NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS132H14

Lot# : 6608_B4Dj

Vector : pGCAP10

Gene	IMMT	
RefSeq_mRNA	NM_001100170.2	2656 bp

● Plasmid DNA purification

Date : 2024/04/23 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/04/24 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/04/24

DNA concentration (O.D.): 364 ng/ul

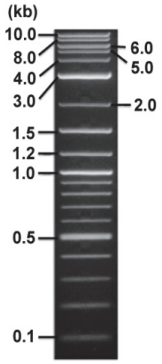
DNA	0.3 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

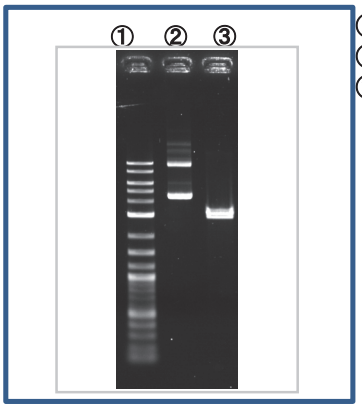
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.9 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 : 2024/05/07

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 : 2024/05/08

DNA (364 ng/ul)	84 ul
10x TE	122 ul
dH_2O	1,017 ul
Total	1,223 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.05.08 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001100170:Homo sapiens inner membrane mitochondrial...

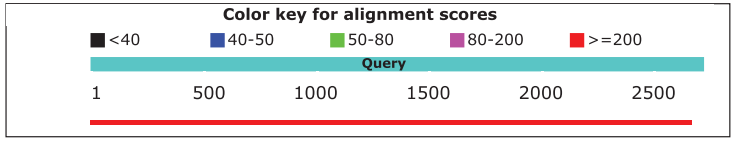
RID 3JZCVWG6114 (Expires on 05-08 09:02 am)

Query ID	NM_001100170.2	**Subject ID**	lcl|Query_6141471
Description	Homo sapiens inner membrane mitochondrial protein (IMMT), transcript variant 3, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2656	**Subject Length**	2677
		Program	BLASTN 2.15.0+

RBdS132H14hts.seq

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	4900	4900	100%	0.0	99.96%	Query_6141471

Alignments

Sequence ID: Query_6141471 Length: 2677 Number of Matches: 1
Range 1: 2 to 2657

Score	Expect	Identities	Gaps	Strand	Frame
4900 bits(2653)	0.0()	2655/2656(99%)	0/2656(0%)	Plus/Plus	

Features:

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Query              1    ACACACGCAAGCACGCCTCCACTTAACTCGCGCCGCCGCGGCAGCTCGAGTCCACCAGCA  60
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               2    ACACACGCAAGCACGCCTCCACTTAACTCGCGCCGCCGCGGCAGCTCGAGTCCACCAGCA  61

CDS:MICOS complex su 1                        M  L  R  A  C  Q  L  S  G  V  T  A  A
Query              61   GCGCCGTCCGCTTGACCGAGATGCTGCGGGCCTGTCAGTTATCGGGTGTGACCGCCGCCG  120
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              62   GCGCCGTCCGCTTGACCGAGATGCTGCGGGCCTGTCAGTTATCGGGTGTGACCGCCGCCG  121

CDS:MICOS complex su 14   A  Q  S  C  L  C  G  K  F  V  L  R  P  L  R  P  C  R  R  Y
Query             121   CCCAGAGTTGTCTCTGTGGGAAGTTTGTCCTCCGTCCATTGCGACCATGCCGCAGATACT  180
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              122   CCCAGAGTTGTCTCTGTGGGAAGTTTGTCCTCCGTCCATTGCGACCATGCCGCAGATACT  181

CDS:MICOS complex su 34   S  T  S  G  S  S  G  L  T  T  G  K  I  A  G  A  G  L  L  F
Query             181   CTACTTCAGGCAGCTCTGGGTTGACTACTGGCAAAATTGCTGGAGCTGGCCTTTTGTTTG  240
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Sbjct              182   CTACTTCAGGCAGCTCTGGGTTGACTACTGGCAAAATTGCTGGAGCTGGCCTTTTGTTTG  241

