

Library Number	RMK001
Library Name	One Carbon Metabolism Library
Old Document Name	190306_1C metabolism library (Brie)
Library Purpose	CRISPR/Cas9 Knockout of genes from one carbon metabolic pathway in mouse T cells
Location	1C Met Screen Box in -20 in B3301
Designer Name	Ayaka Sugiura
Designing Date	3/6/19
Design Reference	Mouse CRISPR Knockout Pooled Library (Brie)
	(Addgene#73632) (Doench et al., 2016)
Usage Reference	Ayaka Sugiura
Species	Mouse (Mus musculus)
Total Gene #	39
Total Target #	166
Gene Group	
1. Negative Controls	10
2. Positive Controls	Tsc2
3. One carbon pathway	39
Target Number	
1. Negative Controls	10*1=10
2. Positive Controls	Tsc2
3. One carbon pathway	39*4=156

Note: Target selected from KEGG pathways

Number	Target Gene Symbol	sgRNA Target Sequence
1	Ada	GTTGTGGATCTTGTGAACCA
2	Ada	ATTCATCGGACCGTCCACGC
3	Ada	CTTCATCTCCACAACTCGT
4	Ada	GCTGCGCAACATTATCGGCA
5	Ahcy	GCGCACCTGACAGAAGCTGT
6	Ahcy	TGTCAACGATTCTGTCACCA
7	Ahcy	TGACCCTATCATACCCTCCA
8	Ahcy	TGTGATGATTGCGGGCAAGG
9	Aldh1l1	CCAGCCAGCGAAGTATCGGA
10	Aldh1l1	AGTACCATAAACCCAACGGA
11	Aldh1l1	TTGGATCCTACAGATCAACT
12	Aldh1l1	TCCAGGCCTAGTCACCAAAG
13	Amt	AAATGGTGGCGTTTGCAGGG
14	Amt	TTGTAAGCAATACTTCTGAG
15	Amt	TGCGGAACTAAGGCCTAACC
16	Amt	TGTAACACCTGTGTTGCCGT
17	Atic	AGACGACTGTCACTCGAGCG
18	Atic	GAGATGTGTCTGAGCTAACA
19	Atic	AATTGCTTCATCGTATTGAG
20	Atic	TTCTTTCAAGCACGTCAGCC
21	Bhmt	TCCCTCGGGCCCAATGCACA
22	Bhmt	CGTGGACTTCCTCATTGCAG
23	Bhmt	ACCTGCCTCAGGATGCTCCA
24	Bhmt	GCAGTTCACGCCGACAATGG
25	Bhmt2	CCATGTGCATCGGCCAGAG
26	Bhmt2	TGAAGACAATATGGCCAGCA
27	Bhmt2	TCACACAGAATTCTTGAGAG
28	Bhmt2	AGAGAGGCTTCGTGAAGGCG
29	Cbs	ACACTACGATGACACCGCCG
30	Cbs	TCGCCATGCCACTCCCACGT
31	Cbs	GTGAGTTCTTCAATGCGGGT
32	Cbs	ATAATGTGGGGAGTCCGCCA
33	Cth	TGCATGGATGAAGTGTATGG
34	Cth	GCAATGGAATTCTCGTGCCG
35	Cth	TTCCAAAACCAAATTGCTAG
36	Cth	TTTGTGGACAATTTGTGCGC
37	Dhfr	GACATGGTTTGGATAGTCGG
38	Dhfr	AACCTCAGAGAACCACCACG
39	Dhfr	TCGCCGTGTCCCAAATATG
40	Dhfr	CAGCCCGGCCAATACCTGAG
41	Ftcd	CAGGTTAAGAGCAATACGGT
42	Ftcd	CCGAACAAAACCGCGCAGTG

