NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe49A12

Lot# : 7672_B3Jr

Vector : pKA1U5

Gene	COL18A1	
RefSeq_mRNA	NM_130445.4	5399 bp

● Plasmid DNA purification

Date : 2023/10/26 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/10/27 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/10/27

DNA concentration (O.D.): 369 ng/ul

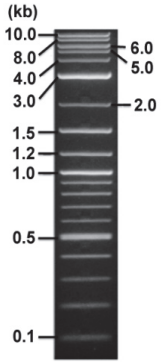
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

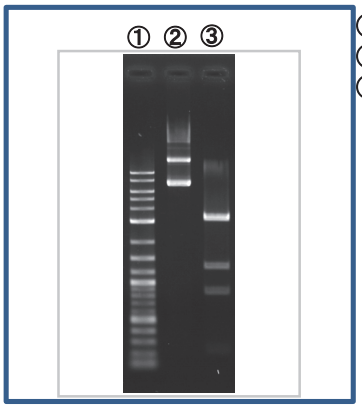
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 3.2, 1.3, 0.9, 0.2 kb (unsure)

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

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





①:Marker
②:uncut
③:BamHI

● Confirmation of the insertion sequence

Date : 2023/11/06

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

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2023/12/13

DNA (369 ng/ul)	80 ul
10x TE	118 ul
dH_2O	983 ul
Total	1,181 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '23.12.13 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_130445.4|

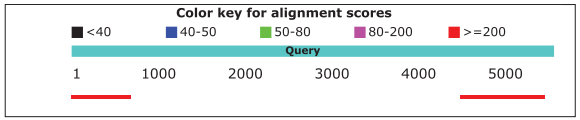
RID M3PFPRWK114 (Expires on 11-02 12:54 pm)

Query ID NM_130445.4
Description Homo sapiens collagen type XVIII alpha 1 chain (COL18A1), transcript variant 2, mRNA
Molecule type rna
Query Length 5399

Subject ID 3 subjects
Description See details
Molecule type dna
Subject Length 1706
Program BLASTN 2.14.1+

Graphic Summary

Distribution of the top 2 Blast Hits on 2 subject sequences



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'23.11.06
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Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
primerC (Reverse)	1755	1755	17%	0.0	99.90%	Query_25199
primerA (Forward)	1227	1227	12%	0.0	100.00%	Query_25198

Alignments

primerC (Reverse)
Sequence ID: Query_25199 Length: 960 Number of Matches: 1
Range 1: 8 to 960

Score	Expect	Identities	Gaps	Strand	Frame
1755 bits(950)	0.0()	953/954(99%)	1/954(0%)	Plus/Minus	

Features:

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Query  4489  CTGTTAGCAGACAGGCCCCGTGAGGCAATGGGAGCTGAGGCCACACTCAGCACAAGGCCA  4548
Sbjct  900   CTGTTAGCAGACAGGCCCCGTGAGGCAATGGGAGCTGAGGCCACACTCAGCACAAGGCCA  841
Query  4549  TCTGGGCTCCTCCAGGGTGTGTGCTCGCCCTGCGGTAGATGGGAGGGAGGCTCAGGTCCC  4608
Sbjct  840   TCTGGGCTCCTCCAGGGTGTGTGCTCGCCCTGCGGTAGATGGGAGGGAGGCTCAGGTCCC  781
Query  4609  TGGGGCTAGGGGGAGCCCCTTCTGCTCAGCTCTGGGCCATTCTCCACAGCAACCCCAGGC  4668
Sbjct  780   TGGGGCTAGGGGGAGCCCCTTCTGCTCAGCTCTGGGCCATTCTCCACAGCAACCCCAGGC  721
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Sbjct  660   CACCAAGCACAGCAGCCTGGGGCTGGCCTCCCAAATGAGCCATGAGATGATACATCCAAA  601
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Sbjct  600   GCAGACAGCTCCACCCTGGCCGAGTCCAAGCTGGGAGATTCAAGGGACCCATGAGTTGGG  541
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Sbjct  360   GCCCATGGACAGGCTGGCTCCAGATGCAGGGCAGTCATTGGCTGTCTCCTAGGAAACCCA  301
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primerA (Forward)
Sequence ID: Query_25198 Length: 742 Number of Matches: 1
Range 1: 79 to 742

