

APP-201

Donor Template WT -> SNV

Protospacer Sequence

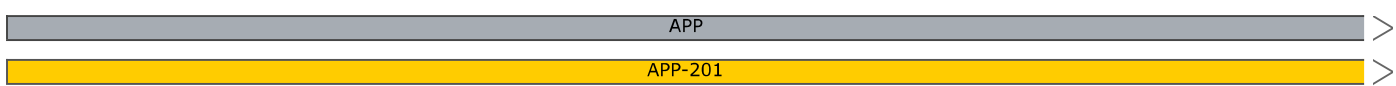
SNV

INK2S00119_APP_V717I_A10_BB
6468 bp

5'
3'

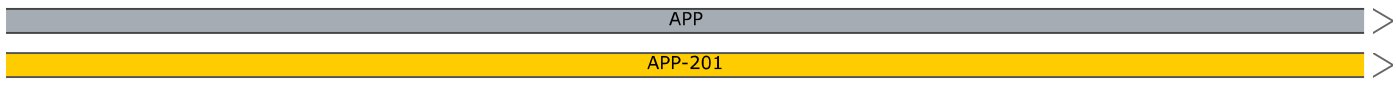
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85



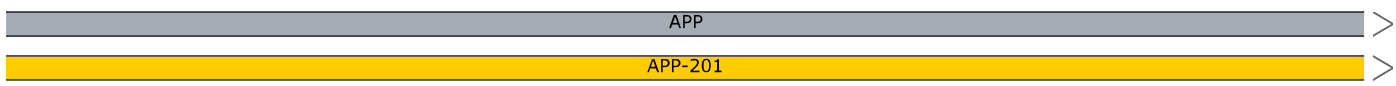
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170



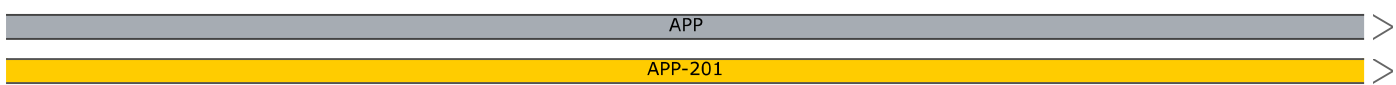
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255



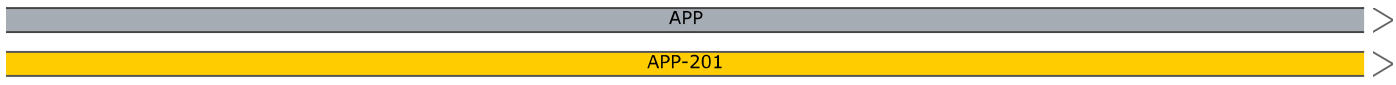
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340



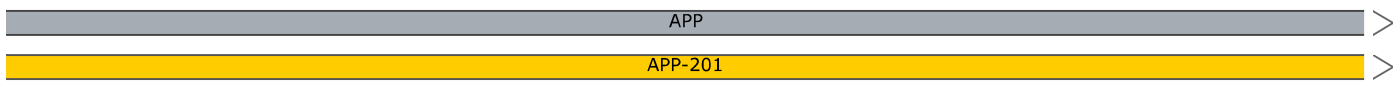
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425



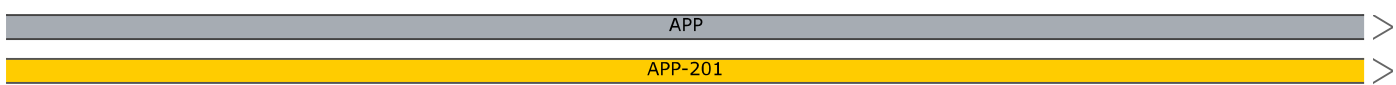
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510



