

INK2S00026.2R_APOE_R158C_A08_AA
 3603 bp

GAGTCCTACTCAGCCCCAGCGGAGGTGAAGGACGTCCTTCCCCAGGACCGGGTGAAGAAGCCAGTGAAGCTCAGGGGCGCTCTAGAAAGAGCTGGGACCCCTGGGAAACCCCTGGCCCTCAAGTT
CTCAGGATGAGTCGGGGTCGCCCTCCACTTCTGCAAGGAAAGGGTCTCTGGCCACTCTTTCGCGTCAAGCCCCGCTGCCCCACTCTCGAGTCCCCGGAGATCTTCTCGACCCCTGGGACCCCTGGGGACCCGGAGGTTCCA

135

APOE

APOE-201

AGTCTCAGGAGAGCTACTCGGGTTCGGCTTGGGGAGAGGAGGAGCGGGGGTGAAGCAAGCAGCAGGGGACTGGACCTGGGAAGGGCTGGGCAGCAGAGACGACCCGACCCGCTAGAAGTGGGGTGGGGAGAGC
TCAGAGTCTCTCGATGAGCCCCAGCCCGAACCCCTCTCCTCTGCCCCCACTCGTTCGTCGCTGCCCTGACCTGGACCCCTCCCGACCCGCTGCTCTGCTGGGCTGGGCGATCTTCCACCCCACTCCCTCTC

270

APOE

APOE-201

AGCTGGACTGGGATGTAAGCCATAGCAGGACTCCACGAGTTGTCACTATCATTATTCGAGCACCTACTGGGTGCCCAAGTGTCTCAGATCTCCATAACTGGGGAGCCAGGGGACGACACGGTAGCTAGCCG
TCGACCTGACCCCTACATTGATCGTCTCGTCTGAGGTCCTAACAGTGATAGTAAATAGCTCGTGGATGACCCACAGGGGTCACAGGAGTCTAGAGGTATTGACCCCTCGGTCCCGCTGCTGTGCCATCGATCGGC

405

APOE

APOE-201

TCGATTGGAGAACTTTAAATGAGGACTGAATTAGCTCATAAATGGAACACGGCGCTTAACCTGTGAGGTTGGAGCTTAGAATGTGAAGGGAGAAATGAGGAATGCGAGACTGGGACTGAGATGGAACCGCGGTGG
AGCTAACCTCTTGAATTTTACTCTGACTTAATCGAGTATTTACCTTGTGCCGCAATTGACACTCAAACCTCGAATCTTACACTTCCCTCTTACTCTTACGCTCTGACCCGACTCTACCTTGGCCGCCACC

540

APOE

APOE-201

GGAGGGGGTGGGGGATGGAATTTGAACCCCGGAGAGGAAGATGGAATTTCTATGGAGGCCGACTGGGGATGGGGAGATAAGAGAAGACCAAGAGGGAGTTAAATAGGGAATGGGTTGGGGCGGCTTGGTA
CCTCCCCACCCCTACCTTAACTTGGGGCCCTCTCTTACCTTAAAGATACCTCGGCTGGACCCCTACCCCTCTATTCTTCTGGTCTCCCTCAATTTATCCCTTACCACCCCGCCGCAACCAT

675

APOE

APOE-201

AATGTGCTGGGATTAGGCTGTTGACAGATAATGCAACAAGGCTTGAAGGCTAACCTGGGGTGAAGCCGGGTTGGGGCCGGGCTGGGGGTGGGAGGAGTCTCACTGGCGGTTGATTGACAGTTTCTCTTCCCCA
TTACAGGACCTAATTCGACAACTCTATTACGTTGTTCCGAACCTTCCGATTGGACCCCACTCGGCCAACCCCGGCCCGACCCACCCCTCTCAGGAGTGAACCCCACTAACTGTCAAAGAGGAGAGGGGT

810

APOE

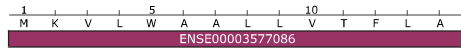
APOE-201

GACTGGCCAATCACAGGACGGAAGATGAAGTTCTGTGGGCTGCGTTGCTGGTCACTTCTGGCAGGATGGGGGCGGGCTTGGCTGGTTCCCCCGCTCTCTCCCTCTCATCTCACCTCAACCTCCTGGC
CTGACCAGTTAGTGTCCGTCCTTCTACTTCCAAGACACCCGACGCAACGACCAAGTGAAGGACCGTCCATACCCCGCCCGAACGAGCCAAGGGGGGCGAGGAGGGGGAGAGTAGGAGTGGAGTTGGAGGACCG

