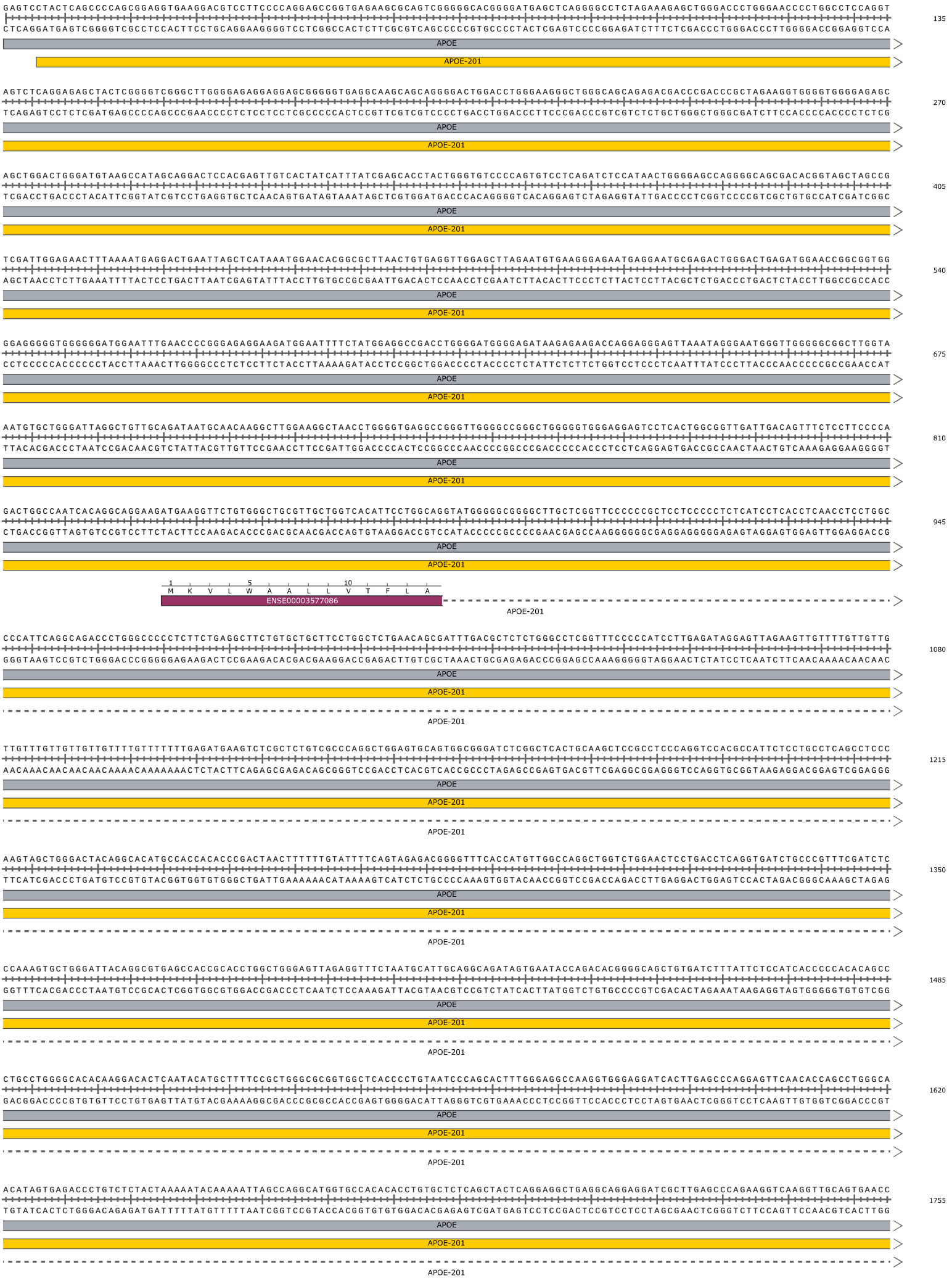
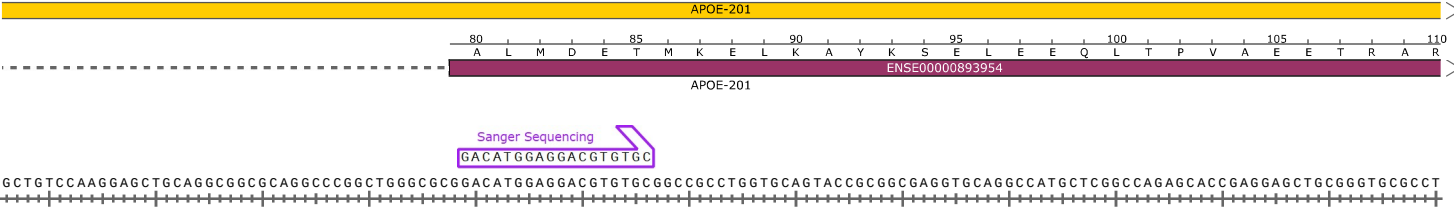
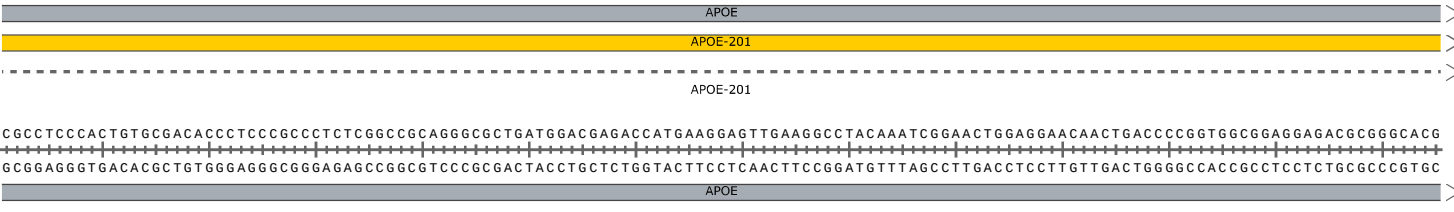
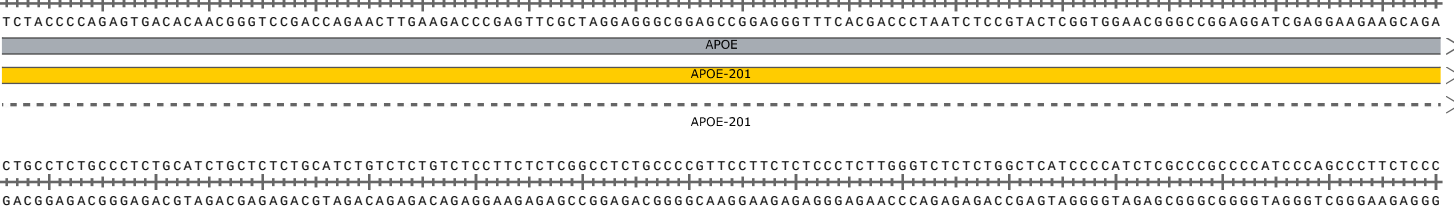
