

INK2S00027.2_APP_A673T_A02_AB
4564 bp

5'
3'

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GGGATATTTTTATTACAGTCTTTCCAAGCAAAGTCGTCTTACTCAACTTTGAATTGGTTTTTTATGAATTGTTATAATTTTCATT

85

APP

APP-201

GAAAATAAATAAGAATAGAGAACTCTGTGGGTCTCGTAGCAAGAAGTTGGGGGTTGAGGGTTAGGTCATTGAGAGGACCAGAGTT
CTTTTATTTATTCTTATCTCTTGAGACACCCAGAGCATCGTTCTTCAACCCCCAACTCCCAATCCAGTAACTCTCCTGGTCTCAA

170

APP

APP-201

AAAGAATGAGAAAAGGAAACTGTCCCACTTCCATTGTGCCTTTTATGTCTATATTAAGAGAATGAACTTCTGATGAAAAGGAAAT
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255

APP

APP-201

TAAAGCCCGAGATAGATCAACATGAGAAAAGAAAGCCCTAGCCATTAGTTACCTATTGCTACGTAGCAAATAACGCGAGAATTT
ATTTCCGGCTCTATCTAGTTGTACTCTTTTCTTTCCGGATCGGGTAATCAATGGATAACGATGCATCGTTTATTGCGCTCTTAAA

340

APP

APP-201

AGCAGCTTAAAAACAACAAGCATTAGTTTCTTACAGTTTTTATAGGTCAGGATTTGGGATGTGGTTTAGCTGGATGGTTCTGGCAC
TCGTGCAATTTTGTGTTTCTGTAATCAAAGAATGTCAAAAATATCCAGTCTTAAACCCTACACCAAATCGACCTACCAAGACCGTG

425

APP

APP-201

AGTGTCCGTCATGTGGTTGCAGTTAAGACTGCCTGAGCTAAAGTCATCTGAAGGTTTATTGGACCTGGTGGGCTCTGTTTCCA
TCACAGGCAGTACACCAACGTCAATTCTGTGACGGACTCGATTTTCACTAGACTTCCAAACTAACCTGGACCACCCAGACAAAAGGT

510

APP

APP-201

ACGTGGCTCACTCACGTCCTGTTACTAAGAGACCTCAGTATCTTACCATGTGAACTCTGTAATGCTGCTTGAGCGTCCCTACAA
TGCACCGAGTGAGTGCAGTGACAATGATTCTCTGGAGTCATAGAATGGTACACTTGAGACATTACGACGAACTCGCAGGGATGTT

595

APP

APP-201

CATGGCATCTCGCACCCCTGCACCAAGAGGTCCAGGAAAAGAGATTAAGGAAGTTTTTATGTCCTTTTTTGGCCCACTCTCAGAAGT
GTACCGTAGAGCGTGGGGACGTGGTTCTCCAGGTCCTTTCTCTAATTCTTCAAATCACGGAAAAAACCGGGTCAGAGTCTTCA

680

APP

APP-201

CATACCCATCACTTCTATCATGCTCTGTTCACTAGAGCAAGTCACTACATCCCGACCACATTCGAAGGAAGGGAATCAAGTTCT
GTATGTGGTAGTGAAGATAGTACGAGACAAGTGATCTCGTTCACTGATGTAGGGCTGGTGTAAAGCTTCTTCCCTTAGTTCAAGA

765

APP

APP-201

CCCTCTTGAAGGAAGGAGTATCAGCAAATTTGTGGATATATTTAACTATGACATCTTGTACCCAAGTCCAAGTTCTTATGAC
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850

APP

APP-201

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935

APP

APP-201

AGGAAAATGAAGTTCTGAATAGCAAAAAGGAGAGAAGATAGCTTCACAATCTGTAAGCCAGGTATAGAGTGACATTGATTGTGGG
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1020

