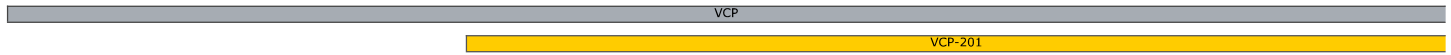


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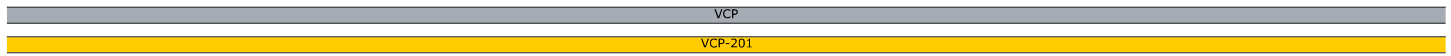
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135



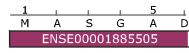
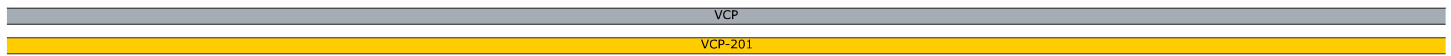
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270



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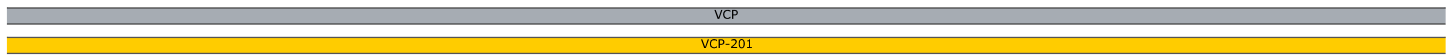
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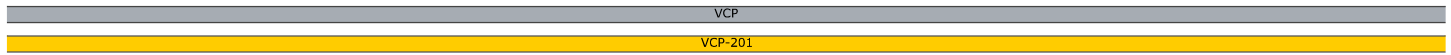
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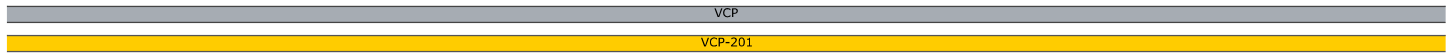
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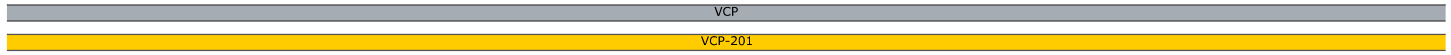
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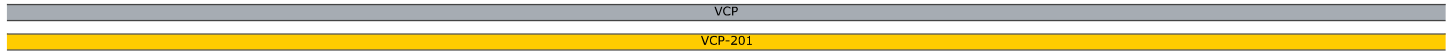
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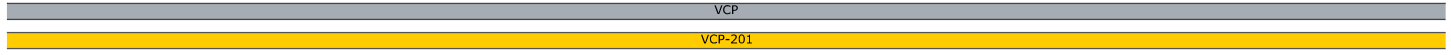
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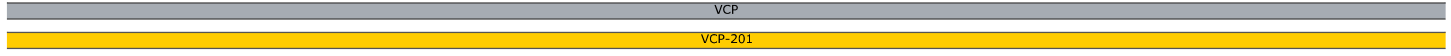
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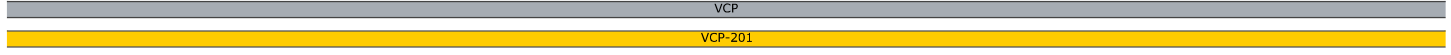
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1350



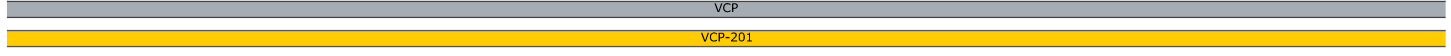
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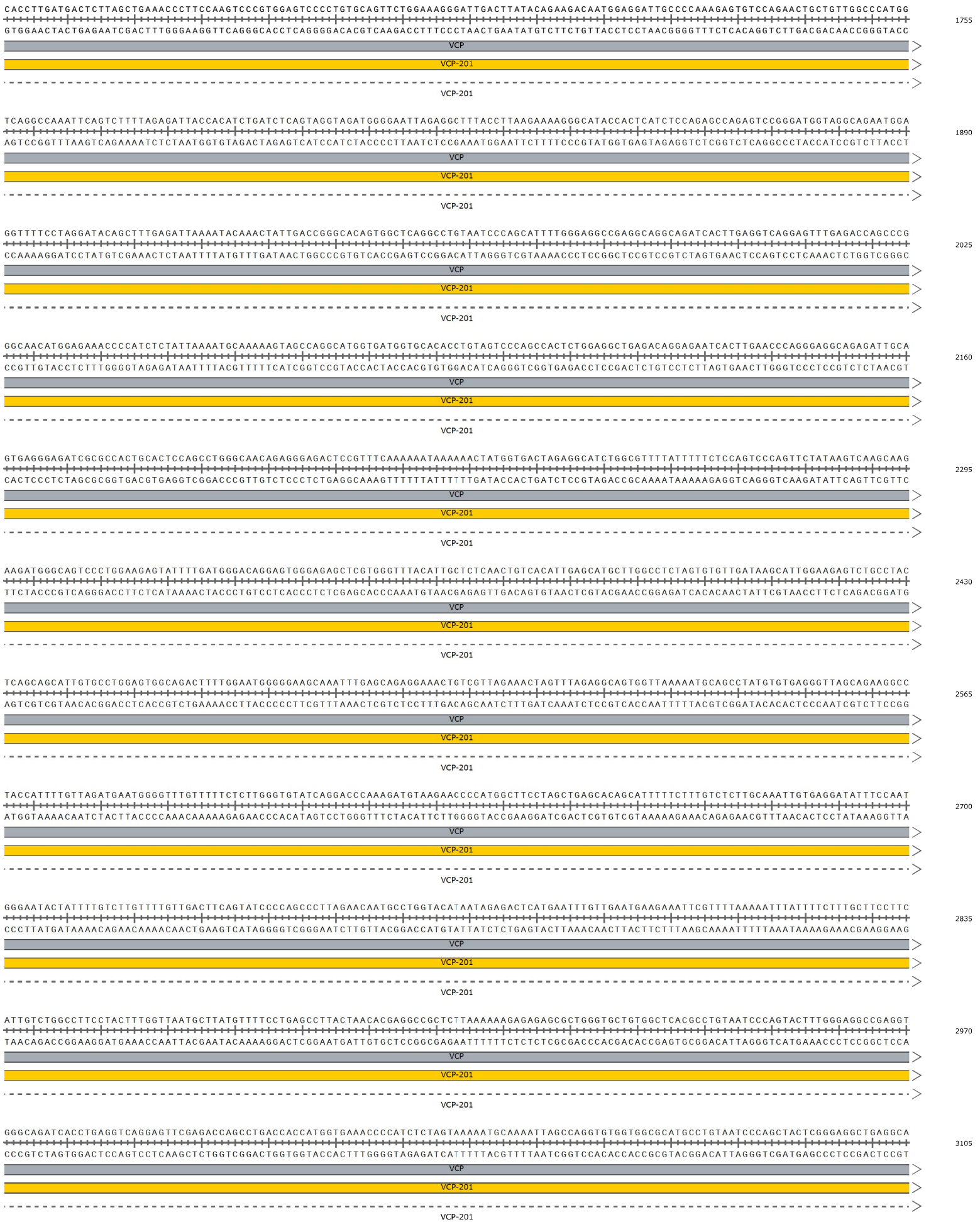