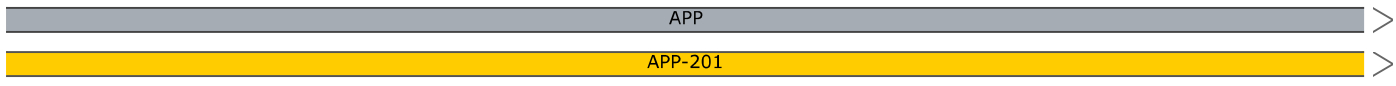
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595



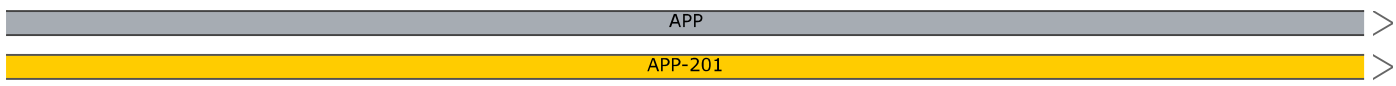
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680



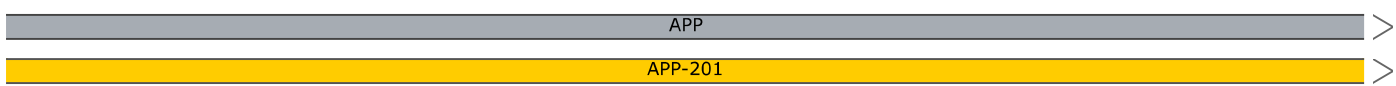
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765



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850



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CTACAAGTGACGACGTCCGATTAGGTCCACCACCGACGACTCCAAACACCACCGACACCGTTAAAGGATTTTATTCTGTTATTAC

935

APP

APP-201

AAGTTTGCTGCATCGATTGACTCTTCCTTTACAAAAAGATGTCTCTGTAGCATGTGATGCTGTTTGATAGCATTTTGCTCACAG
TTCAAACGACGTAGCTAACTGAGAAGGAAAAGTGTTTTTCTACAGAGACATCGTACACTACGACAAACTATCGTAAAACGAGTGTC

1020

APP

APP-201

TAGAACAGCTTTCAAATTTGGAGTCAGTCTTCGCAAACTAGCCACTGCTTCATCGAGTTTATGTGATATCCTAAATCCTTTGTT
ATCTTGTCGAAAGTTTTAACCTCAGTCAGAAGCGTTTAGATCGGTGACGAAGTAGCTCAAATACACTATAGGATTTAGGAAACAA

1105

APP

APP-201

GTCATTTCAACAGTGTTTCATAGCATCTTCACCAAGAGTAGATTCCATTGCAAGAAACCACTTTCTTTGCTCATCCATAAGAGGTA
CAGTAAAGTTGTCACAAGTATCGTAGAAGTGGTTCTCATCTAAGGTAACGTTCTTTGGTGAAAGAAACGAGTAGGTATTCTCCAT

1190

APP

APP-201

ACTCCTCATCCATTCAAGTTTGATCATGAGATGGTAGCAGTTCAGTCATGTCTTTAGGCTCCACTTCTAATTCTAGTTCTCTTGT
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1275

APP

APP-201

TATTTCCACCACATCTGCTGTGACATCCTTTACTGAAGTCTTGAAGTCTCAAAGTCACCCATGAGAGTTGGAATCATTGTCTTC
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1360

APP

APP-201

CAAACCTCCCGTTATTGCTGATGTTTTGATCTCCCATGGATCACAGATGTTCTTAATGGCATCTGGAATGGTGAATCCTTTTTAGA
GTTTGAGGGCAATAACGACTACAAAACCTAGAGGGTACCTAGTGTCTACAAGAATTACCGTAGACCTTACCACCTTAGGAAAAATCT

1445

APP

APP-201

AGGTTTGCAAGTTTACTTTGCCAGATCCATTAGAGGAATCGCTATCTATGGCAGTGAATAGCCCTACAAAATATATTTGAAATAT
TCCAAACGTCAAATGAAACGGGTCTAGGTAATCTCCTTAGCGATAGATACCGTCACTTATCGGGATGTTTTATATAAACTTTATA

