Supplementary information for: Effective CRISPR interference of an endogenous gene via a single transgene in mice

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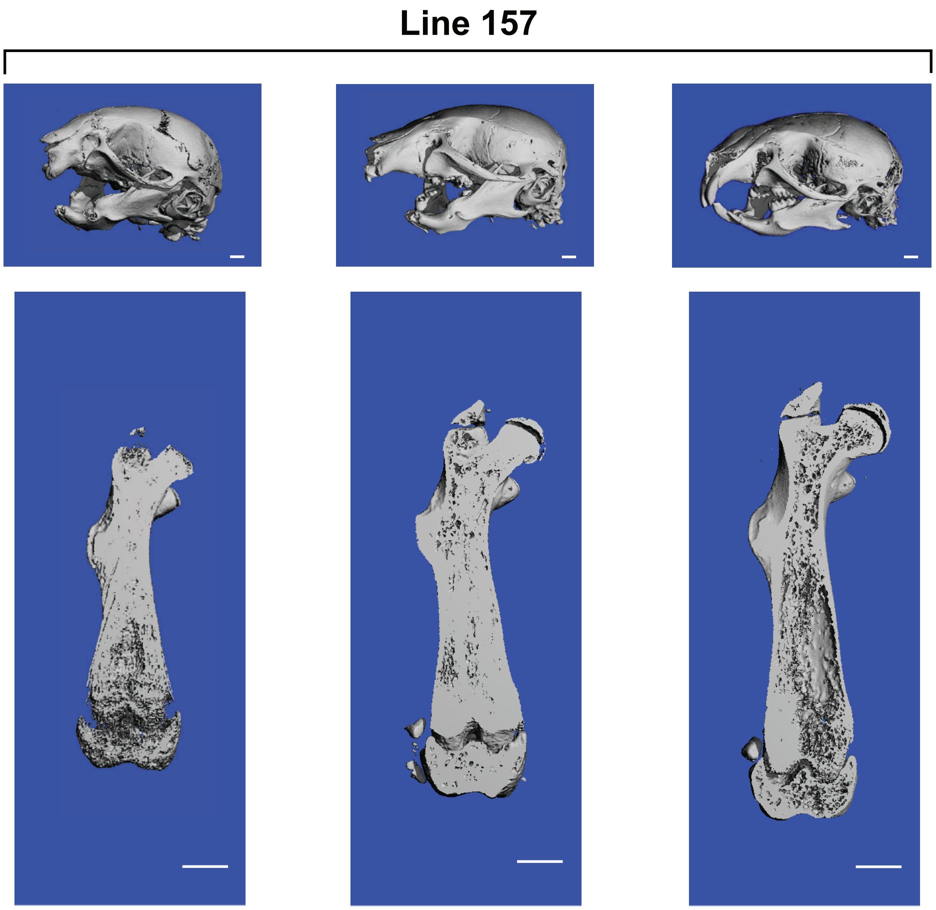
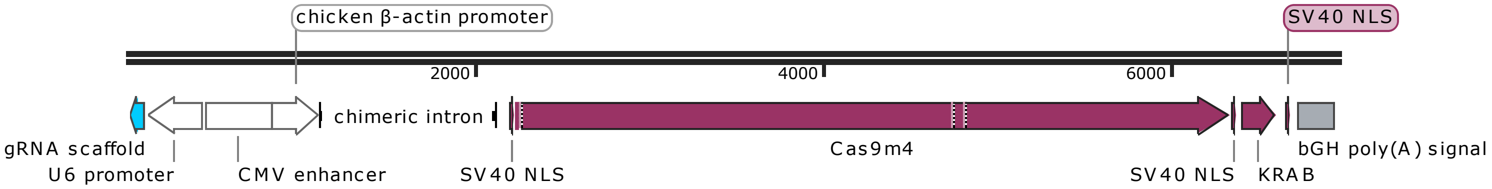


Supplementary Figure S1. Animal-to-animal variance within lines of CRISPRi mice. Micro-CT generated images of skulls and femurs of three different transgenic mice from line 157.

Supplementary Figure S1

Supplementary Figure S2. Diagram and annotated sequence of CRISPRi transgene.



CAG-sg4 Transgene
6968 bp

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                                    gRNA scaffold

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    gRNA scaffold                                               U6 promoter

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                                        U6 promoter

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                                        U6 promoter

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                                        U6 promoter

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                  U6 promoter                                   CMV enhancer

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                CMV enhancer                      chicken β-actin promoter
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chicken β-actin promoter

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chicken β-actin promoter

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chicken β-actin promoter    chimeric intron

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chimeric intron

cccacaggtgagcgggcgggacggcccttctcctccgggctgtaattagcgcttggtttaatgacggcttgtttcttttc    1280
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chimeric intron

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chimeric intron
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                                                 Pro Lys Lys Lys Arg Lys Val Gly Arg
                                                 SV40 NLS

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Cas9m4

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Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile Gly Ala Leu Leu Phe
Cas9m4

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Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile
Cas9m4

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Cas9m4
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Cas9m4 >
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Cas9m4 >
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Cas9m4 >
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Cas9m4 >
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Cas9m4 >
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Cas9m4 >
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320 325 330 335 340 345
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Cas9m4

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Cas9m4

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Cas9m4

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Cas9m4

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Cas9m4

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Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu

Cas9m4

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Cas9m4

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Cas9m4

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Cas9m4

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Cas9m4

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Phe Asn Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu
Cas9m4

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Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr
Cas9m4

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Cas9m4

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Ile Asn Gly Ile Arg Asp Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala Asn Arg Asn Phe
Cas9m4

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Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser
Cas9m4

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Leu His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu
Cas9m4
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Cas9m4

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     775          780          785          790          795
Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His
Cas9m4

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800          805          810          815          820          825
Pro Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu Gln Asn Gly Arg Asp Met Tyr Val Asp Gln
Cas9m4

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Cas9m4

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Asn Lys Val Leu Thr Arg Ser Asp Lys Ala Arg Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met
Cas9m4

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Lys Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly
Cas9m4

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Cas9m4

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Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys
Cas9m4
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Cas9m4
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CGGATGGACTTACGTCACCATCCGTGACGTGAATAGTTTTTTATAGGGTTCGAACTTAGACTTAAACAAATGCCTCTGAT
            990                 995                 1000                1005                1010
Ala Tyr Leu Asn Ala Val Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe Val Tyr Gly Asp Tyr
Cas9m4
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TAAAGTGTACGATGTTAGGAAAATGATCGCAAAGTCTGAGCAGGAAATAGGCAAGGCCACCGCTAAGTACTTCTTTTACA    5360
ATTTCACATGCTACAATCCTTTTACTAGCGTTTCAGACTCGTCCTTTATCCGTTCCGGTGGCGATTCATGAAGAAAATGT
    1015                1020                1025                1030                1035
Lys Val Tyr Asp Val Arg Lys Met Ile Ala Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr
Cas9m4
```