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1620



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3240

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3375

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VCP-201

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3510

VCP

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3645

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3780

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4050

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4185

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4320

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S K G D
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4455

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4590

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4725

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4860

VCP

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VCP-201

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4995

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5130

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5265

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5400

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5535

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5670

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5805

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5940

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6075

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VCP-201

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6210

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6345

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6480

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6615

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6750

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6885

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7020

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PCR Reverse
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7155

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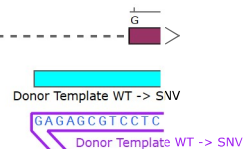
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7290

VCP

VCP-201

VCP-201



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8640

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8775

VCP

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8910

VCP

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9045

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VCP-201

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9180

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9450

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VCP-201

VCP-201

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9585

VCP

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9720

VCP

VCP-201

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VCP-201

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10,125

VCP

VCP-201

VCP-201

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10,260

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10,395

VCP

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ENSE00001091832

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10,665

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10,800

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VCP-201

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10,935

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C C T G A T C T A C T C G G G A C A A A T A C A A A C A C A T A C A G G G T G T C C A G C G A A A C T G C C C C C A T C T A T A A C C T T A A G G A C T A C A T G T C C T G C G A A T C T C T A A G A A G T C T A G G T A T G G T T C T T G A C T T C G A C C G

11,070

VCP

VCP-201

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11,205

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VCP-201

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VCP-201

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11,340

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11,475

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VCP-201

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11,610

VCP

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11,880

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12,015

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12,150

VCP

VCP-201

-495
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VCP-201

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12,285

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ENSE00003550122

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12,420

VCP

VCP-201

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ENSE00003550122

VCP-201

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12,555

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12,690

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VCP-201

VCP-201

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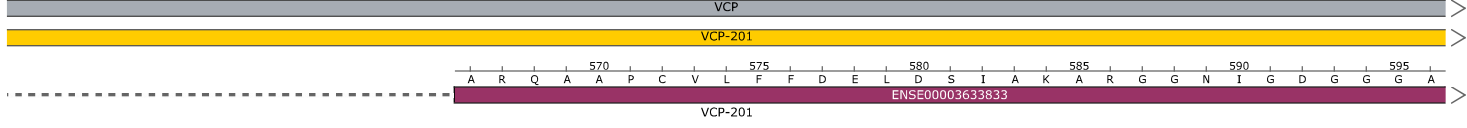
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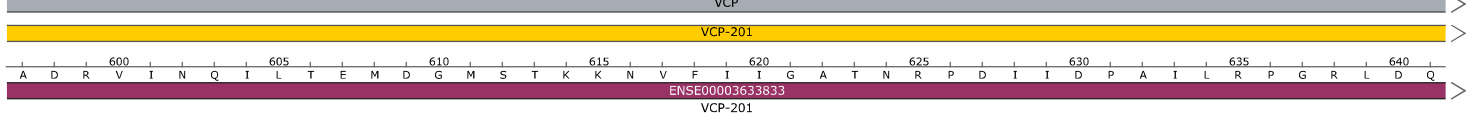
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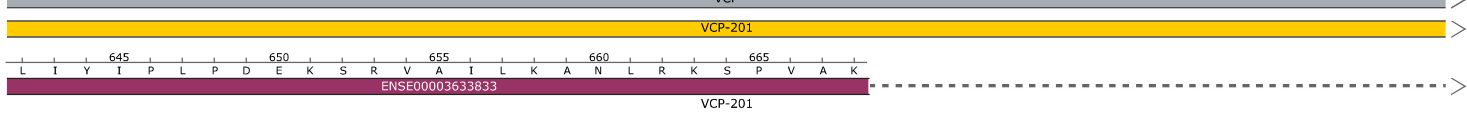
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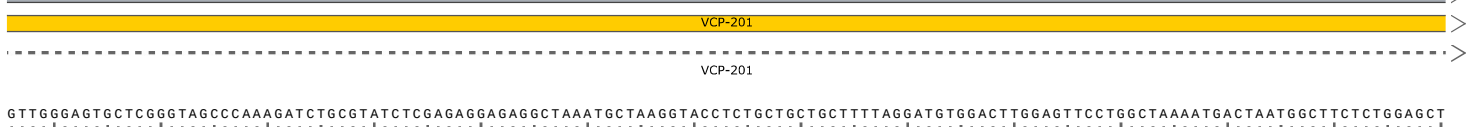
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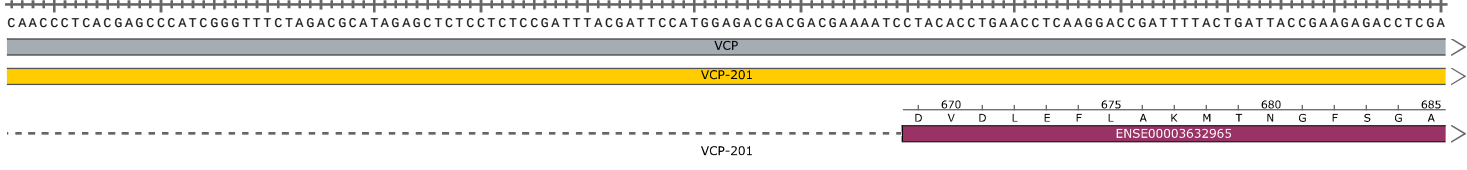


