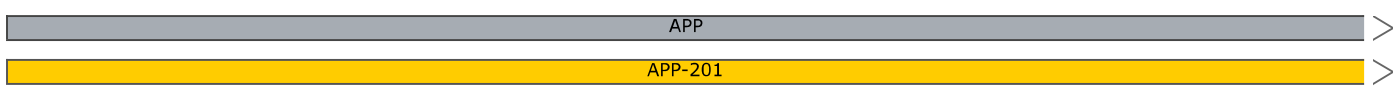


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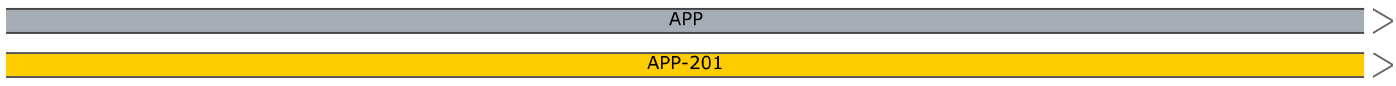
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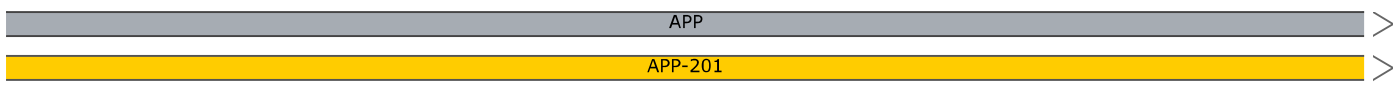
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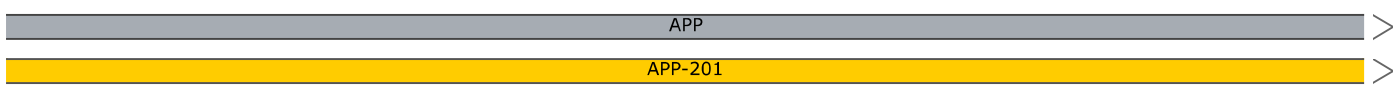
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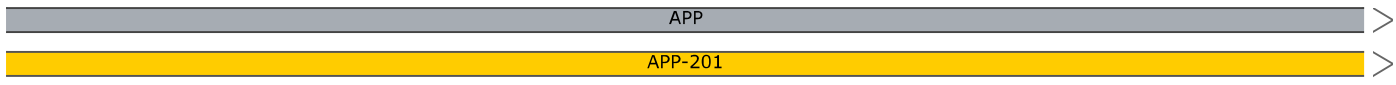
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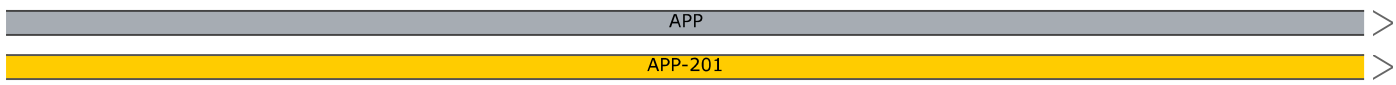
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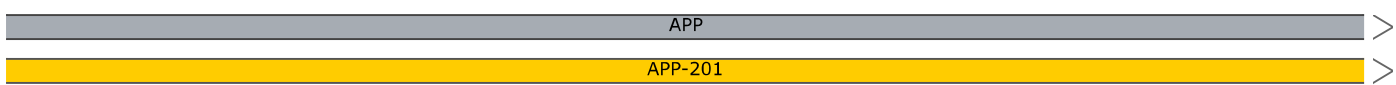
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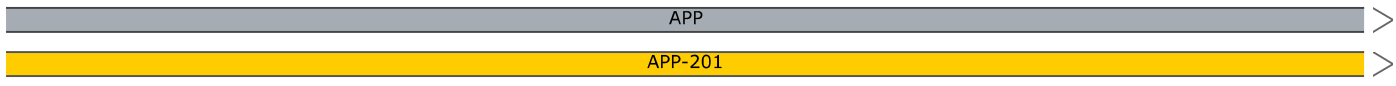
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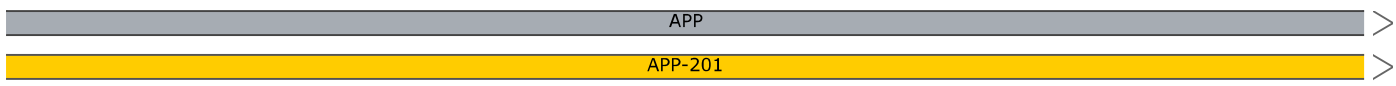
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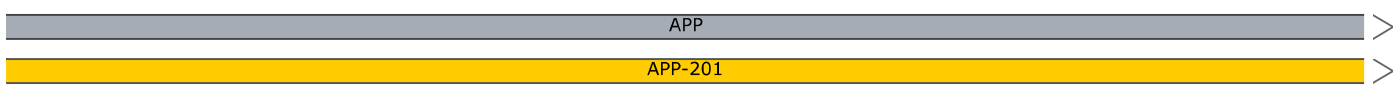
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765



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935

APP

APP-201

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APP

APP-201

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APP

APP-201

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APP-201

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APP

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APP-201

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APP-201

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1785

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APP-201

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2125

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APP-201

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APP

APP-201

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2380

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APP-201

E P V 640

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APP-201

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2550

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APP-201

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APP-201

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APP-201

APP-201

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APP-201

APP-201

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APP-201

APP-201

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APP-201

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2975

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APP-201

APP-201

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APP-201

APP-201

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APP-201

APP-201

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APP-201

APP-201

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APP-201

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APP-201

APP-201

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3485

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APP-201

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APP-201

APP-201

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3655

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APP-201

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APP-201

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APP-201

APP-201

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APP-201

APP-201

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4080

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APP-201

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APP-201

APP-201

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APP-201

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APP-201

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APP-201

APP-201

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4590

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APP-201

APP-201

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4675

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APP-201

APP-201

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4760

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APP-201

APP-201

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4845

APP

APP-201

APP-201

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4930

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APP-201

APP-201

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5015

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APP-201

APP-201

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5100

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APP-201

APP-201

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5185

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APP-201

APP-201

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5270

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APP-201

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5355

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APP-201

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5440

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APP-201

APP-201

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5525

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APP-201

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5610

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APP-201

APP-201

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APP-201

APP-201

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5780

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APP-201

APP-201

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5865

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APP-201

APP-201

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5950

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APP-201

APP-201

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6035

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APP-201

APP-201

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6120

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APP-201

APP-201

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6205

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APP-201

APP-201

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6290

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APP-201

APP-201

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6375

APP

APP-201

APP-201

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6460

APP

APP-201

APP-201

CCGCCTCAGCCTCCCAAAGGCTGGGATTACAGGCATGAGTCACTGCACCTGGCCGAGAGCTCATTCTTTTTTTTTTTTTTTTTTGA
GGCGGAGTCGGAGGGTTTTCCGACCCCTAATGTCCGTAAGTCACTGACGTGGACCGGCTCTCGAGTAAGAAAAAAAAAAAAAAAAAACT

6545

APP

APP-201

APP-201

GATGGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCAGTGGCACGAATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTACACC
CTACCTCAGAGTGAGACAGCGGGTCCGACCTCACGTACCGTGCTTAGAGCCGAGTGACGTTTCGAGACGGAGGACCCAAGTGTGG

6630

APP

APP-201

APP-201

ATTCTCCTGCCTAAGCCTCTAGTAGCTGGGACTACAGGTGCCTGCCACCACGTCCGGCTAATTTTTTGTATTTTTAGTAGAGACG
TAAGAGGACGGATTTCGGAGATCATCGACCCTGATGTCCACGGACGGTGGTGCAGGCCGATTAACAAAAACATAAAAAATCATCTCTGC

6715

APP

APP-201

APP-201

GGGTTTCACCATGGTCTTGATCTCTTGACCTCGTGATCCTCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCAC
CCCAAAGTGGTACCAGAAGTAGAGAAGTGGAGCACTAGGAGGGCGGAGCCGGAGGGTTTCACGACCCTAATGTCCACACTCGGTG

6800

APP

APP-201

APP-201

TGTGCCCGGCCAGAGCTCATTCTTTACTTTTTATTTTTTCAGTATAAATATTTGGCTCCAAATCTAAAAGGGAAGACTCTTCAAAC
ACACGGGCCGGTCTCGAGTAAGAAATGAAAATAAAAAGTCATATTTATAAACCGAGGTTTTAGATTTTCCCTTCTGAGAAGTTTG

6885

APP

APP-201

APP-201

TGTTCAAGAAAGTTTTCTTAAAAATCTCAGAAATATAGTTCTAACCTATTGTGTTGCTAGATCTTTTTATTTATTTATTTATTTTT
ACAAGTTCTTTCAAAGAATTTTTAGAGTCTTTATATCAAGATTGGATAACACAACGATCTAGAAAAATAATAAATAAATAAAAA

6970

APP

APP-201

APP-201

GGAGACAGAGTCTCATTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTCAGCTCACTGCAACCTCCACCTGCCGGGTTCAAG
CCTCTGTCTCAGAGTAAGACAGTGGGTCCGACCTCACGTACCCTGTTAGAGTTCGAGTGACGTTGGAGGTGGACGGCCCAAGTTC

7055

APP

APP-201

APP-201

CGATTCTTATGCCTCAGCCTTCTGGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTTTTTTTTTTTTTTT
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7140

APP

APP-201

APP-201

TTTTTTTTTTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGACCAGGCTGGTCTCAAACCTCTGACCTCAAGTGATCCAC
AAAAACAAAAACATAAAAAATCATCTCTGTCCCAAAGTGGTACAACCTGGTCCGACCAGAGTTTGAGGACTGGAGTTCACTAGGTG

7225

APP

APP-201

APP-201

CCAGCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCTTGGCACGTTGCCAGATCTTAATAACAGAAAAGGAG
GGTCGAACCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTGGCACGAACCGTGCAACGGTCTAGAATTATTGTCTTTTCTC

7310

APP

APP-201

APP-201

TGAGCTCTAAAGAAATCACTGGTTATATAAGGATCTCAGATTTAAAGGGCTATAGAAAGATTAAATATACAGCCAGTGAGAAT
ACTCGAGATTTCTTTAGTGACCAATATATTCCTAGAGTCTAAATTTTCCCGATATCTTTCTAATTTTATATGTCTGGTCACTCTTA