APP

APP-201

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1105

APP

APP-201

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1190

APP

APP-201

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1275

APP

APP-201

AATCCCTGGGAGCCAAAAGGAATTGGGAATGTGTAGCCCAAGTAAGACAAGAACCAGCAGGAACATGCCTCTCCTTAGGGTCGT
TTAAGGGGACCCCTCGGTTTCTTAACCCTTACACATCGGGTTCATTCTGTTCTTGGTCGTCCTTGTACGGAGAGGAATCCCAGCA

1360

APP

APP-201

GATACCTGTTCAAGGTTTTAATGTGGAAGGGAGGATTAGGCTTGCTCTGTGTTGAATCAGGCTCAAAGGATGGAAGTTACAGGGA
CTATGGACAAGTTCCAAAATTACACCTTCCCTCCTAATCCGAACGAGACACA AACTTAGTCCGAGTTTCTACCTTCAATGTCCCT

1445

APP

APP-201

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1530

APP

APP-201

TGTTCAAACAGGAACTGACAATCTGCCCTGGGTGGGAACACGGTAGAGAAGATGACTTCAAAGCCCTTTTCATCCTAAAATTC
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1615

APP

APP-201

TGATGTTTGATAATTAATGTTATAGCATGGACACTGACATTTACATTTTTTACTTATGTTTTTGGTTTTTAAATGACTCTGCAT
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1700

APP

APP-201

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1785

APP

APP-201

AGGAAGAGTTCGTAGGTTATAAATTCTGTTAGTTGCTAAGAAGCATTTTTAAAATTATGTACTATAGCTCTTTATTTCAGCAGACG
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1870

APP

APP-201

AACCAATTACAATCTGTGTAAGTACTAGAACACTTGACTAAAATTATATAATTTTTTACAACGCTTCACTGCATAGATACATGAACATA
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1955

APP

APP-201

ATTTATTTGTAATTGGAACAAAGCCCCAAAGTAGCAGTTTTGTTCTACCAGGTAATTAATGCTCATTTTTAAAGCCTTTTATTAT
TAAATAAACATTAACCTTGTTTCGGGGTTTCATCGTCAAAACAAGATGGTCCATTAATTACGAGTAAAAATTCGGAAAAATAATA

2040

APP

APP-201

TATTTCTGAAGTAATGAGTGCACATGGAAAAAGACACATAATAGGCTAAACAATAAGCCCGTAAGCCAAGCCAACATATTCCAGG
ATAAAGACTTCATTACTCACGTGTACCTTTTTCTGTGTATTATCCGATTTGTTATTTCGGGCATTTCGGTTTCGGTTGTATAAGGTCC

2125

APP

APP-201

AACAAATCCTTGCCAACCTCTCAACCAGGATTTAACTTCTGCTTTTCCCCATTTTCAAAAATTATAGCATGTATTTAAAGGCAG
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2210

APP

APP-201

PCR Reverse

AGCCTTACTTTTCAGGTTTCCCT

CAGAAGCCTTACTTTTCAGGTTTCCCTTACCCTTTTCATTTCTTTTTGTTTCAAAATAGGTAGTAATTGAAGTTTTAAATATAGGGTA
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2295

APP

APP-201

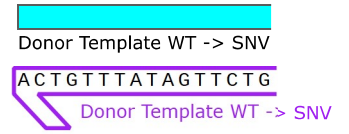
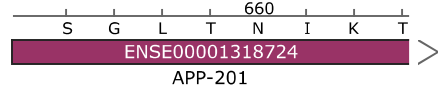
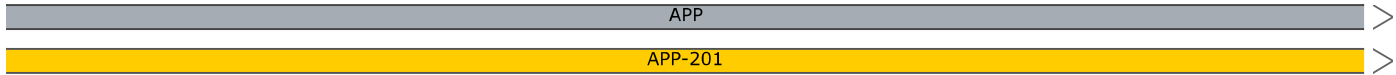
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2380