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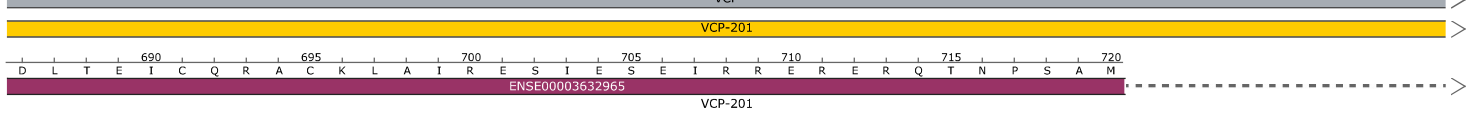


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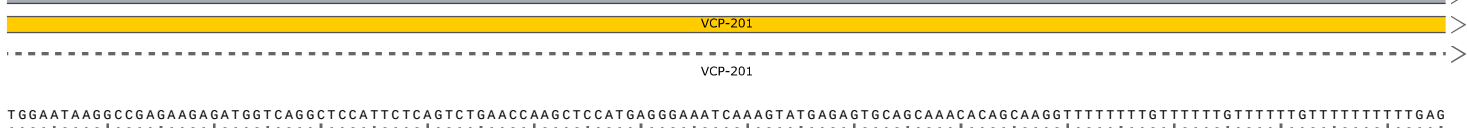
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13,635

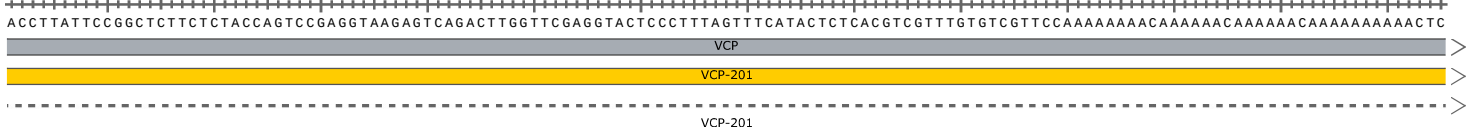


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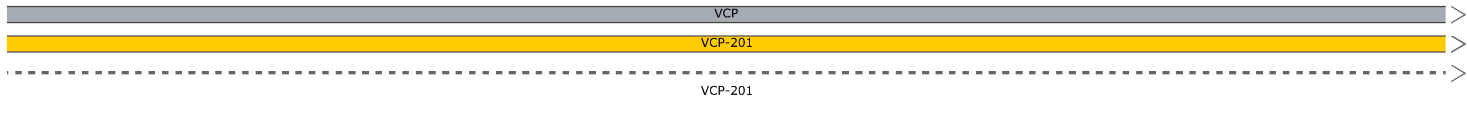


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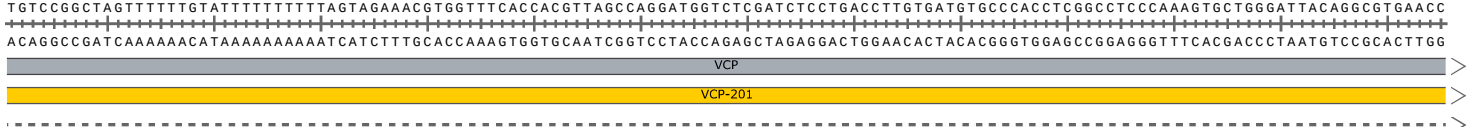


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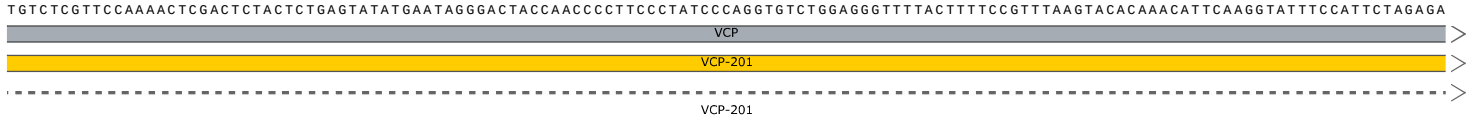