7395

APP

APP-201

APP-201

TAAGAGAGTTTTAGCATCACTACCCTATAAAAAAAGTGTCAGAAAGGTTTCGTTTTCAGCAGAATGAGTTGAAACTTAACCAAAAA
ATTCTCTCAAAATCGTAGTGATGGGATATTTTTATTACAGTCTTTCCAAGCAAAGTCGTCTTACTCAACTTTGAATTGGTTTTT

7480

APP

APP-201

APP-201

ATACTTAACAATATTAAGTAAGAAAAATAAATAAGAATAGAGAACTCTGTGGGTCTCGTAGCAAGAAGTTGGGGGTTGAGGGTTA
TATGAATTGTTATAATTTCACTCTTTTATTCTTATCTCTTGAGACACCCAGAGCATCGTTCTTCAACCCCCAACTCCCAAT

7565

APP

APP-201

APP-201

GGTCATTGAGAGGACCAGAGTTAAAGAATGAGAAAGGGAAACTGTCCCACTTCCATTGTGCCTTTTATGTCTATATTAAGAGAA
CCAGTAACTCTCCTGGTCTCAATTTCTTACTCTTTCCCTTTGACAGGGTGAAGGTAACACGGAAAAATACAGATATAATTTCTCTT

7650

APP

APP-201

APP-201

TGAACTTCTGATGAAAGGAAATTAAGCCCGAGATAGATCAACATGAGAAAAGAAAGCCCTAGCCCATTAGTTACCTATTGCTAC
ACTTGAAGACTACTTTCTTTAATTTCTGGGCTCTATCTAGTTGTACTCTTTTCTTTCTGGGATCGGGTAATCAATGGATAACGATG

7735

APP

APP-201

APP-201

GTAGCAAATAACGCGAGAATTTAGCAGCTTAAACAACAAGCATTAGTTTCTTACAGTTTTTATAGGTCAGGATTTGGGATGTGG
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7820

APP

APP-201

APP-201

TTTAGCTGGATGGTTCTGGCACAGTGTCCGTCATGTGGTTGCAGTTAAGACACTGCCTGAGCTAAAGTCATCTGAAGGTTTGGATT
AAATCGACCTACCAAGACCCTGTGCACAGGCAGTACACCAACGTCAATTCTGTGACGGACTCGATTTTCAGTAGACTTCCAAACTAA

7905

APP

APP-201

APP-201

GGACCTGGTGGGTCTGTTTTCCAACGTGGCTCACTCACGTCCTGTTACTAAGAGACCTCAGTATCTTACCATGTGAACTCTGTAA
CCTGGACCACCCAGACAAAAGGTTGCACCGAGTGAGTGCAGTGACAATGATTCTCTGGAGTCATAGAATGGTACACTTGAGACATT

7990

APP

APP-201

APP-201

TGCTGCTTGAGCGTCCCTACAACATGGCATCTCGCACCCCTGCACCAAGAGGTCCAGGAAAGAGATTAAGGAAGTTTTAGTGCCT
ACGACGAACTCGCAGGGATGTTGTACCGTAGAGCGTGGGGACGTGGTTCTCCAGGTCCTTTCTCTAATTCTTCAAAAATCACGGA

8075

APP

APP-201

APP-201

TTTTTGGCCAGTCTCAGAAGTCATACCCATCACTTCTATCATGCTCTGTTCACTAGAGCAAGTCACTACATCCCGACCACATT
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8160

APP

APP-201

APP-201

CGAAGGAAGGGAATCAAGTTCTCCCTCTTGAAGGAAGGAGTATCAGCAAATTTGTGGATATATTTTAAACTATGACATCTTGCTA
GCTTCTTCCCTTAGTTCAAGAGGGGAGAACTTCCCTTCCCTCATAGTCGTTTAAACACCTATATAAAATTTGATACTGTAGAACGAT

8245

APP

APP-201

APP-201

CCCAAGTCCAAGTTCTTATGACCCAGACCAACTGCAGGCTAAGAGAAGTTGAAGGGGAAGTAGCACCATTGCCTGTGGTCTTTGT
GGGTTCAAGTTCAAGAATACTGGGTCTGGTTGACGTCCGATTCTTGAAGTTCCCTTTCATCGTGGAACGGACACCAGAAAACA

8330

APP

APP-201

APP-201

GGAAAGCTGGGAAGGTAGGGATAGGAAAATGAAGTTCTGAATAGCAAAAAGGAGAGAAGATAGCTTCACAATCTGTAAGCCAGGT
CCTTCGACCCTTCCATCCCTATCCTTTTACTTCAAGACTTATCGTTTTTCTCTCTTCTATCGAAGTGTTAGACATTCCGGTCCA

8415

APP

APP-201

APP-201

ATAGAGTGACATTGATTGTGGGTCTCTTTTCAAATAGGTTATCAAGTGGGAAGCTTTTTGAACAATTGGATGAGGAAATGGTGCTA
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8500

APP

APP-201

APP-201

GGTCACAACCAGCGTGGATTTCTAGGTTTTGTCAGATTATCCTTACCTTCTCCTTGTATAGGCTGTGCTCTTAGACTGGCACAT
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8585

APP

APP-201

APP-201

CATATGCTGTGGACATTGTGCTTTTTCAGTGTGCAAGATGTGTCACAAGTTTTCCAGAAATCTCGTAGACAAGATTGAAAGAGTG
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8670

APP

APP-201

APP-201

ATTAGGCCAAGAGCAGGAAGTGAATTCCCCTGGGAGCCAAAAGGAATTGGGAATGTGTAGCCCAAGTAAGACAAGAACCAGCAGGA
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8755

APP

APP-201

APP-201

ACATGCCTCTCCTTAGGGTCGTGATACCTGTTCAAGGTTTTAATGTGGAAGGGAGGATTAGGCTTGCTCTGTGTTGAATCAGGCT
TGTACGGAGAGGAATCCCAGCACTATGGACAAGTTCAAAATTACACCTTCCCTCCTAATCCGAACGAGACACAACCTTAGTCCGA

8840

APP

APP-201

APP-201

CAAAGGATGGAAGTTACAGGGAAGCTGATTCTGGCTTCATGTAAAAAAGGACAGTTTGGGCAGGCAAATCTATCAAAAAATGGA
GTTTCTACCTTCAATGTCCCTTCGACTAAGACCGAAGTACATTTTTTCTGTCAAACCCGTCCGTTTAGATAGTTTTTTTACCT

8925

APP

APP-201

APP-201

GGGAAATTGATACATTCTCTATGTTCAAACAGGAACTGACAATCTGCCCTGGGTGGGAACACGGTAGAGAAGATGACTTCAA
CCCTTTAACTATGTAAGGAGATACAAGTTTGTCTTACTGTTAGACGGGGACCCACCTTGTGCCATCTCTTCTACTGAAGTTT

9010

APP

APP-201

APP-201

AGCCCTTTTCATCCTAAAATTCTGATGTTTGATAATTAATGTTATAGCATGGACACTGACATTTACATTTTTTACTTATGTTTT
TCGGGAAAAGTAGGATTTTAAGACTACAAACTATTAATTTACAATATCGTACCTGTGACTGTAAATGTAAAAAATGAATACAAAA

9095

APP

APP-201

APP-201

TGGTTTTTAAATGACTCTGCATTTTGTTTTAAGCTTCAAATTATTATTTGAATAATGAAATTCATCAGAACAATTAGTGTTAAGA
ACCAAAAATTTACTGAGACGTAAAAACAAAATTCGAAGTTTAATAATAAACTTATTACTTTAAGTAGTCTTGTTAATCACAATTCT

9180

APP

APP-201

APP-201

ATCATATAGCAATTTATAGAAAAGGAAGAGTTCGTAGGTTATAAATCTGTTAGTTGCTAAGAAGCATTTTTAAAATTATGTACT
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9265

APP

APP-201

APP-201

ATAGCTCTTTATTCAGCAGACGAACCAATTACAATCTGTGTAAGTACTAGAACACTTGACTAAAATTATATAATTTTTACAACGCTTC
TATCGAGAAATAAGTCGTCTGCTTGGTTAATGTTAGACACATTGATCTTGTGAAGTATTTAATATATTAAAAATGTTGCGAAG

9350

APP

APP-201

APP-201

ACTGCATAGATACATGAACATAATTTATTTGTAATTGGAACAAAGCCCCAAAGTAGCAGTTTTGTTCTACCAGGTAATTAATGCT
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9435

APP

APP-201

APP-201

CATTTTTAAAGCCTTTTATTATTATTTCTGAAGTAATGAGTGCACATGGAAAAAGACACATAATAGGCTAAACAATAAGCCCGTA
GTAAAAATTTTCGGAAAAATAATAAAAGACTTCATTACTCACGTGTACCTTTTTCTGTGTATTATCCGATTTGTTATTTCGGGCAT

9520

APP

APP-201

APP-201

AGCCAAGCCAACATATTCCAGGAACAAATCCTTGCCAACCTCTCAACCAGGATTTAACTTCTGCTTTTCCCCCATTTTCAAAAAT
TCGGTTCGGTTGTATAAGGTCCTTGTTTAGGAACGGTTGGAGAGTTGGTCTAAATTGAAGACGAAAAGGGGGTAAAAGTTTTTA

9605

APP

APP-201

APP-201

PCR Reverse

AGCCTTACTTTTCAGGTTTCCTT

TATAGCATGTATTTAAAGGCAGCAGAAAGCCTTACTTTTCAGGTTTCCTTACCCTTTTCATTTCTTTTTGTTCAAATAAGGTTAGTAA
ATATCGTACATAAAATTTCCGTCGTCTTCGGAATGAAAAGTCCAAAGGGAATGGGAAAAGTAAAGAAAAACAAGTTTTATCCATCATT

9690

APP

APP-201

APP-201

TTGAAGTTTTAAATATAGGGTATCATTCTTTAAGAGTCATTTATCAATTTCTTCTAACTTCAGGCCTAGAAAGAAGTTTTG
AACTTCAAATTTATATCCCATAGTAAAAAGAAATTTCTCAGTAAATAGTTAAAAAGAAGATTGAAGTCCGGATCTTTCTTCAAAC

9775

APP

APP-201

APP-201

GGTAGGCTTTGCTTACAGTGTTATTATTTATGAGTAAACTAATTGGTTGTCCTGCATACTTTAATTATGATGTAATACAGGTT
CCATCCGAAACAGAATGTCACAATAATAAATACTCATTGATTAACCAACAGGACGTATGAAATTAATACTACATTATGTCCAA

9860

APP

APP-201

APP-201

655
G

gRNA Protospacer

CAGAATTCGACATGACTC

CTGGGTTGACAAATATCAAGACGGAGGAGATCTCTGAAGTGAAGATGGATGCAGAATTCGACATGACTCAGGATATGAAGTTCA
GACCCAACACTGTTTATAGTTCTGCCTCCTCTAGAGACTTCACTTCTACCTACGTCTTAAGGCTGTAAGTCTTACTTCAAGT

