGACGAAACACCGGCCGACGACGAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_133 GGAAAGGACGAAACACCGTCTCCACGCCAAGACAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_134 GGAAAGGACGAAACACCGATGGGTGACAGTCTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_135 GGAAAGGACGAAACACCGCAGACTGTGAAAGAGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_136 GGAAAGGACGAAACACCGCATGCTTATGGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_137 GGAAAGGACGAAACACCGCGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_138 GGAAAGGACGAAACACCGTACCTCGCTACCTGGAGCACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_139 GGAAAGGACGAAACACCGCGGCGCTGAAGGAGGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_140 GGAAAGGACGAAACACCGCGCGGAGGGCGCGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_141 GGAAAGGACGAAACACCGCACTCAACACAGCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_142 GGAAAGGACGAAACACCGGAGAGTAAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_143 GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_144 GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_145 GGAAAGGACGAAACACCGCTCAAAAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_146 GGAAAGGACGAAACACCGTTTACCCAGAATCCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_147 GGAAAGGACGAAACACCGTACTCGGGCAAGGGCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_148 GGAAAGGACGAAACACCGTCCAGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_149 GGAAAGGACGAAACACCGTCAAAGTAAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_150 GGAAAGGACGAAACACCGCAGCACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_151 GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_152 GGAAAGGACGAAACACCGTAAAGTGAACGGCACACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_153 GGAAAGGACGAAACACCGCATTATGGGGTGTGCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_154 GGAAAGGACGAAACACCGTCTGCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_155 GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_156 GGAAAGGACGAAACACCGAAACTGGAATAGTGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext1_157 GGAAAGGACGAAACACCGTCTTTCATGTTCCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext1_158 GGAAAGGACGAAACACCGTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext1_159 GGAAAGGACGAAACACCGTCTCGAGAACATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext1_160 GGAAAGGACGAAACACCGGAGGCAAGTGTGTAATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_162 GGAAAGGACGAAACACCGGAATAAAACATACCCAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_163 GGAAAGGACGAAACACCGTCCGGAACACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigc_164 GGAAAGGACGAAACACCGGCCGACCTGAAGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGATGCTTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_166 GGAAAGGACGAAACACCGCCACACATCATGAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_167 GGAAAGGACGAAACACCGTAAACCCATAGAACCCCGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_168 GGAAAGGACGAAACACCGTCTATGGCTTAAACCGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_169 GGAAAGGACGAAACACCGTCTAGTCTTCTTCCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_170 GGAAAGGACGAAACACCGTCCGCGCATATCCACGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_171 GGAAAGGACGAAACACCGTGCCGAAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_172 GGAAAGGACGAAACACCGAGGTCTACTACCAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_173 GGAAAGGACGAAACACCGTACTCTGCTATCGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_174 GGAAAGGACGAAACACCGTGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_175 GGAAAGGACGAAACACCGTGTGGTGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_176 GGAAAGGACGAAACACCGTGTACTACGCGTCTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_177 GGAAAGGACGAAACACCGTCACTGCTGTAAGTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_178 GGAAAGGACGAAACACCGAGGGGTTTTAAATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_179 GGAAAGGACGAAACACCGGTTAGCTCAGTGACAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_180 GGAAAGGACGAAACACCGCGGCCAACCGGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_181 GGAAAGGACGAAACACCGGACCTACTCGAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_182 GGAAAGGACGAAACACCGGACGAGAGCTTGCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_183 GGAAAGGACGAAACACCGTCCAGGCCCTCTCTACCAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_184 GGAAAGGACGAAACACCGACTGTGAGTGAAGGAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_185 GGAAAGGACGAAACACCGGATGTGTCACGCTACACAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_186 GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_187 GGAAAGGACGAAACACCGTCCGTTGTAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_188 GGAAAGGACGAAACACCGTAGAGCGGATATGCCCTTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_189 GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_190 GGAAAGGACGAAACACCGTAACTAATCATTTAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_191 GGAAAGGACGAAACACCGAACAAATCTAGTCTAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name	Oligo Sequence
