Library Registration Form

Library Number	RMK018
Library Name	KV iron library
Old Document Name	
Library Purpose	CRISPR/Cas9 knockout of iron metabolism genes in mice
Location (Oligos)	
Location (Bacteria)	N/A
Designer Name	Kelsey Voss
Designing Date	Feb-21
Design Reference	Kelsey Voss
Usage Reference	Kelsey Voss

Species	Mouse (Mus musculus)
Total Gene #	60 (55+5 NTCs)
Total Target #	225
Gene Group	Iron metabolism
1. Negative Controls	5
2. Positive Controls	2
3. Iron metabolism	46
Target Number	
1. Negative Controls	5*1=5
2. Positive Controls	2*4=8
3. Iron metabolism	212

Number	Gene name	Guide sequence
1	Tfrc	CTACACGCTTACAATAGCCC
2	Tfrc	GAATACATACACTCCTCGTG
3	Tfrc	GGGCTCCTACTACAACATAA
4	Tfrc	AACCCTCGGGAGACTCCACT
5	Slc11a1	GGGTGTGCTACCACATACTG
6	Slc11a1	GAGAAGTAGACAGAACCCGC
7	Slc11a1	CCTAGCATGATACCGTCCAG
8	Slc11a1	GAATGGGGATCTTCTCACTC
9	Slc11a2	ATGTCACCGTCAGTATCCCA
10	Slc11a2	AAACACAAAAGTGTCTGCGA
11	Slc11a2	TGAGAAAATCCCCATTCCTG
12	Slc11a2	CCTTGACTAAGGCAGAATGC
13	Fpn, Slc40a1	CAGGGTACGCCTACACTCAG
14	Fpn, Slc40a1	CCTTTGGATTGTGATCGCAG
15	Fpn, Slc40a1	TCATCAGGATGATTCCGCAG
16	Fpn, Slc40a1	CCCATCCATCTCGGAAAGTG
17	Scara5	TAGGTCCATGTCACAAACGG
18	Scara5	CTGGTAGAGTTCCAGCTGTG
19	Scara5	CAGCGCCTTCAAGTCATCTG
20	Scara5	GGGAACACTCCATCGCCTTG
21	Timd2	GATATACGGTCACACATCAG
22	Timd2	GGAATCGTTCCTATGTGTTG
23	Timd2	TGTTGGAAGTTAAACCAGGT
24	Timd2	CTGATCTGGATAAAATGTAG
25	Heph	CATGTGCAAGGGTGATACTG
26	Heph	TTGGAGCATCTACATGCGAG
27	Heph	GTTTATAAGGAATACAGTGA
28	Heph	AAAAGTCACATACTACTGGA
29	Hephl1	ACAGCGGCGCTACTTCATAG
30	Hephl1	GTTTCCCCATATGGCCACAA
31	Hephl1	GTGAAACCTTCACCTACAGG
32	Hephl1	CCCAGAGCAGATATCCTTAG
33	Cp	CATATAAGCATCAATTAGGG
34	Cp	GCTGTGAGGAGCGACCTGGT
35	Cp	ATGAAAAGTGTAGATCCTAG
36	Cp	GCTGAACAAATACCACACGA
37	Fth1	CACCATAGACAGATAGACGT
38	Fth1	AGTGCGCCAGAACTACCACC
39	Fth1	GGAGAGCGGGCTGAATGCAA
40	Fth1	TCTTCAGAGCCACATCATCT
41	Ftl1	GCTGCTCACCAGAGAGAGGT
42	Ftl1	TTGGCCGAGGAGAAGCGCGA
43	Ftl1	GAGTTTCAGAACGATCGCGG
44	Ftl1	TCGTCAGAATTATTCCACCG

Number	Gene name	Guide sequence
45	Steap2	AGTACCGCCGATTTCCCCCG
46	Steap2	TATTAGATGTGGCTACCACG
47	Steap2	TAAATGGTATCAAAGACGCA
48	Steap2	CAGAGAGTAAACAGTCGCAG
49	Steap3	AGCTCAAGTGACTTTCCAGG
50	Steap3	AGCAGCACATAAGCCACACA
51	Steap3	TGGGGTTGCTTACATCCACG
52	Steap3	GGTTTCACACCCCTGGACAT
53	Steap4	TGTGTACTGTGCAATACGAG
54	Steap4	GATAATCAACTAGTTCCGTG
55	Steap4	AATACCAGGGAGGTACACCA
56	Steap4	GTTAAATGCTTTGACCACGT
57	Glrx5	GCACGGTGTTCGCGACTATG
58	Glrx5	GCGTTGCTGAAGCCGCACTG
59	Glrx5	AGGTGGTGGTGTTCCTCAAG
60	Glrx5	GGAGTAGTCTTTAATACCTG
61	Tfr2	GAGGTCGCTCCAGTACAACG
62	Tfr2	AGTGCGTGTCAGTCCACACG
63	Tfr2	TGGTGTACGCCCACTACGGG
64	Tfr2	ACCCCCAGTGAAGATTAGCA
65	Hamp	CACCTGTTGATGGAGATAGG
66	Hamp	AGATACCAATGCAGAAGAGA
67	Hamp	AGAGCTGCAGCCTTTGCACG
68	Hamp	AGAAAGCAGGGCAGACATTG
69	Ncoa4	CGTCGCTGATTGTTGCGCCG
70	Ncoa4	TTCAAGAAGTCAGCATCCAG
71	Ncoa4	GGTCTTAAGGGATCCAAATG
72	Ncoa4	AATTAAAGATAATTTACGAG
73	Hfe	TGCTCCACGTACCCTTACTG
74	Hfe	TTCCTCCCGCACTCACGCGG
75	Hfe	GATCCGTGCCAAACAGAACA
76	Hfe	CATGAAGACAACAGTACCAG
77	Aco1, IRP2	CCACCGCCATTTAGGCCGCG
78	Aco1, IRP2	CATATGCTATTACCAGAGGG
79	Aco1, IRP2	TAGCCCACCACATCAAACCT
80	Aco1, IRP2	GTGTAGCACCTCCGACAAGT
81	Aco2	AGATCCGTGCCACTATTGAG
82	Aco2	GCGTTTACGGCCCGACCGGG
83	Aco2	TGGGTGAGGTCCAACCAGAG
84	Aco2	GATTGAAATTAACCTCAATG
85	IREB2	AATTTGGCAGAAATCGAGAG
86	IREB2	TAAGCTGTCCCATGGATCCG
87	IREB2	TCTAAGAAGCTTCCATGTCG
88	IREB2	TCAATAGTTGCATCTGTCAG

Number	Gene name	Guide sequence
89	Hepb1, Nrf2	GAAACACGGCAAAAGAGACA
90	Hepb1, Nrf2	CCCAAGATCATGAAGTATGT
91	Hepb1, Nrf2	AGGGGGCAAGTTTGCTACTG
92	Hepb1, Nrf2	TGATGAGAGTGTGAAGATCG
93	UCP2	TCTGGGTACCATCCTAACCA
94	UCP2	GTCAAACAGTTCTACACCAA
95	UCP2	AGACCATTGCACGAGAGGAA
96	UCP2	CGGACCTTGGCGGTATCCAG
97	UCP3	GTAGAGGCCAATTCGAATGG
98	UCP3	CCTGACTATGGTGCGCACAG
99	UCP3	TTTCAAGCCATGATACGCCT
100	UCP3	TGCCTACAGAACCATCGCCA
101	Slc25a4, ANT	CCTAGACCTGTTTAACTGTG
102	Slc25a4, ANT	CAGTTTGACCCTCTCGATCG
103	Slc25a4, ANT	GGAAGATCCCTTGCCCACGT
104	Slc25a4, ANT	TTGTGTCGTGAGAATCCCCA
105	Slc25a37, Mitoferrin1	CTGGATTCATTACTGCATCG
106	Slc25a37, Mitoferrin1	CACTGTCCGGATACAACTGA
107	Slc25a37, Mitoferrin1	GATGAAGTGAATTGACTGGA
108	Slc25a37, Mitoferrin1	GCATCTATGGCGCCCTCAAG
109	Mitoferrin2	CAACACGTTCCGATAGCGGG
110	Mitoferrin2	TTGAGTGACGTAATCCACCC
111	Mitoferrin2	CCCGAACACAGTCTGTCACG
112	Mitoferrin2	ACGTCACAGCAACAGGCGCG
113	FXN	AGGGAACCGATCGTAACCTG