945

APOE

APOE-201



APOE-201

CCCATTCAAGGACAGCCCTGGGGCCCTCTTCTGAGGCTTCTGTGCTGCTTCTGGCTCTGAACAGCGATTTGACGCTCTCTGGGCTCGGTTTCCCCATCCTTGAGATAGGAGTAGAAGTTGTTTGTGTTG
GGTAAAGTCCGTCCTGGGACCCGGGGGAGAGACTCCGAAGACACGACGAAGGACCGAGACTTGTGCTAAACTGCGAGAGACCCGGAGCCAAGGGGGTAGGAACCTATCTCTAATCTTCAACAAAACAACAC

1080

APOE

APOE-201

APOE-201

TTGTTTGTGTTGTTGTTTGTGTTTTGAGATGAAGTCTCGCTCTGTGCCCCAGGCTGGAGTGCAAGTGGCGGGATCTGGCTCACTGCAAGCTCCGCCCTCCAGGTCCACGCCATTCTCTGCTCAGCCTCCC
AACAAACAACAACAACAACAAAACAAAACACTCTACTTTCAGAGCGAGACGCGGGTCCGACCTCACGTCACCGCCCTAGAGCCGAGTGACGTTTCGAGGCGGAGGGTCCAGGTGCGGTAAAGAGGACGGATCGGAGGG

1215

APOE

APOE-201

APOE-201

AAGTAGCTGGACTACAGGACATGCCACCACCCGACTAACTTTTTGTATTTTTCAGTAGAGACGGGTTTACCATGTTGGCCAGGCTGGTCTGGAACTCCTGACCTCAGGTGATCTGCCGTTTTGATCTC
TTCATCGACCTGATGTCGCTGTACGTTGTTGGGCTGATTGAAAAACATAAAGTCATCTCTGCCCCAAAGTGGTACAACCCGTCGACCAAGCTTGAAGACTGGAGTCCACTAGACGGGCAAGCTAGAG

1350

APOE

APOE-201

APOE-201

CCAAAGTGTGGGATTAAGCGCTGAGCCACCAGCCTGGCTGGGAGTTAGAGTTTCTAATGCATTGCAGGACAGATAGTGAATACAGACACGGGGCAGCTGTGATCTTTATTCTCCATCACCCCCACACAGCC
GTTTTCAGACCCCTAATGTCCGACTCGGTGGGCTGAGCCGACCCCTCAATCTCCAAAGATTACGTAACGTCGCTATCACTTATGGTCTGTGCCCGCTGACACTAGAAATAAGAGGTAGTGGGGTGTGTCGG

1485

APOE

APOE-201

APOE-201

CTGCCCTGGGACACAAAGGACTCAATACATGCTTTTCCGCTGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCCAAGTGGGAGGATCACTTGAAGCCAGGATTCAACACCAGCCTGGGCA
GACGGACCCCGTGTTCTCTGTGAGTTATGTACGAAAAGGCGACCCGGCCACCAGGTGGGACATTAAGGCTGTAAGGCTGTAAGGCTCAGGACCCCGGTTCCACCCTCTAGTGAACCTCGGGTCTCAAGTTGTGGTGGACCCGT

1620

APOE

APOE-201

APOE-201

ACATAGTGAGACCTGTCTCTACTAAAAATCAAAAAATTAGCCAGGATGTTGCCACACACCTGTGCTCTCAGCTACTCAGGAGGCTGAGGACGAGGATCGCTTGAAGCCAGAAAGTCAAGGTGCAAGTGAACC
TGTATCACTCTGGGACAGAGATGATTTTTATGTTTTTAATCGGTCCGTACCAAGTGTGTGGACACGAGAGTGCATGAGTCCCGACTCCGTCCTCTAGCGAAGCTCGGGTCTTCAAGTTCCAAAGTCACTTGG

1755

APOE

APOE-201

APOE-201

ATGTTCAAGCCCGCTGCACCTCCAAGCCTGGGTGACAGAGCAAGACCCCTGTTTATAAATACATAATGCTTTTCCAAGTGATTAACCCGACTCCCCCTCACCTGCCCCCAAGCAATTTGTGGAGCA
TACAAGTCCGGCGACGTGAGGTGCGGACCCACTGTCTCGTTCTGGGACAAATATTTATGTATTACGAAAGGTTCACTAATTTGGCTGAGGGGGGAGTGGGACGGGTGGTACCGAGGTTTCTTCGTAAACACCTCGT

