NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd47D07

Lot# : 7677_B3Ld

Vector : pGCAP10

Gene	EXOSC3	
RefSeq_mRNA	NM_016042.4	1813 bp

● Plasmid DNA purification

Date : 2023/12/13 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/12/14 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/12/14

DNA concentration (O.D.): 73 ng/ul

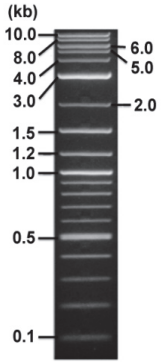
< Size of fragment expected from this clone >

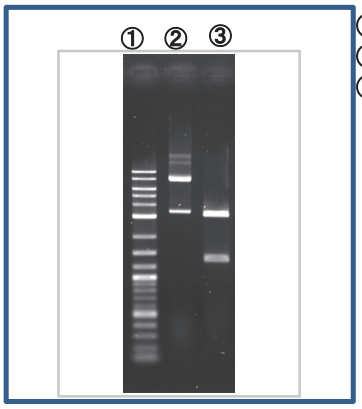
DNA	1.3	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	6.7	ul
Total	10	ul

BamHI 3.1kb (vector), 2.0 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 : 2023/12/20

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 : 2023/12/20

DNA (73 ng/ul)	84	ul
10x TE	25	ul
dH_2O	137	ul
Total	245	ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '23.12.20 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

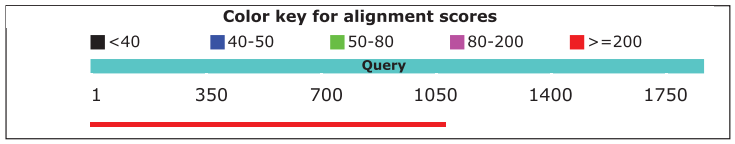
Job title: NM_181503:Homo sapiens exosome component 8...

RID S2FAWD99114 (Expires on 12-20 13:51 pm)

Query ID	NM_016042.4	**Subject ID**	lcl|Query_44123
Description	Homo sapiens exosome component 3 (EXOSC3), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1813	**Subject Length**	1244
		Program	BLASTN 2.14.1+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



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Match to NM_016042.4 (1-1071)
CDS:full/var

Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	1973	1973	59%	0.0	99.91%	Query_44123

Alignments

Sequence ID: Query_44123 Length: 1244 Number of Matches: 1
Range 1: 101 to 1171

Score	Expect	Identities	Gaps	Strand	Frame
1973 bits(1068)	0.0()	1070/1071(99%)	0/1071(0%)	Plus/Plus	

