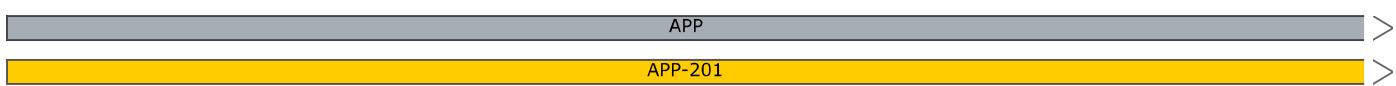


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5'
3'

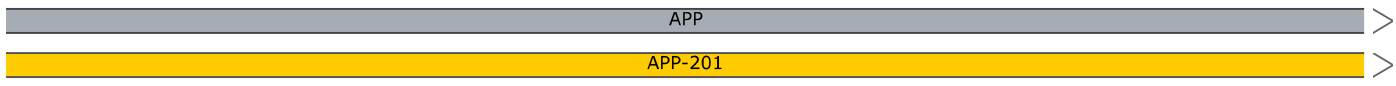
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85



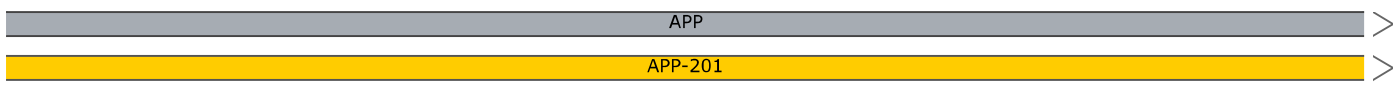
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170



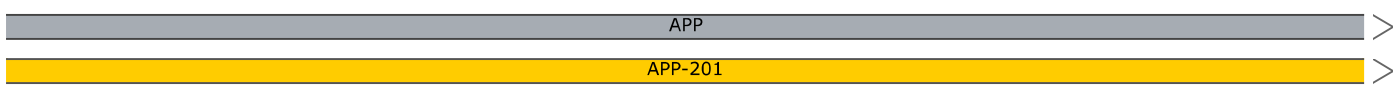
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255



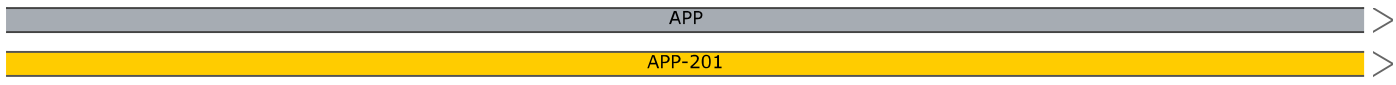
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340



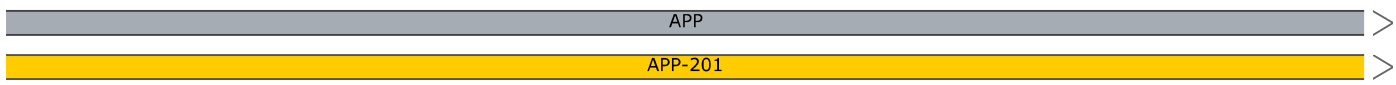
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425



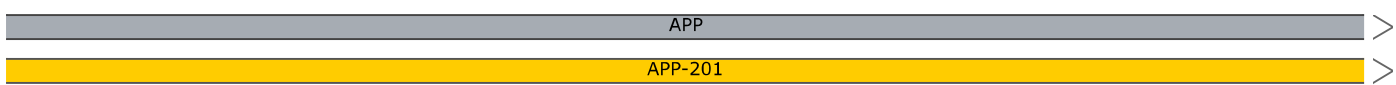
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510



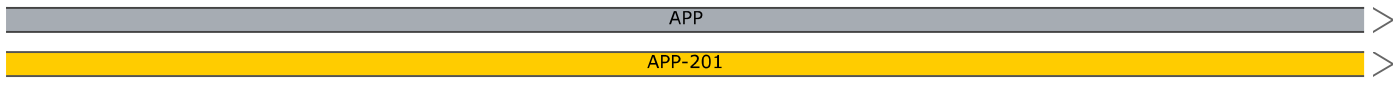
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595



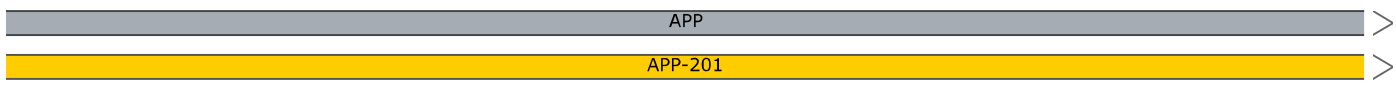
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680



