NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBb50E11

Lot# : 7676_B4Fd

Vector : pGCAP1

Gene	SERP1	
RefSeq_mRNA	NM_014445.4	3022 bp

● Plasmid DNA purification

Date : 2024/06/17 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/06/18 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/06/18

DNA concentration (O.D.): 304 ng/ul

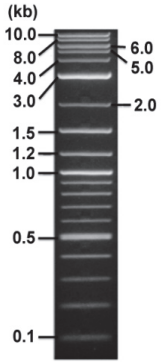
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

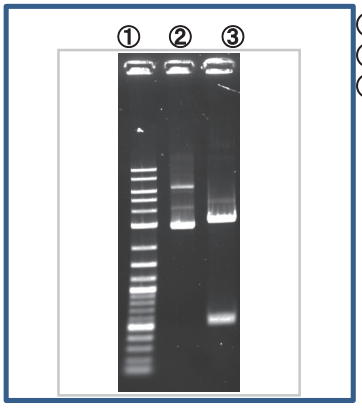
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 0.5, 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 : 2024/06/19

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 : 2024/06/21

DNA (304 ng/ul)	88 ul
10x TE	107 ul
dH_2O	875 ul
Total	1,070 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.06.21 笹沼

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

Blast 2 sequences

Job title: NM_014445:Homo sapiens stress associated endoplasmic...

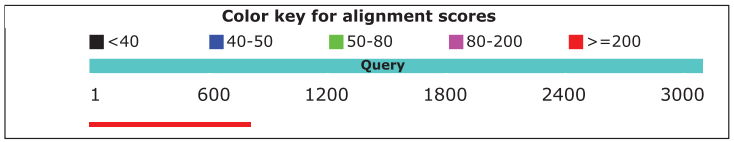
RID 747MSJCV114 (Expires on 06-20 07:56 am)

Query ID	NM_014445.4	**Subject ID**	lcl|Query_6486191
Description	Homo sapiens stress associated endoplasmic reticulum protein 1 (SERP1), mRNA	**Description**	None See details
		Molecule type	dna
Molecule type	nucleic acid	**Subject Length**	953
Query Length	3022	**Program**	BLASTN 2.15.0+

RBb50E11z.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



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Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	1489	1489	26%	0.0	100.00%	Query_6486191

Alignments

Sequence ID: Query_6486191 Length: 953 Number of Matches: 1
Range 1: 107 to 912

Score	Expect	Identities	Gaps	Strand	Frame
1489 bits(806)	0.0()	806/806(100%)	0/806(0%)	Plus/Plus	

Features:

```
Query                  1    AGATCGAGGCGGCGGGGCTGCACATTCCCGTTGTTGCGTTGCGTTTCCTTCCTCTTTCACT  60
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  107  AGATCGAGGCGGCGGGGCTGCACATTCCCGTTGTTGCGTTGCGTTTCCTTCCTCTTTCACT  166
Query                  61   CCGCGCTCAcggcggcggccaaagcggcggcgacggcggcgcgagaacgacccggcggcC  120
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  167  CCGCGCTCACGGCGGCGGCCAAAGCGGCGGCGACGGCGGCGCGAGAACGACCCGGCGGCC  226
Query                  121  AGTTCTCTTCCTCCTGCGCACCTGCCCCGCTCGGTCAGTCAGTCGGCGGCCGGCGCCCGG  180
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  227  AGTTCTCTTCCTCCTGCGCACCTGCCCCGCTCGGTCAGTCAGTCGGCGGCCGGCGCCCGG  286
Query                  181  CTTGTGCTCAGACCTCGCGCTTGCGGCGCCCCAGGCCCAGCGGCCGTAGCTAGCGTCTGGC  240
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  287  CTTGTGCTCAGACCTCGCGCTTGCGGCGCCCCAGGCCCAGCGGCCGTAGCTAGCGTCTGGC  346
Query                  241  CTGAGAACCTCGGCGGCTCCGGCGGCGCGGGCACCACGAGCCGAGCCTCGCAGCGGCTCCA  300
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Sbjct                  347  CTGAGAACCTCGGCGGCTCCGGCGGCGCGGGCACCACGAGCCGAGCCTCGCAGCGGCTCCA  406
Query                  301  GAGGAGGCAGGCGAGTGAGCGAGTCCGAGGGGGTGGCCGGGGCAGGTGGTGGCGCCGCGAA  360
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  407  GAGGAGGCAGGCGAGTGAGCGAGTCCGAGGGGGTGGCCGGGGCAGGTGGTGGCGCCGCGAA  466
CDS:stress-associate   1      M  V  A  K  Q  R  I  R  M  A  N  E  K  H  S  K  N  I  T  Q
Query                  361  GATGGTCGCCAAGCAAAGGATCCGTATGGCCAACGAGAAGCACAGCAAGAACATCACCCA  420
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Sbjct                  467  GATGGTCGCCAAGCAAAGGATCCGTATGGCCAACGAGAAGCACAGCAAGAACATCACCCA  526
CDS:stress-associate   21     R  G  N  V  A  K  T  S  R  N  A  P  E  E  K  A  S  V  G  P
Query                  421  GCGCGGCAACGTCGCCAAGACCTCGAGAAATGCCCCCGAAGAGAAGGCGTCTGTAGGACC  480
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Sbjct                  527  GCGCGGCAACGTCGCCAAGACCTCGAGAAATGCCCCCGAAGAGAAGGCGTCTGTAGGACC  586