Features:

```
CDS:exosome complex   1                                   M  A  E  P  A  S  V  A  A  E  S  L  A
Query                 1   GGTGTTTGGTGGAGCCCGCGATGGCCGAACCTGCGTCTGTCGCGGCTGAATCTCTCGCGG  60
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 101 GGTGTTTGGTGGAGCCCGCGATGGCCGAACCTGCGTCTGTCGCGGCTGAATCTCTCGCGG  160

CDS:exosome complex   14  G  S  R  A  R  A  A  R  T  V  L  G  Q  V  V  L  P  G  E  E
Query                 61  GCAGCAGGGCGCGCGCTGCACGCACAGTACTAGGTCAGGTGGTGCTCCCGGGTGAGGAGC  120
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 161 GCAGCAGGGCGCGCGCTGCACGCACAGTACTAGGTCAGGTGGTGCTCCCGGGTGAGGAGC  220

CDS:exosome complex   34  L  L  L  P  E  Q  E  D  A  E  G  P  G  G  A  V  E  R  P  L
Query                 121 TGCTCCTGCCGGAACAGGAGGACGCGGAAGGCCCTGGGGGTGCAGTGGAGCGACCGTTGA  180
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 221 TGCTCCTGCCGGAACAGGAGGACGCGGAAGGCCCTGGGGGTGCAGTGGAGCGACCGTTGA  280

CDS:exosome complex   54  S  L  N  A  R  A  C  S  R  V  R  R  V  V  C  G  P  G  L  R  R
