

**INK2J00026.1R\_APOE\_R158C\_A05\_AA**  
 3603 bp

GAGTCTACTCAGCCCCAGCGGAGGTGAAGGACGTCTTCCCAAGGACCGGTGAGAAAGCAGTCAGCTCAGGGGCTCTAGAAAGAGCTGGGACCTGGGAACCCCTGGCCCTCAAGTT  
CTCAGGATGAGTCGGGGTGCCTCCACTTCTGCAAGGAGGGTCTCGGCCACTCTTCCGCTCAGCCCCCTGCCCCCTACTCGAGTCCCGGAGATCTTCTCGACCTGGGACCCCTGGGGACCGGGTCCA

135

APOE

APOE-201

AGTCTCAGGAGAGCTACTCGGGTCTGGGCTTGGGAGAGGAGGAGCGGGGGTGAAGCAAGCAGCAGGGGACTGGACCTGGGAAGGGCTGGGACGAGAGACGACCCGACCCGCTAGAAGTGGGGTGGGAGAGC  
TCAGAGTCTCTCGATGAGCCCCAGCCCCGAACCCCTCTCCTCTGCCCCCACTCCGTTGCTGCTCCCTGACCTGGACCCCTCCCGACCCGCTGCTCTGCTGGGCTGGGCGATCTTCCACCCACCCCTCTC

270

APOE

APOE-201

AGCTGGACTGGGATGAAGCCATAGCAGGACTCCACGAGTTGTCACTATCATTATCGAGCACCTACTGGGTGCCCAAGTGCTCCAGATCTCCATAACTGGGGAGCCAGGGGACGACACCGGTAGCTAGCCG  
TCGACCTGACCCCTACATTCGATGATCGTCTGAGGTCCTAACAGTGATAGTAAATAGCTCGTGATGACCCACAGGGGTCAAGAGGATCTAGAGGATTGACCCCTCGGTCGCCGCTGCTGCTCAGATCGAC

405

APOE

APOE-201

TCGATTGGAGAACTTTAAATGAGGACTGAATTAGCTCATAAATGGAAACACGGCGTTAACTGTGAGGTTGGAGCTTAGAATGTGAAGGGAAGAATGAGGAATGCGAGACTGGGACTGAGATGGAACCGCGGTGG  
AGCTAACCTCTTGAATTTTACTCTGACTTAATCGAGTATTACCTTGTGCCGCAATTGACACTCAAACCTCGAATCTTACACTTCCCTCTTACTCTTACGCTCTGACCCGACTCTACTTTGGCCGCCACC

540

APOE

APOE-201

GGAGGGGGTGGGGGATGGAATTTGAACCCCGGAGAGGAAGATGGAATTTCTATGGAGGCCACTGGGGATGGGGAGATAAGAGAAGACAGAGGGGAGTTAAATAGGGAATGGGTTGGGGGCGGCTGGTA  
CCTCCCCACCCCTACCTTAACTTGGGGCCCTCTCTTCTACCTTAAAGATACCTCGGCTGGACCCCTACCCCTCTATTCTTCTGTGCTCCCTCAATTTATCCCTTACCACCCCGCGCAACCAT

675

APOE

APOE-201

AATGTGCTGGGATTAGGCTGTTGACAGATAATGCAACAAGGCTTGAAGGCTAACCTGGGGTGAAGCCGGGTTGGGGCCGGGCTGGGGGTTGGAGGAGTCTCACTGGCGGTTGATTGACAGTTTCTCCTTCCCA  
TTACAGGACCTAATTCGACAAAGTCTATTACGTTGTCCGAACTTCCGATTGGACCCACTCGGGCCAAACCCGGCCCGGACCCACCCCTCTCAGGAGTGACCCGCAACTAAGTGTCAAAAGAGGAGGGGT