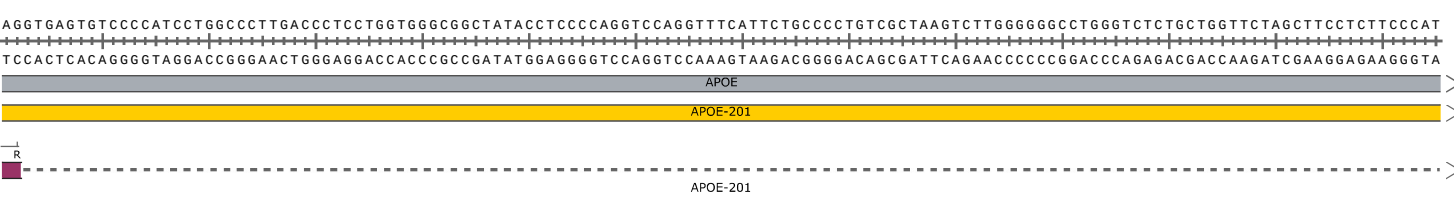
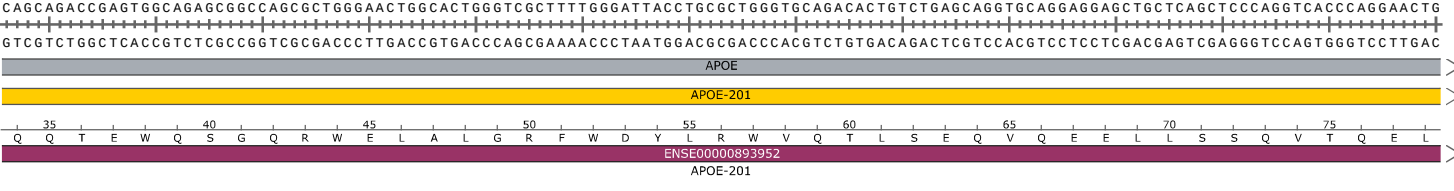
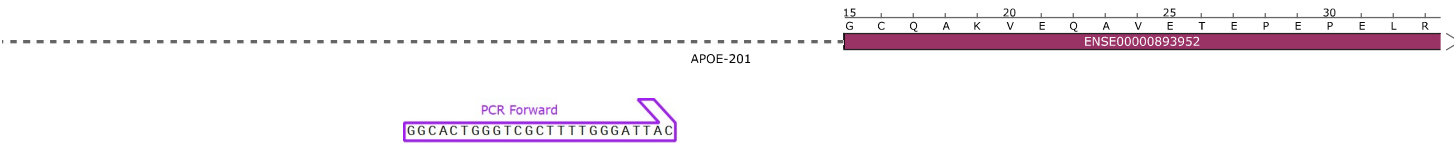
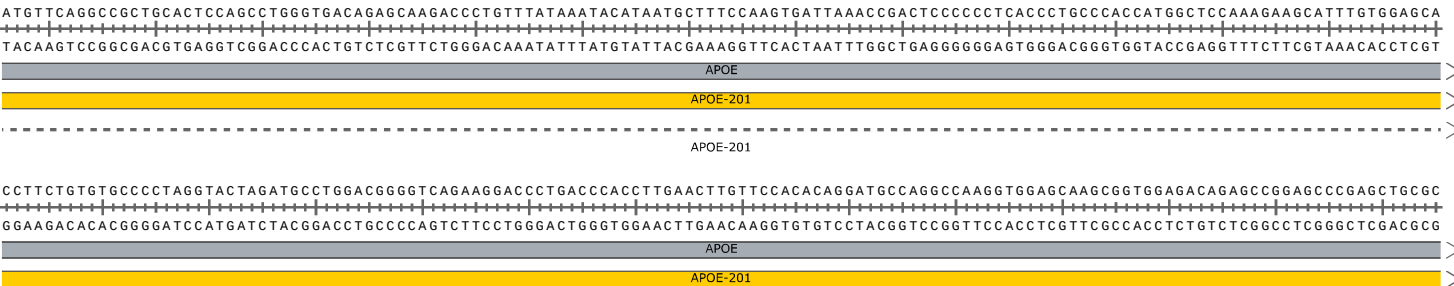


