

**INK2J00025.1\_APOE\_R136S\_C02.1\_BB**  
 3803 bp

3' GAGTCCTACTCAGCCCCAGCGGAGGTGAAGGACGTCTTCCCCAGGACCGGGTGAGAAAGCCAGTGAAGCTCAGGGGCCCTCTAGAAAGAGCTGGGACCCCTGGGAAACCCCTGGCCCTCCAGGT  
CTCAGGATGAGTCGGGGTCCGCTCCACTTCTGCAAGGAAAGGGTCTCTGGCCACTCTTTCGCGTCAAGCCCGTGCCTTACTCGAGTCCCAGAGATCTTCTCGACCTGGGACCCCTGGGGACCGGAGGTCCA

135

APOE

APOE-201

AGTCTCAGGAGAGCTACTCGGGTCTGGGCTTGGGGAGAGGAGGAGCGGGGGTGAAGCAAGCAGCAGGGGACTGGACCTGGGAAGGGCTGGGCAGCAGAGACGACCCGACCCGCTAGAAGTGGGGTGGGGAGAGC  
TCAGAGTCTCTCGATGAGCCCCAGCCCGAACCCCTCTCTCTGCCCCACTCTCTGTCGTCGCTGCCTTGCACCTTCCCGACCCCTTCCCGACCCGCTGCTCTGCTGGGCTGGGCGATCTTCCACCCACCCCTCTCG

270

APOE

APOE-201

AGCTGGACTGGGATGTAAGCCATAGCAGGACTCCACAGTGTGCACTATCATTATTCGAGCACCTACTGGGTGTCCCAAGTGTCTCAGATCTCCATAACTGGGGAGCCAGGGGACGACACACGGTACTAGCCG  
TCGACCTGACCCCTACATTGCGTATCGTCTGAGGTGCTCAACAGTGATAGTAAATAGCTCGTGGATGACCACAGGGGTCACAGGAGTCTAGAGGTATTGACCCCTCGGTCGCCGCTGCTGTCATCGATCGCC

405

APOE

APOE-201

TCGATTGGAGAACTTTAAATGAGGACTGAATTAGCTCATAAATGGAACACGGCGTTAAGTGTGAGGTTGGAGCTTAGAATGTGAAGGGAGAATGAGGAATGCGAGACTGGGACTGAGATGGAACCGCGGTGG  
AGCTAACCTCTTGAAATTTACTCTGACTTAATCGAGTATTTACCTTGTCCCGCAATTGACACTCCAACCTCGAATCTTACACTTCCCTCTTACTCTTACGCTCTGACCCGACTCTACTTTGGCCGCCACC

540

APOE

APOE-201

GGAGGGGGTGGGGGATGGAATTTGAAACCCGGGAGAGGAAGATGGAATTTCTATGGAGGCCACTGGGGATGGGGAGATAAGAGAAGACCAGGAGGAGTAAATAGGGAATGGGTTGGGGGCGGCTGGTA  
CCTCCCCACCCCTTACCTTAAACTTGGGGCCCTCTCTTCTACCTTAAAGATACCTCGGCTGGACCCCTACCCCTCTATTCTTCTTGGTCTCCCTCAATTTATCCCTTACCCAACCCCGCGCAACCAT

675

APOE

APOE-201

AATGTGCTGGGATTAGGCTGTTGACAGATAATGCAACAAGGCTTGAAGGGCTAACCTGGGGTGAAGGCCGGTGGGGCCGGGCTGGGGGTTGGAGGAGTCTCACTGGCGTTGATTGACAGTTTCTCTTCCCA  
TTACAGGACCTAAATCGACAAAGTCTATTACGTTGTTCCGAACTTCCGATTGAGCCCACTCGGCCCAACCCGCGCCGACCCACCCCTCTCAGGAGTGACCGCCAACTAAGTGTCAAAGAGGAAAGGGT