Hprt_192	GGAAAGGACGAAACACCGAGCCCTTGGACACACAGGTTTATAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737505	GGAAAGGACGAAACACCGGAAATTCGCGGATTACGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737693	GGAAAGGACGAAACACCGGAAACCGGCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737637	GGAAAGGACGAAACACCGGAAACGTAATATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000738185	GGAAAGGACGAAACACCGGAAATTCGACCTTCCCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737801	GGAAAGGACGAAACACCGGAAACCCCGCGCGGAGCGTCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737467	GGAAAGGACGAAACACCGGAAACCTAGCGTAGATTCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737848	GGAAAGGACGAAACACCGGAAACGAGGCTGTCGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737609	GGAAAGGACGAAACACCGGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_1	GGAAAGGACGAAACACCGCTGTAGCTAAAGTGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCGGTGCAATATATGCAAGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCGCAAGGCAATGTACCATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCGATTTCACCACTACAGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCGCTACACGTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCGGGCTCCTACTACACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCGCAACCCGCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_9	GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10	GGAAAGGACGAAACACCGTGAACCTGGGAAAGCGTTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11	GGAAAGGACGAAACACCGCGGTGGAATAGGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12	GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13	GGAAAGGACGAAACACCGACTGTCTTCACAGACTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14	GGAAAGGACGAAACACCGTATAGTTCGCTTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15	GGAAAGGACGAAACACCGCAATCGCCTTAAAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16	GGAAAGGACGAAACACCGCTTACGAGTTGGTTACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17	GGAAAGGACGAAACACCGTGACTGTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_18	GGAAAGGACGAAACACCGAGTCGGCCATCATCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_19	GGAAAGGACGAAACACCGTGTGGCCCTTGGCCCACTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_20	GGAAAGGACGAAACACCGCTTACGGGAAAGGCGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_21	GGAAAGGACGAAACACCGGAAACTCACCAACCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_22	GGAAAGGACGAAACACCGCTGTGTACGAACGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_23	GGAAAGGACGAAACACCGGCACAAGTAACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_24	GGAAAGGACGAAACACCGCAACGAAAAATGAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_25	GGAAAGGACGAAACACCGTGGCTGCTAGACGTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_26	GGAAAGGACGAAACACCGTCCAGTGGCCGAAAGCGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_27	GGAAAGGACGAAACACCGACAGCACCTTCACTGCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCGCCAGCGCAGCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCGTGGCCGATGAAACTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCGTCCAGTTATGGCCAAGGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCGGAGCACTCCGAAGCCATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCGTGTGGCCCAATCATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCGAGCATTATCGACATGCCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCGCAGTGCACCACCTAGTCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCGTGTGACCAAGTTTGTACCATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCGTGTGGCACAAGTTACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCGAAGTGCGGTCTTCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCGGAGAGAGGAGCCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCGTCTGTTGGAACCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCGCCCTCCTCGAGTACATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCGCCCTACTTACGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCGAGCGGCCCTTTCGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCGTGTAGCAGAGTGCGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCGGATGTCGGGATGAGGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCGCTTCAAACGTTCCAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCGGCAGCAGTGCAGATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49	GGAAAGGACGAAACACCGGAAACAGCAAAATGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCGTCTTCCGACTGATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCGAGTGAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCGTAAACCATCTCTCCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53	GGAAAGGACGAAACACCGTACGGCCTCACATAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54	GGAAAGGACGAAACACCGAATCTTCAAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55	GGAAAGGACGAAACACCGTACACCATGTAGTGAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56	GGAAAGGACGAAACACCGTGTATGACATACCTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57	GGAAAGGACGAAACACCGGAACTCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58	GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59	GGAAAGGACGAAACACCGAGCAACTATGAACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60	GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61	GGAAAGGACGAAACACCGGATGGATTGAGTTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62	GGAAAGGACGAAACACCGGAACTATGAGTTGTTGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63	GGAAAGGACGAAACACCGCTACTTCAACCCCTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64	GGAAAGGACGAAACACCGGAGGAAACCAAGGTTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65	GGAAAGGACGAAACACCGTTCGCACTCATAGATACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66	GGAAAGGACGAAACACCGACTAGTTCAACTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67	GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68	GGAAAGGACGAAACACCGAAAGCTGAACAGTTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69	GGAAAGGACGAAACACCGCTGTAGTGGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70	GGAAAGGACGAAACACCGTCTTTCGCAAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71	GGAAAGGACGAAACACCGTGAACGATATAGTGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72	GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73	GGAAAGGACGAAACACCGCAAACTGTAGTCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74	GGAAAGGACGAAACACCGGTCGCCGAAAAATGGCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75	GGAAAGGACGAAACACCGGGCCCTCGAGCCAATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76	GGAAAGGACGAAACACCGCTATGTGGCTTGCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77	GGAAAGGACGAAACACCGGACAGATAACTGTCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78	GGAAAGGACGAAACACCGCCGAGTTCGATGTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