```
GCAATATTATGAATTTTTTCAAGACCGAGATTACACTGGCCAATGGAGAGATTCGGAAGCGACCACTTATCGAAACAAAC    5440
CGTTATAATACTTAAAAAAGTTCTGGCTCTAATGTGACCGGTTACCTCTCTAAGCCTTCGCTGGTGAATAGCTTTGTTTG
1040             1045                1050                1055                1060                1065
Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn
Cas9m4
```

```
GGAGAAACAGGAGAAATCGTGTGGGACAAGGGTAGGGATTTCGCGACAGTCCGGAAGGTCCTGTCCATGCCGCAGGTGAA    5520
CCTCTTTGTCCTCTTTAGCACACCCTGTTCCCATCCCTAAAGCGCTGTCAGGCCTTCCAGGACAGGTACGGCGTCCACTT
            1070                1075                1080                1085                1090
Gly Glu Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val Leu Ser Met Pro Gln Val Asn
Cas9m4
```

```
CATCGTTAAAAAGACCGAAGTACAGACCGGAGGCTTCTCCAAGGAAAGTATCCTCCCGAAAAGGAACAGCGACAAGCTGA    5600
GTAGCAATTTTTCTGGCTTCATGTCTGGCCTCCGAAGAGGTTCCTTTCATAGGAGGGCTTTTCCTTGTCGCTGTTCGACT
    1095                1100                1105                1110                1115
Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu
Cas9m4
```

```
TCGCACGCAAAAAAGATTGGGACCCCAAGAAATACGGCGGATTCGATTCTCCTACAGTCGCTTACAGTGTACTGGTTGTG    5680
AGCGTGCGTTTTTTCTAACCCTGGGGTTCTTTATGCCGCCTAAGCTAAGAGGATGTCAGCGAATGTCACATGACCAACAC
1120             1125                1130                1135                1140                1145
Ile Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val Leu Val Val
Cas9m4
```

```
GCCAAAGTGGAGAAAGGGAAGTCTAAAAAACTCAAAAGCGTCAAGGAACTGCTGGGCATCACAATCATGGAGCGATCAAG    5760
CGGTTTCACCTCTTTCCCTTCAGATTTTTTGAGTTTTCGCAGTTCCTTGACGACCCGTAGTGTTAGTACCTCGCTAGTTC
            1150                1155                1160                1165                1170
Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
Cas9m4
```

```
CTTCGAAAAAAACCCCATCGACTTTCTCGAGGCGAAAGGATATAAAGAGGTCAAAAAAGACCTCATCATTAAGCTTCCCA   5840
GAAGCTTTTTTTGGGGTAGCTGAAAGAGCTCCGCTTTCCTATATTTCTCCAGTTTTTTCTGGAGTAGTAATTCGAAGGGT
   1175       1180       1185       1190       1195
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro
Cas9m4

AGTACTCTCTCTTTGAGCTTGAAAACGGCCGGAAACGAATGCTCGCTAGTGCGGGCGAGCTGCAGAAAGGTAACGAGCTG   5920
TCATGAGAGAGAAACTCGAACTTTTGCCGGCCTTTGCTTACGAGCGATCACGCCCGCTCGACGTCTTTCCATTGCTCGAC
1200       1205       1210       1215       1220       1225
Lys Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu
Cas9m4

GCACTGCCCTCTAAATACGTTAATTTCTTGTATCTGGCCAGCCACTATGAAAAGCTCAAAGGGTCTCCCGAAGATAATGA   6000
CGTGACGGGAGATTTATGCAATTAAAGAACATAGACCGGTCGGTGATACTTTTCGAGTTTCCCAGAGGGCTTCTATTACT
         1230       1235       1240       1245       1250
Ala Leu Pro Ser Lys Tyr Val Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser Pro Glu Asp Asn Glu
Cas9m4

GCAGAAGCAGCTGTTCGTGGAACAACACAAACACTACCTTGATGAGATCATCGAGCAAATAAGCGAATTCTCCAAAAGAG   6080
CGTCTTCGTCGACAAGCACCTTGTTGTGTTTGTGATGGAACTACTCTAGTAGCTCGTTTATTCGCTTAAGAGGTTTTCTC
   1255       1260       1265       1270       1275
Gln Lys Gln Leu Phe Val Glu Gln His Lys His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys Arg
Cas9m4

TGATCCTCGCCGACGCTAACCTCGATAAGGTGCTTTCTGCTTACAATAAGCACAGGGATAAGCCCATCAGGGAGCAGGCA   6160
ACTAGGAGCGGCTGCGATTGGAGCTATTCCACGAAAGACGAATGTTATTCGTGTCCCTATTCGGGTAGTCCCTCGTCCGT
1280       1285       1290       1295       1300       1305
Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala
Cas9m4

GAAAACATTATCCACTTGTTTACTCTGACCAACTTGGGCGCGCCTGCAGCCTTCAAGTACTTCGACACCACCATAGACAG   6240
CTTTTGTAATAGGTGAACAAATGAGACTGGTTGAACCCGCGCGGACGTCGGAAGTTCATGAAGCTGTGGTGGTATCTGTC
         1310       1315       1320       1325       1330
Glu Asn Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg
Cas9m4

AAAGCGGTACACCTCTACAAAGGAGGTCCTGGACGCCACACTGATTCATCAGTCAATTACGGGGCTCTATGAAACAAGAA   6320
TTTCGCCATGTGGAGATGTTTCCTCCAGGACCTGCGGTGTGACTAAGTAGTCAGTTAATGCCCCGAGATACTTTGTTCTT
   1335       1340       1345       1350       1355
Lys Arg Tyr Thr Ser Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr Arg
Cas9m4

TCGACCTCTCTCAGCTCGGTGGAGACAGCAGGGCTGACCCCAAGAAGAAGAGGAAGGTGGctagCGATGCTAAGTCACTG   6400
AGCTGGAGAGAGTCGAGCCACCTCTGTCGTCCCGACTGGGGTTCTTCTTCTCCTTCCACCgatcGCTACGATTCAGTGAC
1360       1365                                   130
Ile Asp Leu Ser Gln Leu Gly Gly Asp Ser Arg Ala Asp Pro Lys Lys Lys Arg Lys Val Ala Ser Asp Ala Lys Ser Leu
Cas9m4                                 SV40 NLS      (in frame with SV40 NLS)
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ACTGCCTGGTCCCGGACACTGGTGACCTTCAAGGATGTGTTTGTGGACTTCACCAGGGAGGAGTGGAAGCTGCTGGACAC
                                                                                      6480
TGACGGACCAGGGCCTGTGACCACTGGAAGTTCCTACACAAACACCTGAAGTGGTCCCTCCTCACCTTCGACGACCTGTG
                 15                  20                  25                  30
Thr Ala Trp Ser Arg Thr Leu Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp Thr
KRAB