114	FXN	CGAAGCGCGTACTCACGGCG
115	FXN	GCGCGGGTTCCCGACCCAGG
116	FXN	TGGGGACATTGGACAACCCA
117	Elavl1	CAAACCGCCTAGCAGGCGAG
118	Elavl1	GATGCCAACTTATACATCAG
119	Elavl1	TACCTGTGGTCTGATCCACA
120	Elavl1	TCTCTTATAGGACACAGCTT
121	Elavl2	GATGCAAACTTATACGTCAG
122	Elavl2	CTGGCTACTTACCAGTGACC
123	Elavl2	GTTCCCGGAGTCAACTGGTG
124	Elavl2	TGTGAACTACATTGACCCCA
125	IRF5	CTCACCATCAGCAACCCACA
126	IRF5	AGGGCTTCAGTGGGTCAACG
127	IRF5	AAGGAATAGGGTGCGTTGGG
128	IRF5	CCCAGAACGTAATCATCAGT
129	Fbxl5	CAAACAGGCATACTGCGTGG
130	Fbxl5	GTAAAATATTCCATTAACAT
131	Fbxl5	TACCTCTTGCCCAATGAACA
132	Fbxl5	AAATGCAGAATCAGAAATGT

Number	Gene name	Guide sequence
133	Hmox1	TCGTGCTCGAATGAACACTC
134	Hmox1	TCAGGACCTGACCCCCTGAG
135	Hmox1	ACGCTTTACATAGTGCTGTG
136	Hmox1	TTCCTTGTACCATATCTACA
137	Bdh2	TGCCCGTCCAATCCCTTGAG
138	Bdh2	ATGTGTGTACAGTGCTACCA
139	Bdh2	CATTATCAACATGTCGTCTG
140	Bdh2	TATCAACGAGTCCAAACTCC
141	Tet1	GATTAATCACATCAACGCCG
142	Tet1	TGGCGGCGTAGAATTACATG
143	Tet1	AATTCAAGACAGAATCCGGT
144	Tet1	TTTGCCCAGACCATAAGGAA
145	Tet2	CGAAGCTTGCAAATTCCGGT
146	Tet2	GGTATATCGGAGATCGAGTG
147	Tet2	CTCACAATAATACCCAAGGG
148	Tet2	TGATAACCGTTGAGTCTCTG
149	Gpx1	GGTGTCCGAACTGATTGCAC
150	Gpx1	TCCCTCAAGTACGTCCGACC
151	Gpx1	CTCGGTGTAGTCCCGGATCG
152	Gpx1	CGCGGAGAAGGCATACACGG
153	Gpx2	GCTGGTACCCACCCCCAGGT
154	Gpx2	ACCAGTTCGGACATCAGGTG
155	Gpx2	ATAGACTTCAATACGTTCAG
156	Gpx2	TTCTACGATCTCAGTGCCGT
157	Gpx3	TGGTACCACTCATACCGCCA
158	Gpx3	GTCAACGTAGCCAGCTACTG
159	Gpx3	TGAGAAAGGAGATGTGAACG
160	Gpx3	ATGCACTACAAGAAGAACTT
161	Gpx5	GGTCTGACAATCCAGTACCC
162	Gpx5	AGGTAGCCACATTGACAAAG
163	Gpx5	GCTATGTGCAGACAACCCCC
164	Gpx5	AGAATCTCTAAATTGTCTCC
165	Gch1	GCACCAATGGGTTCTCCGAG
166	Gch1	CCCTTCCTACAAATGGAACA
167	Gch1	GGTGAACCTCCCCAAACTGG
168	Gch1	GTACTTCACCAAGGGATACC
169	Csf2	ATATTCGAGCAGGGTCTACG
170	Csf2	GGATGACATGCCTGTCACGT
171	Csf2	CTGCTCGAATATCTTCAGGC
172	Csf2	CCGGCCTTGGAAGCATGTAG
173	Il17a	CTCAGCGTGTCCAAACACTG
174	Il17a	GAACGGTTGAGGTAGTCTGA
175	Il17a	CTTACGTACTGGAGAGTCCA
176	Il17a	CTGAGCTTCCCAGATCACAG
177	Il17f	GACTTACTTGTAATCCCATG

Number	Gene name	Guide sequence
178	Il17f	TGGGAACTGTCCTCCCCTGG
179	Il17f	AGCGGTTCTGGAATTCACGT
180	Il17f	GGGCCTCAGCGATCTCTGAG
181	Il17ra	ACTGAAGTAGCAAACAACGT
182	Il17ra	ATGAGGCCATACACCCACAG
183	Il17ra	GAAGGTCTGGATCGTCTACT
184	Il17ra	GACCTGGAGATGTTTGAACC
185	Il6ra	CTGTGCGTTGCAAACAGTGT
186	Il6ra	GGGGCAAATCAGGGTAACGG
187	Il6ra	CAGGTATGGCTGATACCACA
188	Il6ra	CACCCCCTCTCCAACCACGA
189	Il1R1	AGCATACAATTGTAGCCGTG
190	Il1R1	CAGCAAGACCCCCATATCAG
191	Il1R1	CGTATGTCCTATACGTTCCG
192	Il1R1	ACTGTGTTAGAGAATGACCC
193	Il2ra	GTGTCTGTATGACCCACCCG
194	Il2ra	ATCTTGCAGATGCTAATAGC
195	Il2ra	GAGAGGTTTCCGAAGACTAA
196	Il2ra	GAATCTTCATGTTTCCAAGG
197	Il23r	TCTATAGTACTTACGTCCAG
198	Il23r	AAACTGCTCTGGTGACATGT
199	Il23r	GGAGATCTTAACATAGCTTG
200	Il23r	CACCAAACTTCCCAGACAGG
201	Rheb	AACAAACTGAATTGTCAATG
202	Rheb	CCATATCCAACAACTTGCCA
203	Rheb	TTCAGCTTGTAGACACAGCG
204	Rheb	TCATAGGATACCTATTATGT
205	Rorc	CTTGAGTATAGTCCAGAACG
206	Rorc	GTCATCTGGGATCCACTACG
207	Rorc	TCTGGGGCACTGCAGAAACT
208	Rorc	GACAAGCAGAGGCCTCGGGT
209	Foxp3	CATACCTGATGCATGAAGTG
210	Foxp3	TCTACCCACAGGGATCAATG
211	Foxp3	AGGTCGGGACCTGCGAAGTG
212	Foxp3	GCAAGAGCTCTTGTCCATTG
213	Tsc2	TGAACCACATGGCTATGACG
214	Tsc2	CACAGGGTGATAATGAACAG
215	Tsc2	CAGCTCCAAAGACCCTTGAG
216	Tsc2	CTGATCCTAGCACACATGTG
217	Tbx21	AGTCTGGGTGGACATATAAG
218	Tbx21	AGGACTACGCATTGCCCGCG
219	Tbx21	GACCCGACCGATCGCCGCGC
220	Tbx21	GGCTTCCAACAATGTGACCC
221	NTC	AAAATTGCACCTTCCCGGCC

Number	Gene name	Guide sequence
222	NTC	AAACCCCCGCGCGGAGCGTC
223	NTC	AAACCTAGCGTAGATTCGGC
224	NTC	AAACGAGGCTGTTCGTACAC
225	NTC	AAACTCATACGTAGCGAATC

Original Doc: Kelsey Iron Library

Gene name	Guide sequence	Twist Order
Tfrc	CTACACGCTTACAATAGCCC	GGAAAGGACGAAACACCGCTACACGCTTACAATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc	GAATACATACACTCCTCGTG	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc	GGGCTCCTACTACAACATAA	GGAAAGGACGAAACACCGGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfrc	AACCCTCGGGAGACTCCACT	GGAAAGGACGAAACACCGAACCCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a1	GGGTGTGCTACCACATACTG	GGAAAGGACGAAACACCGGGGTGTGCTACCACATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a1	GAGAAGTAGACAGAACCCGC	GGAAAGGACGAAACACCGGAGAAGTAGACAGAACCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a1	CCTAGCATGATACCGTCCAG	GGAAAGGACGAAACACCGCCTAGCATGATACCGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a1	GAATGGGGATCTTCTCACTC	GGAAAGGACGAAACACCGGAATGGGGATCTTCTCACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a2	ATGTCACCGTCAGTATCCCA	GGAAAGGACGAAACACCGATGTCACCGTCAGTATCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a2	AAACACAAAAGTGTCTGCGA	GGAAAGGACGAAACACCGAAACACAAAAGTGTCTGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a2	TGAGAAAATCCCCATTCCTG	GGAAAGGACGAAACACCGTGAGAAAATCCCCATTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc11a2	CCTTGACTAAGGCAGAATGC	GGAAAGGACGAAACACCGCCTTGACTAAGGCAGAATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fpn, Slc40a1	CAGGGTACGCCTACACTCAG	GGAAAGGACGAAACACCGCAGGGTACGCCTACACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fpn, Slc40a1	CCTTTGGATTGTGATCGCAG	GGAAAGGACGAAACACCGCCTTTGGATTGTGATCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fpn, Slc40a1	TCATCAGGATGATTCCGCAG	GGAAAGGACGAAACACCGTCATCAGGATGATTCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fpn, Slc40a1	CCCATCCATCTCGGAAAGTG	GGAAAGGACGAAACACCGCCCATCCATCTCGGAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scara5	TAGGTCCATGTCACAAACGG	GGAAAGGACGAAACACCGTAGGTCCATGTCACAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scara5	CTGGTAGAGTTCCAGCTGTG	GGAAAGGACGAAACACCGCTGGTAGAGTTCCAGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scara5	CAGCGCCTTCAAGTCATCTG	GGAAAGGACGAAACACCGCAGCGCCTTCAAGTCATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scara5	GGGAACACTCCATCGCCTTG	GGAAAGGACGAAACACCGGGGAACACTCCATCGCCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Timd2	GATATACGGTCACACATCAG	GGAAAGGACGAAACACCGGATATACGGTCACACATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Timd2	GGAATCGTTCCTATGTGTTG	GGAAAGGACGAAACACCGGGAATCGTTCCTATGTGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Timd2	TGTTGGAAGTTAAACCAGGT	GGAAAGGACGAAACACCGTGTTGGAAGTTAAACCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Timd2	CTGATCTGGATAAAATGTAG	GGAAAGGACGAAACACCGCTGATCTGGATAAAATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Heph	CATGTGCAAGGGTGATACTG	GGAAAGGACGAAACACCGCATGTGCAAGGGTGATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Heph	TTGGAGCATCTACATGCGAG	GGAAAGGACGAAACACCGTTGGAGCATCTACATGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Heph	GTTTATAAGGAATACAGTGA	GGAAAGGACGAAACACCGGTTTATAAGGAATACAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Heph	AAAAGTCACATACTACTGGA	GGAAAGGACGAAACACCGAAAAGTCACATACTACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hephl1	ACAGCGGCGCTACTTCATAG	GGAAAGGACGAAACACCGACAGCGGCGCTACTTCATAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hephl1	GTTTCCCCATATGGCCACAA	GGAAAGGACGAAACACCGGTTTCCCCATATGGCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hephl1	GTGAAACCTTCACCTACAGG	GGAAAGGACGAAACACCGGTGAAACCTTCACCTACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hephl1	CCCAGAGCAGATATCCTTAG	GGAAAGGACGAAACACCGCCCAGAGCAGATATCCTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cp	CATATAAGCATCAATTAGGG	GGAAAGGACGAAACACCGCATATAAGCATCAATTAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cp	GCTGTGAGGAGCGACCTGGT	GGAAAGGACGAAACACCGGCTGTGAGGAGCGACCTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cp	ATGAAAAGTGTAGATCCTAG	GGAAAGGACGAAACACCGATGAAAAGTGTAGATCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cp	GCTGAACAAATACCACACGA	GGAAAGGACGAAACACCGGCTGAACAAATACCACACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fth1	CACCATAGACAGATAGACGT	GGAAAGGACGAAACACCGCACCATAGACAGATAGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fth1	AGTGCGCCAGAACTACCACC	GGAAAGGACGAAACACCGAGTGCGCCAGAACTACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fth1	GGAGAGCGGGCTGAATGCAA	GGAAAGGACGAAACACCGGGAGAGCGGGCTGAATGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fth1	TCTTCAGAGCCACATCATCT	GGAAAGGACGAAACACCGTCTTCAGAGCCACATCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ftl1	GCTGCTCACCAGAGAGAGGT	GGAAAGGACGAAACACCGGCTGCTCACCAGAGAGAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ftl1	TTGGCCGAGGAGAAGCGCGA	GGAAAGGACGAAACACCGTTGGCCGAGGAGAAGCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ftl1	GAGTTTCAGAACGATCGCGG	GGAAAGGACGAAACACCGGAGTTTCAGAACGATCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ftl1	TCGTCAGAATTATTCCACCG	GGAAAGGACGAAACACCGTCGTCAGAATTATTCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap2	AGTACCGCCGATTTCCCCCG	GGAAAGGACGAAACACCGAGTACCGCCGATTTCCCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap2	TATTAGATGTGGCTACCACG	GGAAAGGACGAAACACCGTATTAGATGTGGCTACCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap2	TAAATGGTATCAAAGACGCA	GGAAAGGACGAAACACCGTAAATGGTATCAAAGACGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap2	CAGAGAGTAAACAGTCGCAG	GGAAAGGACGAAACACCGCAGAGAGTAAACAGTCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap3	AGCTCAAGTGACTTTCCAGG	GGAAAGGACGAAACACCGAGCTCAAGTGACTTTCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap3	AGCAGCACATAAGCCACACA	GGAAAGGACGAAACACCGAGCAGCACATAAGCCACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap3	TGGGGTTGCTTACATCCACG	GGAAAGGACGAAACACCGTGGGGTTGCTTACATCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap3	GGTTTCACACCCCTGGACAT	GGAAAGGACGAAACACCGGGTTTCACACCCCTGGACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap4	TGTGTACTGTGCAATACGAG	GGAAAGGACGAAACACCGTGTGTACTGTGCAATACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap4	GATAATCAACTAGTTCCGTG	GGAAAGGACGAAACACCGGATAATCAACTAGTTCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap4	AATACCAGGGAGGTACACCA	GGAAAGGACGAAACACCGAATACCAGGGAGGTACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Steap4	GTTAAATGCTTTGACCACGT	GGAAAGGACGAAACACCGGTTAAATGCTTTGACCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Glrx5	GCACGGTGTTCGCGACTATG	GGAAAGGACGAAACACCGGCACGGTGTTCGCGACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Glrx5	GCGTTGCTGAAGCCGCACTG	GGAAAGGACGAAACACCGGCGTTGCTGAAGCCGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Glrx5	AGGTGGTGGTGTTCCTCAAG	GGAAAGGACGAAACACCGAGGTGGTGGTGTTCCTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Glrx5	GGAGTAGTCTTTAATACCTG	GGAAAGGACGAAACACCGGGAGTAGTCTTTAATACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr2	GAGGTCGCTCCAGTACAACG	GGAAAGGACGAAACACCGGAGGTCGCTCCAGTACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr2	AGTGCGTGTCAGTCCACACG	GGAAAGGACGAAACACCGAGTGCGTGTCAGTCCACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr2	TGGTGTACGCCCACTACGGG	GGAAAGGACGAAACACCGTGGTGTACGCCCACTACGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr2	ACCCCCAGTGAAGATTAGCA	GGAAAGGACGAAACACCGACCCCCAGTGAAGATTAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hamp	CACCTGTTGATGGAGATAGG	GGAAAGGACGAAACACCGCACCTGTTGATGGAGATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hamp	AGATACCAATGCAGAAGAGA	GGAAAGGACGAAACACCGAGATACCAATGCAGAAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hamp	AGAGCTGCAGCCTTTGCACG	GGAAAGGACGAAACACCGAGAGCTGCAGCCTTTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hamp	AGAAAGCAGGGCAGACATTG	GGAAAGGACGAAACACCGAGAAAGCAGGGCAGACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4	CGTCGCTGATTGTTGCGCCG	GGAAAGGACGAAACACCGCGTCGCTGATTGTTGCGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Gene name	Guide sequence	Twist Order
Ncoa4	TTCAAGAAGTCAGCATCCAG	GGAAAGGACGAAACACCGTTCAAGAAGTCAGCATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4	GGTCTTAAGGGATCCAAATG	GGAAAGGACGAAACACCGGGTCTTAAGGGATCCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4	AATTAAAGATAATTTACGAG	GGAAAGGACGAAACACCGAATTAAAGATAATTTACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hfe	TGCTCCACGTACCCTTACTG	GGAAAGGACGAAACACCGTGCTCCACGTACCCTTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hfe	TTCCTCCCGCACTCACGCGG	GGAAAGGACGAAACACCGTTCCTCCCGCACTCACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hfe	GATCCGTGCCAAACAGAACA	GGAAAGGACGAAACACCGGATCCGTGCCAAACAGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hfe	CATGAAGACAACAGTACCAG	GGAAAGGACGAAACACCGCATGAAGACAACAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco1, IRP2	CCACCGCCATTTAGGCCGCG	GGAAAGGACGAAACACCGCCACCGCCATTTAGGCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco1, IRP2	CATATGCTATTACCAGAGGG	GGAAAGGACGAAACACCGCATATGCTATTACCAGAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco1, IRP2	TAGCCCACCACATCAAACCT	GGAAAGGACGAAACACCGTAGCCCACCACATCAAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco1, IRP2	GTGTAGCACCTCCGACAAGT	GGAAAGGACGAAACACCGGTGTAGCACCTCCGACAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco2	AGATCCGTGCCACTATTGAG	GGAAAGGACGAAACACCGAGATCCGTGCCACTATTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco2	GCGTTTACGGCCCGACCGGG	GGAAAGGACGAAACACCGGCGTTTACGGCCCGACCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco2	TGGGTGAGGTCCAACCAGAG	GGAAAGGACGAAACACCGTGGGTGAGGTCCAACCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Aco2	GATTGAAATTAACCTCAATG	GGAAAGGACGAAACACCGGATTGAAATTAACCTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IREB2	AATTTGGCAGAAATCGAGAG	GGAAAGGACGAAACACCGAATTTGGCAGAAATCGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IREB2	TAAGCTGTCCCATGGATCCG	GGAAAGGACGAAACACCGTAAGCTGTCCCATGGATCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IREB2	TCTAAGAAGCTTCCATGTCG	GGAAAGGACGAAACACCGTCTAAGAAGCTTCCATGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IREB2	TCAATAGTTGCATCTGTCAG	GGAAAGGACGAAACACCGTCAATAGTTGCATCTGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hepb1, Nrf2	GAAACACGGCAAAAGAGACA	GGAAAGGACGAAACACCGGAAACACGGCAAAAGAGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hepb1, Nrf2	CCCAAGATCATGAAGTATGT	GGAAAGGACGAAACACCGCCCAAGATCATGAAGTATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hepb1, Nrf2	AGGGGGCAAGTTTGCTACTG	GGAAAGGACGAAACACCGAGGGGGCAAGTTTGCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hepb1, Nrf2	TGATGAGAGTGTGAAGATCG	GGAAAGGACGAAACACCGTGATGAGAGTGTGAAGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP2	TCTGGGTACCATCCTAACCA	GGAAAGGACGAAACACCGTCTGGGTACCATCCTAACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP2	GTCAAACAGTTCTACACCAA	GGAAAGGACGAAACACCGGTCAAACAGTTCTACACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP2	AGACCATTGCACGAGAGGAA	GGAAAGGACGAAACACCGAGACCATTGCACGAGAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP2	CGGACCTTGGCGGTATCCAG	GGAAAGGACGAAACACCGCGGACCTTGGCGGTATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP3	GTAGAGGCCAATTCGAATGG	GGAAAGGACGAAACACCGGTAGAGGCCAATTCGAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP3	CCTGACTATGGTGCGCACAG	GGAAAGGACGAAACACCGCCTGACTATGGTGCGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP3	TTTCAAGCCATGATACGCCT	GGAAAGGACGAAACACCGTTTCAAGCCATGATACGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
UCP3	TGCCTACAGAACCATCGCCA	GGAAAGGACGAAACACCGTGCCTACAGAACCATCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a4, ANT	CCTAGACCTGTTTAACTGTG	GGAAAGGACGAAACACCGCCTAGACCTGTTTAACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a4, ANT	CAGTTTGACCCTCTCGATCG	GGAAAGGACGAAACACCGCAGTTTGACCCTCTCGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a4, ANT	GGAAGATCCCTTGCCCACGT	GGAAAGGACGAAACACCGGGAAGATCCCTTGCCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a4, ANT	TTGTGTCGTGAGAATCCCCA	GGAAAGGACGAAACACCGTTGTGTCGTGAGAATCCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a37, Mitoferrin1	CTGGATTCATTACTGCATCG	GGAAAGGACGAAACACCGCTGGATTCATTACTGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a37, Mitoferrin1	CACTGTCCGGATACAACTGA	GGAAAGGACGAAACACCGCACTGTCCGGATACAACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a37, Mitoferrin1	GATGAAGTGAATTGACTGGA	GGAAAGGACGAAACACCGGATGAAGTGAATTGACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Slc25a37, Mitoferrin1	GCATCTATGGCGCCCTCAAG	GGAAAGGACGAAACACCGGCATCTATGGCGCCCTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mitoferrin2	CAACACGTTCCGATAGCGGG	GGAAAGGACGAAACACCGCAACACGTTCCGATAGCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mitoferrin2	TTGAGTGACGTAATCCACCC	GGAAAGGACGAAACACCGTTGAGTGACGTAATCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mitoferrin2	CCCGAACACAGTCTGTCACG	GGAAAGGACGAAACACCGCCCGAACACAGTCTGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mitoferrin2	ACGTCACAGCAACAGGCGCG	GGAAAGGACGAAACACCGACGTCACAGCAACAGGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FXN	AGGGAACCGATCGTAACCTG	GGAAAGGACGAAACACCGAGGGAACCGATCGTAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FXN	CGAAGCGCGTACTCACGGCG	GGAAAGGACGAAACACCGCGAAGCGCGTACTCACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FXN	GCGCGGGTTCCCGACCCAGG	GGAAAGGACGAAACACCGGCGCGGGTTCCCGACCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FXN	TGGGGACATTGGACAACCCA	GGAAAGGACGAAACACCGTGGGGACATTGGACAACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl1	CAAACCGCCTAGCAGGCGAG	GGAAAGGACGAAACACCGCAAACCGCCTAGCAGGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl1	