810

APOE

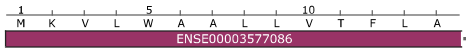
APOE-201

GACTGGCCAATCACAGGCAGGAAGATGAAGGTTCTGTGGGCTCGCTTGTGGTCACATTCCTGGCAGGTATGGGGGCGGGGCTTGGTCTGGTTCCCCCGCTCCTCCCTCTCATCCTCACCTCAACCTCCTGGC  
CTGACCAGTTAGTGCTCGCTTCTACTTCCAAGACACCCGACGCAACGACCAAGTGAAGGACCGTCCATACCCCGCCCGAACGAGCCAAGGGGGGCGAGGAGGGGGAGAGTAGGAGTGGAGTTGGAGGACCG

945

APOE

APOE-201



APOE-201

CCCATTGAGGACGACCCCTGGGCCCTCTTCTGAGGCTCTGTGCTGCTTCTGGCTCTGAACAGCGATTGACGCTCTCTGGGCTCGGTTTCCCCATCCTTGAGATAGGAGTTAGAAGTTGTTTGTGTTG  
GGTAAAGTCCGCTCGGGACCCGGGGGAGAGACTCCGAAAGACACGACGAAGGACCGAGACTTGTGCTAAACTGCGAGAGACCCGGAGCCAAGGGGGTAGGAACCTATCTCTAATCTTCAACAAAACAACAC

1080

APOE

APOE-201

APOE-201

TTGTTTGTGTTGTTGTTTGTGTTTTGTGAGATGAAGTCTCGCTCTGTGCGCCAGGCTGGAGTGACAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCCTCCAGGTCACGCCATCTCTGCTCAGCCTCCC  
AACAAAACAACAACAACAACAAAAAATCTACTTTCAGAGCGAGACGCGGGTCCGACCTCAGCTCAGCGCCCTAGAGCCGAGTGACGTTTCGAGGCGGAGGGTCCAGGTCGGTAAGAGGACGGAGTCGGAGGG

1215

APOE

APOE-201

APOE-201

AAGTAGCTGGGACTACAGGCACATGCCACCACCCGACTAACTTTTTGATTTTTAGTAAAGAGCAGGGTTTACCATTGTTGGCAGGCTGGTCTGGAACCTCCTGACCTCAGGTGATCTGCCGTTTTCGATCTC  
TTCATCGACCCTGATGTCGCTGTACGGTGGTGGGCTGATTGAAAAACATAAAAGTCATCTCTGCCCAAAGTGGTACAACCGGTCGACCAAGACCTTGGGACTGGAGTCCACTAGACGGGCAAGCTAGAG

1350

APOE

APOE-201

APOE-201

CCAAAGTGCTGGGATTACAGCGTGAGCCACCACCCGACTGACTGACTGGGAGTTAGAGGTTTCTAATGCATTGCAAGGAGATAGTAATACCAGACACGGGGCAGCTGTGATCTTTATTCTCCATCACCCACACAGCC  
GGTTTACAGACCCCTAATGTCGCACTCGGTGCGTGGACCGACCTCAATCTCCAAAGATTACGTAACGTCGGTCTATCACTTATGGTCTGTGCCCCGTCGACACTAGAAATAAGAGGTAGTGGGGGTTGTCCG

1485

APOE

APOE-201

APOE-201

CTGCCCTGGGACACAAAGGACACTCAATACATGCTTTTCCGCTGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGAGGATCACTTGAGCCCAAGAGTTCAACACCAGCCTGGGCA  
GACGGACCCCGTGTCTCTGAGTTATGTACGAAAAGGGACCCGCGCCACCGAGTGGGGACTTAGGGTCTGTAAGCCCTCCGGTCCACCCCTCTAGTGAACCTCGGGTCTCAAAGTTGTGGTGGACCCG

1620

APOE

APOE-201

APOE-201

ACATAGTGAGACCCTGTCTCTACTAAAAATCAAAAAATTAGCCAGGCATGGTGCACACACCTGTCTCTCAGCTACTCAGGAGGCTGAGGACGAGGATCGCTTGAGCCCAAGAGGTCAGGTTGCAGTGAAC  
TGTATCACTCTGGGACAGAGATGATTTTTATGTTTTTAAATCGGTCGTAACAGGTTGTGGACAGGAGTGCAGTGAAGTCTCCGACTCCGCTCCTAGCGAACTCGGGTCTTCCAGTTCCAACGTCATTTG