43	Ftcd	GCACTGTCTACACTTTCGTG
44	Ftcd	CACAGCTCAAACAGGCCGAG
45	Gart	ACTCGTAGTTGTCCGACCAG
46	Gart	TGACGGCTTCAGTTGTA CTG
47	Gart	GCTAGAAAGGATCACCGAAG
48	Gart	GGCAAAGTAGTGACCAGCGG
49	Gnmt	TGTGTGGCAGCTGTACATCG
50	Gnmt	AGAACATTGCAAGCATGGTG
51	Gnmt	GAGCCATCCTTTGACAATTG
52	Gnmt	GGGCTTCAGCGTGATGAGCG
53	Mat1a	ACAGGTATGGTGCTACTGTG
54	Mat1a	CTATGCTACTGATGAGACCG
55	Mat1a	GTGTTGCACAGAGATGACGA
56	Mat1a	GACACATTGGGCAATATCTG
57	Mat2a	CCTGATGCTAAAGTGGCTTG
58	Mat2a	GTGCAATATATGCAAGATCG
59	Mat2a	ACCAAGGCAATGTACCATTG
60	Mat2a	ATTACCACCTACAGCCAAG
61	Mtrr	GATGAAGCGGTTGTAATCAG
62	Mtrr	GGTGAGCAAAATAGTCCGTG
63	Mtrr	GAACAAAATGAGACAAACAG
64	Mtrr	CTCGACCGTACTCATGTGCA
65	Dnmt1	TAATGTGAACCGGTTACAG
66	Dnmt1	CAGAGCCCTATCGCATCGGT
67	Dnmt1	CATCACGGCTCACTTCACGA
68	Dnmt1	ACCTCGGGCCAATCAATCAG
69	Dnmt3a	GATCATTGATGAGCGCACAA
70	Dnmt3a	AGTTTACACCGACATGTGGG
71	Dnmt3a	CTTACCAGTATGACGACGAT
72	Dnmt3a	CAGGCCGAATTGTGTCTTGG
73	Dnmt3b	TGGTAGCCGGAAACTCCACA
74	Dnmt3b	CAGCCTTCTGAATTACACGC
75	Dnmt3b	GGAGGGTATGGATACCACAC
76	Dnmt3b	CAGTAGGCTTGAAGCCACCG
77	Mtfmt	GTGTACGAGTGCCCCGACGT
78	Mtfmt	GTGCCTTCGCTATCCCCAA
79	Mtfmt	ACCGTGTGGATTATCGGAGC
80	Mtfmt	GTCAAACTTGGTGCCAACA
81	Mthfd1	ACACCAACGATAGATTCCTG
82	Mthfd1	CACTATGAATCCGTGCACAG
83	Mthfd1	GATTGCCGGAAGGCACGCGG
84	Mthfd1	GGTAGCGTCCAGTAAGAAAG
85	Mthfd1	GGGTGACCGACATCAATCTG

86	Mthfd1	GCCTCACAGACATGAAAGAG
87	Mthfd1	TGGTTGCGGGGTCAATGTTG
88	Mthfd1	TGAGAGCACTCAAACAGACA
89	Mthfd2	TCGATGAGATATTGTGACTG
90	Mthfd2	AGATAATTAAGCGAACAGGT
91	Mthfd2	GCTTTCATGTCATTAACGTG
92	Mthfd2	CTATGTTCTCAACAAAACCA
93	Mthfd2l	ACTAAAATGATACTCAGATG
94	Mthfd2l	GCGGGAAGATCCAAGAACGT
95	Mthfd2l	GAGCTCACTGCAGATACCTG
96	Mthfd2l	AACATGGATCCAAGAGTCAG
97	Mthfr	AGACCCTGTAGGTGACCACT
98	Mthfr	GACTGGGATGAGTTTCCTAA
99	Mthfr	AGGTAACATCTACGAAGAGG
100	Mthfr	CGAAGCTCTCTGCATCGGGG
101	Mthfs	TTGCTCTGGAATTGGTACCG
102	Mthfs	CTTCTCGCACCTTCTGCGTG
103	Mthfs	GATGAGGTCAAGTCCACCTG
104	Mthfs	ATCTTGATGCTTAGAAAGA
105	Mtr	TCAGGTGCTCGATATCAACA
106	Mtr	GGGGTCCGAATGAGACACGC
107	Mtr	TGTGGATAGCATCATAACA
108	Mtr	CTTCAAAAACACTAGCAGGG
109	Phgdh	CCACACTGAGAGCCTACCTG
110	Phgdh	CTCACTTCTGACCAGACTGT
111	Phgdh	TAGTAGCAGACCGACAATG
112	Phgdh	CTGCGATTTCTCCCCACAG
113	Ppat	ACCTTGGAATCGGACATACG
114	Ppat	ATAAGACGCCCCGATGCAGAG
115	Ppat	TGATCACTCTGGGACTCGTG
116	Ppat	AGGGGTGTATGCGAGTAACT
117	Psat1	TGGAAGGAGTGCTGACTACG
118	Psat1	TGCAAACGAGACTGTGCACG
119	Psat1	CAATACAGAGAATCTTGTGA
120	Psat1	CTTTGTAGTCAAGGACTGAT
121	Psph	TTCGTACATTTTACGACTG
122	Psph	CTTATGCCAGGAGTCAGATG
123	Psph	CCTGGACATTACGCTCCTGG
124	Psph	CAGCCTATTGGCAAACACAT
125	Sardh	CCTTGACTACGACTACTACG
126	Sardh	CGTCGTCCTGAGCGCATCG
127	Sardh	AACCGAGTAGTTCTTGGCAT
128	Sardh	CGGTGACTGGCATCCGTGTG

