Library Registration Form

Library Number	
Library Name	tS Phosphoinositol Regulation Library
Old Document Name	
Library Purpose	CRISPR/Cas9 knockout of phosphoinositol regulation genes in mice
Location (Oligos)	KKS Main Lab -20 Freezer, DNA/Plasmids Box
Location (Bacteria)	N/A
Designer Name	KayLee Steiner/ Channing Chi
Designing Date	Jul-21
Design Reference	KayLee Steiner
Usage Reference	KayLee Steiner

Species	Mouse (Mus musculus)
Total Gene #	63 (53+10 NTCs)
Total Target #	222
Gene Group	Phosphoinositol Regulation
1. Negative Controls	JAK1(IL-2)
2. Positive Controls	Pten, TSC2
Phosphoinositol Regulation	53
Target Number	
1. Negative Controls	1*4=4
2. Positive Controls	2*4=8
3. Phosphoinositol Regulation	212

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

This library was designed based on Mtm1 being found in ARP IEI Library as Enriched. This library includes all members of the Myotubularin family, PI3 Kinases, Phosphatases, and some other important genes within the signaling family deemed as important

Number	Target Gene Symbol	Guide sequence
1	Mtm1	AGGGAACCACCAAAAGAGCA
2	Mtm1	TTACCACTCATACCGACAAG
3	Mtm1	ATGGGAGGCGCGACAAGTAG
4	Mtm1	TCTGACCGGTGCCATTCAAG
5	MTMR1	GTCACATTGGCTATCCAATG
6	MTMR1	CAGCGTTGCTGATACCAACA
7	MTMR1	AGCCATGGGGATAATTCTTG
8	MTMR1	AGGGCTTGCCAAATGAGAGT
9	MTMR10	CCTGACGTACTCTAACCACC
10	MTMR10	CTAACGGCAGTGCTCTTGTG
11	MTMR10	TCTGAGTAAGTTTCGAACAG
12	MTMR10	AGCTATTGCAAGGCATACCT
13	MTMR11	GGGTTAGCACGGTCAATGAG
14	MTMR11	TAACCCTCGACTTCAGTGAG
15	MTMR11	ATTACCTGGGAGACAACCAG
16	MTMR11	AAAGGGCCCTCAGTTTCAAG
17	MTMR12	ATGTACTTACTGGTATACCA
18	MTMR12	AATGGATAACGAGCTTCTCG
19	MTMR12	AAACCTTATTACCCAACAGG
20	MTMR12	TCTGTGAACTCAAATGCTGG
21	MTMR14	AATGTGAATGGTGATATCTG
22	MTMR14	GAAGTTGGGGATGTTCAATG
23	MTMR14	GGCCGACCTGCAAATATGCT
24	MTMR14	TGAGATCCTCTACCTGACTG
25	MTMR2	TGCTCGGCCAAGTGTCAATG
26	MTMR2	GCCTTCTGTACTCTAGAAGG
27	MTMR2	GTGGCATCCTTTAGGTCACG
28	MTMR2	GTAATGATTCTCTCATAACA
29	MTMR3	CAAACATACATTCTATCCGG
30	MTMR3	TCGGGACTTTCCCAACGCAG
31	MTMR3	TAGAAGAGCCTACCCACAGG
32	MTMR3	CATAAGTTTGCTGACCGGTG
33	MTMR4	GCACATCCGATGTCGACAGG
34	MTMR4	AGGGCCCGGACATGACACAC
35	MTMR4	ACACTGTCAATCATCCGGAG
36	MTMR4	TCCATATTACAGGACTCTGG
37	MTMR6	ACCTTGCTGCGGAGTATGAG
38	MTMR6	GGAGAGAGTTATAAATATCG
39	MTMR6	GCTAGCCGGCCGGTGATCGT
40	MTMR6	AATCCAACAACAGTGAGCCG
41	MTMR7	GCTGCCAATAATTATCAGGG
42	MTMR7	TCAGAGAGATGTACACGTCG
43	MTMR7	GCCACGGCACACATCATCGT

Number	Target Gene Symbol	Guide sequence
44	MTMR7	AAGTGACTTCATTTATGTCG
45	MTMR9	TGGGCACAATGACAGTTGGT
46	MTMR9	AAACCCACAACATGGACCGG
47	MTMR9	TTCCAGGTGATTATGCGAAG
48	MTMR9	CTCAGCGTACACGATAGCAG
49	PTEN	CCTCCAATTCAGGACCCACG
50	PTEN	TGTGCATATTTATTGCATCG
51	PTEN	ACTATTCCAATGTTCAGTGG
52	PTEN	GGTTTGATAAGTTCTAGCTG
53	TSC2	TGAACCACATGGCTATGACG
54	TSC2	CACAGGGTGATAATGAACAG
55	TSC2	CAGCTCCAAAGACCCTTGAG
56	TSC2	CTGATCCTAGCACACATGTG
57	EGF	TCACCGTAACAGATATGACA
58	EGF	AGACTGTTCTGGACGGACGT
59	EGF	TGTTCATCGCCTGACAATGG
60	EGF	GTGTCACAAAGGATGGATGG
61	inpp4a	AGGTCAGCTACTACGCGGAA
62	inpp4a	CGCACAGACGGAGATCATCG
63	inpp4a	ACTGACCTCCATCAGTACAA
64	inpp4a	TAGTTGGGAAGCGGTACATG
65	INPP5D	TGGGGATCTCAACTACCGCG
66	INPP5D	CCACTATGCGAATGTTCCAG
67	INPP5D	AGAGGCCAGTCCCATCACCA
68	INPP5D	CATCCGAAGGTGTCCCCATG
69	INPP5E	GAGGTCCCTACGGATAAACA
70	INPP5E	AGTGATCGTCACCAGCCAAG
71	INPP5E	CACCGAGGCTGACTACACTC
72	INPP5E	GGAGATACCTAAGTCCCGAA
73	INPP5B	CCCTACACAGTACACGTCGG
74	INPP5B	CAGTCTCGGAATGCACGGCG
75	INPP5B	GTTCTGGTGTGTGAACCAAA
76	INPP5B	TGTGACCGAATCCTGTGGAA
77	INPP1	TGATTGATGACTCCCATTAG
78	INPP1	GGACTTAACTGATCCCACGC
79	INPP1	TTACACACTGAAGTCCGCTG
80	INPP1	TACTGATGACTGCAGAAAAG
81	INPP5A	ATTTGGAGGGAAAAACTACG
82	INPP5A	GGATTCCAAGTCTGTCGTAG
83	INPP5A	CCTGACACCGGAGTACACTG
84	INPP5A	AAGGCTTCATCAGGACGCGG
85	INPP5F	GGAATGCGGTATAAACGAAG
86	INPP5F	GGTGACGAGAAGTTCCACGG

Number	Target Gene Symbol	Guide sequence
87	INPP5F	AGGCATCCTTGAACCGACTG
88	INPP5F	CGAGAATGTTCAAACCCTCA
89	Inppl1	AGAATCCGGTCACACCACGA
90	Inppl1	CCTGGATATCCATGTCTAAG
91	Inppl1	TCACACTGGACGTACTGACG
92	Inppl1	GCAGGGCACAAACAAGACCC
93	ING2	TTGTCATGTGACATAAGTCA
94	ING2	CCGCGCTCCTGACCGGAGAG
95	ING2	CGCTGCCCCACGACATGCAG
96	ING2	GAAGATGGATTCCAGTCAAC
97	PI4KA	GGTATGTACCTCCATCACGC
98	PI4KA	TGTGCTAATGGGATTCGCTG
99	PI4KA	AGGAACCGTGATCCGATAGG
100	PI4KA	ACATCGATCCAGATGTAGTG
101	Pi4kb	GGCTCCCTACCTGATCTACG
102	Pi4kb	CTTGATGAATTCTCGCTCAG
103	Pi4kb	TGATGATGAAGCCTGGTCAG
104	Pi4kb	CCACTCAGCGACACTCGCGA