Query                 181 GCCTGAATGCTAGAGCGTGCTCGCGGGTGCGCGTTGTATGCGGTCCGGGCCTTCGGCGCT  240
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 281 GCCTGAATGCTAGAGCGTGCTCGCGGGTGCGCGTTGTATGCGGTCCGGGCCTTCGGCGCT  340

CDS:exosome complex   74  C  G  D  R  L  L  V  T  K  C  G  R  L  R  H  K  E  P  G  S
Query                 241 GTGGGGACCGCCTGCTGGTCACCAAGTGCGGCCGCCTCCGTCACAAGGAGCCCGGCAGTG  300
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 341 GTGGGGACCGCCTGCTGGTCACCAAGTGCGGCCGCCTCCGTCACAAGGAGCCCGGCAGTG  400

CDS:exosome complex   94  G  S  G  G  G  V  Y  W  V  D  S  Q  Q  K  R  Y  V  P  V  K
Query                 301 GCAGCGGCGGCGGTGTTTACTGGGTGGACTCTCAGCAGAAGCGGTATGTTCCAGTAAAAG  360
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 401 GCAGCGGCGGCGGTGTTTACTGGGTGGACTCTCAGCAGAAGCGGTATGTTCCAGTAAAAG  460

CDS:exosome complex   114 G  D  H  V  I  G  I  V  T  A  K  S  G  D  I  F  K  V  D  V
Query                 361 GAGACCATGTGATTGGCATAGTGACAGCTAAATCTGGAGATATATTCAAAGTTGATGTTG  420