129	Shmt1	TGTAGAATATCATACCAGCA
130	Shmt1	TCGGCTGGCAAATTCTCCG
131	Shmt1	CCCGGAACCTGGACTACGCA
132	Shmt1	AAGCCCATGATTCGCCCATG
133	Shmt2	CGGCAGATACTACGGAGGAG
134	Shmt2	AACATCCGCGTACTTGAAAG
135	Shmt2	AGCCTCATGATCGAATCATG
136	Shmt2	TAGTCGATGAGGCCAGTTTG
137	Tyms	CAGGCACGATACAGCCTGAG
138	Tyms	GACAATTCTACAGATTACTC
139	Tyms	TCACCACATAGAACTGACAG
140	Tyms	TTCAAGAAGGAGGACCGCAC
141	Prkaa1	GAAGATTCGGAGCCTTGACG
142	Prkaa1	GATCGGCCACTACATCCTGG
143	Prkaa1	ATCACCATGAAAATATCAGA
144	Prkaa1	CCTGTGACAATAATCCACAC
145	Tsc2	TGAACCACATGGCTATGACG
146	Tsc2	CACAGGGTGATAATGAACAG
147	Tsc2	CAGCTCCAAAGACCCTTGAG
148	Tsc2	CTGATCCTAGCACACATGTG
149	Slc25a32	CGGATCTTCACGAGGTCGAG
150	Slc25a32	GGTTCTCGTACCGGACGTGG
151	Slc25a32	GGAGTAACCCCGAATGTGTG
152	Slc25a32	AGGTGTGCGTGGATTATACA
153	BRDN0000737380	GCGAGGTATTCGGCTCCGCG
154	BRDN0000737381	GCTTTCACGGAGGTTGACG
155	BRDN0000737382	ATGTTGCAGTTCGGCTCGAT
156	BRDN0000737383	ACGTGTAAGGCGAACGCCTT
157	BRDN0000737384	GACTCCGGGTACTAAATGTC
158	BRDN0000737385	CCGCGCCGTTAGGGAACGAG
159	BRDN0000737386	ATTGTTCGACCGTCTACGGG
160	BRDN0000737387	ACCCATCGGGTGCGATATGG
161	BRDN0000737388	CGGGCGTCACCTGCTAGTAA
162	BRDN0000737389	GCTTCTACTCGCAACGTATT
163	Gldc	CCACTGAAATCCATTTCTGTG
164	Gldc	TTTACTCAACTACCAGACCA
165	Gldc	CTTGATCCAGGGATGCCACA
166	Gldc	AGGCCACAAACAGCTACCAG

**Original Doc name: 190306\_1C metabolism library (Brie)**

Target Gene Symbol	sgRNA Target Sequence
Ada	GTTGTGGATCTTGTGAACCA
Ada	ATTCATCGGACCGTCCACGC
Ada	CTTCATCTCCACAAACTCGT
Ada	GCTGCGCAACATTATCGGCA
Ahcy	GCGCACCTGACAGAAGCTGT
Ahcy	TGTCAACGATTCTGTACCA
Ahcy	TGACCCTATCATACCCTCCA
Ahcy	TGTGATGATTGCGGGCAAGG
Aldh11	CCAGCCAGCGAAGTATCGGA
Aldh11	AGTACCATAAACCCAACGGA
Aldh11	TTGGATCCTACAGATCAACT
Aldh11	TCCAGGCCTAGTCACCAAAG
Amt	AAATGGTGGCGTTTGCAGGG
Amt	TTGTAAGCAATACTTCTGAG
Amt	TGCGGAACTAAGGCCTAACC
Amt	TGTAACACCTGTGTTGCCGT
Atic	AGACGACTGTCACTCGAGCG
Atic	GAGATGTGTCTGAGCTAACA
Atic	AATTGCTTCATCGTATTGAG
Atic	TTCTTTCAAGCACGTCAGCC
Bhmt	TCCCTCGGGCCCAATGCACA
Bhmt	CGTGGACTTCCTCATTGCAG
Bhmt	ACCTGCCTCAGGATGCTCCA
Bhmt	GCAGTTCACGCCGACAATGG
Bhmt2	CCATGTGCATCGGCCAGAG
Bhmt2	TGAAGACAATATGGCCAGCA
Bhmt2	TCACACAGAATTCTTGAGAG
Bhmt2	AGAGAGGCTTCGTGAAGGCG
Cbs	ACACTACGATGACACCGCCG
Cbs	TCGCCATGCCACTCCCACGT
Cbs	GTGAGTTCTTCAATGCGGGT
Cbs	ATAATGTGGGGAGTCCGCCA
Cth	TGCATGGATGAAGTGTATGG
Cth	GCAATGGAATTCTCGTGCCG
Cth	TTCCAAAACCAAATTGCTAG
Cth	TTTGTGGACAATTTGTGCGC
Dhfr	GACATGGTTTGGATAGTCGG
Dhfr	AACCTCAGAGAACCACCACG
Dhfr	TCGCCGTGTCCCAAATATG
Dhfr	CAGCCCGGCCAATACCTGAG
Ftcd	CAGGTTAAGAGCAATACGGT

