NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi18D04

Lot# : 7675_B4Dj

Vector : pGCAP10

Gene	BOK	
RefSeq_mRNA	NM_032515.5	2626 bp

● Plasmid DNA purification

Date : 2024/04/23 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/04/24 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/04/24

DNA concentration (O.D.): 243 ng/ul

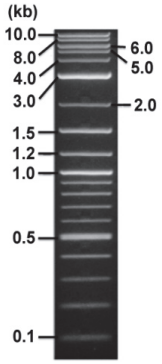
< Size of fragment expected from this clone >

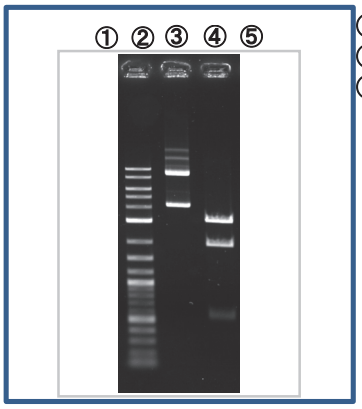
DNA	0.4	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.6	ul
Total	10	ul

BamHI 3.1kb (vector), 2.0, 0.5 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the insert/vector junction sequence

Date : 2024/05/07

Primer A	pGCAP-F
Primer B	pGCAP-R
Primer C	
List of Sequencing Primers	http://dna.brc.riken.jp/en/NRCDhum2en.html

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/05/08

DNA (243 ng/ul)	82	ul
10x TE	80	ul
dH_2O	635	ul
Total	797	ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.05.08 笹沼

http://dna.brc.riken.jp/index.html

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_032515:Homo sapiens BCL2 family apoptosis...

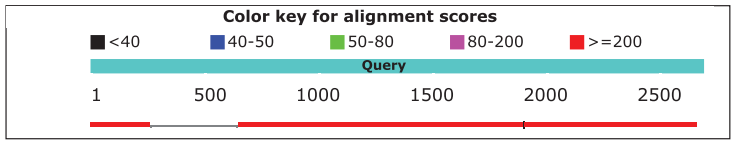
RID 3KCYX6GD114 (Expires on 05-08 12:53 pm)

Query ID	NM_032515.5	**Subject ID**	lcl|Query_2673021
Description	Homo sapiens BCL2 family apoptosis regulator BOK (BOK), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2626	**Subject Length**	2309
		Program	BLASTN 2.15.0+

ARi18D04hts.seq

Graphic Summary

Distribution of the top 31 Blast Hits on 1 subject sequences



検
'24.05.07
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Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	2459	19622	85%	0.0	98.50%	Query_2673021

Alignments

Sequence ID: Query_2673021 Length: 2309 Number of Matches: 31
Range 1: 883 to 2276

Score	Expect	Identities	Gaps	Strand	Frame
2459 bits(1331)	0.0()	1376/1397(98%)	6/1397(0%)	Plus/Plus	

Features:

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Query  1220  GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1278
Sbjct  883   GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  942
Query  1279  GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1338
Sbjct  943   GGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1001
Query  1339  TGAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1398
Sbjct  1002  TGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1061
Query  1399  CC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1457
Sbjct  1062  CCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1121
Query  1458  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1517
Sbjct  1122  CCTGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGG  1180
Query  1518  GGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC-CGGAACACCTGCTCT  1576
Sbjct  1181  GGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCT  1240
Query  1577  CACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAA  1636
Sbjct  1241  CACCTCAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAA  1299
Query  1637  GGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTC  1696
Sbjct  1300  GGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTC  1359
Query  1697  TCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAA  1756
Sbjct  1360  TCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAA  1419
Query  1757  GGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTG  1816
Sbjct  1420  GGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTG  1479
Query  1817  TCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTCTCACCTGAACCCGGGGGTCCCA  1876
Sbjct  1480  TCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTCTCACCTGAACCCGGGGGTCCCA  1539
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Sbjct  1540  TCCCAGGAAGAAGGGCCATCTCAGGACATGAGTCCTCAGGGGCCCTGCACATTCAATCTG  1599
Query  1937  AAGGTGACCCTGGCCTGGCTGAAGCTGGAAGAGCTGTGGGGACTCAGCCTGTAAACAGAG  1996
Sbjct  1600  AAGGTGACCCTGGCCTGGCTGAAGCTGGAAGAGCTGTGGGGACTCAGCCTGTAAACAGAG  1659
Query  1997  CGTAAGGTTCACATGCTGGTTGCTTAATCCGTTTCTGGAGGAAGAGTATGACACCCACTT  2056
Sbjct  1660  CGTAAGGTTCACATGCTGGTTGCTTAATCCGTTTCTGGAGGAAGAGTATGACACCCACTT  1719
Query  2057  GTGATGGGGTCCTTGTGCGGTGGGGACCGGGGCCGGCGGGCTCCAGGCCAGCACACCTAA  2116
Sbjct  1720  GTGATGGGGTCCTTGTGCGGTGGGGACCGGGGCCGGCGGGCTCCAGGCCAGCACACCTAA  1779
Query  2117  CCCATGGATGTGGAACCTACGGCCGAGAAGGAATGTTGCATGAGTCGGATCCCAGTCCAT  2176
Sbjct  1780  CCCATGGATGTGGAACCTACGGCCGAGAAGGAATGTTGCATGAGTCGGATCCCAGTCCAT  1839
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Query  2177  TGTCAGTGGAGGGTGAGGGTGACCCCATCTGCTATTTTTGTGCTCATCCTCATACAACCA  2236
Sbjct  1840  TGTCAGTGGAGGGTGAGGGTGACCCCATCTGCTATTTTTGTGCTCATCCTCATACAACCA  1899
Query  2237  TTTGGGGATGTGCCTATTAGGGCTCCGTAAGAACTCAGATGCCTGGGAAGCCCAGCCCCT  2296
Sbjct  1900  TTTGGGGATGTGCCTATTAGGGCTCCGTAAGAACTCAGATGCCTGGGAAGCCCAGCCCCT  1959
Query  2297  CAGGTGCCCCCACACACAGCCTTCCCTTGACGCCTACATTTCTAGGCACATGTGAGGCAT  2356
Sbjct  1960  CAGGTGCCCCCACACACAGCCTTCCCTTGACGCCTACATTTCTAGGCACATGTGAGGCAT  2019
Query  2357  CTTTCCTGGAGCCCCGAGCCAGCCCTGTCCCTCCCCAGTGCAGCATGGCACTCAGGAGAT  2416
Sbjct  2020  CTTTCCTGGAGCCCCGAGCCAGCCCTGTCCCTCCCCAGTGCAGCATGGCACTCAGGAGAT  2079
Query  2417  ACAGGCTGGACATGGGGCAGTCGTTCTGGGGAGGCCTGGCCTAGCAGCCACCCACCTGAG  2476
Sbjct  2080  ACAGGCTGGACATGGGGCAGTCGTTCTGGGGAGGCCTGGCCTAGCAGCCACCCACCTGAG  2139
Query  2477  CCCTCCCGGCCAGGCTTCGTGCTGGGGTGGGCCATGTGCCAGGACAGGAGGGTCCCGGCG  2536
Sbjct  2140  CCCTCCCGGCCAGGCTTCGTGCTGGGGTGGGCCATGTGCCAGGACAGGAGGGTCCCGGCG  2199
Query  2537  GAAAGCCAGCCCCGGACTCATCGTGACATTGAGATCCCACTGGAGGGTAGGGGTGGTAAT  2596
Sbjct  2200  GAAAGCCAGCCCCGGACTCATCGTGACATTGAGATCCCACTGGAGGGTAGGGGTGGTAAT  2259
Query  2597  AAACTTCTCCAAACGAT  2613
Sbjct  2260  AAACTTCTCCAAACGAT  2276
```

Range 2: 249 to 1491

Score	Expect	Identities	Gaps	Strand	Frame
2217 bits(1200)	0.0()	1230/1244(99%)	4/1244(0%)	Plus/Plus	

Features:

```
CDS:bcl-2-related ov  117   G  I  T  W  G  K  V  V  S  L  Y  A  V  A  A  G  L  A  V  D
Query                626   AGGCATCACGTGGGGCAAGGTGGTGTCCCTGTATGCGGTGGCCGCGGGGCTGGCCGTGGA  685
Sbjct                249   AGGCATCACGTGGGGCAAGGTGGTGTCCCTGTATGCGGTGGCCGCGGGGCTGGCCGTGGA  308

CDS:bcl-2-related ov  137   C  V  R  Q  A  Q  P  A  M  V  H  A  L  V  D  C  L  G  E  F
Query                686   CTGTGTGAGGCAGGCCCAGCCTGCCATGGTCCACGCCCTCGTGGACTGCCTGGGGGAGTT  745
Sbjct                309   CTGTGTGAGGCAGGCCCAGCCTGCCATGGTCCACGCCCTCGTGGACTGCCTGGGGGAGTT  368

CDS:bcl-2-related ov  157   V  R  K  T  L  A  T  W  L  R  R  R  G  G  W  T  D  V  L  K
Query                746   CGTGCGCAAGACCCTGGCAACCTGGCTGCGGAGACGCGGCGGATGGACTGATGTCCTCAA  805
Sbjct                369   CGTGCGCAAGACCCTGGCAACCTGGCTGCGGAGACGCGGCGGATGGACTGATGTCCTCAA  428

CDS:bcl-2-related ov  177   C  V  V  S  T  D  P  G  L  R  S  H  W  L  V  A  A  L  C  S
Query                806   GTGTGTGGTCAGCACAGACCCTGGCCTCCGCTCCCACTGGCTGGTGGCTGCACTCTGCAG  865
Sbjct                429   GTGTGTGGTCAGCACAGACCCTGGCCTCCGCTCCCACTGGCTGGTGGCTGCACTCTGCAG  488

