NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS015O19

Lot# : 6608_B3Kk

Vector : pGCAP10

Gene	VAMP7	
RefSeq_mRNA	NM_005638.6	2594 bp

● Plasmid DNA purification

Date : 2023/11/21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/11/22 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/11/22

DNA concentration (O.D.): 231 ng/ul

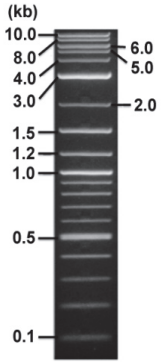
DNA	0.45 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.55 ul
Total	10 ul

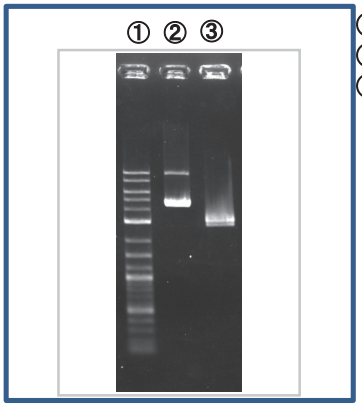
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.8 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 : 2023/12/01

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 : 2023/12/01

DNA (231 ng/ul)	86 ul
10x TE	79 ul
dH_2O	629 ul
Total	795 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '23.12.01 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

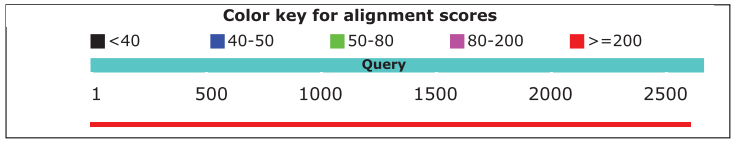
Job title: NM_005638:Homo sapiens vesicle associated...

RID PGDJUBSY114 (Expires on 12-01 14:14 pm)

Query ID	NM_005638.6	**Subject ID**	lcl|Query_83185
Description	Homo sapiens vesicle associated membrane protein 7 (VAMP7), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2594	**Subject Length**	2743
		Program	BLASTN 2.14.1+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



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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	4767	4767	99%	0.0	99.92%	Query_83185

Alignments

Sequence ID: Query_83185 Length: 2743 Number of Matches: 1
Range 1: 100 to 2686

Score	Expect	Identities	Gaps	Strand	Frame
4767 bits(2581)	0.0()	2585/2587(99%)	0/2587(0%)	Plus/Plus	

Features:

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CDS:vesicle-associat 1                                                  M  A
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CDS:vesicle-associat 3    I  L  F  A  V  V  A  R  G  T  T  I  L  A  K  H  A  W  C  G
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Sbjct        220    TTCTTTTGCTGTTGTTGCCAGGGGGACCACTATCCTTGCCAAACATGCTTGGTGTGGAG  279

CDS:vesicle-associat 23   G  N  F  L  E  V  T  E  Q  I  L  A  K  I  P  S  E  N  N  K
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Applied Biosystems

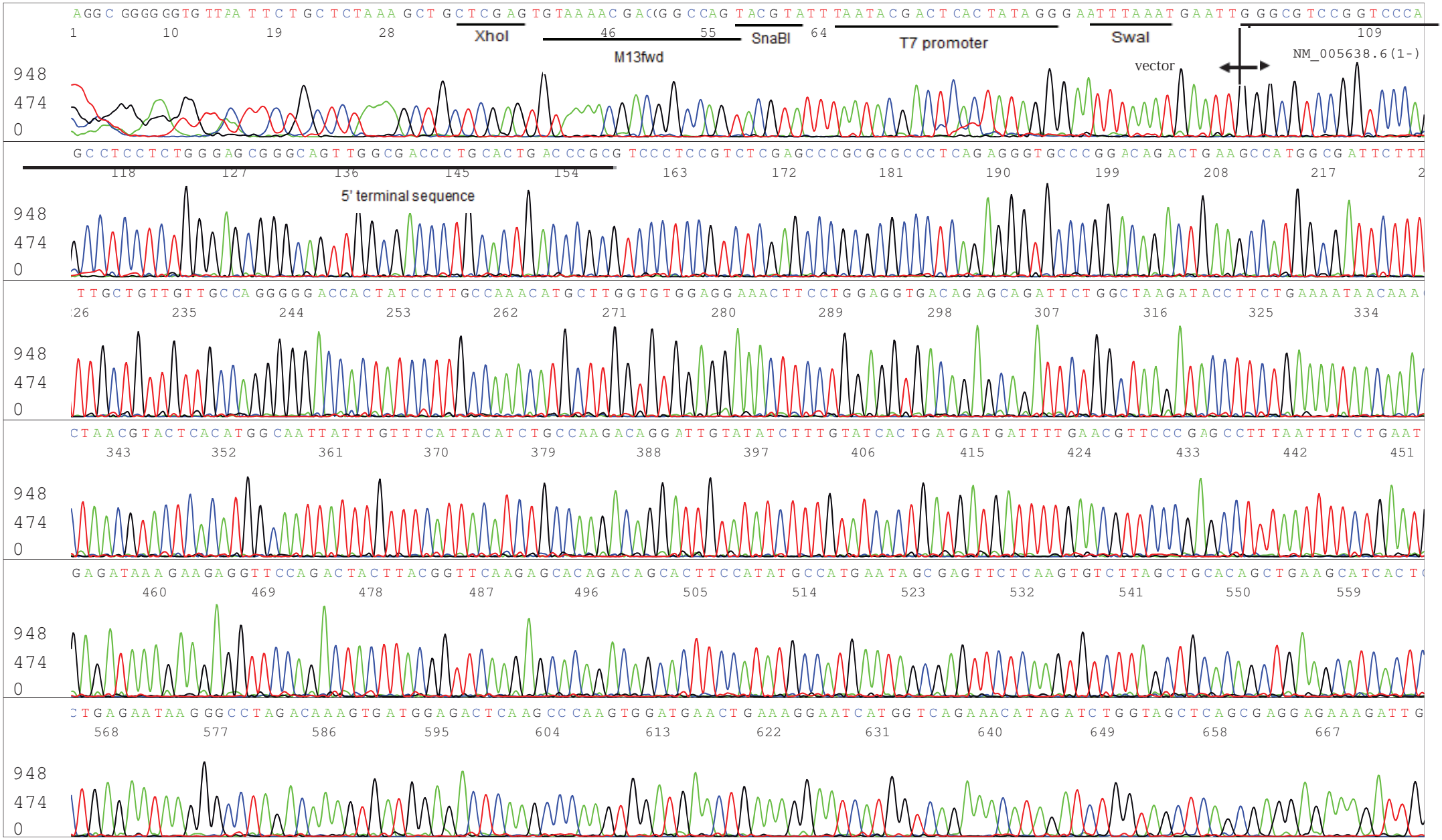
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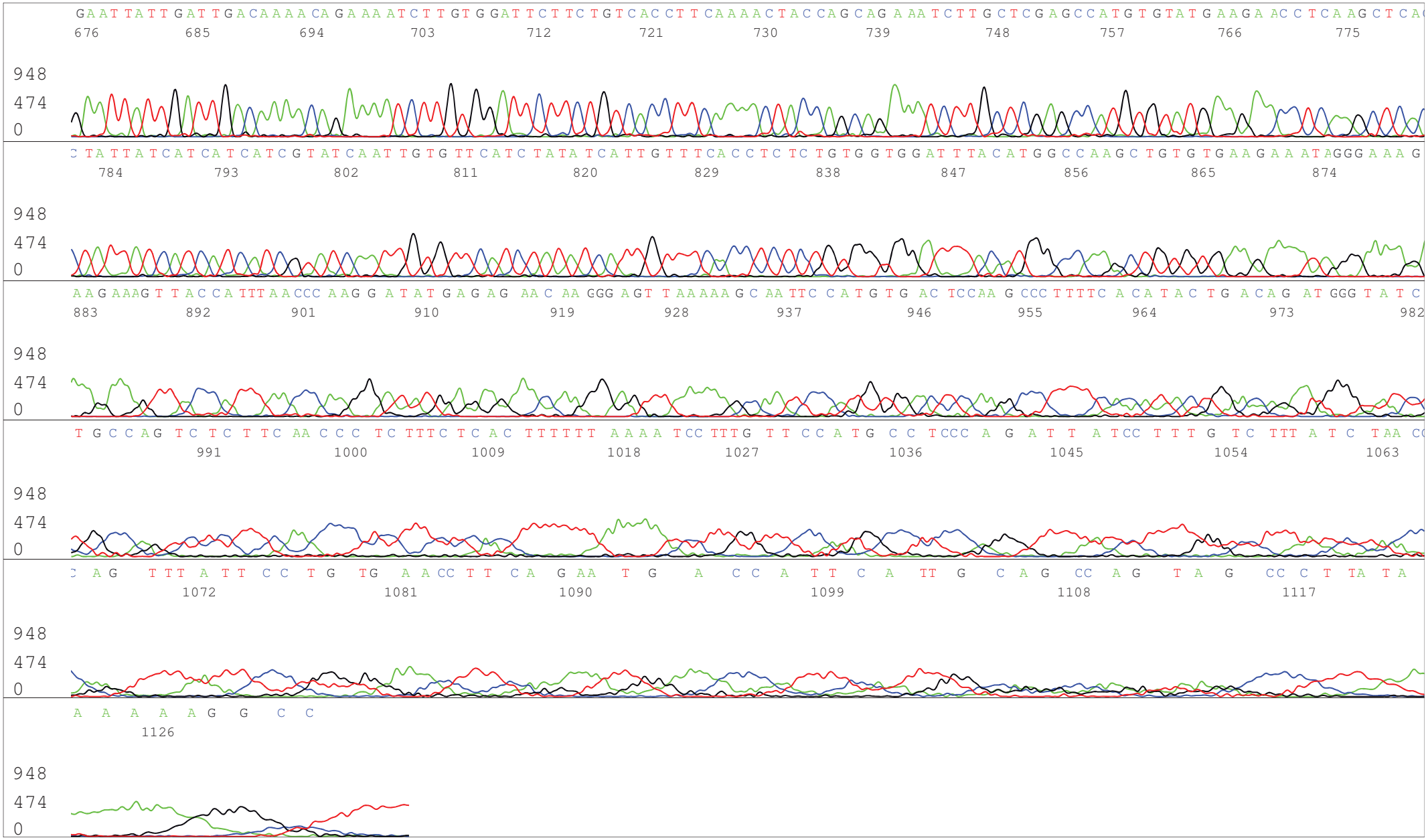