**INK2J00026.1\_APOE\_R158C\_B03\_AB**  
 3603 bp





gRNA Protospacer  
CGATGACCTGCAGAAAGCGCC

CGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCCTGGCAGTGATACAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGCCCTCAGCGCCATCCCGAGCGCCTGGG  
CGGGAGGGTGGACGCGTTCCAGCATTCCGCCGAGGAGCGCTACGGCTACTGGACGCTTTCGGACCGTACATGGTCCGGCCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGCGCTCGCGGACCC

3105

APOE

APOE-201

A S H L R K L R K R L L R D A D D L Q K R L A V Y Q A G A R E G A E R G L S A I R E R L G

ENSE00000893954

APOE-201

Donor Template WT -> SNV

Protospacer Sequence  
PAM

SNV

CGCCGAGGAGCGCTACGGCTACTGGACGCTTTCGGACCGTACATGGTCCGGCCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGCGGCTC  
Donor Template WT -> SNV

GCCCCCTGGTGGAAACAGGGCCGCTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGA  
CGGGGACCACTTGTCCCGGCGCACGCCCGGCGGTGACACCCGAGGGACCGGCCGCTCGCGCATGTCCTCGCCCGGGTCCGGACCCCGCTCGCCGACGCGCGCCCTACCTCCTCTACCCGTCGGCCCTGGGGCGCT

3240

APOE

APOE-201

P L V E Q G R V R A A T V G S L A G Q P L Q E R A Q A W G E R L R A R M E E M G S R T R D

ENSE00000893954

APOE-201

CGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGGCCAAGCTGAGGAGCAGGCCAGCAGATACGCTGACGCGGAGGCCCTCCAGGCCCGCTCAAGAGCTGGTTCCAGCCCTGGTGGAAAGACAT  
GGCGGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGCGGTTCCAGCTCCTCGTCCGGGTCGTCTATGCGGACGTCGGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACCACTTCTGTA

3375

APOE

APOE-201

R L D E V K E Q V A E V R A K L E E Q A Q Q I R L Q A E A F Q A R L K S W F E P L V E D M

ENSE00000893954

APOE-201

GCAAGCCAGTGGGCCGGGCTGGTGGAGAAAGTGCAGGCTGCCGTGGGACACAGCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC  
CGTCCGCGTCAACCGGCCGACCACTTCCACGTCGACGGCACCCGTTGTCGCGGCGGGACACGGGTCGCTGTTAGTGACTTCCGGCTTCGGACGTCGGTACGCTGGGGTGGGTCGGGTCGGGACGAGGACGG

