

**Feng et al Table S5** Benchling off-target list for Gnao1 G203 gRNA

Sequence	PAM	Score	Gene	Chromosome	Mismatches
<i>TGCAGGCTGTTTGACGTCGG</i>	<i>GGG</i>	<i>100</i>	<i>ENSMUSG00000031748</i>	<i>chr8</i>	<i>0</i>
GGCAAGCTGATTGACGTCTG	TAG	0.6189		chr18	4
TGGATGGTGTGGACGTCGG	AAG	0.5200	ENSMUSG00000041390	chr6	4
TGCAGGCTGTTTGAAGTCTG	CAG	0.5076		chr3	2
GGTGGGCTGTTTGACGTGGG	AGG	0.3804		chr1	4
TTCAGGCTGAGTGACGTCAG	TGG	0.3169	ENSMUSG00000032497	chr9	4
AGCAGGCACTTTGAAGTCGG	AAG	0.2931		chr3	4
TTCAGTCTGTTAGACGTCTG	TAG	0.1953		chr1	4
TGCATGGGGTTTGACTTCGG	AGG	0.1929		chr13	4
TGCTGGCTGTTTGAGGTGGG	AAG	0.1923		chr1	3
TCCAGGCTGGTGGACGTGGG	CAG	0.1710		chr1	4
TGATGGCTGTTCGACTTCGG	GAG	0.1556	ENSMUSG00000086805	chr8	4
TACAGAATGTTTGACGTGGG	AGG	0.1543	ENSMUSG00000057614	chr5	4
TTCAGTCTGTTTGAGGTCGT	TGG	0.1515		chrX	4
AGCAGGCTGCTTGACATCGA	GAG	0.1480		chr4	4
TGCAAGCTGGTTGAGGTCAG	GGG	0.1450		chr17	4
TCCAGGATGTTTGATGCCGG	AAG	0.1403		chr18	4
TGCAGGCTGTCTGAAGTCTG	GGG	0.1343	ENSMUSG00000026413	chr1	3
GGCTGGCTGTTTGACCTCAG	AGG	0.1262		chrX	4
AGCAGCCTGTTTGAAGTCTG	TGG	0.1144		chr11	4
GGCAGGCTGTATGAAGGCGG	AGG	0.1127		chr5	4
TGGAGGCTGTTACACGTCAG	CAG	0.1127		chr1	4
TGCTGGCTATTTGAAGTCTG	AGG	0.1004		chr10	4
TGCTGGTTATTTGTCGTCGG	GAG	0.1002		chr11	4
TCCAGGCTGTCTGATGTCAG	GAG	0.0954		chrX	4
TTCAGGATGTTTGACGTATG	CAG	0.0933		chr3	4
TGCACGCTGTGAGACGTGGG	CGG	0.0930	ENSMUSG00000020015	chr10	4
TGCATGCTGTCTGAAGTCAG	AAG	0.0865		chrX	4
TGCAGGCTGTATGACCTCTG	GGG	0.0862		chr2	3
TGCAGTCTCTTTGACGACAG	TGG	0.0836		chr11	4

TGCATGCTGTAGGACCTCGG	AGG	0.0771		chr4	4
CGGAGGCTGTTTGACTTGGG	AGG	0.0754		chr5	4
TCCAGGCTGTTTCAGGACGG	AAG	0.0745		chr8	4
GGCAGCCTGTTTGACATCAG	GAG	0.0744		chr17	4
TGCAAGATGTTTGACCTCAG	AAG	0.0720		chr19	4
TGGAGGTTGTTTGAGGTAGG	AGG	0.0704		chr2	4
TGTGGGCTGTTTGACCTGGG	AGG	0.0693		chr19	4
GGCAGGCTGTTTGAAGCCAG	GGG	0.0669		chr9	4
TCCAGGCTGTTTGAGGGCTG	CAG	0.0647	ENSMUSG00000097637	chr8	4
TGCAGGCTGGCTGACGATGG	TGG	0.0611		chr8	4
TGCAGGATGCTTGACCTCTG	TAG	0.0604		chr2	4
TGCACTCTGTTTGAGGTTGG	AGG	0.0599		chr10	4
TCCAGGCTGTGTGAGGTGGG	AGG	0.0574		chr9	4
GGCAGGCTGTTGGAAGTAGG	GAG	0.0520		chr2	4
TGAAGGCTGTTCGAAGTGGG	GAG	0.0480		chrX	4
TGCAGGCTGATTGATGGCTG	GAG	0.0470		chr7	4
TACAGACTGTTTGACTTGGG	CAG	0.0430		chr3	4
TTCAGGCTGTTTTACTTCTG	AGG	0.0422		chr15	4
AGCAGGATGTTTGTCGTGGG	GAG	0.0420		chr1	4
AGCAGGCTGTGTGACCTGGG	AGG	0.0385		chr6	4