105	Pi4k2a	ATTGATCGAGTAAAGTCCAG
106	Pi4k2a	CACTTTCCGCAAGTACCGGG
107	Pi4k2a	GCTGTCGGTTCGTGTTCTCA
108	Pi4k2a	TTAGGGTTAAGGTGCCCGTA
109	PIP4K2A	GGAAATACGACTTAAAGGTG
110	PIP4K2A	GTATATAGTGGAATGTCATG
111	PIP4K2A	GGGGGGTCAACCATTCGGTA
112	PIP4K2A	CATCAAGACCATTACCAGTG
113	Pip4k2b	CAGTCTTGATGACGAAACGC
114	Pip4k2b	GCATCGCAAATACGACCTGA
115	Pip4k2b	AGCTTACAGCAAGATCAAGG
116	Pip4k2b	GGGCATGTACCGCCTGACCG
117	Pip4k2c	TTTCGTACAGCAGAAAGTGA
118	Pip4k2c	AGTGTCGAGCGAAGATATTG
119	Pip4k2c	TCTGGCAGCAACATCACTGG
120	Pip4k2c	TCCTTGAACTTGAAATGACT
121	Pip5k1a	GTGAGTGATGCCTAACTGGA
122	Pip5k1a	ACAACATGGACCATGCACAG
123	Pip5k1a	TGAAGGGTTCAACTTACAAG
124	Pip5k1a	ACAGCTATGGAATCCATCCA
125	Pip5k1c	TGGTGGCAAGAACATCCGCG
126	Pip5k1c	CCGACGCATCCACGCCTCGG
127	Pip5k1c	TTACCAAATAGTCATCTGGA
128	Pip5k1c	GCCATGGAGTCTATCCAGGG
129	Pip5kl1	GCTTCTTTGTGAAGACCCAA

Number	Target Gene Symbol	Guide sequence
130	Pip5kl1	GGACTCACCTCTCAGAAATG
131	Pip5kl1	CATGACCCAAGTTCACGAAG
132	Pip5kl1	TTTCAGGCGTATACAGTCTG
133	FIG4	CTTGGTGGTAATCGACGACA
134	FIG4	AAATCCGAACAGAGTCATTG
135	FIG4	GAAGGATTAATTACACAGGG
136	FIG4	CACAGGTGGAATGAACTAGG
137	OCRL	TTTCGAATCATATTTGTACG
138	OCRL	CCAATGCAGTAAATATCAGG
139	OCRL	ATTTACCCCAATATGGAACA
140	OCRL	ACGTGGAAGAGTTCGAACGA
141	PDK1	TTGTCGCAGAAACATAAACG
142	PDK1	ATGGCTATGAGAACGCTAGG
143	PDK1	TTGATAGCCTTATTGTTCGG
144	PDK1	AAACACCATGTGATAGAGAT
145	DOK2	GAGGCGGACAACCTTCCGAG
146	DOK2	TTTGAGTTCGAAACACGACA
147	DOK2	AAAGCGTCGAAGAAACCTGT
148	DOK2	GTCCTATACTCTCCGGACCG
149	DOK1	AGGGCCTGGAGGAATTCGCA
150	DOK1	TGCAAGGCTCCTACATACTG
151	DOK1	CCAGTCACTCACCGGAAAGG
152	DOK1	CCATACAAATCCCAATAGAG
153	PIK3CA	AGCAGATCTTCTAACCCATG
154	PIK3CA	TCTTACCTAGGATTGGAACA
155	PIK3CA	GAGGCGAGTTGAGATCCCGC
156	PIK3CA	CAGTTACTCCCATACAGGAC
157	PIK3CB	TATGTCCGGGAATACGCTGT
158	PIK3CB	ATTAGCTTACCTTATCGAAG
159	PIK3CB	CATTCCACAAGGATGAAGTG
160	PIK3CB	ACGGACGGCTCGTGCTCAGG
161	PIK3CD	GTTGTGTGTTCAACTACCGG
162	PIK3CD	AAAACTGGCGCATCTTAGTG
163	PIK3CD	GGAGCGTGGGCGCATCACGG
164	PIK3CD	CACCAAGTGGAATAAACACG
165	PIK3CG	TGCGGGGCGTAACCAGACGG
166	PIK3CG	GGAGCACATAGTCCCCGTGG
167	PIK3CG	CACCCACCAGGTACTCATCG
168	PIK3CG	GATCTATGACAGGTACCAAG
169	Pik3ip1	AGACCGGCGTCCCTGAAAAG
170	Pik3ip1	TGGGCTCGGTGAGCGACTCG
171	Pik3ip1	CCCGATCACTGGCTGCACCT
172	Pik3ip1	AACCCGGACCAGGACCCGCG

Number	Target Gene Symbol	Guide sequence
173	PIK3R1	GAGCTTTATAAGGAGAGGCG
174	PIK3R1	TCCATTAACCTTCAACTCTG
175	PIK3R1	TGGCTACAATGAAACCACTG
176	PIK3R1	CTGGAAATCTGAAAAGCACG
177	Pik3r2	GGAACTCCACGTATGTCCCG
178	Pik3r2	CTTAACAGCATCATACAAGG
179	Pik3r2	ACTGGGCCAGTGATTCGTGG
180	Pik3r2	AGCTGTATGAAGAATACACA
181	PIK3C2A	GTATAAATAATGTCAAACGC
182	PIK3C2A	ACAGTGCAAAGAAACATGTG
183	PIK3C2A	GGAAGGCCCGCATAATCCAG
184	PIK3C2A	GCCTAAGGTAGACTATGTGG
185	PIK3C3	AGCCTGTAAGAACTCAACAC
186	PIK3C3	ATACACATCCCATATAGTCA
187	PIK3C3	CTCACCAAGGCTCATCGGCA
188	PIK3C3	ATGGACCAGGCGATCTACAA
189	JAK1	CGATGCCATTCGAATGACAG
190	JAK1	TGAATAAATCCATCAGACAG
191	JAK1	TCCGAACCGAATCATCACTG
192	JAK1	AAACATATAGTGTACCTCTA
193	Tiam1	AGGTGGAGTCGGCTACCCGG
194	Tiam1	AAACCTACCGTAATTATCAG
195	Tiam1	ATGACACGGAGAAGATCCCG
196	Tiam1	GGAGAACCCTCCGCACCGAG
197	PRKCA	CATGGAATACGTCAACGGCG
198	PRKCA	AAGAAGCACTTACAACGTGA
199	PRKCA	GTGGATAAGTCCATAGAGCA
200	PRKCA	ACCATGCCTTACCCGTGACG
201	PIK3C2B	AGACTGCCAAACTCATAGCG
202	PIK3C2B	GGAAGGCGTCCACCTCATTG
203	PIK3C2B	TGCAAAGTTCCTTGCCACCG
204	PIK3C2B	CCTCACACCTGGACTAGCTG
205	PIK3C2G	AAGTGATCATTTGCATATCG
206	PIK3C2G	TCGCCCACAAGACACAGACC
207	PIK3C2G	ATGGAGTACTTTATTACTGA
208	PIK3C2G	ATGCACAGTGCCGGGTTCAG
209	RAB11A	GAGTGATTTACGTCATCTCA
210	RAB11A	AGATACTATCGTGGAGCAGT
211	RAB11A	TGTTGCAAACTCTACTCCAA
212	RAB11A	CCACGGCCTCACCTTTAAAG
213	BRDN0000737505	AAAAAGTCCGCGATTACGTC
214	BRDN0000737693	AAAACGGCTCGATCGGTGAT
215	BRDN0000737637	AAAACGTAATTATACCGAGC
216	BRDN0000738185	AAAATTGCACCTTCCCGGCC

Number	Target Gene Symbol	Guide sequence
217	BRDN0000737801	AAACCCCCGCGCGGAGCGTC
218	BRDN0000737467	AAACCTAGCGTAGATTCGGC
219	BRDN0000737848	AAACGAGGCTGTTCGTACAC
220	BRDN0000737609	AAACTCATACGTAGCGAATC
221	BRDN0000737434	AAACTCCCGTGTCAACCGAT
222	BRDN0000738254	AAAGACGTGCATTCAGCGAG
223		
224		
225		

Original Doc: Kelsey Iron Library

Gene name	Guide sequence	Twist Order