1530

APP

APP-201

ATTTTGAAATAATAAGAGGCTGAAATAATAAGACTTGAAAGTTGATCCACAGGCTGCAGAATGGATGTTGTGTTAGCAGGCATGA
TAAAACCTTTATTATTCTCCGACTTTATTATTCTGAACTTTCAACTAGGTGTCCGACGCTTACCTACAACACAATCGTCCGTA

1615

APP

APP-201

AAACAACAGTAATCTCCCTGTACCTGTCTTCAGAGCTCTTGGGTGACTAGGTGCTTTGTTAGTGAGCAGTAATATTTTGAAATG
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1700

APP

APP-201

AGTCTTTTCTGAGCAGTAGGTCTCAACAGTGGGTTTAAAAATATTCAGTAAACCATGCTGTTAAGAGATGTGCTGTCATCCCAGTT
TCAGAAAAGACTCGTCATCCAGAGTTGTCACCCAAATTTTATAAGTCATTTGGTACGACAATTCTCTACACGACAGTAGGGTCAA

1785

APP

APP-201

TTGTTCCATTTATAGAGCATGGGCACAGTAGATTTAGAATAATTCTTAAGCGCCCTAGGACTTTTTACAATGGTCAGTCTTGGCTT
AACCAAGGTAAATATCTCGTACCCGTGTCATCTAAATCTTATTAAGAATTCGCGGGATCCTGAAAATGTTACCAGTCAGAACCAGAA

1870

APP

APP-201

CAAAAACAAAGTCGCCAGCTGCATTAGCCCTAACCAAGAGAGTCAGCTTGTCTTTGAAGCTTTGAAGGCAGGACTTCTCTCTAG
GTTTTTGTTCAGCGGTCGACGTAATCGGGGATTGTTCTCTCAGTCGAACAAGAACTTCGAAACTTCCGTCTGAAGAGAGATC

1955

APP

APP-201

TGATGAAAGTCCTAGATGGCATTCTTCCAAAATAAGTCTGTTTCATCTCCACTGAAAATCTGTTATTTAGTGTAGCCACCTTCA
ACTACTTTCAGGATCTACCGTAAAAGAAGGTTTATTTCAGACAAAGTAGAGGTGACTTTTAGACAATAAATCACATCGGTGGAAGT

2040

APP

APP-201

TCAGGAGTCTTATCTAGATCTTCTGGATAACTTATTGCAGCTTCTACATCAGCACTTGCTGCTTCACCTTGCACTTCTGTGTTAT
AGTCTCAGAAATAGATCTAGAAGACCTATTGAATAACGTCGAAGATGTAGTCGTGAACGACGAAGTGGAAACGTGAAGACACAATA

2125

APP

APP-201

GGAGATGGCTTCTTCCCTTAAACCTCATGAAATCAACCTCTCCCACTTTTTTTTTCTTCTGCAGCTTCTTCACCTCTCTCATCCT
CCTCTACCGAAGAAGGGAATTTGGAGTACTTTAGTTGGAGAGGGTTGAAAAAAAAAGAAGACGTCGAAGAAGTGGAGAGAGTAGGA

2210

APP

APP-201

TCATAGAATTGAAGACAGTTGTGGGCCTTGTCTTGATTAGGCTTTGGCCTAAGAGAATGTTGTGGTTGGTTTTGATCTTCCATCC
AGTATCTTAACTTCTGTCAACACCCGGAACAAGAATAATCCGAAACCGGATTCTCTTACAACACCAACCAAATAAGGTTAGG

2295

APP

APP-201

AGACAACATAAAAGTTTTCTCCGTATCAGCAATAAGGCTGTTTTGCTTTATCATTTGTGTGCTCACTGGAGTAGCACTTTTAATCT
TCTGTTGATTTTCAAAGAGGCATAGTCGTTATTCCGACAAAACGAAATAGTAAACACACGAGTGACCTCATCGTGAAAATTAGA

2380

APP

APP-201

CCTTCAAGAGCTTTTCTTTGCATTCACTTGGCTAACTGGCACAAGAATCTTGGCTTTCAATATGCCTTGCCCACTAAGCTTA
GGAAGTTCTCGAAAAGAAACGTAAGTGTGTAACCGATTGACCGTGTCTTAGAACCGAAAGTTATACGGAACGGGTGATTGCAAT

2465

APP

APP-201

ATTATTTCTAGCTTTTGTCTTTAAAGTGAGAGACCTGTGACTCTTCTTTCACTTGAATACTTAAAGAGGCCACTGTAGGGTTATTT
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2550

APP

APP-201

ACTGGCCCACTTTCAATATTGTTGTCTCTCAAGGGATAGGGAGCTGGGAGTTGAGGGGGTGGAGTGGCCAGTTTGGGGGGCAGA
TGACCGGGTGAAAAGTTATAACAACAGAGAGTTCCCTATCCCTCGGACCTCAACTCCCCACCTCACCGGTCAAACCCCCCGTCT

2635

APP

APP-201

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GTCTTGTGTGTGTTGTAATAACTAAATCAAACGACAGAAATACCCGTACAAAAGTACTGTGAGGTTTTGTTAATTTTATCATTGT

2720

APP

APP-201

TCAAAGGCCACTGATCACAGATCACCAAACAGATATAATAATTTTTAATGTTTGAATATTTAAATAATTACCAAATGTGACACA
AGTTTCCGGTGACTAGTGTCTAGTGGTTTTGTCTATATTATAAAAATTACAACTTATAAATTTATTAATGGTTTTACACTGTGT

2805

APP

APP-201

GACATGAAGTGAACCTGTGTTCACTGTTGGAAAAATGGCACCAATAGACTTGTTTCGATGCAGGGTTACCAGAAACCTTTTTGTTT
CTGTACTTCACTTGGACACAAGTGACAACCTTTTTACCGTGGTTATCTGAACAAGCTACGTCCAATGGTCTTTGGAAAAACAAA

2890

APP

APP-201

TTTTTTTTTAAATACTATCTGTAAGCACTACTGTACAATAAAGCTATGTATGCCTGTATTTTCATTAAGTTGCAGAGCAAACGTG
AAAAAAAAATTTATGATAGACATTCGTGATGACATGTTATTTTCGATACATACGGACATAAAAAGTAATTCACGTCTCGTTTTGCAC

2975

APP

APP-201

GTAATATTTAGCTTTAGTTTTACTTTCATCTGGCATAAGATCAACTCCTTATATAACAAGATGATAAAAAGTTGTGGTGTGCTTCTA
CATTATAAATCGAAATCAAATGAAGTAGACCGTATTCTAGTTGAGGAATATATTGTTCTACTATTTTCAACACCACACGAAGAT

3060

APP

APP-201

TAATTTCAATCAAGTAGATAAAGTTGAAAAATAATGACTTGCTTTTATAAACAGTATGAAGCAATGTAGTGCAGTAAATGAAATT
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3145

APP

APP-201

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AATAAGGAAGAAATGTTACAAGAGTTTTAATAAAAATACAAATTAGGTTTATTTCTCGTTCTTATTTTCGTTGTAAGTCTAAAAC

3230

APP

APP-201

GTTTCTGGAGACAATAGTTAGAAAAGCATGAGTTATGAGTGAAGTAAATTTCTGTTGCCTGTACTTCACTTTGAAATAACATTAT
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3315

APP

APP-201

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3400

APP

APP-201

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3485

APP

APP-201

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3570

APP

APP-201

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3655

APP

APP-201

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3740

APP

APP-201

ATAAACTATGATTATCATTCTTAGTAGGAAAATATGTGATTTCTTTTTTTTTTTTTTTTTTTTTTAAAGTAAGCATCAAATATTTGAC
TATTTGATACTAATAGTAAGAATCATCCTTTTATACACTAAAGAAAAAAAAAAAAAAAAAAAAAAAAATTTCAATTCGTAGTTTATAAACTG

