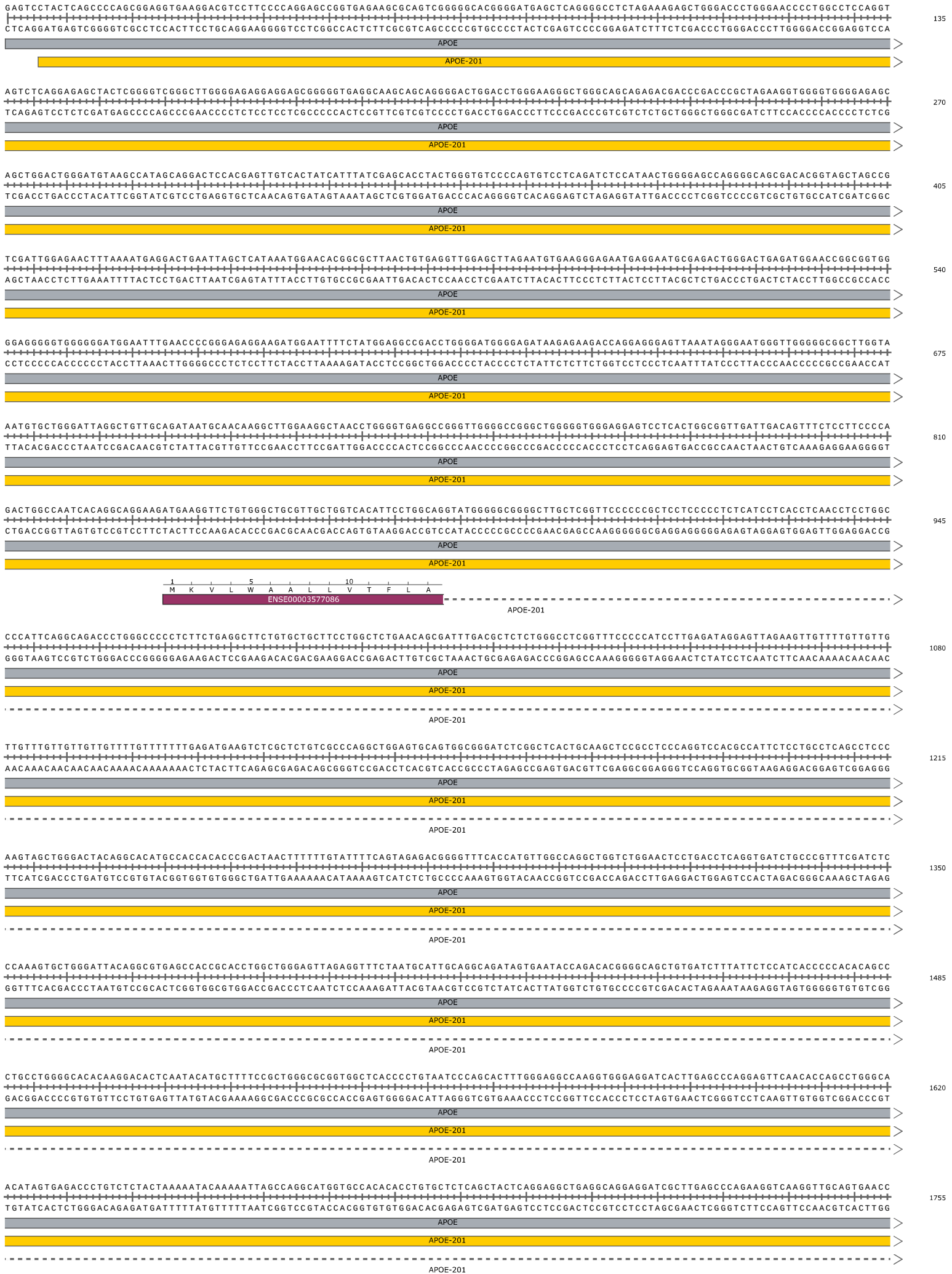


**INK2S00026.2\_APOE\_R158C\_A07\_BB**  
 3603 bp



ATGTTACAGCCCGCTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCCTGTTTATAAATACATAATGCTTTTCCAAGTGATTAACCCGACTCCCCCTCACCTGCCCCACCATGGCTCCAAAGAAGCATTTGTGGAGCA  
TACAAGTCCGGCGACGTGAGGTGCGGACCCACTGTCTCGTTCTGGGACAAATATTTATGTATTACGAAAGGTTCACTAATTTGGCTGAGGGGGGAGTGGGACGGGTGGTACCGAGGTTTCTTCGTAAACACCTCGT