1755

APOE

APOE-201

APOE-201

ATGTTCAAGCCCGCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTTTATAAATACATAATGCTTCCAAGTGATTA AACCGACTCCCCCTCACCTGCCCAACATGGCTCCAAAGAAGCATTGTGGAGCA  
TACAAGTCCGGCGACGTGAGGTCGGACCCACTGTCTCGTTCTGGGACAAATATTTATGTATTACGAAAGGTTCACTAATTTGGCTGAGGGGGAGTGGACGGGTGGTACCGAGGTTTCTTCGTAACACCTCGT

1890

APOE

APOE-201

APOE-201

CCTTCTGTGTGCCCTAGGTAAGTACTAGATGCTGGACGGGGTCAGAAGGACCCCTGACCCACCTTGAACCTTGTTCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGC  
GGAAGACACACGGGGATCCATGATCTACGGACCTGCCCAAGTCTTCTGGGACTGGGTGGAACCTGAACAAGGTGTGTCTACGGTCCGGTTCACCTCTGTTCCGCACCTCTGTCTGGCTCGGGCTCGACGCG

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  
GGCACTGGGTCGCTTTTGGGATTAC

CAGCAGACCAGGTGGCAGAGCGGCCAGCGCTGGGAACCTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTGTCAGACACTGTCTGAGCAGGTGCAAGGAGGAGCTGCTCAGCTCCAGGTCACCCAGGAACTG  
GTCGCTGCTGCTCAGCTGCTCGCGGTCGCGACCTTGACCTGACCCAGCGAAACCTAATGGACGCGACCCAGCTGTGTGACAGACTCGTCCAGCTCCTCTCGACGAGTCTGAGGGTCCAGTGGGTCCTTGAC

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

AGGTGAGTGTCCCATCTGCGCCCTGACCTCTGCTGGGCGGCTATACCTCCCGAGGTCAGGTTTCAATCTGCCCCGTGCTGCTAAGTCTTGGGGGGCCTGGGCTCTGCTGCTTCTAGCTTCTCTTCCCAT  
TCCACTCACAGGGTAGGACCGGGAACCTGGGAGGACCCCGCCGATATGGAGGGTCCAGGTCCAAGTAAAGACGGGGACAGGATTGAGAACCCCGGACCCAGAGACGACCAAGATCGAAGGAGAAGGGTA

2295

APOE

APOE-201

R  
TTCTGACTCCTGGCTTTAGCTCTCTGGAATCTCTCTCTCAGCTTTGTCTCTCTCTCTCCCTTCTGACTCAGTCTCTCACACTCGTCTGGCTCTGTCTCTGTCTTCCCTAGCTCTTTTATATAGAGACAGAG  
AAGACTGAGGACCGAAATCGAGAGACCTTAAGAGAGAGAGTGAAGACAGAGAGAGAGAAGGGAAGACTGAGTCAAGAGAGTGTGAGCAGGACCGAGACAGAGACAGGAAGGATCGAGAAAATATATCTCTGTCTC

2430

APOE

APOE-201

APOE-201

AGATGGGGTCTCACTGTGTTGCCAGGCTGGTCTTGAACCTTCTGGGCTCAAGCGATCTCCCGCCTCGGCTCCCAAAGTGTGGGATTAGAGGCATGAGCCACCTTGCCCGGCCTCTAGCTCCTTCTCTGCTCT  
TCTACCCAGAGTGACACAACGGGTCGACCAAGACTTGAAGACCCGAGTTCCTAGGAGGGCGGAGCCGGAGGGTTTACGACCCCTAATCTCCGTACTCGTGGACGGGCGGAGGATCGAGGAAGAAGCAGA