5'

3'

Oligo Name

Oligo Sequence

5'

3'

Umps_79 GGAAAGGACGAAACACCGAGAGCGTGCACACCGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Umps_80 GGAAAGGACGAAACACCGTCTGTCTGCCGATGTGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gpx4_81 GGAAAGGACGAAACACCGCGTGTGCATGCTACCAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gpx4_82 GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gpx4_83 GGAAAGGACGAAACACCGTGGTCTGGCAGGCACCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gpx4_84 GGAAAGGACGAAACACCGTAAGCCAGCACTGCTGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gale_85 GGAAAGGACGAAACACCGATCTCCACCGATGCCGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gale_86 GGAAAGGACGAAACACCGAGAAGTGGACTTGCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gale_87 GGAAAGGACGAAACACCGTAACTCTATAGTAGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Gale_88 GGAAAGGACGAAACACCGTGGGGTCCCGTACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg13_89 GGAAAGGACGAAACACCGGATCTTGCTATTAGCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg13_90 GGAAAGGACGAAACACCGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg13_91 GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Alg13_92 GGAAAGGACGAAACACCGTTCGACGAGCTCGTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hcfc1_93 GGAAAGGACGAAACACCGGTACCCTTCAACAACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hcfc1_94 GGAAAGGACGAAACACCGCAGCAGTATGTGACTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hcfc1_95 GGAAAGGACGAAACACCGTGGAAAGGCTAGTTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Hcfc1_96 GGAAAGGACGAAACACCGCCAAGTTAGCCACAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc25a22_97 GGAAAGGACGAAACACCGGTGCTTAGCCAGGTGCTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc25a22_98 GGAAAGGACGAAACACCGTACATGCATGCGGAAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc25a22_99 GGAAAGGACGAAACACCGTGATTCAGGTGGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Slc25a22_100 GGAAAGGACGAAACACCGGCACCCAGCTCTCTAAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pten_101 GGAAAGGACGAAACACCGCTCCAATTACAGGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pten_102 GGAAAGGACGAAACACCGTGTGCATATTTATGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pten_103 GGAAAGGACGAAACACCGACTATCCAAATGTTGAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pten_104 GGAAAGGACGAAACACCGGTTGATAAGTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Asah1_105 GGAAAGGACGAAACACCGGCAAGGTGTACGTTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Asah1_106 GGAAAGGACGAAACACCGTAACTAATTTATAACATACCGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Asah1_107 GGAAAGGACGAAACACCGAGTATAAACCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Asah1_108 GGAAAGGACGAAACACCGGATATAAATAAATACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmadhc_109 GGAAAGGACGAAACACCGTCTGAGGCAGTCCCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmadhc_110 GGAAAGGACGAAACACCGTGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAAACAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Agps_113 GGAAAGGACGAAACACCGTACCAATGAGTGAACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Agps_114 GGAAAGGACGAAACACCGTAAACCAAGCCACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Agps_115 GGAAAGGACGAAACACCGTCAAGAGAGGGATGTTTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Agps_116 GGAAAGGACGAAACACCGTCCCTGGAAATTCAGCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pex2_117 GGAAAGGACGAAACACCGTATGCTGTGTGCACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pex2_118 GGAAAGGACGAAACACCGTCCAAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pex2_119 GGAAAGGACGAAACACCGTCTGGGGCTTGAACAAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pex2_120 GGAAAGGACGAAACACCGTGAAGCACTGAGTAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mtm1_121 GGAAAGGACGAAACACCGGGAACCAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mtm1_122 GGAAAGGACGAAACACCGTTACCCTCATACCCGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mtm1_123 GGAAAGGACGAAACACCGTGGGAGGCGGCAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Mtm1_124 GGAAAGGACGAAACACCGTCTGACCGTGCATTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Esr2_125 GGAAAGGACGAAACACCGTGGCGCTTGACTAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Esr2_126 GGAAAGGACGAAACACCGTCTGACCGCTCTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Esr2_127 GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Esr2_128 GGAAAGGACGAAACACCGGCTCACTAGCACATTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Arsb_129 GGAAAGGACGAAACACCGGTGGCAGACTAGGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Arsb_130 GGAAAGGACGAAACACCGGAATGCTGCCGACACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Arsb_131 GGAAAGGACGAAACACCGTACAGCACAGACGATTTATGCGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Arsb_132 GGAAAGGACGAAACACCGCCAGCACGAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Piga_133 GGAAAGGACGAAACACCGTCTCCACGCCAAGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Piga_134 GGAAAGGACGAAACACCGTGGTGGTGCAGTCCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Piga_135 GGAAAGGACGAAACACCGCAGACTGTGAAGAGAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Piga_136 GGAAAGGACGAAACACCGCCATGCTTATGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Coa5_137 GGAAAGGACGAAACACCGCGGTTATGAGGACAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Coa5_138 GGAAAGGACGAAACACCGTACCTGAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Coa5_139 GGAAAGGACGAAACACCGCGGCGTGAAGGAGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Coa5_140 GGAAAGGACGAAACACCGGCGGAGGGCGCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Adar_141 GGAAAGGACGAAACACCGTCACTCAACAAAGCCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Adar_142 GGAAAGGACGAAACACCGAGGTAACCCCAAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Adar_143 GGAAAGGACGAAACACCGTCTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Adar_144 GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pus1_145 GGAAAGGACGAAACACCGCTGCAAAAGAGGTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pus1_146 GGAAAGGACGAAACACCGTACCAGAAATCCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pus1_147 GGAAAGGACGAAACACCGTACTCGGCAAGGGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pus1_148 GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_149 GGAAAGGACGAAACACCGTCAAAGTATAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_150 GGAAAGGACGAAACACCGCAGCACAGCAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_151 GGAAAGGACGAAACACCGAGTTTTATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Dse_152 GGAAAGGACGAAACACCGTAAATGAACGGCACACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_153 GGAAAGGACGAAACACCGCAATTATGGGTGCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_154 GGAAAGGACGAAACACCGAGCTTGCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_155 GGAAAGGACGAAACACCGAAAGCCGTTTCACTGCTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Nr3c1_156 GGAAAGGACGAAACACCGAAACTGGAATAGTGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGCTACCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_158 GGAAAGGACGAAACACCGTGGAGGACTAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_159 GGAAAGGACGAAACACCGTCTGCAGAACATCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ext2_160 GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_162 GGAAAGGACGAAACACCGGAAATAAAACATACCCACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_163 GGAAAGGACGAAACACCGTCCGGAAACATCATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Pigc_164 GGAAAGGACGAAACACCGGCCACTGAAGACTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name	Oligo Sequence