Mtm1	AGGGAACCACCAAAAGAGCA	GGAAAGGACGAAACACCGAGGGAACCACCAAAAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mtm1	TTACCACTCATACCGACAAG	GGAAAGGACGAAACACCGTTACCACTCATACCGACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mtm1	ATGGGAGGCGCGACAAGTAG	GGAAAGGACGAAACACCGATGGGAGGCGCGACAAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Mtm1	TCTGACCGGTGCCATTCAAG	GGAAAGGACGAAACACCGTCTGACCGGTGCCATTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR1	GTCACATTGGCTATCCAATG	GGAAAGGACGAAACACCGGTCACATTGGCTATCCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR1	CAGCGTTGCTGATACCAACA	GGAAAGGACGAAACACCGCAGCGTTGCTGATACCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR1	AGCCATGGGGATAATTCTTG	GGAAAGGACGAAACACCGAGCCATGGGGATAATTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR1	AGGGCTTGCCAAATGAGAGT	GGAAAGGACGAAACACCGAGGGCTTGCCAAATGAGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR10	CCTGACGTACTCTAACCACC	GGAAAGGACGAAACACCGCCTGACGTACTCTAACCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR10	CTAACGGCAGTGCTCTTGTG	GGAAAGGACGAAACACCGCTAACGGCAGTGCTCTTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR10	TCTGAGTAAGTTTCGAACAG	GGAAAGGACGAAACACCGTCTGAGTAAGTTTCGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR10	AGCTATTGCAAGGCATACCT	GGAAAGGACGAAACACCGAGCTATTGCAAGGCATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR11	GGGTTAGCACGGTCAATGAG	GGAAAGGACGAAACACCGGGGTTAGCACGGTCAATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR11	TAACCCTCGACTTCAGTGAG	GGAAAGGACGAAACACCGTAACCCTCGACTTCAGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR11	ATTACCTGGGAGACAACCAG	GGAAAGGACGAAACACCGATTACCTGGGAGACAACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR11	AAAGGGCCCTCAGTTTCAAG	GGAAAGGACGAAACACCGAAAGGGCCCTCAGTTTCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR12	ATGTACTTACTGGTATACCA	GGAAAGGACGAAACACCGATGTACTTACTGGTATACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR12	AATGGATAACGAGCTTCTCG	GGAAAGGACGAAACACCGAATGGATAACGAGCTTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR12	AAACCTTATTACCCAACAGG	GGAAAGGACGAAACACCGAAACCTTATTACCCAACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR12	TCTGTGAACTCAAATGCTGG	GGAAAGGACGAAACACCGTCTGTGAACTCAAATGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR14	AATGTGAATGGTGATATCTG	GGAAAGGACGAAACACCGAATGTGAATGGTGATATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR14	GAAGTTGGGGATGTTCAATG	GGAAAGGACGAAACACCGGAAGTTGGGGATGTTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR14	GGCCGACCTGCAAATATGCT	GGAAAGGACGAAACACCGGGCCGACCTGCAAATATGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR14	TGAGATCCTCTACCTGACTG	GGAAAGGACGAAACACCGTGAGATCCTCTACCTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR2	TGCTCGGCCAAGTGTCAATG	GGAAAGGACGAAACACCGTGCTCGGCCAAGTGTCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR2	GCCTTCTGTACTCTAGAAGG	GGAAAGGACGAAACACCGGCCTTCTGTACTCTAGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR2	GTGGCATCCTTTAGGTCACG	GGAAAGGACGAAACACCGGTGGCATCCTTTAGGTCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR2	GTAATGATTCTCTCATAACA	GGAAAGGACGAAACACCGGTAATGATTCTCTCATAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR3	CAAACATACATTCTATCCGG	GGAAAGGACGAAACACCGCAAACATACATTCTATCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR3	TCGGGACTTTCCCAACGCAG	GGAAAGGACGAAACACCGTCGGGACTTTCCCAACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR3	TAGAAGAGCCTACCCACAGG	GGAAAGGACGAAACACCGTAGAAGAGCCTACCCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR3	CATAAGTTTGCTGACCGGTG	GGAAAGGACGAAACACCGCATAAGTTTGCTGACCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR4	GCACATCCGATGTCGACAGG	GGAAAGGACGAAACACCGGCACATCCGATGTCGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR4	AGGGCCCGGACATGACACAC	GGAAAGGACGAAACACCGAGGGCCCGGACATGACACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR4	ACACTGTCAATCATCCGGAG	GGAAAGGACGAAACACCGACACTGTCAATCATCCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR4	TCCATATTACAGGACTCTGG	GGAAAGGACGAAACACCGTCCATATTACAGGACTCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR6	ACCTTGCTGCGGAGTATGAG	GGAAAGGACGAAACACCGACCTTGCTGCGGAGTATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR6	GGAGAGAGTTATAAATATCG	GGAAAGGACGAAACACCGGGAGAGAGTTATAAATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR6	GCTAGCCGGCCGGTGATCGT	GGAAAGGACGAAACACCGGCTAGCCGGCCGGTGATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR6	AATCCAACAACAGTGAGCCG	GGAAAGGACGAAACACCGAATCCAACAACAGTGAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR7	GCTGCCAATAATTATCAGGG	