GATGCCAACTTATACATCAG	GGAAAGGACGAAACACCGGATGCCAACTTATACATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl1	TACCTGTGGTCTGATCCACA	GGAAAGGACGAAACACCGTACCTGTGGTCTGATCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl1	TCTCTTATAGGACACAGCTT	GGAAAGGACGAAACACCGTCTCTTATAGGACACAGCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl2	GATGCAAACTTATACGTCAG	GGAAAGGACGAAACACCGGATGCAAACTTATACGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl2	CTGGCTACTTACCAGTGACC	GGAAAGGACGAAACACCGCTGGCTACTTACCAGTGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl2	GTTCCCGGAGTCAACTGGTG	GGAAAGGACGAAACACCGGTTCCCGGAGTCAACTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Elavl2	TGTGAACTACATTGACCCCA	GGAAAGGACGAAACACCGTGTGAACTACATTGACCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IRF5	CTCACCATCAGCAACCCACA	GGAAAGGACGAAACACCGCTCACCATCAGCAACCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IRF5	AGGGCTTCAGTGGGTCAACG	GGAAAGGACGAAACACCGAGGGCTTCAGTGGGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IRF5	AAGGAATAGGGTGCGTTGGG	GGAAAGGACGAAACACCGAAGGAATAGGGTGCGTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
IRF5	CCCAGAACGTAATCATCAGT	GGAAAGGACGAAACACCGCCCAGAACGTAATCATCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fbxl5	CAAACAGGCATACTGCGTGG	GGAAAGGACGAAACACCGCAAACAGGCATACTGCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fbxl5	GTAAAATATTCCATTAACAT	GGAAAGGACGAAACACCGGTAAAATATTCCATTAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fbxl5	TACCTCTTGCCCAATGAACA	GGAAAGGACGAAACACCGTACCTCTTGCCCAATGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Fbxl5	AAATGCAGAATCAGAAATGT	GGAAAGGACGAAACACCGAAATGCAGAATCAGAAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hmox1	TCGTGCTCGAATGAACACTC	GGAAAGGACGAAACACCGTCGTGCTCGAATGAACACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hmox1	TCAGGACCTGACCCCCTGAG	GGAAAGGACGAAACACCGTCAGGACCTGACCCCCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hmox1	ACGCTTTACATAGTGCTGTG	GGAAAGGACGAAACACCGACGCTTTACATAGTGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hmox1	TTCCTTGTACCATATCTACA	GGAAAGGACGAAACACCGTTCCTTGTACCATATCTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bdh2	TGCCCGTCCAATCCCTTGAG	GGAAAGGACGAAACACCGTGCCCGTCCAATCCCTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bdh2	ATGTGTGTACAGTGCTACCA	GGAAAGGACGAAACACCGATGTGTGTACAGTGCTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bdh2	CATTATCAACATGTCGTCTG	GGAAAGGACGAAACACCGCATTATCAACATGTCGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bdh2	TATCAACGAGTCCAAACTCC	GGAAAGGACGAAACACCGTATCAACGAGTCCAAACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Gene name	Guide sequence	Twist Order
Tet1	GATTAATCACATCAACGCCG	GGAAAGGACGAAACACCGGATTAATCACATCAACGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet1	TGGCGGCGTAGAATTACATG	GGAAAGGACGAAACACCGTGGCGGCGTAGAATTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet1	AATTCAAGACAGAATCCGGT	GGAAAGGACGAAACACCGAATTCAAGACAGAATCCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet1	TTTGCCCAGACCATAAGGAA	GGAAAGGACGAAACACCGTTTGCCCAGACCATAAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet2	CGAAGCTTGCAAATTCCGGT	GGAAAGGACGAAACACCGCGAAGCTTGCAAATTCCGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet2	GGTATATCGGAGATCGAGTG	GGAAAGGACGAAACACCGGGTATATCGGAGATCGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet2	CTCACAATAATACCCAAGGG	GGAAAGGACGAAACACCGCTCACAATAATACCCAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tet2	TGATAACCGTTGAGTCTCTG	GGAAAGGACGAAACACCGTGATAACCGTTGAGTCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx1	GGTGTCCGAACTGATTGCAC	GGAAAGGACGAAACACCGGGTGTCCGAACTGATTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx1	TCCCTCAAGTACGTCCGACC	GGAAAGGACGAAACACCGTCCCTCAAGTACGTCCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx1	CTCGGTGTAGTCCCGGATCG	GGAAAGGACGAAACACCGCTCGGTGTAGTCCCGGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx1	CGCGGAGAAGGCATACACGG	GGAAAGGACGAAACACCGCGCGGAGAAGGCATACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx2	GCTGGTACCCACCCCCAGGT	GGAAAGGACGAAACACCGGCTGGTACCCACCCCCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx2	ACCAGTTCGGACATCAGGTG	GGAAAGGACGAAACACCGACCAGTTCGGACATCAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx2	ATAGACTTCAATACGTTCAG	