NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd50B08

Lot# : 7677_B4D4

Vector : pGCAP10

Gene	PUM2	
RefSeq_mRNA	NM_001352930.3	6139 bp

● Plasmid DNA purification

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

Date : 2024/04/05 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/04/05

DNA concentration (O.D.): 177 ng/ul

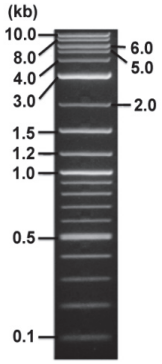
DNA	0..55 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.45 ul
Total	10 ul

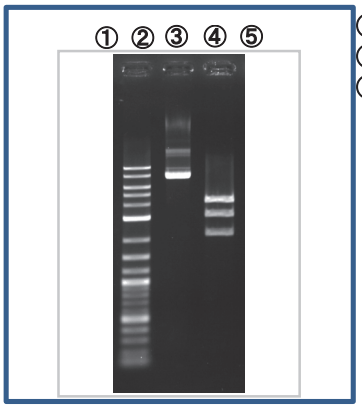
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 4.2, 2.1 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 : 2024/04/09

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

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/04/16

DNA (177 ng/ul)	82 ul
10x TE	58 ul
dH_2O	441 ul
Total	581 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

検 '24.04.16 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

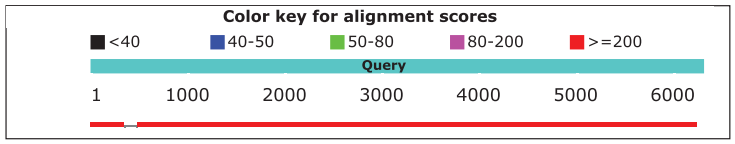
Job title: ref|NM_001352930.3|

RID 195CXCWS114 (Expires on 04-10 09:10 am)

Query ID	NM_001352930.3	**Subject ID**	lcl|Query_3004469
Description	Homo sapiens pumilio RNA binding family member 2 (PUM2), transcript variant 15, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	6139	**Subject Length**	6101
		Program	BLASTN 2.15.0+

Graphic Summary

Distribution of the top 2 Blast Hits on 1 subject sequences





Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	10515	11102	98%	0.0	99.88%	Query_3004469

Alignments

Sequence ID: Query_3004469 Length: 6101 Number of Matches: 2
Range 1: 324 to 6041

Score	Expect	Identities	Gaps	Strand	Frame
10515 bits(5694)	0.0()	5712/5719(99%)	7/5719(0%)	Plus/Plus	