GGAAAGGACGAAACACCGGCTGCCAATAATTATCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR7	TCAGAGAGATGTACACGTCG	GGAAAGGACGAAACACCGTCAGAGAGATGTACACGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR7	GCCACGGCACACATCATCGT	GGAAAGGACGAAACACCGGCCACGGCACACATCATCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR7	AAGTGACTTCATTTATGTCG	GGAAAGGACGAAACACCGAAGTGACTTCATTTATGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR9	TGGGCACAATGACAGTTGGT	GGAAAGGACGAAACACCGTGGGCACAATGACAGTTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR9	AAACCCACAACATGGACCGG	GGAAAGGACGAAACACCGAAACCCACAACATGGACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR9	TTCCAGGTGATTATGCGAAG	GGAAAGGACGAAACACCGTTCCAGGTGATTATGCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
MTMR9	CTCAGCGTACACGATAGCAG	GGAAAGGACGAAACACCGCTCAGCGTACACGATAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PTEN	CCTCCAATTCAGGACCCACG	GGAAAGGACGAAACACCGCCTCCAATTCAGGACCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PTEN	TGTGCATATTTATTGCATCG	GGAAAGGACGAAACACCGTGTGCATATTTATTGCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PTEN	ACTATTCCAATGTTCAGTGG	GGAAAGGACGAAACACCGACTATTCCAATGTTCAGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PTEN	GGTTTGATAAGTTCTAGCTG	GGAAAGGACGAAACACCGGGTTTGATAAGTTCTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
TSC2	TGAACCACATGGCTATGACG	GGAAAGGACGAAACACCGTGAACCACATGGCTATGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
TSC2	CACAGGGTGATAATGAACAG	GGAAAGGACGAAACACCGCACAGGGTGATAATGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
TSC2	CAGCTCCAAAGACCCTTGAG	GGAAAGGACGAAACACCGCAGCTCCAAAGACCCTTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
TSC2	CTGATCCTAGCACACATGTG	GGAAAGGACGAAACACCGCTGATCCTAGCACACATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
EGF	TCACCGTAACAGATATGACA	GGAAAGGACGAAACACCGTCACCGTAACAGATATGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
EGF	AGACTGTTCTGGACGGACGT	GGAAAGGACGAAACACCGAGACTGTTCTGGACGGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
EGF	TGTTCATCGCCTGACAATGG	GGAAAGGACGAAACACCGTGTTCATCGCCTGACAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
EGF	GTGTCACAAAGGATGGATGG	GGAAAGGACGAAACACCGGTGTCACAAAGGATGGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
inpp4a	AGGTCAGCTACTACGCGGAA	GGAAAGGACGAAACACCGAGGTCAGCTACTACGCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
inpp4a	CGCACAGACGGAGATCATCG	GGAAAGGACGAAACACCGCGCACAGACGGAGATCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
inpp4a	ACTGACCTCCATCAGTACAA	GGAAAGGACGAAACACCGACTGACCTCCATCAGTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
inpp4a	TAGTTGGGAAGCGGTACATG	GGAAAGGACGAAACACCGTAGTTGGGAAGCGGTACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5D	TGGGGATCTCAACTACCGCG	GGAAAGGACGAAACACCGTGGGGATCTCAACTACCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5D	CCACTATGCGAATGTTCCAG	GGAAAGGACGAAACACCGCCACTATGCGAATGTTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5D	AGAGGCCAGTCCCATCACCA	GGAAAGGACGAAACACCGAGAGGCCAGTCCCATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5D	CATCCGAAGGTGTCCCCATG	GGAAAGGACGAAACACCGCATCCGAAGGTGTCCCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5E	GAGGTCCCTACGGATAAACA	GGAAAGGACGAAACACCGGAGGTCCCTACGGATAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Gene name	Guide sequence	Twist Order
INPP5E	AGTGATCGTCACCAGCCAAG	GGAAAGGACGAAACACCGAGTGATCGTCACCAGCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5E	CACCGAGGCTGACTACACTC	GGAAAGGACGAAACACCGCACCGAGGCTGACTACACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5E	GGAGATACCTAAGTCCCGAA	GGAAAGGACGAAACACCGGGAGATACCTAAGTCCCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5B	CCCTACACAGTACACGTCGG	GGAAAGGACGAAACACCGCCCTACACAGTACACGTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5B	CAGTCTCGGAATGCACGGCG	GGAAAGGACGAAACACCGCAGTCTCGGAATGCACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5B	GTTCTGGTGTGTGAACCAAA	GGAAAGGACGAAACACCGGTTCTGGTGTGTGAACCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5B	TGTGACCGAATCCTGTGGAA	GGAAAGGACGAAACACCGTGTGACCGAATCCTGTGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP1	TGATTGATGACTCCCATTAG	GGAAAGGACGAAACACCGTGATTGATGACTCCCATTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP1	GGACTTAACTGATCCCACGC	GGAAAGGACGAAACACCGGGACTTAACTGATCCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP1	