

Comparison of BREAKING-CAS with MIT CRISPR FINDER

Species: **Mouse**

Query sequence:

>mouse Tyr exon 1 (210 bp)

**ATGTTCTTGGCTGTTTTGTATTGCCTTCTGTGGAGTTTCCAGATCTCTGATGG
CCATTTTCCTCGAGCCTGTGCCTCCTCTAAGAACTTGTTGGCAAAGAATGC
TGCCACCATGGATGGGTGATGGGAGTCCCTGCGGCCAGCTTTCAGGCAGA
GGTTCCTGCCAGGATATCCTTCTGTCCAGTGCACCATCTGGACCTCAGTTCCCC**

PAM sequence: **NGG**

PAM location: **3'**

Guide length: **20 nt**

mouse Tyr exon 1 (210 bp)

Mus musculus (house mouse, mouse)

Analysis Settings:

-Genome (FASTA)=Mus_musculus.GRCm38.dna.toplevel.MAIN_CHRS.fa
 -Genome (GTF)=Mus_musculus.GRCm38.84.MAIN_CHRS.gtf
 -PAM='NGG'
 -PAM Position=3'
 -Oligo Size=20
 -Positional Weights (1 to 20)=0|0|0.014|0|0|0.395|0.317|0|0.389|0.079|0.445|0.508|0.613|0.851|0.732|0.828|0.615|0.804|0.685|0.583

Filter boxes [?](#) [Export Oligos](#) (text-tabulated format)

START↓	END↓	STRAND↓	OLIGO↓	ONTARGETS↓	OFFTARGETS↓	GENES↓	SCORE↓
136	155	-	CTGCCTGAAAGCTGGCCGCA GGG	1	128	85	83.8
175	194	+	CTTCTGTCCAGTGCACCAT TGG	1	123	88	83.3
137	156	-	TCTGCCTGAAAGCTGGCCG CAGG	1	125	81	82.7
185	204	-	CTGAGGTCAGATGGTGCAC TGG	1	132	90	82.3
168	187	-	CACTGGACAGAAGGATATCC TGG	1	168	101	79.7
77	96	-	TGCCAACAAAGTTCTTAGAGG AGG	1	133	78	77.5
42	61	-	GAAAATGGCCATCAGAGAT TGG	1	161	81	77.1
57	76	-	AGGCACAGGCTCGAGGAA ATGG	1	175	118	75.9
72	91	+	TGCCCTCTAAGAACTTGT TGG	1	159	83	75.4
107	126	+	GCCACCATGGATGGGTG ATGGG	1	124	53	75.3
100	119	+	GAATGCTGCCACCATGG ATGGG	1	138	74	74.8
80	99	-	TTTT GCCAACAAGTCTTAGAG G	1	143	62	74.6
144	163	-	AGGAACCTCTGCCTGAAAG CTGG	1	163	102	74.5
147	166	+	TTCAGGCAGAGGTTCTGC CAGG	1	185	103	74.1
164	183	-	GGACAGAAGGATATCCTG GCAGG	1	176	120	74
130	149	+	AGTCCCTGCGCCAGCTT TCAGG	1	123	86	73.8
115	134	-	GGACTCCATCACCCATC CATGG	1	127	87	72.6
64	83	-	TTAGAGGAGGCACAGG CTGAGG	1	201	131	70.5
106	125	+	TGCCACCATGGATGGGT ATGG	1	174	99	69.2
111	130	-	TCCCATCACCCATCC ATGGTGGG	1	171	89	69.1
112	131	-	CTCCCATCACCCATC ATGGTGG	1	191	123	69
71	90	-	CAAGTTCTTAGAGGAGG CACAGG	1	240	123	67.2
136	155	+	TGCGGCCAGCTTTCAGG CAGAGG	1	155	103	66.8
118	137	+	ATGGGTGATGGGAGTCC CTCGG	1	190	105	64.9
95	114	+	CAAAGAATGCTGCC ACCATGG	1	194	116	63.6
27	46	-	AGATCTGAAACTCCAC AGAAGG	1	240	133	55.3
177	196	-	CAGATGGTGCAC TGGACAGAAGG	1	277	181	54.3
11	30	+	CTG TTTT GTATTGCCT TCTGTGG	1	385	193	54
99	118	+	AGAATGCTGCC ACCATGGATGG	1	235	133	53.5
31	50	+	TGGAGTTTCAGATC TCTGATGG	1	351	172	49.7

CTGCCTGAAAGCTGGCCGCA(GGG)

[Export Targets](#) (text-tabulated format)

100 7:87493196-87493218(+)
 ENSMUSG0000004651 (Tyr): 23 nts overlap

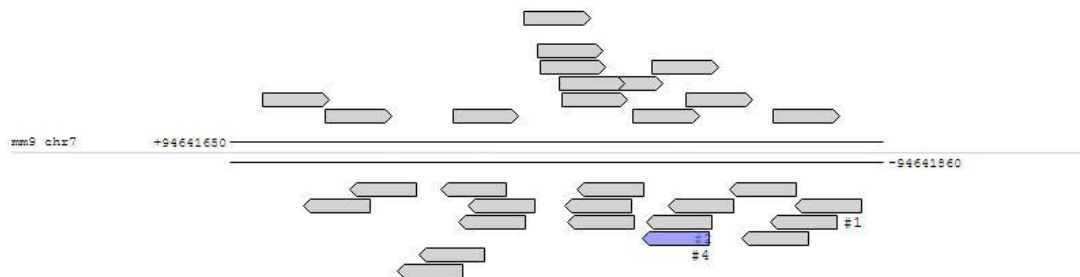
2.3 7:136601377-136601399(-)
 *** Intergenic ***