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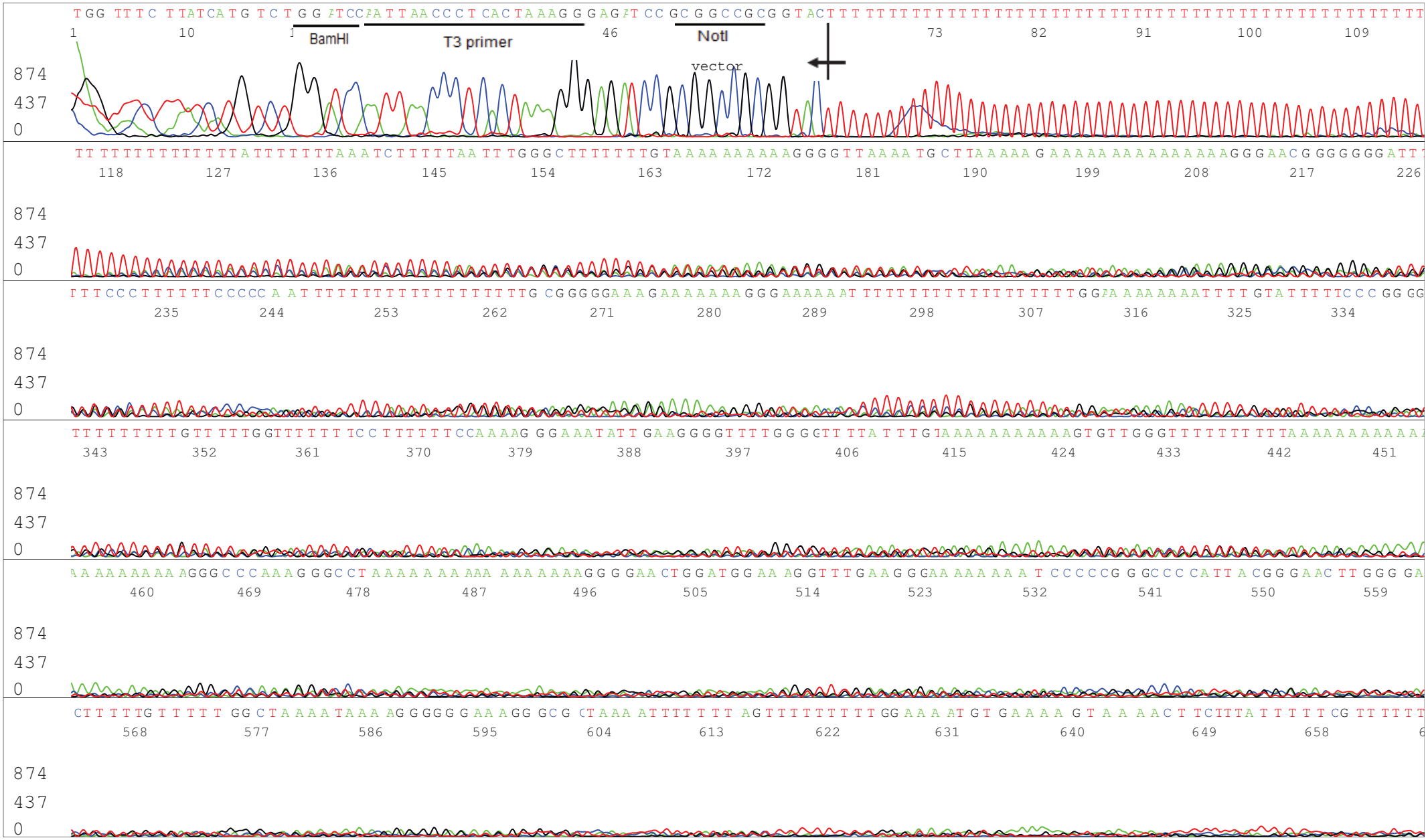
Applied Biosystems