TTACACACTGAAGTCCGCTG	GGAAAGGACGAAACACCGTTACACACTGAAGTCCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP1	TACTGATGACTGCAGAAAAG	GGAAAGGACGAAACACCGTACTGATGACTGCAGAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5A	ATTTGGAGGGAAAAACTACG	GGAAAGGACGAAACACCGATTTGGAGGGAAAAACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5A	GGATTCCAAGTCTGTCGTAG	GGAAAGGACGAAACACCGGGATTCCAAGTCTGTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5A	CCTGACACCGGAGTACACTG	GGAAAGGACGAAACACCGCCTGACACCGGAGTACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5A	AAGGCTTCATCAGGACGCGG	GGAAAGGACGAAACACCGAAGGCTTCATCAGGACGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5F	GGAATGCGGTATAAACGAAG	GGAAAGGACGAAACACCGGGAATGCGGTATAAACGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5F	GGTGACGAGAAGTTCCACGG	GGAAAGGACGAAACACCGGGTGACGAGAAGTTCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5F	AGGCATCCTTGAACCGACTG	GGAAAGGACGAAACACCGAGGCATCCTTGAACCGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
INPP5F	CGAGAATGTTCAAACCCTCA	GGAAAGGACGAAACACCGCGAGAATGTTCAAACCCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Inppl1	AGAATCCGGTCACACCACGA	GGAAAGGACGAAACACCGAGAATCCGGTCACACCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Inppl1	CCTGGATATCCATGTCTAAG	GGAAAGGACGAAACACCGCCTGGATATCCATGTCTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Inppl1	TCACACTGGACGTACTGACG	GGAAAGGACGAAACACCGTCACACTGGACGTACTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Inppl1	GCAGGGCACAAACAAGACCC	GGAAAGGACGAAACACCGGCAGGGCACAAACAAGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
ING2	TTGTCATGTGACATAAGTCA	GGAAAGGACGAAACACCGTTGTCATGTGACATAAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
ING2	CCGCGCTCCTGACCGGAGAG	GGAAAGGACGAAACACCGCCGCGCTCCTGACCGGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
ING2	CGCTGCCCCACGACATGCAG	GGAAAGGACGAAACACCGCGCTGCCCCACGACATGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
ING2	GAAGATGGATTCCAGTCAAC	GGAAAGGACGAAACACCGGAAGATGGATTCCAGTCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PI4KA	GGTATGTACCTCCATCACGC	GGAAAGGACGAAACACCGGGTATGTACCTCCATCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PI4KA	TGTGCTAATGGGATTCGCTG	GGAAAGGACGAAACACCGTGTGCTAATGGGATTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PI4KA	AGGAACCGTGATCCGATAGG	GGAAAGGACGAAACACCGAGGAACCGTGATCCGATAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PI4KA	ACATCGATCCAGATGTAGTG	GGAAAGGACGAAACACCGACATCGATCCAGATGTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4kb	GGCTCCCTACCTGATCTACG	GGAAAGGACGAAACACCGGGCTCCCTACCTGATCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4kb	CTTGATGAATTCTCGCTCAG	GGAAAGGACGAAACACCGCTTGATGAATTCTCGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4kb	TGATGATGAAGCCTGGTCAG	GGAAAGGACGAAACACCGTGATGATGAAGCCTGGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4kb	CCACTCAGCGACACTCGCGA	GGAAAGGACGAAACACCGCCACTCAGCGACACTCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4k2a	ATTGATCGAGTAAAGTCCAG	GGAAAGGACGAAACACCGATTGATCGAGTAAAGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4k2a	CACTTTCCGCAAGTACCGGG	GGAAAGGACGAAACACCGCACTTTCCGCAAGTACCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4k2a	GCTGTCGGTTCGTGTTCTCA	GGAAAGGACGAAACACCGGCTGTCGGTTCGTGTTCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pi4k2a	TTAGGGTTAAGGTGCCCGTA	GGAAAGGACGAAACACCGTTAGGGTTAAGGTGCCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIP4K2A	GGAAATACGACTTAAAGGTG	GGAAAGGACGAAACACCGGGAAATACGACTTAAAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIP4K2A	GTATATAGTGGAATGTCATG	GGAAAGGACGAAACACCGGTATATAGTGGAATGTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIP4K2A	GGGGGGTCAACCATTCGGTA	GGAAAGGACGAAACACCGGGGGGGTCAACCATTCGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIP4K2A	CATCAAGACCATTACCAGTG	GGAAAGGACGAAACACCGCATCAAGACCATTACCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2b	CAGTCTTGATGACGAAACGC	GGAAAGGACGAAACACCGCAGTCTTGATGACGAAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2b	GCATCGCAAATACGACCTGA	GGAAAGGACGAAACACCGGCATCGCAAATACGACCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2b	AGCTTACAGCAAGATCAAGG	GGAAAGGACGAAACACCGAGCTTACAGCAAGATCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2b	GGGCATGTACCGCCTGACCG	GGAAAGGACGAAACACCGGGGCATGTACCGCCTGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2c	