

SI Data File C: Ranked off-target sites for sgRNAs used in this study

Off-target for A146K sgRNA

Sequence	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target
CTGCGGTGCTGACGCTGCGC	AGG	5.146703297	ENSG00000167995	chr11	-1	61955893	2	FALSE
CCTGTGTCTGACGCTGCGC	GGG	1.442307692		chr20	-1	50246956	4	FALSE
CTTTGTTCATGACGCTGCGC	AGG	0.896991699	ENSG00000048471	chr16	-1	12524752	3	FALSE
CTTTGTGCCGACGTTGCGC	GGG	0.762558049		chr4	1	54658402	3	FALSE
CCGCGGTGCTGACGCTGCTC	AGG	0.611313191	ENSG00000090316	chr4	-1	1309855	4	FALSE
CTGTAGTGCAGAGGCTGCGC	TGG	0.582322973		chr2	1	47237604	4	FALSE
TTTTGGTGCTGAAGCTGCCC	AAG	0.54756383		chr8	-1	101982967	3	FALSE
CCATGGGGCTGGCGCTGCGC	AAG	0.543948597	ENSG00000266074	chr17	1	81461477	4	FALSE
CCCTGCTGCTGGCGCTGCGC	TGG	0.477428291	ENSG00000170128	chr1	1	200873893	4	FALSE
CTCTGCTGCCGCCGCTGCGC	GAG	0.431824255	ENSG00000143502	chr1	1	223364152	4	FALSE
CGTTGGTGGCGACGCTGCCC	CGG	0.348889334	ENSG00000204666	chr19	1	50050818	4	FALSE
CTGCGGTGCGGACGCTGGGC	CAG	0.346494543	ENSG00000167608	chr19	-1	54164551	4	FALSE
CTCCGGTCTGATGCTGCGG	GAG	0.343553885	ENSG00000138311	chr10	-1	62374409	4	FALSE
CTTTGGTGACAGCTGCCCC	GAG	0.332111303		chr10	1	15762893	3	FALSE
CTTTCAGGCTTACGCTGCGC	GGG	0.330770661	ENSG00000273079	chr12	1	13563279	4	FALSE
CTGTGGTCTGCCGCTGCTC	TGG	0.30076609	ENSG00000073060	chr12	-1	124787421	4	FALSE
CTTTGGAGAACACGCTGCGC	TAG	0.293406436		chr5	-1	14191003	4	FALSE
CTGTGGTCTGATGCTGGGC	CAG	0.287073004		chr3	1	139829324	3	FALSE
CCTTGGTCCGACGCTGCAG	AAG	0.271059097	ENSG00000112782	chr6	-1	46014623	4	FALSE
CTTTGTTGGAGCCGCTGCGC	GGG	0.241590158	ENSG00000111058	chr12	-1	80937330	4	FALSE
CAGTGGTGGTACGCTGAGC	AGG	0.237659842		chr2	-1	23667620	4	FALSE
ATTTCTGCTGACGCTGGGC	AGG	0.233392956		chr9	-1	35982279	4	FALSE
GTTTGGAGCTGCTGCTGCGC	AGG	0.228221001	ENSG00000132382	chr17	1	4544546	4	FALSE
TTTTGATGCTGAGGCTGCGG	CGG	0.221542787		chr7	1	36242063	4	FALSE
GTCTGGTCTGACGATCCGC	GAG	0.21965615	ENSG00000108465	chr17	1	47973578	4	FALSE
CTGTGGTGC GGAAGCTGCC	AGG	0.215507231		chr5	-1	140677455	4	FALSE
CCTGGGGGCTGACGCGGCGC	CGG	0.214619615	ENSG00000117322	chr1	-1	207454238	4	FALSE
CCTGCTGCTGATGCTGCGG	AGG	0.213387838		chr15	-1	74832344	4	FALSE
CTTCAGTGCTTACGCTGTGC	CAG	0.205041667		chr10	-1	46442968	4	FALSE
CCTGGGTGCTGGCGCTGGGC	TGG	0.198577457		chr17	1	39635341	4	FALSE
