







INK2S00024.2_APOE_C156R_A01_AB
 3603 bp

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	= MSSGASRKSWDPGNPWPP,,DWPITGRKMKVLAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLARMEEMGSRT 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	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLARMEEMGSRTDRDLDEVKEQVAEVRKLEEQAQIRLQAEAFQAR KLVVFRLEVEEQRQVAQVLEKVAAVGTSAAPVPSDNH*		
APOE-202	835 .. 3164	2330 bp	CDS
▶ 3 segments = 658 bp			
/note	= coding sequence ENSP00000410423		
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa		
APOE-204	835 .. 3154	2320 bp	CDS
▶ 3 segments = 648 bp			
/note	= coding sequence ENSP00000413135		
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa		
Donor Template WT -> SNV	2857 .. 2931	75 bp	misc_feature
Protospacer Sequence	2876 .. 2895	20 bp	misc_feature
SNV	2894 .. 2894	1 bp	misc_feature
/note	= WT = T SNV = C		
PAM	2896 .. 2898	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	21-mer		2630 .. 2650		58°C	Aug 31, 2022
/sequence = cgttccttctctccctctTGG 57% GC / 6266.1 Da						
✓ Sanger Sequence Primer	21-mer		2630 .. 2650		58°C	Aug 31, 2022
/sequence = cgttccttctctccctctTGG 57% GC / 6266.1 Da						
✓ Donor Template WT -> SNV	75-mer		2857 .. 2931		87°C	Aug 31, 2022
/sequence = GCGCAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACC GCGGCCGAGGTGCAGGC 79% GC / 23,389.0 Da						
✓ gRNA Protospacer	20-mer		2876 .. 2895		62°C	Aug 31, 2022
/sequence = GCGGACATGGAGGACGTGTG 65% GC / 6263.1 Da						
✓ PCR Reverse	20-mer		3011 .. 3030		59°C	Aug 31, 2022
/sequence = TTCTGCAGGTCATCGGCATC 55% GC / 6084.0 Da						