TGCTCAGCAGATCCTGTACAGAAATGTGATGCTGGAGAACTATAAGAACCTGGTTTCCTTGGGTTATCAGCTTACTAAGC
                                                                                      6560
ACGAGTCGTCTAGGACATGTCTTTACACTACGACCTCTTGATATTCTTGGACCAAAGGAACCCAATAGTCGAATGATTCG
    35                  40                  45                  50                  55
Ala Gln Gln Ile Leu Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys
KRAB

CAGATGTGATCCTCCGGTTGGAGAAGGGAGAAGAGCCCTGGCTGGTGGAGAGAGAAATTCACCAAGAGACCCATCCTGAT
                                                                                      6640
GTCTACACTAGGAGGCCAACCTCTTCCCTCTTCTCGGGACCGACCACCTCTCTCTTTAAGTGGTTCTCTGGGTAGGACTA
60                  65                  70                  75
Pro Asp Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His Gln Glu Thr His Pro Asp
KRAB                                                            (in frame with KRAB)

TCAGAGACTGCATTTGAAATCAAATCATCAGTTCCGAAAAAGAAACGCAAAGttGctagCtgaTAAGaattcctagagct
                                                                                      6720
AGTCTCTGACGTAAACTTTAGTTTAGTAGTCAAGGCTTTTTCTTTGCGTTTCaaCgatcGactATTCttaaggatctcga
                                                      130
Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser Val Pro Lys Lys Lys Arg Lys Val Ala Ser *
(in frame with KRAB)                        SV40 NLS

cgctgatcagcctcgactgtgccttctagttgccagccatctgttgtttgcccctcccccgtgccttccttgaccctgga
                                                                                      6800
gcgactagtcggagctgacacggaagatcaacggtcggtagacaacaaacggggagggggcacggaaggaactgggacct
bGH poly(A) signal

aggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcattgtctgagtaggtgtcattctattctgg
                                                                                      6880
tccacggtgagggtgacaggaaaggattattttactcctttaacgtagcgtaacagactcatccacagtaagataagacc
bGH poly(A) signal

ggggtggggtggggcaggacagcaagggggaggattgggaagagaatagcaggcatgctggggagcggccAACgtacgca
                                                                                      6960
ccccaccccaccccgtcctgtcgttccccctcctaacccttctcttatcgtccgtacgacccctcgccggTTGcatgcgt
bGH poly(A) signal

