

**Table S3. Predicted off-target sites of sgRNA-1 in mouse genome.**

Possible off-target sites were predicted as described in Materials and Methods. Five sites with 3-base mismatches and 5 sites with 4-base mismatches and high-scoring were chosen for Surveyor assay.

<b>sgRNA-1</b>				
TAGTAAGAGCTGAGGTCCGT				
<b>Top genome-wide off-target</b>				
<b>sequence</b>	<b>score</b>	<b>mismatches</b>	<b>label</b>	<b>locus</b>
GAGTCAGAACTGAGGTCCGTGAG	1.6	3MMs [1:5:9]	OT-1	chr1:-107924912
CAGGAAAAGTTGAGGTCCGTGAG	0.9	4MMs [1:4:7:10]	OT-2	chr10:-21145428
TGGAAAGAGGAGAGGTCCGTAGG	0.7	4MMs [2:4:10:11]	OT-3	chr3:-31398650
GAGTAAGAACTGAGGTCCATAAG	0.7	3MMs [1:9:19]	OT-4	chr14:-41981068
GAGGCAGAGCTGAGGTTCGTGGG	0.6	4MMs [1:4:5:17]	OT-5	chr17:-46832870
CAGTAAGTGTTGAGGTTCGTGAG	0.6	4MMs [1:8:10:17]	OT-6	chrX:+163004146
TAGAGAGAGATGAGGTACGTGGG	0.5	4MMs [4:5:10:17]	OT-7	chr1:+186211390
TATACAGAGCTGAGGTCCCTTGGG	0.5	4MMs [3:4:5:19]		chr4:-57026988
TGGTTAGAGGTGAGGTCCCTTGGG	0.5	4MMs [2:5:10:19]		chr1:-195695078
TAGTAACTGAAGAGGTCCGTGGG	0.5	4MMs [7:8:10:11]		chr15:-25943556
TGGAAGGAGCTTAGGTCCGTAGG	0.4	4MMs [2:4:6:12]		chr8:+24267523
CAGTGGGAGCTGAGGTCCGAGGG	0.4	4MMs [1:5:6:20]		chr8:-19312258
TTGTCAGAGGTGAGTTCCTGAG	0.4	4MMs [2:5:10:15]		chr11:+82671514
TAGAGAAAAGCTGAGGTCCCTTAGG	0.3	4MMs [4:5:7:19]		chr8:-89295418
AAGAAAGTGCTGAGGTCTGTGAG	0.3	4MMs [1:4:8:18]		chr1:-113703635
CAGGCAGAGCTGAGGTCTGTGGG	0.3	4MMs [1:4:5:18]		chr15:-72844924
GAGCATGAGCTGAGGTCCCTTGGG	0.3	4MMs [1:4:6:19]		chr11:+115710138
TAGTAAAAGCTAAGGTCCCTTGG	0.3	3MMs [7:12:19]	OT-8	chr13:+69901881
TAGGAATAGATGAGGTCCCTCAG	0.3	4MMs [4:7:10:19]		chr8:-37145519
TGATGAGAGCTGAGGTGAGTGG	0.3	4MMs [2:3:5:18]		chr6:+142822525
AAGTAAGAGCAGAGGCCCGTCCG	0.3	3MMs [1:11:16]	OT-9	chr2:+102053997
TATTGAGAGTTGAGGTGAGTGGG	0.3	4MMs [3:5:10:18]		chr8:-5466752
AAGGCAGAGCTGAGGCCCGTTAG	0.3	4MMs [1:4:5:16]		chr12:+77242731
TAGTAGCGGCTGAGGTCCGAGGG	0.3	4MMs [6:7:8:20]		chr4:-43524738
GAGTGAGAGCTCAGGTCCCTGGG	0.3	4MMs [1:5:12:19]		chr7:-121968004
TGGGAAGAGGTGAGGACCGTAAG	0.2	4MMs [2:4:10:16]		chr7:-116331715
TAGAGAAAAGCTGAGGTGAGTGGG	0.2	4MMs [4:5:7:18]		chr4:+138638448
GAGTAAGAGTTGAGGTCCCTGGG	0.2	4MMs [1:10:19:20]		chr13:-34332518
TAGTCAGAGCTGAGGTCCGTAAG	0.2	3MMs [5:16:17]	OT-10	chr12:+12318505