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Sbjct                 461 GAGACCATGTGATTGGCATAGTGACAGCTAAATCTGGAGATATATTCAAAGTTGATGTTG  520

CDS:exosome complex   134 G  G  S  E  P  A  S  L  S  Y  L  S  F  E  G  A  T  K  R  N
Query                 421 GAGGGAGTGAGCCAGCTTCTTTGTCTTACTTGTCATTTGAAGGTGCAACTAAAAGAAACA  480
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 521 GAGGGAGTGAGCCAGCTTCTTTGTCTTACTTGTCATT[518 G>A]ACTAAAAGAAACA  580

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Sbjct                 581 GACCAAATGTGCAGGTTGGAGATCTCATCTATGGCCAATTTGTGGTTGCTAATAAAGACA  640

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Sbjct                 641 TGGAACCAGAGATGGTCTGTATTGACAGCTGTGGACGAGCCAATGGAATGGGTGTCATTG  700

CDS:exosome complex   194 G  Q  D  G  L  L  F  K  V  T  L  G  L  I  R  K  L  L  A  P
Query                 601 GACAGGATGGTCTGCTTTTTAAAGTGACTCTGGGCTTAATTAGAAAGCTATTAGCTCCAG  660
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Sbjct                 701 GACAGGATGGTCTGCTTTTTAAAGTGACTCTGGGCTTAATTAGAAAGCTATTAGCTCCAG  760

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Sbjct                 761 ATTGTGAAATCATACAGGAAGTGGGAAAACTCTATCCACTGGAGATAGTATTTGGAATGA  820

CDS:exosome complex   234 N  G  R  I  W  V  K  A  K  T  I  Q  Q  T  L  I  L  A  N  I
Query                 721 ATGGAAGAATATGGGTTAAGGCAAAAACCATCCAGCAGACTTTAATTTTGGCAAACATTT  780
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 821 ATGGAAGAATATGGGTTAAGGCAAAAACCATCCAGCAGACTTTAATTTTGGCAAACATTT  880
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Query                 781   TAGAAGCTTGTGAAACACATGACGTCAGATCAAAGAAAACAGATCTTCTCCAGATTGGCAG  840
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 881   TAGAAGCTTGTGAACACATGACGTCAGATCAAAGAAAACAGATCTTCTCCAGATTGGCAG  940

CDS:exosome complex   274   E  S
Query                 841   AAAGTTGATATAGGTGGACTTTTTTACAGGTCAGTTGAGGCAAAAAACTATGGGTTTTTT  900