810

APOE

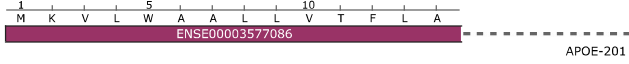
APOE-201

GACTGGCCAATCACAGGACGGAAGATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCTGGCAGGATGGGGGCGGGGCTTGGCTGGTTCCCCCGCTCTCCCTCTCATCTCACCTCAACCTCCTGGC  
CTGACCAGTGTAGTGTCCGCTCTTACTTCCAAGACACCCGACGCAACGACCAAGTGAAGGACCGTCCATACCCCGCCGCAACGAGCCAAAGGGGGGAGGAGGAGGAGTGGAGTGGAGTTGGAGGACCG

945

APOE

APOE-201



CCCATTGAGGACGACCCCTGGGCCCCCTCTTCTGAGGCTTCTGTGCTGCTTCTGGCTCTGAACAGCGATTGACGCTCTCTGGGCTCGGTTTCCCCATCCTTGAGATAGGAGTTAGAAGTTGTTTGTGTTG  
GGTAAAGTCCGCTCGGACCCGGGGAGAGGACTCCGAAGACACGACGAAGGACCGAGACTTGTGCTAAACTGCGAGAGACCCGGAGCCAAAGGGGGTAGGAACCTATCTCTCAATCTTCAACAAAACAACAAC

1080

APOE

APOE-201

APOE-201

TTGTTTGTGTTGTTGTTTGTGTTTTGAGATGAAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCTCCAGGTTCCACGCCATCTCTCTGCTCAGCCTCCC  
AACAAAACAACAACAACAACAAACTCTACTTTCAGAGCGAGACGCGGGTCCGACCTCAGCTCACCGCCCTAGAGCCGAGTGACGTTTCGAGGCGGAGGGTCCAGGTGCGGTAAAGAGGACGGATCGGAGGG

1215

APOE

APOE-201

APOE-201

AAGTAGCTGGGACTACAGGCACATGCCACCACCCGACTAACTTTTTGTATTTTCAAGTAGAGACGGGTTTTACCATGTTGGCCAGGCTGGTCTGGAACCTCCTGACCTCAGGTGATCTGCCGTTTTGATCTC  
TTCATCGACCTGATGTCGCTGTACGGTGGTGTGGCTGATTGAAAAACATAAAGTCATCTCTGCCCAAAGTGGTACAACCGGTCGACCAAGCTTGAGGACTGGAGTCCACTAGACGGGCAAGCTAGAG

1350

APOE

APOE-201

APOE-201

CCAAAGTGCTGGGATTACAGCGTGAGCCACCACCCGACTGACTGCTGGAGTTAGAGTTTCTAATGCATTGACAGGACAGATAGTGAATACCAGACACGGGACAGCTGATCTTTATTCTCCATCACCCCAACAGCC  
GGTTTACAGACCCATAATGTCGCACTCGGTGGGCGGACCCCTCAATCTCCAAAGATTACGTAACGTCGCTATCACTTATGGTCTGTGCCCGCTGACACTAGAAAATAAGAGGTAGTGGGGTGTGTCGG

1485

APOE

APOE-201

APOE-201

CTGCCCTGGGACACAAAGGACACTCAATACATGCTTTTCCGCTGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGAGGATCACTTGAGCCCAAGAGTTCAACACAGCCTGGGCA  
GACGGACCCCGTGTCTCTGTGAGTTATGTACGAAAAGGCGACCCGCGCCACCGAGTGGGGACATTAGGGTCTGTAACCCCTCCGGTTCACCCCTCTAGTGAACCTCGGGTCTCAAGTTGTGGTGGACCCGT

1620

APOE

APOE-201

APOE-201

ACATAGTGAGACCTGTCTCTACTAAAAATCAAAAAATTAGCCAGGATGGTCCACACACCTGTCTCTCAGCTACTCAGGAGGCTGAGGACGAGGATCGCTTGAGCCCAAGAGGTCAAGTTGCAAGTGAACC  
TGTATCACTCTGGGACAGAGATGATTTTTATGTTTTTAAATCGGTCGTAACCGTGTGTGGACAGGAGTGCATGAGTCTCCGACTCCGCTCTCTAGGAACTCGGGTCTTCAAGTTCCAACGTCACCTTGG