CDS:stress-associate   41     W  L  L  A  L  F  I  F  V  V  C  G  S  A  I  F  Q  I  I  Q
Query                  481  CTGGTTATTGGCTCTCTTCATTTTTGTTGTCTGTGGTTCTGCAATTTTCCAGATTATTCA  540
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Sbjct                  587  CTGGTTATTGGCTCTCTTCATTTTTGTTGTCTGTGGTTCTGCAATTTTCCAGATTATTCA  646
CDS:stress-associate   61     S  I  R  M  G  M
Query                  541  AAGTATCAGGATGGGCATGTGAAGTGACTGACCTTAAGATGTTTCCATTCTCCTGTGAAT  600
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Query                  661  CCTGCCTCAGAATGACTTTCCTATCATGCTTCATGTGTCATTCCAAGGTTTCTTCATGAG  720
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Sbjct                  767  CCTGCCTCAGAATGACTTTCCTATCATGCTTCATGTGTCATTCCAAGGTTTCTTCATGAG  826
Query                  721  TCATTCCAAGTTTTCTAGTCCATACCACAGTGCCTTGCAAAAAACACCACATGAATAAAG  780
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Sbjct                  827  TCATTCCAAGTTTTCTAGTCCATACCACAGTGCCTTGCAAAAAACACCACATGAATAAAG  886
Query                  781  CAATAAAATTTGATTGTTAAGATACA  806
                            |||||||||||||||||||||||||
Sbjct                  887  CAATAAAATTTGATTGTTAAGATACA  912
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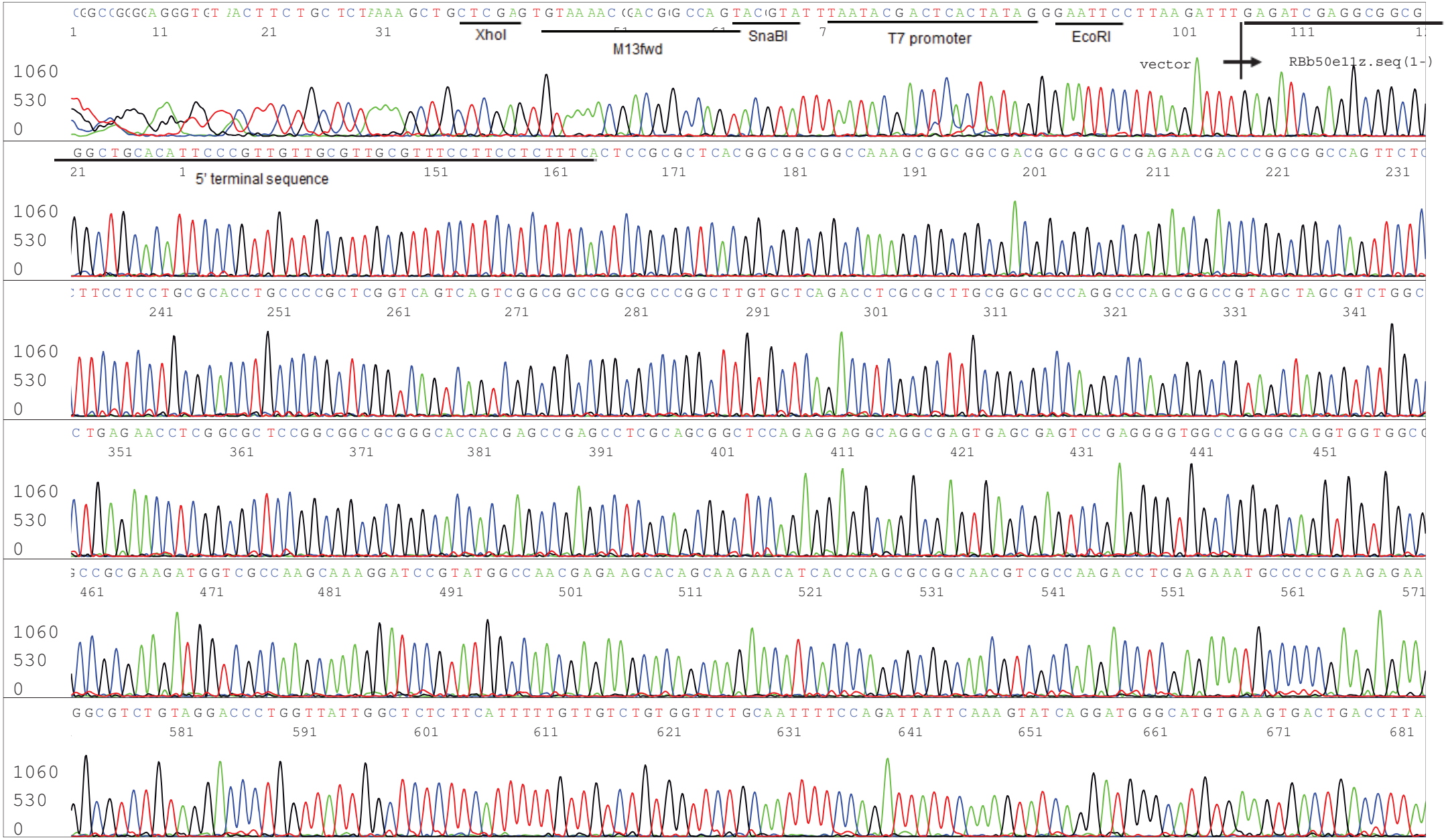
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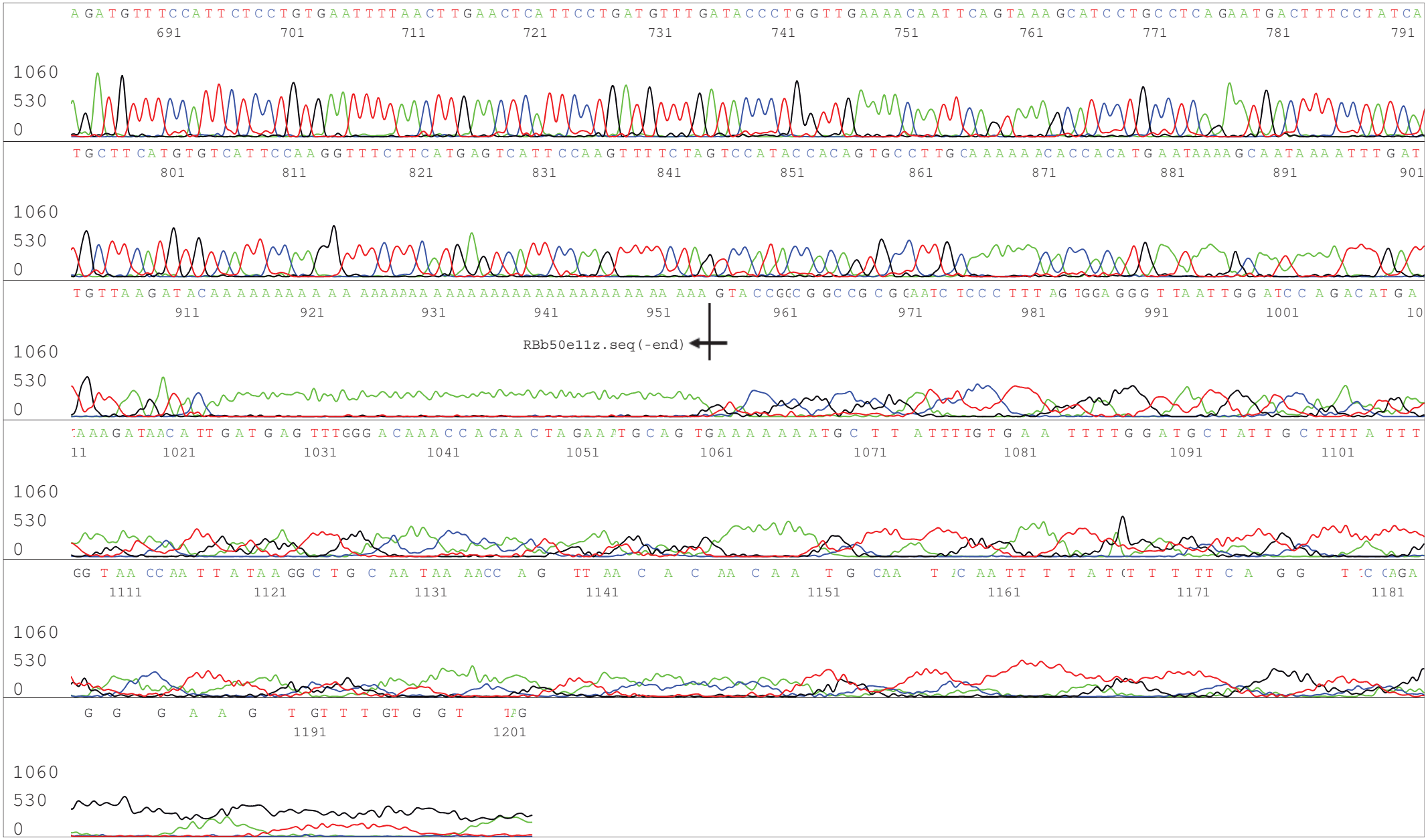
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5' CTCAGTGGATGTTGCCTTTAC 3'

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Version 6.0 HiSQV Bases: 954

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Jun 18,2024 03:21PM, JST
Spacing:12.05 Pts/Panel1350
Plate Name: 20240618_GNP




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530
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S/N G:22 A:32 T:27 C:34
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KB 1.4.1.8 Cap:2

Primer B : pGCAP-R
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Version 6.0 HiSQV Bases: 504

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