SNVs within TAD

Chromosome	Coordinate	SNV
chr14	37695514	c>G
chr14	37700981	a>G
chr14	37703714	a>T
chr14	37715593	C>T
chr14	37715710	T>C
chr14	37730447	A>G
chr14	37755665	g>T
chr14	37762423	A>G
chr14	37781081	c>A
chr14	37785616	c>T
chr14	37787646	A>C
chr14	37803915	a>G
chr14	37829761	g>A
chr14	37857322	G>C
chr14	37870712	g>A
chr14	37884260	T>C
chr14	37887005	A>G
chr14	37887437	G>T
chr14	37888682	a>G
chr14	37888869	g>T
chr14	37890288	G>A
chr14	37903468	t>G
chr14	37904343	A>T
chr14	37905854	A>G
chr14	37906009	T>C
chr14	37918105	G>A
chr14	37925787	A>G
chr14	37941995	g>A
chr14	37952831	c>T
chr14	37966152	a>T
chr14	37975348	g>T
chr14	37997221	C>G
chr14	38008477	a>G
chr14	38012766	g>A
chr14	38015049	C>G
chr14	38022140	c>T
chr14	38022335	a>T
chr14	38036543	A>G
chr14	38037962	G>C
chr14	38051839	G>T

chr14	38055269	C>G
chr14	38055908	T>C
chr14	38056977	T>G
chr14	38059153	G>A
chr14	38060558	C>T
chr14	38061208	G>C
chr14	38061229	A>C
chr14	38061231	A>C
chr14	38061231	A>G
chr14	38061231	A>T
chr14	38061250	G>A
chr14	38061294	G>A
chr14	38061313	C>T
chr14	38061317	G>T
chr14	38061340	A>C
chr14	38061528	c>T
chr14	38061975	G>T
chr14	38062840	C>G
chr14	38072955	C>A
chr14	38082628	c>T
chr14	38097288	g>A
chr14	38099831	g>T
chr14	38103657	g>A
chr14	38107989	t>G
chr14	38109595	T>C
chr14	38127842	t>C
chr14	38145684	a>G
chr14	38151460	a>C
chr14	38152352	T>G
chr14	38161158	a>G
chr14	38165472	A>T
chr14	38165665	A>G
chr14	38178575	t>A
chr14	38193969	T>C
chr14	38197633	a>C