Ehhadh_166	GGAAAGGACGAAACACCGCCACATCATGAGTTACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_167	GGAAAGGACGAAACACCGGTAACCCATAGAACCCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ehhadh_168	GGAAAGGACGAAACACCGTCACTATGGCTCAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_169	GGAAAGGACGAAACACCGTCTAGGTCATTTCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_170	GGAAAGGACGAAACACCGTGGCGCAGCATATCCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_171	GGAAAGGACGAAACACCGTGGCGGAAATAGACGTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mogs_172	GGAAAGGACGAAACACCGGAGGTCCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_173	GGAAAGGACGAAACACCGATACCTCTGCTATCGCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_174	GGAAAGGACGAAACACCGTAGTACATGATACCCGCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_175	GGAAAGGACGAAACACCGATGGTGGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc6a9_176	GGAAAGGACGAAACACCGTGTGTACCAGCGTCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_177	GGAAAGGACGAAACACCGTCACTGCTGTAAAGATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_178	GGAAAGGACGAAACACCGAGGGGTTTTAAATCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_179	GGAAAGGACGAAACACCGCTTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc39a8_180	GGAAAGGACGAAACACCGCGGCCAACCCGGCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_181	GGAAAGGACGAAACACCGCGACCTACTCGAAATGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_182	GGAAAGGACGAAACACCGAGGACAGAGAGCTTGCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_183	GGAAAGGACGAAACACCGTCAAGCCCTCTCTACCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmaa_184	GGAAAGGACGAAACACCGACTTGAGTGAAGGAGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_185	GGAAAGGACGAAACACCGGAGTATGTACGCTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_186	GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_187	GGAAAGGACGAAACACCGTGGGTTAGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Lipe_188	GGAAAGGACGAAACACCGAGCGGATATGCTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_189	GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_190	GGAAAGGACGAAACACCGTATACCTAATCATTTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_191	GGAAAGGACGAAACACCGAACAATCTAGGTCATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hprt_192	GGAAAGGACGAAACACCGAGCCCTCTTAGCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737505	GGAAAGGACGAAACACCGAATAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737693	GGAAAGGACGAAACACCGAACCCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737637	GGAAAGGACGAAACACCGAACCCTAATATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000738185	GGAAAGGACGAAACACCGAATAATGACCTTCCGCGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737801	GGAAAGGACGAAACACCGAACCCTCGCGGAGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737467	GGAAAGGACGAAACACCGAACCCTAGCGTAGTTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737848	GGAAAGGACGAAACACCGAACCCTGTTGCTGATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
BRDN0000737609	GGAAAGGACGAAACACCGAACCCTACAGTACGGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_1	GGAAAGGACGAAACACCGCTGATGCTAAAGTGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_2	GGAAAGGACGAAACACCGTGGCAATATATGCAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_3	GGAAAGGACGAAACACCGACCAAGGCAATGACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mat2a_4	GGAAAGGACGAAACACCGTATTTACCCTACAGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_5	GGAAAGGACGAAACACCGCTACAGCTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_6	GGAAAGGACGAAACACCGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_7	GGAAAGGACGAAACACCGGGCTCCTACTACAACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Tfrc_8	GGAAAGGACGAAACACCGAACCCTCGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_9	GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_10	GGAAAGGACGAAACACCGGAACCTGGGAAGCGTTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_11	GGAAAGGACGAAACACCGCGGTGAATAGGTTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6ap2_12	GGAAAGGACGAAACACCGTGGCAGTGCAGTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_13	GGAAAGGACGAAACACCGACTGCTTCCACAGACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_14	GGAAAGGACGAAACACCGTATAGTTCGCTTTCACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_15	GGAAAGGACGAAACACCGCAATCAGCTTAAAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Vcp_16	GGAAAGGACGAAACACCGCTTCAGGATGTTGTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_17	GGAAAGGACGAAACACCGTACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_18	GGAAAGGACGAAACACCGAGTGGCCATCATACTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_19	GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Atp6v1a_20	GGAAAGGACGAAACACCGCTTACGGGAAAAGGCAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_21	GGAAAGGACGAAACACCGGAAAACCTACCAACCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_22	GGAAAGGACGAAACACCGGCTGTGACGAACGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_23	GGAAAGGACGAAACACCGGCACAAGTAACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Cog4_24	GGAAAGGACGAAACACCGCAACAGAAAATGAACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_25	GGAAAGGACGAAACACCGTGGTCTGAGCAGCTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_26	GGAAAGGACGAAACACCGTCCAGTGGCCGAAAGCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_27	GGAAAGGACGAAACACCGCAGCAGCACCTTCACTCGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCGCCAGCCAGCCGAGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCGTGGCTTCTCAACAAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCGTGGCCGATGAAACTGCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCGTTCGCGATTTAGCCAAAGGATTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCGGAGCACTCCGAAGCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCGTTTTAGCCAAATCATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCGAGCATTTATCGACATGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCGCAGTGCACCAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCGGAAAGTTTTGTACCATCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCGTGTGGCACAAGTTACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCGAAGCTGCGGCTTTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCGGAGAGAGGAGCCCTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCGTCTGTTGTGAACCAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCGCCCTCTCGCAGTACATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCGACCCCTACTTACGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCGAGCGGCTCTTCGCGCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCGTAGCAGATGCGCCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCGGATGTCGGGATGAGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCGCTATGCCAAAGAGTGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCGCTTCAAACGTTCGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_49	GGAAAGGACGAAACACCGGAAACAGCAAAATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCGTTCCTGGACTGATGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCGTAGTAAACATAGCTTCCGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCGTAACCATCTCTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

