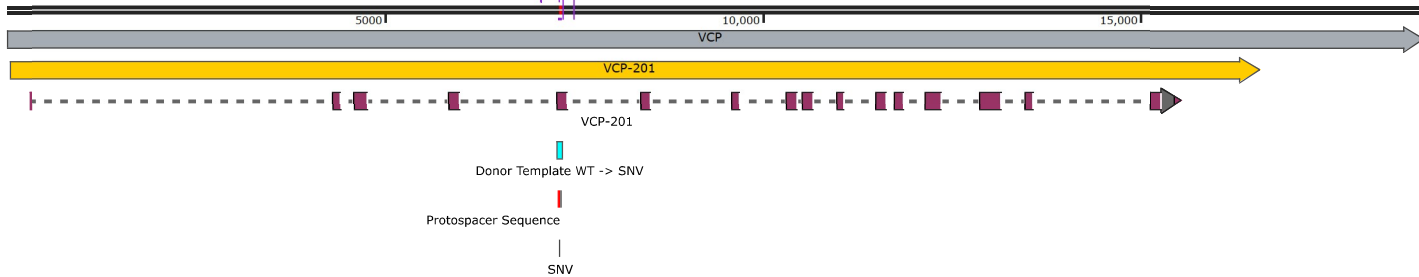
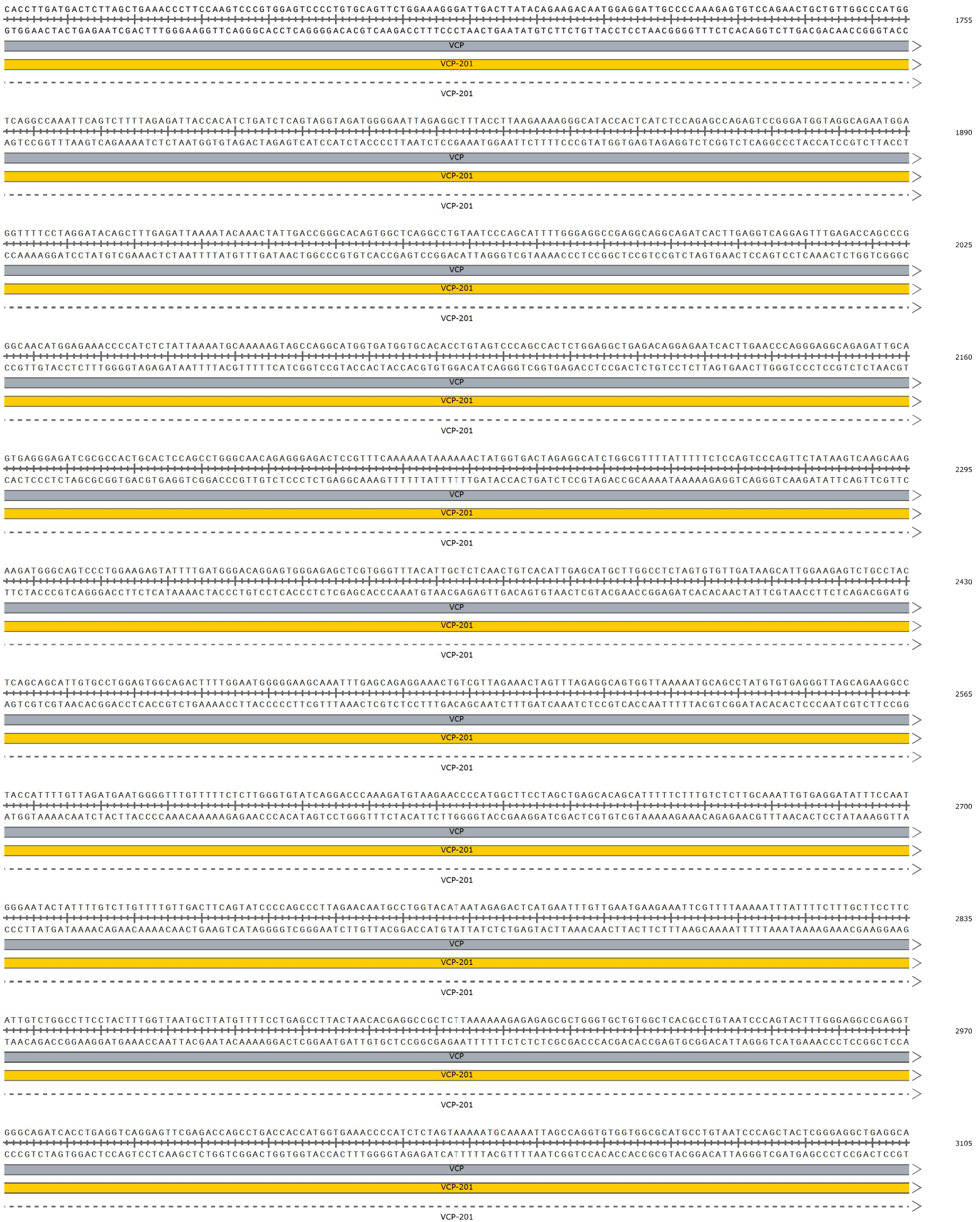