9945

APP

APP-201

S G L T N I K T E E I S E V K M D A E F R H D S G Y E V H

ENSE00001318724

APP-201

Donor Template SNV -> REV

Protospacer Sequence

PAM

SNV

AGACTTCACTTCTACCTACGTCTTAAGGCTGTAAGTCTTACTTCAAGT

Donor Template SNV -> REV

TCATCAAATAATGGTACGTAATAATTTACCTCTTCCACTACTGTTTGTCTTGCCAAATGACCTATTAACCTCTGGTTCATCCT
AGTAGTTTTTAACCATGCATTTTATTAAATGGAGAAAAGGTGATGACAAACAGAACGGTTTACTGGATAATTGAGACCAAGTAGGA

10,030

APP

APP-201

APP-201

685
H Q K L

ENSE00001318724

Donor Template SNV -> REV

AGTAGTTTTTAACCATGCATTTTATTAAATGGAGAAAAGGTGATGACA

Donor Template SNV -> REV

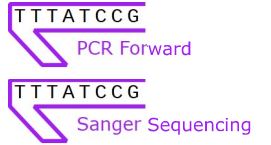
GTGCTAGAAATCAAATTAAGGAAAAAGATAAAAAATACAATGCTTGCCTATAGGATTACCATGAAAACATGAAGAAAAATAAATAGGC
CACGATCTTTAGTTTAAATTCCTTTTTCTATTTTTATGTTACGAACGGATATCCTAATGGTACTTTTTGTACTTCTTTTTATTTATCCG

10,115

APP

APP-201

APP-201



TAGGCTGAGCGCAGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATCACGAGGTCAGAAATTCGAGAC
ATCCGACTCGCGTCACCGAGTTCGGACATTAGGGTCGTGAAACCCCTCCGGTTCGCGCCACCTAGTGCTCCAGTCTTTAAGCTCTG

10,200

APP

APP-201

APP-201

ATccgactcgcg

PCR Forward

ATccgactcgcg

Sanger Sequencing

CAGCCTGGCCAATATGGTGAAACCCCATCTCTACTAAAAATACAAAAAGATTAGCTGGGTGTGGTGGCAAACACCTGTAGTCCC
GTCGGACCGTTATACCACCTTTGGGGTAGAGATGATTTTTATGTTTTTTCTAATCGACCCACACCACCGTTTGTGGACATCAGGG

10,285

APP

APP-201

APP-201

AGCTGCTGGGGAGGCTGACGCAGGAGACTTGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCTAGGCGACAG
TCGACGACCCCTCCGACTGCGTCCTCTGAACGAACTTGGGTCTCCACCTCCAACGTCACCTCGACTCTAGCACGGATCCGCTGTC

10,370

APP

APP-201

APP-201

AGCGAGACTCCATCCCAAAAAAAAAAAGAAAAGAAAGAGGCTGTATGTATAGTTCTTTTCAGACTACAAGGCAGCAAAGTTCGTG
TCGCTCTGAGGTAGGGTTTTTTTTTTTTCTTTCTTTCTCCGACATACATCAAGAAAGTCTGATGTTCCGTCGTTTCAAGCAC

10,455

APP

APP-201

APP-201

CATGACTCGGGACTTAAAGTGGAAATTAATTTCAATATAGCAGCCACTTTGACTTCCACTGTGTTTTCTGGGAAAAATAGGTTTACA
GTA CTGAGCCCTGAATTTACCTTAATTAAGTTATATCGTCCGGTGAACCTGAAGGTGACACAAAAGACCCTTTTATCCAAATGT

10,540

APP

APP-201

APP-201

ATAGGTTTATTTGAAGGATCAAACACATGCATACACTGCTTGGTTTTACAGAACAACCTTTATGTGGCTTAAATTCACATCCGGAAC
TATCCAAATAAACTTCCTAGTTTGTGTACGTATGTGACGAACCAAATGTCTTGTGAAATACACCGAATTTAAGTGTAGGCCTTG

10,625

APP

APP-201

APP-201

TGTCTTCCTTTACCCATTCATTTCTCCCCAGCTCTTTCTTTTCATTCCCTCCCCTACCTCCCATGATTTAACTTCTCTTGCAAG
ACAGAAGGAAATGGGTAAGTAAAGAGGGGGTTCGAGAAAAGAAAAGTAAGGGAGGGGATGGAGGGTACTAAATTGAAGAGAACGTTT

10,710

APP

APP-201

APP-201

AGTAAGATCATGGAGTGAGCAGGACCCCATGATGTTCCCGATAGTGTATTTCATCAAAGGTTTGTGCAAAGAAGACAGCAGCTT
TCATTCTAGTACCTCACTCGTCTGGGGTACTACAAGGGCTATCACAATAAGTAGTTTTCCAAACACGTTTCTTCTGTCTGTCGAA

10,795

APP

APP-201

APP-201

CCTTTTCAGATGAAATCACTTTTCCCCCTAATGTTAGAATTGGAGTAAATCAAAAAGCCACATCTCCTTTGTGGTCAGCTCTAG
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10,880

APP

APP-201

APP-201

TAGTTATATAAAATCCTTTACCAAAAGCTTAGAAATGGAGATAAATCAAATCGTGGATTATGTTAGGGTTCCATCTTATCAGTAG
ATCAATATATTTTAGGAAATGGTTTTCGAATCTTTACCTCTATTTAGTTTAGCACCTAATACAATCCCAAGGTAGAATAGTCATC

10,965

APP

APP-201

APP-201

GTGCAGTAAGAGGGTTAAATTAATGAAGACGACAATTTTATCACATTCAGTGGTGGACAGAAAAATGGTAAGAAAATTTCCATAG
CACGTCATTCTCCCAATTTAATTACTTCTGCTGTTAAAATAGTGTAAGTCAACACCTGTCTTTTTACCATTCTTTTAAAGGTATC

11,050

APP

APP-201

APP-201

CAATAATACTTAAAGTTATCTCAGGCACTTCTTTTGTGTTTTGTTTTGTGTGTGTGTGTGTGTGAGTGTACTTTTTTCCAAGCAGA
GTTATTATGAATTTCAATAGAGTCCGTGAAGAAAACAAAACAAAACACACACACACTCACAATGAAAAAAGGTTTCGTCT

11,135

APP

APP-201

APP-201

AAATGTCTTTTCAATATTCATAAAGTTGATAAATCCTAGTATTAATCTCTAAAAGAAACACCTCCAAATTATTATTTATGCCTTA
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11,220

APP

APP-201

APP-201

CTTGACTCCAAATAATTGTAGCAAATAAAAACTGACTTGGGATTTGGATTTGCATTCTTAACTCCCATAGTTCTTTTTTTGTAG
GAACTGAGGTTTATTAACATCGTTTATTTTTGACTGAACCCTAAACCTAAACGTAAGAATTGAGGGTATCAAGAAAAAACATC

11,305

APP

APP-201

APP-201

AAAGACATTTAGCTTTTTGAAGCATGGTTTTTCATTGGCAAGATAATCTAGTATCAGTTGTTATAAGATCAGGGTTTCTCTTGATG
TTTCTGTAAATCGAAAACTTCGTACCAAAAAGTAACCGTTCTATTAGATCATAGTCAACAATATTCTAGTCCCAAAGAGAACTAC

11,390

APP

APP-201

APP-201

AGGCTGTTGCTGAAGAGGTTAATAAAAACTGGGGAACCACTAAAGAGTTGAAGAGTTGGTGGGGTAGAAAAGCTGACGATTAATGT
TCCGACAACGACTTCTCCAATTATTTTTGACCCCTTGGTGATTTCTCAACTTCTCAACCACCCCATCTTTCGACTGCTAATTACA

11,475

APP

APP-201

APP-201

ACAGATTTGCATTTGTCGGGGCCTGGGGCCTGTGTCATATAAGCCATCCCCACAATTACACTAACGCCTATAATGCGACAGTGA
TGCTAAACGTAAACAGCCCCGGACCCCGGACACAGTATATTCGGGTAGGGGTGTTAATGTGATTGCGGATATTACGCTGTCACT

11,560

APP

APP-201

APP-201

CTAATGGCAGCGGCAGCAATTAGGAGAATCAGCTCCCTCTACTGGACTAGTTAAGATAATGTATTATAATTAGTGCAATGAATAT
GATTACCGTCGCCGTCGTTAATCCTCTTAGTCGAGGGAGATGACCTGATCAATTCTATTACATAATATTAATCACGTTACTTATA

11,645

APP

APP-201

APP-201

TACAAAATTACAGTATTTTTCTTAAAGGCACAGGCATATGTCCAGACTTGTATTTATTCCTGATTACCTCACACTAGTATATTAGC
ATGTTTTAATGTCATAAAGAATTTCCGTGTCCGTATACAGGTCTGAACATAAATAAGGACTAATGGAGTGTGATCATATAATCG

11,730

APP

APP-201

APP-201

TAATTAATGATTTGCTTTTCATAAAAAATGTTGAGCTAGCATATTTGTTTTAGTAAAGGGAATAATTATGAACAATTTCTCATTTTG
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11,815

APP

APP-201

APP-201

TTATAAACCCACGAGTAAAACACTTTTTAGAAGTTGCTTCATTTGCTATATTTTATATTGCCTTTCCAGATTGCTAGTATGTTAGTT
AATATTTGGTGCTCATTTTGTGAAAATCTTCAACGAAGTAAACGATATAAAAATATAACGGAAAAGGTCTAACGATCATACAATCAA

11,900

APP

APP-201

APP-201

TCAGCTTAGAAAAATCAGTTCATTTGACTACCTTGAGGCTAAATTGAAAGAATTTTTAGGGAGGTACAGGCATACCTTGGAAATT
AGTCGAATCTTTTTAGTCAGTAAACTGATGGAACCTCCGATTTAACTTTCTTAAAAAATCCCTCCATGTCCGTATGGAACCTTTAA

11,985

APP

APP-201

APP-201

TCAGAACACCACAATAAAAACAAATTTTGAACAAAAATGTCACACAAATTTTTGGCTTCCCAGTACATATAAAAAGTTATGTTGGC
AGTCTTGTGGTGTTATTTTTGTTTAAAACGTTGTTTTACAGTGTGTTTTAAAAAACCGAAGGGTCATGTATATTTTCAATACAACCG

12,070

APP

APP-201

APP-201

CAGGCACGGTGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGTGGATCACAAGGTCAGGAGGTCGAGAGCATCC
GTCCGTGCCACCGAGTACGGACATTAGGGTTCGTGAAACCTCCGGTTCCGTCCACCTAGTGTTCAGTCTCCAGCTCTCGTAGG

