

Supplementary Table S1. The off-target sites for *GRIK1*, *GRIK2*, and *GRIK4* gRNA.

Target sequence for <i>GRIK1</i> : GGATATAGCAGAGGAAATAGAGG		
Location	Number of mismatches	Sequence (including mismatches)
chr1:151261259 (<i>ZNF687</i> _intron 3)	3	CCCCTAT c T t C c CTGCTATATCC
chr11:24740548 (<i>LUZP2</i> _intron 1)	3	GG g TATAt a AGAGGAAATAGAGG
chr11:121289377	3	GGAT g TAGCAGAGGAA c T g GCGG
chr11:134869848	3	GG gg A g AGCAGAGGAAATAGGGG
chr12:14769329 (<i>GUCY2C</i> _intron 25)	3	GGATAT g GCAGAGGAAAT g c TGG
chr13:48811058 (<i>ITM2B</i> _intron 1)	3	t GATATAG g AGAG a AAATAGTGG
chr14:43133466	3	GG a GAT a c CAGAG t AAATAGGGG
chr14:89886352 (<i>FOXN3</i> _intron 1)	3	GGATAT t g AGAGGAAAT a c GGG
chr16:57583416 (<i>ADGRG5</i> _intron 1)	3	CCCCTATTTCTCT t CT t cATCC
chr16:67968640 (<i>PSMB10</i> _intron 7)	3	CCCCTAT c TCC c CTGCTATAG g CC
chr17:33321885 (<i>LIG3</i> _intron 9)	3	GGATATAGCAG t GGAAA a a TGG
chr2:121266319	2	CCTC g ATTTCTCTGCTAT a c CC
chr20:12024758	3	CCT t TATTTCTC g GCT c TATCC
chr20:34109882	3	GGATAT a c t GAGGA g TAGAGG
chr22:36536844 (<i>APOL3</i> _exon 3)	3	CCGCT g TTT c tTCTGCT g TATCC
chr22:49245727	3	GGAT a g a AGAGGAAA c AGTGG
chr3:58054571 (<i>FLNB</i> _intron 1)	3	GGATATAG a AGAGG c a tTAGAGG
chr3:117677756	3	GGATATAGCAG a g GA c AGGGG
chr4:71771379 (<i>MOB1B</i> _intron 1)	3	GGAT gg AGCAGAGGAAAT a AGGG
chr4:77129747 (<i>SCARB2</i> _intron 1)	3	GG a g a AGCAGAGGAAA a AGTGG
chr5:103041128	3	CCACTATTTCT t TG t TATAT C a

chr6:136174586 (<i>PDE7B</i> _intron 1)	3	CCTC c ATTTCCTCTGCT t TATC t
chr6:147805828	3	GGATAT g GCA a AGGAAAT g GGGG
chr8:26388739 (<i>DPYSL2</i> _intron 1)	3	GGA a A c AGCAGAGGAAAT t GAGG
chr9:6820589 (<i>KDM4C</i> _intron 4)	2	GGATATAGCA t AGGAAT t TAGGGG
chr9:18501127 (<i>ADAMTSL1</i> _intron 1)	3	CCTCTATTTCC c CTGCTA g AT g C
chr9:104416811 (<i>GRIN3A</i> _intron 3)	3	CCACT t TTTCCTCT ca TATATCC
Target sequence for <i>GRIK2</i> : GTGGTCGATGGAACGATTGCAGG		
Location	Number of mismatches	Sequence (including mismatches)
There are no off-targets.		
Target sequence for <i>GRIK4</i> : TCGGCCCCAGATCTGGCAGCACGG		
Location	Number of mismatches	Sequence (including mismatches)
chr11:118663590	3	CCCTGCT t CCAG c TCTGGGCC a A
chr13:82463674	3	CCAG g GCTGCCAGATCTGGG ga GA
chr14:23851992 (<i>MYH6</i> _intron 37)	3	CCATGCTGCC c GATCTGGGCC cc
chr15:31779358 (<i>OTUD7A</i> _intron 13)	3	CCCTGCTGCCAG g TCTGG t CC ca A
chr17:43324175 (<i>FMNL1</i> _intron 26)	3	CCATGCT c CCAG c TCTGGGC g GA
chr17:81143686	3	CCCTGCTGCCAG ca ca GGGCCGA
chr18:56887029	3	c CGGCCCCAGATC a GGCAGC g GGG
chr20:61287978 (<i>SLCO4A1</i> _exon 2)	3	CCC ct CTGCCAG c TCTGGGCCGA
chr4:7817520 (<i>AFAP1</i> _intron 7)	3	TCGGCC a AG g TCTGGCAG g ATGG
chr7:46948287	3	CCATGC a GCCAGATCT t GGCC ca A
chrX:12514161 (<i>FRMPD4</i> _intron 4)	3	CCATGCT a CCAGATCT ca GCCGA
chrX:110478130	3	CCC ct CTGCCAGATCTGGGC a GA

Small bold red letters mean mismatch nucleotide.