3825

APP

APP-201

Sanger Sequencing

CAACCAGTTGGGCAGAGAAT

PCR Reverse

CAACCAGTTGGGCAGAGAAT

CAACCAGTTGGGCAGAGAATATACTGAACTTTTTATATAACCTCATCCAAATGTCCCTGCATTTAAGAAATGAAATTCCTTCTA
GTTGGTCAACCCGTCTCTTATATGACTTTGAAAAATATATTGGAGTAGGTTTACAGGGGACGTA AATTCCTTACTTTAAGAAGAT

3910

APP

APP-201

ATTGCGTTTATAAATTGTA AATTATATTGCATTTAGAAATTA A AATTCCTTTTTCTTAATTTGTTTTCAAGGTGTTCTTTGCAGAA
TAACGCAAATATTTAACATTTAATATAACGTAAATCTTTAATTTTAAGAAAAAGAATTAACAAAAGTTCACAAGAAACGTCTT

3995

APP

APP-201

690
V F F A E
ENSE00003548276
APP-201

gRNA Protospacer

GACAGTGATCGTCATCACCT

GATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGA
CTACACCCAAGTTTGTTCACGTTAGTAACCTGAGTACCACCCGCCACAACAGTATCGCTGTCACTAGCAGTAGTGGAAACCACT

4080

APP

APP-201

D V G S N K G A I I G L M V G G V V I A T V I V I T L V

ENSE00003548276

APP-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

GTAACCTGAGTACCACCCGCCACAACAGTATCGCTGTCACTAGTAGTAGTGGAAACCACT

Donor Template WT -> SNV

TGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGGTGGAGGTAGGTAACCTTGACTGCATGTTTTCCAAGTGGGAATTA
ACGACTTCTTCTTTGTCATGTGTAGGTAAGTAGTACCACACCACCTCCATCCATTTGAACTGACGTACAAAGGTTACCCCTTAAT

4165

APP

APP-201

M L K K K Q Y T S I H H G V V E V G K L D C M F P S G N *

ENSE00003548276

APP-201

(in frame with APP-201)

Donor Template WT -> SNV

ACGACTTCTTCTTTGTCATGTGTAGGTA

Donor Template WT -> SNV

AGACTATGAGAGAATTAGGCTTAGCTTTTTGCTAAGAACTAGCTAAGTATCTCTTTTTAAAAACGAATCAGTGTGCTTCCATGAT
TCTGATACTCTCTTAATCCGAATCGAAAAACGATTCTTGATCGATTCATAGAGAAAATTTTTGCTTAGTCACACGAAGGTA

4250

APP

APP-201

ACGAAGGTA

PCR Forward

GCTTGGGTTACAGTTGTTCTTTTGGTTTTTCATTCATTGCAACTTACCGTGAATATTCTGCTCAAGGTATTGAGAGTGT
CGAACCCAATGTCAACAAGAAAGAACAAAAACAAAAAGTAAGTAACGTTGAATGGCACTTATAAGACGAGTTCATAACTCTCACA

4335

APP

APP-201

CGAACCCA

PCR Forward

GTGTTGTTATCTCAACTTACAATTTGTGTTGAAGTTATCAAAAATAATACAAATGATAATGCATGACTTTAAAAAGCATGATTAC
CACAACAATAGAGTTGAATGTTAAACACAACCTTCAATAGTTTTATTATGTTTACTATTACGTAAGTAAATTTTTTCGTAATAATG

4420

APP

APP-201

TCTTAGACTTTTTTTTTTCAAACACAAGCAACAAAAACAGTACAAGAAGTTAAAAATAAAAAATAGAAGTAGGAAGTTGCTTTTT
AGAATCTGAAAAAAAAGTTTGTGTTTCGTTGTTTTGGTTCATGTTCTTCAATTTTTATTTTTATCTTCATCCTTCAACGAAAA

