

INK2J00092_CHMP2B_Q206H_A04_BB
1263 bp

5' ATAAATTTGTGTTGAAATGAACATTATTCCAGATTTAATGGCTCAAATATGTATTTATCAATTTACTTCACTGACATTTTGAAGGA
 3' TATTA AACACA AACTTTACTTGTAAATAAGGTCTAAATTACCGAGTTTATACATAAATAGTTAAATGAAGTGACTGTAAAACCTCCT

CHMP2B
 CHMP2B-201

85

TTTTTTTAGTTTGTTCCTGAGTTTGCCTTCTGTAATATACAAAATAGTTGGGCTAGACTGTAATATGTAAGTCTAACCTGAAG
 AAAAAAATCAAACAAGTGACTCAAACGGAAGACATTATATGTTTTATCAACCCGATCTGACATTTATACATTCAGATTGGACTTC

CHMP2B
 CHMP2B-201

170

PCR Forward
 GCTCCTTCTCCCATATCCCCTAGTC

TTTGTGTTGAAAGTAACTGCTTTGCTCCTTCTCCCATATCCCCTAGTCAATGATACACTTGATGACATCTTTGACGGTTCTGATGA
 AAACAACTTTCATTGACGAAACGAGGAAGAGGGTATAGGGGATCAGTTACTATGTGAACTACTGTAGAACTGCCAAGACTACT

CHMP2B
 CHMP2B-201

255

N D T L D D I F D G S D D
 145 150 155
 ENSE00001209407
 CHMP2B-201

CGAAGAAGAAAGCCAGGATATTGTGAATCAAGTCTTTGATGAAATTGGAATTGAAATTTCTGGAAAGGTATGAACATCATCTTT
 GCTTCTTCTTTCCGGTCTATAACACTTAGTTCAAGAACTACTTAACTTAACTTAAAGACCTTCCATACTTGTAGTAGAAAA

CHMP2B
 CHMP2B-201

340

E E E S Q D I V N Q V L D E I G I E I S G K
 160 165 170 175
 ENSE00001209407
 CHMP2B-201

CTTAGTTGAAATAGTTTCTGCCTACCACGTTTGTCACTTAATTGTTTTGTTTTACTAGGAGGTGCATGGTTTTTATTTCTGTT
 GAATCAACCTTTATCAAAGACGGATGGTGCAAACAGTGAATTAACAAAACAAAATGATCCTCCACGTACCAAAAATAAAGACAA

CHMP2B
 CHMP2B-201

425

CHMP2B-201

Sanger Sequencing Primer
 GCACATCCTGTATGTCCTAG

TCAAAGTAAATTAACAGACCTTTACAGCACATCTGTATGTCCTAGTCCAATGTTTCTAATGCACGTTTGTCTTTTTCA
 AGTTTTTCATTTAATTTGCTGGAGAAATGTCGTGTAGGACATACAGGATCAGGTTTACAAAGGATTACGTGCAAACAGAAAAAGT

CHMP2B
 CHMP2B-201

510

CHMP2B-201

gRNA Protospacer

A

TTGTTTAATATAGATGGCCAAAGCTCCATCAGCTGCTCGAAGCTTACCATCTGCCTCTACTTCAAAGGCTACAATCTCAGATGAA
AACAAATTATATCTACCGTTTTGAGGTAGTCGACGAGCTTCAATGGTAGACGGAGATGAAGTTTTCCGATGTTAGAGTCTACTT

595

CHMP2B

CHMP2B-201

M A K A P S A A R S L P S A S T S K A T I S D E

CHMP2B-201

Donor Sequence WT -> SNV

gRNA Protospacer Sequence

CCGATGTTAGAGTCTACTT
Donor Template WT -> SNV

gRNA Protospacer

GAGATTGAACGGCAACTCA

GAGATTGAACGGCACTCAAGGCTTTAGGAGTAGATTAGTCAAAGAAGTCATACTATTTTGCTTACTTATAATTATGTAGTATA
CTCTAACTTGCCGTGAGTTCGAAATCCTCATCTAATCAGTTTTCTTCAGTATGATAAAACGAATGAATATTAATACATCATAT

