

**INK2S00027.2\_APP\_A673T\_A07\_BB**  
4054 bp

5'  
3'

ACAGTTTTTATAGGTCAGGATTTGGGATGTGGTTTAGCTGGATGGTCTCTGGCACAGTGTCCGTCATGTGGTTGCAGTTAAGACAC  
TGTCAAAAATATCCAGTCCTAAACCCTACACCAAATCGACCTACCAAGACCGTGTTCACAGGCAGTACACCAACGTCAATTCTGTG

85

APP >

APP-201 >

TGCCTGAGCTAAAGTCATCTGAAGGTTTGGATTGGACCTGGTGGGTCTGTTTTCCAACGTGGCTCACTCACGTCCTGTTACTAAGA  
ACGGACTCGATTTAGTACTTCCAAACTAACCTGGACCACCCAGACAAAAGGTTGCACCGAGTGAGTGCAGTGACAATGATTCT

170

APP >

APP-201 >

GACCTCAGTATCTTACCATGTGAACTCTGTAATGCTGCTTGAGCGTCCCTACAACATGGCATCTCGCACCCCTGCACCAAGAGGT  
CTGGAGTCATAGAATGGTACACTTGAGACATTACGACGAACTCGCAGGGATGTTGTACCGTAGAGCGTGGGGACGTGGTTCTCCA

255

APP >

APP-201 >

CCAGGAAAGAGATTAAGGAAGTTTTAGTGCCTTTTTGGCCAGTCTCAGAAGTCATACACCATCACTTCTATCATGCTCTGTTC  
GGTCCTTTCTCTAATTCCTTCAAAATCACGGAAAAACCGGGTCAGAGTCTTCAGTATGTGGTAGTGAAGATAGTACGAGACAAG

340

APP >

APP-201 >

ACTAGAGCAAGTCACTACATCCCGACCACATTGGAAGGAAGGGAATCAAGTTCTCCCTCTTGAAGGAAGGAGTATCAGCAAATTT  
TGATCTCGTTTCAAGTATGTAGGGCTGGTGTAAAGCTTCCCTTAGTTCAAGAGGGAGAAGTTCCTTCCCTCATAGTCGTTTTAAA

425

APP >

APP-201 >

GTGGATATATTTAAACTATGACATCTTGCTACCCAAGTCCAAGTTCTTATGACCCAGACCAACTGCAGGCTAAGAGAAGTGTGAA  
CACCTATATAAAATTTGATACTGTAGAACGATGGGTTCAAGGTTCAAGAATACTGGGTCTGGTTGACGTCCGATTCTCTTGAAGT

510

APP >

APP-201 >

GGGGAAGTAGCACCATTGCCTGTGGTCTTTGTGGAAAGCTGGGAAGGTAGGGATAGGAAAATGAAGTTCTGAATAGCAAAAAGGA  
CCCCTTCATCGTGGTAACGGACACCAGAAACACCTTTCGACCTTCCATCCCTATCCTTTTACTTCAAGACTTATCGTTTTTCT

595

APP >

APP-201 >

GAGAAGATAGCTTCACAATCTGTAAGCCAGGTATAGAGTGACATTGATTGTGGGTCTCTTTTCAAATAGGTTATCAAGTGGAAAGC  
CTCTTCTATCGAAGTGTTAGACATTCGGTCCATATCTCACTGTAACCTAACACCCAGAGAAAAGTTTATCCAATAGTTCACCTTCG

680

APP >

APP-201 >

TTTTTGAACAATTGGATGAGGAAATGGTGCTAGGTCACAACCAGCGTGGATTTCTAGGTTTTGTGAGATTATCCTTACCTTCTC  
AAAACTTGTAACTACTCCTTTACCACGATCCAGTGTTGGTTCGCACCTAAAGGATCCAAAACAGTCTAATAGGAATGGAAGAG