GCggccGC     3′
                 6968
CGccggCG     5′
```

Supplementary Figure S3. DESKGEN on-target and off-target analysis of *Tnfsf11*-targeted sgRNAs.

Tnfsf11-sg1

Sequence	PAM	Exon	Activity	Off-target
GGAGGCCAGCTCTCTCCACG	AGG	P	73	14

Guide Details	
Cut site	chr14 [+78,308,081 : -78,308,081]
GC %	70
Activity	73
Off-target	14

OFF-TARGET ANALYSIS:

Mismatches	0	1	2	3	Total
Coding	0	0	0	0	0
Non-Coding	0	5	69	598	672

OFF-TARGET HITS:

Sequence	PAM	Similarity	Mism.	Gene	Locus
GGAGGCCAGCTCTCTCCAGG	TGG	32	19	No	chrX@ 108697291-108697314
GGAGGCCAGCTCTCTCCAGG	TGG	32	19	No	chrX@ 20108906-20108929
GGAGGCCAGCTCTCTCCAAG	TGG	32	19	No	chr18@ 39797402-39797425
GGAGGCCAGCTCTCTCCGCG	AGG	20	18	No	chr15@ 33061846-33061869
GGAGGCCAGCTCTCTCCCCG	TGG	20	18	No	chr9@ 9132446-9132469
GGAGACCAGCTCTCTCCACA	CAG	6	5,20	No	chr17@ 23435687-23435710
GGAGACCAGCTCTCTCCACT	CAG	6	5,20	No	chr17@ 23362771-23362794
GGAGTCCAGCTCTCTCCACA	CAG	6	5,20	No	chr9@ 62856165-62856188
GAAGGCCAGCTCTCTCCAGG	TGG	6	2,19	No	chrX@ 118850871-118850894
GGTGGCCAGCTCTCTCCAGG	AGG	5	3,19	No	chr15@ 61496638-61496661
GGGGGCCAGCTCTCTCCAGG	CAG	5	3,19	No	chr7@ 18083920-18083943
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chrX@ 132668125-132668148
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chrX@ 104331095-104331118
GGAGTCCAGCTCTCTCCAGG	TGG	4	5,19	No	chrX@ 115474805-115474828

Sequence	PAM	Similarity	Mism.	Gene	Locus
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chrX@ 162436757-162436780
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chrX@ 158080260-158080283
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chrX@ 16246963-16246986
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chrX@ 16111349-16111372
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr18@ 17560826-17560849
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr18@ 15374510-15374533
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr17@ 81258623-81258646
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr17@ 53050125-53050148
GGAGACCAGCTCTCTCCAGG	CGG	4	5,19	No	chr16@ 56141624-56141647
GGAGACCAGCTCTCTCCAGG	CGG	4	5,19	No	chr16@ 35876138-35876161
GGAGACCAGCTCTCTCCAGG	CGG	4	5,19	No	chr14@ 112135213-112135236
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chr14@ 8829035-8829058
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr12@ 109128063-109128086
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chr12@ 45247102-45247125
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr10@ 125469397-125469420
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr10@ 17187475-17187498
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr10@ 78766165-78766188
GGAGACCAGCTCTCTCCAGG	TAG	4	5,19	No	chr10@ 57550598-57550621
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr9@ 37973121-37973144
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr8@ 59557762-59557785
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr8@ 73742415-73742438
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr7@ 129906529-129906552
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr7@ 65184338-65184361
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr7@ 58282921-58282944
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr6@ 63225175-63225198
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr6@ 129766229-129766252
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr6@ 44688564-44688587
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr5@ 126675997-126676020
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chr5@ 87359227-87359250
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chr5@ 87300749-87300772
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr4@ 73184232-73184255
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr3@ 56335965-56335988
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr3@ 17915223-17915246
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr3@ 58954535-58954558
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr3@ 21256459-21256482
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr3@ 10502946-10502969
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr2@ 14357004-14357027
GGAGACCAGCTCTCTCCAGG	CGG	4	5,19	No	chr2@ 139465469-139465492
GGAGACCAGCTCTCTCCAGG	AAG	4	5,19	No	chr2@ 97696308-97696331
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr2@ 78767220-78767243
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr2@ 40385442-40385465
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr2@ 3549485-3549508
GGAGACCAGCTCTCTCCAGG	TGG	4	5,19	No	chr1@ 99078626-99078649

Sequence	PAM	Similarity	Mism.	Gene	Locus
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr1@ 97535487-97535510
GGAGACCAGCTCTCTCCAGG	AGG	4	5,19	No	chr1@ 153344611-153344634
GGAGACCAGCTCTCTCCAGG	CAG	4	5,19	No	chr1@ 12558470-12558493
GCCGGCCAGGTCTCTCCACG	GAG	2	2,3,10	No	chr4@ 149307232-149307255
TGCAGCCAGCTCTCTCCACG	AGG	2	1,3,4	No	chr3@ 122455163-122455186
GGAGGCCAGTTCTCTCCAGG	AGG	2	10,19	No	chrX@ 20978967-20978990
GGAGGCCAGTTCTCTCCAGG	AGG	2	10,19	No	chrX@ 117739433-117739456
GGAGACCAGCTCTCTCCGCG	CAG	2	5,18	No	chr18@ 21487921-21487944
GGAGACCAGCTCTCTCCTCG	TAG	2	5,18	No	chr9@ 6834090-6834113
GGAGACCAGCTCTCTCCTCG	GGG	2	5,18	No	chr3@ 115174342-115174365
GGTGTCCATCTCTCTCCACG	TGG	2	3,5,9	No	chr3@ 32720611-32720634
AGAAGTCAGCTCTCTCCACG	GAG	2	1,4,6	No	chr2@ 162607400-162607423
GGTGGCCAGATCTCTCCACA	GAG	1	3,10,20	No	chr1@ 75651902-75651925
GCAGGCCAGGTTTCTCCACG	GGG	1	2,10,12	No	chr10@ 74973355-74973378
TGAGACCAGCTCTCTCCAGG	CAG	1	1,5,19	No	chrX@ 168984830-168984853
AGAGACCAGCTCTCTCCAGG	CAG	1	1,5,19	No	chr9@ 9367591-9367614
CGAGACCAGCTCTCTCCAAG	TAG	1	1,5,19	No	chr9@ 36156455-36156478
AGAGACCAGCTCTCTCCAGG	TGG	1	1,5,19	No	chr5@ 86223214-86223237
AGAGACCAGCTCTCTCCAGG	AGG	1	1,5,19	No	chr5@ 39209800-39209823
TGAGCCCAGCTCTCTCCAGG	TGG	1	1,5,19	No	chr3@ 128026647-128026670
GGAGGCCAGCTGTCTCCAGG	CAG	1	12,19	No	chr10@ 30324091-30324114