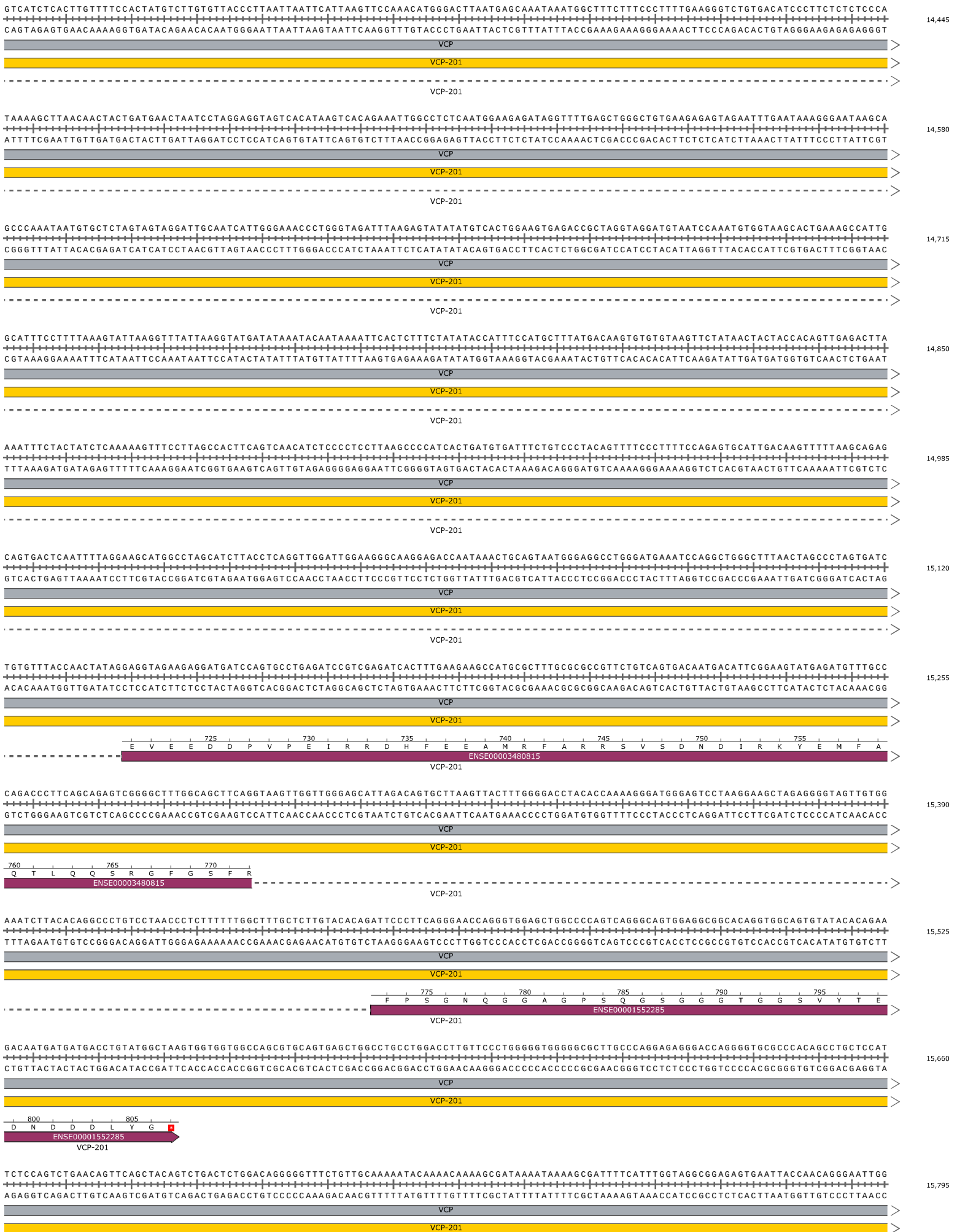
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14,310





GCCTTGGGCCATGCCATTTCTGTTGTAGTTTGGGGCAGTGCAGGGGACCTGTGTGGGGTGTGAACCAAGGCACTACTGCCACCTGCCACAGTAAAGCATCTGCACCTTGACTCAATGCCTCCGGAGCCCTCCCTCGGAACCCGGATACGGTAAAGACAACATCAAACCCCGTACGTCCCTGGACACACCCCACTTGGTTCGGTATGACGGTGGACGGTGCATTTCTGAGACGTGAACAGTACGTTACGACGGGCTCGGGAGGGAA 15,930

VCP

VCP-201

CCCCCTATCCAACCTGGGTAGGTGGGTAGGGGCCACAGTTGCTGGATGTTTATATAGAGAGTAGGTTGATTTATTTTACATGCTTTTGAGTTAAATGTTGGAAAACCTAATCACAAGCAGTTTCTAAACCAAAAAATGGGGGATAGGTTGGACCATCCACCCATCCCGGTGTCAACGACCTACAAATATATCTCTCATCCAATAAATAAATGTACGAAAACCTCAATTACAACCTTTTGATTAGTGTTCGCAAGATTGGTTTTTA 16,065

VCP

VCP-201

GACATGTTGTAAAAGGACAATAAACGTTGGGTCAAAATGGAGCCTGAGTCTGGGCCCTGTGCCTGCTCTTTTCTGGGAACAGCCTTGGGCTACCCACCACTCCAAGGCATTCTTCCAAATGTGAATCCTGCTGTACAACATTTCTGTTATTTGCAACCCAGTTTACCTCGGACTCAGGACCCGGGACAGGACGAAGAAAAGGACCCCTGTGCGAACCCGATGGGTGGTGAAGGTTCCGTAAGAAGGTTTACACTTTAGGAC 16,200

VCP

VCP-201

GAAGTAAGATTGCACCTTCTTCTCTCTGATCAACATCGGTATGATGTCCTGTGGCCTCACCCTTTGCTGCAAGTACTGATGATAGGACTGGTGGAAAGGGAGCAGCCTGACAGAGCTCCAAATGTGGAGA CTTCACTTCAACGTGGAAGAAGGAGAGGACTAGTTGTAGCCATACTACAGAGGACAACGGAGTGGAAAACAGAGCTCATAGTACCTATCTGACCACTTTCCCTGCTGGACTGCTCGAGGTTTACACCTT 16,335

VCP

VCP-201

ATATGGCATCCCTCCACCTATATTTGATGTGGACGGTAAGGCTAGGCCCTGACGATCCCTTATCCTGACCAAGACTGTGTTGGGGTGCCATTTGAAAATCGCAGGGTTGCAAAAAGATAACAATCTTACTTGCAG TATACCGTAGGGAGGTGGATATAAACTACACCTGCCATTCGATCCGGACGTCCTAGGGAATAGGACTGGTTCTGACACAACCCCACTGTAACCTTTAGCGTCCCACTTTTCTTATGTTAGAAATGAACGTC 16,470

VCP

VCP-201

GTGGATATCTCTATACTCTCTTTAATGCATCTAAAAATCCCAAACATCCCTGGTGGTGTGATCACTTACAGTTGGTGCACCTTTATTTTATGTACTTTGATTAATAAAAAAACTTTTGTAAATAAAAA CACCTATAAGAGATATGAGAGAAAAATACGTAGATTTTGGGTTTGTAGGGGACCAACCACTAGTGAATGTCAACACAGGTGGAAAATAAATACATGAACTAATTTTTTTTTTGGAAAACAATTTATTTT 16,605