765

APP >

APP-201 >

CTTGATAGGCTGTGCTCTTAGACTGGCACATCATATGCTGTGGACATTGTGCTTTTTAGTGTGAGCAAGATGTGTCACAAGTTT  
GAACATATCCGACACGAGAATCTGACCGTGTAGTATACGACACCTGTAACACGAAAAGTCAAGTTCGTTCTACACAGTGTTCAAA

850

APP >

APP-201 >

CCCAGAATCTCGTAGACAAGATTGAAAAGAGTGATTAGGCCAAGAGCAGGAAGTGAATTCCCCTGGGAGCCAAAGGAATTGGGAAT  
GGGTCTTAGAGCATCTGTTCTAACTTTCTCACTAATCCGGTTCTCGTCTTCACTTAAGGGGACCCTCGGTTTCTTAACCCCTTA

935

APP

APP-201

GTGTAGCCCAAGTAAGACAAGAACCAGCAGGAACATGCCTCTCCTTAGGGTCGTGATACCTGTTCAAGGTTTTAATGTGGAAGGG  
CACATCGGGTTCATTCTGTTCTTGGTCGTCTTGTACGGAGAGGAATCCCAGCACTATGGACAAGTCCAAAATTACACCTTCCC

1020

APP

APP-201

AGGATTAGGCTTGCTCTGTGTTGAATCAGGCTCAAAGGATGGAAGTTACAGGGAAGCTGATTCTGGCTTCATGTAAAAAAGGAC  
TCCTAATCCGAACGAGACACAACCTTAGTCCGAGTTTCTACCTTCAATGTCCCTTCGACTAAGACCGAAGTACATTTTTTCTCG

1105

APP

APP-201

AGTTTGGGCAGGCAAATCTATCAAAAAATGGAGGGAAATTGATACATTCCTCTATGTTCAAACAGGAACTGACAATCTGCCCTG  
TCAAACCCGTCCGTTTAGATAGTTTTTACCTCCCTTTAACTATGTAAGGAGATACAAGTTTGTCTTGACTGTTAGACGGGGAC

1190

APP

APP-201

GGTGGGAACACGGTAGAGAAGATGACTTCAAAGCCCTTTTCATCCTAAAATTCTGATGTTTGATAATTAAATGTTATAGCATGG  
CCACCCTTGTGCCATCTCTTCTACTGAAGTTTTTCGGGAAAAGTAGGATTTAAGACTACAAACTATTAATTTACAATATCGTACC

1275

APP

APP-201

ACACTGACATTTACATTTTTTACTTATGTTTTTGGTTTTTAAATGACTCTGCATTTTGTTTAAGCTTCAAATTATTATTTGAAT  
TGTGACTGTAAATGTAAAAAATGAATACAAAAACCAAAAATTTACTGAGACGTAAAAACAAAATTCGAAGTTTAATAATAAACTTA

1360

APP

APP-201

AATGAAATTCATCAGAACAATTAGTGTTAAGAATCATATAGCAATTTATAGAAAAGGAAGAGTTCGTAGGTTATAAATCTGTTA  
TTACTTTAAGTAGTCTTGTTAATCACAATTCCTAGTATATCGTTAAATATCTTTTCTTCTCAAGCATCCAATATTTAAGACAAT

1445

APP

APP-201

GTTGCTAAGAAGCATTTTTTAAAATTATGTAATATAGCTCTTTATTTCAGCAGACGAACCAATTACAATCTGTGTAAGTACACT  
CAACGATTCTTCGTAAAAATTTAATACATGATATCGAGAAATAAGTCGTCTGCTTGGTTAATGTTAGACACATTGATCTTGTGA

1530

APP

APP-201

TGACTAAAATTATATAATTTTTACAACGCTTCACTGCATAGATACATGAACATAATTTATTTGTAATTGGAACAAAGCCCCAAAG  
ACTGATTTTTAATATATTTAAAAATGTTGCGAAGTGACGTATCTATGTAATTTGTAATTAATAAACATTAACCTTGTTCGGGGTTTC