12,155

APP

APP-201

APP-201

TGGCCAACATGGTGAAATGCCATCTCTACTAAAAATACAAAAATTAGCTGCATATGGTGGCATGTGCCTGTAGTCCCAGCTACTC
ACCGGTTGTACCACTTTACGGTAGAGATGATTTTTATGTTTTAATCGACGTATACCACCGTACACGGACATCAGGGTCGATGAG

12,240

APP

APP-201

APP-201

GGGAGGCTGAGGCAAGAGAATCTCTTGATCCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCCTGGGCAACAAGA
CCCTCCGACTCCGTTCTCTTAGAGAACTAGGGTCCCTCCGTCTCCAACGTCACTCGGCTCTAGCGTGAGGTCGGACCCGTTGTTCT

12,325

APP

APP-201

APP-201

GCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGTTTGTATTTACTACTACTCTAGTCTGTTACATGTGCAATAGCATTATGTCTAAA
CGTTCTGAGACAGAGTTTTTTTTTTTTTTTTTTTCAAACATAAATGTGATATGAGATCAGACAATGTACACGTTATCGTAATACAGATTT

12,410

APP

APP-201

APP-201

AAAAAAAAAAGCCATGTATATACTTTACTTTTATTAGTAAAATATTTTATTACTAAAAATGCTAATGATCATCTGAGTCTTCAGC
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12,495

APP

APP-201

APP-201

AAGTCCTAATCTTTTTGCTCGTGGAGAATCTTGCCTTGATGTTCACTGCTGCAGGCTAATCCAGGTGGTGGCTGCTGAGGTTTGT
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12,580

APP

APP-201

APP-201

GGTGGCTGTGGCAATTTCTTAAATAAGACAATAATGAAGTTTGTGTCATCGATTGACTCTTCCTTTACAAAAAGATGTCTCTG
CCACCGACACCGTTAAAGGATTTTATTCTGTTATTACTTCAAACGACGTAGCTAACTGAGAAGGAAAGTGTTTTTCTACAGAGAC

12,665

APP

APP-201

APP-201

TAGCATGTGATGCTGTTTGATAGCATTGCTCACAGTAGAACAGCTTTCAAATTTGGAGTCAGTCTTCGCAAATCTAGCCACTG
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12,750

APP

APP-201

APP-201

CTTCATCGAGTTTATGTGATATCCTAAATCCTTTGTTGTCATTTCAACAGTGTTTCATAGCATCTTCACCAAGAGTAGATTCCATT
GAAGTAGCTCAAATACACTATAGGATTTAGGAAACAACAGTAAAGTTGTCACAAGTATCGTAGAAGTGGTTCTCATCTAAGGTAA

12,835

APP

APP-201

APP-201

GCAAGAAACCACTTTCTTTGCTCATCCATAAGAGGTAACCTCCTCATCCATTCAAGTTTGTGATCATGAGATGGTAGCAGTTCAGTCA
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12,920

APP

APP-201

APP-201

TGTCTTTAGGCTCCACTTCTAATTCTAGTTCTCTTGTATTTCCACCACATCTGCTGTGACATCCTTTACTGAAGTCTTGAAGTCT
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13,005

APP

APP-201

APP-201

CTCAAAGTCACCCATGAGAGTTGGAATCATTGTCTTCCAAACTCCCGTTATTGCTGATGTTTTGATCTCCCATGGATCACAGATG
GAGTTTCAGTGGGTACTCTCAACCTTAGTAACAGAAGGTTTGAGGGCAATAACGACTACAAAACCTAGAGGGTACCTAGTGTCTAC

13,090

APP

APP-201

APP-201

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AAGAATTACCGTAGACCTTACCACCTTAGGAAAAATCTTCCAAACGTCAAATGAAACGGGTCTAGGTAATCTCCTTAGCGATAGAT

13,175

APP

APP-201

APP-201

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13,260

APP

APP-201

APP-201

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13,345

APP

APP-201

APP-201

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13,430

APP

APP-201

APP-201

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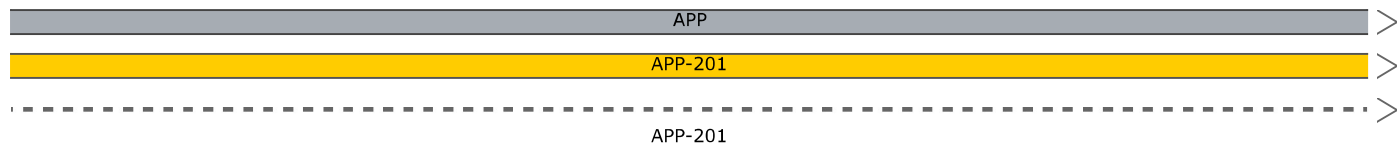
13,515

APP

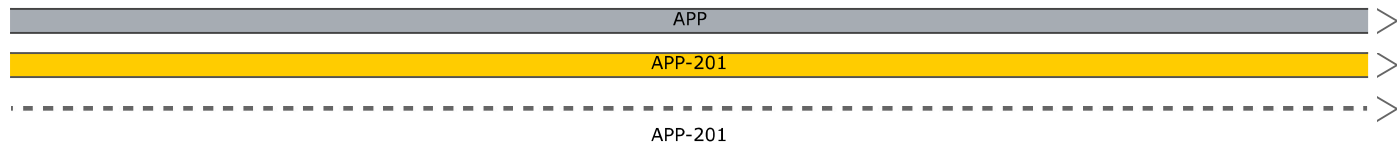
APP-201

APP-201

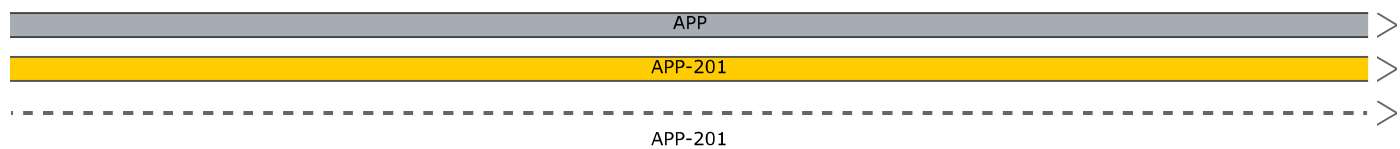
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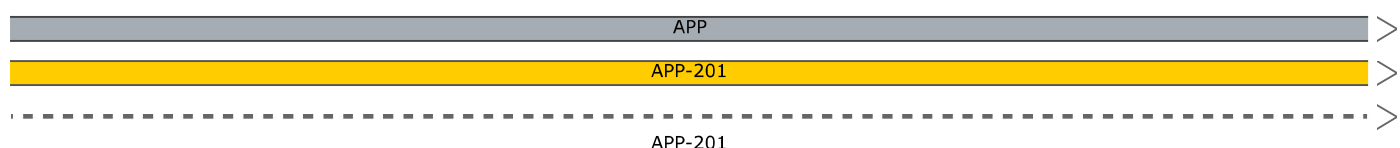
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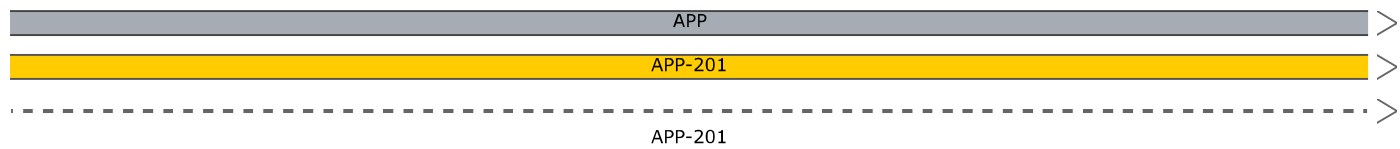
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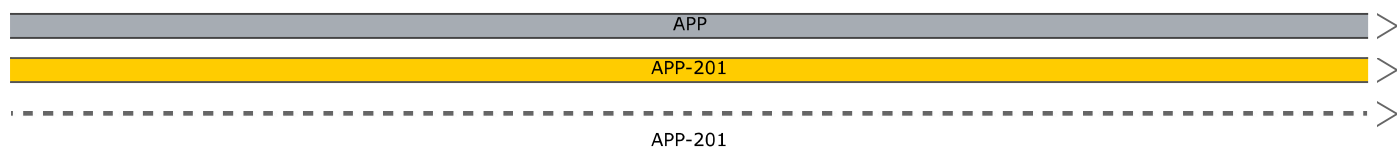
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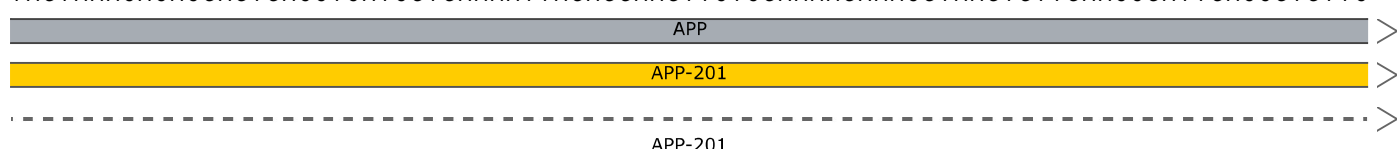
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14,195