4505

APP

APP-201

CCAAAAAACTAAACATGTTTATTCTTGGATTTCTTTTGTCTTAAATAGTCTGGCCTCTCAATACAACCAGGTAATAGTAAATAA
GGTTTTTTTTGATTTGTACAAATAAGAACCCTAAAGAAAAACAGAATTTATCAGACCGGAGAGTTATGTTGGTCCATTATCATTATT

4590

APP

APP-201

TGTGACTTTTTCAGTGCAGACTCTTACCTTTAAAGTTTTCTCAGGAAATCACACTATAACCAATGGCCACCAAAACATACATGATT
ACACTGAAAAGTCACGTCTGAGAATGGAAATTTCAAAGAGTCCTTTAGTGTGATATGGTTTACCGGGTGGTTTTGTATGTACTAA

4675

APP

APP-201

GTTATTTGAGAGTTCTGCAACCTATTACCCTGCACTTCCACCTGAAATATCTTAGTTTCAAGGTGCTATACTAAAAACAAGAAAGA
CAATAAACTCTCAAGACGTTGGATAATGGGACGTGAAGGTGGACTTTATAGAATCAAAGTTCACGATATGATTTTGTCTTTCT

4760

APP

APP-201

GAGAAAGAAAATTTACGAATAAGTTATTTTTATGCATTTGAAATGCCATTTGGATGGGGGAAAAAGTGTAAAAATCTCACAGTAT
CTCTTTCTTTTAAATGCTTATTCAATAAAAAATACGTAAACTTTACGGTAAACCTACCCCTTTTTTCACAATTTTAGAGTGTACATA

4845

APP

APP-201

ATGCAACTTTTTAGGAAACTGTCTTGCAGAGAGTATAGTGTAAACATAACTTTTTATATGCACAGGGAAACTGAAAAATTTGTGTG
TACGTTGAAAAATCCTTTGACAGAACGTCTCTCATATCACATTTGTATTGAAAAATATACGTGTCCCTTTGACTTTTTAAACACAC

4930

APP

APP-201

ACATTTAATTGCGATATTTAAGAGTTATGGAATTTTTAGAGCTGAAAGATTTATTGATGATGACCAATCAAATTGATCTTCTCA
TGTAATTAACGCTATAAAATTTCTCAATACCTTAAAAATCTCGACTTTCTAAATAACTACTACTGGTTAGTTTAACTAGAAAGAT

5015

APP

APP-201

TCTTGTAGATGAGGGAACTGAGGCCGAGACAGAAGGGTTCAAATTATGCAAGGTCAAGCTCAGAGTCCAGATTTCCCTCATATT
AGAACATCTACTCCCTTGACTCCGGCTCTGTCTTCCCAAGTTTAAATACGTTCCAGTTCGAGTCTCAGGTCTAAAGGGGAGTATAA

5100

APP

APP-201

CCCCATTGCTTTTTTTTTTTTTTTTTTTTGGAGACAGTCTCGCGCTGTTGCCAGGCTGGATCTTGGCTCACTGCAACCTCTGCCTCCT
GGGGTAACGAAAAAAAAAAAAAAAAAACTCTGTGACAGCGCGACAACGGGTCCGACCTAGAACCGAGTGACGTTGGAGACGGAGGA

5185

APP

APP-201

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CCCAAGTTTCGTTAAGAGAACAGAGTCTGAAGGACTCATCGACCTTGATACCGTGTGCGGTGGTACGGGCCGATTAAAAACA AAAA

5270

APP

APP-201

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TCATCTCTGTCCCAAAGTGGTATAACCAGTCCGACCAGAGCTTGAGGACTGGAGTCCACTAGGTGGGCGGAACCGAAGGGTTTTCA