1615

APP

APP-201

TAGCAGTTTTGTTCTACCAGGTAATTAATGCTCATTTTTAAAGCCTTTTATTATTATTTCTGAAGTAATGAGTGCACATGGAAAA  
ATCGTCAAAACAAGATGGTCCATTAATTACGAGTAAAAATTTTCGGAAAATAATAATAAAGACTTCATTACTCACGTGTACCTTTT

1700

APP

APP-201

AGACACATAATAGGCTAAACAATAAGCCCCTAAGCCAAGCCAACATATTTCCAGGAACAAATCCTTGCCAACCTCTCAACCAGGAT  
TCTGTGTATTATCCGATTTTGTATTTCGGGCATTTCGGTTTCGGTTGTATAAGGTCCTTGTTTAGGAACGGTTGGAGAGTTGGTCTTA

1785

APP

APP-201

PCR Reverse

AGCCTTACTTTTCAGGTTTCCCT

TAACTTCTGCTTTTCCCCCATTTTCAAAAATTATAGCATGTATTTAAAGGCAGCAGAAGCCTTACTTTTCAGGTTTCCCTTACCC  
AATTGAAGACGAAAAGGGGGTAAAAGTTTTAATATCGTACATAAATTTCCGTCGTCTTCGGAATGAAAAGTCCAAAAGGGAATGGG

1870

APP

APP-201

TTTCATTTCTTTTTGTTCAAAATAGGTAGTAATTGAAGTTTTAAATATAGGGTATCATTTTTCTTTAAGAGTCATTTATCAATTT  
AAAGTAAAGAAAAACAAGTTTTATCCATCATTAACTTCAAAAATTTATATCCCATAGTAAAAAGAAATTTCTCAGTAAATAGTTAAA

1955

APP

APP-201

TCTTCTAACTTCAGGCCTAGAAAAGAAGTTTTGGGTAGGCTTTGTCTTACAGTGTTATTATTTATGAGTAAACTAATTTGGTTGTC  
AGAAGATTGAAGTCCGGATCTTTCTTCAAAACCCATCCGAAACAGAATGTCACAATAATAAATACTCATTTTTGATTAACCAACAG

2040

APP

APP-201

gRNA Protospacer

GGAGATCTCTGAAGTGAAGA

CTGCATACTTTAATTATGATGTAATACAGGTTCTGGGTTGACAAATATCAAGACGGAGGAGATCTCTGAAGTGAAGATGGATGCA  
GACGTATGAAATTAATACTACATTATGTCCAAGACCCAACCTGTTTATAGTTCTGCCTCCTCTAGAGACTTCACTTCTACCTACGT

2125

APP

APP-201

S G L T 660 I K T E 665 I S E V 670 K M D A

ENSE00001318724

APP-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

ACTGTTTATAGTTCTGCCTCCTCTAGAGACTTCACTTCTACCTAAGT

Donor Template WT -> SNV

GAATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAATTTGGTACGTAAAATAATTTACCTCTTTCCACTACTGTTTGTCT  
CTTAAGGCTGTAAGTCTGAGTCTTCAAGTAGTAGTTTTAACCATGCATTTTATTAATGGAGAAAAGGTGATGACAAACAGA

2210

APP

APP-201

E F R H D S 675 G Y E V 680 H H Q K L V R K I I Y L F P L L F V 685

ENSE00001318724

APP-201

(in frame with APP-201)

Donor Template WT -> SNV

CTTAAGGCTGTAAGTCTGAGTCTTCAAGTAGTAGTTTTT


Donor Template WT -> SNV

TGCCAAATGACCTATTAACCTCTGGTTCATCCTGTGCTAGAAATCAAATTAAGGAAAAGATAAAAAATACAATGCTTGCCTATAGGA  
ACGGTTTACTGGATAATTGAGACCAAGTAGGACACGATCTTTAGTTTAATTCCTTTTTCTATTTTTATGTTACGAACGGATATCCT