5'

3'

Oligo Name

Oligo Sequence

5'

3'

Pgm3_53 GGAAAGGACGAAACACCGTACGGCTCACATAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54 GGAAAGGACGAAACACCGAATCTTCAAGGTACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55 GGAAAGGACGAAACACCGTACACCATGTAGTCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56 GGAAAGGACGAAACACCGTGTATGCATACCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57 GGAAAGGACGAAACACCGGAACCTCCCGTACTTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58 GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59 GGAAAGGACGAAACACCGAGGCAACTATGAACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60 GGAAAGGACGAAACACCGGGTCAGAAACATCATAGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61 GGAAAGGACGAAACACCGGATGGATTGAGTTTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62 GGAAAGGACGAAACACCGAATCTATGAGTTGGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63 GGAAAGGACGAAACACCGCTACTCTCAACCCCTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64 GGAAAGGACGAAACACCGGGAGGAACCAAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65 GGAAAGGACGAAACACCGTGGCCACTCATAGATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66 GGAAAGGACGAAACACCGGACTAGTTCCAACTATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67 GGAAAGGACGAAACACCGGTAAGTGAAGACCTTGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68 GGAAAGGACGAAACACCGAAAGCTGAACAGTTCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69 GGAAAGGACGAAACACCGTCCCGCTGTAGTGGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70 GGAAAGGACGAAACACCGTCTTCCGCAAAAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71 GGAAAGGACGAAACACCGTGCAGGATATAGATGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72 GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73 GGAAAGGACGAAACACCGCAACTGTAGTCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74 GGAAAGGACGAAACACCGGTCGCCAGAAAATGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75 GGAAAGGACGAAACACCGGGCCCTCGAGCCAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76 GGAAAGGACGAAACACCGGTATGTGGCTTGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77 GGAAAGGACGAAACACCGGACAGATAAAGTTCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78 GGAAAGGACGAAACACCGCCGAGGTGATGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_79 GGAAAGGACGAAACACCGGAGCGTGCACACCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_80 GGAAAGGACGAAACACCGTCTGTCCGATGTGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_81 GGAAAGGACGAAACACCGGTGTGCATCGTCCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_82 GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_83 GGAAAGGACGAAACACCGTGTCTGGCAGCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_84 GGAAAGGACGAAACACCGTAAGCCAGCACTGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_85 GGAAAGGACGAAACACCGATCTTCCCGATGCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_86 GGAAAGGACGAAACACCGGAACCTTGGACTTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_87 GGAAAGGACGAAACACCGTAACTCTATAGTAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_88 GGAAAGGACGAAACACCGTGGGGTCCCGTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_89 GGAAAGGACGAAACACCGGATCTTGTCTATTAGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_90 GGAAAGGACGAAACACCGTGAATGACTCAGTACGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_91 GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_92 GGAAAGGACGAAACACCGTTTCGACGAGCTCGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_93 GGAAAGGACGAAACACCGGTACTCTTCCACCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_94 GGAAAGGACGAAACACCGGACAGCAGTATGTGACTCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_95 GGAAAGGACGAAACACCGTGGAGGGTATGTCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_96 GGAAAGGACGAAACACCGCCCAAGTTAGCCACAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_97 GGAAAGGACGAAACACCGTGTCTTAGCCAGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_98 GGAAAGGACGAAACACCGATACATGCCAAGTAGCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_99 GGAAAGGACGAAACACCGTGTTCAGTTGGCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_100 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_101 GGAAAGGACGAAACACCGCTCCAATTACGACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_102 GGAAAGGACGAAACACCGTGTGCATATTTATGCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_103 GGAAAGGACGAAACACCGACTATTCCAATGTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_104 GGAAAGGACGAAACACCGGTTTTGATAAGTTCTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_105 GGAAAGGACGAAACACCGCAAGGTGTACGTTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_106 GGAAAGGACGAAACACCGTAACATTTATAACATACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_107 GGAAAGGACGAAACACCGAGTGATAAACCCCTACCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_108 GGAAAGGACGAAACACCGGAATAATAATAAACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_109 GGAAAGGACGAAACACCGTCTGTGAGGCACTCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_110 GGAAAGGACGAAACACCGGTGTGGCCTGATGAAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_111 GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_112 GGAAAGGACGAAACACCGTATGTAATGAGTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_113 GGAAAGGACGAAACACCGTACCAATGAGTCAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_114 GGAAAGGACGAAACACCGTAAAAACCAAGCCACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_115 GGAAAGGACGAAACACCGTCAAGAAAGGGATGTTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_116 GGAAAGGACGAAACACCGTCCCTGGAATTCAGCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_117 GGAAAGGACGAAACACCGTATGCTGTGTGCCACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_118 GGAAAGGACGAAACACCGTCCCAAAAGACGCTAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_119 GGAAAGGACGAAACACCGTCTGGGGCTTGAATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pex2_120 GGAAAGGACGAAACACCGATGAAAGCACTGAGTAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_121 GGAAAGGACGAAACACCGAGGGAACCAAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_122 GGAAAGGACGAAACACCGTACCCTCATACCGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_123 GGAAAGGACGAAACACCGATGGGAGGCGGCAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mtm1_124 GGAAAGGACGAAACACCGTCTGACCGTGCATTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_125 GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_126 GGAAAGGACGAAACACCGTCTGTGACGGCTCTCATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_127 GGAAAGGACGAAACACCGGAAGTGAATGGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Esr2_128 GGAAAGGACGAAACACCGGCTCACTAGCACATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arbs_129 GGAAAGGACGAAACACCGGTGGGCACTAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arbs_130 GGAAAGGACGAAACACCGAATGTCTGCCGACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arbs_131 GGAAAGGACGAAACACCGAGCACAGCAGTATTTATGSCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Arbs_132 GGAAAGGACGAAACACCGGCCAGCAGCAAGACCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_133 GGAAAGGACGAAACACCGTCTTCCACGCCAAGACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_134 GGAAAGGACGAAACACCGTGGTGCAGGTCCTATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_135 GGAAAGGACGAAACACCGCAGACTGTGAAAGAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Piga_136 GGAAAGGACGAAACACCGCATGCTTATGGAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_137 GGAAAGGACGAAACACCGCGTATTATGAGGACAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_138 GGAAAGGACGAAACACCGTCTACTGGAGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Coa5_139 GGAAAGGACGAAACACCGGGCGGTGAAGGAGGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Coa5_140 GGAAAGGACGAAACACCGCCGGAGGCGGCGCGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Adar_141 