5355

APP

APP-201

GCTGGGATTACAGGCGTGAGCCACCGCGTCTGGCCCCATTGCTTTTTCCATCAGAGAAAAGTCCAGGTGTTTCTAGGGAGTTGA
CGACCCTAATGTCCGCACTCGGTGGCGCAGACCGGGGTAACGAAAAAGGTAGTCTCTTTTTCAGGTCCACAAAAGATCCCTCAACT

5440

APP

APP-201

AGATTCCACTATCCCCAAGGAAATGGGCTCTAAACCATTCTTGATTAGAAGAGGACAGGCAGAGTTTTAAATAAATGAAATTTGTG
TCTAAGGTGATAGGGGTTCTTTACCCGAGATTTGGTAAGAACTAATCTTCTCCTGTCCGTCTCAAATTTATTTACTTTAAACAC

5525

APP

APP-201

GTGAAGCCAGAAAATTTCATTTTGCTCAGCAATTA AACCTCTGCAGACTACAACAGAAGCTGCTGATGGAAATTTGGGGTGGAGCC
CACTTCGGTCTTTAAAGTAAAACGAGTCGTTAATTTTGGAGACGTCTGATGTTGTCTTCGACGACTACCTTTAACCCACCTCGG

5610

APP

APP-201

TCATTTCCCCATTCATACTGACGTGGATGAGCAGTGTGAGGAAGGAAACCAAGAGAACAGCAGGCAGCAGGGTGGAAAGGAACGG
AGTAAAGGGGTAAGTATGACTGCACCTACTCGTCACACTCCTTCTTTGGTTCTTGTCTCGTCCGTCGTCCACCTTTCTTTGCC

5695

APP

APP-201

ACTGACCCATAGATCAGAGTGTGAGCACATAAAAAGCAATGACCCCACTGTCATGTTTGGCCATTGCACCTTTTGTGATAGTATCT
TGACTGGGTATCTAGTCTCACACTCGTGTATTTTCTGTTACTGGGGTGACAGTACAAAACGGTAACGTGGAAAAACACTATCATAGA

5780

APP

APP-201

AAGCTTATGTCCCTCAAAACAGTGTAAAGATAGGTTTTTCATTAGTATCAGCTTATTTCAATTTCTGCTCAAATTAATTTTTAAAAA
TTCGAATACAGGGAGTTTTGTACATTCTATCCAAAAGTAATCATAGTCAATAAAGTAAAGACGAGTTTAATTAATAATTTTTTT

5865

APP

APP-201

ATTTAATTCCATATTTGAGCAAATAAAGATGTCTTCATACTTGAGTAATTCAGACCCCTTTTTTGTCTGCTGTTGTTGTTTTGGT
TAAATTAAGGTATAAACTCGTTTTATTTCTACAGAAGTATGAACTCATTAAGTTCTGGGGAAAAAACGACGACAACAACAAAACCA

5950

APP

APP-201

TTTTTTCATGGTTTTGTTGTTTTCTTTTGTGTTGTTGTTTCTTTGTTTTTGGAGATGGAGTCTTGCTCTTTTCACCCAGGCTGGA
AAAAAAGTACCAAAACAACAAAAGAAAACAACAACAACAAGAAAACAAAAACTCTACCTCAGAACGAGAAAGTGGGTCCGACCT

6035

APP

APP-201

GTGCAGTGGCATGATCTCCGCTCACTGCAACCTCCACCTCCAGGTTCAAGCGATTCTCCTACCTCACTCTCAGCCTCCTGAGTA
CACGTCAACGTAAGAGGCGAGTGACGTTGGAGGTGGAGGGTCCAAGTTTCGTAAGAGGATGGAGTGAGAGTCCGGAGGACTCAT

6120

APP

APP-201

ACTGGGATTACAGGGGCATACCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTGCCATGTTGGCCAGGCTG
TGACCCTAATGTCCCGTATGGTGGTGCAGGACCGATTAAAAACATAAAAAATCATCTCTGTCCCAAAACGGTACAACCGGTCCGAC

