

Table S3a. The potential off-targets accessed using the Cas-OFFinder off-target searching tool

sgRNA	Target Sequence	Bulge Type	Bulge Size	Mismatch	Number of Found Targets
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	2	1
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	4	5
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	5	26
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	6	321
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	7	2624
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	8	16176
sgRNA-1	CACCACAAATCAGCCAAACTCTGTNRG	X	0	9	83760
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	3	1
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	4	9
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	5	127
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	6	794
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	7	4868
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	8	26948
sgRNA-2	CACCCTCATCATTTTCAATATGAANRG	X	0	9	120873

Table S3b. The potential mismatch ≤ 4 off-target regions accessed using the Cas-OFFinder off-target searching tool

Target DNA sequence	Chromosome	Position	Location	Direction	Mismatches	Nearby Gene	Position to Gene
aAgCACAAATCAGCCAAACTCTGTTGG	chr6	134979327	chr6:134,979,127-134,979,527	-	2	HBS1L	Intron 14-15
CACCCTCATCATTTTCAatTGAATAG	chr14	75029254	chr14:75029054-75029454	+	3	MLH3	Intron 9-10
CACCCTCATCATcTTCAAgTGAATAG	chr3	2319531	chr3:2319331-2319731	-	4	CNTN4	Intron 1-2
CAcCCTCATCATcTTCAAatTGAATAG	chr6	65029636	chr6:65029436-65029836	-	4	EYS	Intron 13-14
CACCACAcAgCAGCCAgAtTCTGTGGG	chr15	26660595	chr15:26660395-26660795	+	4	GABRB3	Intron 3-4
actaCTCATCATTTTCAATATGAATGG	chr6	134979362	chr6:134979162-134979562	+	4	HBS1L	Intron 13-14
CACCcCAAATCAGCaAAAtTCTGgCAG	chr2	12481111	chr2:12480911-12481311	+	4	MIR3681HG	Intron 4-5
CcCCCTCATCATTTTCAtaAgGAACAG	chr20	4630067	chr20:4,629,867-4,630,267	-	4	RPS4XP2	Intron 1-2
CACCCTCATCATcTTCAtcATGcACAG	chr20	10241310	chr20:10241110-10241510	+	4	SNAP25	Intron 1-2
CACCCTCAaCtTcTTCAATATcAATAG	chr5	35769486	chr5:35,769,286-35,769,686	-	4	SPEF2	Intron 26-27
CACCACAAaCAGCtcAACTCTGaAAG	chr9	113099568	chr9:113,099,368-113,099,768	+	4	amorph	
CcCCACAAATCAGaaAAGCTCTGTAAG	chr10	3671670	chr10:3,671,470-3,671,870	+	4	amorph	
CAGcAgAAATCAGCCAAACTCTaaGAG	chr18	24354628	chr18:24,354,428-24,354,828	+	4	amorph	
CACCCTCATCATcTTCAiTTGAgTAG	chr7	88609588	chr7:88609388-88609788	-	4	amorph	
CAcCCTCATCATcTTCAcTTTGAATAG	chr2	161620915	chr2:161620715-161621115	-	4	amorph	
CAttCaCATCATTTTCAAgATGAATGG	chr14	26367404	chr14:26367204-26367604	-	4	amorph	