Supplementary Table S1 Top ten genome-wide off-target sites used in this study

	Sequence	Score	Mismatches	Locus
OT1	GGCTGTGGAGTGCATGTGCGAAGGT	5.0	2MMs [8:10]	chr10:-79469902
OT2*	TGCATTGTAATGCATGTGCACAGGG	0.7	4MMs [1:4:5:20]	chr13:-12962821
OT2*	TGCATTGTAATGCATGTGCACAGGG	0.7	4MMs [1:4:5:20]	chr13:-13174810
OT2*	TGCATTGTAATGCATGTGCACAGGG	0.7	4MMs [1:4:5:20]	chr13:+13206983
OT2*	TGCATTGTAATGCATGTGCACAGGG	0.7	4MMs [1:4:5:20]	chr13:-27869407
OT3	TGCAGTGTAGTGCATGTGCACAGGG	0.7	4MMs [1:4:10:20]	chr4:-152973806
OT4	GACTGTGCACTGCATGTGCCAGGGT	0.6	4MMs [2:8:10:20]	chr1:-134765564
OT5	GGCAATGCAATGCATGTGAGTGGTC	0.5	4MMs [4:5:8:19]	chr9:-115822056
OT6	GCGTGTGTGAGGCATGTGCGAGGCA	0.5	4MMs [2:3:9:11]	chr15:-99017711
OT7	GCCTGTGCAGTGCATGTGTGGAGAC	0.5	4MMs [2:8:10:19]	chr1:+94173408

Off-target sites were predicted using the CRISPR Design server (http://crispr.mit.edu). Ten sites were chosen based on sequence similarity. PAM sequences are underlined.

*Duplicated region in the annotated mouse genome.