CCTTGGCGCTGATGCTTCGC	AGG	0.19810534	ENSG00000131759	chr17	-1	40355405	4	FALSE
CTTTGGTGGGGCCGCTGCGG	TGG	0.191301516	ENSG00000279685	chr17	1	45897419	4	FALSE
CTGTGATGCTGGCGCTGCC	GGG	0.186075653		chr2	1	144508184	4	FALSE
CTTGGGCGCTGAGGCTTCGC	AGG	0.185914242		chr4	1	1168570	4	FALSE
CTGTTGTGCTGACGATGCTC	TGG	0.175464972		chr18	1	2857771	4	FALSE
CTTTGCTACTGTGGCTGCGC	AAG	0.174629839		chr4	1	71438039	4	FALSE
CTTTGGGGCTGACGCAGCGG	AGG	0.171411114	ENSG00000072952	chr11	-1	10652138	3	FALSE
ATGTGGTCTGAGGCTGAGC	AAG	0.163459897		chr11	-1	109641742	4	FALSE
CCTGGGTGCTGAGGCTGGGC	CAG	0.158025	ENSG00000139880	chr14	1	23055784	4	FALSE
GTTTGGGGCTGACGTTGCTC	CAG	0.127583658		chr19	-1	17997337	4	FALSE
CTGTGGGGCTGGCGCTGAGC	CGG	0.125055252	ENSG00000135100	chr12	-1	120999611	4	FALSE
TTTTGGTCTGACTCTGAGC	AGG	0.124133333		chr2	-1	45393365	3	FALSE
GTTTGGTCTGCAGCTGCAC	CGG	0.122096565	ENSG00000125457	chr17	-1	75266944	4	FALSE
CTCTGGAGCTGACGCTGGGG	GAG	0.121791994		chr14	-1	94370120	4	FALSE
CTCTGGAGCTGACGCTGGGG	GAG	0.121791994		chr14	-1	94361639	4	FALSE
TTTTGCTGCTGCCGCTGTGC	TGG	0.1215445		chr5	1	179212942	4	FALSE
CATTGGTGCAGACTGCGG	GGG	0.120628554		chr4	1	8581829	4	FALSE
CTTTGGTCTGGCGCTGGGT	GGG	0.115238422	ENSG00000258986	chr14	-1	104594792	3	FALSE
CCTTGGTCTGAGGGTGCAG	AGG	0.11344589	ENSG00000052749	chr10	1	97373604	4	FALSE
ATGTGGTCTGACTCTGCAC	AGG	0.106364551		chr13	-1	51223383	4	FALSE

Off-target for N296H sgRNA Off-target for N296H sgRNA

Sequence	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target
CTTCATCATCTCCAAAGGGG	AAG	6.69014085		chr9		-1 90546396	2	FALSE
CAGCATGCTCTCCAAAGGGG	AAG	4.04915253		chr18		1 37665117	2	FALSE
CATGCTCCTCTCCAAAGGGC	AGG	1.68216561		chr5		1 172749869	3	FALSE
CATAATCATCTCCAAAGGGC	TAG	1.68216561		chrX		1 79627241	3	FALSE
CACCCTCCTCCCAAAGGGG	CAG	1.56823077		chr2		1 74347940	3	FALSE
GAATATCGTCTCCAAAGGGG	TAG	1.45752075		chr4		1 164866636	4	FALSE
CATTATCCTACCCAAAGGGG	AGG	1.41367467		chr5		-1 37917393	3	FALSE
CGTCATCCTGTACAAAGGGG	AGG	1.39992		chr13		-1 32175536	3	FALSE
CTCCTTCCTTTCCAAAGGGG	CAG	1.38846679	ENSG000001	chr14		-1 21405293	4	FALSE
ATACCTCCTCTCCAAAGGGG	TAG	1.35622587		chr3		1 113192849	4	FALSE
CAGCATTCTCCCAAAGGGG	CAG	1.07110162	ENSG000000	chr17		-1 48057103	3	FALSE
CAACAACCTCTCCAAAGGGA	AGG	1.05733942		chr15		-1 62599769	3	FALSE