Ftcd	CCGAACAAAACCGCGCAGTG
Ftcd	GCACTGTCTACACTTTCGTG
Ftcd	CACAGCTCAAACAGGCCGAG
Gart	ACTCGTAGTTGTCCGACCAG
Gart	TGACGGCTTCAGTTGTACTION
Gart	GCTAGAAAGGATCACCGAAG
Gart	GGCAAAGTAGTGACCAGCGG
Gnmt	TGTGTGGCAGCTGTACATCG
Gnmt	AGAACATTGCAAGCATGGTG
Gnmt	GAGCCATCCTTTGACAATTG
Gnmt	GGGCTTCAGCGTGATGAGCG
Mat1a	ACAGGTATGGTGCTACTGTG
Mat1a	CTATGCTACTGATGAGACCG
Mat1a	GTGTTGCACAGAGATGACGA
Mat1a	GACACATTGGGCAATATCTG
Mat2a	CCTGATGCTAAAGTGGCTTG
Mat2a	GTGCAATATATGCAAGATCG
Mat2a	ACCAAGGCAATGTACCATTG
Mat2a	ATTTACCACCTACAGCCAAG
Mtrr	GATGAAGCGGTTGTAATCAG
Mtrr	GGTGAGCAAAATAGTCCGTG
Mtrr	GAACAAAATGAGACAAACAG
Mtrr	CTCGACCGTACTCATGTGCA
Dnmt1	TAATGTGAACCGGTTACACAG
Dnmt1	CAGAGCCCTATCGCATCGGT
Dnmt1	CATCACGGCTCACTTCACGA
Dnmt1	ACCTCGGGCCAATCAATCAG
Dnmt3a	GATCATTGATGAGCGCACAA
Dnmt3a	AGTTTACACCGACATGTGGG
Dnmt3a	CTTACCAGTATGACGACGAT
Dnmt3a	CAGGCCGAATTGTGTCTTGG
Dnmt3b	TGGTAGCCGGAAACTCCACA
Dnmt3b	CAGCCTTCTGAATTACACGC
Dnmt3b	GGAGGGTATGGATACCACAC
Dnmt3b	CAGTAGGCTTGAAGCCACCG
Mtfmt	GTGTACGAGTGGCCCGACGT
Mtfmt	GTGCCTTCGCTATCCCCAA
Mtfmt	ACCGTGTGGATTATCGGAGC
Mtfmt	GTCAAAACTTGGTGCCAACA
Mthfd1	ACACCAACGATAGATTCCTG
Mthfd1	CACTATGAATCCGTGCACAG
Mthfd1	GATTGCCGGAAGGCACGCGG
Mthfd1	GGTAGCGTCCAGTAAGAAAG