CDS:bcl-2-related ov  197   F  G  R  F  L  K  A  A  F  F  V  L  L  P  E  R
Query                866   CTTCGGCCGCTTCCTGAAGGCTGCCTTCTTCGTGCTGCTGCCAGAGAGATGAGCTGCCCA  925
Sbjct                489   CTTCGGCCGCTTCCTGAAGGCTGCCTTCTTCGTGCTGCTGCCAGAGAGATGAGCTGCCCA  548
Query                926   CCTGGCAGTGGCCGCAGCCTGGCCCTCTGGGCCCAACGCAGGAGGCCCTCAGCACCCGAA  985
Sbjct                549   CCTGGCAGTGGCCGCAGCCTGGCCCTCTGGGCCCAACGCAGGAGGCCCTCAGCACCCGAA  608
Query                986   CACATCTTCCTCCTCCCCACCCGAGCCTGGAGCACTCTAACCCTCGGAGACCCCCTAAGC  1045
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Query                1106  CCTGGAGCTGGGCTTTGGGGCAGCCTGCGACCCTCCCCGCTTGTGTCCCTTCTCCTGTGA  1165
Sbjct                729   CCTGGAGCTGGGCTTTGGGGCAGCCTGCGACCCTCCCCGCTTGTGTCCCTTCTCCTGTGA  788
Query                1166  TCTCTGTGTTTTCCCTTTTCTTTCTGGGGCCAGGAAGTCAGGGTCAACTCCCAGGCCTCA  1225
Sbjct                789   TCTCTGTGTTTTCCCTTTTCTTTCTGGGGCCAGGAAGTCAGGGTCAACTCCCAGGCCTCA  848
Query                1226  GATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACA  1285
Sbjct                849   GATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACA  908
Query                1286  CCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCC  1345
Sbjct                909   CCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCC  968
Query                1346  CAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAAC  1405
Sbjct                969   CAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAAC  1028
Query                1406  ACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCC  1465
Sbjct                1029  ACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCC  1088
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Query                1466  CCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCCAGA  1525
Sbjct                1089  CCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCCGGA  1148
Query                1526  ACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGC  1585
Sbjct                1149  ACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGC  1208
Query                1586  CCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGGCCCGG  1645
Sbjct                1209  CCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGGCCCGG  1268
Query                1646  AACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAG  1705
Sbjct                1269  AACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAG  1328
Query                1706  CCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG  1765
Sbjct                1329  CCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCCCGG  1388
Query                1766  AACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAG  1825
Sbjct                1389  AACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCACCTGAG  1448
Query                1826  CCCCAGGTGAAGGGGCCCGGGAACACCTC-T--CACCTGAACCC  1866
Sbjct                1449  CCCCAGGTGAAGGGGCCCGG-AACACCTCCTGTCACCTGAGCCC  1491
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Range 3: 843 to 1451

Score	Expect	Identities	Gaps	Strand	Frame
941 bits(509)	0.0()	580/613(95%)	10/613(1%)	Plus/Plus	

Features:

```
Query  1260  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1319
Sbjct  843   GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  901
Query  1320  GGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1378
Sbjct  902   GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  961
Query  1379  TGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1438
Sbjct  962   TGAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1021
Query  1439  CCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1498
Sbjct  1022  CC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1080
Query  1499  CCTGAACCCCAGGTGAAGGGGCCCA-GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGG  1557
Sbjct  1081  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1140
Query  1558  GGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCT  1617
Sbjct  1141  GGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCT  1199
Query  1618  CACCTGAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAA  1676
Sbjct  1200  CACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAA  1259
Query  1677  GGGGCCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTC  1736
Sbjct  1260  GGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTC  1319
Query  1737  TCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAA  1796
Sbjct  1320  TCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAA  1379
Query  1797  GGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTC-T  1855
Sbjct  1380  GGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTCCT  1438
Query  1856  C--ACCTGAACCC  1866
Sbjct  1439  CTCACCTGAGCCC  1451
```

Range 4: 924 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
928 bits(502)	0.0()	579/614(94%)	13/614(2%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1278
Sbjct  924   GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC  983
Query  1279  GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1338
Sbjct  984   -GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1041
Query  1339  TGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1397
```

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Sbjct  1042  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1101
Query  1398  CCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTC  1456
Sbjct  1102  CCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTC  1160
Query  1457  ACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAG  1516
Sbjct  1161  ACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAG  1219
Query  1517  GGGCC-CAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTC  1575
Sbjct  1220  GGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGGCCCGGAACACTTGCTC  1279
Query  1576  TCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGA  1635
Sbjct  1280  TCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGA  1338
Query  1636  AGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCT  1695
Sbjct  1339  AGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCGGTGAAGGGGCCCGGAACACTTGCT  1398
Query  1696  CTCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGA  1755
Sbjct  1399  CTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGA  1458
Query  1756  AGGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTCC  1814
Sbjct  1459  AGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTC-  1517
Query  1815  TGTCACCTGAGCCC  1828
Sbjct  1518  T--CACCTGAACCC  1529
```

Range 5: 966 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
896 bits(485)	0.0()	543/570(95%)	8/570(1%)	Plus/Plus	