CATCCTTCTACCAAAGGGG	AAG	1.01297257		chr16		-1 86594199	3	FALSE
AAAAATTCTCTCCAAAGGGG	AAG	0.97130481		chr5		1 54721830	4	FALSE
CAGCGTGTCTCCAAAGGGG	CAG	0.95582585		chr5		1 14191020	4	FALSE
GCTCCTCCACTCCAAAGGGG	CAG	0.94228896		chr17		1 49558343	4	FALSE
AGTCATCATCTCCAAAGGGC	AGG	0.93431604		chr5		-1 10046165	4	FALSE
CTTCATTCTCTCCAAAGGAG	TAG	0.91448658	ENSG000000	chr11		-1 75798251	3	FALSE
AGTCATCCTGTCCAAAGGGA	AAG	0.88271165		chr18		-1 51768352	4	FALSE
GATACTCCTCTCCAAAGGGC	AAG	0.87903107		chr15		1 66408966	4	FALSE
CATTCTCTGCTCCAAAGGGG	GAG	0.87417169		chr10		-1 90779223	4	FALSE
GCACATCCTCTCCAAAGGGA	AGG	0.86672463		chr9		1 88700535	4	FALSE
CTTAGTCCTCTCCAAAGGGC	GAG	0.84889286		chr16		-1 54391594	4	FALSE
TCTCATCTTCTACAAAGGGG	GAG	0.84673913		chrX		-1 149295005	4	FALSE
CATTTGCCTATCCAAAGGGG	GAG	0.80366106		chr8		1 65982123	4	FALSE
CATCGTCTCTTCCAAAGGGG	GGG	0.79238308	ENSG000001	chr16		-1 87956795	4	FALSE
CACCCTCCTTCCCAAAGGGG	CAG	0.79096733		chr2		1 74347104	4	FALSE
CATTTTCCTAGCCAAAGGGG	TAG	0.78154064	ENSG000001	chr11		-1 47109311	4	FALSE
CACAATCATCTACAAAGGGG	CAG	0.77498274		chr13		1 60717346	4	FALSE
CTTTATCCTTTACAAAGGGG	AAG	0.75787923		chr17		1 68574649	4	FALSE
CTTCCTCATCTCCAAAGGG	AGG	0.72569444		chr8		1 140074446	4	FALSE
CTTCGTCCTCTCCAATGGGG	AGG	0.62967245		chr2		-1 136402449	3	FALSE
AAGCATCCTATCAAAGGGG	AGG	0.62914291		chr20		-1 58404478	4	FALSE
CTGCATCCTATCTAAAGGGG	CAG	0.61072897		chr5		-1 173795919	4	FALSE
TATCTTTCTCTCCAAAGGGT	GGG	0.60756838		chr2		-1 229408453	4	FALSE
CACCTTCTTCTCCAAAGGAG	CAG	0.60463217		chr17		1 35998658	4	FALSE
TATCATATTCTCCAAAGGGC	AAG	0.60037822		chr11		1 63668189	4	FALSE
GATCTATCTCTCCAAAGGGG	AAG	0.59598317		chr18		-1 57046457	4	FALSE
GATCACTTTTCCAAAGGGG	AGG	0.59204552		chr12		1 83596582	4	FALSE
CACTATCCTGTCAAAGGGG	AAG	0.58779079		chr12		1 79892649	4	FALSE
CCTCATCCTCTCAAAGGG	CAG	0.5719		chr1		-1 245981290	3	FALSE
CATCATCTTCCCAAAGGAG	AAG	0.56204315	ENSG000000	chr17		1 4960280	3	FALSE
GATAATGCTTTCAAAGGGG	TAG	0.56203204		chr8		-1 87976851	4	FALSE
CAACAAACTTTCAAAGGGG	CAG	0.55469015		chr3		1 184027869	4	FALSE
CAACATCCTCTCAAAGGAA	TGG	0.55051556		chr3		1 113407849	3	FALSE
CATGATGTTCTCCAAAGGGC	TGG	0.5425878	ENSG000002	chr3		1 15475283	4	FALSE
CAGCAGCACCTCCAAAGGGG	TGG	0.52998343		chr20		-1 24296403	4	FALSE