Score	Expect	Identities	Gaps	Strand	Frame
1227 bits(664)	0.0()	664/664(100%)	0/664(0%)	Plus/Plus	

Features:

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CDS:collagen alpha-1 39   S  E  E  V  G  L  L  Q  L  L  G  D  P  P  P  Q  Q  V  T  Q
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Sbjct                 259  AGCGAGGAGGTGGGGCTGCTGCAGCTCCTTGGGGACCCCCCGCCCCAGCAGGTCACCCAG  318

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Sbjct                 379  GTGGCCCGGTACCACTTCCCCAGCCTCTTCTTCCGTGACTTCTCACTGCTGTTCCACATC  438

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HHS Vulnerability Disclosure

Applied Biosystems

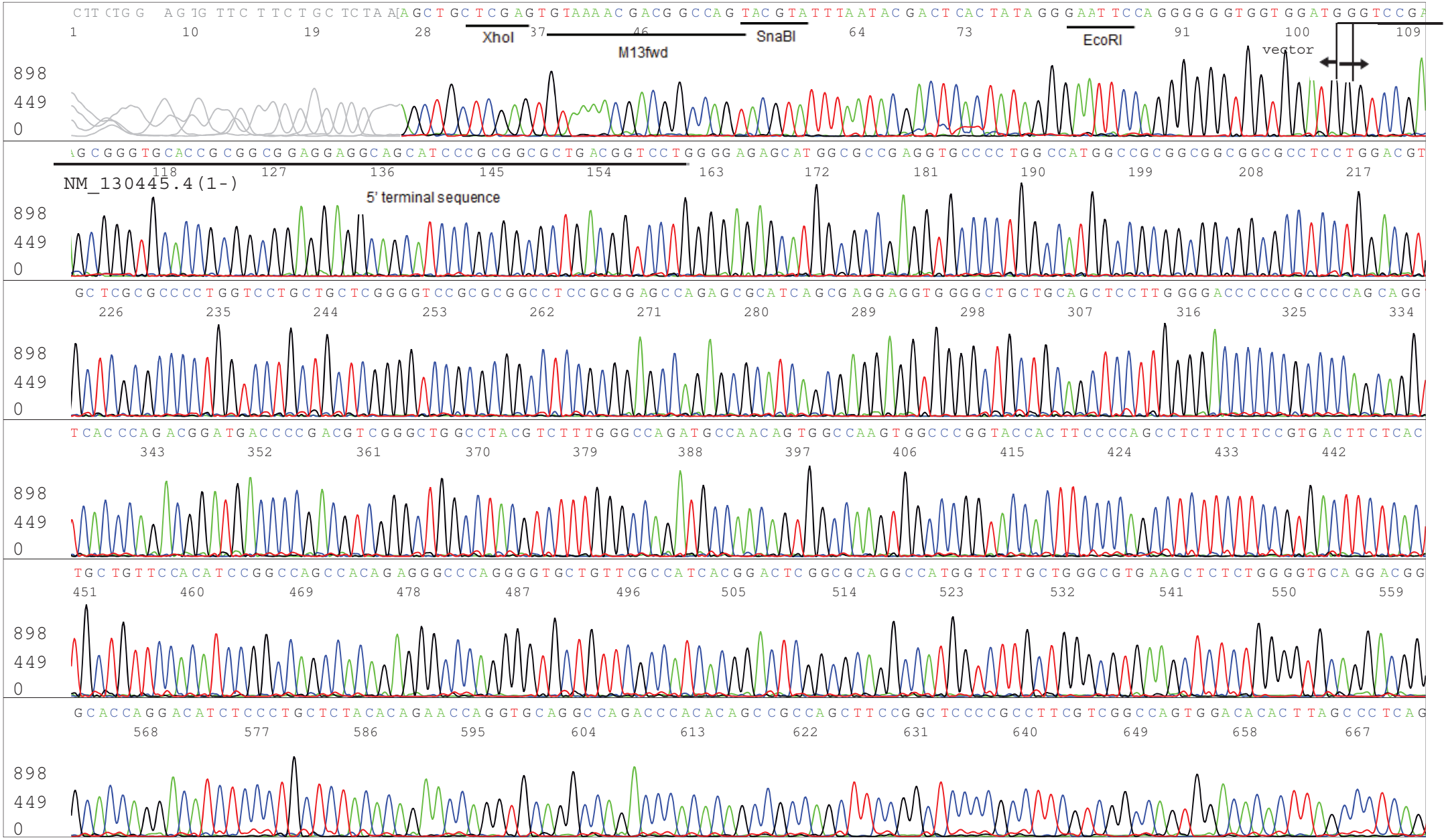
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KB 1.4.1.8 Cap:17