1890

APOE

APOE-201

APOE-201

CCTTCTGTGTGCCCTTAGGTAAGTACTAGATGCTGGACGGGGTTCAGAAAGACCCCTGACCCACCTTGAACCTTGTTCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGC
GGAAGACACACGGGGATCCATGATCTACGGACCTGCCCAAGTCTTCTGGGACTGGGTGGAACCTTGAACAAGGTGTCTCTACGGTCCGGTTCCACCTCGTTCCGCCACCTCTGTCTCGGCCCTCGGGCTCGACGCG

2025

APOE

APOE-201

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

CAGCAGACCGAGTGGCAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTACCCAGGAACTG
GTCGTCTGGCTCACCGTCTCGCCGGTTCGCGACCCCTTGACCCTGACCCAGCGAAAACCTAATGGACGCGACCCACGCTGTGTGACAGACTGTCACGCTCCCTCCTCGACGAGTTCGAGGGTCCAGTGGGTCTTGTGAC

2160

APOE

APOE-201

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

AGGTGAGTGTCCCATCCTGGCCCTTGAACCTCCTGGTGGGGGGCTATACCTCCCCAGGTCCAGGTTTCAATCTGCCCCCTGTCGCTAAGTCTTGGGGGGCCTGGGTCTCTGCTGGTTCTAGCTTCTCTTCCCAT
TCCACTCACAGGGGTAGGACCGGGAACCTGGGAGGACCAACCGCGATATGGAGGGGTCCAGGTTCAAAGTAAAGACGGGACAGCGATTTCAGAAACCCCGGACCCAGAGACGACCAAGATCGAAGGAGAAGGGTA

2295

APOE

APOE-201

APOE-201

TTCTGACTCCTGGCTTTAGCTCTCTGGAATTTCTCTCTCAGCTTTGCTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCTGCTCTGTCTCTGCTCTTCCCTAGCTCTTTTATATAGAGACAGAG
AAGACTGAGGACCGAAATCGAGAGACCTTAAGAGAGAGAGTCGAAACAGAGAGAGAGAAGGGAAGACTGAGTTCAGAGAGTGTGAGCAGGACCGAGACAGAGACAGGAAAGGATCGAGAAAATATATCTCTGTCTC

2430

APOE

APOE-201

APOE-201

AGATGGGGTCTCACTGTGTGCCAGGCTGGTCTTGAACCTTCTGGGCTCAAGCGATCTCCCGCCTCGGCCCTCCAAAGTCTGGGATTAGAGGCATGAGCCACCTTGCCCGGCCCTCCTAGCTCCTTCTCTGCTCT
TCTACCCAGAGTGACACAACGGGTCCGACCCAGAACTTGAAGACCCGAGTTCGCTAGGAGGGCGGAGCCGGAGGGTTTTCAGGACCCCTAATCTCCGTAAGTCTGGTGAACGGGCGGAGGATCGAGGAAGAAGCAGA

2565

APOE

APOE-201

APOE-201

CTGCCTCTGCCCTCTGCATCTGCTCTCTGCATCTGTCTCTGTCTCTCTTCTCTCGGCCCTGCCCCGTTCTCTTCTCTCCCTCTGGGTCTCTCTGCTCATCCCATCTCGCCCGCCCATCCAGCCCTTCTCCC
GACGGAGACGGGAGACGTAGACGAGAGACGTAGACAGAGACAGAGGAAGAGAGCCGGAGACGGGCAAGGAAAGAGAGGGAGAACCAGAGAGACCGAGTAGGGGTAGAGCGGGCGGGGTAGGGTCTGGGAAGAGGG

2700

APOE

APOE-201

APOE-201

Sanger Sequencing
CTGGAGGAACAAGTACCC
PCR Forward
CTGGAGGAACAAGTACCC

CGCCTCCCACTGTGCGACACCTCCCGCCCTCTCGGCCGAGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCACAAATCGGAACTGGAGGAACAAGTACCCCGGTTGGCGGAGGAGACGGGGCACG
GCGGAGGGTGACACGCTGTGGGAGGGCGGAGAGCCGGCTCCCGGACTACCTGCTCTGGTACTTCTCAACTTCCGGATGTTAGCCTTGACCTCCTTGTGACTGGGGCCACCGCCTCCTCTGCGCCCGTGC

2835

APOE

APOE-201

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 E E T R A R
ENSE00000893954