● (7279 .. 7357) Donor Template WT -> SNV
(7304 .. 7323) gRNA Protospacer
(7059 .. 7081) PCR Reverse
PCR Forward (7480 .. 7499)
Sanger Sequencing Primer (7480 .. 7499)



JIPSC1070_SnappeneDNA_INK2S00112_VCP_R159H_SNVWT
18,741 bp



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3240

VCP

VCP-201

VCP-201

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ACTCAGATCATTCACTGTGCACCTTTGCCGATCCATTATTAACACAGTACAGACCACTTACTAGGATCGAAGATCCTTTATTGTGACTCACATCTGGGTCAGCTGAAACTAAACCCACTCTCCCTAAACCT

3375

VCP

VCP-201

VCP-201

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3510

VCP

VCP-201

VCP-201

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3645

VCP

VCP-201

VCP-201

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3780

VCP

VCP-201

VCP-201

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3915

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VCP-201

VCP-201

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4050

VCP

VCP-201

VCP-201

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4185

VCP

VCP-201

VCP-201

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4320

VCP

VCP-201

VCP-201

10
S K G D
ENSE00003685641

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4455

VCP

VCP-201

VCP-201

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D L S T A I L K Q K N R P N R L I V D E A I N E D N S V V S L S Q
ENSE00003685641

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4590

VCP

VCP-201

VCP-201

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4725

VCP

VCP-201

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VCP-201

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4860

VCP

VCP-201

85 90 95 100
M N R V V R N N L R M G D V I S

VCP-201

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4995

VCP

VCP-201

VCP-201

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5130

VCP

VCP-201

VCP-201

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5265

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VCP-201

VCP-201

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5400

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VCP-201

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5535

VCP

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VCP-201

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5670

VCP

VCP-201

VCP-201

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5805

VCP

VCP-201

VCP-201

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5940

VCP

VCP-201

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VCP-201

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6075

VCP

VCP-201

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VCP-201

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8640

VCP

VCP-201

235
G V K
ENSE0000360...

VCP-201

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8775

VCP

VCP-201

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8910

VCP

VCP-201

VCP-201

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9045

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9180

VCP

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9315

VCP

VCP-201

VCP-201

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9450

VCP

VCP-201

VCP-201

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9585

VCP

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9720

VCP

VCP-201

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ENSE00003523069

VCP-201

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9855

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9990

VCP

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VCP-201

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

10,125

VCP

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VCP-201

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

10,260

VCP

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VCP-201

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

10,395

VCP

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ENSE00001091832

VCP-201

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

10,530

VCP

VCP-201

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ENSE00001091832

VCP-201

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

10,665

VCP

VCP-201

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ENSE00001091840

VCP-201

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

10,800

VCP

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VCP-201

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

10,935

VCP

VCP-201

VCP-201

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

G R F D R E V D I G I P D A T G R L E I L Q I H T K N M K L A
ENSE00003519681

VCP-201

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

11,205

VCP

VCP-201

D D V D L E Q
ENSE00003519681

VCP-201

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

11,340

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A A C C C A G C C C A T A A A G G T A T T G A T A G T A T A T A T T C A A G G A A A T G A G A G A C C C A G G G A T A G C A G T C A G G G G A A G G A T T C T A T T G T C T G A G C C T C C T G C A G A C T G G G T C T T T G A G G C A G C A T A G T A A G T A G
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11,475