TTTCGTACAGCAGAAAGTGA	GGAAAGGACGAAACACCGTTTCGTACAGCAGAAAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2c	AGTGTCGAGCGAAGATATTG	GGAAAGGACGAAACACCGAGTGTCGAGCGAAGATATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2c	TCTGGCAGCAACATCACTGG	GGAAAGGACGAAACACCGTCTGGCAGCAACATCACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip4k2c	TCCTTGAACTTGAAATGACT	GGAAAGGACGAAACACCGTCCTTGAACTTGAAATGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1a	GTGAGTGATGCCTAACTGGA	GGAAAGGACGAAACACCGGTGAGTGATGCCTAACTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1a	ACAACATGGACCATGCACAG	GGAAAGGACGAAACACCGACAACATGGACCATGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1a	TGAAGGGTTCAACTTACAAG	GGAAAGGACGAAACACCGTGAAGGGTTCAACTTACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1a	ACAGCTATGGAATCCATCCA	GGAAAGGACGAAACACCGACAGCTATGGAATCCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1c	TGGTGGCAAGAACATCCGCG	GGAAAGGACGAAACACCGTGGTGGCAAGAACATCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1c	CCGACGCATCCACGCCTCGG	GGAAAGGACGAAACACCGCCGACGCATCCACGCCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1c	TTACCAAATAGTCATCTGGA	GGAAAGGACGAAACACCGTTACCAAATAGTCATCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5k1c	GCCATGGAGTCTATCCAGGG	GGAAAGGACGAAACACCGGCCATGGAGTCTATCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5kl1	GCTTCTTTGTGAAGACCCAA	GGAAAGGACGAAACACCGGCTTCTTTGTGAAGACCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5kl1	GGACTCACCTCTCAGAAATG	GGAAAGGACGAAACACCGGGACTCACCTCTCAGAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5kl1	CATGACCCAAGTTCACGAAG	GGAAAGGACGAAACACCGCATGACCCAAGTTCACGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pip5kl1	TTTCAGGCGTATACAGTCTG	GGAAAGGACGAAACACCGTTTCAGGCGTATACAGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FIG4	CTTGGTGGTAATCGACGACA	GGAAAGGACGAAACACCGCTTGGTGGTAATCGACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FIG4	AAATCCGAACAGAGTCATTG	GGAAAGGACGAAACACCGAAATCCGAACAGAGTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FIG4	GAAGGATTAATTACACAGGG	GGAAAGGACGAAACACCGGAAGGATTAATTACACAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
FIG4	CACAGGTGGAATGAACTAGG	GGAAAGGACGAAACACCGCACAGGTGGAATGAACTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
OCRL	TTTCGAATCATATTTGTACG	GGAAAGGACGAAACACCGTTTCGAATCATATTTGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
OCRL	CCAATGCAGTAAATATCAGG	GGAAAGGACGAAACACCGCCAATGCAGTAAATATCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
OCRL	ATTTACCCCAATATGGAACA	GGAAAGGACGAAACACCGATTTACCCCAATATGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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OCRL	ACGTGGAAGAGTTCGAACGA	GGAAAGGACGAAACACCGACGTGGAAGAGTTCGAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PDK1	TTGTCGCAGAAACATAAACG	GGAAAGGACGAAACACCGTTGTCGCAGAAACATAAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PDK1	ATGGCTATGAGAACGCTAGG	GGAAAGGACGAAACACCGATGGCTATGAGAACGCTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PDK1	TTGATAGCCTTATTGTTCGG	GGAAAGGACGAAACACCGTTGATAGCCTTATTGTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PDK1	AAACACCATGTGATAGAGAT	GGAAAGGACGAAACACCGAAACACCATGTGATAGAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK2	GAGGCGGACAACCTTCCGAG	GGAAAGGACGAAACACCGGAGGCGGACAACCTTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK2	TTTGAGTTCGAAACACGACA	GGAAAGGACGAAACACCGTTTGAGTTCGAAACACGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK2	AAAGCGTCGAAGAAACCTGT	GGAAAGGACGAAACACCGAAAGCGTCGAAGAAACCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK2	GTCCTATACTCTCCGGACCG	GGAAAGGACGAAACACCGGTCCTATACTCTCCGGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK1	AGGGCCTGGAGGAATTCGCA	GGAAAGGACGAAACACCGAGGGCCTGGAGGAATTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK1	TGCAAGGCTCCTACATACTG	GGAAAGGACGAAACACCGTGCAAGGCTCCTACATACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK1	CCAGTCACTCACCGGAAAGG	GGAAAGGACGAAACACCGCCAGTCACTCACCGGAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