GGAAAGGACGAAACACCGACTCCAACAAGCCGCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Adar_142 GGAAAGGACGAAACACCGAGAGGTAAACCCAGTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Adar_143 GGAAAGGACGAAACACCGTTCTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Adar_144 GGAAAGGACGAAACACCGTGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pus1_145 GGAAAGGACGAAACACCGCTCGCAAGAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pus1_146 GGAAAGGACGAAACACCGCTACCCAGAATCCGAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pus1_147 GGAAAGGACGAAACACCGTACTCGGGCAAGGGTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pus1_148 GGAAAGGACGAAACACCGTCCAGGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Dse_149 GGAAAGGACGAAACACCGTCAAGTATAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Dse_150 GGAAAGGACGAAACACCGCAGCACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Dse_151 GGAAAGGACGAAACACCGAGTTTCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Dse_152 GGAAAGGACGAAACACCGTAAATGAACGGCACACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_153 GGAAAGGACGAAACACCGCATTATGGGGTGTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_154 GGAAAGGACGAAACACCGAGCTTGCCCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_155 GGAAAGGACGAAACACCGAAAGCCCTTCTACTGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_156 GGAAAGGACGAAACACCGGAAACTGGAATAGGTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGCTACCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ext2_158 GGAAAGGACGAAACACCGCTGGAGGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ext2_159 GGAAAGGACGAAACACCGTCTGCAGAACATCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ext2_160 GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pigc_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pigc_162 GGAAAGGACGAAACACCGGAAATAAAAATACCCCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pigc_163 GGAAAGGACGAAACACCGTCCGGAAAAACATCTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pigc_164 GGAAAGGACGAAACACCGCCGACCTGAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ehhadh_166 GGAAAGGACGAAACACCGCCACATCATGAGTTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ehhadh_167 GGAAAGGACGAAACACCGTAAACCCATAGAACCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ehhadh_168 GGAAAGGACGAAACACCGTCACTATGGCTTCAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mogs_169 GGAAAGGACGAAACACCGTCTAGTTCATTTCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mogs_170 GGAAAGGACGAAACACCGCTCGGCAGCATATCCAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mogs_171 GGAAAGGACGAAACACCGTGCCGAAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mogs_172 GGAAAGGACGAAACACCGGAGGTCTACTACCAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc6a9_173 GGAAAGGACGAAACACCGTACTCCTGCTATCCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc6a9_174 GGAAAGGACGAAACACCGTAGTACATGATACCCGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc6a9_175 GGAAAGGACGAAACACCGATGGTGTGTCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc6a9_176 GGAAAGGACGAAACACCGTGTGCTACCAGCGTCTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc39a8_177 GGAAAGGACGAAACACCGTCACTGCTGTAAGTACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc39a8_178 GGAAAGGACGAAACACCGAGGGGTTTTAAAATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc39a8_179 GGAAAGGACGAAACACCGGTTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc39a8_180 GGAAAGGACGAAACACCGCGGCCCAACCGGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mmaa_181 GGAAAGGACGAAACACCGGACCTACTCGAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mmaa_182 GGAAAGGACGAAACACCGAGGACAGAGGCTTGCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mmaa_183 GGAAAGGACGAAACACCGTCAGGCCCTCTCCTACCAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mmaa_184 GGAAAGGACGAAACACCGACTTGAAGTGAAGGAGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lipe_185 GGAAAGGACGAAACACCGGAGTATGTCACGCTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lipe_186 GGAAAGGACGAAACACCGCACTTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lipe_187 GGAAAGGACGAAACACCGTGCCTTGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lipe_188 GGAAAGGACGAAACACCGAGAGCGGATAGCCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hprt_189 GGAAAGGACGAAACACCGTATGAATGATCAGTACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hprt_190 GGAAAGGACGAAACACCGTATACCTAATCATTATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hprt_191 GGAAAGGACGAAACACCGCAAAATCTAGGTCTAACCCTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hprt_192 GGAAAGGACGAAACACCGTGGCCCTTGAACACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737505 GGAAAGGACGAAACACCGAAAAATGCCGATTACGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737693 GGAAAGGACGAAACACCGAAAAACCGCTCGATCGGTGATTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737637 GGAAAGGACGAAACACCGAAACCGTAATATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000738185 GGAAAGGACGAAACACCGAAAAATGCACTTCCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737801 GGAAAGGACGAAACACCGAAACCCCGCGCGGAGCGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737467 GGAAAGGACGAAACACCGAAACCTAGCGTAGATTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737848 GGAAAGGACGAAACACCGAAACGAGGCTGTTGCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737609 GGAAAGGACGAAACACCGAAACTCATACGTAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mat2a_1 GGAAAGGACGAAACACCGCCTGATGCTAAAGTGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mat2a_2 GGAAAGGACGAAACACCGTGCATATATGCAAGATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mat2a_3 GGAAAGGACGAAACACCGAACCAAGCAATGTACCAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mat2a_4 GGAAAGGACGAAACACCGATTTACCACCTACAGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc_5 GGAAAGGACGAAACACCGTACACGTTCAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc_6 GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc_7 GGAAAGGACGAAACACCGGGCTCCTACTACAACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc_8 GGAAAGGACGAAACACCGAACCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6ap2_9 GGAAAGGACGAAACACCGTTAGCATATTAAGATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6ap2_10 GGAAAGGACGAAACACCGTGAACCTGGGAAGCGTTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6ap2_11 GGAAAGGACGAAACACCGCCGTTGGAATAGTTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6ap2_12 GGAAAGGACGAAACACCGTGGACAGTGCAGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vcp_13 GGAAAGGACGAAACACCGACTCTTCCACAGCTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vcp_14 GGAAAGGACGAAACACCGTATAGGTCGTTTTGACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vcp_15 GGAAAGGACGAAACACCGCAATGCCTTAAAGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vcp_16 GGAAAGGACGAAACACCGTTCAGGAGTGGTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6v1a_17 GGAAAGGACGAAACACCGTGACTGCTGATATCCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6v1a_18 GGAAAGGACGAAACACCGAGTGCCTCATCTACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6v1a_19 GGAAAGGACGAAACACCGATGTTGCCCCACGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Atp6v1a_20 GGAAAGGACGAAACACCGTTACGGGAAAGGGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cog4_21 GGAAAGGACGAAACACCGGAAACTACCAACCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cog4_22 GGAAAGGACGAAACACCGCTGTGTACGAACGACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cog4_23 GGAAAGGACGAAACACCGGACCAAGTAAACGATGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cog4_24 GGAAAGGACGAAACACCGCAACGAAAAAATGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nus1_25 GGAAAGGACGAAACACCGTGTGCTGACGCTAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nus1_26 GGAAAGGACGAAACACCGTCCAGGTGCCGAGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Oligo Name