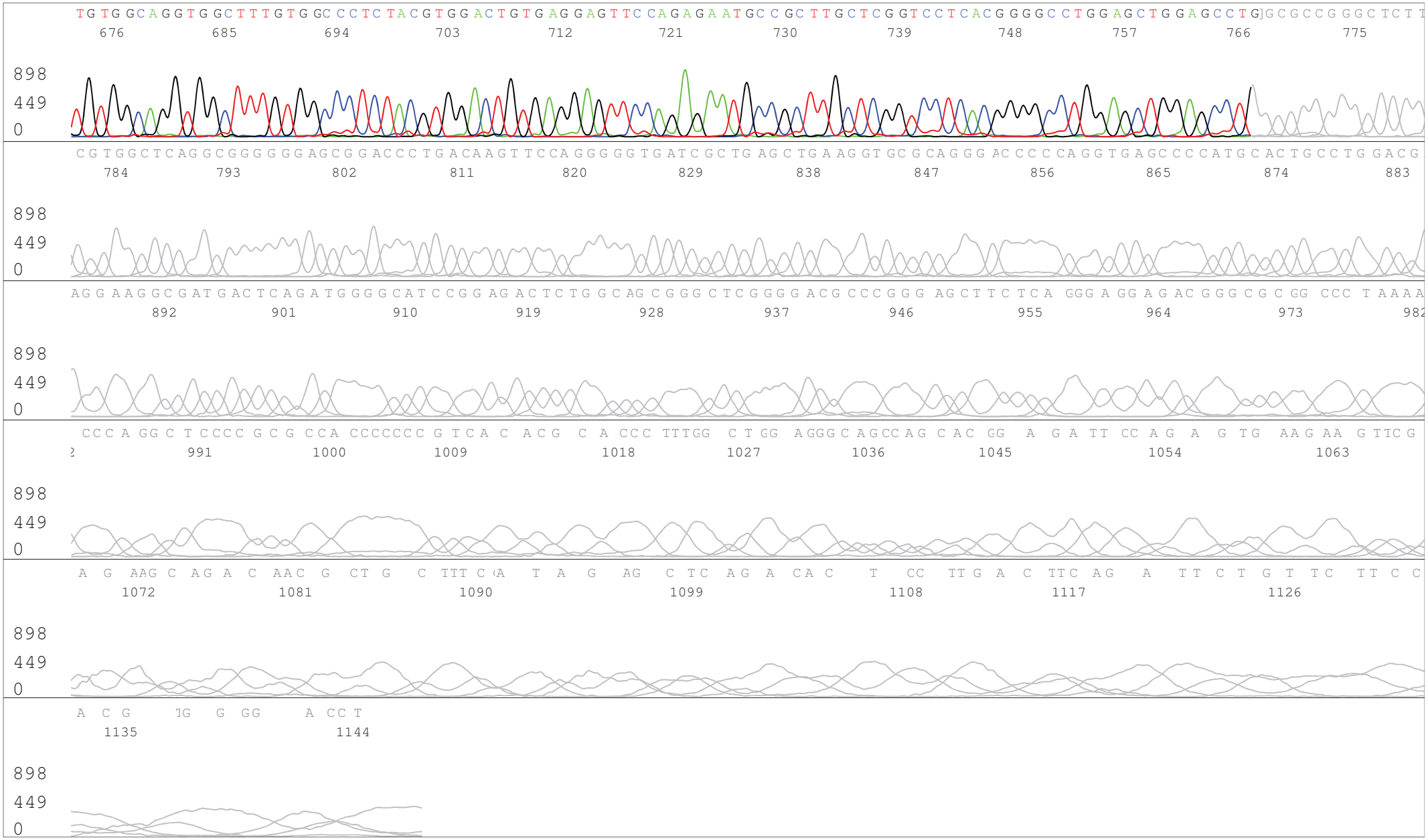
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5' CTCAGTGGATGTTGCCTTTAC 3'

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Pts 1377 to 13057 Pk1 Loc:1354
Version 6.0 HiSQV Bases: 902

Gray line indicates quality value (QV) < 40.