VCP

VCP-201

TTTTAGTATTGAATTTTTTTTTTCCAAACAGAAAAAGACTATCCTCTCAACAGTAATCACTTAGTGCTTCTAGGGTCAGTACAGTGCCTTACCAGAGAGAGTAGTGACAGAAAAATAAATACTA AAAATCAAACTTAAAAAAAAGGTTGCTTTTATCTGATAGGAGAAGTTGCTATTAGTGAATCAGCAAGATCCCACTGTCACCTACGGAATGGGTCTCTCTCATACGTCCTTTTATTTAATGAT 16,740

VCP

VCP-201

AATTAATATATGTTGATTGGCTTTGGGACATAATCTCAAAGACAGTCTGACACCCGTAATTTGAATAAAATCTGTAATCTCAAAGATCAAAATCCCTAAAGTCTAAAATCTGAAAATCACAATCCCAA TTAATTTATATACAACTAACCGAAACCTGTATTAGAGTTTTCTGTGAGGACTGTGGCATTAAAACCTATTTTATGACATTAGAGGTTCTAGTTTTAGGGATTTAGAGTTTTAAGACTTTTAGTGTAGGGTT 16,875

VCP

VCP-201

AAGGTCAAAATCCAAAATACAATTTCTGGAAGAATACTAAACATTTCTCGAAAATTTACTTACATTTTTAAAGCGTATTTATTTGAGAAAACAACAACAGAACGTTTTCATAGGCCACTACACGATAAAATAG TTCCAGTTTAGGGTTTATGTTAAGACCTCTTTATGATTGTAAGAAGCTTTAAATGAATGAAAAATTTTCGCATAAATAAATCTTTGTTGTGTTGCTTGCAAGATACCGGTGATGCTATTTTATC 17,010

VCP

VCP-201

GGAAATAGTAACATTTTTGCAAGATAAACTCAGGTATACCAATGACAGTTGCACGGATATAACGGTGTGAGCAGATGAAACATTCATAAAGAAATAGGTCAAAAAGTAAAATGATAAATGCTTTGCACTAT CCTTATCATTTGAAAAACGTTCTATTTGAGTCCATATGGTTACTGTCAACGTCCTATATTGCCACTACTCGTCTACTTTGTAAGTATTTCTTTATCCAGTTTTCACTTTACATATTTACGAAACAGTGATA 17,145

VCP

VCP-201

GCCTGGTAATTGTGGGCACCTAGCTTTATATACTGGTCACTGTAACTACTGTGACAGAAAACCTAAGTCTTGATGAGATGGTTCAAAAACCTGTTGCGTTACCCTGCACTTCTCCAAAAGAGACGAGGTCTTG CGAACCATTAACACCCGTTGGATGAAAATATATTGACCACTGACATTATGACACTGCTCTTTGGATTGCAAGTACTCTACCAAGTTTTTGACAACGCAATGGTGACGTAACAGAGGGTTTCTGCTCCAGAAC 17,280

VCP

VCP-201

AGAAATTTTATCCTTCAAAATGACAGTGTACAAAAACAGATGCTCTCTCGTTTATTGAGGAACCTTCAACATTTTATGACACATATAAATGCTTACACACAGAGTCAACATTTGCGGTTCATGGAGTCAAAATTT TCTTTAAATAGGAAGTGTACGTGCACATGTTTTTGTCTACAGAGAAGCAAATAACTCCTTGAAGTTGTAATAAATACGTGTGATATTACGAATGTGTCTCAGTTGTAACGCCAGTACCTCAGTTAAA 17,415

VCP

VCP-201

TAAATGTCGAAGGCACGAGAAAAATCTGTCTAGGCTGGGCATGGTGGCTCATGCTTAAATCCAGCACTTTGGGATGCTGAGGCGGGCAGATCACCTGAGGTCGGGAGCTCAAGACCAGCCTGACCAAAA AATTACAGGTTCCGTGGTCTCTTTTATAGACAGGATCCGACCCGTACCACCGAGTACGGACATTAGGGTCTGAAACCTACGACTCCGCCCTCTAGTGGACTCCAGCCCTCGAGTTCTGGTGGACTGGTTTT 17,550

VCP

VCP-201

TGGAGAAACCCATCTCTACTACAATACAAAATAGCCAGGCGTGGTGGCCTTGCCTGTACTCCAGCTACTTGGGAGGCTGAGGCAGAGAAATAGCTTGAACCCGGGAGGCGGAGGTTGCTGTAGCTGAGAT ACCTCTTTGGGGTAGAGATGATGTTTATGTTTTAATCGGTCCGACACCCGCAACGGACATGAGGGTCGATGAAACCTCCGACTCCGTCTTTATCGAACTTGGGCCCTCCGCCCTCAACAGCACTCGACTCTA 17,685

VCP

VCP-201

GGAGCCATTGCACTCCAGCCTGGGCAACAAGAGCAAACTCAATCTAAAAAAGAAAGAAAATCTATCCTACCTCTAGAGACCAATTTGCTTCTGTATTTGTTCTCTGGGCCCCCGCTGTTGGATGGTAC CTTCCGTAACGTGAGGTCGGACCCGTTGTTCTGTTTTGAGTTAGAAATTTTTCTTCTTTTATAGATAGGATGGAGAATCTCTGGTTAAACGGAAAGACATAAACAAGAGAGACCCGGGGCGGACAACCTACCATG 17,820

VCP

VCP-201

CCACCAACATTGAAGGCAGATCTTCCCACTCAGTCCACTCAGACTTACAACTAATCCCGGAAAACAACCTCACAGACACACCCAGATAATGCTTTACCAAGTTTCTAAATACTCCTTAATCCAGTAAAATTTGA GGTGGTTGTAACCTCCGTCTAGAAAGGGGTGAGTCAAGTGAAGTGAATGTTGATTAGGGGCCCTTTGTTGGAGTGTCTGTGGGCTATTACGAAATGGTCCAAAGATTTATAGGAATTAGGTCATTTAACT 17,955