CCTCATCACCAACCAAAGGGG	AGG	0.5275378		chr16		1 31128217	4	FALSE
CATCAGATTGTCCAAAGGGG	AAG	0.52346882		chr2		1 205279527	4	FALSE
CCTCAGCATCTCCAAAGGGA	AGG	0.51951752	ENSG000001	chr9		-1 87707435	4	FALSE

Off-target for R218C sgRNA

Sequence	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target
GTGTCCACACTGAGTACGCA	AGG	19.6	ENSG00000167995	chr11	-1	61957403	1	FALSE
ATGTCCACACTGAGTACACC	TGG	10.425		chr7	1	10314123	2	FALSE
GTGTGTAACACTGAGTACACA	AGG	1.46807152		chr10	-1	21984870	3	FALSE
ATGCACACAGTGAAGTACACA	GAG	1.432778384		chr17	-1	48247156	4	FALSE
GAAGCCAGACTGAGTACACA	GAG	1.422115385		chr20	1	48165409	4	FALSE
GTGTTCCACCTGAGTACACT	TAG	0.977970303		chr2	1	111459080	3	FALSE
GTGTTCCACCTGAGTACACT	TAG	0.977970303		chr2	-1	87491157	3	FALSE
CTTCCACACTGAGCACACA	GGG	0.967381888		chr9	1	109316353	3	FALSE
ATTCCCACCTGAGTACACA	TAG	0.9132825		chr9	1	120468910	4	FALSE
GAATCCATACTGAGTACACT	GAG	0.877104566		chr7	-1	115541230	4	FALSE
GTGGGGAGACTGAGTACACA	CAG	0.832166988		chr6	1	2149828	4	FALSE
GTCTCCAGGGTGAAGTACACA	CAG	0.820192107		chr15	-1	72867267	4	FALSE
GTGATTACAATGAGTACACA	AAG	0.803661058		chr6	1	131742399	4	FALSE
GCATGCACACTCAGTACACA	CGG	0.781996154		chr7	-1	151819824	4	FALSE
ATGTCCAGAGTGAAGTAAACA	GAG	0.682815709		chr4	-1	121016770	4	FALSE
CTGGCCACACTGAGTCCACA	GGG	0.66020202		chr2	1	101414147	3	FALSE
GGCCCCACACTGAGTACAGA	TAG	0.611313191		chr7	-1	134144846	4	FALSE
GTCTCCACTGGGTACACA	GAG	0.609590078		chr22	1	43615713	4	FALSE
CTGCCTACTCTGAGTACACA	GAG	0.565191389		chr5	1	144359039	4	FALSE
GTGTACTCTGTGAGTACACA	TGG	0.545509974		chr10	-1	48556885	4	FALSE
GTGTACAGAATGAGTACAGA	TGG	0.524636897		chr4	1	121633689	4	FALSE
GAGTCCACACTGTGTACAGA	GGG	0.51816443		chr4	-1	7581742	3	FALSE
TTTTCCACACTGATTACACA	CAG	0.51406372	ENSG00000198131	chr19	-1	58261673	3	FALSE
GTCTCCTCACTGAGTACCCA	GGG	0.506643053		chr20	-1	59381089	3	FALSE
CAGTCCAGACTGAGAACACA	AAG	0.50515873		chr2	1	30924911	4	FALSE
TGGTTCACACTGAGGACACA	CAG	0.489615385		chr2	1	1373795	4	FALSE
ATGAACACACTGAGCACACA	TGG	0.479773869	ENSG00000231508	chr10	1	97393296	4	FALSE
GTCACCCCACTGAGTAAACA	GAG	0.473672978		chr10	1	49351882	4	FALSE
GTGTTCCACTGTGTACAAA	CAG	0.446280347		chr3	-1	168181081	3	FALSE
GTGTACAGACTGACTACACA	CAG	0.443035994		chr20	-1	15444572	3	FALSE
GTTTGCACACAAAGTACACA	CAG	0.437971408		chr10	1	63488170	4	FALSE