S/N G:12 A:22 T:21 C:16
KB.bcp
KB 1.4.1.8 Cap:4

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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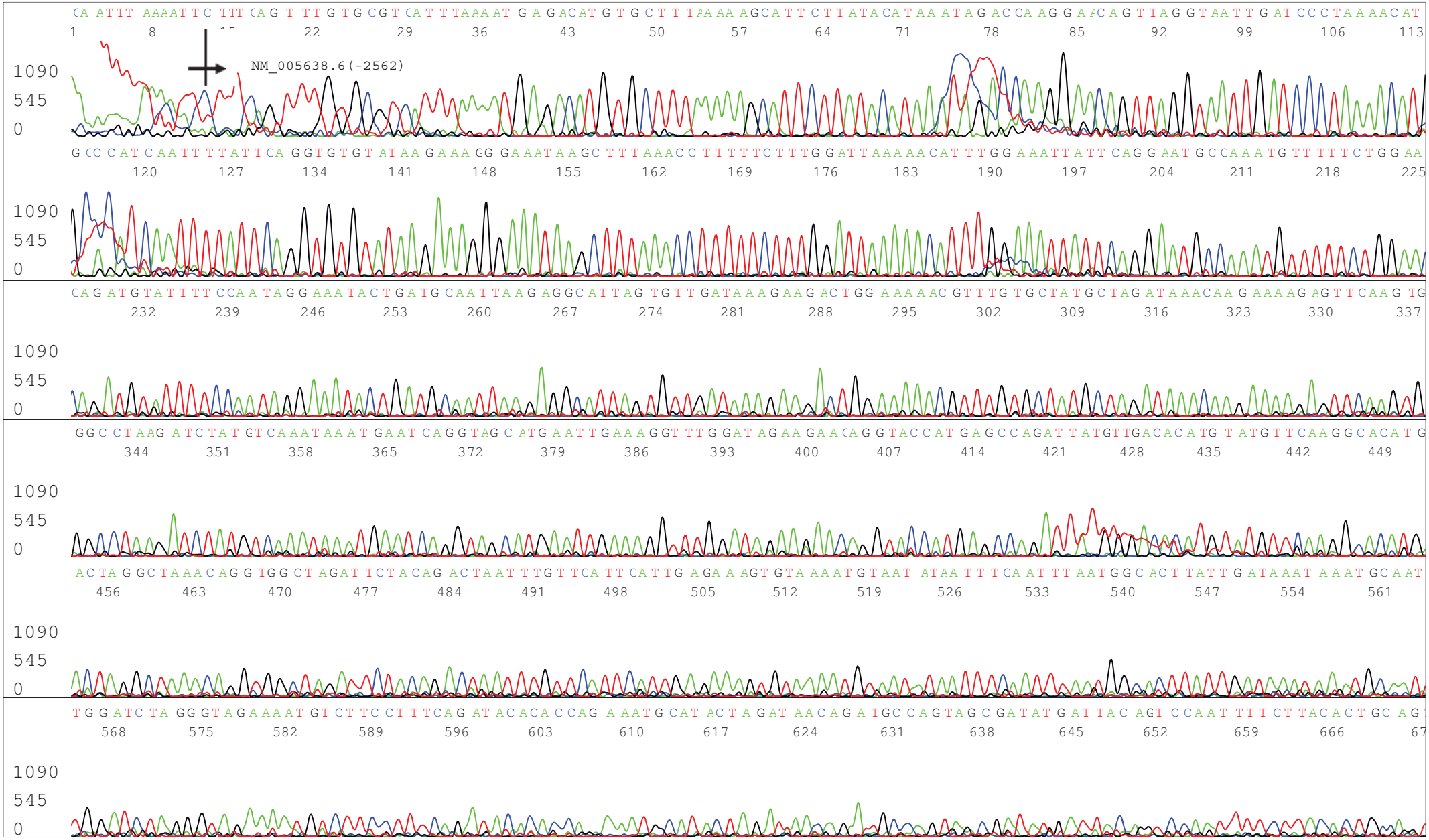
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