VCP

VCP-201

CACCTAAAATTAAGTCCAAATCTGCTCATTGGCAACTTGGACCCCTTATGTGTCTAAACATACTTAAAGACAATAACAAGGTAATACTTCTGTATAACATGATGCAACTGCTCTGTTTACAGGAAAAACATA GTGGATTTAATTCAGGTGTTAAGACGAGTAACCGTTGAACCGTGGGAATACACAGATTTGGTATGAATTTCTGTTATTGTTCCATTATGAAGACATATTGACTACGTTGACAGAAACAAATGTTGCTTTTTGTAT 18,090

VCP

VCP-201

CTAATCTTTCCCGAATTTGAAATTTTTTGTCCAGGTTGTGATTTAAGGATTTGATCTTTTGGACTTCAACATTTGGGGTTATGGTGTGGGATTGTGCTTCCAGGATTTATGATCAACACTGGTA GATTAGGAAAGGGTCTTAACTTTAAAAATAAACAGGTCCAACACTAAAATCCTAAAACCTAGAAAACCTGAAGTTGTAACCCCAATACCACAACCCTAACACAGGAAGTCTAATACTAGTTGTGACCA 18,225

VCP

VCP-201

TTAGTCATCCTAGACTTTATGCTAGGCAAGACCAGGCTCCGTTTTGGTCTACATAGATAATCTTCAAGGATGCAATGATACTTACACTGGTTGACTAAACTGGAGCAGCTCTGGAACCTCATGCTGTGAAATGGGTA
AATCAGTAGGATCTGAAATACGATCCGTTCTGGTCCGAGGCAAAACCAGATGTATCTATTAGAAGTTCCACGTACTATGAATGTGACCAACTGATTTGACCTCGTCGAGACCTTGAGTACGACACTTTACCCAT

18,360

VCP

TTTTGCACCTTTTGGTATTTGTTATTTTCAGGAGGTTTTAGGGAACAGGTGGTGGTTGGTTACGTGAATAAGTTCTTTAGTGGTGATTTCTAAGATTTTGGTGCACCTGTCATCTGAGCGGTGTACACCGTACCC
AAAAACGTGAAAACCATAAACAATAAAGTCTCCAAAAATCCCTTGTCCACCACCAACCAATGCACTTATTCAAGAAATCACCACATAAAGATTCTAAAACACGTTGGACAGTAGACTCGCCACATGTGGCATGGG

18,495

VCP

AATGTGTAGTCTTTTATCCCTCACGCCCCCCCCACCTTTTCCCTGAGTCCCAGAGTCCGTTGTATCATTCTTACGCCTTTGCATTCTCATAGCTTAGCTCCCATGTACGAGTGAGAACGTATGATGTTTGGTTT
TTACACATCAGAAAATAGGGAGTGGCGGGGGGTGGAAAAGGGACTCAGGGGTCTCAGGCAACATAGTAAGAATGCGGAAACGTAAGAGTATCGAATCGAGGGTACATGCTCACTCTTGCATACTACAAACAAA

18,630

VCP

TCCATTCCTGAGTGAGTTCACCTTAGAATAATGGTATTCCAGTTGCTGCAAAATGCCATTATTTTCGTTCCCTTCTTATGGCTGAGTAGTATTCCTGGATGTATATATACCACA
AGGTAAGGACTCACTCAAGTGAATCTTATTACCATAAGGTCAACGACGTTTACGGTAATAAAGCAAGGAAGAATACCGACTCATCATAAGGGACCTACATATATATGGTGT

3' 18,741
5'