2295

APP

APP-201

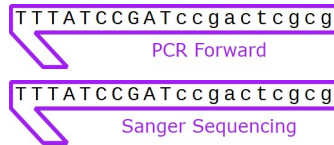
L P N D L L T L V H P V L E I K L R K R   
----- (in frame with APP-201) ----->

TTACCATGAAAACATGAAGAAAATAAATAGGCTAGGCTGAGCGCAGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCAAG  
AATGGTACTTTTGTACTTCTTTATTTATCCGATCCGACTCGCGTCACCGAGTTCGGACATTAGGGTCGTGAAACCTCCGGTTC

2380

APP

APP-201



GCGGGTGGATCACGAGGTCAGAAATTCGAGACCAGCCTGGCCAATATGGTGAAACCCCATCTCTACTAAAAATACAAAAAGATT  
CGCCACCTAGTGCTCCAGTCTTTAAGCTCTGGTCGGACCGTTATACCACTTTGGGGTAGAGATGATTTTTATGTTTTTTCTAA

2465

APP

APP-201

AGCTGGGTGTGGTGGCAAACACCTGTAGTCCCAGCTGCTGGGGAGGCTGACGCAGGAGACTTGCTTGAACCCAGGAGGTGGAGGT  
TCGACCCACACCACCGTTTGTGGACATCAGGGTCGACGACCCCTCCGACTGCGTCCTCTGAACGAACTTGGGTCTCCACCTCCA

2550

APP

APP-201

TGCAGTGAGCTGAGATCGTGCCTAGGCGACAGAGCGAGACTCCATCCCAAAAAAAAAAAGAAAAGAAAGAGGCTGTATGTATAG  
ACGTCACTCGACTCTAGCACGGATCCGCTGTCTCGCTCTGAGGTAGGGTTTTTTTTTTTTCTTTCTTTCTCCGACATACATATC

2635

APP

APP-201

TTCTTTTCAGACTACAAGGCAGCAAAGTTTCGTGCATGACTCGGGACTTAAAGTGGAAATTAATTTCAATATAGCAGCCACTTTGACT  
AAGAAAGTCTGATGTTCCGTCGTTTCAAGCACGTAAGTTCACCTTAATTAAGTTATATCGTCGGTGAAACTGA

2720

APP

APP-201

TCCACTGTGTTTTCTGGGAAAAATAGGTTTACAATAGGTTTATTTGAAGGATCAAACACATGCATACACTGCTTGGTTTTACAGAA  
AGGTGACACAAAAGACCCTTTTATCCAAATGTTATCCAAATAAACTTCCTAGTTTGTGTACGTATGTGACGAACCAAAATGTCTT

2805

APP

APP-201

CACTTTATGTGGCTTAAATTCACATCCGGAAGTGTCTTCTTTACCCATTCATTTCTCCCCAGCTCTTTCTTTTCATTCCCTCC  
GTGAAATACACCGAATTTAAGTGTAGGCCTTGACAGAAGGAAATGGGTAAGTAAAGAGGGGGTTCGAGAAAAGAAAAGTAAGGGAGG

2890

APP

APP-201

CCTACCTCCCATGATTTAACTTCTTTCGCAAGAGTAAGATCATGGAGTGAGCAGGACCCCATGATGTTCCCGATAGTGTATTCA  
GGATGGAGGGTACTAAATTTGAAGAGAACGTTCTCATTCTAGTACCTCACTCGTCTGGGGTACTACAAGGGCTATCACAAATAAGT

2975

APP

APP-201

TCAAAAAGGTTTGTGCAAAGAAGACAGCAGCTTCTTTTTTCAGATGAAATCACTTTTTCCCCCTAATGTTAGAATTGGAGTAAATCA  
AGTTTTCCAAACACGTTTCTTCTGTCGTCGAAGGAAAAGTCTACTTTAGTGAAAAGGGGGGATTACAATCTTAACCTCATTAGT