1890

APOE

APOE-201

APOE-201

CCTTCTGTGTGCCCTAGGTAAGTACTAGATGCCTGGACGGGTGAGAAAGACCCCTGACCCACCTTGAACCTTGTTCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGC  
GGAAGACACACGGGGATCCATGATCTACGGACCTGCCCAAGTCTTCTGGGACTGGGTGGAACCTTGAACAAGGTGTCTCTACGGTCCGGTTCCACCTCGTTCCGCCACCTCTGTCTCGGCCCTCGGGCTCGACGGC

2025

APOE

APOE-201

APOE-201

15 20 25 30  
G C Q A K V E Q A V E T E P E P E L R  
ENSE00000893952

CAGCAGACCGAGTGGCAGAGCGGCCAGCGCTGGGAACGGCACTGGGTGCGCTTTTGGGATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTACCCAGGAACTG  
GTCGTCTGGCTCACCGTCTCGCCGGTTCGCGACCCCTTGACCGTGACCCAGCGAAAACCTAATGGACGCGACCCACGCTGTGTGACAGACTCGTCCACGTCCTCTCGACGAGTTCGAGGGTCCAGTGGGTCTTGTGAC

2160

APOE

APOE-201

APOE-201

35 40 45 50 55 60 65 70 75  
Q Q T E W Q S G Q R W E L A L G R F W D Y L R W V Q T L S E Q V Q E E L L S S Q V T Q E L  
ENSE00000893952

AGGTGAGTGTCCCATCCTGGCCCTTGACCCCTCTGGTGGGGGGCTATACCTCCCCAGGTCCAGGTTTCAATCTGCCCCGTGCGCTAAGTCTTGGGGGGCCTGGGTCTGCTGGTTCTAGCTTCTCTTCCCAT  
TCCACTCACAGGGGTAGGACCGGGAACCTGGGAGGACCAACCGCGATATGGAGGGGTCCAGGTTCAAAGTAAAGACGGGACAGCGATTTCAGAAACCCCGGACCCAGAGACGACCAAGATCGAAGGAGAAGGGTA

2295

APOE

APOE-201

APOE-201

TTCTGACTCCTGGCTTTAGCTCTCTGGAATTTCTCTCTCAGCTTTGCTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCTGCTGCTCTGCTCTTCCCTAGCTCTTTTATATAGAGACAGAG  
AAGACTGAGGACCGAAATCGAGAGACCTTAAGAGAGAGAGTCGAAACAGAGAGAGAGAAGGGAAGACTGAGTTCAGAGAGTGTGAGCAGGACCGAGACAGAGACAGGAAAGGATCGAGAAAATATATCTCTGTCTC

2430

APOE

APOE-201

APOE-201

AGATGGGGTCTCACTGTGTGCCAGGCTGGTCTTGAACCTTCTGGGCTCAAGCGATCTCCCGCCTCGGCCCTCCAAAGTCTGGGATTAGAGGCATGAGCCACCTTGCCCGGCCCTCCTAGCTCCTTCTCTGCTCT  
TCTACCCAGAGTGACACAACGGGTTCGACCCAGAACTTGAAGACCCGAGTTTCGCTAGGAGGGCGGAGCCGGAGGGTTTTCAGGACCCCTAATCTCCGTAAGTCTGGTGAACGGGCGGAGGATCGAGGAAGAAGCAGA

2565

APOE

APOE-201

APOE-201

CTGCCTCTGCCCTCTGCATCTGCTCTCTGCATCTGTCTCTGTCTCTCTTCTCTCGGCCCTGTCGCCCGTTCTTCTCTCCCTCTTGGGTCTCTCTGCTCATCCCATCTCGCCCGCCCATCCAGCCCTTCTCCC  
GACGGAGACGGGAGACGTAGACGAGAGACGTAGACAGAGACAGAGGAAGAGAGCCGGAGACGGGCAAGGAAGAGAGGGGAGAACCCAGAGAGACCGAGTAGGGGTAGAGCGGGCGGGGTAGGGTCTGGGAAGAGGG

2700

APOE

APOE-201

APOE-201

Sanger Sequencing  
CTGGAGGAACAAGTACCC  
PCR Forward  
CTGGAGGAACAAGTACCC

CGCCTCCCACTGTGCGACACCCCTCCCGCCCTCTCGGCCGAGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCACAAATCGGAAGTGGAGGAACAAGTACCCCGGTGGCGGAGGAGACGGGGCACG  
GCGGAGGGTGACACGCTGTGGGAGGGCGGAGAGCCGGCTCCCGGACTACCTGCTCTGGTACTTCTCAACTTCCGGATGTTAGCCTTGACCTCCTTGTGACTGGGGCCACCGCCTCCTCTGCGCCCGTGC

