

5' TTGTTTGCTATAAGATAATTTGTGTTGAAATGAACATTATCCAGATTTAATGGCTCAAATATGTATTTATCAATTTACTTCACT  
 3' AACAAACGATATTCTATTAACACAACCTTTACTTGTAAATAAGGTCTAAATTACCGAGTTTATACATAAATAGTTAAATGAAGTGA

CHMP2B  
 CHMP2B-201

85

GACATTTTGAAGGATTTTTTTAGTTTGTTCCTGAGTTTGCCTTCTGTAATATACAAAATAGTTGGGCTAGACTGTAATATGTA  
 CTGTA AAACTTCTCTAAAAAATCAAACAAGTGACTCAAACGGAAGACATTATATGTTTTATCAACCCGATCTGACATTTATACAT

CHMP2B  
 CHMP2B-201

170

PCR Forward  
GCTCCTTCTCCCATATCCCCTAGTC

AGTCTAACCTGAAGTTTGTGTTGAAAGTAACTGCTTTGCTCCTTCTCCCATATCCCCTAGTCAATGATACACTTGATGACATCTTT  
 TCAGATTGGACTTCAAACAACTTTCATTGACGAAACGAGGAAGAGGGTATAGGGGATCAGTTACTATGTGAACTACTGTAGAAA

CHMP2B  
 CHMP2B-201

255

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

GACGGTTCTGATGACGAAGAAGAAAGCCAGGATATTGTGAATCAAGTCTTGGATGAAATTGGAATTGAAATTTCTGGAAAGGTAT  
 CTGCCAAGACTACTGCTTCTTCTTTCGGTCTATAACACTTAGTTCAAGAACTACTTTAACCTTAACTTTAAAGACCTTCCATA

CHMP2B  
 CHMP2B-201

340

155 160 165 170 175  
 D G S D D E E E S Q D I V N Q V L D E I G I E I S G K  
ENSE00001209407  
 CHMP2B-201

GAACATCATCTTTTCTTAGTTGAAATAGTTTCTGCCTACCACGTTTGTCACTTAATTGTTTTGTTTTACTAGGAGGTGCATGG  
 CTTGTAGTAGAAAAGAATCAACCTTATCAAAGACGGATGGTGCAAACAGTGAATTAACAAAACAAAAATGATCCTCCACGTACC

CHMP2B  
 CHMP2B-201

425

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 CHMP2B-201

Sanger Sequencing Primer  
GCACATCCTGTATGTCCTAG

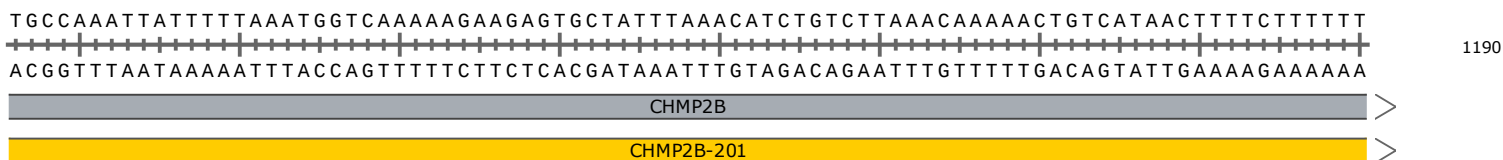
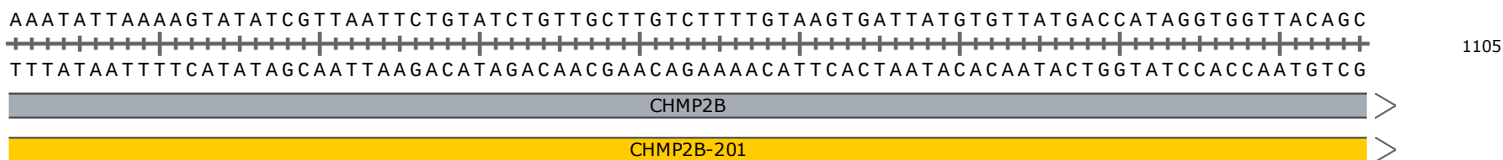
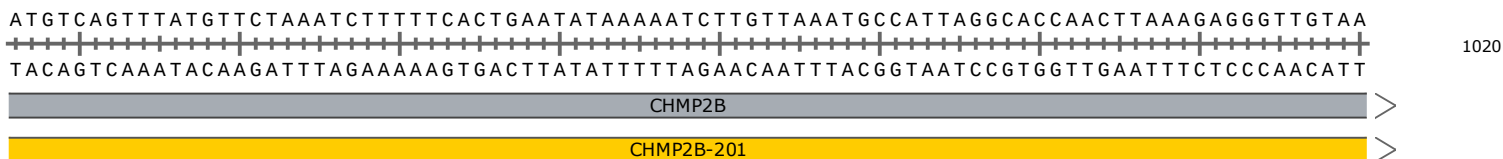
TTTTTATTTCTGTTTCAAAGTAAATTAACAGACCTTTTACAGCACATCCTGTATGTCCTAGTCCAAATGTTTCTTAATGCAC  
 AAAAAATAAAGACAAAGTTTTCAATTAATTTGCTGGAGAAATGTCGTGTAGGACATACAGGATCAGGTTTACAAAGGATTACGTG

CHMP2B  
 CHMP2B-201

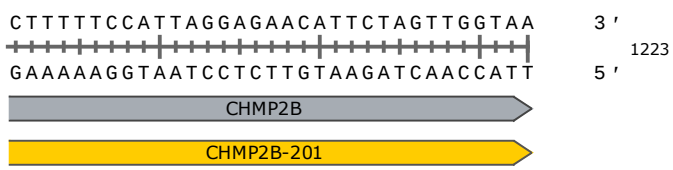
510

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 CHMP2B-201








ACGGTTTAA  
PCR Reverse



Feature	Location	Size	Start	End	Type
✓ <b>CHMP2B</b>	1 .. 1223	1223 bp	■	→	gene
/note = gene <a href="#">ENSG00000083937</a> Protein coding					
✓ <b>CHMP2B-201</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000263780</a>					
<b>CHMP2B-203</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000471660</a>					
<b>CHMP2B-204</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000472024</a>					
<b>CHMP2B-206</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000676705</a>					
<b>CHMP2B-208</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000677929</a> Retained intron					
<b>CHMP2B-210</b>	1 .. 1223	1223 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000678859</a> Retained intron					
<b>CHMP2B-205</b>	1 .. 1050	1050 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000494980</a>					
<b>CHMP2B-202</b>	1 .. 739	739 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000466696</a> Retained intron					
✓ <b>CHMP2B-201</b>	230 .. 648	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000263780</a>					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
<b>CHMP2B-203</b>	230 .. 648	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000419998</a>					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
<b>CHMP2B-204</b>	230 .. 648	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000480032</a>					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
<b>CHMP2B-205</b>	230 .. 648	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000418920</a>					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
<b>CHMP2B-206</b>	230 .. 648	419 bp	■	→	CDS
▶ 2 segments = 218 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000504098</a>					
/translation = NDTLDDIFDGSDDDEESQDIVNQVLDEIGIEISGK, ,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 71 amino acids = 7.6 kDa					
✓ <b>Donor Sequence WT -&gt; SNV</b>	591 .. 690	100 bp	■		misc_feature
✓ <b>gRNA Protospacer Sequence</b>	609 .. 628	20 bp	■		misc_feature

Feature	Location	Size		Type
✓ <b>SNV</b>  /note = WT = A SNV = C	624 .. 624	1 bp		misc_feature
✓ <b>PAM</b>	629 .. 631	3 bp		misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer	207 .. 231 →	62°C	Aug 15, 2023
/sequence = GCTCCTTCTCCCATATCCCCTAGTC 56% GC / 7439.9 Da				
✓ <b>Sanger Sequencing Primer</b>	20-mer	470 .. 489 →	54°C	Aug 15, 2023
/sequence = GCACATCCTGTATGTCCTAG 50% GC / 6068.0 Da				
✓ <b>Donor Template WT -&gt; SNV</b>	100-mer	591 .. 690 ←	69°C	Aug 15, 2023
/sequence = CTACATAATTATAAGTAAGCAAATAGTATGACTTCTTTTGACTAATCTACTCCTAAAGCCTTGAGGTGCCGTTCAATCTTTCATCTGAGATTGTAGCC 36% GC / 30,688.1 Da				
✓ <b>gRNA Protospacer</b>	20-mer	609 .. 628 →	56°C	Aug 15, 2023
/sequence = AGAGATTGAACGGCAACTCA 45% GC / 6159.1 Da				
✓ <b>PCR Reverse</b>	25-mer	1090 .. 1114 ←	60°C	Aug 15, 2023
/sequence = AATTTGGCAGCTGTAACCACTATG 44% GC / 7641.0 Da				