GGAGGCCAGCTTTCTCCAAG	TGG	1	12,19	No	chr3@ 16784007-16784030
GAAGACCAGCTCTCTCCAGG	GAG	1	2,5,19	No	chr8@ 62433436-62433459
GAAGACCAGCTCTCTCCAGG	TAG	1	2,5,19	No	chr8@ 65240531-65240554
GGTGACCAGCTCTCTCCAAG	CGG	1	3,5,19	No	chr4@ 21595857-21595880
GGTGACCAGCTCTCTCCAGG	TGG	1	3,5,19	No	chr2@ 55899886-55899909
GGAAACCAGCTCTCTCCAAG	TAG	1	4,5,19	No	chr19@ 19374333-19374356
GGAAACCAGCTCTCTCCAGG	CAG	1	4,5,19	No	chr17@ 53050344-53050367
GGAAACCAGCTCTCTCCAGG	AGG	1	4,5,19	No	chr16@ 45505898-45505921
GGAAACCAGCTCTCTCCAGG	CAG	1	4,5,19	No	chr15@ 17733445-17733468
GGAAACCAGCTCTCTCCAGG	CAG	1	4,5,19	No	chr12@ 4324463-4324486
GGAGACCCGCTCTCTCCAGG	TGG	1	5,8,19	No	chrX@ 140785952-140785975
GGAGACCTGCTCTCTCCAGG	CAG	1	5,8,19	No	chr18@ 31098351-31098374
GGAGACCTGCTCTCTCCAGG	AGG	1	5,8,19	No	chr17@ 54034089-54034112
GGAGACCTGCTCTCTCCAGG	CAG	1	5,8,19	No	chr16@ 60071452-60071475
GGAGACCTGCTCTCTCCAGG	TGG	1	5,8,19	No	chr14@ 36417759-36417782
GGAGACCTGCTCTCTCCATG	CAG	1	5,8,19	No	chr3@ 44087956-44087979
GGAGGCAAGCTCTCTGCACG	TGG	1	7,16	No	chr15@ 100587086-100587109
AGAGGCCAACTCTCTCCACT	GAG	1	1,9,20	No	chr3@ 52257491-52257514
GGAGACTAGCTCTCTCCACT	GAG	1	5,7,20	No	chr7@ 62494843-62494866
GGAGACTAGCTCTCTCCACT	GAG	1	5,7,20	No	chr4@ 25357948-25357971
GGAGACTAGCTCTCTCCACT	GAG	1	5,7,20	No	chr3@ 4114639-4114662
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chrX@ 89780376-89780399

Sequence	PAM	Similarity	Mism.	Gene	Locus
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chrX@ 46929236-46929259
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chrX@ 109208577-109208600
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chrX@ 115820033-115820056
GGAGACCAGTTCTCTCCAAG	AGG	1	5,10,19	No	chrX@ 137220364-137220387
GGAGACCAGTTCTCTCCAGG	TGG	1	5,10,19	No	chr19@ 9795872-9795895
GGAGACCAGGTCTCTCCAGG	TGG	1	5,10,19	No	chr18@ 16849295-16849318
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr18@ 58746595-58746618
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr18@ 33126397-33126420
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr18@ 37470174-37470197
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr18@ 81780362-81780385
GGAGACCAGTTCTCTCCATG	TGG	1	5,10,19	No	chr18@ 44163004-44163027
GGAGACCAGTTCTCTCCATG	AGG	1	5,10,19	No	chr17@ 42680247-42680270
GGAGACCAGTTCTCTCCATG	AGG	1	5,10,19	No	chr16@ 14562339-14562362
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 65127167-65127190
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 90638819-90638842
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 14429112-14429135
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr16@ 47348780-47348803
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 44023929-44023952
GGAGACCAGGTCTCTCCAGG	CGG	1	5,10,19	No	chr16@ 15713440-15713463
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 9179674-9179697
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr16@ 37341680-37341703
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr14@ 38243427-38243450
GGAGACCAGATCTCTCCAGG	CAG	1	5,10,19	No	chr14@ 13713691-13713714
GGAGACCAGTTCTCTCCATG	AGG	1	5,10,19	No	chr13@ 82547471-82547494
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr13@ 11252799-11252822
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr12@ 29504143-29504166
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr12@ 70463955-70463978
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr12@ 78629466-78629489
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr12@ 97573977-97574000
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr12@ 70381198-70381221
GGAGACCAGTTCTCTCCAGG	TGG	1	5,10,19	No	chr12@ 28264762-28264785
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr11@ 29437206-29437229
GGAGACCAGTTCTCTCCATG	AGG	1	5,10,19	No	chr11@ 18659856-18659879
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr11@ 40935581-40935604
GGAGACCAGGTCTCTCCATG	AAG	1	5,10,19	No	chr11@ 14954692-14954715
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr10@ 8163467-8163490
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr10@ 109235117-109235140
GGAGACCAGTTCTCTCCAGG	TGG	1	5,10,19	No	chr10@ 17187678-17187701
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr9@ 33737079-33737102
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr9@ 3989472-3989495
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr9@ 90468558-90468581
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr9@ 71987228-71987251
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GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr7@ 5281841-5281864
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr7@ 53761800-53761823
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr6@ 106934863-106934886
GGAGACCAGTTCTCTCCAGG	CAG	1	5,10,19	No	chr6@ 122260887-122260910
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr6@ 24805249-24805272
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GGAGACCAGTTCTCTCCAAG	TGG	1	5,10,19	No	chr5@ 7094456-7094479
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GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr4@ 61550975-61550998
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr4@ 60694051-60694074
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr4@ 61468936-61468959
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GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr4@ 60728036-60728059
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GGAGACCAGTTCTCTCCAGG	CAG	1	5,10,19	No	chr4@ 6099047-6099070
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GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr4@ 60567099-60567122
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr4@ 61213163-61213186
GGAGACCAGATCTCTCCATG	AGG	1	5,10,19	No	chr3@ 134151759-134151782
GGAGACCAGATCTCTCCAGG	CAG	1	5,10,19	No	chr3@ 4811857-4811880
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr3@ 126175718-126175741

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GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr3@ 26868466-26868489