Oligo Sequence

5'

3'

Nus1_27	GGAAAGGACGAAACACCGACAGCACCTTCACTGCCGAAGTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Nus1_28	GGAAAGGACGAAACACCGCCAGCGCAGCCGAGGATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_29	GGAAAGGACGAAACACCGGTGGCTTCTCAACAAACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_30	GGAAAGGACGAAACACCGGTGCCGATGAACTGCACCAAGTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_31	GGAAAGGACGAAACACCGTTCGCGATTATGGCCAGGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gmppb_32	GGAAAGGACGAAACACCGGAGCACTCCGAAGCCATTGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_33	GGAAAGGACGAAACACCGTTCGAGCCAAATCATGCCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_34	GGAAAGGACGAAACACCGAGCATTATCGACATGCCTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_35	GGAAAGGACGAAACACCGAGCTGCACTAGTCCCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogt_36	GGAAAGGACGAAACACCGGAAAGTTTGTACCATCATCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_37	GGAAAGGACGAAACACCGTGTGGCACAAGTTACCACGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_38	GGAAAGGACGAAACACCGAAGCTGCGGCTTTCCCGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_39	GGAAAGGACGAAACACCGGGAGAGAGGAGCCCTTAAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gfpt1_40	GGAAAGGACGAAACACCGTCTGTGTGAACCAATGAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_41	GGAAAGGACGAAACACCGGCCCTCTCGCAGTACATCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_42	GGAAAGGACGAAACACCGACCCCTACTTACGCACGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_43	GGAAAGGACGAAACACCGGACCCGCTCTTCGCCCTACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc7a5_44	GGAAAGGACGAAACACCGGTAGCAGAGTGCGCCACGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_45	GGAAAGGACGAAACACCGGATGTGCGGATGAGGAGAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_46	GGAAAGGACGAAACACCGCTATGCCAAGAAGTGTACAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_47	GGAAAGGACGAAACACCGCTTCAAACGTCCAAAGAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Dhdds_48	GGAAAGGACGAAACACCGGCAGCAGATGCAGATCACCCTTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg1_49	GGAAAGGACGAAACACCGGGAACACAGCAATGCCCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_50	GGAAAGGACGAAACACCGTTCCTGGACTGATGATATGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_51	GGAAAGGACGAAACACCGTAGTGAACATAGCTCCGACTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg11_52	GGAAAGGACGAAACACCGTAACCATATCCTCTCACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_53	GGAAAGGACGAAACACCGTACGGCTCACATACCCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_54	GGAAAGGACGAAACACCGAAGCTTCTCAAGGTACCCGCTTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_55	GGAAAGGACGAAACACCGTACCCATGTAGTCAACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pgm3_56	GGAAAGGACGAAACACCGCTGTATGACATACCCTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_57	GGAAAGGACGAAACACCGGAACTCCCGTACTTAAATGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_58	GGAAAGGACGAAACACCGCCAGATAAACCAATCACCCTTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_59	GGAAAGGACGAAACACCGGAGCAACTATGAACAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ddost_60	GGAAAGGACGAAACACCGGTCAGAAACATCATAGTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_61	GGAAAGGACGAAACACCGGATGGATTGAGTTTCCCGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_62	GGAAAGGACGAAACACCGGAECTATGAGTTTGGACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_63	GGAAAGGACGAAACACCGTACTTCCACACCCCTATCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Rnf31_64	GGAAAGGACGAAACACCGGAGGAAACCAAGTGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_65	GGAAAGGACGAAACACCGTTCGCCCCTCATAGATACGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_66	GGAAAGGACGAAACACCGGACTAGTTCGAACATGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_67	GGAAAGGACGAAACACCGTAAAGTGAAGACCTTGTCAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Ogdh_68	GGAAAGGACGAAACACCGGAAGCTGAACAGTTCTACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_69	GGAAAGGACGAAACACCGTCAACCCTGTAGTGGACCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_70	GGAAAGGACGAAACACCGCTGTCTTCCGCAAAAAGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_71	GGAAAGGACGAAACACCGGTGCAAGGTATAGATGAGAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc35a2_72	GGAAAGGACGAAACACCGGCCACTGGATCAGAACCCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_73	GGAAAGGACGAAACACCGCAAACTGTAGTCACTGGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_74	GGAAAGGACGAAACACCGGTCGCCAGAAAATGGCGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_75	GGAAAGGACGAAACACCGGGCCCTCGAGCCCAACAGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pisd_76	GGAAAGGACGAAACACCGCTATGTGGCTTGCAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_77	GGAAAGGACGAAACACCGGAGCAGATAACTGTCCGACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_78	GGAAAGGACGAAACACCGCCGCAAGTGTAGTGTAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_79	GGAAAGGACGAAACACCGGAGCGTGCACACGCGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Umps_80	GGAAAGGACGAAACACCGTCTGTCTGCCGATGTGTCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_81	GGAAAGGACGAAACACCGCGTGTGCATCGTCAACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_82	GGAAAGGACGAAACACCGCATGCCGATATGCTGAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_83	GGAAAGGACGAAACACCGTGGCTGGCAGCCACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gpx4_84	GGAAAGGACGAAACACCGTAAGCCAGCAGTGTGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_85	GGAAAGGACGAAACACCGTCTTCCAGATGCGCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_86	GGAAAGGACGAAACACCGAAGCTTGGACTTGGCTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_87	GGAAAGGACGAAACACCGTAACTTAACTATAGTAGTCCAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Gale_88	GGAAAGGACGAAACACCGTGGGGTTCGCCGTACCGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_89	GGAAAGGACGAAACACCGGATCTTGTCTTACCGACGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_90	GGAAAGGACGAAACACCGGTAATGACTCAGTACGGAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_91	GGAAAGGACGAAACACCGGTTGTAACCCAGACTCTCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Alg13_92	GGAAAGGACGAAACACCGTTCGACGAGCTGTGCGACGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_93	GGAAAGGACGAAACACCGGATACCTTCCACCACTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_94	GGAAAGGACGAAACACCGACAGCAGTATGTACTCCCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_95	GGAAAGGACGAAACACCGTGGAGGGCTAGTTGCACAAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Hcfc1_96	GGAAAGGACGAAACACCGCCCAAGTTAGCCACAACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_97	GGAAAGGACGAAACACCGTGTCTTAGCCAGTGTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_98	GGAAAGGACGAAACACCGATACATGCCGAAGTAGCCCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_99	GGAAAGGACGAAACACCGTGATTTCAGGTTGGCAACAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Slc25a22_100	GGAAAGGACGAAACACCGGACACCGCTCTCTAAGGATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_101	GGAAAGGACGAAACACCGCCTCCAATTACGAGCCACCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_102	GGAAAGGACGAAACACCGTGTGCATATTTATTGCATCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_103	GGAAAGGACGAAACACCGACTTCCAATGTTCAAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Pten_104	GGAAAGGACGAAACACCGGTTTGTAAATGTTAGTCTAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_105	GGAAAGGACGAAACACCGCAAGGTGACGTTACCTAGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_106	GGAAAGGACGAAACACCGTAACATTTATAACATACCCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_107	GGAAAGGACGAAACACCGGATGATAAACCTACCCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Asah1_108	GGAAAGGACGAAACACCGGAATAATAAATAACCACTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_109	GGAAAGGACGAAACACCGTCTGTGAGGCGTCCCTTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_110	GGAAAGGACGAAACACCGTGTGGCTGTGAAACTATGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_111	GGAAAGGACGAAACACCGTCACTAAAGAACAAAATCCTGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Mmadhc_112	GGAAAGGACGAAACACCGTATAATGATTTCAAGTGGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC
Agps_113	GGAAAGGACGAAACACCGTACCAATGAGTGCAAAGCGTTTTATAGAGCTAGAAATAGCAAGTTAAAAAAGGC

Oligo Name

Oligo Sequence

5'

3'