6205

APP

APP-201

GTCTTGAATTCTGGCCTCAAGTGATCCGCCCTCCCAACCTCCCAAGGTGCTGGGATTACAGGCATGAGCCACCATGCCTGGCC
CAGAACTTAAGGACCGGAGTTCACCTAGGCGGGAGGGGTTGGAGGGTTCCACGACCCTAATGTCCGTA CT CGGTGGTACGGACCGG

6290

APP

APP-201

TTCAAGAGCACTTTTTAGTTTATTTAATAATAATTCTCTTTGTTGCCGGTCTGTCCGTTGAAGTTGCCTTCTTTGATGCCAGAGGC
AAGTTCTCGTGAAAAATCAAATAAATTATATTAAGAGAAACAACGGCCAGACAGGCAACTTCAACGGAAGAAACTACGGTCTCCG

6375

APP

APP-201

CAAAGACTTGGCTTCCTCGGGCTTCCATAACAAAGTAACACAGATGGGTGGATTAAGCAACAGAAATTTACCCTCTCACATTTCT
GTTTCTGAACCGAAGGAGCCCGAAGGTATTGTTTCATTGTGTCTACCCACCTAATTCGTTGTCTTTAAATGGGAGAGTGTAAGA

6460






























APP














APP-201








GGAGTGTA 3'
CCTCACAT 5' 6468

APP

APP-201

Feature		Location	Size			Type
✓ APP		1 .. 6468	6468 bp			gene
/note	= gene ENSG00000142192 Protein coding					
APP-DT		1 .. 6468	6468 bp			gene
/note	= gene ENSG00000273492 lncRNA					
✓ APP-201		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000346798					
APP-202		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000348990					
APP-203		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000354192					
APP-204		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000357903					
APP-205		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000358918					
APP-206		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000359726					
APP-208		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000439274					
APP-209		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000440126					
APP-213		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000464867 Retained intron					
APP-DT-201		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000608591 lncRNA					
APP-DT-202		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000609365 lncRNA					
APP-DT-203		1 .. 6468	6468 bp			prim_transcript
/note	= primary transcript ENST00000664668 lncRNA					
✓ APP-201		3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000284981					
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa					
APP-202		3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000345463					
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa					
APP-203		3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000346129					
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa					
APP-204		3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000350578					
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa					
APP-205		3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000351796					
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa					

Feature	Location	Size			Type
APP-206	3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000352760				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-208	3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000398879				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-209	3981 .. 4127	147 bp			CDS
/note	= coding sequence ENSP00000387483				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
✓ Donor Template WT -> SNV	4022 .. 4108	87 bp			misc_feature
✓ Protospacer Sequence	4055 .. 4074	20 bp			misc_feature
✓ SNV	4065 .. 4065	1 bp			misc_feature
/note	= WT = G SNV = A				
✓ PAM	4075 .. 4077	3 bp			misc_feature

Primer	Length		Binding Sites		Tm	Date Added
✓ PCR Reverse	20-mer		3826 .. 3845		57°C	Jan 10, 2023
/sequence = CAACCAAGTTGGGCAGAGAAT 50% GC / 6175.1 Da						
✓ Sanger Sequencing	20-mer		3826 .. 3845		57°C	Jan 10, 2023
/sequence = CAACCAAGTTGGGCAGAGAAT 50% GC / 6175.1 Da						
✓ Donor Template WT -> SNV	87-mer		4022 .. 4108		75°C	Jan 10, 2023
/sequence = ATGGATGTGTAAGTCTTTCTTCTTCAGCATCACCAAGGTGATGATGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAATG 47% GC / 26,706.4 Da						
✓ gRNA Protospacer	20-mer		4055 .. 4074		56°C	Jan 10, 2023
/sequence = GACAGTGATCGTCATCACCT 50% GC / 6077.0 Da						
✓ PCR Forward	20-mer		4239 .. 4258		57°C	Jan 10, 2023
/sequence = ACCCAAGCATCATGGAAGCA 50% GC / 6104.0 Da						