GGAGACCAGTTCTCTCCATG	AGG	1	5,10,19	No	chr3@ 37100399-37100422
GGAGACCAGGTCTCTCCAAG	AGG	1	5,10,19	No	chr2@ 47779375-47779398
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr2@ 23934305-23934328
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GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr1@ 97428908-97428931
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr1@ 60965911-60965934
GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr1@ 30460014-30460037
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GGAGACCAGTTCTCTCCAGG	AGG	1	5,10,19	No	chr1@ 138313954-138313977
GGAGACCAGTTCTCTCCAGG	AAG	1	5,10,19	No	chr1@ 150879970-150879993
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GGAAGCCAGCCTTCTCCACG	TAG	1	4,11,12	No	chr3@ 9326204-9326227
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GGAGACTAGCTCTCTCCAGG	CGG	1	5,7,19	No	chr17@ 80591622-80591645
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GGAGACTAGCTCTCTCCAGG	CAG	1	5,7,19	No	chr10@ 53135537-53135560
GGAGACTAGCTCTCTCCAGG	CAG	1	5,7,19	No	chr6@ 14544131-14544154
GGAGACTAGCTCTCTCCAGG	TGG	1	5,7,19	No	chr1@ 3189390-3189413
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GGAGACCATCTCTCTCCAAG	TGG	1	5,9,19	No	chr7@ 13105394-13105417
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GGAGAACAGCTCTCTCCAGG	CAG	1	5,6,19	No	chr13@ 81212528-81212551
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GGAGAGCAGCTCTCTCCAAG	TGG	1	5,6,19	No	chr11@ 18100814-18100837
GGAGATCAGCTCTCTCCAAG	CAG	1	5,6,19	No	chr10@ 19058379-19058402
GGAGGCAAGGTCTCTCCATG	TAG	1	7,10,19	No	chr18@ 77053921-77053944
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GGAGACCAGCTGTCTCCAGG	AAG	0	5,12,19	No	chr19@ 11437379-11437402
GGAGACCAGCTTTCTCCAGG	CAG	0	5,12,19	No	chr15@ 5626736-5626759
GGAGACCAGCTTTCTCCAGG	TGG	0	5,12,19	No	chr12@ 33529852-33529875
GGAGACCAGCTGTCTCCAGG	CAG	0	5,12,19	No	chr12@ 74960697-74960720
GGAGACCAGCTTTCTCCAGG	TGG	0	5,12,19	No	chr11@ 99975672-99975695
GGAGACCAGCTGTCTCCATG	TGG	0	5,12,19	No	chr4@ 12209796-12209819
GGAGACCAGCTATCTCCAGG	GGG	0	5,12,19	No	chr4@ 17397847-17397870
GGAGACCAGCTGTCTCCAGG	TGG	0	5,12,19	No	chr3@ 9386462-9386485
GGAGACCAGCTCTCTCCAGA	AGG	0	5,19,20	No	chr15@ 48874169-48874192
GGAGACCAGCTCTCTCCAGA	CAG	0	5,19,20	No	chr13@ 79852067-79852090
GGAGACCAGCTCTCTCCAGT	AGG	0	5,19,20	No	chr13@ 84143776-84143799
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GGAGACCAGCTCTCTCCAGA	CAG	0	5,19,20	No	chr11@ 19125885-19125908
GGAGACCAGCTCTCTCCAGA	CAG	0	5,19,20	No	chr9@ 36454737-36454760
GGAGACCAGCTCTCTCCAGA	TAG	0	5,19,20	No	chr2@ 49230167-49230190
GGAGGCCAGTTTTCTCCAGG	AGG	0	10,12,19	No	chr9@ 8532588-8532611
GGAGGCCAGTTTTCTCCAGG	AGG	0	10,12,19	No	chr2@ 23420508-23420531
GGAGACCAGCTCTCTCTAGG	CAG	0	5,17,19	No	chrX@ 160751952-160751975
GGAGACCAGCTCTCTCTAGG	CAG	0	5,17,19	No	chrX@ 158080467-158080490
GGAGACCAGCTCTCTCTAAG	CAG	0	5,17,19	No	chr17@ 54865520-54865543
GGAGACCAGCTCTCTCAAGG	TGG	0	5,17,19	No	chr3@ 72132813-72132836
GGAGACCAGCTCTCTCTAGG	TAG	0	5,17,19	No	chr2@ 39633461-39633484
GGAGACCAGCTCTCTCTAGG	TGG	0	5,17,19	No	chr1@ 113834491-113834514
GGAGACCAGCTCTCTCTAGG	CAG	0	5,17,19	No	chr1@ 99175859-99175882
GGAGTCCAACTCTCTCCTCG	TGG	0	5,9,18	No	chr17@ 91345646-91345669
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GGAGGCCAGCTCTCTCCCAG	TGG	0	18,19	No	chr1@ 5630490-5630513
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GGAGACCAGCTCTCCCCAGG	AAG	0	5,15,19	No	chr11@ 10737105-10737128
GGAGACCAGCTCTCCCCAAG	CAG	0	5,15,19	No	chr9@ 3667331-3667354
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chrX@ 40027631-40027654
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chrX@ 24373068-24373091
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GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr17@ 41676952-41676975
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GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr6@ 61482264-61482287
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr5@ 14552258-14552281
GGAGACCAGCTCTCTCCTCA	TGG	0	5,18,20	No	chr5@ 5919297-5919320
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr4@ 29359308-29359331
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr4@ 13680420-13680443
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GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr3@ 41786597-41786620
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr2@ 10952649-10952672
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr2@ 5275979-5276002
GGAGACCAGCTCTCTCCTCT	GAG	0	5,18,20	No	chr1@ 107233146-107233169
GGAGGCTAGCTGTCACCACG	GGG	0	7,12,15	No	chr19@ 32726447-32726470
GGAGACCAGCTCACTCCCCG	TGG	0	5,13,18	No	chr16@ 15921746-15921769
AGAGGCCAGCTCTCTCCTGG	TGG	0	1,18,19	No	chrX@ 38840120-38840143
TGAGGCCAGCTCTCTCCTAG	CAG	0	1,18,19	No	chr14@ 107171340-107171363
GGAAGCCAGCTCTCTCCTGG	CAG	0	4,18,19	No	chrX@ 110974290-110974313
GGAAGCCAGCTCTCTCCCAG	TGG	0	4,18,19	No	chr18@ 39169211-39169234
GGAAGCCAGCTCTCTCCTGG	CAG	0	4,18,19	No	chr17@ 43290143-43290166
GGAGGCCAGCCCTCTCCAGA	GGG	0	11,19,20	No	chr17@ 84860919-84860942
GGAGGCCAGCACTCTCCAAA	CAG	0	11,19,20	No	chr17@ 52668262-52668285
GGAGACCAGCTCTCTCCCAG	CAG	0	5,18,19	No	chrX@ 104515425-104515448
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chrX@ 103048235-103048258
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chrX@ 71508862-71508885
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GGAGACCAGCTCTCTCCTGG	TAG	0	5,18,19	No	chrX@ 14091184-14091207
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GGAGACCAGCTCTCTCCCGG	AGG	0	5,18,19	No	chr18@ 14959871-14959894
GGAGACCAGCTCTCTCCCTG	TGG	0	5,18,19	No	chr18@ 14454726-14454749
GGAGACCAGCTCTCTCCTAG	CAG	0	5,18,19	No	chr18@ 33421439-33421462
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr18@ 9757563-9757586
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GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr18@ 79613577-79613600