DOK1	CCATACAAATCCCAATAGAG	GGAAAGGACGAAACACCGCCATACAAATCCCAATAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CA	AGCAGATCTTCTAACCCATG	GGAAAGGACGAAACACCGAGCAGATCTTCTAACCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CA	TCTTACCTAGGATTGGAACA	GGAAAGGACGAAACACCGTCTTACCTAGGATTGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CA	GAGGCGAGTTGAGATCCCGC	GGAAAGGACGAAACACCGGAGGCGAGTTGAGATCCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CA	CAGTTACTCCCATACAGGAC	GGAAAGGACGAAACACCGCAGTTACTCCCATACAGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CB	TATGTCCGGGAATACGCTGT	GGAAAGGACGAAACACCGTATGTCCGGGAATACGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CB	ATTAGCTTACCTTATCGAAG	GGAAAGGACGAAACACCGATTAGCTTACCTTATCGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CB	CATTCCACAAGGATGAAGTG	GGAAAGGACGAAACACCGCATTCCACAAGGATGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CB	ACGGACGGCTCGTGCTCAGG	GGAAAGGACGAAACACCGACGGACGGCTCGTGCTCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CD	GTTGTGTGTTCAACTACCGG	GGAAAGGACGAAACACCGGTTGTGTGTTCAACTACCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CD	AAAACTGGCGCATCTTAGTG	GGAAAGGACGAAACACCGAAAACTGGCGCATCTTAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CD	GGAGCGTGGGCGCATCACGG	GGAAAGGACGAAACACCGGGAGCGTGGGCGCATCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CD	CACCAAGTGGAATAAACACG	GGAAAGGACGAAACACCGCACCAAGTGGAATAAACACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CG	TGCGGGGCGTAACCAGACGG	GGAAAGGACGAAACACCGTGCGGGGCGTAACCAGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CG	GGAGCACATAGTCCCCGTGG	GGAAAGGACGAAACACCGGGAGCACATAGTCCCCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CG	CACCCACCAGGTACTCATCG	GGAAAGGACGAAACACCGCACCCACCAGGTACTCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3CG	GATCTATGACAGGTACCAAG	GGAAAGGACGAAACACCGGATCTATGACAGGTACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3ip1	AGACCGGCGTCCCTGAAAAG	GGAAAGGACGAAACACCGAGACCGGCGTCCCTGAAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3ip1	TGGGCTCGGTGAGCGACTCG	GGAAAGGACGAAACACCGTGGGCTCGGTGAGCGACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3ip1	CCCGATCACTGGCTGCACCT	GGAAAGGACGAAACACCGCCCGATCACTGGCTGCACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3ip1	AACCCGGACCAGGACCCGCG	GGAAAGGACGAAACACCGAACCCGGACCAGGACCCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3R1	GAGCTTTATAAGGAGAGGCG	GGAAAGGACGAAACACCGGAGCTTTATAAGGAGAGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3R1	TCCATTAACCTTCAACTCTG	GGAAAGGACGAAACACCGTCCATTAACCTTCAACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3R1	TGGCTACAATGAAACCACTG	GGAAAGGACGAAACACCGTGGCTACAATGAAACCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3R1	CTGGAAATCTGAAAAGCACG	GGAAAGGACGAAACACCGCTGGAAATCTGAAAAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3r2	GGAACTCCACGTATGTCCCG	GGAAAGGACGAAACACCGGGAACTCCACGTATGTCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3r2	CTTAACAGCATCATACAAGG	GGAAAGGACGAAACACCGCTTAACAGCATCATACAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3r2	ACTGGGCCAGTGATTCGTGG	GGAAAGGACGAAACACCGACTGGGCCAGTGATTCGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pik3r2	AGCTGTATGAAGAATACACA	GGAAAGGACGAAACACCGAGCTGTATGAAGAATACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2A	GTATAAATAATGTCAAACGC	GGAAAGGACGAAACACCGGTATAAATAATGTCAAACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2A	ACAGTGCAAAGAAACATGTG	GGAAAGGACGAAACACCGACAGTGCAAAGAAACATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2A	GGAAGGCCCGCATAATCCAG	GGAAAGGACGAAACACCGGGAAGGCCCGCATAATCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2A	GCCTAAGGTAGACTATGTGG	GGAAAGGACGAAACACCGGCCTAAGGTAGACTATGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C3	AGCCTGTAAGAACTCAACAC	GGAAAGGACGAAACACCGAGCCTGTAAGAACTCAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C3	ATACACATCCCATATAGTCA	GGAAAGGACGAAACACCGATACACATCCCATATAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C3	CTCACCAAGGCTCATCGGCA	GGAAAGGACGAAACACCGCTCACCAAGGCTCATCGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C3	ATGGACCAGGCGATCTACAA	GGAAAGGACGAAACACCGATGGACCAGGCGATCTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
JAK1	CGATGCCATTCGAATGACAG	GGAAAGGACGAAACACCGCGATGCCATTCGAATGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
JAK1	TGAATAAATCCATCAGACAG	GGAAAGGACGAAACACCGTGAATAAATCCATCAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
JAK1	TCCGAACCGAATCATCACTG	GGAAAGGACGAAACACCGTCCGAACCGAATCATCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