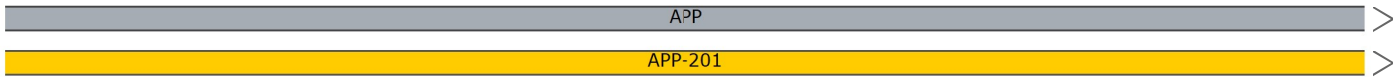
APP

APP-201

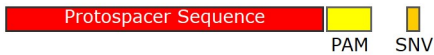
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GGAGGAGATCTCTGAAGTGAAGATGGATGCAGAAATTCGACATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTACGTAAA
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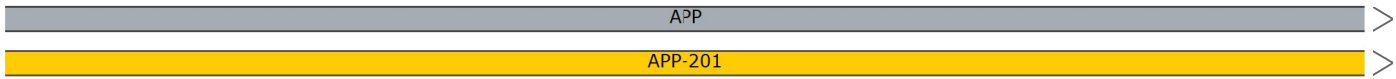


E E I S E V K M D A E F R H D S G Y E V H Q K L V R K
ENSE00001318724
APP-201



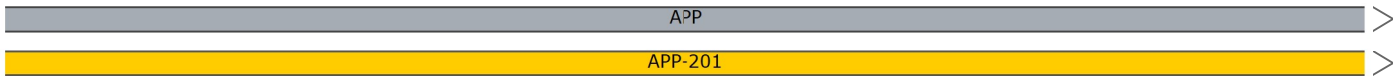
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Donor Template WT -> SNV

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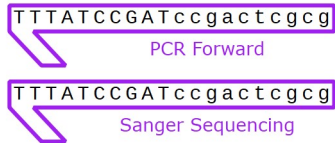


I I Y L F P L L F V L P N D L L T L V H P V L E I K L R
(in frame with APP-201)

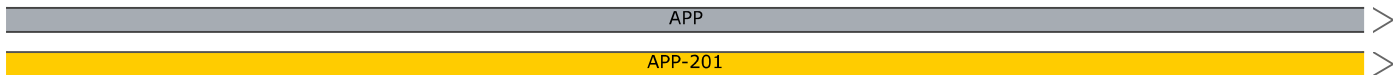
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K R *



GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATCACGAGGTCAGAAATTCGAGACCAGCCTGGCCAATATGGTGAAA
CGGACATTAGGGTCGTGAAACCTCCGGTTCCGCCACCTAGTGCTCCAGTCTTTAAGCTCTGGTCGGACCGGTTATACCACTTT



CCCCATCTCTACTAAAAATACAAAAAAGATTAGCTGGGTGTGGTGGCAAACACCTGTAGTCCCAGCTGCTGGGGAGGGCTGACGCA
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2890

APP

APP-201

GGAGACTTGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCTAGGCGACAGAGCGAGACTCCATCCCCAAAA
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2975

APP

APP-201

AAAAAAGAAAAGAAAAGAGGGCTGTATGTATAGTTCTTTTCAGACTACAAGGCAGCAAAGTTCGTGCATGACTCGGGACTTAAAGTGG
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3060

APP

APP-201

AATTAATTTCAATATAGCAGCCACTTTGACTTCCACTGTGTTTTCTGGGAAAAATAGGTTTACAATAGGTTTATTTGAAGGATCAA
TTAATTAAGTTATATCGTCGGTGAAACTGAAGGTGACACAAAAGACCCTTTTATCCAAATGTTATCCAAATAAACTTCCTAGTT

3145

APP

APP-201

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3230

APP

APP-201

TCTCCCCAGCTCTTTCTTTTCATTCCCTCCCTACCTCCCATGATTTAACTTCTCTTGCAAGAGTAAGATCATGGAGTGAGCAG
AGAGGGGGTTCGAGAAAAGAAAAGTAAGGGAGGGGATGGAGGGTACTAAATTGAAGAGAACGTTCTCATTCTAGTACCTCACTCGTC

3315

APP

APP-201

GACCCCATGATGTTCCCGATAGTGTATTTCATCAAAAGGTTTGTGCAAAGAAGACAGCAGCTTCCTTTTCAGATGAAATCACTTT
CTGGGGTACTACAAGGGCTATCACAATAAGTAGTTTTCCAAACACGTTTCTTCTGTCGTCGAAGGAAAAGTCTACTTTAGTGAAA