GTGTACACAATGATTACACA	AGG	0.40803615		chr8	1	113125227	3	FALSE
CTGTCCAGGCTGTGTACACA	CAG	0.399231309		chr16	-1	80654292	4	FALSE
CTCTCCACTGAGTAGACC	TGG	0.394359707		chr1	-1	175504570	4	FALSE
GTTTCAACAGTGAAGTACACA	GGG	0.390436322		chr5	1	179960628	4	FALSE
TTCTCCACTAAGTAAACA	GGG	0.38910025		chr2	1	34814827	4	FALSE
GTTTCCACAAGCAGTACACA	GAG	0.385757183		chr7	-1	21421854	4	FALSE
GTCTCCATCCTGAGTACAGA	GAG	0.361528006	ENSG00000151348	chr11	1	44124841	4	FALSE
GTGTACAGGCTGTGTACACA	AAG	0.35845875		chr11	-1	103603253	4	FALSE
GTGTGTTGCTGAGTACACA	GAG	0.347274102		chr16	1	10566772	4	FALSE
GTATCTTCACTGAGTACACT	AGG	0.33439929		chr5	-1	39906309	4	FALSE
TTGTCCACAGAGCGTACACA	GGG	0.333991947	ENSG00000197989	chr1	-1	28582390	4	FALSE
GTGACCACACTGGGCACACA	TGG	0.333435533		chr2	1	131536773	3	FALSE
GTGACCACACTGGGCACACA	TGG	0.333435533		chr2	1	131202725	3	FALSE
GTGACCACACTGGGCACACA	TGG	0.333435533		chr2	-1	130136194	3	FALSE
GTGTATGCACAGAGTACACA	CAG	0.330770661		chr10	-1	105461678	4	FALSE
GTGTACACTGTGTGTACACA	GGG	0.330140509		chr2	1	207287915	4	FALSE
GTATACACACTCGGTACACA	CAG	0.316975285		chr19	-1	46319193	4	FALSE
CTCTACACACTGAGTCCACA	CAG	0.316320157		chr14	1	94544044	4	FALSE
CTGTCAGCACTGAGTATACA	GGG	0.303074972		chr13	-1	23985245	4	FALSE

Off-target for AAVS1 sgRNA

Sequence	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target
GGGGCCACTAGGGACAGGAT	TGG		100	chr19	-1	55115755	0	TRUE
GGAGACATTAGGGACAGGAT	AAG	2.548843537		chr10	1	119439186	3	FALSE
GAGGGCTCTAGGGACAGGAT	GAG	1.765578231		chr9	-1	90086414	3	FALSE
GGCCCCACTAGGGACAGGAC	GAG	1.747668456		chr7	1	122844142	3	FALSE
GGGACCATCAGGGACAGGAT	GGG	1.579455782		chr6	1	36797704	3	FALSE
CAGGGCACTGGGGACAGGAT	CAG	1.45825		chr14	1	92970608	4	FALSE
GGGGCCAGTGGGGACAGGAG	CAG	1.286963492		chr11	1	2127694	3	FALSE
GGGGCCAGTGGGGACAGGAA	GGG	1.286963492		chr2	-1	231959836	3	FALSE
GGGGCCAATTAGGACAGGAT	GGG	1.240350575		chr13	1	105960580	3	FALSE
GGGGTCACTGGGGACAAGAT	TGG	1.188203704		chr15	-1	45535701	3	FALSE
TGGGCCACTATGGACAGGAA	TGG	1.102071429		chr12	-1	108187905	3	FALSE
GGGACCACTGGGCACAGGAT	CGG	1.059798592		chr15	-1	25222754	3	FALSE
GGGGATGCTAGGGACAGGAT	GAG	0.972872986		chr2	1	204531421	3	FALSE
ACTGCCTCTAGGGACAGGAT	AGG	0.971304808		chr15	-1	36995662	4	FALSE
AGTGCCAACAGGGACAGGAT	GGG	0.945468667		chr4	1	22172000	4	FALSE