VCP

Feature	Location	Size	Type
VCP	1 .. 18,741	18,741 bp	gene
/note	= gene ENSG00000165280		
			Protein coding
VCP-203	1 .. 16,605	16,605 bp	prim_transcript
/note	= primary transcript ENST00000448530		
VCP-217	24 .. 16,093	16,070 bp	prim_transcript
/note	= primary transcript ENST00000679647		
VCP-214	34 .. 4418	4385 bp	prim_transcript
/note	= primary transcript ENST00000679392		
VCP-223	34 .. 4418	4385 bp	prim_transcript
/note	= primary transcript ENST00000680108		
VCP-225	34 .. 4418	4385 bp	prim_transcript
/note	= primary transcript ENST00000680575		
VCP-211	44 .. 17,293	17,250 bp	prim_transcript
/note	= primary transcript ENST00000678465		
			Nonsense mediated decay
VCP-201	44 .. 16,605	16,562 bp	prim_transcript
/note	= primary transcript ENST00000358901		
VCP-231	44 .. 16,092	16,049 bp	prim_transcript
/note	= primary transcript ENST00000681335		
VCP-229	44 .. 16,073	16,030 bp	prim_transcript
/note	= primary transcript ENST00000680916		
			Nonsense mediated decay
VCP-235	44 .. 16,017	15,974 bp	prim_transcript
/note	= primary transcript ENST00000681690		
			Retained intron
VCP-206	44 .. 12,921	12,878 bp	prim_transcript
/note	= primary transcript ENST00000480327		
			Retained intron
VCP-222	44 .. 5994	5951 bp	prim_transcript
/note	= primary transcript ENST00000680079		
			Nonsense mediated decay
VCP-232	44 .. 4778	4735 bp	prim_transcript
/note	= primary transcript ENST00000681386		
VCP-221	46 .. 18,741	18,696 bp	prim_transcript
/note	= primary transcript ENST00000679902		
VCP-216	46 .. 16,048	16,003 bp	prim_transcript
/note	= primary transcript ENST00000679599		
			Retained intron
VCP-208	53 .. 15,985	15,933 bp	prim_transcript
/note	= primary transcript ENST00000676836		
			Retained intron
VCP-219	58 .. 16,035	15,978 bp	prim_transcript
/note	= primary transcript ENST00000679862		
VCP-209	68 .. 17,293	17,226 bp	prim_transcript
/note	= primary transcript ENST00000677257		
VCP-218	78 .. 17,293	17,216 bp	prim_transcript
/note	= primary transcript ENST00000679800		
			Retained intron
VCP-210	101 .. 17,293	17,193 bp	prim_transcript
/note	= primary transcript ENST00000678018		
			Nonsense mediated decay
VCP-212	108 .. 17,293	17,186 bp	prim_transcript
/note	= primary transcript ENST00000678650		
VCP-220	108 .. 4418	4311 bp	prim_transcript
/note	= primary transcript ENST00000679901		
VCP-207	120 .. 15,799	15,680 bp	prim_transcript
/note	= primary transcript ENST00000493886		
			Retained intron
VCP-213	227 .. 16,011	15,785 bp	prim_transcript
/note	= primary transcript ENST00000679204		
			Nonsense mediated decay
VCP-217	316 .. 15,692	15,377 bp	CDS
▶ 16 segments = 2202 bp			
/note	= coding sequence ENSP00000506216		
/translation	= MASGAD,,SKGDDLSTA ILKQKRNPNRLIV DEAINEDNSVVSLSQ,,PKMDELQ LFRGDTVLLKGGKRRREAV CIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDV KYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEA YRPIRK,,GDI FLVRGGMRAVEFKV VETDPSYICIVA PDTVIHCEGEP IKRE,,DEESLNEVGYDDIGGCRKQLAQ IKEMVELPLRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGES NLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLLTMDGLKQRAHVIVMAATNRPNSIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKNMKLADDDVLEQ,,VANETHGHV GADLAALCSEAALQAIIRK MDLIDLEDETIDA EVMNSLAVTMDDFR,,WALSQSNPSALRET VVEVPQVTWEDIGGLE DVKRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELTMWFGESEANVREIFDK,,A RQAAPCVLFFDELDSIAKARGGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAK,,DVDFLEAKMTNGFSGDALTEICQRA,,LSWPAWT LFPGGGGA QSGSGGGRPAFSSLSFAT*		
VCP-201	316 .. 15,552	15,237 bp	CDS
▶ 17 segments = 2421 bp			
/note	= coding sequence ENSP00000351777		
/translation	= MASGAD,,SKGDDLSTA ILKQKRNPNRLIV DEAINEDNSVVSLSQ,,PKMDELQ LFRGDTVLLKGGKRRREAV CIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDV KYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEA YRPIRK,,GDI FLVRGGMRAVEFKV VETDPSYICIVA PDTVIHCEGEP IKRE,,DEESLNEVGYDDIGGCRKQLAQ IKEMVELPLRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGES NLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLLTMDGLKQRAHVIVMAATNRPNSIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKNMKLADDDVLEQ,,VANETHGHV GADLAALCSEAALQAIIRK MDLIDLEDETIDA EVMNSLAVTMDDFR,,WALSQSNPSALRET VVEVPQVTWEDIGGLE DVKRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELTMWFGESEANVREIFDK,,A RQAAPCVLFFDELDSIAKARGGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAK,,DVDFLEAKMTNGFSGDALTEICQ RACKLAIRSEISEIRRE REBQSNMREDEDPYRDRDHFEEAMRFARRVSDN DIRKYEMFAQLTQSRGFSFR,,FPSGNQGGAGPSQGS GGGTGGSVYTEDNDDLYG*		

Feature	Location	Size	Type
VCP-209	316 .. 15,552	15,237 bp	CDS
▶ 17 segments = 2415 bp			
/note	= coding sequence ENSP00000504354		
/translation	= MASGAD,,SKGDDLSTAILKQKNRPNRLIVDEAINEDNSVVSLSQ,,MDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,VEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-231	316 .. 15,552	15,237 bp	CDS
▶ 16 segments = 2265 bp			
/note	= coding sequence ENSP00000505230		
/translation	= MASGAD,,SKGDDLSTAILKQKNRPNRLIVDEAINEDNSVVSLSQ,,PKMDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-221	316 .. 15,297	14,982 bp	CDS
▶ 16 segments = 2319 bp			
/note	= coding sequence ENSP00000506338		
/translation	= MASGAD,,SKGDDLSTAILKQKNRPNRLIVDEAINEDNSVVSLSQ,,PKMDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-202	464 .. 16,081	15,618 bp	prim_transcript
/note	= primary transcript ENST00000417448		
	1506 .. 7330	5825 bp	gene
/note	= gene ENSG00000288699 Protein coding		
	1506 .. 7330	5825 bp	prim_transcript
/note	= primary transcript ENST00000681845 Nonsense mediated decay		
VCP-215	4307 .. 4778	472 bp	CDS
▶ 2 segments = 321 bp			
/note	= coding sequence ENSP00000506658		
/translation	= FKR**PINSHSQTEEPSQSVNC**SHQ*GQCQGLVLP,,AQ*PKGLNFLSSAQDG*IAVVR*HSV AERKEETRSC LHRPF**YLF**EDSDE*SCSE*PSC TPRGCHQ 107 codons (14 internal stop codons)		
VCP-228	4307 .. 4778	472 bp	CDS
▶ 2 segments = 306 bp			
/note	= coding sequence ENSP00000505674		
/translation	= FKR**PINSHSQTEEPSQSVNC**SHQ*GQCQGLVLP,,GLNFLSSAQDG*IAVVR*HSV AERKEETRSC LHRPF**YLF**EDSDE*SCSE*PSC TPRGCHQ 102 codons (13 internal stop codons)		
VCP-215	4307 .. 4778	472 bp	prim_transcript
/note	= primary transcript ENST00000679449		
VCP-228	4307 .. 4778	472 bp	prim_transcript
/note	= primary transcript ENST00000680900		
VCP-226	4606 .. 8515	3910 bp	prim_transcript
/note	= primary transcript ENST00000680731 Nonsense mediated decay		
VCP-202	4612 .. 15,552	10,941 bp	CDS
▶ 15 segments = 2286 bp			
/note	= coding sequence ENSP00000399456		
/translation	= MDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-203	4612 .. 15,552	10,941 bp	CDS
▶ 15 segments = 2286 bp			
/note	= coding sequence ENSP00000392088		
/translation	= MDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-212	4612 .. 15,552	10,941 bp	CDS
▶ 15 segments = 2286 bp			
/note	= coding sequence ENSP00000503426		
/translation	= MDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		
VCP-219	4612 .. 15,552	10,941 bp	CDS
▶ 15 segments = 2283 bp			
/note	= coding sequence ENSP00000504990		
/translation	= MDELQLFRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVIS,,IQPCPDVYKYGRIHVLPIDDTVEGITGNLFEVYLPKPYFLEAYRPIRK,,GDI FLV RGGMRAVEFKV VETDPSYCI VAPDTVIHCEGEP IKRE,,DEEESLNEVGYDDIGGCRKQLAQIKEMVELPRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGESENLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLTLM DGLKQRAHVIVMAATNRPN SIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKMKLADDDVLEQ,,VANETHGHV GADLAALCSEAA LQAI RKKMDLIDLEDETIDA EVMNSLAVT MDDFR,,WALSQSNPSALRET VVEVPQVTWEDI GGLEDV KRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIA NECQANFISIKGPELLTMWFGESEANVREIFDK,,ARQAAPCVLFFDELDSIAKARGNIGDGGGAADRVINQILTEM DGMSTKKNVFIIGATNRPD IIDPAILRPRGLDQLIYIPLPDEKSRVA I LKANLRKSPVAK,,DVDFLEFLAKMTNGFSGADLTEICQ RACKLA IRESIESEIRRERERQTNPSAM,,EVEEDDPVPEIRRDHFEEAMRFARRSVSDN DIRKYEMFAQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR* AQT LQSRGFSFR*		