VCP

VCP-201

VCP-201

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11,610

VCP

VCP-201

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ENSE00003669115

VCP-201

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11,745

VCP

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VCP-201

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11,880

VCP

VCP-201

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ENSE00003597683

VCP-201

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12,015

VCP

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12,150

VCP

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VCP-201

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12,285

VCP

VCP-201

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ENSE00003550122

VCP-201

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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

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12,825

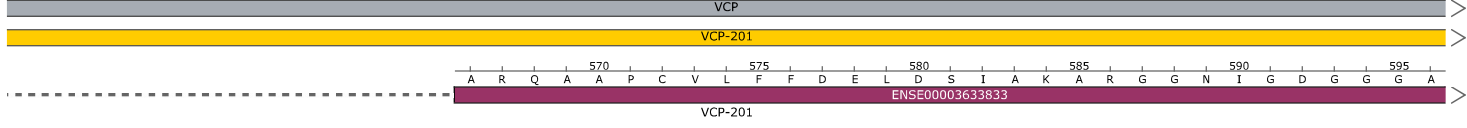
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VCP-201

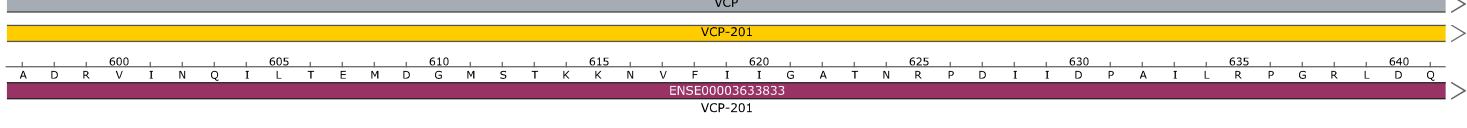
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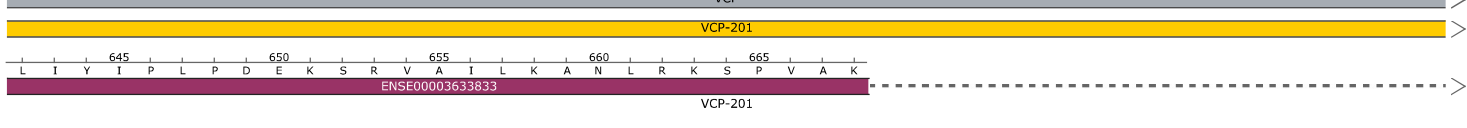
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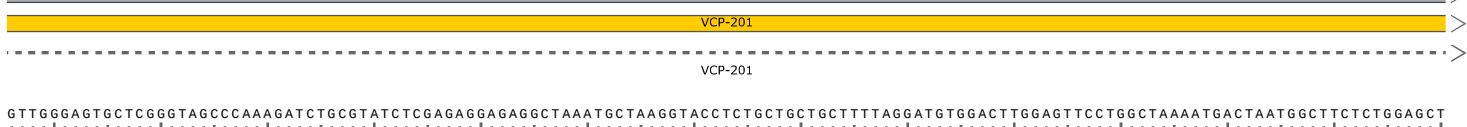
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13,230



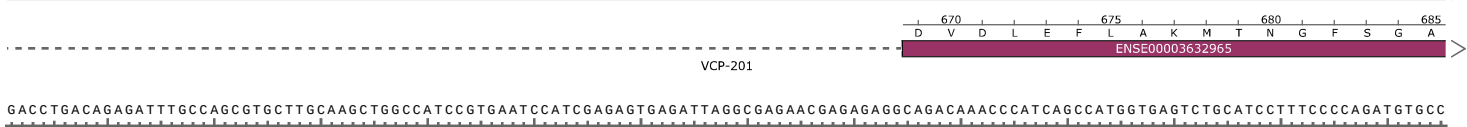
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13,365