Features:

```
Query          427   ACCATTCAATGTCCCAGCCTATTATGGTACAGAGAAGATCTGGACAGGGTTTTCATGGAA  486
Sbjct          324   ACCATTCAATGTCCCAGCCTATTATGGTACAGAGAAGATCTGGACAGGGTTTTCATGGAA  383

Query          487   ACAGTGAAGTAAATGCAATACTGTCTCCGCGATCAGAAAGTGGAGGCCTTGGTGTGAGCA  546
Sbjct          384   ACAGTGAAGTAAATGCAATACTGTCTCCGCGATCAGAAAGTGGAGGCCTTGGTGTGAGCA  443

Query          547   TGGTAGAATATGTATTAAGTTCTTCTCCTGCTGATAAATTGGATTCTCGATTTAGGAAGG  606
Sbjct          444   TGGTAGAATATGTATTAAGTTCTTCTCCTGCTGATAAATTGGATTCTCGATTTAGGAAGG  503

Query          607   GAAATTTTTCGTACTCCTGGAAGTCGTCAAGCCTCTCCAACTGAAGTAGTTGAGCGCTTG  666
Sbjct          504   GAAA-TTTTCGTACTCCTGGAAGTCGTCAAGCCTCTCCAACTGAAGTAGTTGAGCGCTTG  562

Query          667   GGCCCCAATACTAATCCCTCAGAAGGACTGGGGCCTCTTCCTAATCCTACAGCTAATAAA  726
Sbjct          563   GGCCCCAATACTAATCCCTCAGAAGGACTGGGGCCTCTTCCTAATCCTACAGCTAATAAA  622

CDS:pumilio homolog 1                                                  M  E  Q  V
Query          727   CCACTTGTTGAAGAATTTTCAAATCCTGAAACTCAGAATCTGGATGCCATGGAACAAGTT  786
Sbjct          623   CCACTTGTTGAAGAATTTTCAAATCCTGAAACTCAGAATCTGGATGCCATGGAACAAGTT  682

CDS:pumilio homolog 5     G  L  E  S  L  Q  F  D  Y  P  G  N  Q  V  P  M  D  S  S  G
Query          787   GGTCTGGAATCCTTACAGTTTGACTATCCTGGTAATCAGGTACCAATGGACTCTTCAGGA  846
Sbjct          683   GGTCTGGAATCCTTACAGTTTGACTATCCTGGTAATCAGGTACCAATGGACTCTTCAGGA  742

CDS:pumilio homolog 25    A  T  V  G  L  F  D  Y  N  S  Q  Q  Q  L  F  Q  R  T  N  A
Query          847   GCTACTGTAGGCCTTTTTGACTACAATTCCCAGCAGCAGCTCTTTCAGAGGACTAATGCA  906
Sbjct          743   GCTACTGTAGGCCTTTTTGACTACAATTCCCAGCAGCAGCTCTTTCAGAGGACTAATGCA  802

CDS:pumilio homolog 45    L  T  V  Q  Q  L  T  A  A  Q  Q  Q  Q  Y  A  L  A  A  A  Q
Query          907   CTAACAGTTCAACAGTTAACTGCAGCTCAACAGCAGCAATATGCATTAGCAGCAGCTCAG  966
Sbjct          803   CTAACAGTTCAACAGTTAACTGCAGCTCAACAGCAGCAATATGCATTAGCAGCAGCTCAG  862

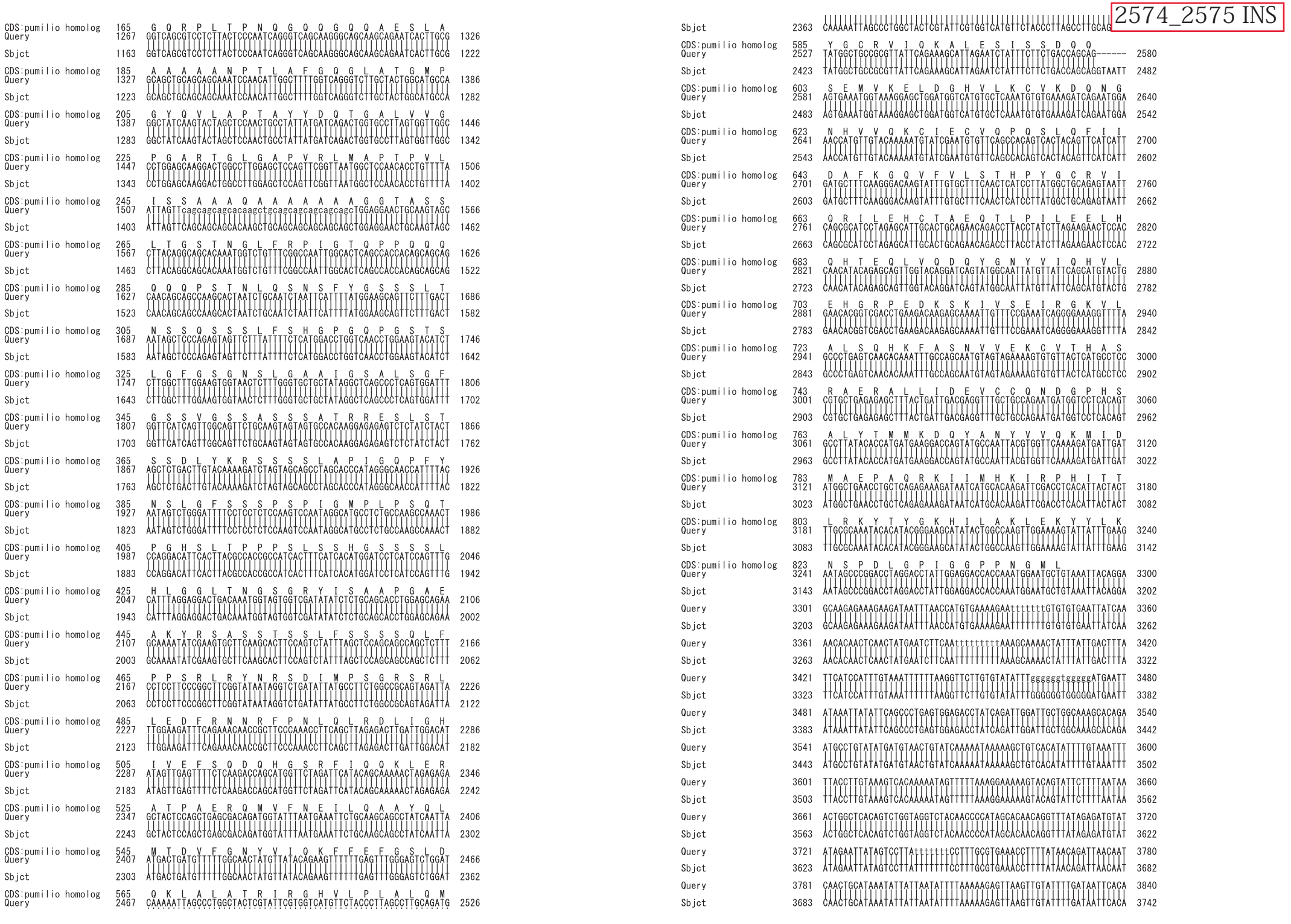
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Query          967   CAGCCACATATAGCTGGTGTATTCTCAGCAGGCCTTGCTCCAGCTGCATTTGTGCCAAAT  1026
Sbjct          863   CAGCCACATATAGCTGGTGTATTCTCAGCAGGCCTTGCTCCAGCTGCATTTGTGCCAAAT  922

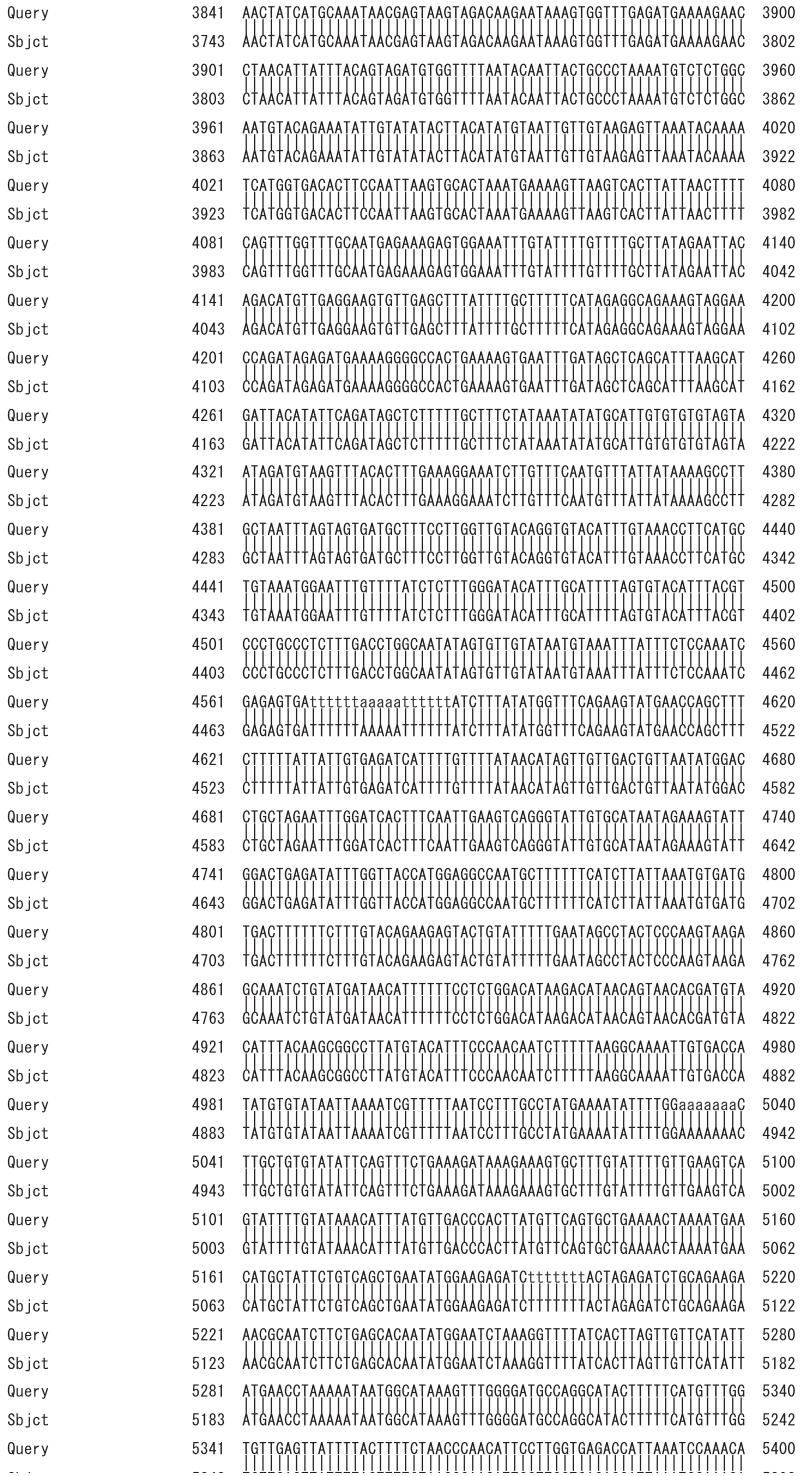