1755

APOE

APOE-201

APOE-201

ATGTTACAGCCCGCTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCCTGTTTATAAATACATAATGCTTTTCCAAAGTATTAAACCCGCTCCCCCTCACCCCTGCCACCATGGCTCCAAAGAACATTTGTGGAGCA  
TACAAGTCCGGCGACGTGAGGTGCGGACCCACTGTCTCGTTCTGGGACAAATATTTATGTATTACGAAAGGTTCACTAATTTGGCTGAGGGGGAGTGGACGGGTGGTACCGAGGTTTCTTCGTAACACCTCGT

1890

APOE

APOE-201

APOE-201

CCTTCTGTGTGCCCTTAGGTAAGATGCCTGGACGGGTGCAAGGACCCCTGACCCACCTTGAACCTTGTTCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGC  
GGAAGACACACGGGGATCCATGATCTACGGACCTGCCCAAGTCTTCTGGGACTGGGTGGAACCTTGAACAAAGGTGTCTCTACGGTCCGGTTCACCTCGTTCCGACCTCTGTCTCGGCTCGGGCTCGACGCG

2025

APOE

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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

CAGCAGACCAGGTGGCAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTGCGAGACTGTCTGAGCAGGTGCAGGAGGAGTGTCTAGCTCCCAAGTCCACCAAGAACTG  
GTCGTCTGGCTACCAGTCTCGCCGGTCCGACCCCTTGACCGTGACCCAGCGAAAACCTAATGGACGGCACCACGCTGTGACAGACTGTCACGTCCTCCTCGACGAGTCGAGGGTCCAGTGGGCTCCTTGAC

2160

APOE

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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

AGGTGAGTGTCCCATCTG6CCCTTACCCTCTGGTGGGCGGCTATACCTCCCAAGTCCAGGTTTCACTTCTGCCCTGTGCTAAAGTCTTGGGGGGCTGGGTTCTGCTGTTCTAGCTTCTCTTCCCAT  
TCCACTCACAGGGGTAGGACCGGGAACCTGGGAGGACCCCGCGGATATGGAGGGTCCAGGTCCAAAGTAAAGACGGGACAGCGATTCAGAAACCCCGGACCCAGAGACGACCAAGATCGAAGGAGAAGGGTA

2295

APOE

APOE-201

APOE-201

TTCTGACTCTGGCTTTAGCTCTCTG6AATTTCTCTCTCTCAGCTTTGTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCTG6CTCTGTCTCTGCTCTTCCCTAGCTCTTTATATAGAGACAGAG  
AAGACTGAGGACCGAAATCGAGAGACCTTAAGAGAGAGAGTCAAACAGAGAGAGAGAAGGGAAGACTGAGTCAAGAGAGTGTGAGCAGGACCGAGACAGAGACAGGAAAGGATCGAGAAAATATATCTGTCTC

2430

APOE

APOE-201

APOE-201

AGATGGGGTCTCACTGTGTTGCCAGGCTGGTCTTGAACCTTCTGGGCTCAAGCGATCCTCCCGCTCGGCTCCCAAAGTGTGGGATTAGAGGCATGAGCCACCTTGCCTGGCCCTCCTAGCTCCTTCTCGTCT  
TCTACCCAGAGTGACACAAACGGTCCGACGAGAACTTGAAGACCCGAGTTTCGCTAGGAGGGCGGAGCCGGAGGGTTTACGACCCCTAATCTCGTACTCGGTGGAACGGGCGGAGGATCGAGGAAGAAGCAGA

2565

APOE

APOE-201

APOE-201

CTGCCCTCGCCCTCTGCATCTGCTCTCTG6CATCTGTCTCTGTCTCTTCTCTCGGCTCTGCCCGTTCTTCTCTCCCTTCTG6GTTCTCTG6CTCATCCCATCTCGCCCGCCCATCCAGCCCTTCTCCC  
GACGGAGACGGGAGACGTAGACGAGAGACGTAGACAGAGACAGAGGAAGAGAGCCGAGAGCGGGCAAGGAAAGAGAGGAGAAACCCAGAGAGACCAGTGGGGTAGAGCGGGCGGGGTAGGGTGGGAAGAGGG

