

INK2J00024.1_APOE_C156R_C01_BB
3603 bp

ATGTTCAAGCCCGCTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCCTGTTTATAAATACATAATTTTCCAAGTGATTAACCCGACTCCCCCTCACCTGCCACCATGGCTCCAAAGAAGCATTTGTGGAGCA
TACAAGTCCGGCGACGTGAGGTGCGGACCCACTGTCTCGTTCTGGGACAAATATTTATGTATTACGAAAGGTTCACTAATTTGGCTGAGGGGGAGTGGACGGGTGGTACCGAGGTTTCTTCGTAACACCTCGT

1890

APOE

APOE-201

APOE-201

CCTTCTGTGTGCCCTTAGTACTAGATGCCTGGACGGGGTTCAGAAAGACCCCTGACCCACCTTGAACCTTGTCCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGC
GGAAGACACACGGGGATCCATGATCTACGGACCTGCCCCAGTCTTCTGGGACTGGGTGGAACCTTGAACAAGGTGTCTCTACGGTCCGGTTCACCTCGTTTCGCCACCTCTGTCTCGGCCTCGGGCTCGACGGC

2025

APOE

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

APOE-201

PCR Forward
GGCACTGGGTGCTTTTGGGATTAC

CAGCAGACCAGGTGGCAGAGCGGCCAGCGCTGGGAACCTGGCACTGGGTGCTTTTGGGATTACCTGCCTGGGTGCAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCAGGTCACCCAGGAACCTG
GTCGCTGCTGCTCACCCTCGCCGGTCCGACCTTACCCTGACCGTACCCAGCGAAAACCTAATGGACGCGACCCACGCTGTGTACAGACTCGTCCAGTCTCTCGACGAGTGCAGGGTCCAGTGGTCTTGCAC

2160

APOE

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

APOE-201

AGGTGAGTGTCCCATCTCGCCCTTGACCCTCTGGTGGGCGGCTATACCTCCCGAGGTCAGGTTTTCATTCTGCCCTGTGCTAAGTCTTGGGGGGCTGGTCTCTGCTGGTTCTAGCTTCTCTTCCCAT
TCCACTCACAGGGTAGGACCGGGAACCTGGGAGGACCCCGCCGATATGGAGGGTCCAGGTCCAAGTAAGACGGGGACAGCGATTACAGAACCCCGGACCCAGAGACGACCAAGATCGAAGGAGAAGGGTA

2295

APOE

APOE-201

R
TTCTGACTCCTGGCTTTAGCTCTCTGGAATTTCTCTCTCAGCTTTGTCTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCTGGCTGTCTCTGCTGCTCCTCCCTAGCTCTTTTATATAGAGACAGAG
AAGACTGAGGACCGAAATCGAGAGACCTTAAGAGAGAGAGTGAACACAGAGAGAGAGAAGGGAAGACTGAGTCAAGAGAGTGTGAGCAGGACCGAGACAGAGACAGGAAGGATCGAGAAAATATATCTCTGTCTC

2430

APOE

APOE-201

APOE-201

AGATGGGGTCTCACTGTGTTGCCAGGCTGGTCTTGAACCTTCTGGGCTCAAGCGATCCTCCCGCCTCGGCCCTCCCAAAGTGTGGGATTAGAGGCATGAGCCACCTTGGCCGGCTCTAGCTCCTTCTCTGCTCT
TCTACCCAGAGTGACACAACGGGTCGGACCGAAGTTGAAGACCCGAGTTCGCTAGGAGGGCGGAGCCGGAGGGTTTACAGACCTAATCTCCGTAAGTGGTGGACGGGGCGGAGGATCGAGGAAGAAGCAGA

2565

APOE

APOE-201

APOE-201

CTGCCCTGCCCCCTGCACTGCTGCTCTGCACTGTCTCTGCTCTCTCTCTCTGCGCCCTGTCGCCCGTTCCCTTCTCTCCCTCTTGGGTCTCTCTGCTCATCCCCATCTCGCCCGCCCATCCCAAGCCCTTCTCCC
GACGGAGACGGGAGACGTAGACGAGAGACGTAGACAGAGACAGAGGAAGAGAGCCGGAGACGGGGCAAGGAGAGAGGGAGAACCCAGAGAGACCGAGTAGGGGTAGAGCGGGCGGGTAGGGTGGGAAAGAGGG