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GGAGTCCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr16@ 71751401-71751424
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chr16@ 4245235-4245258
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GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr15@ 60358105-60358128
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GGAGACCAGCTCTCTCCTGG	AGG	0	5,18,19	No	chr11@ 30637254-30637277
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr11@ 21620283-21620306
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GGAGACCAGCTCTCTCCCAG	CAG	0	5,18,19	No	chr10@ 19305515-19305538
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chr10@ 26225496-26225519
GGAGACCAGCTCTCTCCTAG	CAG	0	5,18,19	No	chr10@ 8034987-8035010
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GGAGTCCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr8@ 79102629-79102652
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chr8@ 63402446-63402469
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr8@ 82606210-82606233
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr8@ 99140150-99140173
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr8@ 79814061-79814084
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GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr8@ 112526570-112526593
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GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr5@ 20505322-20505345
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr5@ 23157131-23157154
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GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr3@ 20346501-20346524
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GGAGACCAGCTCTCTCCTGG	TAG	0	5,18,19	No	chr1@ 103930379-103930402
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr1@ 15757515-15757538
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GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr1@ 47353386-47353409
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr1@ 55552544-55552567
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr1@ 16756203-16756226
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr1@ 54208112-54208135
GGAGACCAGCTCTCTCCTGG	AGG	0	5,18,19	No	chr1@ 16860570-16860593
GGAGACCAGCTCTCTCCCTG	TGG	0	5,18,19	No	chr1@ 47231303-47231326
GGAGACCAGCTCTCTCCCAG	TAG	0	5,18,19	No	chr1@ 77571061-77571084
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chr1@ 10823266-10823289
GGAGACCAGCTCTCTCCCAG	TGG	0	5,18,19	No	chr1@ 176157669-176157692
GGAGACCAGCTCTCTCCTTG	TGG	0	5,18,19	No	chr1@ 15862176-15862199
GGAGACCAGCTCTCTCCTAG	TGG	0	5,18,19	No	chr1@ 31428081-31428104
GGAGACCAGCTCTCTCCTAG	AGG	0	5,18,19	No	chr1@ 5675370-5675393
GGAGACCAGCTCTCTCCTAG	TGG	0	5,18,19	No	chr1@ 5549675-5549698
GGAGACCAGCTCTCTCCTGG	TGG	0	5,18,19	No	chr1@ 44244715-44244738
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr1@ 54631810-54631833
GGAGACCAGCTCTCTCCTGG	CAG	0	5,18,19	No	chr1@ 4233464-4233487
GGAGACCAGCTCTCTCCTGG	TAG	0	5,18,19	No	chr1@ 26258462-26258485
GGAGGCCAGATCTCTACACT	GAG	0	10,16,20	No	chr9@ 32416081-32416104
GGAGGCCAGCACTCTCTATG	TGG	0	11,17,19	No	chr6@ 53643668-53643691
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chrX@ 70666396-70666419
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chrX@ 132792325-132792348
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chrX@ 91197687-91197710
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr18@ 59496434-59496457
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr17@ 77301479-77301502
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr16@ 61101473-61101496
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr14@ 98241800-98241823
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr14@ 97338402-97338425
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr14@ 89331000-89331023
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr13@ 106663917-106663940
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr13@ 29237155-29237178
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr10@ 70890076-70890099
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr10@ 33314070-33314093
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr6@ 109098957-109098980
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr6@ 72036337-72036360
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr6@ 132422192-132422215
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr3@ 70052308-70052331

Sequence	PAM	Similarity	Mism.	Gene	Locus
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr3@ 7483195-7483218
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr3@ 47377717-47377740
GGAGGCAAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr2@ 139439394-139439417
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr2@ 63641606-63641629
GGAGGCTAGCTCTCTCCTCT	GAG	0	7,18,20	No	chr2@ 138845504-138845527
GGAGACCAGCTCTCTTCAGG	TGG	0	5,16,19	No	chr19@ 29757054-29757077
GGAGACCAGCTCTCTTCAGG	TGG	0	5,16,19	No	chr18@ 5906535-5906558
GGAGACCAGCTCTCTTCAGG	CAG	0	5,16,19	No	chr18@ 8255187-8255210
GGAGACCAGCTCTCTTCAGG	AGG	0	5,16,19	No	chr16@ 59858894-59858917
GGAGACCAGCTCTCTGCAGG	TGG	0	5,16,19	No	chr3@ 61572672-61572695
GCAGGCCAGCTCTGTCCATG	GGG	0	2,14,19	No	chr2@ 128085118-128085141
GGAGGCCAGTTCTCTCCTTG	CAG	0	10,18,19	No	chr11@ 57834333-57834356
GGAGGCCAGTTCTCTCCTGG	CAG	0	10,18,19	No	chr9@ 73701854-73701877
GGAGGCCAGGTCTCTCCTGG	CAG	0	10,18,19	No	chr5@ 23194590-23194613
GGAGCCCAGCTCTTTCCATG	AGG	0	5,14,19	No	chrX@ 81606549-81606572
GGAGACCAGCTCTTTCCAGG	CAG	0	5,14,19	No	chr10@ 27837442-27837465
GGAGACCAGCTCTGTCCAGG	CAG	0	5,14,19	No	chr10@ 90662942-90662965
GGAGACCAGCTCTGTCCAGG	TGG	0	5,14,19	No	chr10@ 47380065-47380088
GGAGACCAGCTCTTTCCAGG	TGG	0	5,14,19	No	chr9@ 14434569-14434592
GGAGACCAGCTCTTTCCAAG	TGG	0	5,14,19	No	chr3@ 99890769-99890792
GGAGACCAGCTCTTTCCAGG	AGG	0	5,14,19	No	chr2@ 37096430-37096453