Guide RNA for Clonal and Transient CRISPR/Cas9 and dCas9-KRAB experiments

Target	gRNA for Cas9 targeting	Location (Hg19)
CRE1_1	GTGGAGGTTTAATTGAAACC	chr14:37886718-37886737
CRE1_2	AACATGACCATAGACCTACT	chr14:37886860-37886879
CRE1_3	CCAATTTCCATTCATGGTCT	chr14:37887321-37887340
CRE1_4	ACCCATTTTTCAATCACGTA	chr14:37887646-37887665
CRE1_5	TATTGAAATGTGGTCTTCTA	chr14:37887034-37887053
CRE1_6	CATAATTCCAGGTGACATAA	chr14:37887749-37887768
CRE2_1	TGACTATAGCTGGTGTTCAC	chr14:37905489-37905508
CRE2_2	CAGGTGAATAAAGTCTACTC	chr14:37905215-37905234
CRE2_3	ATTTACTAATGCATGTGTCA	chr14:37905617-37905636
CRE2_4	AACTTAACAGCAGGTTGCCT	chr14:37904850-37904869
CRE2_5	GCATTAAGCTTAATTTGTGC	chr14:37905060-37905079
CRE2_6	CAGAAGCAGGATTCTGTGAC	chr14:37905425-37905444
CRE2_7	TGGCAGTACAGTCAGATATC	chr14:37905915-37905934
CRE2_8	CTTAGGTTTGGAATAGTCAG	chr14:37906218-37906237
CRE3_1	CACTATTTCTCGATCCAAAC	chr14:38035926-38035945
CRE3_2	GCGGTAAATACTAGAAATTT	chr14:38036041-38036060
CRE3_3	GTTTCTGGGAACCTGTTAGT	chr14:38036102-38036121
CRE3_4	GAGTCCGCCTTATCTCCACA	chr14:38036347-38036366
CRE3_5	GTCCTTTAAGACTCCATATG	chr14:38036460-38036479
CRE3_6	CTTCTATCCCCTTATCTAAA	chr14:38036572-38036591
CRE4_1	CCTTCGTGCGACACGTAGTT	chr14:38053998-38054017
CRE4_2	TGATGCTAATGCTCGGTCCT	chr14:38054179-38054198
CRE4_3	TAACCCGGATCCTTAGCGGA	chr14:38054385-38054404
CRE4_4	CGAGGCCCTGCGCTACAATA	chr14:38054499-38054518
CRE4_5	CGCAGCGGTAGTTGGCGCCC	chr14:38054577-38054596
CRE4_6	AACTGACCCGGGATATGAGC	chr14:38054901-38054920
CRE5_1	CACAGGTGTTCGGAAGTAGA	chr14:38056803-38056822
CRE5_2	AAATGTTTGCTCGGTAGCGT	chr14:38057009-38057028
CRE5_3	TCGCCAGCTCCCGAAGACCA	chr14:38057208-38057227
CRE5_4	CCGCAGGAGCCGTAACGAGG	chr14:38057452-38057471
CRE5_5	CCCGCGCGCGTCCTAACGCG	chr14:38057639-38057658
CRE5_6	CTTCCGAGGTCTCCAAATTA	chr14:38058088-38058107
CRE6_1	AGTTTAAGCTTTGTTGAACC	chr14:38127236-38127255
CRE6_2	GTTAGTCATTTTATGGGATC	chr14:38127547-38127566
CRE6_3	ACATTTTTGTCTGACCTTGC	chr14:38127651-38127670
CRE6_4	ACACACATGGATGTAGTGTA	chr14:38127732-38127751
CRE6_5	TTCAGACATTTTACTTACCC	chr14:38127948-38127967
CRE6_6	GTTGGAGCTAAATTACACAA	chr14:38128193-38128212
FOXA1(+)_1	TCTTTGTGCGGCGGACAAAT	chr14:38064525-38064544
FOXA1(+)_2	GAGTTCAATCCAGTATCGCC	chr14:38066997-38067016

