



INK2J00024.1_APOE_C156R_G09_AB
 3603 bp

CGCCCTCCACCTGCGCAAGCTGCGTAAGCGGGTCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGATCCAGGCCGGGGCCCGCAGGGCCGCGAGCGCGGCTCAGCGCCATCCCGCAGCGCCTGGG
GCGGAGGGTGGACGCGTTTCGACGCAATTCGCCGAGGAGGCGCTACGGCTACTGGACGTCCTTCGCGGACCGTACACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGGGCTCGCGGACCC

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

GCCCTGGTGGAAACAGGGCCGCGTGGGGCCGCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTGCGCGCGGGATGGAGGAGATGGGCAGCCGACCCGCGA
CGGGACCACTTGTCCCGGCGCACGCCGGCGGTGACACCCGAGGGACCGGCCGCTCGCGATGTCCTCGCCGGGTCCGGACCCCGCTCGCGCAGCGCGCGCTACCTCTCTACCCGTCGGCTGGGGCT

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

CGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGGCCAAGCTGGAGGAGCAGGCCAGCAGATACGCTCGAGGCCGAGGCCCTTCAGGCCCGCTCAAGAGCTGGTTGAGGCCCTGGTGGAAAGACAT
GGCGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGGTTTCGACCTCTCGTCCGGGTGCTCTATGCGGACGTCGGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGACCACTTCTGTA

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

GCAGGCCAGTGGGCCGGGCTGGTGGAGAGGTGCAGGCTGCCGTGGCCACCAGCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCTGCC
CGTCCGCGGTACCCGGCCGACCACTTCTCCACGTCGACGGCACCCGTGGTCCGCGGCGGGACACGGGTGCTGTTAGTGACTTGCGGCTTCGGACGTCGGTACGCTGGGGTGGGGCACGGAGGACGG

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

GGGTCGCTGTTAGTGACTTGGGCT
PCR Reverse

TCCGCGCAGCCTGCAGCGGGAGACCCTGTCCCGCCCAAGCCGCTCTCTGGGGTGGACCTAGTTTAATAAAGATTACCAAGTTTCACGCA
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGCGGGGTGCGCAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

3'

3603

5'

APOE

APOE-201

Feature	Location	Size	Color	Strand	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,DWPITGRKMV LWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 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,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRLDDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLK 517 amino acids = 58.4 kDa				
APOE-202	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence ENSP00000410423				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa				
APOE-204	835 .. 3154	2320 bp	■	→	CDS
▶ 3 segments = 648 bp					
/note	= coding sequence ENSP00000413135				
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa				
Donor Template WT -> SNV	2866 .. 2965	100 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	25-mer	2064 .. 2088 →	65°C	Oct 12, 2022
/sequence = GGCAC TGGGT CGCTTTTGGGATTAC 56% GC / 7720.1 Da				
✓ Sanger Sequencing Primer	20-mer	2748 .. 2767 →	56°C	Oct 12, 2022
/sequence = TGATGGACGAGACCATGAAG 50% GC / 6215.1 Da				
✓ Donor Template WT -> SNV	100-mer	2866 .. 2965 ←	88°C	Oct 12, 2022
/sequence = CACCCGACGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGGTACTGCACCAGGCGGCCGCGCACGTCCTCCATGTCCGCGCCAGCCGG 75% GC / 30,531.6 Da				
✓ gRNA Protospacer	20-mer	2876 .. 2895 →	62°C	Oct 12, 2022
/sequence = GCGGACATGGAGGACGTGTG 65% GC / 6263.1 Da				
✓ PCR Reverse	25-mer	3443 .. 3467 ←	67°C	Oct 12, 2022
/sequence = TCGGCGTTCAGTGATTGTCGCTGGG 60% GC / 7736.1 Da				