2700

APOE

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APOE-201

Sanger Sequencing Primer
TGATGGACGAGACCATGAA

CGCCTCCCACTGTGCGACACCCTCCCGCCCTCTCGGCCGAGGGCGGTGATGGACGAGACCATGAAAGGATTGAAGCCCTACAAATCGGAAGTGGAGGAACAAGTACCCCGGTGGCGGAGGAGACGCGGGCACG
GCGGAGGGTACACGCTGTGGGAGGGCGGGAGAGCCGGCTCCCGCACTACCTGCTCTGTTACTTCTCAACTTCCGGATGTTAGCCTTGACCTCCTTGTGACTGGGGCCACCGCTCTCTGCGCCCGTGC

2835

APOE

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 A E E T R A R
ENSE00000893954

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gRNA Protospacer
GCGGACATGGAGGACGTGTG

GCTGTCCAAGGAGCTGCAGGCGGCCGAGGCGCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCCGCTGGTGCAGTACCAGCGGAGGAGTGCAGGCGCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCAGCT
CGACAGGTTCTCGACGTCGCGCGCTCCGGCCGACCCGCGCTGTACCTCTGCACGCGCCGGCGGACCGTGTGCGCGCGCTCCAGCTCCGGTACGAGCCGGTCTCGTGGCTCTCGACGCCACCGGGA

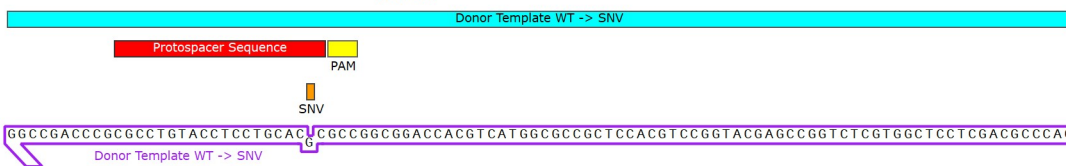
2970

APOE

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

APOE-201



CGCCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGATCCAGGCCGGGGCCCGCAGGGCCGCGAGCGCGGCTCAGCGCCATCCCGCAGCGCCTGGG
GCGGAGGGTGGACGCGTTTCGACGCAATTCGCCGAGGAGGCGCTACGGCTACTGGACGTCCTCGCGGACCGTACACATGGTCCGGCCCGGGGCGCTCCCGCGGCTCGCGCCGGAGTCGCGGTAGGGCTCGCGGACCG

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

GCCCTGGTGGAAACAGGGCCGCGTGGGGCCGCGCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTGCGCGCGGGATGGAGGAGATGGGCAGCCGACCCGCGA
CGGGACCACTTGTCCCGGCGCACGCCGGCGGTGACACCCGAGGGACCGGCCGCTCGCGATGTCCTCGCCGGGTCCGGACCCCGCTCGCCGACGCGCGCGCTACCTCCTCTACCCGTCGGCTGGGGCT

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
GGCGGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGGTTTCGACCTCCTCGTCCGGGTGCTCTATGCGGACGTCGGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACCACTTCTGTA

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

GCAGGCCAGTGGGCCGGGCTGGTGGAGAGGTGCAGGCTGCCGTGGCCACCAGCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC
CGTCCGCGTCAACCGGCCGACCACTTCTCCACGTCGACGGCACCCGTGGTCCGCGGCGGGACACGGGTGCTGTTAGTGACTTGCGGCTTCGGACGTCGGTACGCTGGGGTGGGGTGGGGCACGGAGGACGG

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

TCCGCGCAGCCTGCAGCGGGAGACCCTGTCCCGCCCGAGCCGCTCCTCGGGTGGACCTAGTTTAAATAAGATTACCAAGTTTCACGCA
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGGCGGGTCCGCAAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

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,,DWPITGRKMVLWAALLVTFLA,,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	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRDLDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLK 517 amino acids = 58.2 kDa				
APOE-202	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence ENSP00000410423				
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa				
APOE-204	835 .. 3154	2320 bp	■	→	CDS
▶ 3 segments = 648 bp					
/note	= coding sequence ENSP00000413135				
/translation	= MKVLWAALLVTFLA,,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
TEC	3585 .. 9178	5594 bp	■	→	gene
/note	= gene ENSG00000280087 TEC				
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	=	GGCACTGGGTCGCTTTTGGGATTAC 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	=	CACCCGACGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGGTACTGCACCAGCGGCCGCGCACGTCCTCCATGTCCGCGCCAGCCGG 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	=	TCGGCTTCAGTGATTGTCGCTGGG 60% GC / 7736.1 Da					