3060

APP

APP-201

AAAAGCCACATCTCCTTTGTGGTCAGCTCTAGTAGTTATATAAAATCCTTTACCAAAGCTTAGAAATGGAGATAAATCAAATCG  
TTTTCGGTGTAGAGGAAACACCAGTCGAGATCATCAATATATTTAGGAAATGGTTTTCGAATCTTTACCTCTATTTAGTTTAGC

3145

APP

APP-201

TGGATTATGTTAGGGTCCATCTTATCAGTAGGTGCAGTAAGAGGGTTAAATTAATGAAGACGACAATTTTATCACATTCAGTGG  
ACCTAATACAATCCCAAGGTAGAATAGTCATCCACGTCATTCTCCAATTTAATTACTTCTGCTGTTAAAATAGTGTAAGTCACC

3230

APP

APP-201

TGGACAGAAAAATGGTAAGAAAAATTTCCATAGCAATAATACTTAAAGTTATCTCAGGCACTTCTTTTTGTTTTGTTTTGTGTGTGT  
ACCTGTCTTTTTACCATTCTTTTAAAGGTATCGTTATTATGAATTTCAATAGAGTCCGTGAAGAAAAACAAAACAAACACACACA

3315

APP

APP-201

GTGTGTGTGAGTGTTACTTTTTTCCAAGCAGAAAAATGCTTTTTCAATATTCATAAAGTTGATAAATCCTAGTATTAATCTCTAAA  
CACACACACTCACAATGAAAAAAGGTTTCGCTTTTTACAGAAAAAGTTATAAGTATTTCAACTATTTAGGATCATAATTAGAGATTT

3400

APP

APP-201

AGAAACACCTCCAAATTATTATTTATGCCTTACTTGACTCCAAATAATTGTAGCAAATAAAAACTGACTTGGGATTTGGATTTG  
TCTTTGTGGAGGTTTAATAATAAATACGGAATGAACTGAGGTTTATTAACATCGTTTTATTTTTGACTGAACCCTAAACCTAAAC

3485

APP

APP-201

CATTCTTAACTCCCATAGTTCTTTTTTTGTAGAAAGACATTTAGCTTTTTGAAGCATGGTTTTTCATTGGCAAGATAATCTAGTAT  
GTAAGAATTGAGGGTATCAAGAAAAAACATCTTCTGTAAATCGAAAACTTCGTACCAAAGTAACCGTTCTATTAGATCATA

3570

APP

APP-201

CAGTTGTTATAAGATCAGGGTTTTCTCTTGATGAGGCTGTTGCTGAAGAGGTTAATAAAAACTGGGGAACCACTAAAGAGTTGAAG  
GTCAACAATATTCTAGTCCCAAAGAGAAGTACTCCGACAACGACTTCTCCAATTTTTTTGACCCCTTGGTGATTTCTCAACTTC

3655

APP

APP-201

AGTTGGTGGGGTAGAAAAGCTGACGATTAATGTACAGATTTGCATTTGTCGGGGCCTGGGGCCTGTGTCATATAAGCCCATCCCCA  
TCAACCACCCCATCTTTGACTGCTAATTACATGTCTAAACGTAAACAGCCCCGGACCCCGGACACAGTATATTCGGGTAGGGGT

3740

APP

APP-201

CAATTACACTAACGCCTATAATGCGACAGTGACTAATGGCAGCGGCAGCAATTAGGAGAATCAGCTCCCTCTACTGGACTAGTTA  
GTTAATGTGATTGCGGATATTACGCTGTCACTGATTACCGTCGCCGTCGTTAATCCTCTTAGTCGAGGGGAGATGACCTGATCAAT

3825

APP

APP-201

AGATAATGTATTATAATTAGTGCAATGAATATTACAAAATTACAGTATTTTCTTAAAGGCACAGGCATATGTCCAGACTTGTATT  
TCTATTACATAATATTAATCACGTTACTTATAATGTTTTAATGTCATAAAAAGAATTTCCGTGTCCGTATACAGGTCTGAACATAA