EOVA1/1) 2	CGCAGTACCTGAGCGGCACT	chr14:38067708-38067727
FOXA1(+)_3 FOXA1(+)_4	ACGTCTGCGAATTAAACGGT	chr14:38063687-38063706
· ·	CCCGACTCTCGCAGCCGGAG	chr14:38063887-38063906
FOXA1(+)_5	GTAGTAGCTGTTCCAGTCGC	
FOXA1(+)_6		chr14:38064121-38064140
AAVS1 (-)_1	ATTCCCAGGGCCGGTTAATG	chr19:55627186-55627205
AAVS1 (-)_2	GTCCCCTCCACCCCACAGTG	chr19:55627139-55627158
AAVS1 (-)_3	GGGGCCACTAGGGACAGGAT	chr19:55627120-55627139
AAVS1 (-)_4	ACTAGGAAGGAGGCCTA	chr19:55627077-55627096
AAVS1 (-)_5	CGTGGGGTACCCTAAGAACT	chr19:55625766-55625785
AAVS1 (-)_6	GATTCCCTTCTCAGGTTACG	chr19:55626035-55626054
chr14 different TAD non-targeting (-		
)_1	AAACGTCACTAATGTTGGGG	chr14:30211476-30211495
chr14 different TAD non-targeting (-		
)_2	AAGAGCCCTCACCCCCATGA	chr14:30212122-30212141
chr14 different TAD non-targeting (-	00040700444470700747	
)_3	GCGAGTCCAAAATCTGCTAT	chr14:30211558-30211577
chr14 different TAD non-targeting (-	GTATTTATCTAGCTCTCAGT	chr14:30212024-30212043
)_4 chr14 different TAD non-targeting (-	GIATTIATCIAGCICICAGI	CIII 14.30212024-30212043
)_5	GCCGTACAGCATTTTACAAG	chr14:30211388-30211407
chr14 different TAD non-targeting (-	decarrender	CIII 14.30211300 30211407
)_6	GCATATCTCAGACCTTCATG	chr14:30212137-30212156
Within_TAD_Neg1_1	CATATCAGCTGTAGTGTATG	chr14:37812350-37812369
Within_TAD_Neg1_2	TATTCCAAGTTATTGTAATG	chr14:37812510-37812529
Within_TAD_Neg1_3	TTCACATTGACACCAAAGTT	chr14:37812661-37812680
Within_TAD_Neg1_4	AGAGTTGTATCACATCCAAG	chr14:37812733-37812752
Within_TAD_Neg1_5	TAAAAACTTAGACGATGTTA	chr14:37812833-37812852
Within_TAD_Neg1_6	GCTGGTATCATGAATCCTTA	chr14:37813115-37813134
Within_TAD_Neg2_1	AGCCACCCCACAGTTGTTAA	chr14:38151715-38151734
Within_TAD_Neg2_2	GCATGCTTGAAACTAAGCAT	chr14:38151841-38151860
Within_TAD_Neg2_3	TTTCCAACAGAGCGTGCATA	chr14:38151953-38151972
Within_TAD_Neg2_4	TACCGTTAAAGACACCCACT	chr14:38152153-38152172
Within_TAD_Neg2_5	CCATACGTTGGTCCTTGCCT	chr14:38152244-38152263
Within_TAD_Neg2_6	GAAGTGCAAGTTGCCCACTT	chr14:38152312-38152331
Within_TAD_Neg3_1	CATTTTAGCTAAGGACTTGC	chr14:37875337-37875356
Within_TAD_Neg3_1 Within_TAD_Neg3_2	GTATAGAAGAAATTCTACCC	chr14:37875447-37875466
Within_TAD_Neg3_3	GTTTGGTTCAGCATGTGTTC	chr14:37875530-37875549
Within_TAD_Neg3_4	TTACGACTCAAGTGTAAAGG	chr14:37875669-37875688
Within_TAD_Neg3_5	GTACCAGAGAGCTTAGTGAA	chr14:37875775-37875794
Within_TAD_Neg3_6	TACCAAGCCAACTGTTCTTG	chr14:37875913-37875932

Region		Sequence
CRE1	Forward Reverse	GACTGAGGAACCTCATTATCTCTG
	Complement	GCCCAAACTTTCTGCCTATAATG
CRE2_Lenti	Forward Reverse	GCAGGTTGCCTGGGAAGTGAG
	Complement	CTGCCAGTGCCACCCAGTC
CRE2_EverythingElse	Forward Reverse	GCAGGTTGCCTGGGAAGTG
	Complement	AGCCAGTCCCTATCCCTAGGC
CRE3	Forward Reverse	GCACATGGAAAGGGGATGTG
	Complement	CAACCAGGCTGTTATGCTGG
CRE4	Forward Reverse	CTGGCGTAGCGCAGGAGATC
	Complement	CACTCCTCCCCTTGCAGTC
CRE5	Forward Reverse	GGCATGCTCTTAACTCCATTTAGTTGC
	Complement	GCCTTCTGTGTTTCCTTTGAGCC
CRE6	Forward Reverse	GGTTCATTTTAGAGATGCATTTGTTC
	Complement	CCCCTGAACCTAAAATAAAAAAATTTTTAAAG
TAD1-	Forward Reverse	GTG CTG ATA TGT TGC CTA ATG G
	Complement	GCAGCAGGCTGAAAATACC
TAD2-	Forward Reverse	CAT AGT ATT TGG TAT TGT ATG CCA TC
	Complement	GGTTGACACTAGAAACCCTC
TAD3-	Forward Reverse	CTT TCT TTA TAG CCT ATG CAC C
	Complement	CACTGACTATTTCACTGGTTTC