Features:

```
Query  1221  CCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG  1280
Sbjct  966   CCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-G  1024
Query  1281  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTG  1340
Sbjct  1025  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTG  1084
Query  1341  AACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1399
Sbjct  1085  AGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCC  1144
Query  1400  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1459
Sbjct  1145  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1203
Query  1460  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1519
Sbjct  1204  TGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGG  1263
Query  1520  CCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1579
Sbjct  1264  CCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1323
Query  1580  CTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGG  1639
Sbjct  1324  CTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCGGTGAAGGG  1382
Query  1640  GCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCA  1699
Sbjct  1383  GCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCA  1442
Query  1700  CCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGG  1759
Sbjct  1443  CCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGG  1502
Query  1760  GCCCGG-AACACCTCCTCTCACCTGAGCCC  1788
Sbjct  1503  GCCCGGGAACACCTC-TC--ACCTGAACCC  1529
```

Range 6: 843 to 1411

Score	Expect	Identities	Gaps	Strand	Frame
870 bits(471)	0.0()	542/574(94%)	13/574(2%)	Plus/Plus	

Features:

```
Query  1301  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC  1360
Sbjct  843   GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  901
Query  1361  -GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1418
Sbjct  902   GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  961
```

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Query  1419  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1478
Sbjct  962   TGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1020
Query  1479  CCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC-AGAACACCTGCTCTC  1537
Sbjct  1021  CCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTC  1079
Query  1538  ACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAG  1596
Sbjct  1080  ACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAG  1139
Query  1597  GGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGGCCCGGAACACTTGCTC  1656
Sbjct  1140  GGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTC  1198
Query  1657  TCACCTGAGCCCCAGGTGAAGGGGCC-CGGAACACCTGCTCTCACCTGAGCCCCCGGTGA  1715
Sbjct  1199  TCACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGA  1258
Query  1716  AGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCT  1775
Sbjct  1259  AGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCT  1318
Query  1776  CTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGA  1835
Sbjct  1319  CTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCGGTGA  1378
Query  1836  AGGGGCCCGGGAACAC---CTCTCACCTGAACCC  1866
Sbjct  1379  AGGGGCCCGG-AACACTTGCTCTCACCTGAGCCC  1411
```

Range 7: 1005 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
835 bits(452)	0.0()	505/530(95%)	6/530(1%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1279
Sbjct  1005  GCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1064
Query  1280  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1339
Sbjct  1065  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1124
Query  1340  GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1399
Sbjct  1125  GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1184
Query  1400  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1459
Sbjct  1185  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACC  1244
Query  1460  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1519
Sbjct  1245  TCAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1303
Query  1520  CCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1579
Sbjct  1304  CCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1363
Query  1580  CTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGG  1639
Sbjct  1364  CTGAGCCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGG  1422
Query  1640  GCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCA  1699
Sbjct  1423  GCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCA  1482
Query  1700  CCTGAGCCCCCGGTGAAGGGGCCCGG-AACACTTGCTCTCACCTGAGCCC  1748
Sbjct  1483  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACAC---CTCTCACCTGAACCC  1529
```

Range 8: 844 to 1371

Score	Expect	Identities	Gaps	Strand	Frame
817 bits(442)	0.0()	502/530(95%)	8/530(1%)	Plus/Plus	

Features:

```
Query  1343  CCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-G  1401
Sbjct  844   CCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG  903
Query  1402  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTG  1461
Sbjct  904   GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTG  963
Query  1462  AGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCC  1521
Sbjct  964   AACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1022
Query  1522  CAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1580
```

```
Sbjct  1023  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1082
Query  1581  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGG  1640
Sbjct  1083  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1142
Query  1641  CCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1700
Sbjct  1143  CCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1202
Query  1701  CTGAGCCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGG  1759
Sbjct  1203  CTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGG  1262
Query  1760  GCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCA  1819
Sbjct  1263  GCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCA  1322
Query  1820  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--ACCTGAACCC  1866
Sbjct  1323  CCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTGCTCTCACCTGAGCCC  1371
```

Range 9: 843 to 1331

Score	Expect	Identities	Gaps	Strand	Frame
767 bits(415)	0.0()	466/490(95%)	6/490(1%)	Plus/Plus	

Features:

```
Query  1382  GCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1441
Sbjct  843   GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  902
Query  1442  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1501
Sbjct  903   GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  962
Query  1502  GAACCCCAGGTGAAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1561
Sbjct  963   GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1022
Query  1562  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1621
Sbjct  1023  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1082
Query  1622  TGAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1680
Sbjct  1083  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1142
Query  1681  CCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTCAC  1740
Sbjct  1143  CCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCAC  1202
Query  1741  CTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGG  1799
Sbjct  1203  CTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGG  1262
Query  1800  GCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--  1856
Sbjct  1263  GCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTGCTCTC  1321
Query  1857  ACCTGAACCC  1866
Sbjct  1322  ACCTGAGCCC  1331
```

Range 10: 1045 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
734 bits(397)	0.0()	462/492(94%)	10/492(2%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1278
Sbjct  1045  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1104
Query  1279  GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1338
Sbjct  1105  GGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1163
Query  1339  TGAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1398
Sbjct  1164  TGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1223
Query  1399  CC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1457
Sbjct  1224  CTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCA  1282
Query  1458  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1517
Sbjct  1283  CCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGG  1341
Query  1518  GGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTC  1577
Sbjct  1342  GGCCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCCCGGAACACTTGCTCTC  1401
```