2700

APOE

APOE-201

APOE-201

PCR Forward  
TACAAATCGGAACCTGGAGGAACAAC

CGCCTCCCACTGTGCGACACCTCCCGCCCTCTCGGCGCAGGGCGGCTGATGGACGAGACCATGAAAGGAGTTGAAGGCCACAAATCGGAACCTGGAGGAACAACACTGACCCCGGTGGCGGAGGAGACGCGGGCACG  
GCGGAGGGTGACACGCTGTGGGAGGGCGGGAGAGCCGGCTCCCGGACTACCTGCTCTGGTACTCTCTCAACTCCGGATGTTTAGCCTTGACCTCCTTGTGACTGGGGCCACCGCTCCTTGCGCCCGTGC

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

Donor Template WT -> SNV

CGTGTGCGGCCGCTTGGTGCAGTACCGCGGAGGTCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTCAAGCCT

GCTGTCAAAGGAGCTGCAAGGCGGCGAGGCGCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCTGGTGCAGTACCGCGGAGGTCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTCAAGCCT  
CGACAGGTTCTCGACGTCGCGCGGCTCGGGCCGACCCGCGCTGTACCTCCTGCACACGCGGCGGACACGTCATGGCGCCGCTCCAGCTCCGTTACGAGCCGGTCTGCTGGCTCCTCGACGCCACCGGGA

2970

APOE

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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

Donor Template WT -> SNV

Protospacer Sequence

SNV

TCCTCGACGCCACCGGGA  
gRNA Protospacer

Donor Template WT -> SNV

CGCCTCCACCTGCGCAAAG

CGCCTCCACCTGCGCAAAGTGCCTAAGCGGCTCCTCCGCGATGCGGATGACCTGCAGAAGCGCCTGGCAGTGTACCAAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGG  
GCGGAGGGTGGACCGCTTCGACGCATTCCGCCGAGGAGCGCTACGGCTACTGGACGCTTTCGCGGACCGTACATGGTCCGGCCCCGGGGCGCTCCCGCGGCTCGCGCCGAGTCCGGGTAGCGGCTCGCGGACCC

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

PAM  
Protospacer Sequence

gRNA Protospacer

GCCCTGGTGGAAACAGGGCCGCTGCGGGCCGCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCAGGCCCTGGGGCGAGCGGCTGCGCGCGGGATGGAGGAGATGGGCAGCCGACCCGCGA  
CGGGGACACCTTGTCCCGGGCGACGCCCGGGGTGACACCCGAGGAGCCGGCCGGTCCGCGATGTCCTCGCCGGGTCCGGACCCCGCTCGCCGACCGCGCGCTACCTCCTCTACCCGTCGGCTGGGGCGCT

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

CCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCAAGCTGGAGGAGCAGGCCAGCAGATACGCTGACGGCCGAGGCCCTCCAGGCCGCTCAAGAGCTGGTTGAGCCCTGGTGGAAAGCAT  
GGCGACCTGCTCCACTTCTCGTCCACCGCTCCACGCGCGGTTGACCTCCTCGTCCGGGTGCTCTATGCGGACGTCCGGCTCCGGAAAGTCCGGGCGGAGTTCTCGACCAAGCTCGGGGACACCTTCTGTA

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 Q A R L K S W F E P L V E D M

ENSE0000893954

APOE-201

GCAAGCCAGTGGGCCGGGCTGGTGGAGGAGGTGCAAGGCTGCCGTGGGCACAGCGCCGCCCTGTGCCAGCGACAATCACTGAACGCCGAAAGCTGCAAGCCATGCGACCCACGCCACCCCGTGCCTCCTGCC  
CGTCCGGGTCAACCGGCCGACCACTTCTCCAGTCCGACGCGACCCGTGGTCCGGCGGGGACACGGGTGCTGTTAGTGACTTCGCGCTTCGGACGTCGGTACGCTGGGGTCCGGTGGGGCACGGAGGACGG