TCGCCCACAGGGACAGGAT	CAG	0.934200644	ENSG00000140983	chr16	-1	668379	4	FALSE
GTGTCCAAGAGGGACAGGAT	GGG	0.92625		chr1	-1	154829128	4	FALSE
GCAGCCAGGAGGGACAGGAT	GGG	0.921121835		chr12	1	49891231	4	FALSE
GAGGGCAGCAGGGACAGGAT	GGG	0.918433544		chr12	1	131827329	4	FALSE
GGCCCCAAGAGGGACAGGAT	GAG	0.890545176		chr8	1	141604148	4	FALSE
GGTTCCAGCAGGGACAGGAT	CAG	0.890545176	ENSG00000113303	chr5	1	180947683	4	FALSE
GGAGCCAGTAGGGAGAGGAT	AGG	0.885487125		chr16	1	33884580	3	FALSE
GGAGCCAGTAGGGAGAGGAT	AGG	0.885487125		chr16	-1	32969375	3	FALSE
GTGGCCAGCTGGGACAGGAT	AGG	0.85307625		chr9	1	34350240	4	FALSE
GGAGGGAGTAGGGACAGGAT	GAG	0.839975543		chr11	1	113401727	4	FALSE
GGGGGAAGTAGTGACAGGAT	AGG	0.823222707		chr20	-1	43709929	3	FALSE
GAACCTACTAGGGACAGGAT	GAG	0.820516651		chr6	-1	157966901	4	FALSE
GAGGCCACAGGGACAGGCT	GGG	0.818083893		chr5	-1	170084415	3	FALSE
GGGCACAGTAGGGACAGGAA	GAG	0.811782787		chr8	-1	17472023	4	FALSE
GAGGCCAGTGGGGACAGGAC	AGG	0.790868822		chrX	-1	150758233	4	FALSE
GGGGATATTGGGGACAGGAT	TGG	0.79085371		chr4	-1	47212824	4	FALSE
GGAGGCACTGGTGACAGGAT	GAG	0.720218458	ENSG00000223995	chrX	-1	128838711	4	FALSE
GGGGACAGTGGGGACAGGAG	GGG	0.716336682		chr8	-1	608459	4	FALSE
GGTGCCACTAGGCACAGGAG	CGG	0.676347693		chr8	1	143802967	3	FALSE
GCGGCCAATGGGGACATGAT	GGG	0.661366001	ENSG00000063978	chr4	1	2469079	4	FALSE
GAGGACAGTAGGGACAGGTT	AAG	0.634004237		chr18	1	8749311	4	FALSE
CAGGCCCTAGGGACAGGAG	CAG	0.630210675		chr10	1	48519097	4	FALSE
GCAGCCCCAAGGGACAGGAT	GGG	0.623771948	ENSG00000166126	chr14	-1	102932045	4	FALSE
AGGGGCACTGGGGACAGGCT	TGG	0.618883046	ENSG00000126461	chr19	-1	49658572	4	FALSE
GCTGCCACTGGGTACAGGAT	CAG	0.610728971		chr9	-1	89227532	4	FALSE
AGGGCCCTTATGGACAGGAT	GGG	0.605569086	ENSG00000174951	chr19	-1	48749680	4	FALSE
TGGGCCAGTGGGGACAGGGT	GGG	0.597418895		chr2	-1	121052619	4	FALSE
GGGGCTTCTAAGGACAGGAT	GGG	0.592837031		chr19	-1	16064183	3	FALSE
GAGGGCCCTAGGGACAGGAG	AGG	0.58649664		chr12	-1	125092753	4	FALSE
GGTGGCTCTAGGGACAGGAA	GAG	0.558901809		chr3	1	46366887	4	FALSE
GAGGCCGCTGGGGACAGGAC	GGG	0.546481106		chr16	-1	715574	4	FALSE
GGGCCCTATAGGGACAGGAA	AGG	0.542587801		chr3	-1	48569139	4	FALSE
GGTGCCACCAGGGAGAGGAT	GGG	0.541032634		chr22	-1	44303224	3	FALSE
GGAGCCACCAGGGAAAGGAT	GAG	0.541032634		chr13	-1	99628492	3	FALSE
ATGGCCACTAAGGACAGGAA	AGG	0.538880515		chr12	1	107092504	4	FALSE