GGAGGTCAGCTCTCTTCACT	GAG	0	6,16,20	No	chr11@ 84396647-84396670
GGAGGGCAGCTCTCTCTGCG	CAG	0	6,17,18	No	chr8@ 119006123-119006146
GGAGGCCATCTCTCTTCACC	TGG	0	9,16,20	No	chr16@ 28834580-28834603
GGAGGCGAGCTCTCTCCTAG	CGG	0	7,18,19	No	chrX@ 85281240-85281263
GGAGGCAAGCTCTCTCCTGG	CAG	0	7,18,19	No	chrX@ 96785875-96785898
GGAGGCAAGCTCTCTCCTGG	CAG	0	7,18,19	No	chrX@ 95806571-95806594
GGAGGCTAGCTCTCTCCTGG	TGG	0	7,18,19	No	chr17@ 82983562-82983585
GGAGGCTAGCTCTCTCCCTG	CAG	0	7,18,19	No	chr14@ 46861414-46861437
GGAGGCTAGCTCTCTCCTGG	CGG	0	7,18,19	No	chr11@ 41847667-41847690
GGAGGTCAGCTCTCTCCTGG	CAG	0	6,18,19	No	chr16@ 23695473-23695496
GGAGGTCAGCTCTCTCCTGG	AGG	0	6,18,19	No	chr10@ 37122749-37122772
GGAGGACAGCTCTCTCCTTG	AGG	0	6,18,19	No	chr6@ 64089717-64089740
GGAGGTCAGCTCTCTCCTGG	CAG	0	6,18,19	No	chr4@ 37518990-37519013
GGAGGCAAGCTCTCTTCAGG	GAG	0	7,16,19	No	chr13@ 82221819-82221842
GGAGGCCATCTCTCTCCTGG	CAG	0	9,18,19	No	chrX@ 117033005-117033028
GGAGGCCAACTCTCTCCCGG	TAG	0	9,18,19	No	chr1@ 10415719-10415742
GGAGGCCGGCTCTGGCCACG	TGG	0	8,14,15	No	chr14@ 51282439-51282462
GGAGACCAGCTCTCTTCCCG	TGG	0	5,16,18	No	chr13@ 92069186-92069209
GGAGGCAAGCTCTGTCCAGG	CAG	0	7,14,19	No	chr7@ 107995743-107995766
GGAGGCTAGCTCTTTCCAGG	CAG	0	7,14,19	No	chr3@ 10504161-10504184
GGAGACCAGCTCTTTCCTCG	TGG	0	5,14,18	No	chr17@ 93275166-93275189
GGAGGCCAGCTATCTCCTGG	CAG	0	12,18,19	No	chr19@ 9322638-9322661

Tnfsf11-sg2

Sequence	PAM	Exon	Activity	Off-target
GCCATCTCTCCCACGTCCCG	GGG	1	58	92

Guide Details	
Cut site	chr14 [+78,308,026 : -78,308,026]
GC %	70
Activity	58
Off-target	92

OFF-TARGET ANALYSIS:

Mismatches	0	1	2	3	Total
Coding	0	0	0	3	3
Non-Coding	0	0	1	27	28

OFF-TARGET HITS:

Sequence	PAM	Similarity	Mism.	Gene	Locus
GCCCTCTCCCCCACGTCCCC	CAG	1	4,9,20	Yes	chr7@ 4836174-4836197
GCCAGCTCTGCCAGGTCCCG	AAG	0	5,10,14	Yes	chr11@ 102064626-102064649
GCCAGCTCTCCCACCTCCAG	CAG	0	5,15,19	Yes	chr6@ 125031822-125031845
CCCATCTCGCCCACGTCCCC	GGG	1	1,9,20	No	chr6@ 118335281-118335304
ACCATCTCTCCCACGTCCAT	CAG	0	1,19,20	No	chr15@ 103328649-103328672
GCCTTTTCTCCCACTTCCCG	CAG	0	4,6,15	No	chr17@ 34030421-34030444
CCCATCTCTCCCACATCCCA	CAG	0	1,15,20	No	chr1@ 48043227-48043250
GCCAGCTCTCCCACGTGCTG	CAG	0	5,17,19	No	chrX@ 137165367-137165390
GCCAACTCTCCCACCTCCCA	AAG	0	5,15,20	No	chr9@ 57331002-57331025
GCCAGCTCTCCCACTTCCCT	TAG	0	5,15,20	No	chr8@ 113518567-113518590
GCCAGCTCTCCCACCTGCCG	CAG	0	5,15,17	No	chr5@ 49788664-49788687
GCCATACCTCCCACTTCCCG	TGG	0	6,7,15	No	chr5@ 84540224-84540247
GCCATCTCTCCCACCTCACG	GGG	0	15,18	No	chr1@ 133548365-133548388
GGCATCTCTCCCACTTCCTG	GAG	0	2,15,19	No	chr8@ 13430493-13430516
GCCACCTCTCCCACCTCCAG	TGG	0	5,15,19	No	chr12@ 30124249-30124272
GCGATCTCACCCAAGTCCCG	GGG	0	3,9,14	No	chrX@ 105289388-105289411
GCCATCCCTCCCACCTCCCT	AGG	0	7,15,20	No	chr1@ 76141909-76141932
GCCAGCTCTCCCACGGCCCT	GGG	0	5,16,20	No	chr4@ 63137888-63137911

Sequence	PAM	Similarity	Mism.	Gene	Locus
GCCAGCTCTCCCAAGTCCCA	CAG	0	5,14,20	No	chr11@ 99272497-99272520
GCCAGCTCTCCCAGGTCCCT	CAG	0	5,14,20	No	chr10@ 41008104-41008127
GCCAACTCTCCCAGGTCCCC	TAG	0	5,14,20	No	chr9@ 73125106-73125129
GCCATCTCTCAAACTTCCCG	AAG	0	11,12,15	No	chr8@ 88393082-88393105
GCCATCTCTCCAACGTCCAT	GGG	0	12,19,20	No	chr6@ 34778065-34778088
GCCATCACTCCCACCTCCTG	CAG	0	7,15,19	No	chr7@ 49255346-49255369
GTCATCTCTCCCAACTCCCG	CAG	0	2,14,15	No	chr18@ 67741223-67741246
GCCATCTCTCCAACCTCCTG	TAG	0	12,15,19	No	chr2@ 116194052-116194075
GCCATCTCTCCCACCTTCCC	AAG	0	15,17,20	No	chr1@ 69109072-69109095
GCCATCTCTCTCACGCCCTG	CAG	0	11,16,19	No	chr19@ 6825810-6825833
GCCATCTCTCCAACGCCCGG	TAG	0	12,16,19	No	chr12@ 83018950-83018973

Tnfsf11-sg3

Sequence	PAM	Exon	Activity	Off-target
GAGCCAATCAGCCTCCAGGA	GGG	P	67	77

Guide Details	
Cut site	chr14 [+78,308,116 : -78,308,116]
GC %	60
Activity	67
Off-target	77

OFF-TARGET ANALYSIS:

Mismatches	0	1	2	3	Total
Coding	0	0	0	0	0
Non-Coding	0	0	1	32	33

OFF-TARGET HITS:

Sequence	PAM	Similarity	Mism.	Gene	Locus
CAGCCAATCAGCGTCCAGGA	CAG	4	1,13	No	chr7@ 52576531-52576554
TTGCCAAACAGCCTCCAGGA	AGG	3	1,2,8	No	chr13@ 78227477-78227500
GACCAAAGCAGCCTCCAGGA	AGG	2	3,5,8	No	chr4@ 11676087-11676110
GAAGGAATCAGCCTCCAGGA	CAG	2	3,4,5	No	chr11@ 77740518-77740541
GCTCCCATCAGCCTCCAGGA	CAG	1	2,3,6	No	chr4@ 124624488-124624511
GAGAAAATCAACCTCCAGGA	AAG	1	4,5,11	No	chr3@ 92534116-92534139
CAGCCAAACAGACTCCAGGA	GAG	1	1,8,12	No	chr6@ 131455389-131455412
AAGCCAAGCAGCTTCCAGGA	AAG	1	1,8,13	No	chr15@ 54942196-54942219
GAGCCAAACCGTCTCCAGGA	AGG	1	8,10,12	No	chr17@ 69224111-69224134
GTGACAATCAGCCTCCAGCA	AAG	1	2,4,19	No	chr7@ 139751433-139751456
GAGACAAGCAGCATCCAGGA	GAG	1	4,8,13	No	chr6@ 81756928-81756951
TAGCCCCTCAGCCTCCAGGA	AAG	1	1,6,7	No	chr18@ 21894445-21894468
GAGACATTCAGCCTCCTGGA	TAG	1	4,7,17	No	chr2@ 66836841-66836864
GATCCAAGCAGCCTTCAGGA	GAG	1	3,8,15	No	chr6@ 125518531-125518554
GAGACAAACAGCCTGCAGGA	AGG	1	4,8,15	No	chr17@ 32080924-32080947
GAGCCCACCAGGCTCCAGGA	AGG	1	6,8,12	No	chr9@ 114553929-114553952
GAACCCATCAGCCTCCAGCA	CGG	1	3,6,19	No	chr7@ 46246433-46246456
GAGCCCCTGAGCCTCCAGGA	AGG	1	6,7,9	No	chr5@ 105560828-105560851
GACCCACTCAGCCTACAGGA	GGG	1	3,7,15	No	chr6@ 34281356-34281379
GTGCCAATCAGGCTCCAGCA	AGG	1	2,12,19	No	chr14@ 24760455-24760478

Sequence	PAM	Similarity	Mism.	Gene	Locus
GAGATAATCAGCCTCAAGGA	AGG	1	4,5,16	No	chr6@ 65926362-65926385
GAGCAAAGCAGCCTCAAGGA	TGG	0	5,8,16	No	chrX@ 71141650-71141673
GAGCCAATCTGTCTCCTGGA	AGG	0	10,12,17	No	chr2@ 150736290-150736313
AAGCCAATCAGCTTCCAGCA	TGG	0	1,13,19	No	chr7@ 123844813-123844836
GACCCAAGCAGCCCCCAGGA	TGG	0	3,8,14	No	chr5@ 130150526-130150549
GAGCTAATCACCCTTCAGGA	CAG	0	5,11,15	No	chr5@ 29898425-29898448
GAGCAACTCAGCCCCCAGGA	TGG	0	5,7,14	No	chr4@ 120869839-120869862
GAGCCAGTCAGCCTCCAGTT	GGG	0	7,19,20	No	chr9@ 34683131-34683154
GAGCCAATCAAGCTCCTGGA	AGG	0	11,12,17	No	chr17@ 44547438-44547461
GAGCCAAGCAGCCTGCAGCA	GAG	0	8,15,19	No	chr5@ 130466815-130466838
CAGCCAATCAGCTACCAGGA	AGG	0	1,13,14	No	chrX@ 129911572-129911595
GAGCCAATCAGCATGCAGAA	GGG	0	13,15,19	No	chr17@ 7782714-7782737