RT-PCR mRNA Expression Primers

Gene	Primer Forward	Primer Reverse
FOXA1	GAA GAT GGA AGG GCA TGA AA	GCC TGA GTT CAT GTT GCT GA
TBP	TGC ACA GGA GCC AAG AGT GAA	CAC ATC CAC AGC TCC CCA CCA
SNAI2	ACGCCTCCAAAAAGCCAAAC	ACTCACTCGCCCCAAAGATG
ACPP	CTTTCAGGAACTGCCCTCGT	GGTGCAGCCTCTTCTGGAAT
MIPOL1	CCATCGCAAGGTTCTCAAGG	CCCTGGCCATTCTGTGTTCT
TTC6	AAAGCTGTCCCTTTTGGGCT	CCTTGAGATTCTGCAACCTTGG
GRIN3A	CGGAGACTTTGCAAATGGGC	AGACCAAATCCAATGCACAGC

Guide RNA for lentiviral-based CRISPR/Cas9 deletion proliferation assays

Target	gDNA for Cas9 targeting	Location (Hg19)
CRE1	AACATGACCATAGACCTACT	chr14:37886860-37886879
CRE1	ACCCATTTTTCAATCACGTA	chr14:37887646-37887665
CRE2	ATTTACTAATGCATGTGTCA	chr14:37905617-37905636
CRE2	GCATTAAGCTTAATTTGTGC	chr14:37905060-37905079
CRE3	TCTATGTTGTTATTAACTAG	chr14:38035682-38035701
CRE3	TTCCACTAGGAACAATAATG	chr14:38036962-38036981
CRE4	CCTTCGTGCGACACGTAGTT	chr14:38053998-38054017
CRE4	AACTGACCCGGGATATGAGC	chr14:38054901-38054920
CRE5	TGTGATCCCTCAATGTCAAC	chr14:38056269-38056288
CRE5	GAGTGGGGCGATCAAAGTAA	chr14:38058291-38058310

CRE6	AGTTTAAGCTTTGTTGAACC	ab = 1.4.2012722C 201272E
CREO	AGITTAAGCTTTGTTGAACC	chr14:38127236-38127255
CRE6	TTCAGACATTTTACTTACCC	chr14:38127948-38127967
FOXA1 Promoter (+)	TCTTTGTGCGGCGGACAAAT	chr14:38064525-38064544
FOXA1 Promoter (+)	ACGTCTGCGAATTAAACGGT	chr14:38063687-38063706
AAVS1 (-)	ATTCCCAGGGCCGGTTAATG	chr19:55627186-55627205
AAVS1 (-)	ACTAGGAAGGAGGCCTA	chr19:55627077-55627096
chr14 non-targeting (-)	AAACGTCACTAATGTTGGGG	chr14:30211476-30211495
chr14 non-targeting (-)	AAGAGCCCTCACCCCCATGA	chr14:30212122-30212141

Primers for MAMA ChIP-qPCR

Name	Primer Sequence
Constant, pGL3 Promoter, after BamHI_ Reverse Complement	GAAGACAGTCATAAGTGCGG
7005_A_F_MAMA	GGT TAC TCT GGA AAT AAC TCT ATT AAA A
7005_G_F_MAMA	GGT TAC TCT GGA AAT AAC TCT ATT AA <mark>TG</mark>
7437_G_F_MAMA	CAA GAT CTC AAG GAG AGA TAA AAG T <mark>GG</mark>
7437_T_F_MAMA	CAA GAT CTC AAG GAG AGA TAA AAG T <mark>CT</mark>
5854_A_F_MAMA	GCC ACT GCT GTC ATA AAA AGC TTA
5854_G_F_MAMA	GCC ACT GCT GTC ATA AAA AGC TAG
6009_T_F_MAMA	CCCAAAATGATGAATGTTTACCTAT
6009_C_F_MAMA	CCCAAAATGATGAATGTTTACCTTC
6543_A_F_MAMA	GAACCAAGATCTGTGAAAGAAAAG <mark>TA</mark>
6543_G_F_MAMA	GAACCAAGATCTGTGAAAGAAAAG <mark>AG</mark>
7842_T_F_MAMA	CTTAATGAGTACATTGGGTTATTT
7842_C_F_MAMA	CTTAATGAGTACATTGGGTTATGC
5269_C_F_MAMA	CGC ATT CCA CCT GGA TTC
5269_G_F_MAMA	CGC ATT CCA CCT GGA TTG
5908_T_F_MAMA	GCTTTACCTTTCCAAATCAATTCTATTT
5908_C_F_MAMA	GCTTTACCTTTCCAAATCAATTCTATGC
6977_T_F_MAMA	CCC CTG TCC TAT GCT CAC T
6977_G_F_MAMA	CCC CTG TCC TAT GCT CAAG
4343_A_F_MAMA	CCAGATGTATGTTGTGATATTACTTATAA
4343_T_F_MAMA	CCAGATGTATGTTGTGATATTACTTATCT