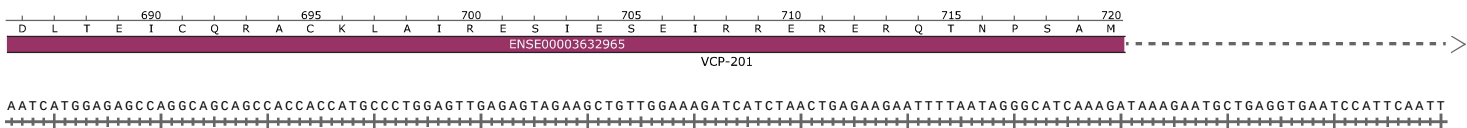
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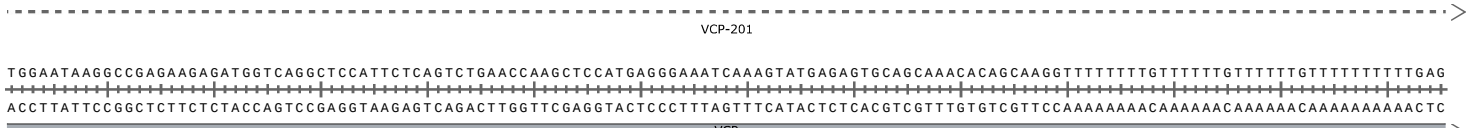
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13,635



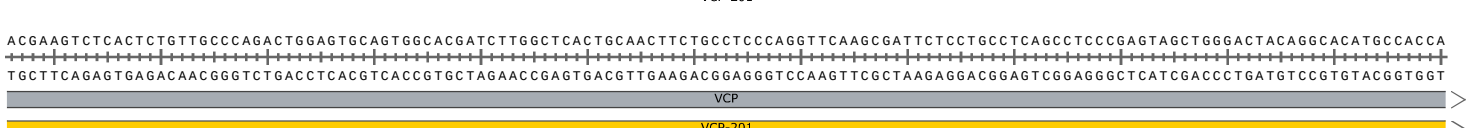
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13,770



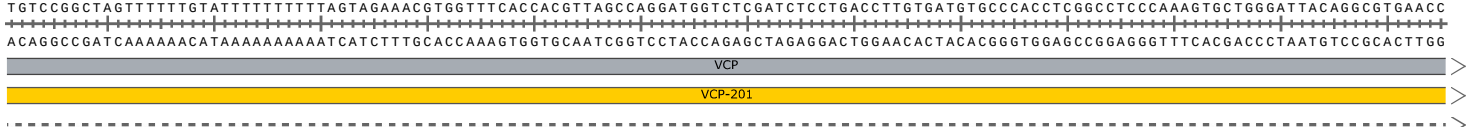
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13,905



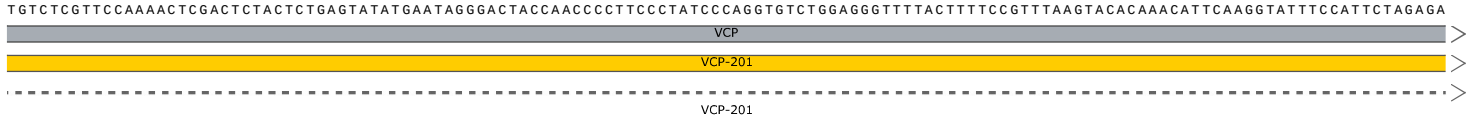
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14,040