JAK1	AAACATATAGTGTACCTCTA	GGAAAGGACGAAACACCGAAACATATAGTGTACCTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tiam1	AGGTGGAGTCGGCTACCCGG	GGAAAGGACGAAACACCGAGGTGGAGTCGGCTACCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tiam1	AAACCTACCGTAATTATCAG	GGAAAGGACGAAACACCGAAACCTACCGTAATTATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tiam1	ATGACACGGAGAAGATCCCG	GGAAAGGACGAAACACCGATGACACGGAGAAGATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tiam1	GGAGAACCCTCCGCACCGAG	GGAAAGGACGAAACACCGGGAGAACCCTCCGCACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PRKCA	CATGGAATACGTCAACGGCG	GGAAAGGACGAAACACCGCATGGAATACGTCAACGGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PRKCA	AAGAAGCACTTACAACGTGA	GGAAAGGACGAAACACCGAAGAAGCACTTACAACGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PRKCA	GTGGATAAGTCCATAGAGCA	GGAAAGGACGAAACACCGGTGGATAAGTCCATAGAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PRKCA	ACCATGCCTTACCCGTGACG	GGAAAGGACGAAACACCGACCATGCCTTACCCGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2B	AGACTGCCAAACTCATAGCG	GGAAAGGACGAAACACCGAGACTGCCAAACTCATAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2B	GGAAGGCGTCCACCTCATTG	GGAAAGGACGAAACACCGGGAAGGCGTCCACCTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2B	TGCAAAGTTCCTTGCCACCG	GGAAAGGACGAAACACCGTGCAAAGTTCCTTGCCACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2B	CCTCACACCTGGACTAGCTG	GGAAAGGACGAAACACCGCCTCACACCTGGACTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2G	AAGTGATCATTTGCATATCG	GGAAAGGACGAAACACCGAAGTGATCATTTGCATATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2G	TCGCCCACAAGACACAGACC	GGAAAGGACGAAACACCGTCGCCCACAAGACACAGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2G	ATGGAGTACTTTATTACTGA	GGAAAGGACGAAACACCGATGGAGTACTTTATTACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
PIK3C2G	ATGCACAGTGCCGGGTTCAG	GGAAAGGACGAAACACCGATGCACAGTGCCGGGTTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
RAB11A	GAGTGATTTACGTCATCTCA	GGAAAGGACGAAACACCGGAGTGATTTACGTCATCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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RAB11A	AGATACTATCGTGGAGCAGT	GGAAAGGACGAAACACCGAGATACTATCGTGGAGCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
RAB11A	TGTTGCAAACTCTACTCCAA	GGAAAGGACGAAACACCGTGTTGCAAACTCTACTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
RAB11A	CCACGGCCTCACCTTTAAAG	GGAAAGGACGAAACACCGCCACGGCCTCACCTTTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737505	AAAAAGTCCGCGATTACGTC	GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737693	AAAACGGCTCGATCGGTGAT	GGAAAGGACGAAACACCGAAAACGGCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737637	AAAACGTAATTATACCGAGC	GGAAAGGACGAAACACCGAAAACGTAATTATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000738185	AAAATTGCACCTTCCCGGCC	GGAAAGGACGAAACACCGAAAATTGCACCTTCCCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737801	AAACCCCCGCGCGGAGCGTC	GGAAAGGACGAAACACCGAAACCCCCGCGCGGAGCGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737467	AAACCTAGCGTAGATTCGGC	GGAAAGGACGAAACACCGAAACCTAGCGTAGATTCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737848	AAACGAGGCTGTTCGTACAC	GGAAAGGACGAAACACCGAAACGAGGCTGTTCGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737609	AAACTCATACGTAGCGAATC	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000737434	AAACTCCCGTGTCAACCGAT	GGAAAGGACGAAACACCGAAACTCCCGTGTCAACCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
BRDN0000738254	AAAGACGTGCATTCAGCGAG	GGAAAGGACGAAACACCGAAAGACGTGCATTCAGCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Gene family/pathway	Gene (mouse)	
MyotubularinFamily	Mtm1	
	Mtmr1	
	Mtmr10	
	Mtmr11	
	Mtmr12	
	Mtmr14	
	Mtmr2	other IEM gene. Charcot-Marie Tooth Syndrome. Mtmr2 involved possibly to promote invasion nd metastasis .
	Mtmr3	
	Mtmr4	Involved in STING signaling
	Mtmr6	
	Mtmr7	
	Mtmr9	Was found in a T cell screen with AKT signaling
Kinases	Pi4ka	
	Pi4kb	
	Pi4k2a	
	Pip4k2a	
	Pip4k2b	
	Pip4k2c	
	Pip5k1a	
	Pip5k1c	
	Pip5kl1	
	Pdk1	
	Pik3ca	
	Pik3cb	
	Pik3cd	
	Pik3cg	
	Pik3ip1	
	Pik3r1	
	Pik3r2	
	Pik3c2a	
	Pik3c3	Also known as Vps34
	Prkca	
	Pik3c2b	
	Pik3c2g	
Other Phosphatases	Inpp4a	
	Inpp5d	PI(3,4)P2. PI(3,4P2 is onvolved in AKT signaling and endocytic trafficking

	Inpp5e	
	Inpp5b	
	Inpp1	
	Inpp5a	
	Inpp5f	
	Inppl1	
	Fig4	
	Ocrl	
Other	Egf	
	Ing2	
	Dok1	
	Dok2	
	Tiam1	
	Rab11a	
Controls	Jak1	
	Tsc2	
	Pten	
	NTCs (multiple)	