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Oct 31,2023 11:58AM, JST
Oct 31,2023 12:24PM, JST
pacing:11.68 Pts/Panel1350
Plate Name: 20231031_MGE




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892 901 910 919 928 937 946 955 964 973
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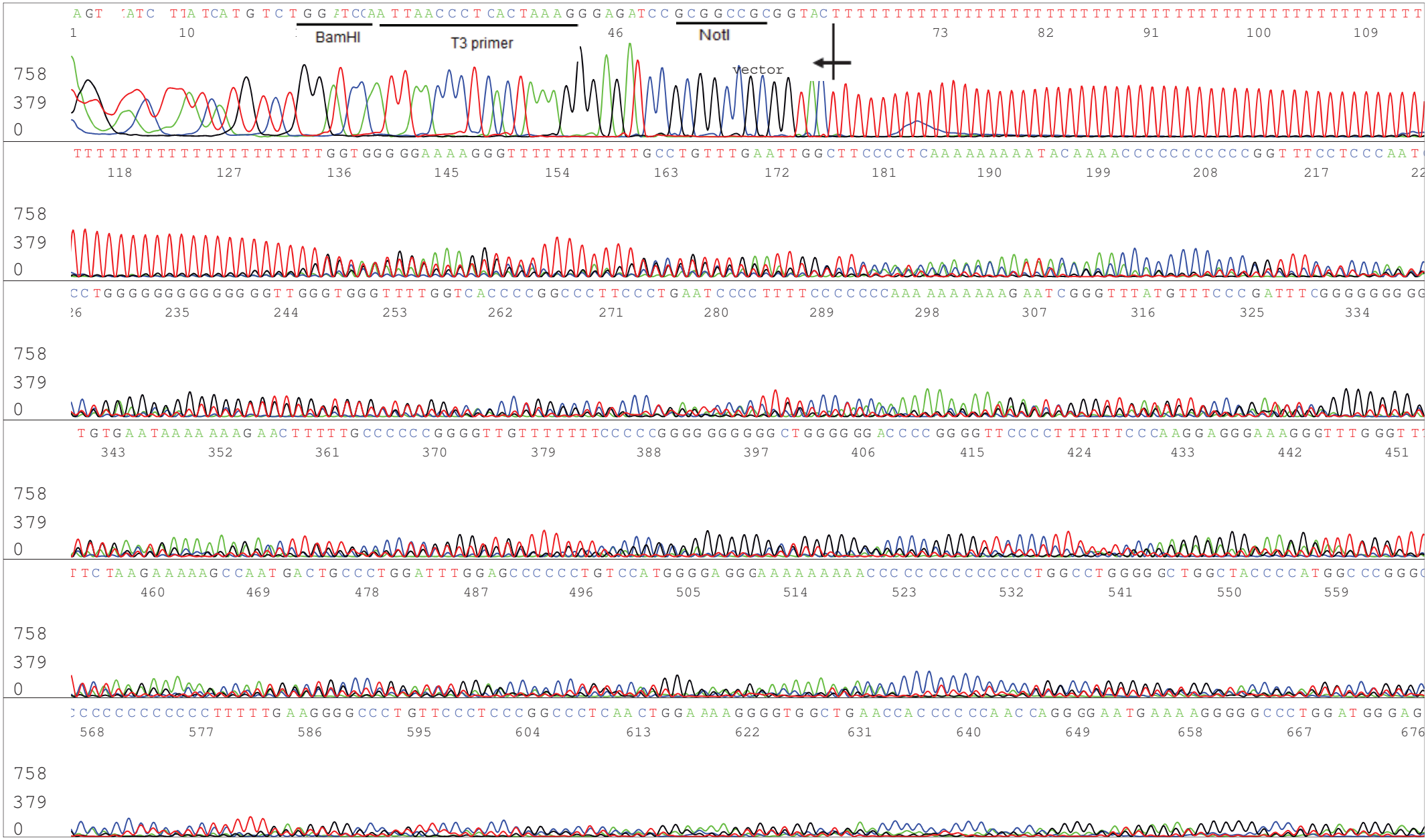
Applied Biosystems

S/N G:101 A:87 T:103 C:119
KB.bcp
KB 1.4.1.8 Cap:20

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1380 to 13190 Pk1 Loc:1357
Version 6.0 HiSQV Bases: 110