3400

APP

APP-201

TCCCCCTAATGTTAGAAATGGAGTAAATCAAAAAGCCACATCTCCTTTGTGGTCAGCTCTAGTAGTTATATAAAATCCTTTACC
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3485

APP

APP-201

AAAAGCTTAGAAATGGAGATAAATCAAATCGTGGATTATGTTAGGGTTCCATCTTATCAGTAGGTGCAGTAAGAGGGTTAAATTA
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3570

APP

APP-201

ATGAAGACGACAATTTTATCACATTCAGTGGTGGACAGAAAAATGGTAAGAAAAATTTCCATAGCAATAATACTTAAAGTTATCTC
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3655





































APP

APP-201

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3'
4564
5'



Feature		Location	Size			Type
✓ APP		1 .. 4564	4564 bp			gene
/note	= gene ENSG00000142192 Protein coding					
APP-DT		1 .. 4564	4564 bp			gene
/note	= gene ENSG00000273492 lncRNA					
✓ APP-201		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000346798					
APP-202		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000348990					
APP-203		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000354192					
APP-204		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000357903					
APP-205		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000358918					
APP-206		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000359726					
APP-208		1 .. 4564	4564 bp			prim_transcript
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APP-209		1 .. 4564	4564 bp			prim_transcript
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APP-DT-201		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000608591 lncRNA					
APP-DT-202		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000609365 lncRNA					
APP-DT-203		1 .. 4564	4564 bp			prim_transcript
/note	= primary transcript ENST00000664668 lncRNA					
APP-213		2131 .. 4564	2434 bp			prim_transcript
/note	= primary transcript ENST00000464867 Retained intron					
✓ APP-201		2441 .. 2541	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence ENSP00000284981					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
APP-202		2441 .. 2541	101 bp			CDS
/codon_start	= 1					
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/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
APP-203		2441 .. 2541	101 bp			CDS
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/note	= coding sequence ENSP00000346129					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					
APP-204		2441 .. 2541	101 bp			CDS
/codon_start	= 1					
/note	= coding sequence ENSP00000350578					
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa					

Feature	Location	Size			Type
APP-205	2441 .. 2541	101 bp			CDS
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/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
APP-206	2441 .. 2541	101 bp			CDS
/codon_start	= 1				
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/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
APP-208	2441 .. 2541	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000398879				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
APP-209	2441 .. 2541	101 bp			CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000387483				
/translation	= SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL 33 amino acids = 3.8 kDa				
✓ Donor Template WT -> SNV	2450 .. 2538	89 bp			misc_feature
✓ Protospacer Sequence	2469 .. 2488	20 bp			misc_feature
✓ PAM	2489 .. 2491	3 bp			misc_feature
✓ SNV	2494 .. 2494	1 bp			misc_feature
/note	= WT = G SNV = A				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Reverse	22-mer	2215 .. 2236	58°C	Jan 10, 2023
/sequence = AGCCTTACTTTCAGGTTTCCTT 45% GC / 6627.4 Da				
✓ Donor Template WT -> SNV	89-mer	2450 .. 2538	71°C	Jan 10, 2023
/sequence = TTTTGGATGATGAACCTTCATATCCTGAGTCATGTCGGAATTCTGTATCCATCTTCACTTCAGAGATCTCCTCCGTCTTGATATTTGTCA 38% GC / 27,232.8 Da				
✓ gRNA Protospacer	20-mer	2469 .. 2488	52°C	Jan 10, 2023
/sequence = GGAGATCTCTGAAGTGAAGA 45% GC / 6230.1 Da				
✓ PCR Forward	20-mer	2691 .. 2710	60°C	Jan 10, 2023
/sequence = gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da				
✓ Sanger Sequencing	20-mer	2691 .. 2710	60°C	Jan 10, 2023
/sequence = gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da				