gBlock Sequences for Luciferase Assays

Mu Wild tati Type or

on Mutant gBlock Sequence

chr		AACCAACGGATCCATCCTAGTAGGTCTATGGTCATGTTCTTTGAGAAATCATCTAACT
14:		TGATGTATTGTTTGAAGATACCCAATTATATATTTTATAGATGTTTTAATAGTGCTA
378		GCTTAATCATATATTTTATGGTTACTCTGGAAATAACTCTATTAAA $oldsymbol{A}$ TAACTATCAC
870 05		ACATATTAAATTATACCATATTGAAATGTGGTCTTCTATGGTAAAATAAGCAATGTTT
(A>	Wild	TCTGGATACTTGTTAGTTCCAACTTTCTTTCTAACCATCTATGAAACCTTGGACAATTT
(, t,	Туре	CCAAATGTTTCCCTGAACATGTTGGATCCTAGAGAGGGG
,	, ·	AACCAACGGATCCATCCTAGTAGGTCTATGGTCATGTTCTTTGAGAAATCATCTAACT TGATGTATTGTTTGAAGATACCCAATTATATATTTTATAGATGTGTTTAATAGTGCTA
		gcttaatcatatatattatggttactctggaaataactctattaaaGtaactatcac
		ACATATTAAATTATACCATATTGAAATGTGGTCTTCTATGGTAAAATAAGCAATGTTT
		TCTGGATACTTGTTAGTTCCAACTTTCTTTCTAACCATCTATGAAACCTTGGACAATTT
	Mutant	CCAAATGTTTCCCTGAACATGTTGGATCCTAGAGAGGGG
chr		AACCAACGGATCCCATAACATCAGATGTCTCTGTTCTAAGATAAAAACCAATTTCCAT
14:		TCATGGTCTTGGAGTTACTAAAACAAGGCTTAACTGTATCAGACTATAACTATTAAAA
378 874		ACACATTTAAACCAAACATAACAAGATCTCAAGGAGAGATAAAAGTG $oldsymbol{G}$ TTTATCCAC
37		AATACTGGTTAAGAATAGCGCTTAGTGATGTGAACAGTGTGGTCTTTTCTTTGTCATT
(G>	Wild	CTGAGTTACTAGATTAAGCTCCAGTGAAACAATGTAGTTCATTTCTGATACAGTCCCA
T)	Type	ACACAAATGGCTGTCCTATTTAGATGGATCCTAGAGAGGGG
		AACCAACGGATCCCATAACATCAGATGTCTCTGTTCTAAGATAAAAACCAATTTCCAT
		TCATGGTCTTGGAGTTACTAAAACAAGGCTTAACTGTATCAGACTATAACTATTAAAA
		acacatttaaaccaaacataacaagatctcaaggagagataaaagtg $oldsymbol{T}$ tttatccac
		AATACTGGTTAAGAATAGCGCTTAGTGATGTGAACAGTGTGGTCTTTTCTTTGTCATT
		CTGAGTTACTAGATTAAGCTCCAGTGAAACAATGTAGTTCATTTCTGATACAGTCCCA
	Mutant	ACACAAATGGCTGTCCTATTTAGATGGATCCTAGAGAGGGG
chr		AACCAACGGATCCAGGTAAAAATTACCCTCTCTAAAAGGGGCATGCACTTGCCATTT
14: 379		CACCACACTTTCTATTCCACCTACTTTGTGAATTTAAAGTCATCTTCCTCAACCCTGTA
043		GGTATTTAATTTTATGACCCCAGATGTATGTTGTGATATTACTTATA $oldsymbol{A}$ AATGGATGTT
43		TGTACACGTATACATATACTCTGGCCCCTGGCTACCTCTAACCTTATTTCTTAACAT
(A>	Wild	GTTTCTACTCTTGGTTCACTCCAGCCACACTAGGTTCCTTAATAACTCAAATATTCTAG
T)	Type	GTGTGCTCCCATCCCAGGGCCCGGATCCTAGAGAGGGG
		AACCAACGGATCCAGGTAAAAATTACCCTCTCTAAAAGGGGCATGCACTTGCCATTT
		CACCACACTTTCTATTCCACCTACTTTGTGAATTTAAAGTCATCTTCCTCAACCCTGTA
		ggtatttaattttatgaccccagatgtatgttgtgatattacttata ${\sf T}$ aatggatgtt
		TGTACACGTATACATATACTCTGGCCCCTGGCTACCTCTCTAACCTTATTTCTTAACAT
		GTTTCTACTCTTGGTTCACTCCAGCCACACTAGGTTCCTTAATAACTCAAATATTCTAG
	Mutant	GTGTGCTCCCATCCCAGGGCCCGGATCCTAGAGAGGGG
chr		ΛΛCCΛΛCCCΛTCCΛTTCΛΛCΛCTTTCTTCΛCCΛΛCΛTTCTCΛTTΛΛTTCΛTTΛΛTTCΛΛ
14:	Wild	AACCAACGGATCCATTGAAGACCTTTGTTCAGGAACATTCTGATTCATTAATTGCAAA
379	Type	AACAATAAATGTTAAACATACAGTACAAGATCTAATAAACTGAGATCTTTAAGCTAGT