2565

APOE

APOE-201

APOE-201

CTGCCCTGCGCCCTGCACTGCTCTGCACTGTCTCTGCTCTCTCTCGGCTCTGCGCCCTGCTCTCCCTCTTGGGCTCTCTGCTGCTCATCCCATCTGCGCCCGCCCATCCAGCCCTTCTCC  
GACGGAGACGGGAGACGTAGACGAGAGACGTAGACAGAGACAGAGGAAGAGAGCCGGAGACGGGGCAAGGAGAGAGGGAGAACCAGAGAGACCGAGTAGGGGTAGAGCGGGCGGGTAGGGTCTGGGAAGAGGG

2700

APOE

APOE-201

APOE-201

CGCCTCCCACTGTGCGACACCTCCCGCCCTCTCGGCGCAGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCACAAATCGGAACTGGAGGAACAACCTGACCCCGGTGGCGGAGGAGACGGGGCAG  
GCGGAGGGTGACACGCTGTGGGAGGGCGGAGAGCCGGCTCCCGGACTACTGCTCTGTTACTTCTCAACTTCCGGATGTTTAGCCTTGACCTCCTTGTGACTGGGGCCACCGCCTCTCTGCGCCCGTGC

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 E E T R A R  
ENSE00000893954

APOE-201

Sanger Sequencing  
GACATGGAGGACGTGTGC

GCTGTCAAAGGAGCTGCAAGGCGGCGAGGCGCCGGCTGGGCGCGGACATGGAGGACGTGTGCAGGCGGCTGGTGCAGTACCGCGGCGAGGTCGAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGC  
CGACAGGTTCTCTGACGCTCGCGCGCTCCGGGCGGACCCGCGCTGTACTCTCTGACACGCCGGCGGACCACTCATGGCGGCTCCAGCTCGGATACGAGCCGGTCTGCTGGCTCTCTGACGCGCCACCGCGGA

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

gRNA Protospacer

CCATCACTGCAGAACTGCC

CGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCCTGGCAGTGTACAGGCCGGGGCCCGCGAGGGGCCGAGCGCGCCTCAGCGCCATCCGCGAGCGCCTGGG  
GCGGAGGGTGGACGCGTTCCAGCGCATTCCGCGAGGAGGCGCTACGGCTACTGGACGTCTTCGCGAACCGTACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGATCGCGGTAGGCGCTCGCGAACCC

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 WT -> SNV

Protospacer Sequence

PAM

SNV

CGCCGAGGAGGCGCTACGGCTACTGGACGTCTTCGCGAACCGTACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAAGTCGCGGTAGGCGCTC

Donor Template SNV -> REV

GCCCCTGGTGGAAACAGGGCCGCGTGGCGGCCGCGCACTGTGGGCTCCTTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGA  
CGGGGACCACCTTGTCCCGGCGCACGCCCGGCGGTGACACCCGAGGAGCACGGCCGGTCCGCGATGTCTCTCGCCGGGTCCGGACCCCGCTCGCGCAGCGCGCGCTACCTCCTCTACCCGTCGGCTGGGGCGCT

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

CCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCAAGCTGGAGGAGCAGGCCAGCAGATACGCTGCAGGCCGAGGCCCTTCCAGGCCCGCCTCAAGAGCTGGTTCCGAGCCCTGGTGGAAAGACAT  
GGCGGACCTGCTCCACTTCTCGTCCACCGCCTCCACGCGG6TTGACCTCCTCGTCCGGGTGCTCTATGCGGACGTCCGGCTCCGGAAGGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACCACCTTCTGTA

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

GCAGCGCCAGTGGGCCGGGCTGGTGGAGAAAGGTGCAAGGCTGCCGTGGGCACAGCGCCGCCCTGTGCCAGCGCAATCACTGAACGCCGAAAGCTGCAAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC  
CGTCCGCGGTCACCCGGCCGACCACTTCTCCAGTCCGACGGCACCCGTGTCGCGGCGGGACACGGGTCGCTGTTAGTGACTTCCGGCTTCCGACGTCGGTACGCTGGGGTCCGGTGGGGCACGGAGGACGG