3910

APP

APP-201

TATTCCTGATTACCTCACACTAGTATATTAGCTAATTAATGATTTGCTTTTCATAAAAATGTTGAGCTAGCATATTTGTTTAGTA  
ATAAGGACTAATGGAGTGTGATCATATAATCGATTAATTACTAAACGAAAAGTATTTTACAACCTCGATCGTATAAACAAATCAT

3995

APP

APP-201

AAGGGAATAATTATGAACAATTTCTCATTGTTATAAACCACGAGTAAAACACTTTTA  
TTCCCTTATTAATACTTGTAAAGAGTAAAACAATATTTGGTGCTCATTGTTGAAAAAT





































3'

4054

5'








APP

APP-201

Feature		Location	Size			Type
✓ <b>APP</b>		1 .. 4054	4054 bp			gene
/note	= gene <a href="#">ENSG00000142192</a> Protein coding					
<b>APP-DT</b>		1 .. 4054	4054 bp			gene
/note	= gene <a href="#">ENSG00000273492</a> lncRNA					
✓ <b>APP-201</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000346798</a>					
<b>APP-202</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000348990</a>					
<b>APP-203</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000354192</a>					
<b>APP-204</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000357903</a>					
<b>APP-205</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000358918</a>					
<b>APP-206</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000359726</a>					
<b>APP-208</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000439274</a>					
<b>APP-209</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000440126</a>					
<b>APP-DT-201</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000608591</a> lncRNA					
<b>APP-DT-202</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000609365</a> lncRNA					
<b>APP-DT-203</b>		1 .. 4054	4054 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000664668</a> lncRNA					
<b>APP-213</b>		1760 .. 4054	2295 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000464867</a> Retained intron					
✓ <b>APP-201</b>		2070 .. 2170	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence <a href="#">ENSP00000284981</a>					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
<b>APP-202</b>		2070 .. 2170	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence <a href="#">ENSP00000345463</a>					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
<b>APP-203</b>		2070 .. 2170	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence <a href="#">ENSP00000346129</a>					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
<b>APP-204</b>		2070 .. 2170	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence <a href="#">ENSP00000350578</a>					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					



Feature	Location	Size			Type
<b>APP-205</b>	2070 .. 2170	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000351796</a>				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
<b>APP-206</b>	2070 .. 2170	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000352760</a>				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
<b>APP-208</b>	2070 .. 2170	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000398879</a>				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
<b>APP-209</b>	2070 .. 2170	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000387483</a>				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
✓ <b>Donor Template WT -&gt; SNV</b>	2079 .. 2167	89 bp			misc_feature
✓ <b>Protospacer Sequence</b>	2098 .. 2117	20 bp			misc_feature
✓ <b>PAM</b>	2118 .. 2120	3 bp			misc_feature
✓ <b>SNV</b>	2123 .. 2123	1 bp			misc_feature
/note	= WT = G SNV = A				

Primer	Length		Binding Sites		Tm	Date Added
✓ <b>PCR Reverse</b>	22-mer		1844 .. 1865		58°C	Jan 10, 2023
/sequence	= AGCCTTACTTTCAGGTTCCCT 45% GC / 6627.4 Da					
✓ <b>Donor Template WT -&gt; SNV</b>	89-mer		2079 .. 2167		71°C	Jan 10, 2023
/sequence	= TTTTGGATGATGAACATTCATATCCTGAGTCATGTCGGAATTCTGTATCCATCTTCACTTCAGAGATCTCCTCCGTCTTGATATTTGTCA 38% GC / 27,232.8 Da					
✓ <b>gRNA Protospacer</b>	20-mer		2098 .. 2117		52°C	Jan 10, 2023
/sequence	= GGAGATCTCTGAAGTGAAGA 45% GC / 6230.1 Da					
✓ <b>PCR Forward</b>	20-mer		2320 .. 2339		60°C	Jan 10, 2023
/sequence	= gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da					
✓ <b>Sanger Sequencing</b>	20-mer		2320 .. 2339		60°C	Jan 10, 2023
/sequence	= gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da					