GGAAAGGACGAAACACCGATAGACTTCAATACGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx2	TTCTACGATCTCAGTGCCGT	GGAAAGGACGAAACACCGTTCTACGATCTCAGTGCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx3	TGGTACCACTCATACCGCCA	GGAAAGGACGAAACACCGTGGTACCACTCATACCGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx3	GTCAACGTAGCCAGCTACTG	GGAAAGGACGAAACACCGGTCAACGTAGCCAGCTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx3	TGAGAAAGGAGATGTGAACG	GGAAAGGACGAAACACCGTGAGAAAGGAGATGTGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx3	ATGCACTACAAGAAGAACTT	GGAAAGGACGAAACACCGATGCACTACAAGAAGAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx5	GGTCTGACAATCCAGTACCC	GGAAAGGACGAAACACCGGGTCTGACAATCCAGTACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx5	AGGTAGCCACATTGACAAAG	GGAAAGGACGAAACACCGAGGTAGCCACATTGACAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx5	GCTATGTGCAGACAACCCCC	GGAAAGGACGAAACACCGGCTATGTGCAGACAACCCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gpx5	AGAATCTCTAAATTGTCTCC	GGAAAGGACGAAACACCGAGAATCTCTAAATTGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gch1	GCACCAATGGGTTCTCCGAG	GGAAAGGACGAAACACCGGCACCAATGGGTTCTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gch1	CCCTTCCTACAAATGGAACA	GGAAAGGACGAAACACCGCCCTTCCTACAAATGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gch1	GGTGAACCTCCCCAAACTGG	GGAAAGGACGAAACACCGGGTGAACCTCCCCAAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gch1	GTACTTCACCAAGGGATACC	GGAAAGGACGAAACACCGGTACTTCACCAAGGGATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Csf2	ATATTCGAGCAGGGTCTACG	GGAAAGGACGAAACACCGATATTCGAGCAGGGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Csf2	GGATGACATGCCTGTCACGT	GGAAAGGACGAAACACCGGGATGACATGCCTGTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Csf2	CTGCTCGAATATCTTCAGGC	GGAAAGGACGAAACACCGCTGCTCGAATATCTTCAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Csf2	CCGGCCTTGGAAGCATGTAG	GGAAAGGACGAAACACCGCCGGCCTTGGAAGCATGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a	CTCAGCGTGTCCAAACACTG	GGAAAGGACGAAACACCGCTCAGCGTGTCCAAACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a	GAACGGTTGAGGTAGTCTGA	GGAAAGGACGAAACACCGGAACGGTTGAGGTAGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a	CTTACGTACTGGAGAGTCCA	GGAAAGGACGAAACACCGCTTACGTACTGGAGAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a	CTGAGCTTCCCAGATCACAG	GGAAAGGACGAAACACCGCTGAGCTTCCCAGATCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17f	GACTTACTTGTAATCCCATG	GGAAAGGACGAAACACCGGACTTACTTGTAATCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17f	TGGGAACTGTCCTCCCCTGG	GGAAAGGACGAAACACCGTGGGAACTGTCCTCCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17f	AGCGGTTCTGGAATTCACGT	GGAAAGGACGAAACACCGAGCGGTTCTGGAATTCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17f	GGGCCTCAGCGATCTCTGAG	GGAAAGGACGAAACACCGGGGCCTCAGCGATCTCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17ra	ACTGAAGTAGCAAACAACGT	GGAAAGGACGAAACACCGACTGAAGTAGCAAACAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17ra	ATGAGGCCATACACCCACAG	GGAAAGGACGAAACACCGATGAGGCCATACACCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17ra	GAAGGTCTGGATCGTCTACT	GGAAAGGACGAAACACCGGAAGGTCTGGATCGTCTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17ra	GACCTGGAGATGTTTGAACC	GGAAAGGACGAAACACCGGACCTGGAGATGTTTGAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il6ra	CTGTGCGTTGCAAACAGTGT	GGAAAGGACGAAACACCGCTGTGCGTTGCAAACAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il6ra	GGGGCAAATCAGGGTAACGG	GGAAAGGACGAAACACCGGGGGCAAATCAGGGTAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il6ra	CAGGTATGGCTGATACCACA	GGAAAGGACGAAACACCGCAGGTATGGCTGATACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il6ra	CACCCCCTCTCCAACCACGA	GGAAAGGACGAAACACCGCACCCCCTCTCCAACCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il1R1	AGCATACAATTGTAGCCGTG	GGAAAGGACGAAACACCGAGCATACAATTGTAGCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il1R1	CAGCAAGACCCCCATATCAG	GGAAAGGACGAAACACCGCAGCAAGACCCCCATATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il1R1	CGTATGTCCTATACGTTCCG	GGAAAGGACGAAACACCGCGTATGTCCTATACGTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il1R1	ACTGTGTTAGAGAATGACCC	GGAAAGGACGAAACACCGACTGTGTTAGAGAATGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il2ra	