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

CGCTGTTAGTGACTTGGCGCTTCGG

PCR Reverse

TCCGCGCAGCCTGCAAGCGGGAGACCCTGTCCCGGCCAGCCGCTCCTTGGGGTGGACCTAGTTTAAATAAGATTACCAAGTTTCACGCA  
AGGCGCGTGGACGTCGCCCTCTGGGACAGGGGCGGGGTCCGCAAGGAGGCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

3'




3603

5'

APOE

APOE-201

Feature	Location	Size	Type
<b>APOE</b>	1 .. 3603	3603 bp	gene
/note	= gene <a href="#">ENSG00000130203</a> Protein coding		
<b>APOE-204</b>	1 .. 3154	3154 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000446996</a>		
<b>APOE-201</b>	6 .. 3603	3598 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000252486</a>		
<b>APOE-205</b>	6 .. 1536	1531 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000485628</a> Retained intron		
<b>APOE-203</b>	22 .. 3235	3214 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000434152</a>		
<b>APOE-203</b>	79 .. 3235	3157 bp	CDS
▶ 4 segments = 807 bp			
/note	= coding sequence <a href="#">ENSP00000413653</a>		
/translation	= MSSGASRKSWDPGNPWPP,,DWPITGRKMVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 269 amino acids = 30.6 kDa		
<b>APOE-202</b>	570 .. 3164	2595 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000425718</a>		
<b>APOE-201</b>	835 .. 3460	2626 bp	CDS
▶ 3 segments = 954 bp			
/note	= coding sequence <a href="#">ENSP00000252486</a>		
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRDLDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLKSIVFPHHFDNRQVAGLVKQAAVGTSAAPVPSDNH*		
<b>APOE-202</b>	835 .. 3164	2330 bp	CDS
▶ 3 segments = 658 bp			
/note	= coding sequence <a href="#">ENSP00000410423</a>		
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 219 amino acids = 24.9 kDa		
<b>APOE-204</b>	835 .. 3154	2320 bp	CDS
▶ 3 segments = 648 bp			
/note	= coding sequence <a href="#">ENSP00000413135</a>		
/translation	= MKVLWAAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa		
<b>Donor Template WT -&gt; SNV</b>	2998 .. 3097	100 bp	misc_feature
<b>Protospacer Sequence</b>	3016 .. 3035	20 bp	misc_feature
<b>SNV</b>	3032 .. 3032	1 bp	misc_feature
/note	= SNV = T REV = C		
<b>PAM</b>	3036 .. 3038	3 bp	misc_feature
	3585 .. 9178	5594 bp	gene
/note	= gene <a href="#">ENSG00000280087</a> TEC		
	3585 .. 9178	5594 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000623895</a> TEC		

Primer		Length		Binding Sites		Tm	Date Added
✓ <b>PCR Forward</b>		25-mer		2064 .. 2088		65°C	Oct 13, 2022
/sequence	=	GGCACTGGGTCGCTTTTGGGATTAC 56% GC / 7720.1 Da					
✓ <b>Sanger Sequencing</b>		18-mer		2879 .. 2896		57°C	Oct 13, 2022
/sequence	=	GACATGGAGGACGTGTGC 61% GC / 5604.7 Da					
✓ <b>Donor Template SNV -&gt; REV</b>		100-mer		2998 .. 3097		90°C	Oct 13, 2022
/sequence	=	CTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCCGGCCTGGTACACTGCCAGGC GCTTCTGCAGGTCATCGGCATCGCGGAGGAGCCGC 76% GC / 30,827.8 Da					
✓ <b>gRNA Protospacer</b>		20-mer		3016 .. 3035		57°C	Oct 13, 2022
/sequence	=	CGATGACCTGCAGAAGTGCC 60% GC / 6127.0 Da					
✓ <b>PCR Reverse</b>		25-mer		3447 .. 3471		66°C	Oct 13, 2022
/sequence	=	GGCTTCGGCGTTCAGTGATTGTCGC 60% GC / 7696.0 Da					