Aggs_114 GGAAAGGACGAAACACCGGTAAACCAAGCCACTAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Aggs_115 GGAAAGGACGAAACACCGTCCAGAAAGGGATGTTTAGAGTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Aggs_116 GGAAAGGACGAAACACCGTCCCTGGAAATTCAGCACCGCTGTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_117 GGAAAGGACGAAACACCGGTATGCTGTGTGCACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_118 GGAAAGGACGAAACACCGTCCCAAAAGACGCTAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_119 GGAAAGGACGAAACACCGTTCCTGGGCTTGCAAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pex2_120 GGAAAGGACGAAACACCGATGAAAGCACTGAGTAACTGTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_121 GGAAAGGACGAAACACCGAGGGAACCAAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_122 GGAAAGGACGAAACACCGTACCCTATACCACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_123 GGAAAGGACGAAACACCGATGGGAGGCGCGCAAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mtm1_124 GGAAAGGACGAAACACCGTCTGACCGGTGCCATTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_125 GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_126 GGAAAGGACGAAACACCGTTCGTGACGGCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_127 GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Esr2_128 GGAAAGGACGAAACACCGCGCTACTAGCACATTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_129 GGAAAGGACGAAACACCGGTGGGACAGACTAGGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_130 GGAAAGGACGAAACACCGGAATGTCTGCCGACACGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_131 GGAAAGGACGAAACACCGACACAGACTATTTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Arsb_132 GGAAAGGACGAAACACCGGCGACGACGAAGACCACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_133 GGAAAGGACGAAACACCGTCTCCACGCCAAGACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_134 GGAAAGGACGAAACACCGATGGGTGACAGTCTATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_135 GGAAAGGACGAAACACCGCAGACTGTGAAAGAGAGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Piga_136 GGAAAGGACGAAACACCGCATGTCTTATGAAATCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_137 GGAAAGGACGAAACACCGCGGTATTATGAGGACAAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_138 GGAAAGGACGAAACACCGTACCTCGCTACCTGGACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_139 GGAAAGGACGAAACACCGCGGGCGTGAAGGAGGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Coa5_140 GGAAAGGACGAAACACCGGCGGAGGGCGGCGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_141 GGAAAGGACGAAACACCGTACCTCAACAAAGCCGCTACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_142 GGAAAGGACGAAACACCGAGAGTAAACCCAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_143 GGAAAGGACGAAACACCGTCTTGTAGGGTGAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Adar_144 GGAAAGGACGAAACACCGGTATCCAGGAATCCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_145 GGAAAGGACGAAACACCGCTGCAAGAGGGTCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_146 GGAAAGGACGAAACACCGTACCAGAATCCGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_147 GGAAAGGACGAAACACCGTACTCGGCAAGGGCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pus1_148 GGAAAGGACGAAACACCGTCCAGCCCTCACGTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_149 GGAAAGGACGAAACACCGTCAAAAGTAAAGCATGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_150 GGAAAGGACGAAACACCGCAGCACAGAACATTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_151 GGAAAGGACGAAACACCGATTTCCATACATATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Dse_152 GGAAAGGACGAAACACCGTAAATGAACGGCACACCATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_153 GGAAAGGACGAAACACCGCATTATGGGGTGTGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_154 GGAAAGGACGAAACACCGAGCTTGGCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_155 GGAAAGGACGAAACACCGGAAGCCGTTTTCACTGTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Nr3c1_156 GGAAAGGACGAAACACCGAAACTGGAATAGTGCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_157 GGAAAGGACGAAACACCGTGTTCGATGCTACCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_158 GGAAAGGACGAAACACCGCTGGAGACTCAATGGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_159 GGAAAGGACGAAACACCGTCTGCAGAACATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ext2_160 GGAAAGGACGAAACACCGAGGGCAGTGTGTAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigg_161 GGAAAGGACGAAACACCGTGTACTGACAGACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigg_162 GGAAAGGACGAAACACCGGAATAAAACATACCCAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigg_163 GGAAAGGACGAAACACCGTCCGGAATAAACATCTATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Pigg_164 GGAAAGGACGAAACACCGGCGCACCTGAAGAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_165 GGAAAGGACGAAACACCGTTCATATGGATGCTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_166 GGAAAGGACGAAACACCGGAAGTACTAGGTTACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_167 GGAAAGGACGAAACACCGTAAACCCATAGAACCCCGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Ehhadh_168 GGAAAGGACGAAACACCGTCACTATGGCTCAACCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_169 GGAAAGGACGAAACACCGTCTAGTCACTTCTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_170 GGAAAGGACGAAACACCGTCCGACATATCCACGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_171 GGAAAGGACGAAACACCGTCCGAAATAGACGTGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mogs_172 GGAAAGGACGAAACACCGGAGTCTACTACAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_173 GGAAAGGACGAAACACCGTACTCTGCTATCGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_174 GGAAAGGACGAAACACCGGTAGTACATGATACCCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_175 GGAAAGGACGAAACACCGTGTGGTGTCCACATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc6a9_176 GGAAAGGACGAAACACCGTGTGTACCAGCTCTACGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_177 GGAAAGGACGAAACACCGTCACTGCTGTAAGATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_178 GGAAAGGACGAAACACCGGGGTTAAATCAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_179 GGAAAGGACGAAACACCGCTTAGGCTCAGTGACAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Slc39a8_180 GGAAAGGACGAAACACCGGCGCCACCCGAGCCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_181 GGAAAGGACGAAACACCGACCTACTCGAAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_182 GGAAAGGACGAAACACCGAGGACAGAGCTTGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_183 GGAAAGGACGAAACACCGTCCAGGCCCTCTCCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Mmaa_184 GGAAAGGACGAAACACCGACTGAGTGAAGGAGCATTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_185 GGAAAGGACGAAACACCGGAGTATGTCACGCTACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_186 GGAAAGGACGAAACACCGCACITTAGAGAGTACGCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_187 GGAAAGGACGAAACACCGTCCGTTAGAAGCCACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Lipe_188 GGAAAGGACGAAACACCGAGCGGATATGCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_189 GGAAAGGACGAAACACCGTGAATGATCAGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_190 GGAAAGGACGAAACACCGTATACCTAATCATTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_191 GGAAAGGACGAAACACCGAACAATCTAGGTCTAACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 Hprt_192 GGAAAGGACGAAACACCGAGCCCTTGGACACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737505 GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737693 GGAAAGGACGAAACACCGTCCAGGCCCTCCTACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737637 GGAAAGGACGAAACACCGAAACGTAATTTAACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000738185 GGAAAGGACGAAACACCGAAATTCACCTTCCCGCGCTTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737801 GGAAAGGACGAAACACCGAACCCCGCGGAGCGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737467 GGAAAGGACGAAACACCGAACCTAGCTAGATTCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737848 GGAAAGGACGAAACACCGAACGAGGCTGTTCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC
 BRDN0000737609 GGAAAGGACGAAACACCGAAACTACATACGAGTAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAAAAGGC