

Supplementary information, Table S1. Predicted off-target sites of sgRNA-m3 in human and mouse genomes.

		sequence	score	mismatches	locus
	sgRNA-m3	TTTTCTCTTTGCAGGTCC G T			
Human Genome	h-H530R	TTTTCTCTTTGCAGGTCC G TCGG		0 MisMatches	chr7:-151257690
	h-WT	TTTTCTCTTTGCAGGTCC A TCGG	31.5	1MMs [19]	chr7:-151257690
	h-OT1	TTTTATCTTTGCAGGTCTGTCAG	2.2	2MMs [5:18]	chr11:+101612313
	h-OT2	CGGCCTCTTTGCAGGTCCGTGGG	1.3	4MMs [1:2:3:4]	chr12:-110035578
	h-OT3	CTGCCTCTCTGCAGGTCCGTAAG	0.8	4MMs [1:3:4:9]	chr3:+46905238
	h-OT4	TCTTTTCACTGCAGGTCCGTGGG	0.8	4MMs [2:5:8:9]	chr3:-127607473
	h-OT5	TTTTCTCTTTTCAGGTCTGTTAG	0.8	2MMs [11:18]	chr13:+23769655
	h-OT6	TTTTCTGCTTGCAGGTTCGTCAG	0.7	3MMs [7:8:17]	chr2:-121996474
	h-OT7	ATTCCTCGTTGCGGGTCCGTGGG	0.6	4MMs [1:4:8:13]	chr18:-72591353
	h-OT8	TCTTCTTTTTGCAGTCCGTTGG	0.6	3MMs [2:7:15]	chr22:+39410049
	h-OT9	CTTCTCTTTGAAGTCCTTTGG	0.6	3MMs [1:12:19]	chr7:-127073516
h-OT10	TTGCATCTTTGCAGGTCC T TAAG	0.5	4MMs [3:4:5:19]	chr12:-119535004	
Mouse genome	m-H530R	TTTTCTCTTTGCAGGTCC G TCGG		0 MisMatches	chr5:-24371977
	m-WT	TTTTCTCTTTGCAGGTCC A TCGG	31.5	1MMs [19]	chr5:-24371977
	m-OT1	TTGTTTTTTTGCAGGTCCGTCAG	1.6	3MMs [3:5:7]	chr13:-99614562
	m-OT2	TTGGGTCTTGGCAGGTCCGTTGG	1.3	4MMs [3:4:5:10]	chr4:+83633358
	m-OT3	TTTTTTTTTTCCAGGTCCGTAAG	1	3MMs [5:7:11]	chr18:+87323263
	m-OT4	CTTTTTCCTTGCAGGTCCCTCAG	0.5	4MMs [1:5:8:19]	chr6:+97421046
	m-OT5	ATTCGTCTTTGCAGGTCC T TTAG	0.5	4MMs [1:4:5:19]	chr15:-99158189
	m-OT6	TTTTCTAAAGGCAGGTCCGTGGG	0.5	4MMs [7:8:9:10]	chr17:+44236548
	m-OT7	TTTTTTCTTTGGAGGTCCCTGGG	0.5	3MMs [5:12:19]	chr6:+70814826
	m-OT8	TTTTCTCTTTGCAGGTCTGCGAG	0.4	2MMs [18:20]	chr1:+176431598
	m-OT9	TTTGTTCTGTGTAGGTCCGTCAG	0.4	4MMs [4:5:9:12]	chr3:+19457592
m-OT10	CATTTTCTTTGCAGTCCGTTAG	0.4	4MMs [1:2:5:15]	chr19:+9189444	