GTGTCTGTATGACCCACCCG	GGAAAGGACGAAACACCGGTGTCTGTATGACCCACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il2ra	ATCTTGCAGATGCTAATAGC	GGAAAGGACGAAACACCGATCTTGCAGATGCTAATAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il2ra	GAGAGGTTTCCGAAGACTAA	GGAAAGGACGAAACACCGGAGAGGTTTCCGAAGACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il2ra	GAATCTTCATGTTTCCAAGG	GGAAAGGACGAAACACCGGAATCTTCATGTTTCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il23r	TCTATAGTACTTACGTCCAG	GGAAAGGACGAAACACCGTCTATAGTACTTACGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il23r	AAACTGCTCTGGTGACATGT	GGAAAGGACGAAACACCGAAACTGCTCTGGTGACATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il23r	GGAGATCTTAACATAGCTTG	GGAAAGGACGAAACACCGGGAGATCTTAACATAGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il23r	CACCAAACTTCCCAGACAGG	GGAAAGGACGAAACACCGCACCAAACTTCCCAGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rheb	AACAAACTGAATTGTCAATG	GGAAAGGACGAAACACCGAACAAACTGAATTGTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rheb	CCATATCCAACAACTTGCCA	GGAAAGGACGAAACACCGCCATATCCAACAACTTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rheb	TTCAGCTTGTAGACACAGCG	GGACGAAACACCGGTTCAGCTTGTAGACACAGCGGGGAAATTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rheb	TCATAGGATACCTATTATGT	GGAAAGGACGAAACACCGTCATAGGATACCTATTATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc	CTTGAGTATAGTCCAGAACG	GGAAAGGACGAAACACCGCTTGAGTATAGTCCAGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc	GTCATCTGGGATCCACTACG	GGAAAGGACGAAACACCGGTCATCTGGGATCCACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc	TCTGGGGCACTGCAGAAACT	GGAAAGGACGAAACACCGTCTGGGGCACTGCAGAAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc	GACAAGCAGAGGCCTCGGGT	GGAAAGGACGAAACACCGGACAAGCAGAGGCCTCGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3	CATACCTGATGCATGAAGTG	GGAAAGGACGAAACACCGCATACCTGATGCATGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3	TCTACCCACAGGGATCAATG	GGAAAGGACGAAACACCGTCTACCCACAGGGATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3	AGGTCGGGACCTGCGAAGTG	GGAAAGGACGAAACACCGAGGTCGGGACCTGCGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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Foxp3	GCAAGAGCTCTTGTCCATTG	GGAAAGGACGAAACACCGGCAAGAGCTCTTGTCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tsc2	TGAACCACATGGCTATGACG	GGAAAGGACGAAACACCGTGAACCACATGGCTATGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tsc2	CACAGGGTGATAATGAACAG	GGAAAGGACGAAACACCGCACAGGGTGATAATGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tsc2	CAGCTCCAAAGACCCTTGAG	GGAAAGGACGAAACACCGCAGCTCCAAAGACCCTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tsc2	CTGATCCTAGCACACATGTG	GGAAAGGACGAAACACCGCTGATCCTAGCACACATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21	AGTCTGGGTGGACATATAAG	GGAAAGGACGAAACACCGAGTCTGGGTGGACATATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21	AGGACTACGCATTGCCCGCG	GGAAAGGACGAAACACCGAGGACTACGCATTGCCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21	GACCCGACCGATCGCCGCGC	GGAAAGGACGAAACACCGGACCCGACCGATCGCCGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21	GGCTTCCAACAATGTGACCC	GGAAAGGACGAAACACCGGGCTTCCAACAATGTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC	AAAATTGCACCTTCCCGGCC	GGAAAGGACGAAACACCGAAAATTGCACCTTCCCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC	AAACCCCCGCGCGGAGCGTC	GGAAAGGACGAAACACCGAAACCCCCGCGCGGAGCGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC	AAACCTAGCGTAGATTCGGC	GGAAAGGACGAAACACCGAAACCTAGCGTAGATTCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC	AAACGAGGCTGTTCGTACAC	GGAAAGGACGAAACACCGAAACGAGGCTGTTCGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC	AAACTCATACGTAGCGAATC	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Gene family/pathway	Gene (mouse)
Transporters and scavengers	Tfrc
	Slc11a1
	Slc11a2
	Fpn, Slc40a1
	Scara5
	Tim-2
	Heph
	Cp
Main Machinery	Fth
	Ftl
	Steap3
Homeostasis	Ncoa4
	Hfe
	Hamp
	IRP1
	IRP2
	Nrf2
Mitochondrial	Glrx5
	UCP2
	ANT
	Heph
	Mitoferrin1
	Mitoferrin2
	FXN
Secondary effects/RNA binding proteins	Elavl1 (HuR)
	Elavl2
	Fbxl5
	HIF1
	HIF2
	IRF5
	HO-1
	BDH2
	Tet1
	Tet2
	Tet3
	Gpx4
	Gch1

Biological Controls	Il17
	Il6
	Il1
	Csf2
	Il2ra
	Il23r
	Tbx21
	Rorc
	Foxp3
Controls	Tsc2
	rheb
	NTCs (multiple)