```
Query  1578  ACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAG  1637
Sbjct  1402  ACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACCTGAGCCCCAGGTGAAG  1460
Query  1638  GGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTGCTC  1696
Sbjct  1461  GGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC  1519
Query  1697  TCACCTGAGCCC  1708
Sbjct  1520  --ACCTGAACCC  1529
```

Range 11: 843 to 1291

Score	Expect	Identities	Gaps	Strand	Frame
665 bits(360)	0.0()	423/452(94%)	10/452(2%)	Plus/Plus	

Features:

```
Query  1422  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1481
Sbjct  843   GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  901
Query  1482  GGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCCA-GAACACCTGCTCTCACC  1540
Sbjct  902   GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  961
Query  1541  TGAGCCCCAGGTGAAGGGGCCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1600
Sbjct  962   TGAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1021
Query  1601  CCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCA  1659
Sbjct  1022  CC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1080
Query  1660  CCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGG  1718
Sbjct  1081  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1140
Query  1719  GGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTC  1778
Sbjct  1141  GGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTC  1200
Query  1779  ACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTGTCACCTGAGCCCCAGGTGAAG  1837
Sbjct  1201  ACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAG  1260
Query  1838  GGGCCCGGGAACAC---CTCTCACCTGAACCC  1866
Sbjct  1261  GGGCCCGG-AACACTTGCTCTCACCTGAGCCC  1291
```

Range 12: 1086 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
658 bits(356)	0.0()	422/452(93%)	11/452(2%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1278
Sbjct  1086  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC  1145
Query  1279  GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1338
Sbjct  1146  -GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1203
Query  1339  TGAACCCCAGGTGAAGGGGCC-CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1397
Sbjct  1204  TGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGG  1263
Query  1398  CCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1457
Sbjct  1264  CCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCA  1322
Query  1458  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1517
Sbjct  1323  CCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGG  1381
Query  1518  GGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTC  1577
Sbjct  1382  GGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTC  1441
Query  1578  ACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAG  1637
Sbjct  1442  ACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTGTCACCTGAGCCCCAGGTGAAG  1500
Query  1638  GGGCCCGG-AACACTTGCTCTCACCTGAGCCC  1668
Sbjct  1501  GGGCCCGGGAACAC---CTCTCACCTGAACCC  1529
```

Range 13: 1128 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
621 bits(336)	0.0()	385/408(94%)	6/408(1%)	Plus/Plus	

Features:

```
Query  1221  CCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG  1280
             ||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1128  CCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-G  1186

Query  1281  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGGAACACCTGCTCTCACCTG  1340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1187  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTCTCACCTC  1246

Query  1341  AACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1247  AGCCCCTGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1306

Query  1401  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1307  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCT  1365

Query  1461  GAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGC  1520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1366  GAGCCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGC  1424

Query  1521  CCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACC  1580
             ||| |||||||| ||||||||||||||||||||||||||||||||||| ||| ||||||
Sbjct  1425  CCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACC  1484

Query  1581  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCC  1628
             |||||||||||||||||||||||||||| ||| |||||| |||
Sbjct  1485  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--ACCTGAACCC  1529
```

Range 14: 843 to 1239

Score	Expect	Identities	Gaps	Strand	Frame
603 bits(326)	2e-175()	376/399(94%)	7/399(1%)	Plus/Plus	

Features:

```
Query  1463  GCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGCCC  1522
             ||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  843   GCCTCAGATGCAGGGGCCC-AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  901

Query  1523  -AGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACC  1580
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  902   GGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  961

Query  1581  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGG  1640
             ||| |||||||||||||||||| |||||||||||||||||||||| |||||||||||||
Sbjct  962   TGAACCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGG  1020

Query  1641  CCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTGCTCTCA  1699
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  1021  CCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCA  1080

Query  1700  CCTGAGCCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGG  1758
             |||||||||| |||||||||||| |||||||| |||||||||||||||||||||||||||
Sbjct  1081  CCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGG  1140

Query  1759  GGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTC  1818
             ||||||||||||| ||||||||||||||||||||||||||||||||||||| |||| |||
Sbjct  1141  GGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTC  1200

Query  1819  ACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC  1856
             ||||||||||||||||||||||||||||||||||| |||
Sbjct  1201  ACCTGAGCCCCAGGTGAAGGGGCCTGGGAACACCTGCTC  1239
```

Range 15: 844 to 1210

Score	Expect	Identities	Gaps	Strand	Frame
562 bits(304)	3e-163()	348/368(95%)	7/368(1%)	Plus/Plus	