0.8 11:102724060-102724082(+)
 *** Intergenic ***

"Lluis Montoliu"

Spacers

Interactive results: mouse over a guide or explore below for details



all guides

scored by inverse likelihood of offtarget binding
 mouse over for details ... [show legend](#)

	score	sequence	
Guide #1	77	CTGAGGTCCAGATGGTGCAC	TGG
Guide #2	76	TCTGCCTGAAAGCTGGCCGC	AGG
Guide #3	76	GCCCACCATGGATGGGTGAT	GGG
Guide #4	73	CTGCCTGAAAGCTGGCCGCA	GGG
Guide #5	72	GAATGCTGCCACCATGGAT	GGG
Guide #6	71	CTTCTGTCCAGTGCACCATC	TGG
Guide #7	70	TGCCACCATGGATGGGTGA	TGG
Guide #8	69	TGCCTCCTCTAAGAACTTGT	TGG
Guide #9	69	CACTGGACAGAAGGATATCC	TGG
Guide #10	68	TTAGAGGAGGCACAGGCTCG	AGG
Guide #11	68	TGCCAACAAAGTTCTTAGAGG	AGG
Guide #12	68	TCCCATCACCATCCATGGT	GGG
Guide #13	66	CTCCCATCACCATCCATGG	TGG
Guide #14	64	TTTTGCCAACAAAGTTCTTAG	AGG
Guide #15	63	TGCGGCCAGCTTTCAGGCAG	AGG
Guide #16	63	GGACAGAAGGATATCCTGSC	AGG
Guide #17	62	GAAATATGGCCATCAGAGATC	TGG
Guide #18	61	AGTCCTTGCGCCAGCTTTC	AGG

guide #4 quality score: 73

guide sequence: CTGCCTGAAAGCTGGCCGCA GGG
 on-target locus: chr7:-94641782
 number of offtarget sites: 229 (24 are in genes)

top 20 genome-wide off-target sites show all exonic

sequence	score	mismatches	UCSC gene	locus
GTCCCTGAAAGCTGGCTGCAAAG	1.3	3MMs [1:3:17]		chrX:-135679050
CTTCATGGCAGCTGGCCGCAGGG	0.8	4MMs [3:5:8:9]		chr14:+29349169
CTACTTGGCAGCTGGCCGCAGGG	0.8	4MMs [3:5:8:9]		chr11:+102585372
TGCCCAGAAAGCTGGCCGCAGAG	0.8	4MMs [1:2:3:6]		chr15:+93343392
CTGTCCGGATGCTGGCCGCACAG	0.8	4MMs [4:6:8:10]		chr13:+103605462
CAGCTTGAAGACTGGCCGCAGAG	0.7	4MMs [2:5:10:11]		chr14:+65437075
CTATCTGCAAGCTGGCCGCCAG	0.7	4MMs [3:4:8:20]		chr8:+120998629
CTGCCAGGAAGCTGGCAGCACAG	0.7	3MMs [6:8:17]		chr15:+83365454
CTGGCTGGATGGTGGCCGCAAAG	0.6	4MMs [4:8:10:12]	NM_029930	chr6:-42629140
CCCTCTGAAAGCTGGCAGCAGAG	0.6	4MMs [2:3:4:17]		chr14:-31513008
TTGCAGTAAAGCTGGCCGCAGAG	0.6	4MMs [1:5:6:7]		chr11:-114621273
CAGGCTGAAGGCTGGCCGCAGAG	0.6	4MMs [2:4:10:17]		chr8:-127838725
CTTCCTGCAGGCTGGCAGCACAG	0.5	4MMs [3:8:10:17]		chr17:+30505775
ATGCCCGGCAGCTGGCCGCAGGG	0.5	4MMs [1:6:8:9]		chr4:+132611438
CTGCCTTGCTGCTGGCCGCAGAG	0.5	4MMs [7:8:9:10]		chr2:-168430232
CTGGTTGCAAGCTGCCCGCAAGG	0.4	4MMs [4:5:8:15]		chr2:-69882811

Comparing suggested guides

Guide sequence	Breaking-Cas SCORE	Breaking-Cas POSITION	CRISPR-MIT SCORE	CRISPR-MT POSITION
CTGCCTGAAAGCTGGCCGCA	83.8	1	73	4
CTTCTGTCCAGTGCACCATC	83.3	2	71	6
TCTGCCTGAAAGCTGGCCGC	82.7	3	76	2
CTGAGGTCCAGATGGTGCAC	82.3	4	77	1
CACTGGACAGAAGGATATCC	79.7	5	69	9
TGCCAACAAGTTCTTAGAGG	77.5	6	68	11
GAAAATGGCCATCAGAGATC	77.1	7	62	17
AGGCACAGGCTCGAGGAAAA	75.9	8	60	22
TGCCTCCTCTAAGAACTTGT	75.4	9	69	8
GCCCACCATGGATGGGTGAT	75.3	10	76	3



All these MIT guides in “green” zone