GCTGTCCAAGGAGCTGACGGCGGCGAGGCCGGCTGGGCGCGGACATGAGGACGCTGTGCGGCCGCTGGTGCAGTACCGCGGCGAGGTGACGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGGCCCT
CGACAGGTTCTCTGACGCTCCGCGCGCTCGGGCCGACCCGCGCTGTACTCTCTGACACCGCCGGACCCACGTCATGGCGCCGCTCCACGTCGCGTACGAGCCGGTCTCGTGCTCTCTGACGCCACCGCGGA

2970

APOE

APOE-201

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

gRNA Protospacer

CCATCACTGCAGAACTGCC

CGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCCTGGCAGTGTACAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCTCAGCGCCATCCGCGAGCGCCTGGG
GCGGAGGGTGGACGCGTTTCGACGCATTTCGCGAGGAGGCGCTACGGCTACTGGACGCTTTCGCGAACCGTACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTTCGCGGTAGGCGCTCGCGAACCC

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

Donor Template SNV -> REV

Protospacer Sequence

PAM

SNV

CGCCGAGGAGGCGCTACGGCTACTGGACGCTTTCGCGAACCGTACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTTCGCGGTAGGCGCTC

Donor Template SNV -> REV

GCCCCGGTGGAAACAGGGCCGCGTGGCGGCCGCGCACTGTGGGCTCCTTGGCCGCGCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTCGCGCGCGGATGGAGGAGATGGGCAGCCGACCCGCGA
CGGGGACCACTTGTCCCGGCGCACGCCCGGGGCGGACACCCGAGGGACCGGCCGGTCCGCGATGTCCTCGCCGGGTCGGGACCCCGCTCGCGCAGCGCGCGCTACCTCCTTACCCGTCGGCCTGGGGCGCT

3240

APOE

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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

CTACCTCCTTACCCGTCG

PCR Reverse

CCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCAAGCTGGAGGAGCAGGCCAGCAGATACGCCTGCAGGCCGAGGCCCTTCCAGGCCCGCCTCAAGAGCTGGTTTCGAGCCCTGGTGGAAAGACAT
GGCGGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGGGTTCGACCTCCTCGTCCGGTCTGCTATGCGGACGTCGGCTCCGGAAGTCCGGCGGAGTTCTCGACCAAGCTCGGGGACCACTTCTGTA

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

GCAGCGCAGTGGGCCGGGCTGGTGGAGAAGGTGCAGGCTGCCGTTGGGCACAGCGCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC
CGTCCGGTCCACCGGCCGACCACTTCCACGTCGACGGCACCCGTTGGTTCGCGGGGACACGCGGTCGCTGTTAGTGACTTCCGGCTTCGGACGTCGGTACGCTGGGGTGGGGTGGGGCACGGAGGACGG

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

TCCGCGCAGCCTGCAGCGGGAGACCCTGTCCCGGCCAGGCCGTCCTTGGGGTGGACCCTAGTTTAAATAAGATTACCAAGTTTCACGCA
AGGCAGGTCGGACGTCGCCCTCTGGGACAGGGGCGGGTCCGCGAGGAGGCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

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,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 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,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRDLDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLK 517 amino acids = 58.4 kDa				
APOE-202	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence ENSP00000410423				
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa				
APOE-204	835 .. 3154	2320 bp	■	→	CDS
▶ 3 segments = 648 bp					
/note	= coding sequence ENSP00000413135				
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa				
Donor Template SNV -> REV	2998 .. 3097	100 bp	■	⇌	misc_feature
Protospacer Sequence	3016 .. 3035	20 bp	■	⇌	misc_feature
SNV	3032 .. 3032	1 bp	■	⇌	misc_feature
/note	= SNV = T REV = C				
PAM	3036 .. 3038	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	20-mer	2792 .. 2811 →	58°C	Oct 13, 2022
/sequence =	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da			
✓ Sanger Sequencing	20-mer	2792 .. 2811 →	58°C	Oct 13, 2022
/sequence =	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da			
✓ Donor Template SNV -> REV	100-mer	2998 .. 3097 ←	90°C	Oct 13, 2022
/sequence =	CTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCCGGCCTGGTACACTGCCAGGC GCTTCTGCAGGTCATCGGCATCGCGGAGGAGCCGC 76% GC / 30,827.8 Da			
✓ gRNA Protospacer	20-mer	3016 .. 3035 →	57°C	Oct 13, 2022
/sequence =	CGATGACCTGCAGAAAGTGCC 60% GC / 6127.0 Da			
✓ PCR Reverse	19-mer	3211 .. 3229 ←	59°C	Oct 13, 2022
/sequence =	GCTGCCCATCTCCTCCATC 63% GC / 5635.7 Da			