CDS:pumilio homolog 85    P  Y  I  I  S  A  A  P  P  G  T  D  P  Y  T  A  A  G  L  A
Query          1027  CCATACATTATTAGTGCTGCTCCTCCAGGGACCGATCCGTATACTGCAGCAGGATTGGCT  1086
Sbjct          923   CCATACATTATTAGTGCTGCTCCTCCAGGGACCGATCCGTATACTGCAGCAGGATTGGCT  982

CDS:pumilio homolog 105   A  A  A  T  L  A  G  P  A  V  V  P  P  Q  Y  Y  G  V  P  W
Query          1087  GCAGCAGCTACATTAGCAGGTCCAGCAGTGGTTCCACCTCAGTATTACGGCGTTCCATGG  1146
Sbjct          983   GCAGCAGCTACATTAGCAGGTCCAGCAGTGGTTCCACCTCAGTATTACGGCGTTCCATGG  1042

CDS:pumilio homolog 125   G  V  Y  P  A  N  L  F  Q  Q  Q  A  A  A  A  A  A  N  N  T  A
Query          1147  GGGGTGTATCCAGCCAACTTATTTCAGCAGCAAGCTGCAGCTGCGGCAAATAACACAGCC  1206
Sbjct          1043  GGGGTGTATCCAGCCAACTTATTTCAGCAGCAAGCTGCAGCTGCGGCAAATAACACAGCC  1102

CDS:pumilio homolog 145   S  Q  Q  A  A  S  Q  A  Q  P  G  Q  Q  Q  V  L  R  A  G  A
Query          1207  AGTCAGCAAGCAGCATCACAAGCTCAGCCTGGACAGCAACAGGTTCTCCGTGCTGGAGCA  1266
Sbjct          1103  AGTCAGCAAGCAGCATCACAAGCTCAGCCTGGACAGCAACAGGTTCTCCGTGCTGGAGCA  1162
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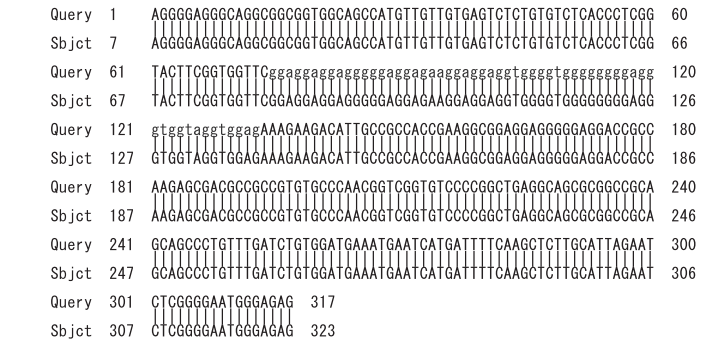