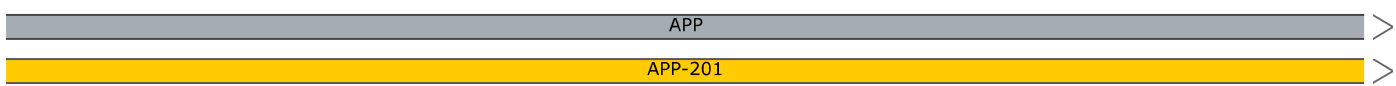
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765



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850



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935

APP

APP-201

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1020

APP

APP-201

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1105

APP

APP-201

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1190

APP

APP-201

ACTCCTCATCCATTCAAGTTTGATCATGAGATGGTAGCAGTTCAGTCATGTCTTTAGGCTCCACTTCTAATTCTAGTTCTCTTGT
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1275

APP

APP-201

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1360

APP

APP-201

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1445

APP

APP-201

AGGTTTGCAAGTTTACTTTGCCAGATCCATTAGAGGAATCGCTATCTATGGCAGTGAATAGCCCTACAAAATATATTTGAAATAT
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1530

APP

APP-201

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1615

APP

APP-201

AAACAACAGTAATCTCCCTGTACCTGTCTTCAGAGCTCTTGGGTGACTAGGTGCTTTGTTAGTGAGCAGTAATATTTTGAAATG
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1700

APP

APP-201

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1785

APP

APP-201

TTGTTCCATTTATAGAGCATGGGCACAGTAGATTTAGAATAATTCTTAAGCGCCCTAGGACTTTTTACAATGGTCAGTCTTGGCTT
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1870

APP

APP-201

CAAAAACAAAGTCGCCAGCTGCATTAGCCCTAACCAAGAGAGTCAGCTTGTCTTTGAAGCTTTGAAGGCAGGACTTCTCTCTAG
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1955

APP

APP-201

TGATGAAAGTCCTAGATGGCATTCTTCCAAAATAAGTCTGTTTCATCTCCACTGAAAATCTGTTATTTAGTGTAGCCACCTTCA
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2040

APP

APP-201

TCAGGAGTCTTATCTAGATCTTCTGGATAACTTATTGCAGCTTCTACATCAGCACTTGCTGCTTCACCTTGCACTTCTGTGTTAT
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2125

APP

APP-201

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2210

APP

APP-201

TCATAGAATTGAAGACAGTTGTGGGCCTTGTTCTTGATTAGGCTTTGGCCTAAGAGAATGTTGTGGTTGGTTTTGATCTTCCATCC
AGTATCTTAACTTCTGTCAACACCCGGAACAAGAATAATCCGAAACCGGATTCTCTTACAACACCAACCAAATAAGGTTAGG

2295

APP

APP-201

AGACAACATAAAGTCTTCTCCGTATCAGCAATAAGGCTGTTTTGCTTTATCATTTGTGTGCTCACTGGAGTAGCACTTTTAATCT
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2380

APP

APP-201

CCTTCAAGAGCTTTTCTTTGCATTCACTTGGCTAACTGGCACAAGAATCTTGGCTTTCAATATGCCTTGCCCACTAAGCTTA
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2465

APP

APP-201

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2550

APP

APP-201

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2635

APP

APP-201

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2720

APP

APP-201

TCAAAGGCCACTGATCACAGATCACCAAACAGATATAATAATTTTTAATGTTTGAATATTTAAATAATTACCAAATGTGACACA
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2805

APP

APP-201

GACATGAAGTGAACCTGTGTTCACTGTTGGAAAAATGGCACCAATAGACTTGTTTCGATGCAGGGTTACCAGAAACCTTTTTGTTT
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2890

APP

APP-201

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2975

APP

APP-201

GTAATATTTAGCTTTAGTTTTACTTTCATCTGGCATAAGATCAACTCCTTATATAACAAGATGATAAAAGTTGTGGTGTGCTTCTA
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3060

APP

APP-201

TAATTTCAATCAAGTAGATAAAGTTGAAAAATAATGACTTGCTTTTATAAACAGTATGAAGCAATGTAGTGCAGTAAATGAAATT
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3145

APP

APP-201

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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