Mthfd1l	GGGTGACCGACATCAATCTG
Mthfd1l	GCCTCACAGACATGAAAGAG
Mthfd1l	TGGTTGCGGGGTCAATGTTG
Mthfd1l	TGAGAGCACTCAAACAGACA
Mthfd2	TCGATGAGATATTGTGACTG
Mthfd2	AGATAATTAAGCGAACAGGT
Mthfd2	GCTTTCATGTCATTAACGTG
Mthfd2	CTATGTTCTCAACAAAACCA
Mthfd2l	ACTAAAATGATACTCAGATG
Mthfd2l	GCGGGAAGATCCAAGAACGT
Mthfd2l	GAGCTCACTGCAGATACCTG
Mthfd2l	AACATGGATCCAAGAGTCAG
Mthfr	AGACCCTGTAGGTGACCACT
Mthfr	GACTGGGATGAGTTTCCTAA
Mthfr	AGGTAACATCTACGAAGAGG
Mthfr	CGAAGCTCTCTGCATCGGGG
Mthfs	TTGCTCTGGAATTGGTACCG
Mthfs	CTTCTCGCACCTTCTGCGTG
Mthfs	GATGAGGTCAAGTCCACCTG
Mthfs	ATCTTGCATGCTTAGAAAGA
Mtr	TCAGGTGCTCGATATCAACA
Mtr	GGGGTCCGAATGAGACACGC
Mtr	TGTGGATAGCATCATACACA
Mtr	CTTCAAAAACACTAGCAGGG
Phgdh	CCCACTGAGAGCCTACCTG
Phgdh	CTCACTTCTGACCAGACTGT
Phgdh	TAGTAGCAGACCGGACAATG
Phgdh	CTGCGATTTCTCCCCACAG
Ppat	ACCTTGGAATCGGACATACG
Ppat	ATAAGACGCCCGATGCAGAG
Ppat	TGATCACTCTGGGACTCGTG
Ppat	AGGGGTGTATGCGAGTAACT
Psat1	TGGAAGGAGTGCTGACTACG
Psat1	TGCAAACGAGACTGTGCACG
Psat1	CAATACAGAGAATCTTGTGA
Psat1	CTTTGTAGTCAAGGACTGAT
Psph	TTCGTACATTTTCAGACACTG
Psph	CTTATGCCAGGAGTCAGATG
Psph	CCTGGACATTACGCTCCTGG
Psph	CAGCCTATTGGCAAACACAT
Sardh	CCTTGACTACGACTACTACG
Sardh	CGTCGTCCTGAGCGCATCG
Sardh	AACCGAGTAGTTCTTGGCAT



Sardh	CGGTGACTGGCATCCGTGTG
Shmt1	TGTAGAATATCATAACCAGCA
Shmt1	TCGGCTGGCAAATTCTCCG
Shmt1	CCCGGAACCTGGACTACGCA
Shmt1	AAGCCCATGATTGCCCCATG
Shmt2	CGGCAGATACTACGGAGGAG
Shmt2	AACATCCGCGTACTTGAAAG
Shmt2	AGCCTCATGATCGAATCATG
Shmt2	TAGTCGATGAGGCCAGTTTG
Tyms	CAGGCACGATACAGCCTGAG
Tyms	GACAATTCTACAGATTACTC
Tyms	TCACCACATAGAACTGACAG
Tyms	TTCAAGAAGGAGGACCGCAC
Prkaa1	GAAGATTCGGAGCCTTGACG
Prkaa1	GATCGGCCACTACATCCTGG
Prkaa1	ATCACCATGAAAATATCAGA
Prkaa1	CCTGTGACAATAATCCACAC
Tsc2	TGAACCACATGGCTATGACG
Tsc2	CACAGGGTGATAATGAACAG
Tsc2	CAGCTCCAAAGACCCTTGAG
Tsc2	CTGATCCTAGCACACATGTG
Slc25a32	CGGATCTTCACGAGGTCGAG
Slc25a32	GGTTCTCGTACCGGACGTGG
Slc25a32	GGAGTAACCCCGAATGTGTG
Slc25a32	AGGTGTGCGTGGATTATACA
BRDN0000737380	GCGAGGTATTCGGCTCCGCG
BRDN0000737381	GCTTTCACGGAGGTTGACG
BRDN0000737382	ATGTTGCAGTTCGGCTCGAT
BRDN0000737383	ACGTGTAAGGCGAACGCCTT
BRDN0000737384	GACTCCGGGTACTAAATGTC
BRDN0000737385	CCGCGCCGTTAGGGAACGAG
BRDN0000737386	ATTGTTGACCGTCTACGGG
BRDN0000737387	ACCCATCGGGTGCGATATGG
BRDN0000737388	CGGGCGTCACCTGCTAGTAA
BRDN0000737389	GCTTCTACTCGCAACGTATT
Gldc	CCACTGAAATCCATTTGCTG
Gldc	TTTACTCAACTACCAGACCA
Gldc	CTTGATCCAGGGATGCCACA
Gldc	AGGCCACAAACAGCTACCAG