Features:

```
Query  1505  CCCCAGGTGAAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-G  1563
             |||| |||| |||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  844   CCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG  903

Query  1564  GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGGAACACCTGCTCTCACCTG  1623
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  904   GAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGGAACACCTGCTCTCACCTG  963

Query  1624  AGCCCCTGGTGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1683
             ||||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  964   AACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC  1023

Query  1684  GGAACACCTGCTCTCACCTGAGCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACCT  1742
             |||||||||||||||||||||||||| |||||||||||| ||||||| |||||||||||
Sbjct  1024  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1083

Query  1743  GAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGC  1801
             ||||||||||||||||||||| |||||||| |||||||||||||||||||||||||||||
Sbjct  1084  GAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGGC  1143

Query  1802  CCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--AC  1858
             |||||||||||| ||||||||||||||||||||||||||||||||||||| ||| |||
Sbjct  1144  CCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTGCTCTCAC  1202

Query  1859  CTGAACCC  1866
             ||||||||
Sbjct  1203  CTGAGCCC  1210
```

Range 16: 1167 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
542 bits(293)	4e-157()	345/369(93%)	7/369(1%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1279
             ||| |||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  GCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCTG  1226

Query  1280  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGGAACACCTGCTCTCACCT  1339
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  GGAACACCTGCTCTCACCTCAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCT  1285

Query  1340  GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1399
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  GAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1345

Query  1400  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1459
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  1346  CGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCCC-GGAACACTTGCTCTCACC  1404

Query  1460  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1519
             |||||||||||||||||||| |||||||| |||||||| |||||||||||||||||||||
Sbjct  1405  TGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGG  1463

Query  1520  CCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGG-AACACCTGCTCTCA  1578
             ||| |||||||| || ||||||||||||||||||||||||||||| |||||||| |||||
Sbjct  1464  CCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--A  1520

Query  1579  CCTGAGCCC  1587
             ||||| |||
Sbjct  1521  CCTGAACCC  1529
```

Range 17: 843 to 1170

Score	Expect	Identities	Gaps	Strand	Frame
484 bits(262)	6e-140()	308/329(94%)	7/329(2%)	Plus/Plus	

Features:

```
Query  1544  GCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1603
             ||| |||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  843   GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  902

Query  1604  GGAACACCTGCTCTCACCTGAGCCCCTGGTGAAGGGGCCC-GGAACACTTGCTCTCACCT  1662
             |||||||||||||||||||||||||||||||||||||||| |||||||| |||||||||||
Sbjct  903   GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  962

Query  1663  GAGCCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCCGGTGAAGGGGCC  1722
             |||| |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  963   GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1022

Query  1723  CGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACC  1781
             ||||||| |||||||||||||||||||||||||||||||| ||||||| |||| ||||||
Sbjct  1023  CGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACC  1082

Query  1782  TGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGG  1840
             ||||||||||||||||||||| |||||||| || |||||| |||||||||||||||||||
Sbjct  1083  TGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCAGGTGAAGGGG  1142

Query  1841  CCCGGGAACACCT-CTC--ACCTGAACCC  1866
             ||||| |||||||| |||  |||||| |||
Sbjct  1143  CCCGG-AACACCTGCTCTCACCTGAGCCC  1170
```

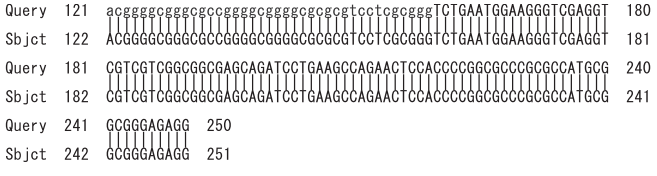
Range 18: 2 to 251

Score	Expect	Identities	Gaps	Strand	Frame
462 bits(250)	3e-133()	250/250(100%)	0/250(0%)	Plus/Plus	

Features:

```
Query  1     CTCTCGCCAGCTGGGAGTCGCGCGCTGCCCACCTCGCTGCCCAGGCCCCCGACGCCGCGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     CTCTCGCCAGCTGGGAGTCGCGCGCTGCCCACCTCGCTGCCCAGGCCCCCGACGCCGCGG  61

Query  61    CAGGAGCCCCCCAAGAGCGCGGGAAGCCCCGTGGACCTgggcgctccggctcgggcgtgg  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62    CAGGAGCCCCCCAAGAGCGCGGGAAGCCCCGTGGACCTGGCGCTCCGGGCTCGGGCGTGG  121
```



Range 19: 1207 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
457 bits(247)	1e-131()	304/330(92%)	9/330(2%)	Plus/Plus	

Features:



Range 20: 1256 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
429 bits(232)	3e-123()	265/280(95%)	6/280(2%)	Plus/Plus	

Features:

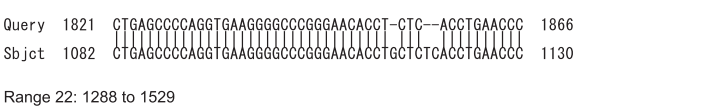


Range 21: 843 to 1130

Score	Expect	Identities	Gaps	Strand	Frame
422 bits(228)	5e-121()	270/289(93%)	7/289(2%)	Plus/Plus	

Features:

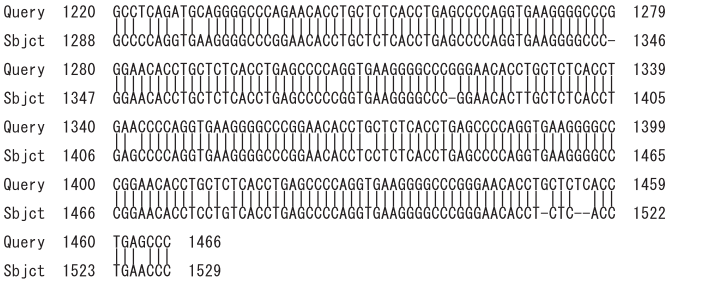




Range 22: 1288 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
363 bits(196)	3e-103()	231/247(94%)	5/247(2%)	Plus/Plus	

Features:



Range 23: 851 to 1089

Score	Expect	Identities	Gaps	Strand	Frame
353 bits(191)	2e-100()	224/239(94%)	5/239(2%)	Plus/Plus	

Features:



Range 24: 843 to 1048

Score	Expect	Identities	Gaps	Strand	Frame
283 bits(153)	2e-79()	190/207(92%)	6/207(2%)	Plus/Plus	

Features:



Range 25: 1328 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
283 bits(153)	2e-79()	190/207(92%)	6/207(2%)	Plus/Plus	

Features:



```
Query  1280  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1339
Sbjct  1387  GGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTCTCACCT  1445
Query  1340  GAACCCCAGGTGAAGGGGCCCGGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCC  1399
Sbjct  1446  GAGCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCC  1505
Query  1400  CGG-AACACCTGCTCTCACCTGAGCCC  1425
Sbjct  1506  CGGGAACACCT-CTC--ACCTGAACCC  1529
```

Range 26: 851 to 1008

Score	Expect	Identities	Gaps	Strand	Frame
211 bits(114)	1e-57()	145/159(91%)	6/159(3%)	Plus/Plus	

Features:

```
Query  1713  TGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACC  1771
Sbjct  851   TGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACC  910
Query  1772  TCCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTGTCACCTGAGCCCCA  1830
Sbjct  911   TGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCA  970
Query  1831  GGTGAAGGGGCCCCGGGAACACCT-CTC--ACCTGAACCC  1866
Sbjct  971   GGTGAAGGGGCCCGG-AACACCTGCTCTCACCTGAGCCC  1008
```

Range 27: 1376 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
211 bits(114)	1e-57()	145/159(91%)	6/159(3%)	Plus/Plus	

Features:

```
Query  1228  TGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACC  1287
Sbjct  1376  TGAAGGGGCCCGGAACACTTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACC  1434
Query  1288  TGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCTGAACCCCA  1347
Sbjct  1435  TCCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-GGAACACCTCCTGTCACCTGAGCCCCA  1493
Query  1348  GGTGAAGGGGCCCGG-AACACCTGCTCTCACCTGAGCCC  1385
Sbjct  1494  GGTGAAGGGGCCCGGGAACACCT-CTC--ACCTGAACCC  1529
```

Range 28: 843 to 968

Score	Expect	Identities	Gaps	Strand	Frame
169 bits(91)	7e-45()	115/126(91%)	4/126(3%)	Plus/Plus	

Features:

```
Query  1745  GCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-  1803
Sbjct  843   GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  902
Query  1804  GGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--ACCT  1860
Sbjct  903   GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  962
Query  1861  GAACCC  1866
Sbjct  963   GAACCC  968
```

Range 29: 1408 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
169 bits(91)	7e-45()	115/126(91%)	4/126(3%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1279
Sbjct  1408  GCCCCAGGTGAAGGGGCCCGGAACACCTCCTCTCACCTGAGCCCCAGGTGAAGGGGCCC-  1466
Query  1280  GGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCTGCTCTCACCT  1339
Sbjct  1467  GGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCGGGAACACCT-CTC--ACCT  1523
Query  1340  GAACCC  1345
Sbjct  1524  GAACCC  1529
```

Range 30: 843 to 927

Score	Expect	Identities	Gaps	Strand	Frame
99.0 bits(53)	9e-24()	75/85(88%)	3/85(3%)	Plus/Plus	

Features:

```
Query  1785  GCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCG  1844
Sbjct  843   GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  902
Query  1845  GGAACACCT-CTC--ACCTGAACCC  1866
Sbjct  903   GGAACACCTGCTCTCACCTGAGCCC  927
```

Range 31: 1448 to 1529

Score	Expect	Identities	Gaps	Strand	Frame
99.0 bits(53)	9e-24()	75/85(88%)	3/85(3%)	Plus/Plus	

Features:

```
Query  1220  GCCTCAGATGCAGGGGCCCAGAACACCTGCTCTCACCTGAGCCCCAGGTGAAGGGGCCCG  1279
Sbjct  1448  GCCCCAGGTGAAGGGGCCCGGAACACCTCCTGTCACCTGAGCCCCAGGTGAAGGGGCCCG  1507
Query  1280  GGAACACCTGCTCTCACCTGAGCCC  1304
Sbjct  1508  GGAACACCT-CTC--ACCTGAACCC  1529
```