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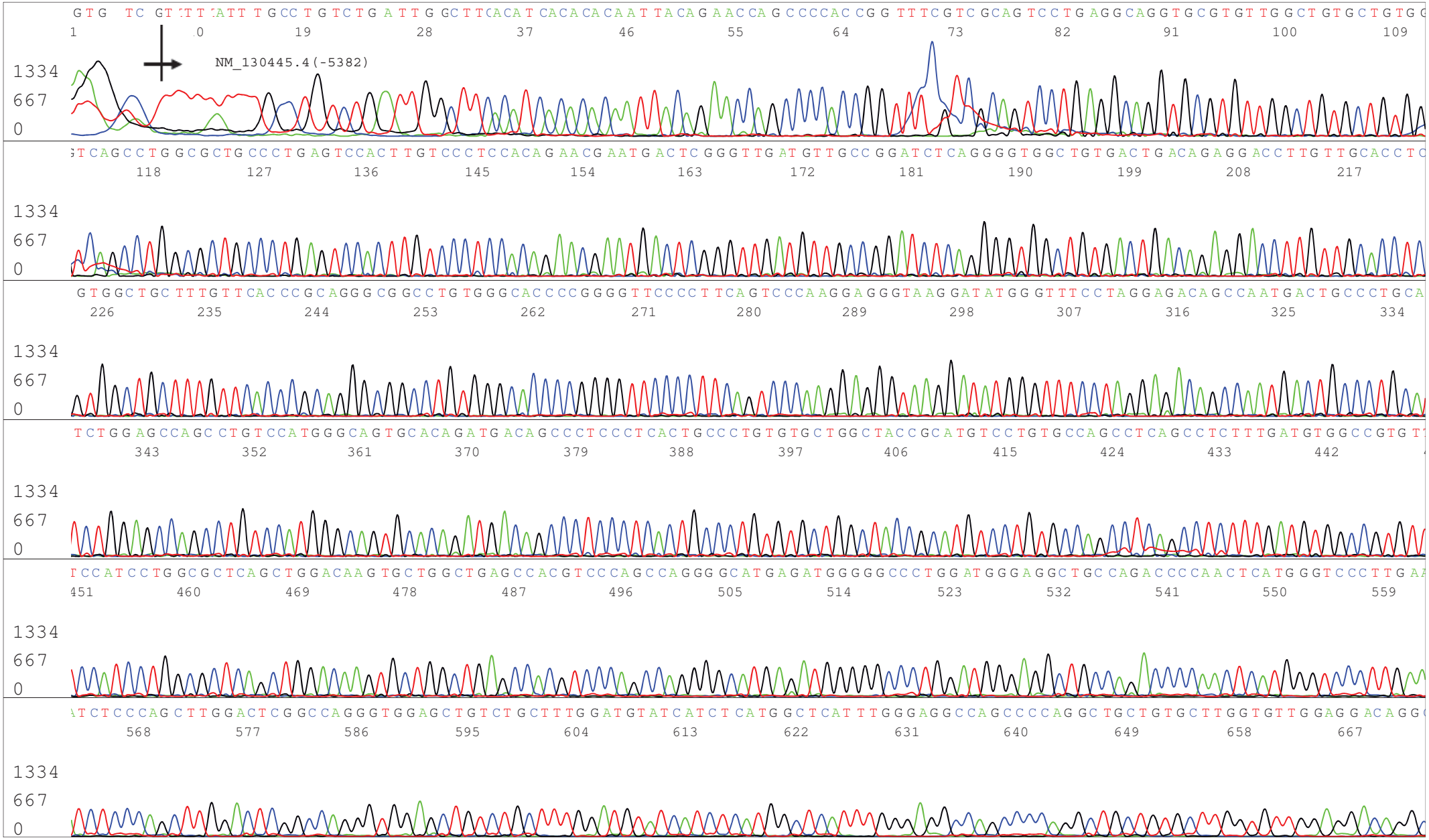
Applied Biosystems