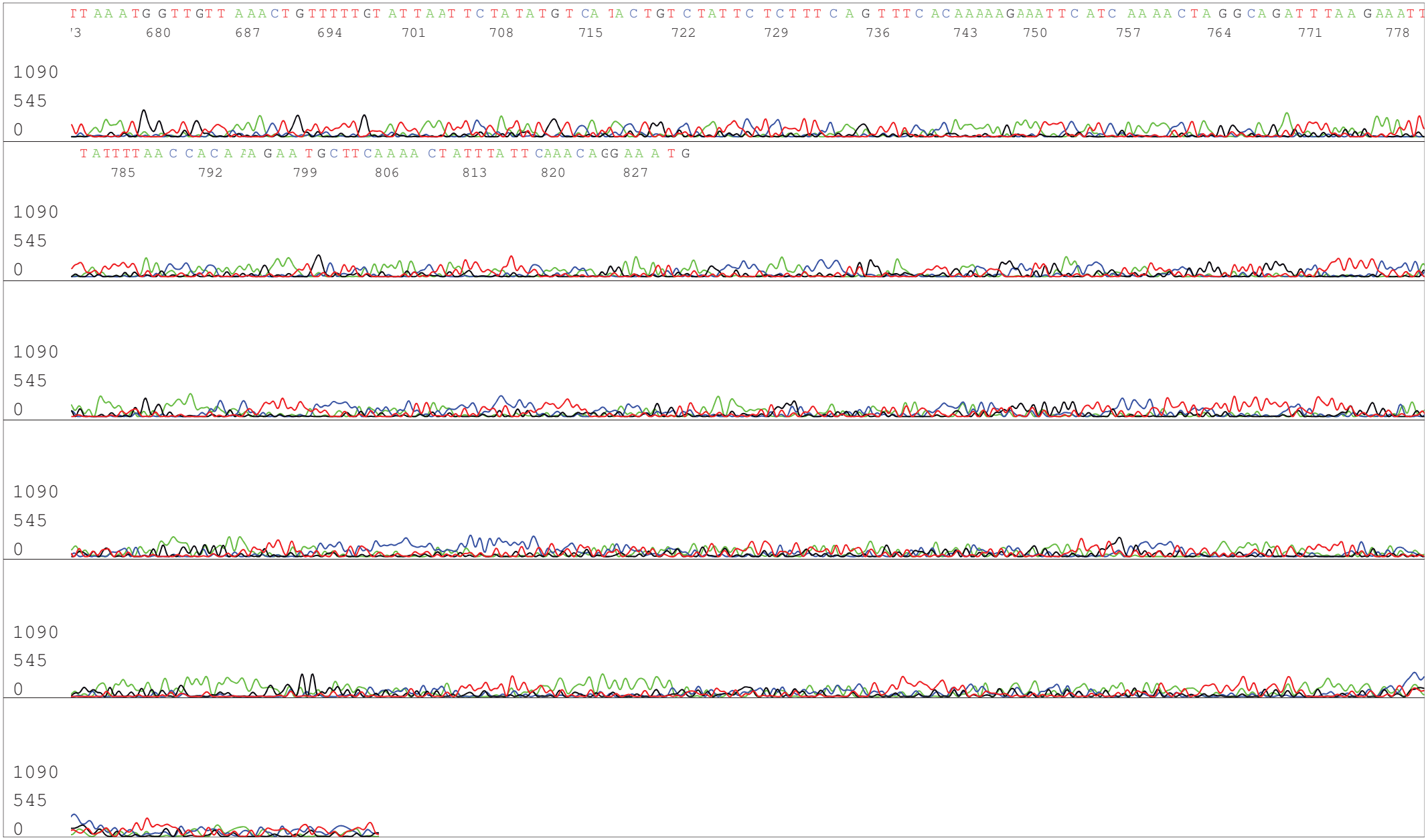
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KB.bcp
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Primer C : Poly(A) region primer #0
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