680

CHMP2B

CHMP2B-201

E I E R Q L K A L G V D *
ENSE00001945124
CHMP2B-201

Donor Sequence WT -> SNV

gRNA Protospacer Sequence PAM

SNV

CTCTAACTTGCCGTGAGTTCGAAATCCTCATCTAATCAGTTTTCTTCAGTATGATAAAACGAATGAATATTAATACATC

Donor Template WT -> SNV

AACCAAGCACAGTGCAGATTTCTTTTACAAAACACATGTATTTTGCAAAAAAAAAAAAAAAAAATGAAGACCATGAGTGAACAGTTGTT
TTGGTTCGTGTCACGTCTAAAGAAAATGTTTTGTGTACATAAAACGTTTTTTTTTTTTTTTACTTCTGGTACTCAGTTGTCAACAA

765

CHMP2B

CHMP2B-201

TCCTAACCCATGGCTATTTAGAATCTTTTGCCAAAGAATGACAATGATGCAAAAATGGGAACAGTTTGGATTTTAATTAGAAGT
AGGATTGGGTACCGATAAATCTTAGAAAACGGTTTCTTACTGTTACTACGTTTTTACCCTTGTCAAACCTAAAATTAATCTTGAC

850

CHMP2B

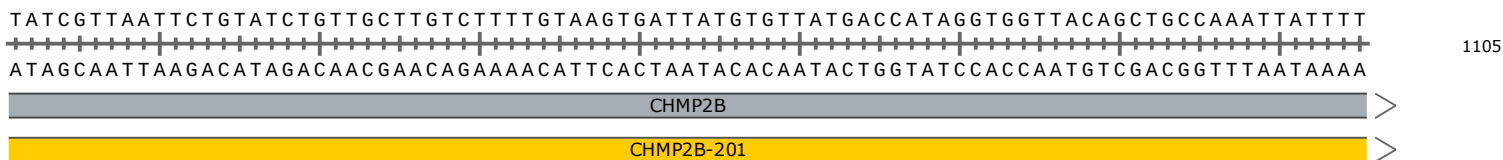
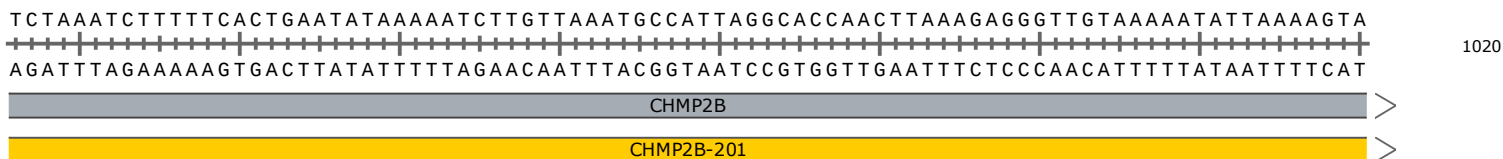
CHMP2B-201

TTTAGGAGTGATGATGTGTAAAAAGTTGACTTCTCTTTGTCATGGCACAGAGAAATTATATTCCTTACTTTCATGTCAGTTTATGT
AAATCCTCACTACTACACATTTTCAACTGAAGAGAAAACGTACCGTGTCTCTTTAATATAAGGAATGAAGTACAGTCAAATACA