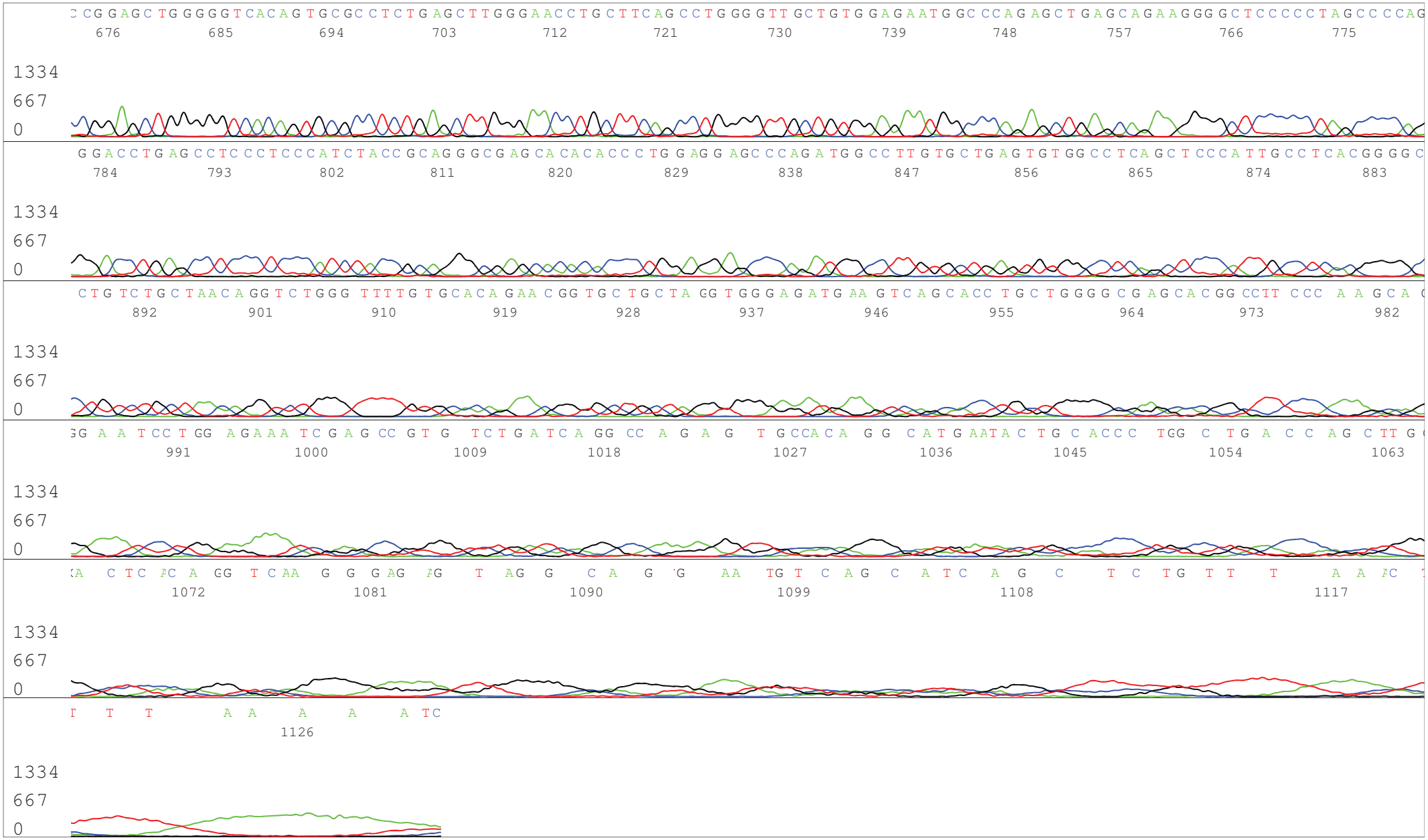
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KB.bcp
KB 1.4.1.8 Cap:23

Primer C : Poly(A) region primer #0
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Pts 1399 to 13248 Pk1 Loc:1376
Version 6.0 HiSQV Bases: 840

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Oct 31,2023 12:24PM, JST
Spacing:11.85 Pts/Panel1350
Plate Name: 20231031_MGE




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676 685 694 703 712 721 730 739 748 757 766 775
1334
667
0
G G A C C T G A G C C T C C C T C C C A T C T A C C G C A G G G C G A G C A C A C A C C C T G G A G G A G C C C A G A T G G C C C T T G T G C T G A G T G T G G C C T C A G C T C C C A T T G C C T C A C G G G G C
784 793 802 811 820 829 838 847 856 865 874 883
1334
667
0
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892 901 910 919 928 937 946 955 964 973 982
1334
667
0
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1334
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