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 941   AAAGTTGATATAGGTGGACTTTTTTACAGGTCAGTTGAGGCAAAAAACTATGGGTTTTTT  1000

Query                 901   CAGGTGAACCTCCCCCATTTAAATACTCAGAAGATAAGGTGTGAATGTATGTATTATTAG  960
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Sbjct                 1121  CATTGCAAAATCATTTTTTTTTGTTCGGTACAATAAAGTTTACTAAAAAACA  1171
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Applied Biosystems

S/N G:91 A:101 T:72 C:92
KB.bcp
KB 1.4.1.8 Cap:1

Primer A : pGCAP-F
5' CTCAGTGGATGTTGCCTTTAC 3'

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Pts 1271 to 13695 Pk1 Loc:1248
Version 6.0 HiSQV Bases: 975

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Dec 14,2023 03:50PM, JST
Spacing:12.08 Pts/Panel1350
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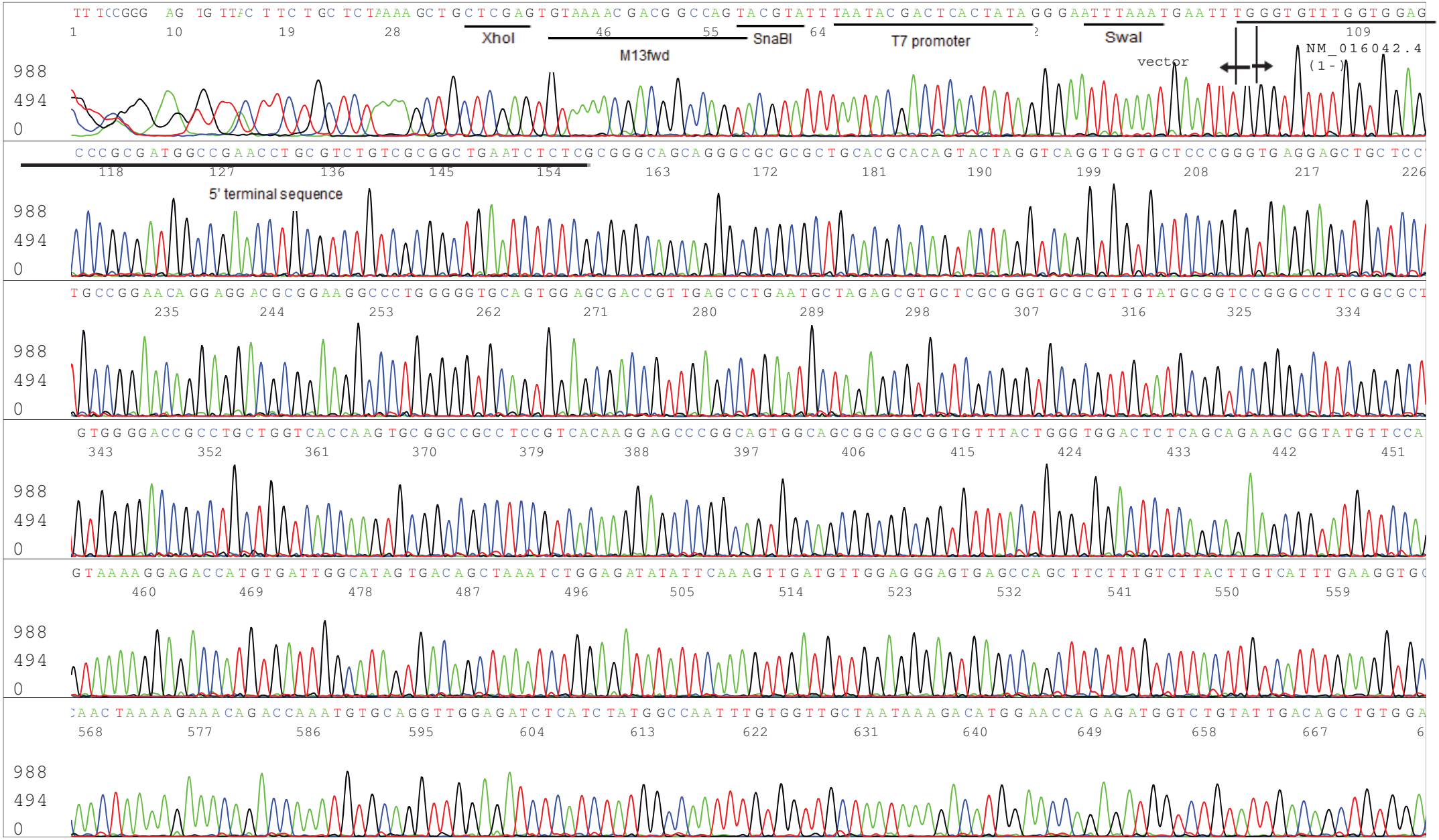

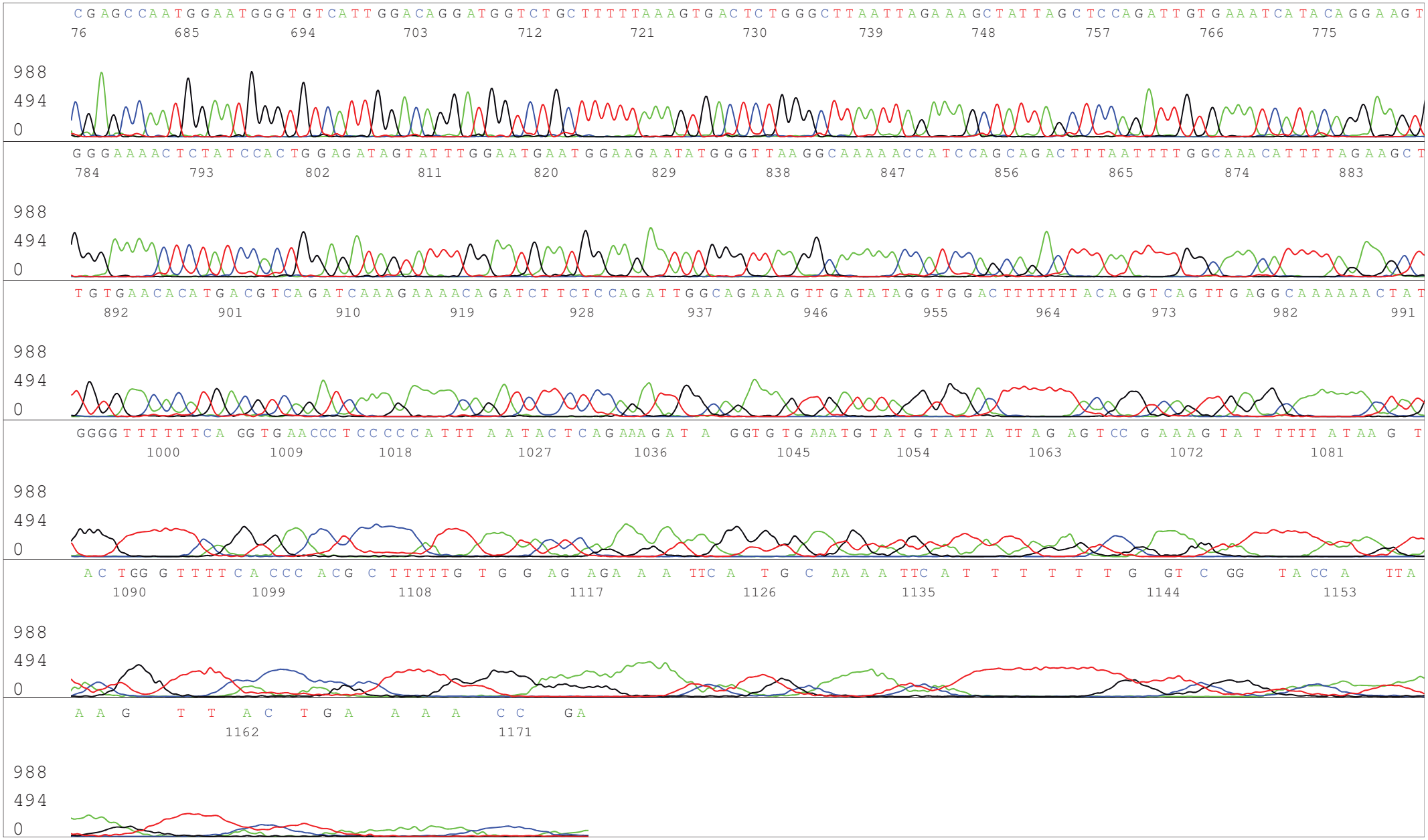
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988
494
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988
494