058 54 (A> G)	Mutant	TTTGATTTCTATAAACTTTCTAATGCCACTGCTGTCATAAAAAAGCTT A GTAAATATTG ACTGAGGATGATGACGATCCGTCAGTATTTTTAAGACTGGGTGGCACTGGCAG TACAGTCAGATATCCGGGACTTAACATTGTTATTTTGCCATGAGGCCCTTCCACCTGG CCCTATCCCAAAATGATGAAGATGTTTAGGATCCTAGAGAGGGG AACCAACGGATCCATTGAAGACCTTTGTTCAGGAACATTCTGATTCATTAATTGCAAA AACAATAAATGTTAAACATACAGTACAAGATCTAATAAACTGAGATCTTTAAGCTAGT TTTGATTTCTATAAACTTTCTAATGCCACTGCTGTCATAAAAAAGCTT G GTAAATATTG ACTGAGGATGATGATGACGATCCGTCAGTATTTTTAAGACTGGGTGGCACTGGCAG TACAGTCAGATATCCGGGACTTAACATTGTTATTTTGCCATGAGGCCCTTCCACCTGG CCCTATCCCAAAATGATGAATGTTTAGGATCCTAGAGAGGGG
	macane	
chr 14: 379 060 09 (T> C)	Wild Type	AACCAACGGATCCATATTGACTGAGGATGATGATGACGATCCGTCAGTATTTTTAAG ACTGGGTGGCACTGGCAGTACAGTCAGATATCCGGGACTTAACATTGTTATTTTGCC ATGAGGCCCTTCCACCTGGCCCTATCCCAAAATGATGAATGTTTACCTATAGTTAAGTTTAAATGTGTAAATATTCCAGATTCAATTATATGTGAGGTAGCTAGAGTTTTCAT TCCTTAAATCATGAACTAGTTCTCTAAAGTTTAAATGATTTACAAGTCTGCAAGGGTC AAAATTGACTTGAC
	Mutant	AAAATTGACTTGACTGAATGTTTTCCCGGATCCTAGAGAGGGG
chr 14: 380 365 43 (A> G)	Wild Type Mutant	AACCAACGGATCCAATTTATTATGAAATGCTTTGTTTGTGTTAACATATATCTTCTCTG GGAAGCTGGAAACAAAGGCATGTCCTTTAAGACTCCATATGGGGAAAACACACTCCT CCTTTGGAATTTAACCTTAATTTGAACCAAGATCTGTGAAAGAAA
chr 14: 380 552 69	Wild Type	AACCAACGGATCCCCCTGATGTGTAATCTTGAAGGGGAGTTGAGAGACGTAAAAAG TTAAACCAAGGCAACCTCACACTTAAATTCTGAGTCAGGCCTGCCGTTGGTGTCACT GGCCTGGTTCTTGATTTCGCCAGTGACTTGACCCGCATTCCACCTGGATT \mathbf{C} TGATGT ATTCGAGCACGATTCTACTTAAGCCCTTTCCTTCCTGGATTTTGAGGGAGAATATCTT

