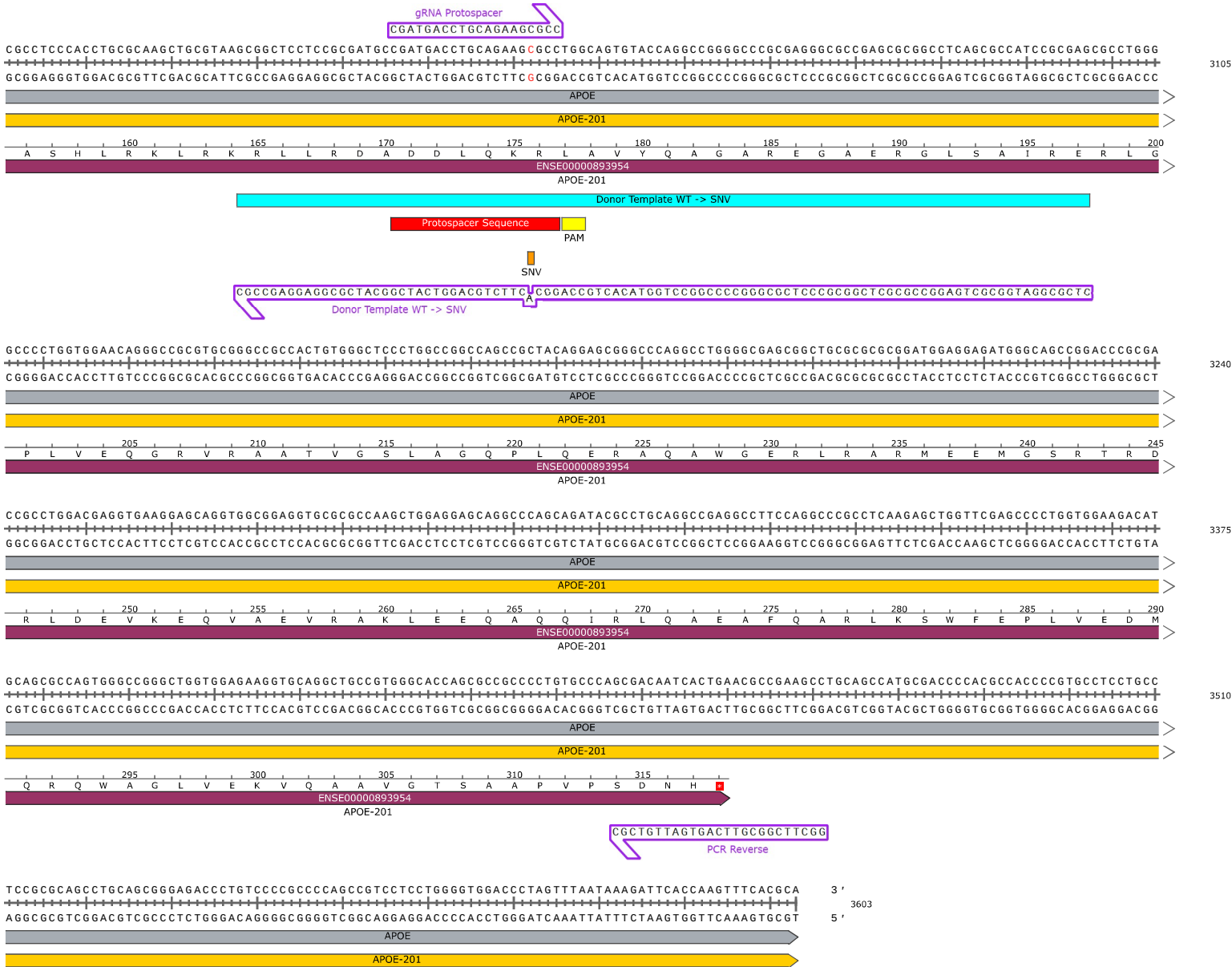

























[illegible]





Feature		Location	Size		Type
✓ APOE		1 .. 3603	3603 bp	 →	gene
/note	= gene ENSG00000130203 Protein coding				
APOE-204		1 .. 3154	3154 bp	 →	prim_transcript
/note	= primary transcript ENST00000446996				
✓ APOE-201		6 .. 3603	3598 bp	 →	prim_transcript
/note	= primary transcript ENST00000252486				
APOE-205		6 .. 1536	1531 bp	 →	prim_transcript
/note	= primary transcript ENST00000485628 Retained intron				
APOE-203		22 .. 3235	3214 bp	 →	prim_transcript
/note	= primary transcript ENST00000434152				
APOE-203		79 .. 3235	3157 bp	 →	CDS
▶ 4 segments = 807 bp					
/note	= coding sequence ENSP00000413653				
/translation	= MSSGARKSWDPGNPWPP,,DWPITGRKMKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 269 amino acids = 30.6 kDa				
APOE-202		570 .. 3164	2595 bp	 →	prim_transcript
/note	= primary transcript ENST00000425718				
✓ APOE-201		835 .. 3460	2626 bp	 →	CDS
▶ 3 segments = 954 bp					
/note	= coding sequence ENSP00000252486				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRDLDEVKEQVAEVRAKLEEQAQQIRLQAEAFQARLK SVFSPHVEFMRQVAGLVKQAAVGTSAAPVPSDNH*				
APOE-202		835 .. 3164	2330 bp	 →	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence ENSP00000410423				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa				
APOE-204		835 .. 3154	2320 bp	 →	CDS
▶ 3 segments = 648 bp					
/note	= coding sequence ENSP00000413135				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSL 216 amino acids = 24.6 kDa				
✓ Donor Template WT -> SNV		2998 .. 3097	100 bp	 ⇌	misc_feature
✓ Protospacer Sequence		3016 .. 3035	20 bp	 ⇌	misc_feature
✓ SNV		3032 .. 3032	1 bp	 ⇌	misc_feature
/note	= WT = C SNV = T				
✓ PAM		3036 .. 3038	3 bp	 ⇌	misc_feature
		3585 .. 9178	5594 bp	 →	gene
/note	= gene ENSG00000280087 TEC				
		3585 .. 9178	5594 bp	 →	prim_transcript
/note	= primary transcript ENST00000623895 TEC				

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