2574_2575 INS



Range 2: 7 to 323

Score	Expect	Identities	Gaps	Strand	Frame
586 bits(317)	1e-169()	317/317(100%)	0/317(0%)	Plus/Plus	

Features:



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Applied Biosystems

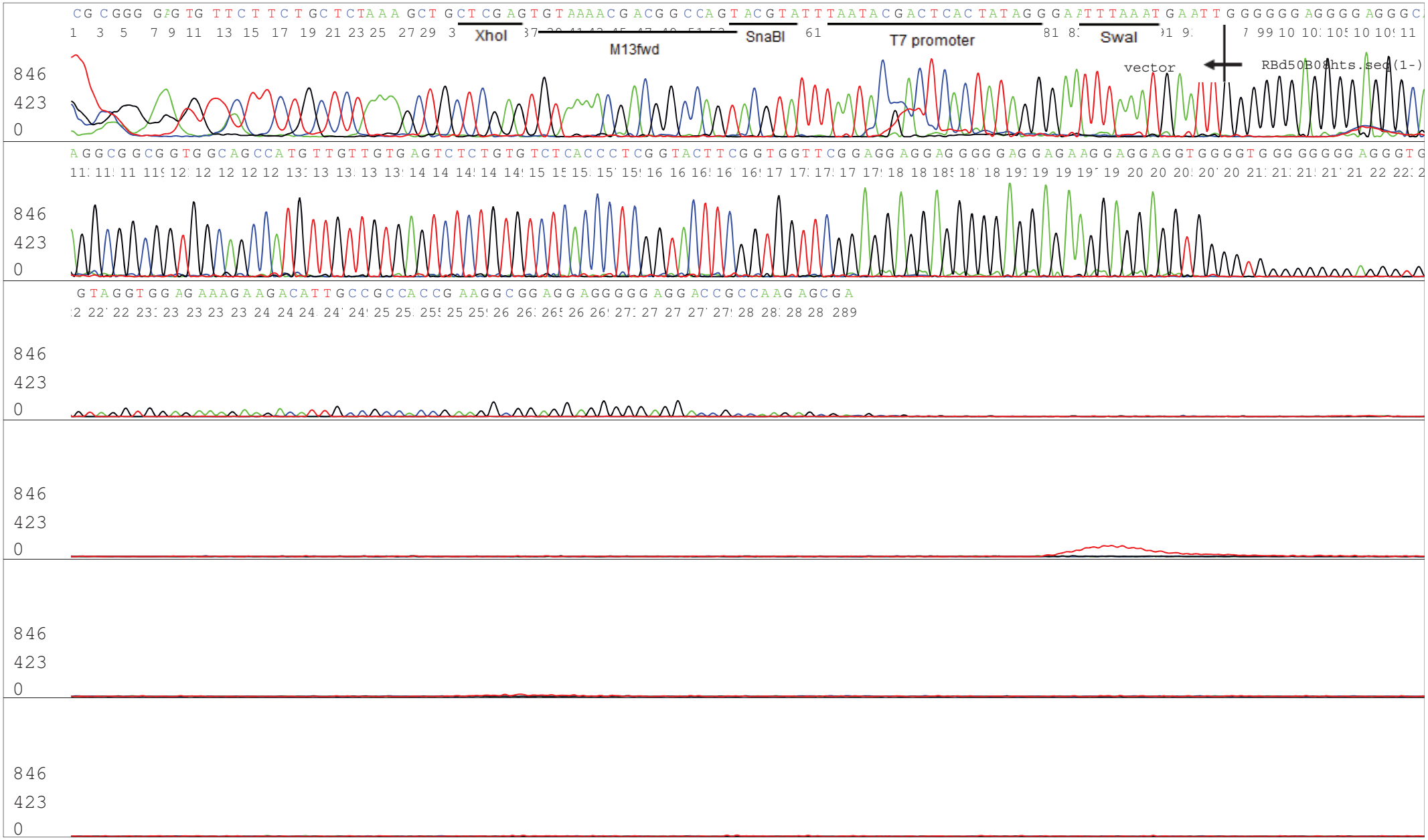
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KB.bcp
KB 1.4.1.8 Cap:18

Primer A : pGCAP-F

5' CTCAGTGGATGTTGCCTTTAC 3'

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7677_RBd50B08_B4D4_pGCAP_F
KB_3500_POP7_BDTv3.mob
Pts 1650 to 11259 Pk1 Loc:1627
Version 6.0 HiSQV Bases: 255

Inst Model/Name 3500/3500 Instrument
Apr 05,2024 03:08PM, JST
Apr 05,2024 03:36PM, JST
Spacing:11.89 Pts/Panel1350
Plate Name: 20240405_MGE2



Applied Biosystems

S/N G:20 A:46 T:33 C:29
KB.bcp
KB 1.4.1.8 Cap:21

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

7677_RBd50B08_B4D4_pGCAP_R_G03_21_ABI24
7677_RBd50B08_B4D4_pGCAP_R
KB_3500_POP7_BDTv3.mob
Pts 1644 to 12323 Pk1 Loc:1621
Version 6.0 HiSQV Bases: 67

Inst Model/Name 3500/3500 Instrument
Apr 05,2024 03:08PM, JST
Apr 05,2024 03:36PM, JST
Spacing:13.25 Pts/Panel1350
Plate Name: 20240405_MGE2