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14,175



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14,310

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14,445

VCP

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14,580

VCP

VCP-201

VCP-201

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14,715

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14,850

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14,985

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VCP-201

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15,120

VCP

VCP-201

VCP-201

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15,255

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VCP-201

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15,390

VCP

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VCP-201

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15,525

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VCP-201

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15,660

VCP

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VCP-201

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ENSE00001552285

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15,795

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VCP

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VCP

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18,360

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18,495

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18,630

VCP

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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 VETDPSYCIVA PDTVIHCEGEP IKRE,,DEESLNEVGYDDIGGCRKQLAQ IKEMVELPLRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGES NLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLLTMDGLKQRAHVIVMAATNRPNSIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKNMKLADDDVLEQ,,VANETHGHV GADLAALCSEAALQAI RKKMDLIDLEDETIDA EVMNSLAVTMDDFR,,WALSQSNPSALRET VVEVPQVTWEDIGGLEVDVKRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIANECQANFISIKGPELTMWFGESEANVREIFDK,,A RQAAPCVLFFDELDSIAKARGGNIGDGGGAADRVINQLTMDGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAK,,DVDFLEFLAKMTNGFSGDALTEICQRA,,LSWPAWTLPFGGGGA QSGSGGGTGGSVYTEDNDDDLYG* | | |
| 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 VETDPSYCIVA PDTVIHCEGEP IKRE,,DEESLNEVGYDDIGGCRKQLAQ IKEMVELPLRHPALFKAIGVK,,PPRGILLYGPPGTGKTLIARAVANETGAFFFLIN,,GPEIMSKLAGES NLRKAFEEAEKNAPAIIFIDELDAIAPKREK,,THGEVERRIVSQLLTMDGLKQRAHVIVMAATNRPNSIDPALRRF,,GRFDREV DIGIPDATGRLEILQIHTKNMKLADDDVLEQ,,VANETHGHV GADLAALCSEAALQAI RKKMDLIDLEDETIDA EVMNSLAVTMDDFR,,WALSQSNPSALRET VVEVPQVTWEDIGGLEVDVKRELQ ELVQ,,YPVEHPDKFLKFGMTPSKGVLFY GPPGCGKTLAKAIANECQANFISIKGPELTMWFGESEANVREIFDK,,A RQAAPCVLFFDELDSIAKARGGNIGDGGGAADRVINQLTMDGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPEKSRVA ILKANLRKSPVAK,,DVDFLEFLAKMTNGFSGDALTEICQ RACKLAIRSEISEIRRE REBQSNRQREEDQYKRDHDFEAMRFARRVSDNDIRKYEMFAQLTQSRGFSFR,,FPSGNQGGAGPSQGS GGTTGGSVYTEDNDDDLYG* | | |

| Feature | Location | Size | Color | Symbol | Type |
|------------------------------------|--|---------|-------|--------|-----------------|
| VCP-232 | 4612 .. 4778 | 167 bp | ■ | → | CDS |
| /note | = coding sequence ENSP00000505509 | | | | |
| /translation | = MDELQ L FRGDTVLLKGGKRRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVI 55 amino acids = 6.4 kDa | | | | |
| VCP-234 | 5852 .. 7418 | 1567 bp | ■ | → | CDS |
| ▶ 3 segments = 328 bp | | | | | |
| /note | = coding sequence ENSP00000505893 | | | | |
| /translation | = HPAAMP*CEVRQTYPCAAH**HSGRHYW*SLRGIP*AVLPGSVSTHPES,,RDGVSPCWSGSSRTL L DLR,,RHFSCPWWDACCGVQSGGNRS*PL L HCCSRHSDPLRRGAYQTR 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 L R T SWNRKDPDCSSCSK*DWSLLLLDQW,,S*DHEQIGW*V*EQPS*SL*GG*EECSCHHLH**ARCHRSQKRE,,NSWRGGAAHCITVVDPHGWPKAEGTCD C YGSNQQTQ Q H *PSSTA I W,,SL*QGGRYWNS*CYRTL R DSSDPYQEHEAGR*CGPGT,,GSQ*DSRACGC*LSSPVL R GC S A S HPQEDGSH*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 M R F A R RSVSDN D IRKYEMFAQTLQ Q SRGFGSFR,,EPGWSWPQSGQ W RRHRWQ C I H RRQ* 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 | = CCGTGGTGGGATGCGTGCTG 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 | | | |