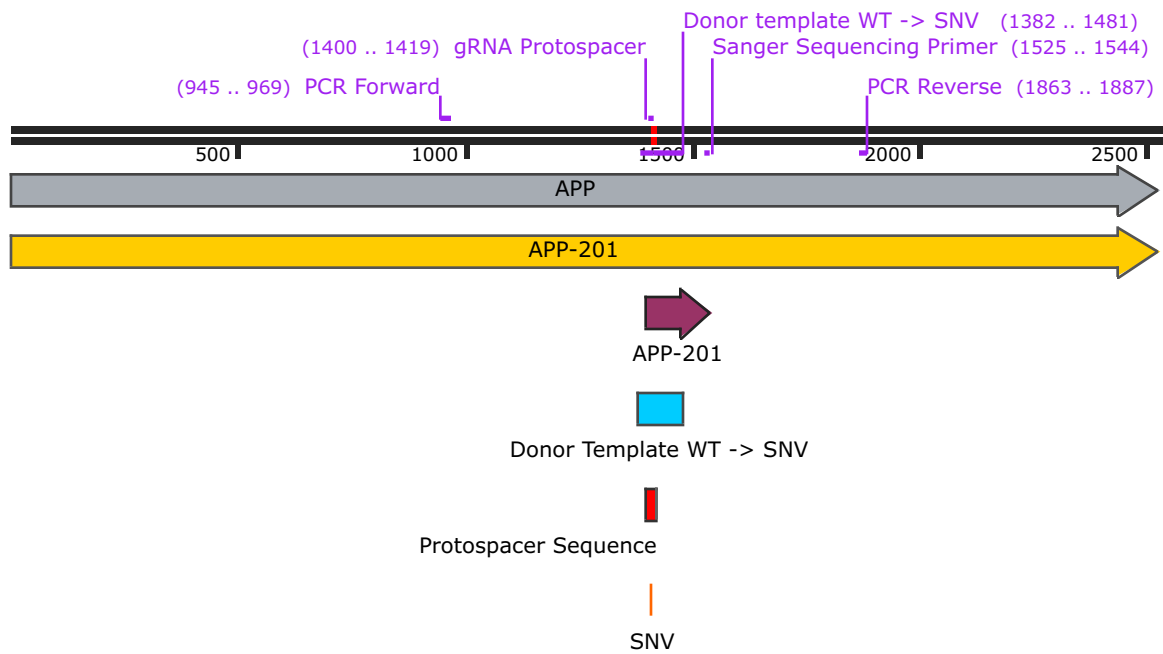


Sequence: INK2J00097_APP_A692G_A09_BB.dna (Linear / 2525 bp)

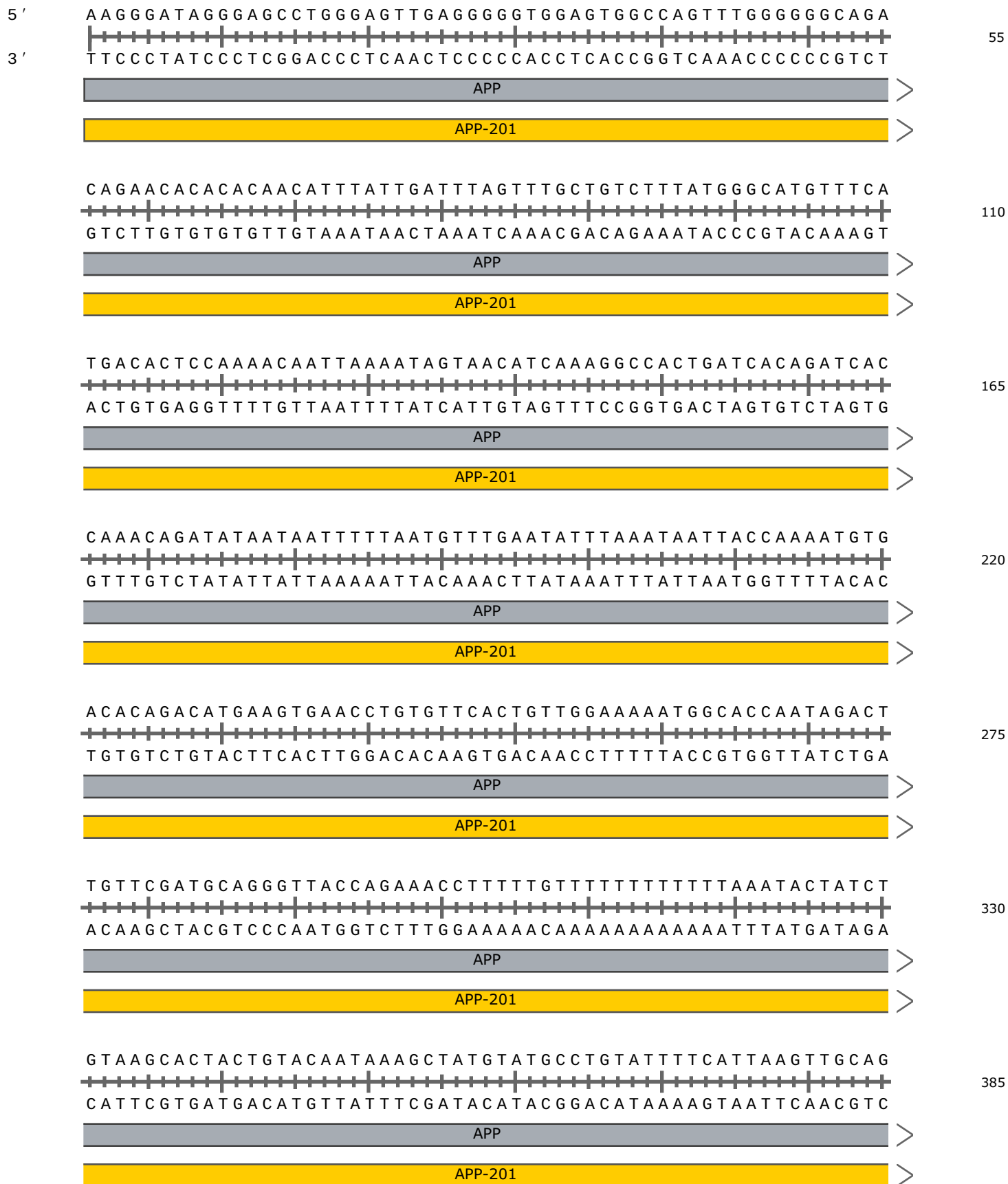
Features: 29 total

Primers: 5 total

amyloid beta precursor protein [Source:HGNC Symbol;Acc:HGNC:620]



INK2J00097_APP_A692G_A09_BB
2525 bp



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 TCGTTTGCACCATTATAAATCGAAATCAAATGAAGTAGACCGTATTCTAGTTGA



CCTTATATAACAAGATGATAAAAGTTGTGGTGTGCTTCTATAATTTCAATCAAGT
 GGAATATATTGTTCTACTATTTTCAACACCACACGAAGATATTAAGTAAGTTCA



AGATAAAGTTGAAAAATAATGACTTGCTTTTATAAACAGTATGAAGCAATGTAGT
 TCTATTTCAACTTTTTATTACTGAACGAAAATATTTGTCATACTTCGTTACATCA



GCAGTAAATGAAATTTTATTCCTTCTTTACAATGTTCTCAAATTTATTTTATGT
 CGTCATTTACTTTAAAATAAGGAAGAAATGTTACAAGAGTTTTAATAAAAATACA



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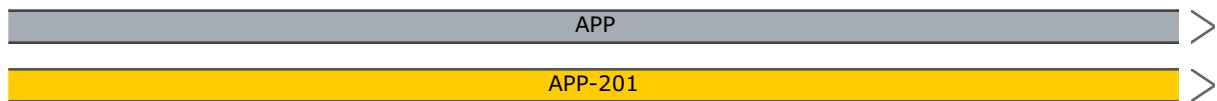
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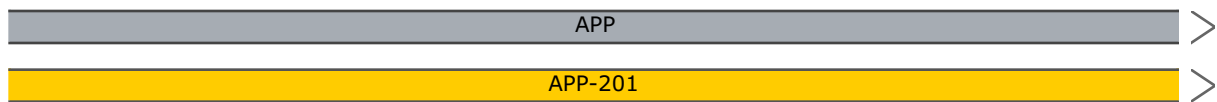
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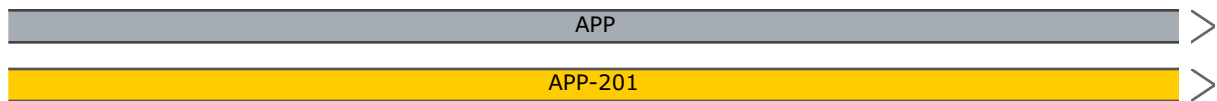
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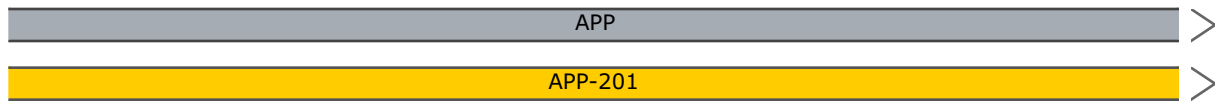


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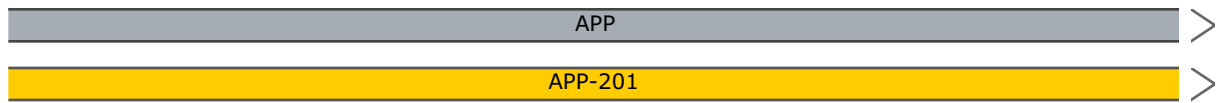


PCR Forward
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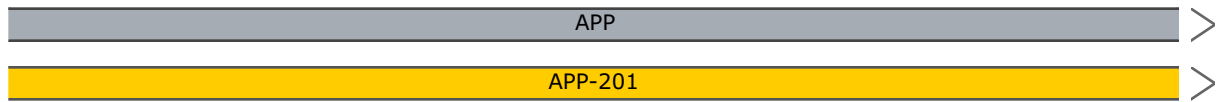
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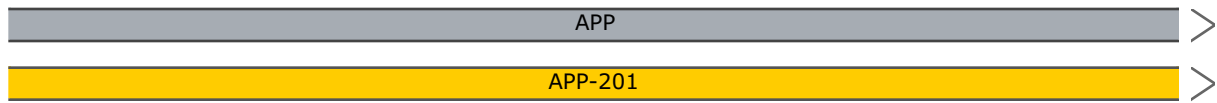
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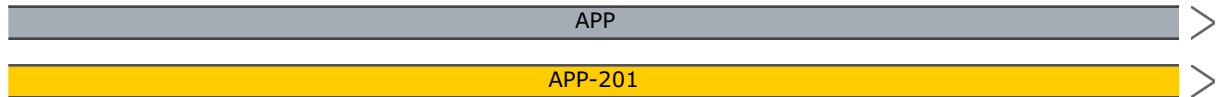
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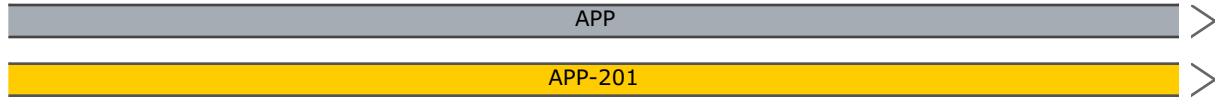
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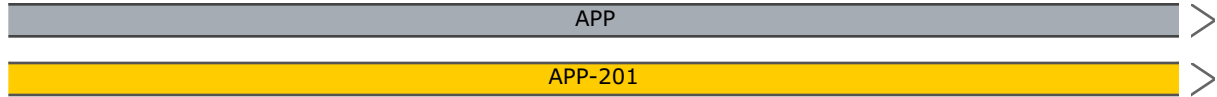
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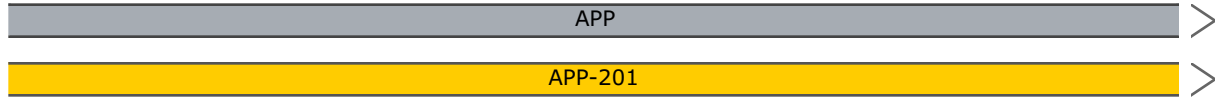
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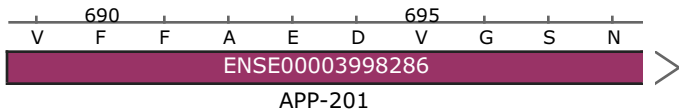
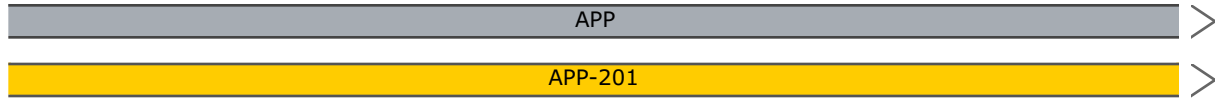


AATTCTTCTAATTGCGTTTATAAATTGTAAATTATATTGCATTTAGAAATTA AAA
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gRNA Protospacer
 GGTGTTCTTTGCAGAAGATG

TTCTTTTTCTTAATTTGTTTTCAAGGTGTTCTTTG CAGAAGATGTGGGTTCAAAC
 AAGAAAAAGAATTAACAAAAGTTCCACAAGAAAC G TCTTCTACACCCAAGTTTG



Donor Template WT -> SNV



SNV

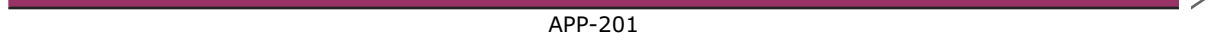
AAGAATTAACAAAAGTTCCACAAGAAAC C TCTTCTACACCCAAGTTTG

Donor template WT -> SNV

AAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCG
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700 705 710 715
 K G A I I G L M V G G V V I A T V I



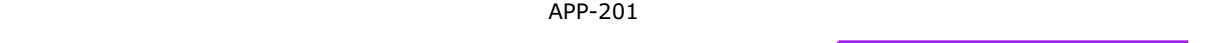
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Donor template WT -> SNV

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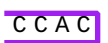
720 725 730 735
 V I T L V M L K K Q Y T S I H H G V



GGTGGAGGTAGGTAAACTTGA CTGCATGTTTCCAAGTGGGAATTAAGACTATGAG
 CCACCTCCATCCATTTGAACTGACGTACAAAGGTTTACCCTTAATTCTGATACTC



V E V G K L D C M F P S G N *
 ENSE00... (in frame with APP-201)



Sanger Sequencing Primer

AGAATTAGGCTTAGCTTTTTGCTAAGAACTAGCTAAGTATCTCTTTTAAAAAACG
 TCTTAATCCGAATCGAAAAACGATTCTTGATCGATTTCATAGAGAAAATTTTGTG



AATCAGTGTGCTTCCATGATGCTTGGGTTACAGTTGTTCTTTCTTGTTTTGGTTT
TTAGTCACACGAAGGTA CTACGAACCCAATGTCAACAAGAAAGAACAAAACCAA

1705



TCATTCATTGCAACTTACCGTGAATATTCTGCTCAAGGTATTGAGAGTGTGTGT
AGTAAGTAACGTTGAATGGCACTTATAAGACGAGTTCCATAACTCTCACACACAA

1760



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1815



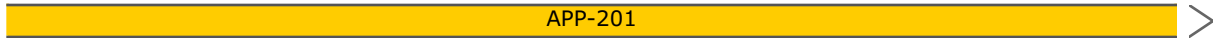
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GTA CTGAAATTTTTTCGTACTAATGAGAATCTGAAAAAAAAGTTTGTGTTTCGT

1870



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1925



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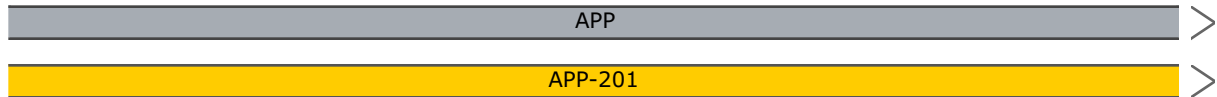
PCR Reverse

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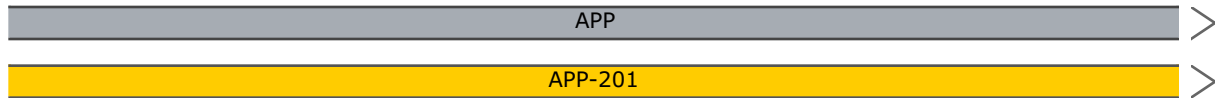
1980



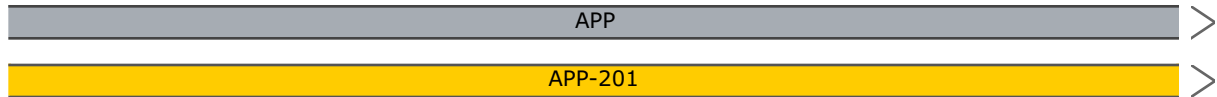
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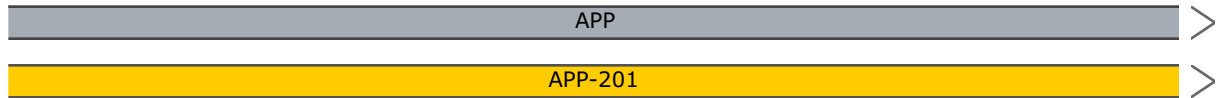
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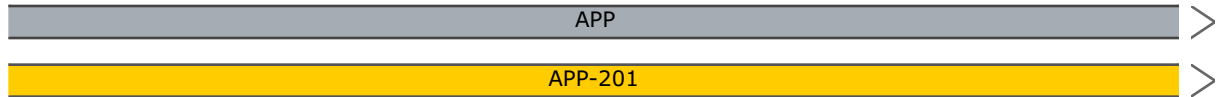
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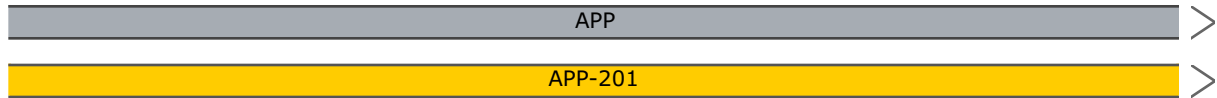
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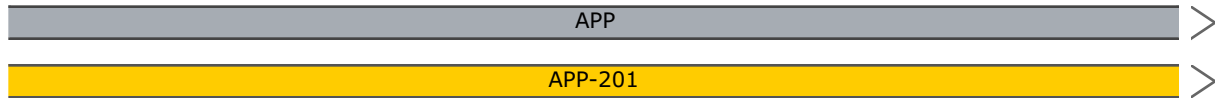
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ATAACTTTTATATGCACAGGGAAACTGAAAAATTTGTGTGACATTTAATTGCGAT
 TATTGAAAATATACGTGTCCCTTTGACTTTTAAACACACTGTAAATTAACGCTA