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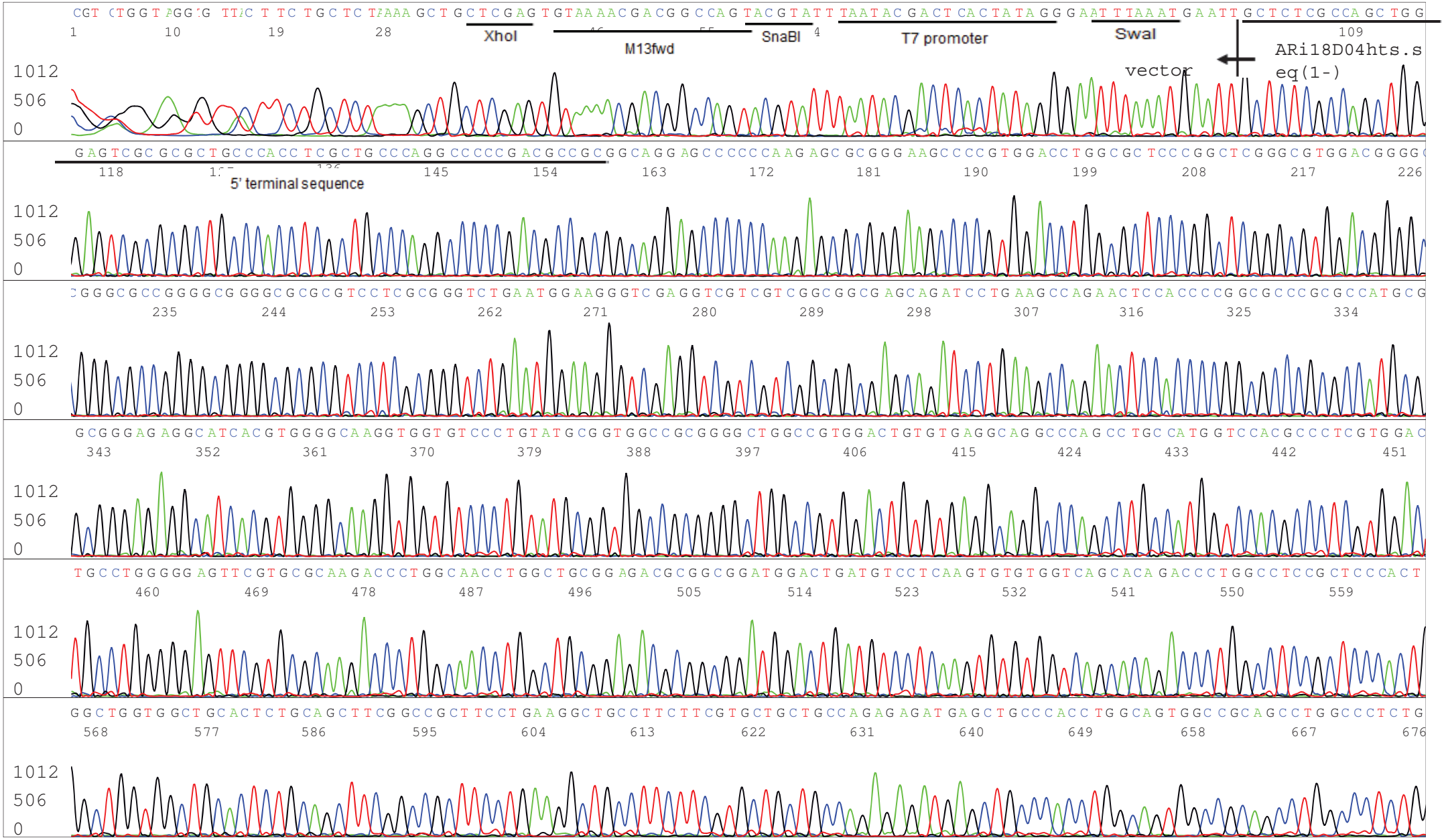
Applied Biosystems

S/N G:342 A:422 T:269 C:507
KB.bcp
KB 1.4.1.8 Cap:2

Primer A : pGCAP-F
5' CTCAGTGGATGTTGCCTTTAC 3'

7675_ARi18D04_B4Dj_pGCAP_F_A02_02_ABI24
7675_ARi18D04_B4Dj_pGCAP_F
KB_3500_POP7_BDTv3.mob
Pts 1419 to 13561 Pk1 Loc:1396
Version 6.0 HiSQV Bases: 923

Inst Model/Name 3500/3500 Instrument
Apr 24,2024 03:16PM, JST
Apr 24,2024 03:43PM, JST
Spacing:11.96 Pts/Panel1350
Plate Name: 20240424_GNP



Applied Biosystems

S/N G:39 A:50 T:49 C:57
KB.bcp
KB 1.4.1.8 Cap:5

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

7675_ARi18D04_B4Dj_pGCAP_R_B02_05_ABI24
7675_ARi18D04_B4Dj_pGCAP_R
KB_3500_POP7_BDTv3.mob
Pts 1431 to 13626 Pk1 Loc:1408
Version 6.0 HiSQV Bases: 108

Inst Model/Name 3500/3500 Instrument
Apr 24,2024 03:16PM, JST
Apr 24,2024 03:43PM, JST
Spacing:12.17 Pts/Panel1350
Plate Name: 20240424_GNP