3510

APOE

APOE-201

Q R Q W A G L V E K V Q A A V G T S A A P V P S D N H

ENSE00000893954

APOE-201

CGCTGTTAGTGACTTGGCGCTTCGG  
PCR Reverse

TCCGCGCAGCCTGCAGCGGGAGACCCTGTCCCGCCCGAGCCGCTCCTCGGGGTGGACCTAGTTTAAATAAGATTCCACCAAGTTTCACGCA  
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGGCGGGGTCGGCAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGTTCAAAGTGCGT

3'








3603

5'

APOE

APOE-201

Feature	Location	Size	Color	Strand	Type
<b>APOE</b>	1 .. 3603	3603 bp	■	→	gene
/note	= gene <a href="#">ENSG00000130203</a> Protein coding				
<b>APOE-204</b>	1 .. 3154	3154 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000446996</a>				
<b>APOE-201</b>	6 .. 3603	3598 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000252486</a>				
<b>APOE-205</b>	6 .. 1536	1531 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000485628</a> Retained intron				
<b>APOE-203</b>	22 .. 3235	3214 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000434152</a>				
<b>APOE-203</b>	79 .. 3235	3157 bp	■	→	CDS
▶ 4 segments = 807 bp					
/note	= coding sequence <a href="#">ENSP00000413653</a>				
/translation	= MSSGASRKSWDPGNPWPP,,DWPITGRKMV LWA ALLV TFLA,,GCQA KVEQAVETEPEPELRQ QTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 269 amino acids = 30.6 kDa				
<b>APOE-202</b>	570 .. 3164	2595 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000425718</a>				
<b>APOE-201</b>	835 .. 3460	2626 bp	■	→	CDS
▶ 3 segments = 954 bp					
/note	= coding sequence <a href="#">ENSP00000252486</a>				
/translation	= MKV LWA ALLV TFLA,,GCQA KVEQAVETEPEPELRQ QTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRLDDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLKSIVFPHKFDNRQVAGLVKVAAVGTSAAVPVPSDNH*				
<b>APOE-202</b>	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence <a href="#">ENSP00000410423</a>				
/translation	= MKV LWA ALLV TFLA,,GCQA KVEQAVETEPEPELRQ QTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ				
219 amino acids = 24.9 kDa					
<b>APOE-204</b>	835 .. 3154	2320 bp	■	→	CDS
▶ 3 segments = 648 bp					
/note	= coding sequence <a href="#">ENSP00000413135</a>				
/translation	= MKV LWA ALLV TFLA,,GCQA KVEQAVETEPEPELRQ QTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS				
216 amino acids = 24.6 kDa					
<b>Donor Template WT -&gt; SNV</b>	2998 .. 3097	100 bp	■	↔	misc_feature
<b>Protospacer Sequence</b>	3016 .. 3035	20 bp	■	↔	misc_feature
<b>SNV</b>	3032 .. 3032	1 bp	■	↔	misc_feature
/note	= WT = C SNV = T				
<b>PAM</b>	3036 .. 3038	3 bp	■	↔	misc_feature
<b>TEC</b>	3585 .. 9178	5594 bp	■	→	gene
/note	= gene <a href="#">ENSG00000280087</a> TEC				
<b>TEC</b>	3585 .. 9178	5594 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000623895</a> TEC				

Primer		Length		Binding Sites		Tm	Date Added
✓ <b>PCR Forward</b>		25-mer		2064 .. 2088		65°C	Oct 13, 2022
/sequence	=	GGCACTGGGTCGCITTTGGGATTAC 56% GC / 7720.1 Da					
✓ <b>Sanger Sequencing</b>		18-mer		2879 .. 2896		57°C	Oct 13, 2022
/sequence	=	GACATGGAGGACGTGTGC 61% GC / 5604.7 Da					
✓ <b>Donor Template WT -&gt; SNV</b>		100-mer		2998 .. 3097		88°C	Oct 13, 2022
/sequence	=	CTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCCGGCCTGGTACACTGCCAGGCACTTCTGCAGGTCATCGGCATCGCGGAGGAGCCGC 75% GC / 30,811.8 Da					
✓ <b>gRNA Protospacer</b>		20-mer		3016 .. 3035		63°C	Oct 13, 2022
/sequence	=	CGATGACCTGCAGAAAGCGCC 65% GC / 6112.0 Da					
✓ <b>PCR Reverse</b>		25-mer		3447 .. 3471		66°C	Oct 13, 2022
/sequence	=	GGCTTCGGCGTTCAGTGATTGTCGC 60% GC / 7696.0 Da					