

INK2S00024.2_APOE_C156R_A08_BB
3603 bp

3' GAGTCTACTCAGCCCCAGCGGAGGTGAAGGACGTCTTCCCCAGGAGCCGGTGAGAAGCCAGTGAAGCTCAGGGGCCCTAGAAAAGACTGAGCCTCGGGACCCCTGGGAAACCCCTGGCCCTCAAGGT

135

APOE

APOE-201

AGTCTCAGGAGAGCTACTCGGGGTCGGGCTTGGGGAGAGGAGGAGCGGGGGTGAAGCAAGCAGCAGGGGACTGGACCTGGGAAGGGCTGGGCAGCAGAGACGACCCGACCCGCTAGAAGTTGGGGTGGGAGAGC

270

APOE

APOE-201

AGCTGGACTGGGATGTAAGCCATAGCAGGACTCCACAGTGTGTACTATCATTATCGAGCACCTACTGGGTGTCCCCAGTGCTCTCAGATCTCCATAACTGGGGAGCCAGGGGCAGCGACACGGTAGCTAGCCG

405

APOE

APOE-201

TCGATTGGAGAACTTTAAATGAGGACTGAATTAGCTCATAAATGGAAACACGGCGTTAAGTGTGAGGTTGGAGCTTAGAAATGTTGAAGGGAAGAATGAGGAATGCGAGACTGGGACTGAGATGGAACCGCCGGTGG

540

APOE

APOE-201

GGAGGGGGTGGGGGATGGAAATTTGAACCCCGGAGAGGAAGATGGAAATTTCTATGGAGGCCACCTGGGGATGGGGAGATAAGAGAAGACAGGAGGGAGTTAAATAGGGAATGGGTTGGGGGCCGTGGTA

675

APOE

APOE-201

AATGTGCTGGGATTAGGCTGTTGCAGATAATGCAACAAGGCTTTGGAAGGCTAAGCTGGGGTGAAGGCCGGTTGGGGCGGGCTGGGGGTGGGAGGAGTCTCACTGGCCGTTGATTGACAGTTTCTCCTTCCC

810

APOE

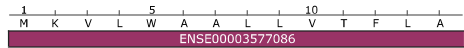
APOE-201

GACTGGCCAATCACAGGCAGGAAGATGAAGTTCTGTGGGCTGCGTTGCTGGTACATTCCTGGCAGGTATGGGGCGGGGCTTGCTCGGTTCCCCCGCTCCTCCCCCTCTCATCCTCACCTCAACCTCCTGGC

945

APOE

APOE-201



APOE-201

CCCATTAGGACGACCCCTGGGGCCCTCTTCTGAGGCTTCTGTGCTGCTTCTGGCTGTAACAGCGATTGACGCTCTCTGGCCCTCGGTTTCCCCATCCTTGAAGTAGGAGTTAGAAGTTGTTTGTGTTG

1080

APOE

APOE-201

APOE-201

TTGTTTGTGTTGTTGTTTGTGTTTTTTGAGATGAAGTCTGCTCTGTGCGCCAGGCTGGAGTGCAAGTGGCGGGATCTGGCTCACTGCAAGCTCCGCCCTCCAGGTTCCAGGCCATTTCTGCTCAGCCTCCC

1215

APOE

APOE-201

APOE-201

AAGTAGCTGGGACTACAGGCACATGCCACCACCCGACTAATTTTTGATTTTTAGTAGAGACGGGTTTTACCATGTTGGCCAGGCTGGTCTGGAACCTCCTGACCTCAGGTGATCTGCCGTTTTGATCTC

1350

APOE

APOE-201

APOE-201

CCAAAGTGTGGGATACAGCGTGAAGCCACCCGACTGCTGGAGTTAGAGGTTTCTAATGCAATGCAAGCCAGATAGTGAATACCAGACACGGGGCAGCTGTGATCTTTATCTCCATCACCCCCACACAGCC

1485

APOE

APOE-201

APOE-201

CTGCTGGGGACACAAAGGACACTCAATACATGCTTTTCCGCTGGGCGCGGTGGTCAACCCCTGTAATCCAGCACTTTGGAGGCGCAAGGTGGGAGGATCACTTGAGCCACAGAGTTCAACACAGCCCTGGCA

