

**INK2S00026.2\_APOE\_R158C\_A01\_AB**  
3603 bp





gRNA Protospacer  
CGATGACCTGCAGAAAGCGCC

Donor Template WT -> SNV

AGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGC  
CGCCTCCACCTGGCGAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGC  
CGGGAGGGTGGACGCGTTCCGCGATTCCGCGAGGAGGCGCTACGGCTACTGGACGCTTTCGGGACCGTTCACATGGTCCGGCCCGGGCGCTCCCGCGGCTCGCGCCGGAGTCGGGTAGGGCTCGCGACCC

3105

APOE

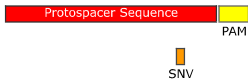
APOE-201

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



GCCCTGGTGGAAACAGGGCCGCTGGGGCCGCCACTGTGGGCTCCTGCGCGGCGAGCCGCTACAGGAGCGGGCCAGCCCTGGGGCGAGGGCTCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGA  
CGGGAGCCACCTTGTCCCGCGCACGCCGGCGGTGACACCCGAGGGAGCCGGCCGCTCGGCGATGTCCTCGCCCGGGTCCGGACCCCGCTCGCCGACGCGCGCCCTACCTCTCTACCCGTCGCGCTGGGCGCT

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

CTACCTCTCTACCCGTCG  
PCR Reverse

CGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAAGCTGGAGGAGCAGGCCAGCAGATACGCTCGAGGCCGAGGCCCTTCCAGGCCCGCCTCAAGAGCTGGTTTCGAGCCCTGGTGGAAAGCAT  
GGCGGACCTGCTCCACTTCTCCTGTCACCGCCTCCACGCGGGTTCGACCTCCTGTCGGGTCGCTCTATGCGGACGTCGGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACCCACTTCTGTGA

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

GCAGGCCAGTGGGCCGGGCTGGTGGAGAAAGTGCAGGCTGCCGTGGGCACCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAGCTGCAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC  
CGTCGCGGTCACCCGGCCGACCACTCTTCCAGTCCGACGGCACCCGTGGTTCGGGCGGGGACACGGGTCGCTGTTAGTGACTTGGCGCTCGGACGTCGGTACGCTGGGGTGGGGCACGGAGGACGG

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

TCCGGCAGCCTGCAGCGGGAGACCTGTCCCGCCCGAGCCGTCCTCCTGGGGTGGACCTAGTTTAATAAAGATTACCAAGTTTCACGCA  
AGGCGGTCGGACGTCGCCCTCTGGGACAGGGCGGGGTCGGCAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCT

3'  
3603  
5'

APOE

APOE-201

Feature	Location	Size	Color	Strand	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,DWPITGRKMVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRT 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	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRLDDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLKS 269 amino acids = 30.6 kDa				
<b>APOE-202</b>	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence <a href="#">ENSP00000410423</a>				
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQ 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	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa				
<b>Donor Template WT -&gt; SNV</b>	2997 .. 3067	71 bp	■	⇌	misc_feature
<b>Protospacer Sequence</b>	3016 .. 3035	20 bp	■	⇌	misc_feature
<b>SNV</b>	3032 .. 3032	1 bp	■	⇌	misc_feature
/note	= WT = C SNV = T				
<b>PAM</b>	3036 .. 3038	3 bp	■	⇌	misc_feature
<b>TEC</b>	3585 .. 9178	5594 bp	■	→	gene
/note	= gene <a href="#">ENSG00000280087</a> TEC				
<b>TEC</b>	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>	20-mer	2792 .. 2811 →	58°C	Oct 13, 2022
/sequence =	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da			
✓ <b>Sanger Sequencing</b>	20-mer	2792 .. 2811 →	58°C	Oct 13, 2022
/sequence =	CTGGAGGAACAACCTGACCCC 60% GC / 6096.0 Da			
✓ <b>Donor Template WT -&gt; SNV</b>	71-mer	2997 .. 3067 →	85°C	Oct 13, 2022
/sequence =	AGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGTGCCTGGCAGTGTACCAAGCCGGGGCCCGCAGGGC 72% GC / 21,950.1 Da			
✓ <b>gRNA Protospacer</b>	20-mer	3016 .. 3035 →	63°C	Oct 13, 2022
/sequence =	CGATGACCTGCAGAAGCGCC 65% GC / 6112.0 Da			
✓ <b>PCR Reverse</b>	19-mer	3211 .. 3229 ←	59°C	Oct 13, 2022
/sequence =	GCTGCCCATCTCCTCCATC 63% GC / 5635.7 Da			