(C> G)	Mutant	GCCTCTGTCCTTTAGGTTGACTGGAACATAGAGAACCCCAAAAGATCACGGAGTGG CACCCAGAAAAAGGAGGGCTCCTTATTTCCGGATCCTAGAGAGGGG AACCAACGGATCCCCCTGATGTGTAATCTTGAAGGGGAGTTGAGAGACGTAAAAAG TTAAACCAAGGCAACCTCACACTTAAATTCTGAGTCAGGCCTGCCGTTGGTGTCACT GGCCTGGTTCTTGATTTCGCCAGTGACTTGACCCGCATTCCACCTGGATTGTGATGT ATTCGAGCACGATTCTACTTAAGCCCTTTCCTTCCTGGATTTTGAGGGAGAATATCTT GCCTCTGTCCTTTAGGTTGACTGGAACATAGAGAACCCCAAAAGATCACGGAGTGG CACCCAGAAAAAAGGAGGGCTCCTTATTTCCGGATCCTAGAGAGAG
chr 14: 380 559 08 (T> C)	Wild Type Mutant	AACCAACGGATCCCCCAAACTTAGCTATTTGGAAGAAAAAACACAAGATTTAAGGTA ATCTGTTGTTAAATGTTATTTGGATACACTAACATCGTGCATGAAAATAAAACTTGTG TAAGTGGCTACTTTAAGAAACGCTTTACCTTTCCAAATCAATTCTATT T ATAAACAGG AAGATTGTGAAATATTCATGTTTTTTTCATTTCA
chr 14: 380 569 77 (T> G)	Wild Type Mutant	AACCAACGGATCCTTTAGTTTTTGCTGAATAGAACTGGTGAGCTTTTCTTCTCCTA TCTTTGGTTCTGTTTTTTGTCACCTTAAAAATGTTTCATACCTGCCCTTCCTAAATGCAA GGTGAGAGTAACAATTGCAGCTCCCCTCCC
chr 14: 381 278 42 (T> C)	Wild Type	AACCAACGGATCCATTTTAGAAAAGCCCTGGGTAGCTGGGAGCTGAATAATGTACA CACATGGATGTAGTATGGAATGACAGACAGTGGAGACTTGGCAGGGTGAGAGG GTTGGCAGGAAATGGAGATAAGAAATTACTTAATGAGTACATTGGGTTATT T GGG TGAAAGATACCTTAAAAGCCTTGACTTCTACACAATCTATGCACATAGCAAAAACTAC ATTTACACACCATACATTTAAACAAGAAAAGAA

AACCAACGGATCCATTTTAGAAAAGCCCTGGGTAGCTGGAGCTGAATAATGTACA CACATGGATGTAGTGTATGGAATGACAGACAGTGGAGACTTGGCAGGGTGAGAGG ${\tt GTTGGCAGGAAATGGAGGATAAGAAATTACTTAATGAGTACATTGGGTTATT} \textbf{\textbf{C}}{\tt GGG}$ TGAAAGATACCTTAAAAGCCTTGACTTCTACACAATCTATGCACATAGCAAAAACTAC Mutant GTCTGAAAAAGCCTTTAAAAATTTTTTTATTTGGATCCTAGAGAGGGG