1620

APOE

APOE-201

APOE-201

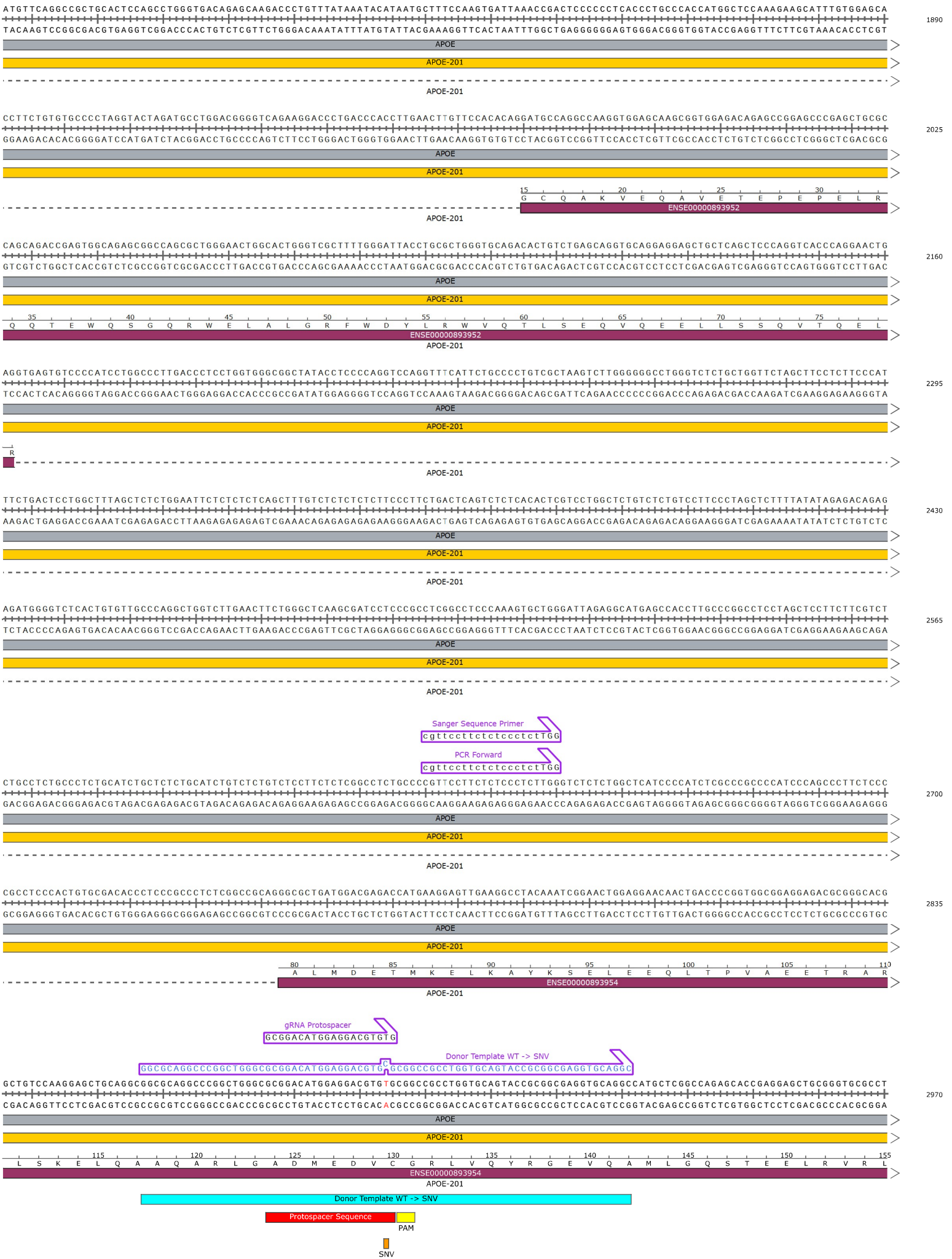
ACATAGTGAGACCCTGTCTCTACTAAAAATCAAAAAATTAGCCAGGCATGGTCCACACACCTGTGCTCTCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGCCCAAGAGTCAAGGTTGCAGTGAAC

1755

APOE

APOE-201

APOE-201



CGCCCTCCCACTTGGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGATACCAAGCCGGGGCCCGCAAGGGCCGCGAGCGCGGCTCAGCGCCATCCCGAGCGCCTGGG
GCAGGAGGGTGGACGCGTTGACGCGATTGCGCCGAGGAGGCGCTACGGCTACTGGACGTCCTCGCGGACCGTCACATGGTCCGGCCCGGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGGGCGCTCGCGGACCC

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

CTACGGCTACTGGACGTCCT
PCR Reverse

GCCCTGGTGGAAACAGGGCCGCGTGGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGA
CGGGACCACTTGTCCCGGCGACGCCCGCGGTGACACCCGAGGGACCGCGGTCGGCGATGTCTCGCCGGGTCCGGACCCGCTCGCGGACGCGCGGCTACCTCCTACCCGTCGGGCTGGGCGCT

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

CCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCAAGCTGGAGGAGCAGGCCAGCAGATACGCTGCAAGGCGAGGCCCTCAAGAGCTGGTTGAGCCCTGGTGGAGACAT
GGCGGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGGGTTCGACCTCCTCGTCCGGGTCTGTCTATGCGGACGTCGGGCTCCGGAAGGTCGGGGCGGAGTTCTCGACCAAGCTCGGGACCACTTCTGTGTA

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

GCAGCGCCAGTGGGGCCGGGCTGGTGGAGAAAGTGCAGGCTGCCGTGGGCACCGCGCCCGCTGTGCCAGCGCAATCACTGAACGCCGAAAGCCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC
CGTCCGGTCAACCGCCGACCACTTCCACGTCGACGGCACCCGTTGTCGGCGGGGACACGGGTCGCTGTTAGTGACTTGGGCTTCGGACGTCGGTACGCTGGGGTGGCGTGGGGCACGGAGGACGG

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

TCCGCGCAGCCTGCAGCGGGAGACCTGTCCCGCCCGAGCCGTCCTCGGGTGGACCTAGTTTAAATAAGATTACCAAGTTTCACGCA
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGGCGGGTGGGACAGGAGGACCCACCTGGGATCAAATTTCTAAGTGGTTCAAAGTGCCT

3'



3603

5'

APOE

APOE-201

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,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 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,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRDLDEVKEQVAEVRKLEEQAQIRLQAEAFQAR MKVLRRLVEEELRQVAQVLEKVAAVGTSAAPVPSDNH*		
APOE-202	835 .. 3164	2330 bp	CDS
▶ 3 segments = 658 bp			
/note	= coding sequence ENSP00000410423		
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa		
APOE-204	835 .. 3154	2320 bp	CDS
▶ 3 segments = 648 bp			
/note	= coding sequence ENSP00000413135		
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEVQVEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGLVEQGRVRAATVGSLS 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	=	GGCGCAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACC 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				