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494
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988
494
0
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1162 1171
988
494
0

Applied Biosystems

S/N G:16 A:26 T:25 C:20
KB.bcp
KB 1.4.1.8 Cap:2

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1284 to 13000 Pk1 Loc:1261
Version 6.0 HiSQV Bases: 118

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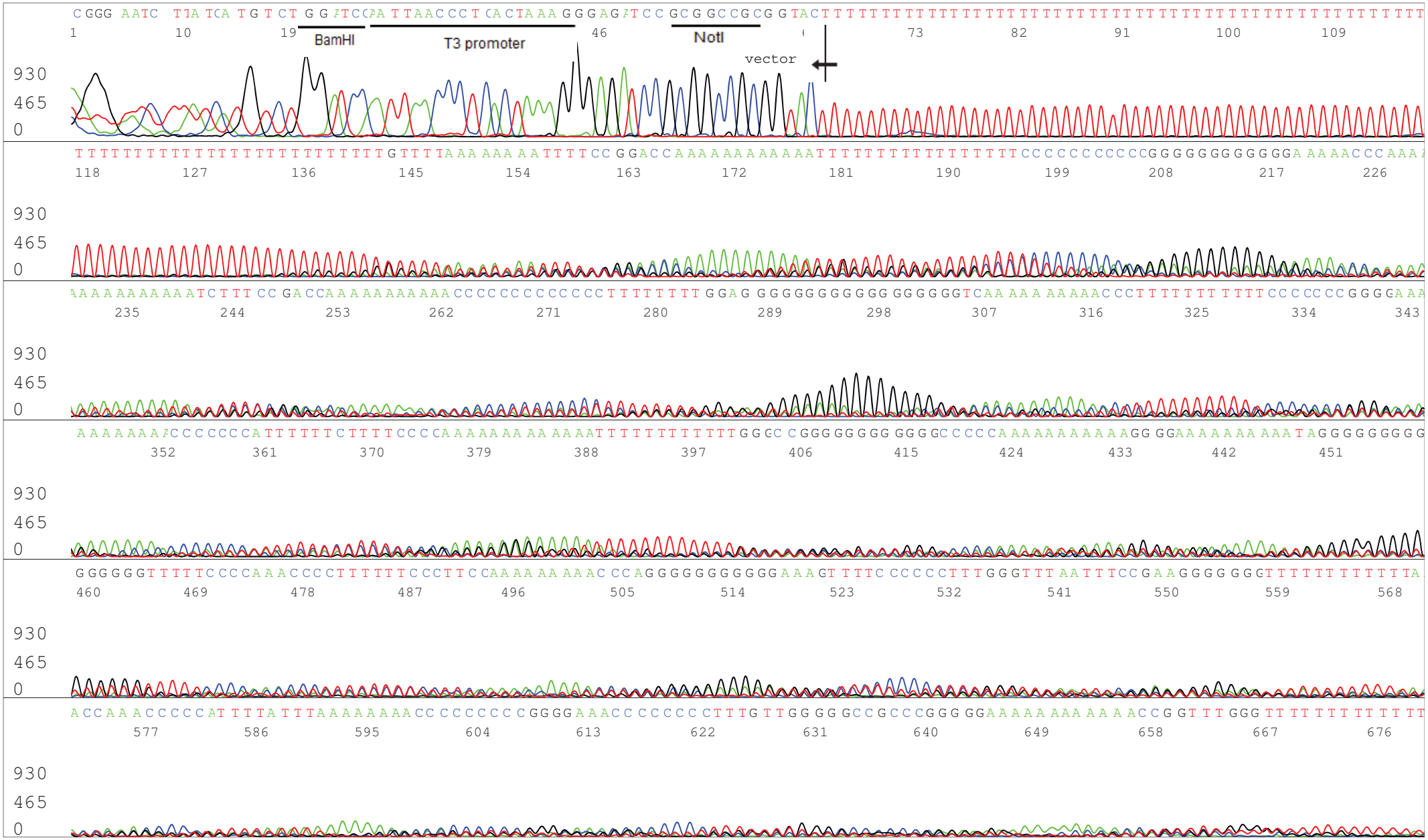

Applied Biosystems

S/N G:8 A:12 T:9 C:11
KB.bcp
KB 1.4.1.8 Cap:3

Primer C : Poly(A) region primer #0
5' TTTTTTTTTTTTTTTTTTTTTVNN 3'

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Version 6.0 HiSQV Bases: 757

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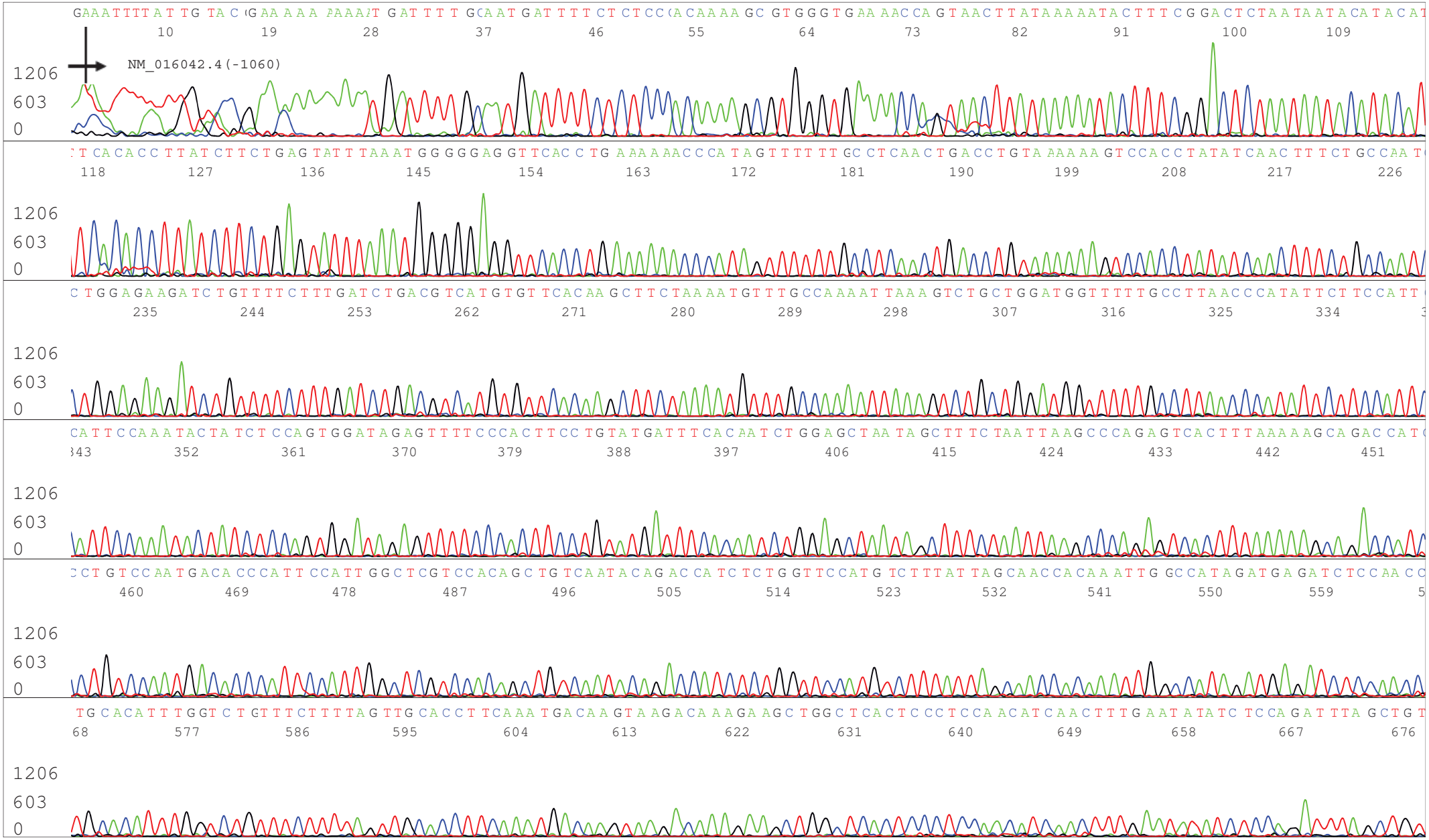

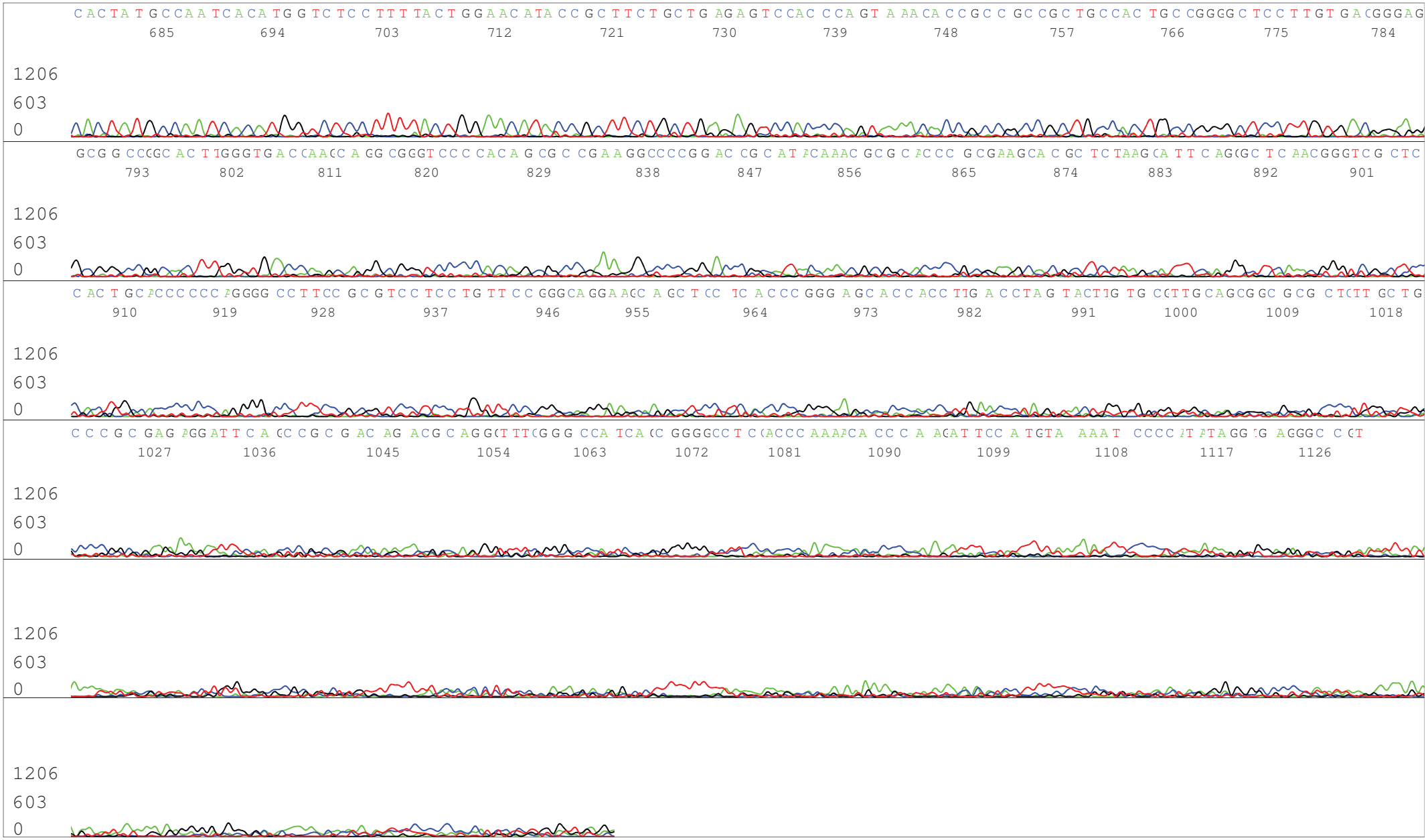
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910 919 928 937 946 955 964 973 982 991 1000 1009 1018
1027 1036 1045 1054 1063 1072 1081 1090 1099 1108 1117 1126
1206
603
0