Feature	Location	Size	Color	Symbol	Type
VCP-232	4612 .. 4778	167 bp	■	→	CDS
/note	= coding sequence ENSP00000505509				
/translation	= MDELQLFRGDTVLLKGGKRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVI 55 amino acids = 6.4 kDa				
VCP-234	5852 .. 7418	1567 bp	■	→	CDS
▶ 3 segments = 328 bp					
/note	= coding sequence ENSP00000505893				
/translation	= HPAMP*CEVRQTYPCAAH**HSGRHYW*SLRGIP*AVLPGSVSTHPES,,RDGVSPCWSGSSRTLDLR,,RHFSCPWWDACCGVQSGGNRS*PLHCCSRHSDPLRRGAYQTR 109 codons (6 internal stop codons)				
VCP-234	5852 .. 7418	1567 bp	■	→	prim_transcript
/note	= primary transcript ENST00000681562				
Donor Template WT -> SNV	7279 .. 7357	79 bp	■	⇌	misc_feature
VCP-224	7288 .. 9691	2404 bp	■	→	prim_transcript
/note	= primary transcript ENST00000680520 Nonsense mediated decay				
VCP-236	7288 .. 9691	2404 bp	■	→	prim_transcript
/note	= primary transcript ENST00000681789 Nonsense mediated decay				
Protospacer Sequence	7304 .. 7323	20 bp	■	⇌	misc_feature
SNV	7318 .. 7318	1 bp	■	⇌	misc_feature
/note	= WT=G SNV=A				
PAM	7324 .. 7326	3 bp	■	⇌	misc_feature
VCP-227	7361 .. 11,654	4294 bp	■	→	CDS
▶ 6 segments = 709 bp					
/note	= coding sequence ENSP00000506387				
/translation	= LHCCSRHSDPLRRGAYQTR,,AS*RNPA LRTSWNRKDPDCSSCSK*DWSLLLLDQW,,S*DHEQIGW*V*EQPS*SL*GG*EECSCHHLH**ARCHRSQKRE,,NSWRGGAAHCITVVDPHGWPKAEGTCDGCGSNQQTQQH *PSSTA IW,,SL*QGGRYWNS*CYRTL RDSSDPYQ EHEAGR*CGPGT,,GSQ*DSRACGC*LSSPVLRGCSA SHPQEDGSH*PRG*DH*CRGHELSSSYG*LP 236 codons (20 internal stop codons)				
VCP-227	7361 .. 11,654	4294 bp	■	→	prim_transcript
/note	= primary transcript ENST00000680834				
VCP-230	10,319 .. 11,654	1336 bp	■	→	prim_transcript
/note	= primary transcript ENST00000681125 Nonsense mediated decay				
VCP-205	12,645 .. 15,762	3118 bp	■	→	prim_transcript
/note	= primary transcript ENST00000479300 Retained intron				
VCP-204	14,836 .. 15,496	661 bp	■	→	prim_transcript
/note	= primary transcript ENST00000466100 Retained intron				
VCP-233	15,139 .. 16,605	1467 bp	■	→	prim_transcript
/note	= primary transcript ENST00000681537				
VCP-233	15,139 .. 15,533	395 bp	■	→	CDS
▶ 2 segments = 231 bp					
/note	= coding sequence ENSP00000505847				
/translation	= EVEEDDPVPEIRRDHFEEA MRFARRVSDNDIRKYEMFAQTLQQRGFGSFR,,EPGWSWPQSGQWRRHRWQCIHRRQ* 76 amino acids = 9.4 kDa				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Reverse	23-mer	7059 .. 7081	58°C	Jun 15, 2022
/sequence = TCAGGTTTTGTTCACTGACCTCT 43% GC / 6971.6 Da				
✓ Donor Template WT -> SNV	79-mer	7279 .. 7357	76°C	Jun 15, 2022
/sequence = GGGCTAGGATCTGTTTCCACCACTTTGAACTCCACAGCATGCATCCCACCGGACAAGAAAAATGTCTCCTGCGAGAG 52% GC / 24,232.8 Da				
✓ gRNA Protospacer	20-mer	7304 .. 7323	67°C	Jun 15, 2022
/sequence = CCGTGGTGGGATGCCTGCTG 70% GC / 6221.1 Da				
✓ PCR Forward	20-mer	7480 .. 7499	55°C	Jun 15, 2022
/sequence = GCACCCAGTCCTGACAGTTA 55% GC / 6062.0 Da				
✓ Sanger Sequencing Primer	20-mer	7480 .. 7499	55°C	Jun 15, 2022
/sequence = GCACCCAGTCCTGACAGTTA 55% GC / 6062.0 Da				