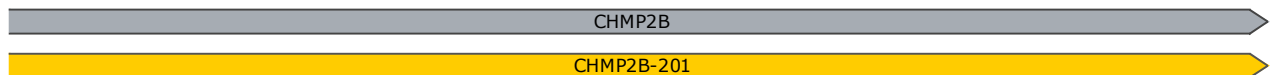





GTTATGACCATAGGTGGTTACAGCTGCCAAATTATTTTTAAATGGTCAAAAAGAAGAGTGCTATTTAAACATCTGTCTT
CAATACTGGTATCCACCAATGTCGACGGTTTAATAAAAATTTACCAGTTTTTCTTCTCACGATAAATTTGTAGACAGAA

3 '
1099
5 '



G T A T C C A C C A A T G T C G A C G G T T T A A
PCR Reverse

Feature	Location	Size	Start	End	Type
✓ CHMP2B	1 .. 1099	1099 bp	■	→	gene
/note = gene ENSG00000083937 Protein coding					
✓ CHMP2B-201	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000263780					
CHMP2B-203	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000471660					
CHMP2B-204	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000472024					
CHMP2B-206	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000676705					
CHMP2B-208	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000677929 Retained intron					
CHMP2B-210	1 .. 1099	1099 bp	■	→	prim_transcript
/note = primary transcript ENST00000678859 Retained intron					
CHMP2B-205	1 .. 989	989 bp	■	→	prim_transcript
/note = primary transcript ENST00000494980					
CHMP2B-202	1 .. 678	678 bp	■	→	prim_transcript
/note = primary transcript ENST00000466696 Retained intron					
✓ CHMP2B-201	169 .. 587	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000263780					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-203	169 .. 587	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000419998					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-204	169 .. 587	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000480032					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-205	169 .. 587	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000418920					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
CHMP2B-206	169 .. 587	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence ENSP00000504098					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
✓ Donor Sequence SNV -> Rev	530 .. 629	100 bp	■		misc_feature
✓ gRNA Protospacer Sequence	548 .. 567	20 bp	■		misc_feature

Feature	Location	Size		Type
✓ SNV /note = SNV = C REV = A	563 .. 563	1 bp		misc_feature
✓ PAM	568 .. 570	3 bp		misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = GCTCCTTCTCCCATATCCCCTAGTC 56% GC / 7439.9 Da	25-mer	146 .. 170 →	62°C	Aug 15, 2023
✓ Sanger Sequencing Primer /sequence = GCACATCCTGTATGTCCTAG 50% GC / 6068.0 Da	20-mer	409 .. 428 →	54°C	Aug 15, 2023
✓ Donor Template SNV -> Rev /sequence = CTACATAATTATAAGTAAGCAAATAGTATGACTTCTTTTGACTAATCTACTCCTAAAGCCTTGAGTTGCCGTTCAATCTTTCATCTGAGATTGTAGCC 35% GC / 30,663.1 Da	100-mer	530 .. 629 ←	69°C	Aug 15, 2023
✓ gRNA Protospacer /sequence = AGAGATTGAACGGCACCTCA 50% GC / 6135.1 Da	20-mer	548 .. 567 →	48°C	Aug 15, 2023
✓ PCR Reverse /sequence = AATTTGGCAGCTGTAACCACTATG 44% GC / 7641.0 Da	25-mer	1029 .. 1053 ←	60°C	Aug 15, 2023