APP

APP-201

APP-201

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14,280

APP

APP-201

APP-201

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14,365

APP

APP-201

APP-201

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14,450

APP

APP-201

APP-201

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14,535

APP

APP-201

APP-201

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14,620

APP

APP-201

APP-201

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14,705

APP

APP-201

APP-201

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14,790

APP

APP-201

APP-201

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14,875

APP

APP-201

APP-201

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14,960

APP

APP-201

APP-201

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15,045

APP

APP-201

APP-201

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15,130

APP

APP-201

APP-201

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15,215

APP

APP-201

APP-201

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15,300

APP

APP-201

APP-201

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15,385

APP

APP-201

APP-201

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15,470

APP

APP-201

APP-201

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15,555

APP

APP-201

APP-201

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15,640

APP

APP-201

APP-201

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15,725

APP

APP-201

V F F A E D 690 695 700 705
V V G S N K G A I I G L M V G G
ENSE00003548276

APP-201

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15,810

APP

APP-201

710 715 720 725 730 735
V V I A T V I V I T L V M L K K Q Y T S I H H G V V E
ENSE00003548276

APP-201

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15,895

APP

APP-201

APP-201

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15,980

APP

APP-201

APP-201

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16,065

APP

APP-201

APP-201

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16,150

APP

APP-201

APP-201

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16,235

APP

APP-201

APP-201

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16,320

APP

APP-201

APP-201

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16,405

APP

APP-201

APP-201

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16,490

APP

APP-201

APP-201

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16,575

APP

APP-201

APP-201

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16,660

APP

APP-201

APP-201

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16,745

APP

APP-201

APP-201

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16,830

APP

APP-201

APP-201

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16,915

APP

APP-201

APP-201

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17,000

APP

APP-201

APP-201

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17,085

APP

APP-201

APP-201

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17,170

APP

APP-201

APP-201

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17,255

APP

APP-201

APP-201

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17,340

APP

APP-201

APP-201

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17,425

APP

APP-201

APP-201

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17,510

APP

APP-201

APP-201

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17,595

APP

APP-201

APP-201

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17,680

APP

APP-201

APP-201

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17,765

APP

APP-201

APP-201

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17,850

APP

APP-201

APP-201

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17,935

APP

APP-201

APP-201

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18,020

APP

APP-201

APP-201

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18,105

APP

APP-201

APP-201

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18,190

APP

APP-201

APP-201

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18,275

APP

APP-201

APP-201

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18,360

APP

APP-201

APP-201

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18,445

APP

APP-201

APP-201

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18,530

APP

APP-201

APP-201

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18,615

APP

APP-201

APP-201

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18,700

APP

APP-201

APP-201

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18,785

APP

APP-201

APP-201

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18,870

APP

APP-201

APP-201

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18,955

APP

APP-201

APP-201

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19,040

APP

APP-201

APP-201

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19,125

APP

APP-201

APP-201

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19,210

APP

APP-201

APP-201

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19,295

APP

APP-201

APP-201

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19,380

APP

APP-201

APP-201

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19,465

APP

APP-201

APP-201

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CTTCAGTACTACTTTTCGAAACCAAAGGTCCTCTAAAAAACAAAAATCTCACTTTTTTACGGGGCGTCTTCTAGTGCTCTATCCTTG

19,550

APP

APP-201

APP-201

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19,635

APP

APP-201

APP-201

CTGAGAAATGTGGCATGGGGCGGTTTGATCGCTGTGCAAACATCATAAAGTACATGTACATAAATCTAGATGGTATAGCCTGCTA
GACTCTTTACACCGTACCCCGCCAAACTAGCGACACGTTTGTAGTATTTTCATGTACATGTATTTAGATCTACCATATCGGACGAT

19,720

APP

APP-201

APP-201

CACACCTGGGCTACACACCTACAACCTATTGCTCCTAGGCTCCACACCTGTGCAGCATATTGCTGCACTGAATACTATAGACAGTT
GTGTGGACCCGATGTGTGGATGTTGATAACGAGGATCCGAGGTGTGGACACGTCGTATAACGACGTGACTTATGATATCTGTCAA

19,805

APP

APP-201

APP-201

GTAACACACTGGCAGGGATTTGCGTATCTAAACAACTAGAAAAAGGTACAGTAAAAAATACGGTATTATGGGGCCACCATCATAT
CATTGTGTGACCGTCCCTAAACGCATAGATTTGTTTGATCTTTTCCATGTCAATTTTTTATGCCATAATACCCCGGTGGTAGTATA

19,890

APP

APP-201

APP-201

GTTTGGTCTGTCGTGGACTAAAAATGTCATTATGTGGCCCACTGATTTTTTATTGGTAGAGTTGTTAGCATTGGAAATGAGC
CAAACCAGACAGCACCTGATTTTACAGTAATACACCGGGTATTGACATAAAAAATAACCATCTCAACAATCGTAAACCTTTACTCG

19,975

APP

APP-201

APP-201

ACTTGCTAGTTGTTGTTTTTTTTTTTTTTTTTTTTTTTCAAATAAGCAGGAAATATTGACTTACTGAATTTACTTAGCCATAAGG
TGAACGATCAACAACAAAAAAGTTTATTCGTCCTTTATAACTGAATGACTTAAATGAATCGGTATTCC

20,060

APP

APP-201

APP-201

CCAGAGAGTCACTCTGTGAGCCATTGGCCACGCTTTCCCAAGGAGGTAAGTGTGCCTTATTGGTGCTTCAAGCAGTGAAGCAATA
GGTCTCTCAGTGAGACACTCGGTAACCGGTGCGAAAGGGTTCTCCATTGACACGGAATAACCACGAAGTTCGTCACTTCGTTAT

20,145

APP

APP-201

APP-201

GCCCTTTATTATTACCACTCCCCAAATGTGCCCTCCATGTCAGAATAGCCCTCTGGTGGCTGGAAATCTCAGCACTAGCTGAATT
CGGGAAATAATAATGGTGAGGGGTTTACACGGGAGGTACAGTCTTATCGGGAGACCACCGACCTTTAGAGTCGTGATCGACTTAA

20,230

APP

APP-201

APP-201

AACCACCTTGCTCCTGTTTTAGGACGTTTCTGCAAAGCCCACTAATCCCAGGATCTGTTTAGTAGCAAGCGGTACTTTTTCTACAT
TTGGTGGAAACGAGGACAAAATCCTGCAAGGACGTTTCGGGTGATTAGGGTCTTAGACAAATCATCGTTTCGCCATGAAAAGATGTA

20,315

APP

APP-201

APP-201

TCACATACATAGACACTGGATATTTAAAAATACGTATTGTAGCTCTTTCTGCTACTCTCCCCAGACATGTCACCTTTAATAAGGA
AGTGTATGTATCTGTGACCTATAAATTTTTATGCATAACATCGAGAAAGACGATGAGAGGGGTCTGTACAGTGGAAATTATTCTT

20,400

APP

APP-201

APP-201

GAAGTTGGGGGCACAGCTTCTCTTTATTATAGGATGTGAAAAAGTTTTCTCTCACAGATCTGATCACTTGAACACCAGAAGTCT
CTTCAACCCCGTGTGCGAAGAGAAAATAATATCCTACACTTTTTCAAAGGAGAGTGTCTAGACTAGTGAACCTTGTGGTCTTCAGA

20,485

APP

APP-201

APP-201

CCCCGCCCCACCTCCTGGTTATCTCATTAAATGATCTAAATAAGAAGAGAGTTCCTTTTTATTTGGCTTTTATGGAGGTATGGCAT
GGGGCGGGGGTGGAGGACCAATAGAGTAATTACTAGATTTATTCTTCTCTCAAGGAAAATAAACCGAAAATACCTCCATACCGTA

20,570

APP

APP-201

APP-201

ATGACTTTTTCTAAGTAATATGCTGTCACACTGGTGACTGTATAAAAAGATGTCCTTAGAGGTCTTTCTTCCCAGCCAGAAGCT
TACTGAAAAAGATTCAATTATACGACAGTGTGACCACTGACATATTTTTCTACAGGAATCTCCAGGAAAGAAGGGCCGGTCTTCGA

20,655

APP

APP-201

APP-201

GACCCACCAGGATACAGACGCACTGACGTTGGCATTGTAGAGTAGTTGGAGAGAGTGGTCAGGTTGAATGGAAAGCCACGATAAG
CTGGGTGGTCTATGTCTGCGTGACTGCAACCGTAACATCTCATCAACCTCTCTCACCAGTCCAACCTTACCTTTTCGGTGCTATTC

20,740

APP

APP-201

APP-201

GAAAAGTGAGGGGGGGTGCAGAACCTAGGAGTGGCTTACAGTGAGCAGCAGGAAGAGAAATTGGAAGATCAAAGGAAAGCATCAA
CTTTTCACTCCCCCCCACGTCTTGGATCCTCACCGAATGTCACCTCGTCGTCCTTCTCTTTAACCTTCTAGTTTTCCTTTCGTAAGTT

20,825

APP

APP-201

APP-201

AAATGATCACAGGCCAGGCGTGGTGGCTCACACCTGTAATCCCAGCATTTGGGGAGGCCAAGGCAGGTGGATCACTTGAGGCTAG
TTTACTAGTGTCCGGTCCGCACCACCGAGTGTGGACATTAGGGTCGTA AACCCCTCCGGTTCGTCACCTAGTGA ACTCCGATC

20,910

APP

APP-201

APP-201

GAGTTCGAGTCCAGCCTGGCCAACATGGTGAGACCCTGTCTCTAATAAAAAATACAAAAAATTAGCCAGGCGTGGTGGCATGCGCC
CTCAAGCTCAGGTCGGACCGGTTGTACCACTCTGGGACAGAGATTATTTTTATGTTTTTAAATCGGTCGACACCACCGTACGCGG

20,995

APP

APP-201

APP-201

TGTAGTCGCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGATGGAGGCTGCAGTGAGCCAAAATCACGCCA
ACATCAGCGTCGATGAGTCCTCCGACTCCGTCTCTTAGCGA ACTTGGGTCCTCTACCTCCGACGTCACCTCGGTTTTAGTGC GGT

21,080

APP

APP-201

APP-201

CTGCACTCCAGCCTGGGTGACAGAGCAAGACTGTCTTAAAAAAAAAAAAAAAAATTATGAAGGGATAGCAAAGGAGTTCCTGAACCTG
GACGTGAGGTCGGACCCACTGTCTCGTTCTGACAGAATTTTTTTTTTTTAAATACTCCCTATCGTTTTCTCAAGGACTTGGAC

21,165

APP

APP-201

APP-201

CCTGAAGAATTGCTTGATGTTGGCCATAAACATAGTCAACTGCCTTCTAGTTATATATAACTATAGAGAGATGGCATCAA AATTA
GGACTTCTTAACGAACTACAACCGGTATTTGTATCAGTTGACGGAAGATCAATATATATTGATATCTCTCTACCGTAGTTTTAAT

21,250

APP

APP-201

APP-201

GGAAAAACAAGCATCTATACAACCTAGGTAGCAGGCAGTTACTGGGAGGTTACGAGGGGATAAGTCACTAGCTTGAAAACTTCCTATT
CCTTTTGTTCGTAGATATGTTGATCCATCGTCCGTCAATGACCCTCCAATGCTCCCTATTCAGTGATCGAACTTTTGAAGGATAA

21,335

APP

APP-201

APP-201

TTCTTTGCTTTTATTTTTTTTTTCCGCAGACTTGTGGCTCCTTTGATGTGTCACACTATTGTTGTATTGTTTCGCCTTAGTTCCCT
AAGAAACGAAAAATAAAAAAAAAAAGGCGTCTGAACACCGAGGAACTACACAGTGTGATAACAACATAACAAGCGGAATCAAGGGA

21,420

APP

APP-201

APP-201

TACCCCTCTTTACTCGTCTGGTCCATCTCAATGACAGGATTCTGTCTGTTTGGCCTGACTCAGTCCCTTGATATAAAGGACATCTA
ATGGGAGGAAATGAGCAGACCAGGTAGAGTTACTGTCTTAAGACAGCAAACCGGACTGAGTCAGGGAACATATTTTCTGTAGAT

21,505

APP

APP-201

APP-201

TTAATCCACATCCTGCTGGTTACTGTACATAATAAAATGTAAACGTGGTGTTCCTGCCTCTCCTCCAAGCTCACACACCCGCAT
AATTAGGTGTAGGACGACCAATGACATGTATTATTTTACATTTGCACCACAAAGGACGGAGAGGAGGTTTCGAGTGTGTGGGCGTA

21,590

APP

APP-201

APP-201

GTAAATACTCTAGGGGCAATAGGAGGAGACCTAGAAACTAAGGTCACCCAAATAGAATCTTGTCCCTGCAGGCGGATAGCTGAGC
CATTTATGAGATCCCCGTTATCCTCCTCTGGATCTTTGATTCCAGTGGGTTTATCTTAGAACAGGGACGTCCGCCTATCGACTCG

21,675

APP

APP-201

APP-201

TCTAAATACTCTGGATACAGTGAAGGACTAAATGGTTCCAATGAATCAAGTTCAGGGAGAAAAGGGTCAGGGGGTATGGAGGTT
AGATTTAATGAGACCTATGTCACTTCCTGATTTACCAAGGTTACTTAGTTCAAGTCCCTCTTTTCCCAGTCCCCCATACTCCAA

21,760

APP

APP-201

APP-201

AGCCAAAGAGTGTCAAACGTTCTCCTCAAAGCTATTTTAGAACAAAGGCTGGTCAGGCTATTTGGGCTCAGCTCTTTTCAGCGTGT
TCGGTTTCTCACAGTTTGAAGAGGAGTTTCGATAAAATCTTGTTCGACCAGTCCGATAAACCCGAGTCGAGAAAAGTCGCACA

21,845

APP

APP-201

APP-201

GTCATAGGCAGCAGCCAGTTGAAGCCATGCCACCATGCAGTGCAGGGGTCCAGGTCTCAGGAAGGTGCAGCGTACCGAGAGTCAC
CAGTATCCGTCGTCGGTCAACTTCGGTACGGTGGTACGTACCGTCCCGAGGTCCAGAGTCCCTTCCACGTGCGATGGCTCTCAGTG

21,930

APP

APP-201

APP-201

ATGAAGACCTCAGATCATTTCCTGCTGCTGTGTAATCCAGGCAGTCTGGGAAGAGAATGAATATTCAGTGGTTGTATGTATGTGT
TACTTCTGGAGTCTAGTAAAGGACGACGACACATTAGGTCCGTCAGACCCTTCTCTTACTTATAAGTCACCAACATACATACACA

22,015

APP

APP-201

APP-201

GTCTTCATCCCAGCAAGTGACAGATGTTCCCTGCCAGTTGGAAATGGAAATTCGACTTCATTGTCTTATCATTCCCTTCCAGAA
CAGAAGTAGGGTCGTTCACTGTCTACAAGGACGGGTCAACCTTTTACCTTTAAGACTGAAGTAACAGAATAGTAAGGAAGGTCTT

22,100

APP

APP-201

APP-201

CAAGCACCATGGGCTCAAACCCTCCCTGGCTCTGCTTTAAGGGAAATAATATTGTGTCTGTGCAGAGGCCCTGTCTGCACAGGGT
GTTCTGGTACCCGAGTTTGGGAGGGACCGAGACGAAATCCCTTTATTATAACACAGACACGTCTCCGGGACAGACGTGTCCCA

22,185

APP

APP-201

APP-201

CGTGGTAGGGCTGGCCTTCACATGGTGGCCCATGCCACTGCTGTAGCTTAGCCATGAGGAAGAGATTGGTGAGCCTGCTGGAGAG
GCACCATCCCGACCGGAAGTGTACCACCGGGTACGGTGACGACATCGAATCGGTACTCCTTCTCTAACCCTCGGACGACCTCTC

22,270

APP

APP-201

APP-201

GAAGGCTACCCTTACTTGGTGCTCCTCCTTTATCCATAGACATGAGTACTCAGATTTTCGCATCTAGCTTTCAAGGGGCTGGAGA
CTTCCGATGGGAATGAACCACGAGGAGGAAATAGGTATCTGTACTCATGAGTCTAAAAGCGTAGATCGAAAAGTCCCCGACCTCT

22,355

APP

APP-201

APP-201

TTAAAGATCCAATCCATACTCCTTGGATGCCCTTTTGTCAAGATAATCCCTTCTTCTGTAGCTCCTAAGCCCTCTAAGGTCTGAG
AATTTCTAGGTTAGGTATGAGGAACCTACGGGAAAACAGTTCTATTAGGGAAGAAGACATCGAGGATTCCGGGAGATTCCAGACTC

22,440

APP

APP-201

APP-201

GGCCAAGCTGCCCATGGCAGGAATGGCAAAATGTAGCTGTCTCTCAGTGGCAAAAGGTAATAGGATTATCAAGTAGCAAAACA
CCGGTTCGACGGGGTACCGTCCTTACCGTTTTACATCGACAGGAGAGTACCAGTTTTCCATTATCCTAATAGTTTCATCGTTTTGT

22,525

APP

APP-201

APP-201

GAAGCCAAGAAAAGACAGGAGAGTTAGAGGTCTGGATTGTGCACCAGCCTTGGAGCCTCGCATCTCTAGCAGGGCACTCTTAAGC
CTTCGGTTCCTTTCTGTCTCTCAATCTCCAGACCTAACACGTGGTCGGAACCTCGGAGCGTAGAGATCGTCCCCTGAGAATTCG

22,610

APP

APP-201

APP-201

GTTAGGCTTTGGAGTTTGAAGAGGAGATAAACCTATCAAATTGCCAGGTGTTCCCTTGCCTTGATGCATGCAAATGATTGTTGA
CAATCCGAAACCTCAAACCTTCTCCTCTATTTGGATAGTTAACGGTCCACAAGGGGACGGGAACCTACGTACGTTTACTAACAACT

22,695

APP

APP-201

APP-201

CAGCCAGTGTGATGGTAGATGTGCCTCCTGGAAGAAATAAAAGTATAATATTCACAACATCAAGCAGCATTGTGGCTTTTTTCTA
GTCGGTCACACTACCATCTACACGGAGGACCTTCTTTATTTTCATATTATAAGGTTGTTAGTTCGTCGTAACACCGAAAAAAGAT

22,780

APP

APP-201

APP-201

CAATCAGAAACATAGCAGCTTTGTGCTTGATCTCCTAAGCAAGATAATTTTTTTAACTGGGCATTCTTTGAGTTCTCAGTTTC
GTTAGTCTTTGTATCGTCGAAACACGAACTAGAGGATTCTTTCTATTAATAAAAAAATTGGACCCGTAAGAAACTCAAGAGTCAAAG

22,865

APP

APP-201

APP-201

GAGGTGATGGGGAGCAAAAATGATGCCCAAGTTCAAATGGCGTACTGCTGCAGATAGGCTGTCTCCTGGCACACAGATTTACAGA
CTCCACTACCCCTCGTTTTTACTACGGGTTCAAGTTTACCGCATGACGACGTCTATCCGACAGAGGACCGTGTGTCTAAATGTCT

22,950

APP

APP-201

APP-201

GTGAATGAAATCTCTCATTATTGGTGCTAATCTTTAACCATGGTTTTTAACTTACAAGTTGGAGGCTAATTACACAGTTACCAAGT
CACTTACTTTAGAGAGTAATAACCACGATTAGAAATTGGTACCAAAAATTGAATGTTCAACCTCCGATTAATGTGTCAATGGTCA

23,035

APP

APP-201

APP-201

TAAAGCCAGGTGACCTCATTGTTGACAACAGTGCACAGCAAAGGAAAGAGGAGAGGATAAGGAAAATATCTGTGATTTGCTCCC
ATTTGCGGTCCACTGGAGTAAACAACCTGTTGTACAGTGTCTGTTTCTTTCTCCTCTCCTATTCTTTTATAGACACTAAACGAGGG

23,120

APP

APP-201

APP-201

AGAAGGACAGTGAAGCTGAGCATCCATTTGAGCAGAGTCCTCTGAGTACTGGCCTTGGTCAGAGCTTGTGGTGGGAGTGTGCTA
TCTTCTGTCACTTCGACTCGTAGGTAACCTCGTCTCAGGAGACTCATGACCGGAACCAGTCTCGAACAAACCACCTCACACGAT

23,205

APP

APP-201

APP-201

AGGGGAGATGCCTAGGTCTGTCAATTGGAGTAAGCTGAGGGTTTGGATGCAGGGGAACCTCAGGCAGCTCTGAGCCACAGGGTGGTA
TCCCTCTACGGATCCAGACAGTAACCTCATTTCGACTCCCAAACCTACGTCCCCTTGAGTCCGTTCGAGACTCGGTGTCCACCAT

23,290

APP

APP-201

APP-201

GATGGGAGGGATTACAGTGGCGCACAGTCTCTTCCATAAATGGAAACGTAAGAATCGGGGCACATGGCCATGGCGGCTCATGCC
CTACCCTCCCTAAGTGTACCCGCGTGTTCAGAGAAGGTATTTACCTTTGCATTCTTAGCCCCGTGTACCGGTACCGCCGAGTACGG

23,375

APP

APP-201

APP-201

TGTAGTCCTAGTGCTACTTTAGGAGGCCGAGGTAGGCGGATCACCTGAGGTCAGTTTGTAGACCAGCATGGCCAACATGGTGA AAC
ACATCAGGATCACGATGAAATCCTCCGGCTCCATCCGCCTAGTGGACTCCAGTCAAACCTCTGGTTCGTACCGGTTGTACCACTTTG

23,460

APP

APP-201

APP-201

CCCATCTCTACTAAAAATACAAAAATTAGCCAGGCGTAGTGGCGGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAG
GGGTAGAGATGATTTTTATGTTTTAATCGGTCCGCATCACCGCCACGGACATTAGGGTTCGATGAGCCCTCCGACTCCGTCTCTC

23,545

APP

APP-201

APP-201

AATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATTGCCTGGGCAACAAGAGCAAGACTCCAACCTCAAAAAAATGG
TTAGTGAACCTGGACCTCCGTCTCCAACGTCACTCGGCTCTAACGGACCCGTTGTTCTCGTTCTGAGGTTGAGTTTTTTTTACC

23,630

APP

APP-201

APP-201

GCACATAATGGATGGAACATTCTGTCCCAAGGGATGAGGGGAGCTGTATATCTACCTATTCCAGCTGCCTTGGGATTAGCCACTGG
CGTGTATTACCTACCTTGTAAAGACAGGGTTCCCTACTCCCTCGACATATAGATGGATAAAGGTCGACGGAACCCCTAATCGGTGACC

23,715

APP

APP-201

APP-201

TAGTCATTCCACCTCACTCCCAGACTGAAAAGAGTCAATCACTTCATGAAGTGGGGCTATCCGAAGGGACCACAGGGGACCTGAT
ATCAGTAAGGTGGAGTGAGGGTCTGACTTTTCTCAGTTAGTGAAGTACTTCACCCCGATAGGCTTCCCTGGTGTCCCCTGGACTA

23,800

APP

APP-201

APP-201

TATACTGACAGATTTATTTTTATTTATTTACTTTTTTTGAGACAGAGTCTCCCTCTGTTGCCCAGGCCGGAGTGCAGTGGCACGA
ATATGACTGTCTAAATAAAAAATAAATAAATGAAAAAACTCTGTCTCAGAGGGAGACAACGGGTCCGGCCTCACGTCACCGTGCT

23,885

APP

APP-201

APP-201

TCTTGGCTCACTGCAGCCTCAGCCTCCTGGGTTCAAGCAGTTCTTCTGCCTCAGCCTCTGGAGTAGCTGGGACTACAGGCACGTG
AGAACCAGAGTGACGTCGGAGTCGGAGGACCCAAGTTCGTCAAGAAGACGGAGTCGGAGACCTCATCGACCCTGATGTCCGTGCAC

23,970

APP

APP-201

APP-201

CTACTGTGCCTGGCTAAATTTTTTTGTATTTTTGTTAAAGATGGGGTTTTCACTATGTTGGCCAGGCGTGCTCAAACCTCCCGACC
GATGACACGGACCGATTTAAAAAACATAAAAAACAATTTCTACCCCAAAGTGATACAACCGGTCCGCACAGAGTTTGAGGGCTGG

24,055

APP

APP-201

APP-201

TCGTGATCCACCCGCCTTGGCCTCCCAAAAGGGCTGGGATTTTGGACCCACCTCACCTGGCCTTTTTTTTTCTTGGAGATGGAGTCT
AGCACTAGGTGGGCGGAACCGGAGGGTTTTCCCGACCCTAAAACCTCGGTGGAGTGGACCGGAAAAAAGAACCTCTACCTCAGA

24,140

APP

APP-201

APP-201

CACTCTGTCTCCCAGGCTGGAGTGCAGTGGCACAAATCTTGGCTCACTGCAAACCTCCACCCCCCAAGTTCAAGCCATTCTCCTGCC
GTGAGACAGAGGGTCCGACCTCACGTCACCGTGTTAGAACCGAGTGACGTTTGGAGTGGGGGGTTCAAGTTCGGTAAGAGGACGG

24,225

APP

APP-201

APP-201

TCCGCCTGTGGAGCAGCTGGGATTACAGGCGTGCACCACCACGCCTGGCTAATTTTTTGTATTTTTTAGTAGAGACAAGGTTTTACC
AGGCGGACACCTCGTCGACCCTAATGTCCGCACGTGGTGGTGC GGACCGATTAAAAACATAAAAAATCATCTCTGTTCCAAAAGTGG

24,310

APP

APP-201

APP-201

ATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGACGCACCCACCTCAGGCTCCCAAAGTGCTGGGATTACAGGAGTGAG
TACAACCGGTCCGACCAGAGTTTGAGGACTGGAGTTCACTGCGTGGGTGGAGTCCGAGGGTTTTACGACCCTAATGTCTCTCACTC

24,395

APP

APP-201

APP-201

CCACTGCACCCGGCCATATTGACAGATCTTTTAGTCTGAATTGTTATCAGCCAGTGTGGTCTAGTCATGACATATCTAGCTCCAT
GGTGACGTGGGCCGGTATAACTGTCTAGAAAATCAGACTTAACAATAGTCGGTTCACACCAGATCAGTACTGTATAGATCGAGGTA

24,480

APP

APP-201

APP-201

CTCGAGACCTCATGTCTTACTGCTGACACTACATCCTCGCTGGTACTTTTTCTTCCTTGGCTTCAGGGGCATTGCTGTGTAGGCT
GAGCTCTGGAGTACAGAATGACGACTGTGATGTAGGAGCGACCATGAAAAAGAAGGAACCGAAGTCCCCGTAACGACACATCCGA

24,565

APP

APP-201

APP-201

CAGATCCATGCCAGATGGGGTGTGTAGGGGGAAAAAGCTGCATAAGGGAGGAATGTCACTTGGCAACACTCAACAAGGGGGAATGG
GTCTAGGTACGGTCTACCCACACATCCCCCTTTTCGACGTATTCCTCCTTACAGTGAACCGTTGTGAGTTGTTCCCCCTTACC

24,650

APP

APP-201

APP-201

GCCTGCAGTATTCTCCAGAGATGAATGAGCAGCCATTCTAGGAAATATCCCTTTGAAGGAATATCTTCTCTATGGTACATCCA
CGGACGTCATAAGAGGGTCTCTACTTACTCGTCGGGTAAGATCCTTTATAGGGAACTTCCTTATAGAAGAGATACCATGTAGGT

24,735

APP

APP-201

APP-201

AACTTTTCTCTGGAAAACATGCCTCTTCATTCTGATGACTTTCTATTTATTCTCTTCATCTTACCATGGTTTTACAAAAGAGGAA
TTGAAAAGAGACCTTTTGTACGGAGAAGTAAGACTACTGAAAGATAAATAAGAGAAGTAGAATGGTACCAAAATGTTTTCTCCTT

24,820

APP

APP-201

APP-201

TTTTAACATACTCATTTCAGCAGAGTTAAGGACCTCCTCTCTTCTGCGAACGGGGAGAGGTATAACAAATATAGTAAAAACAAGAAC
AAAATTGTATGAGTAAGTCGTCTCAATTCCTGGAGGAGAGAAGACGCTTGCCCTCTCCATATTGTTTATATCATTGTTCTTG

24,905

APP

APP-201

APP-201

AGCCACTGCCACGTTGTAGGGGTAAGTACCCTGCCAACCTGCAGACAGTAAATGCCACACACAGCTCTAACAGTGACAGGGGG
TCGGTGACGGGTGCAACATCCCCATTCATGGGACGGGTGGACGTCTGTCATTTACGGTGTGTGTCGAGATTGTCACCTGTCCCC

24,990

APP

APP-201

APP-201

AGAAAAACGTCTTCAGTTACTGGCCTGACCTTAGAGGTAAAGCAACATATTAACAGAGAGGGTCTGATTTTAACTTTGAGCTGA
TCTTTTTGCAGAAGTCAATGACCGGACTGGAATCTCCATTTGTTGTATAATTGTCTCTCCAGACTAAAATTTGAAACTCGACT

25,075

APP

APP-201

APP-201

ACATACTTCTATAGTATCTTAATTCTCAGTTTTTAAAAAATTACATCATCTAGAATGGCGTCGTCCTTGCTCTTCTTTTTTCTT
TGTATGAAGATATCATAGAATTAAGAGTCAAAAATTTTTAATGTAGTAGATCTTACCGCAGCAGGAACGAGAAGGAAAAAAGAA

25,160

APP

APP-201

APP-201

GTGCCAAATAATAGCCCCCTTTGGTATATGTTATTGTTTTAATTGATTCTCAAACCTCTCCTTAACATTTTAAACAAACATAAAAT
CACGGTTTTATTATCGGGGGAAACCATATACAATAACAAAATTAACCTAAGAGTTTGGAGAGGAATTGTAATAATTGTTTGTATTTA

25,245

APP

APP-201

APP-201

TTGATAGAAATGGGCTAGACTAAATTCAGCAGTCCAGGAAATCGAGTATTTTTCTACACAGATTTGAGTGTACCCCAAGATACAG
AACTATCTTTACCGGATCTGATTTAAGTCGTCAGGTCCTTAGCTCATAAAAAGATGTGTCTAAACTCACAGTGGGTTCTATGTC

25,330

APP

APP-201

APP-201

TATACTTTGCTGAATCTCCCTCCATGATACTCTTGTGGTTTTATCTATTTTACCAAAACACTTCCACGTAAAACAGGCTTCCGTT
ATATGAAACGACTTAGAGGGAGGTACTATGAGAACACCAAAAATAGATAAAAATGGTTTTGTGAAGGTGCATTTTGTCCGAAGGCAA

25,415

APP

APP-201

APP-201

GACTCTGTTTGTCTTTATGGACCCAACAGGGGAGGAAAAAATACCATTGCACTGGGTTTATCCACTTACTGTGGAGTTGGGGAA
CTGAGACAAACAGGAAATACCTGGGTTGTCCCTCCTTTTTTATGGTAACGTGACCCAAATAGGTGAATGACACCTCAACCCCTT

25,500

APP

APP-201

APP-201

CCAGAAACAACCACTGGACACGTTGCAAGCGCGTCAAGGTTTCCACCGCCACCTGGTGGCTAGATGGAGCACAGCATCTGTGTAA
GGTCTTTGTTGGTGACCTGTGCAACGTTTCGCGCAGTTCCAAAGGTGGCGGTGGACCACCGATCTACCTCGTGTCTGTAGACACATT

25,585

APP

APP-201

APP-201

CTGGTGGGCAAAGGCGTTCTGCTCCAAGATGTCAAAGTGGGGGAGAAAATTATGGGTGTTCTGCAATCTTGGCAAAGAAGAGTA
GACCACCCGTTTCCGCAAGACGAGGTTCTACAGTTTACCCCTCTTTTAATACCCACAAGACGTTAGAACCGTTTTCTTCTCAT

25,670

APP

APP-201

APP-201

CTGTACTCCTTATCTTTTTACTGCTTCTCCATGTTACCCCTTAAAAGATTGATTTTTATTTTTACTCAGCTCTCCTCTTGT
GACATGAGGAATAGAAAAATGACGAAGAGGTACAAGTGGGAATTTCTAACTAAAAATAAAAAATGAGTCGAGAGGAGAACAAAA

25,755

APP

APP-201

APP-201

TCAGGTTGACGCCGCTGTCACCCAGAGGAGCGCCACCTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTC
AGTCCAACCTGCGGCACAGTGGGGTCTCCTCGCGGTGGACAGGTTCTACGTCGTCCTTGGCGATGCTTTTAGGTTGGATGTTCAAG