ATTTTAAGAGTTATGGAATTTT TAGAGCTGAAAGATTTATTGATGATGACCAATC 2420
 TAAAATTCTCAATACCTTAAAAATCTCGACTTTCTAAATAACTACTACTGGTTAG



AAATTGATCTTCTCATCTTGTAGATGAGGGA ACTGAGGCCGAGACAGAAGGGTTC 2475
 TTTAACTAGAAGAGTAGAACATCTACTCCCTTGACTCCGGCTCTGTCTTCCCAAG



AAATTATGCAAGGTCAAGCTCAGAGTCCAGATTTCCCTCATATTCCCA 3'
 TTTAATACGTTCCAGTTCGAGTCTCAGGTCTAAAGGGGAGTATAAGGGGT 5' 2525



Feature	Location	Size			Type
✓ APP	1 .. 2525	2525 bp			gene
/note	= gene ENSG00000142192 Protein coding				
APP-DT	1 .. 2525	2525 bp			gene
/note	= gene ENSG00000273492 lncRNA				
✓ APP-201	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000346798				
APP-202	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000348990				
APP-203	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000354192				
APP-204	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000357903				
APP-205	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000358918				
APP-206	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000359726				
APP-208	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000439274				
APP-209	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000440126				
APP-213	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000464867 Retained intron				
APP-218	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000707132 protein_coding_CDS_not_defined				
APP-219	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000707133 protein_coding_CDS_not_defined				
APP-220	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000707134 protein_coding_CDS_not_defined				
APP-DT-201	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000608591 lncRNA				
APP-DT-202	1 .. 2525	2525 bp			prim_transcript
/note	= primary transcript ENST00000609365 lncRNA				

Feature	Location	Size		±	Type
APP-DT-203	1 .. 2525	2525 bp	■	←	prim_transcript
/note	= primary transcript ENST00000664668 lncRNA				
✓ Donor Template WT -> SNV	1382 .. 1481	100 bp	■	⇄	misc_feature
✓ Protospacer Sequence	1400 .. 1419	20 bp	■	⇄	misc_feature
✓ APP-201	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000284981				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-202	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000345463				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-203	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000346129				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-204	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000350578				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-205	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000351796				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-206	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000352760				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-208	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000398879				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
APP-209	1401 .. 1547	147 bp	■	→	CDS
/note	= coding sequence ENSP00000387483				
/translation	= VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHGGVVE 49 amino acids = 5.2 kDa				
✓ SNV	1411 .. 1411	1 bp	■	⇄	misc_feature
/note	= WT = C SNV = G				
✓ PAM	1420 .. 1422	3 bp	■	⇄	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	945 .. 969	61°C	Jun 18, 2024
/sequence = TCAGGGCTCAGAGTGCTATGACTAG 52% GC / 7722.1 Da				
✓ Donor template WT -> SNV	100-mer	1382 .. 1481	74°C	Jun 18, 2024
/sequence = CACTGTCGCTATGACAACACCGCCACCATGAGTCCAATGATTGCACCTTTGTTTGAACCCACATCTTCTCCAAGAACACCTTGAAAA CAAATTAAGAA 43% GC / 30,538.9 Da				
✓ gRNA Protospacer	20-mer	1400 .. 1419	54°C	Jun 18, 2024
/sequence = GGTGTTCTTTGCAGAAGATG 45% GC / 6203.1 Da				
✓ Sanger Sequencing Primer	20-mer	1525 .. 1544	55°C	Jun 18, 2024
/sequence = CACCACCCATGATGAATGG 50% GC / 6095.0 Da				
✓ PCR Reverse	25-mer	1863 .. 1887	59°C	Jun 18, 2024
/sequence = CTTGTACTGGTTTTTGTGCTTGTG 40% GC / 7682.1 Da				