2835

APOE

APOE-201

APOE-201

80 85 90 95 100 105 110  
A L M D E T M K E L K A Y K S E L E E Q L T P V A E E T R A R  
ENSE00000893954

GCTGTCAAAGGAGCTGACGGCGGCGAGGCCGGCTGGGCGGGACATGAGGACGCTGTGCGGCCGCTGGTGCAGTACCGCGGCGAGGTGACGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGGCCCT  
CGACAGGTTCTCTGACGTCGCGCGGCTCGGGGCGGACCCGCGCTGTACTCTCTGACACCGCCGGACCCACGTCATGGCGCCGCTCCACGTCGCGTACGAGCCGGTCTCGTGCTCTCTGACGCCACCGCGGA

2970

APOE

APOE-201

APOE-201

115 120 125 130 135 140 145 150 155  
L S K E L Q A A Q A R L G A D M E D V C G R L V Q Y R G E V Q A M L G Q S T E E L R V R L  
ENSE00000893954

gRNA Protospacer  
CGATGACCTGCAGAAAGCGCC

Donor Template WT -> SNV

AGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGCCCGAGGGCCGGCCCTCAGCGCCATCCGCGAGGGCCTGGG  
CGCCTCCACCTGGCGAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGCCCGAGGGCCGGCCCTCAGCGCCATCCGCGAGGGCCTGGG  
GCGGAGGGTGGACGCGTTCGACGCATTCGCCGAGGAGGGCTACGGCTACTGGACGCTTTCGCGGACCGTTCACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGGGCTCGCGACCC

3105

APOE

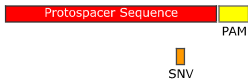
APOE-201

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

ENSE0000893954

APOE-201

Donor Template WT -> SNV



GCCCCTGGTGGAAACAGGGCCGCTGGGGCCGCCACTGTGGGCTCCCTGCCCAGGAGCCGCTACAGGAGCGGGCCCAAGCCCTGGGGCGAGGGCTCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGA  
C666GACCACTTGTCCCGCGCACGCCGGCGGTGACACCCGAGGGAGCCGGCCGCTCGGCGATGTCCTCGCCCGGGTCCGGACCCCGCTCGCCGACGCGCGCCCTACCTCTCTACCCGTCG66CTGG6CGCT

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

ENSE0000893954

APOE-201

CTACCTCCTCTACCCGTCG  
PCR Reverse

CGCCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAAGCTGGAGGAGCAGGCCACGAGATACGCCCTGACGGCCGAGGCCCTTCCAGGCCCGCCTCAAGAGCTGGTTGAGGCCCTGGTGGAAAGCAT  
GGCGGACCTGCTCCACTTCTCGTCCACCGCCTCCACGCGGGTTCGACCTCCTCGTCCGGGTCGCTCTATGCGGACGTCGGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACCACTTCTGTAT

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

ENSE0000893954

APOE-201

GCAGCGCCAGTGGGCCGGGCTGGTGGAGAAAGTGCAGGCTGCCGTGGGCACAGCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC  
CGTCGCGGTCACCCGGCCGACCACTTCTCCAGTCCGACGGCACCCGTGGTTCGGGCGGGGACACGGGTCGCTGTTAGTGACTTGGCGCTCGGACGTCGGTACGCTGGGGTGGGGGACGAGGACGG

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

ENSE0000893954

APOE-201

TCCGGCAGCCTGCAGCGGGAGACCTGTCCCGCCCGAGCCGTCCTCCTGGGGTGGACCTAGTTTAATAAAGATTACCAAGTTTCACGCA  
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGGCGGGGTCGGCAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

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,DWPITGRKMVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,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	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRLDDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLKSIVFSPHFDNRQVAGLVKVAAVGTSAAVPVPSDNH*				
<b>APOE-202</b>	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence <a href="#">ENSP00000410423</a>				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,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	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa				
<b>Donor Template WT -&gt; SNV</b>	2997 .. 3067	71 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>		20-mer		2792 .. 2811	→	58°C	Oct 13, 2022
/sequence	=	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da					
✓ <b>Sanger Sequencing</b>		20-mer		2792 .. 2811	→	58°C	Oct 13, 2022
/sequence	=	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da					
✓ <b>Donor Template WT -&gt; SNV</b>		71-mer		2997 .. 3067	→	85°C	Oct 13, 2022
/sequence	=	AGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGTGCCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGC 72% GC / 21,950.1 Da					
✓ <b>gRNA Protospacer</b>		20-mer		3016 .. 3035	→	63°C	Oct 13, 2022
/sequence	=	CGATGACCTGCAGAAGCGCC 65% GC / 6112.0 Da					
✓ <b>PCR Reverse</b>		19-mer		3211 .. 3229	←	59°C	Oct 13, 2022
/sequence	=	GCTGCCCATCTCCTCCATC 63% GC / 5635.7 Da					