25,840

APP

APP-201

ENSE00001725664

APP-201

V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F

TTTGAGCAGATGCAGAACTAGACCCCGCCACAGCAGCCTCTGAAGTTGGACAGCAAAACCATTGCTTCACTACCCATCGGTGTC
AAACTCGTCTACGTCCTTGATCTGGGGGCGGTGTCGTCGGAGACTTCAACCTGTCGTTTTGGTAACGAAGTGATGGGTAGCCACAG

25,925

APP

APP-201

765 F E Q M Q N 770

ENSE00001725664

APP-201

CATTTATAGAATAATGTGGGAAGAAACAAACCCGTTTTATGATTTACTCATTATCGCCTTTTGACAGCTGTGCTGTAACACAAGT
GTAATAATCTTATTACACCCTTCTTTGTTGGGCAAAATACTAAATGAGTAATAGCGGAAAACCTGTCGACACGACATTGTGTTCA

26,010

APP

APP-201

AGATGCCTGAACTTGAATTAATCCACACATCAGTAATGTATTCTATCTCTTTACATTTTGGTCTCTATACTACATTATTAATG
TCTACGGACTTGAACCTAATTAGGTGTGTAGTCATTACATAAGATAGAGAGAAATGTAAAACCAGAGATATGATGTAATAATTAC

26,095

APP

APP-201

GGTTTTGTG TACTGTAAAGAATTTAGCTGTATCAAAC TAGTGCATGAATAGATTCTCTCCTGATTATTTATCACATAGCCCCTTA

CCAAAACACATGACATTTTCTTAAATCGACATAGTTTGATCACG TACTTATCTAAGAGAGGACTAATAAATAGTGTATCGGGGAAT

26,180

APP

APP-201

GCCAGTTGTATATTATTCTTGTGGTTTTGTGACCCAATTAAGTCCTACTTTACATATGCTTTAAGAATCGATGGGGGATGCTTCAT

CGGTCAACATATAATAAGAACACCAAACACTGGGTTAATTCAGGATGAAATGTATACGAAATTCCTTAGCTACCCCCTACGAAGTA

26,265

APP

APP-201

GTGAACGTGGGAGTTCAGCTGCTTCTCTTGCCTAAGTATTCCTTTCTGATCACTATGCATTTTAAAGTTAAACATTTTTAAGTA

CACTTGCACCCTCAAGTCGACGAAGAGAACGGATTATAAGGAAAGGACTAGTGATACGTAAAATTTCAATTTGTAAAAATTCAT

26,350

APP

APP-201

TTTCAGATGCTTTAGAGAGATTTTTTTTTCCATGACTGCATTTTACTGTACAGATTGCTGCTTCTGCTATATTTGTGATATAGGAA

AAAGTCTACGAAATCTCTCTAAAAAAAAGGTACTGACGTAAAATGACATGTCTAACGACGAAGACGATATAAACACTATATCCTT

26,435

APP

APP-201

TTAAGAGGATACACACGTTTGTTCCTCGTGCCTGTTTTATGTGCACACATTAGGCATTGAGACTTCAAGCTTTTCTTTTTTGT

AATTCTCCTATGTGTGCAAAACAAAGAAGCACGGACAAAATACACGTGTGTAATCCGTAACTCTGAAGTTCGAAAAGAAAAAACA

26,520

APP

APP-201

CCACGTATCTTTGGGTCTTTGATAAAGAAAAGAATCCCTGTTTCATTGTAAGCACTTTTACGGGGCGGGTGGGGAGGGGTGCTCTG

GGTGCATAGAAACCCAGAAACTATTTCTTTTCTTAGGGACAAGTAACATTCTGTGAAAATGCCCGGCCACCCCTCCCCACGAGAC

26,605

APP

APP-201

CTGGTCTTCAATTACCAAGAATTCTCCAAAACAATTTCTGCAGGATGATTGTACAGAATCATTGCTTATGACATGATCGCTTTC

GACCAGAAGTTAATGGTTCTTAAGAGGTTTTGTTAAAAGACGTCTACTAACATGTCTTAGTAACGAATACTGTACTAGCGAAAG

26,690

APP

APP-201

TACACTGTATTACATAAAATAAATTAATAAAAATAACCCCGGGCAAGACTTTTCTTTGAAGGATGACTACAGACATTAATAATCG

ATGTGACATAATGTATTTATTTAATTTATTTTATTGGGGCCCGTCTGAAAAGAACTTCTACTGATGTCTGTAATTTATTAGC

26,775

APP

APP-201

AAGTAATTTTGGGTGGGGAGAAGAGGCAGATTCAATTTTCTTTAACCAGTCTGAAGTTTCATTTATGATACAAAAGAAGATGAAA

TTCATTA AAAACCCACCCCTCTTCTCCGTCTAAGTTAAAAGAAATTTGGTCAGACTTCAAAGTAAATACTATGTTTTCTTCTACTTT

26,860

APP

APP-201

ATGGAAGTGGCAATATAAGGGGATGAGGAAGGCATGCCTGGACAAACCTTCTTTAAGATGTGTCTTCAATTTGTATAAAATGG

TACCTTACCCTTATATTCCCTACTCCTTCCGTACGGACCTGTTTGGGAAGAAAATTTCTACACAGAAGTTAAACATATTTTACC

26,945

APP

APP-201

TGTTTTTCATGTAAATAAATACATTCTTGGAGGAGCA

ACAAAAGTACATTTATTTATGTAAGAACCTCCTCGT

3 '
26,981
5 '



Feature	Location	Size		Type
✓ APP	1 .. 26,981	26,981 bp	→	gene
/note	= gene ENSG00000142192 Protein coding			
APP-DT	1 .. 26,981	26,981 bp	←	gene
/note	= gene ENSG00000273492 lncRNA			
✓ APP-201	1 .. 26,981	26,981 bp	→	prim_transcript
/note	= primary transcript ENST00000346798			
APP-202	1 .. 26,981	26,981 bp	→	prim_transcript
/note	= primary transcript ENST00000348990			
APP-203	1 .. 26,981	26,981 bp	→	prim_transcript
/note	= primary transcript ENST00000354192			
APP-204	1 .. 26,981	26,981 bp	→	prim_transcript
/note	= primary transcript ENST00000357903			
APP-DT-201	1 .. 26,981	26,981 bp	←	prim_transcript
/note	= primary transcript ENST00000608591 lncRNA			
APP-DT-202	1 .. 26,981	26,981 bp	←	prim_transcript
/note	= primary transcript ENST00000609365 lncRNA			
APP-DT-203	1 .. 26,981	26,981 bp	←	prim_transcript
/note	= primary transcript ENST00000664668 lncRNA			
APP-206	1 .. 26,980	26,980 bp	→	prim_transcript
/note	= primary transcript ENST00000359726			
APP-209	1 .. 26,200	26,200 bp	→	prim_transcript
/note	= primary transcript ENST00000440126			
APP-208	1 .. 26,199	26,199 bp	→	prim_transcript
/note	= primary transcript ENST00000439274			
APP-205	1 .. 25,921	25,921 bp	→	prim_transcript
/note	= primary transcript ENST00000358918			
✓ APP-201	2454 .. 25,861	23,408 bp	→	CDS
▶ 4 segments = 404 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000284981			
/translation	= EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN* 133 amino acids = 14.8 kDa			
APP-202	2454 .. 25,861	23,408 bp	→	CDS
▶ 4 segments = 404 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000345463			
/translation	= EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN* 133 amino acids = 14.8 kDa			
APP-203	2454 .. 25,861	23,408 bp	→	CDS
▶ 4 segments = 404 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000346129			
/translation	= EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQQMN* 133 amino acids = 14.8 kDa			

Feature	Location	Size	Color	Symbol	Type
APP-204	2454 .. 25,861	23,408 bp	■	→	CDS
▶ 4 segments = 404 bp					
/codon_start = 1					
/note = coding sequence ENSP00000350578					
/translation = EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN* 133 amino acids = 14.8 kDa					
APP-206	2454 .. 25,861	23,408 bp	■	→	CDS
▶ 4 segments = 404 bp					
/codon_start = 1					
/note = coding sequence ENSP00000352760					
/translation = EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN* 133 amino acids = 14.8 kDa					
APP-208	2454 .. 25,861	23,408 bp	■	→	CDS
▶ 4 segments = 404 bp					
/codon_start = 1					
/note = coding sequence ENSP00000398879					
/translation = EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN* 133 amino acids = 14.8 kDa					
APP-209	2454 .. 25,861	23,408 bp	■	→	CDS
▶ 4 segments = 404 bp					
/codon_start = 1					
/note = coding sequence ENSP00000387483					
/translation = EPVDARPAADRGLTTRP,,GSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYT SIHHGVVE,,VDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN* 133 amino acids = 14.8 kDa					
APP-213	9548 .. 26,017	16,470 bp	■	→	prim_transcript
/note = primary transcript ENST00000464867 Retained intron					
APP-205	9858 .. 25,861	16,004 bp	■	→	CDS
▶ 3 segments = 350 bp					
/codon_start = 1					
/note = coding sequence ENSP00000351796					
/translation = SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL,,VFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKKKQYTSIHHGVVE,,VDAAVTPEER HLSKMQQNGYENPTYKFFEQMQN* 115 amino acids = 12.9 kDa					
✓ Donor Template SNV -> REV	9893 .. 9992	100 bp	■	⇌	misc_feature
✓ Protospacer Sequence	9911 .. 9930	20 bp	■	⇌	misc_feature
✓ SNV	9911 .. 9911	1 bp	■	⇌	misc_feature
/note = REV = G SNV = A					
✓ PAM	9931 .. 9933	3 bp	■	⇌	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Reverse	22-mer	9632 .. 9653	58°C	Jan 10, 2023
/sequence = AGCCTTACTTTCAGGTTTCCCT 45% GC / 6627.4 Da				
✓ Donor Template SNV -> REV	100-mer	9893 .. 9992	71°C	Jan 10, 2023
/sequence = ACAGTAGTGGAAAGAGGTAAATTATTTTACGTACCAATTTTGGATGATGAACTTCATATCCTGAGTCATGTCGGAATTCTGCATCCATCT 36% GC / 808.2 Da				
✓ gRNA Protospacer	20-mer	9912 .. 9930	53°C	Jan 10, 2023
/sequence = ACAGAATTCCGACATGACTC 45% GC / 6070.0 Da				
✓ PCR Forward	20-mer	10,108 .. 10,127	60°C	Jan 10, 2023
/sequence = gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da				
✓ Sanger Sequencing	20-mer	10,108 .. 10,127	60°C	Jan 10, 2023
/sequence = gcgctcagccTAGCCTATTT 55% GC / 6044.0 Da				