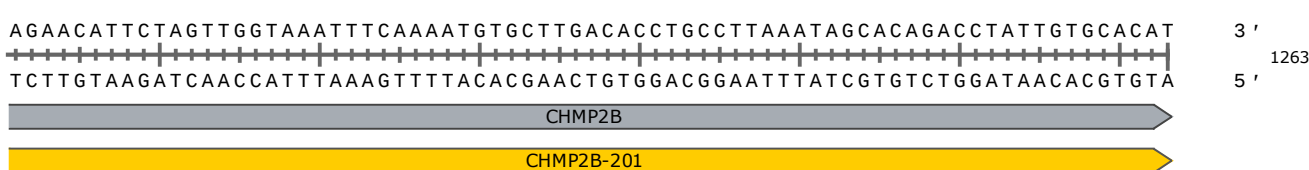
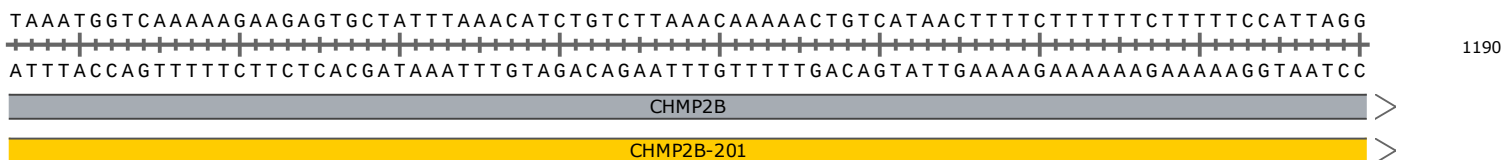
935

CHMP2B




CHMP2B-201



GTATCCACCAATGTCGACGGTTTAA
 PCR Reverse



Feature	Location	Size	Start	End	Type
✓ CHMP2B	1 .. 1263	1263 bp	■	➔	gene
/note = gene ENSG00000083937 Protein coding					
✓ CHMP2B-201	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000263780					
CHMP2B-203	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000471660					
CHMP2B-204	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000472024					
CHMP2B-206	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676705					
CHMP2B-208	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000677929 Retained intron					
CHMP2B-210	1 .. 1263	1263 bp	■	➔	prim_transcript
/note = primary transcript ENST00000678859 Retained intron					
CHMP2B-205	1 .. 1036	1036 bp	■	➔	prim_transcript
/note = primary transcript ENST00000494980					
CHMP2B-202	1 .. 725	725 bp	■	➔	prim_transcript
/note = primary transcript ENST00000466696 Retained intron					
✓ CHMP2B-201	216 .. 634	419 bp	■	➔	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000263780					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-203	216 .. 634	419 bp	■	➔	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000419998					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-204	216 .. 634	419 bp	■	➔	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000480032					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-205	216 .. 634	419 bp	■	➔	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000418920					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-206	216 .. 634	419 bp	■	➔	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000504098					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
✓ Donor Sequence WT -> SNV	577 .. 676	100 bp	■	⌊	misc_feature
✓ gRNA Protospacer Sequence	595 .. 614	20 bp	■	⌊	misc_feature

Feature	Location	Size		Type
✓ SNV /note = WT = A SNV = C	610 .. 610	1 bp		misc_feature
✓ PAM	615 .. 617	3 bp		misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = GCTCCTTCTCCCATATCCCCTAGTC 56% GC / 7439.9 Da	25-mer	193 .. 217 →	62°C	Aug 15, 2023
✓ Sanger Sequencing Primer /sequence = GCACATCCTGTATGTCCTAG 50% GC / 6068.0 Da	20-mer	456 .. 475 →	54°C	Aug 15, 2023
✓ Donor Template WT -> SNV /sequence = CTACATAATTATAAGTAAGCAAATAGTATGACTTCTTTTGACTAATCTACTCCTAAAGCCTTGAGGTGCCGTTCAATCTTTCATCTGAGATTGTAGCC 36% GC / 30,688.1 Da	100-mer	577 .. 676 ←	69°C	Aug 15, 2023
✓ gRNA Protospacer /sequence = AGAGATTGAACGGCAACTCA 45% GC / 6159.1 Da	20-mer	595 .. 614 →	56°C	Aug 15, 2023
✓ PCR Reverse /sequence = AATTTGGCAGCTGTAACCACTATG 44% GC / 7641.0 Da	25-mer	1076 .. 1100 ←	60°C	Aug 15, 2023