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

TCCGCGCAGCTCGAGCGGGAGACCCTGTCCCGCCGCCAGCGCTCCTCGGGGTGGACCTAGTTTAAAGATTACCAAGTTTCACGCATCTGCTGGCCCTCCCTGTGATTTCTCTAAGCCCCAGCCTC  
AGCCGCGTCGGACGTCGCCCTCTGGGACAGGGGCGGGTCCGCAAGGAGGACCCACCTGGGATCAAATATTTCTAAGTGGTTCAAAGTGCCTAGACGACCGGAGGGGACACTAAGGAGATTTCGGGTCCGGAG

3645

APOE

APOE-201

AGTTTCTCTTTCTGCCACATACTGGCCACACAATTCAGCCCCCTCCTCCTCATCTGTGTCTGTGTATCTTTCTCTCTGCCCTTTTTTTTTTTTTAGACGGAGTCTGGCTCTGTACCCAGGCTAGAGTG  
TCAAAGAGAAAGACGGGTGATGACCGGTGTTAAGAGTCCGGGGAGGAGAGGTAGACACAGACACACATAGAAAGAGAGACGGGAAAAAAAAAAAAAATCTGCCTCAGACCGAGACAGTGGGTCCGATCTCAC

3780

GAGGTAGACACAGACACATAGAA

PCR Reverse

GAGGTAGACACAGACACATAGAA

Sanger Sequencing Primer

CAGTGGCAGGATCTTGGCTCACT 3'  
3803  
GTCACCGTGTAGAACCGAGTGA 5'

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,,DWPITGRKMKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,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,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAGQPLQERAQAWGERLRARMEEMGSRTDRLDDEVKEQVAEVRALKLEEQAQQIRLQAEAFQARLK SVFSPHFDNRQVAGLVKVAAVGTSAAVPSDNH*				
<b>APOE-202</b>	835 .. 3164	2330 bp	■	→	CDS
▶ 3 segments = 658 bp					
/note	= coding sequence <a href="#">ENSP00000410423</a>				
/translation	= MKVLWAALLVTFLA,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,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,,GCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELR,,ALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLS 216 amino acids = 24.6 kDa				
<b>Donor Template WT -&gt; SNV</b>	2890 .. 2989	100 bp	■	⇌	misc_feature
<b>Protospacer Sequence</b>	2952 .. 2971	20 bp	■	⇌	misc_feature
<b>SNV</b>	2966 .. 2966	1 bp	■	⇌	misc_feature
/note	= WT = C SNV = A				
<b>PAM</b>	2972 .. 2974	3 bp	■	⇌	misc_feature
	3585 .. 9378	5794 bp	■	→	gene
/note	= gene <a href="#">ENSG00000280087</a> TEC				
	3585 .. 9378	5794 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000623895</a> TEC				

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer	2780 .. 2804	59°C	Oct 13, 2022
/sequence = TACAAATCGGAACTGGAGGAACAAC 44% GC / 7717.1 Da				
✓ <b>Donor Template WT -&gt; SNV</b>	100-mer	2890 .. 2989	88°C	Oct 13, 2022
/sequence = CGTGTGCGGCCGCCTGGTGCAGTACCGCGGCAGGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGAGCCTCGCCTCCACCTGCGCAAAG 73% GC / 30,908.9 Da				
✓ <b>gRNA Protospacer</b>	20-mer	2952 .. 2971	69°C	Oct 13, 2022
/sequence = GAGGCGCACCCGCAGTCCT 75% GC / 6064.0 Da				
✓ <b>PCR Reverse</b>	25-mer	3696 .. 3720	58°C	Oct 13, 2022
/sequence = AAGATACACACAGACACAGATGGAG 44% GC / 7726.1 Da				
✓ <b>Sanger Sequencing Primer</b>	25-mer	3696 .. 3720	58°C	Oct 13, 2022
/sequence = AAGATACACACAGACACAGATGGAG 44% GC / 7726.1 Da				