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3825

APP

APP-201

Sanger Sequencing

CAACCAGTTGGGCAGAGAAT

PCR Reverse

CAACCAGTTGGGCAGAGAAT

CAACCAGTTGGGCAGAGAATATACTGAACTTTTTATATAACCTCATCCAAATGTCCCTGCATTTAAGAAATGAAATTCCTTCTA
GTTGGTCAACCCGTCTCTTATATGACTTTGAAAAATATATTGGAGTAGGTTTACAGGGGACGTA AATTCCTTACTTTAAGAAGAT

3910

APP

APP-201

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TAACGCAAATATTTAACATTTAATATAACGTAAATCTTTAATTTTAAGAAAAAGAATTAACAAAAGTTCACAAGAAACGTCTT

3995

APP

APP-201

690
V F F A E
ENSE00003548276
APP-201

gRNA Protospacer

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GATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTTCATAGCGACAGTGATCGTCATCACCTTGGTGA
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
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4590

APP

APP-201

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4675

APP

APP-201

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CAATAAACTCTCAAGACGTTGGATAATGGGACGTGAAGGTGGACTTTATAGAATCAAAGTTCACGATATGATTTTGTCTTTCT

4760

APP

APP-201

GAGAAAGAAAATTTACGAATAAGTTATTTTTATGCATTTGAAATGCCATTTGGATGGGGGAAAAAGTGTAAAAATCTCACAGTAT
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4845

APP

APP-201

ATGCAACTTTTTAGGAAACTGTCTTGCAGAGAGTATAGTGTAAACATAACTTTTTATATGCACAGGGAAACTGAAAAATTTGTGTG
TACGTTGAAAAATCCTTTGACAGAACGTCTCTCATATCACATTTGTATTGAAAAATATACGTGTCCCTTTGACTTTTTAAACACAC

4930

APP

APP-201

ACATTTAATTGCGATATTTAAGAGTTATGGAATTTTTAGAGCTGAAAGATTTATTGATGATGACCAATCAAATTGATCTTCTCA
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5015

APP

APP-201

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5100

APP

APP-201

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5185

APP

APP-201

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5270

APP

APP-201

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5355

APP

APP-201

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5440

APP

APP-201

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5525

APP

APP-201

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5610

APP

APP-201

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5695

APP

APP-201

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5780

APP

APP-201

AAGCTTATGTCCCTCAAAACAGTGTAAAGATAGGTTTTTCATTAGTATCAGCTTATTTCAATTTCTGCTCAAATTAATTTTTAAAAA
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5865

APP

APP-201

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5950

APP

APP-201

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6035

APP

APP-201

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6120

APP

APP-201

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6205

APP

APP-201

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6290

APP

APP-201

TTCAAGAGCACTTTTTAGTTTATTTAATAATAATTCTCTTTGTTGCCGGTCTGTCCGTTGAAGTTGCCTTCTTTGATGCCAGAGGC
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6375

APP

APP-201

CAAAGACTTGGCTTCCTCGGGCTTCCATAACAAAGTAACACAGATGGGTGGATTAAGCAACAGAAATTTACCCTCTCACATTTCT
GTTTCTGAACCGAAGGAGCCCGAAGGTATTGTTTCATTGTGTCTACCCACCTAATTCGTTGTCTTTAAATGGGAGAGTGTAAGA

6460

APP

APP-201

GGAGTGTAAGATCAAGGTATCAGCCAGGTTGGTTCCTCCCCAGGCATCTCTCCTTGGTTTGCAGATGCCTGT
CCTCACATTCTAGTTCATAGTCGGTCCAACCAAGGAGGGGTCCGTAGAGAGGAACCAAACGTCTACGGACA

3'
















6532








5'

APP

APP-201

Feature	Location	Size			Type
✓ APP	1 .. 6532	6532 bp			gene
/note	= gene ENSG00000142192 Protein coding				
APP-DT	1 .. 6532	6532 bp			gene
/note	= gene ENSG00000273492 lncRNA				
✓ APP-201	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000346798				
APP-202	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000348990				
APP-203	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000354192				
APP-204	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000357903				
APP-205	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000358918				
APP-206	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000359726				
APP-208	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000439274				
APP-209	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000440126				
APP-213	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000464867 Retained intron				
APP-DT-201	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000608591 lncRNA				
APP-DT-202	1 .. 6532	6532 bp			prim_transcript
/note	= primary transcript ENST00000609365 lncRNA				
APP-DT-203	1 .. 6532	6532 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						