CDS:MICOS complex su 54   V  G  G  I  G  G  T  I  L  Y  A  K  W  D  S  H  F  R  E
Query             241   TTGGTGGAGGTATTGGTGGCACTATCCTATATGCCAAATGGGATTCCCATTTCCGGGAAA  300
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              242   TTGGTGGAGGTATTGGTGGCACTATCCTATATGCCAAATGGGATTCCCATTTCCGGGAAA  301

CDS:MICOS complex su 74   S  V  E  K  T  I  P  Y  S  D  K  L  F  E  M  V  L  G  P  A
Query             301   GTGTAGAGAAAACCATACCTTACTCAGACAAACTCTTCGAGATGGTTCTTGGTCCTGCAG  360
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              302   GTGTAGAGAAAACCATACCTTACTCAGACAAACTCTTCGAGATGGTTCTTGGTCCTGCAG  361

CDS:MICOS complex su 94   A  Y  N  V  P  L  P  K  K  S  I  Q  S  G  P  L  K  I  S  S
Query             361   CTTATAATGTTCCATTGCCAAAGAAATCG                                 420
                        ||||||||||||||||||||||||||||
Sbjct              362   CTTATAATGTTCCATTGCCAAAGAAATCG                                 389

CDS:MICOS complex su 114  V  S  E  V  M  K  E  S  K  Q  P  A  S  Q  L  Q  K  Q  K  G
Query             421   TATCAGAAGTAATGAAAGAATCTAAACAGCCTGCCTCACAACTCCAAAAACAAAAGGGAG  480
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              422   TATCAGAAGTAATGAAAGAATCTAAACAGTCTGCCTCACAACTCCAAAAACAAAAGGGAG  481

CDS:MICOS complex su 134  D  T  P  A  S  A  T  A  G  D  T  L  S  V  P  A  P  A  V  Q
Query             481   ATACTCCAGCTTCAGCAACAGCAGGTGATACCCTGTCGGTCCCAGCCCCTGCAGTTCAGC  540
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              482   ATACTCCAGCTTCAGCAACAGCAGGTGATACCCTGTCGGTCCCAGCCCCTGCAGTTCAGC  541

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Query             541   CTGAGGAATCTTTAAAAACTGATCACCCTGAAATTGGTGAAGGAAAACCCACACCTGCAC  600
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              542   CTGAGGAATCTTTAAAAACTGATCACCCTGAAATTGGTGAAGGAAAACCCACACCTGCAC  601

CDS:MICOS complex su 174  L  S  E  E  A  S  S  S  S  I  R  E  R  P  P  E  E  V  A  A
Query             601   TTTCAGAAGAAGCATCCTCATCTTCTATAAGGGAGCGACCACCTGAAGAAGTTGCAGCTC  660
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Sbjct              602   TTTCAGAAGAAGCATCCTCATCTTCTATAAGGGAGCGACCACCTGAAGAAGTTGCAGCTC  661

CDS:MICOS complex su 194  R  L  A  Q  Q  E  K  Q  E  Q  V  K  I  E  S  L  A  K  S  L
Query             661   GCCTTGCACAACAGGAAAAACAAGAACAAGTTAAAATTGAGTCTCTAGCCAAGAGCTTAG  720
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Sbjct              662   GCCTTGCACAACAGGAAAAACAAGAACAAGTTAAAATTGAGTCTCTAGCCAAGAGCTTAG  721

CDS:MICOS complex su 214  E  D  A  L  R  Q  T  A  S  V  T  L  Q  A  I  A  A  Q  N  A
Query             721   AAGATGCTCTGAGGCAAACTGCAAGTGTCACTCTGCAGGCTATTGCAGCTCAGAATGCTG  780
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct              722   AAGATGCTCTGAGGCAAACTGCAAGTGTCACTCTGCAGGCTATTGCAGCTCAGAATGCTG  781
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450 C>T (P124S)

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CDS:MICOS complex su  234   A V Q A V N A H S N I L K A A M D N S E
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                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 782   CGGTCCAGGCTGTCAATGCACACTCCAACATATTGAAAGCCGCCATGGACAATTCTGAGA  841

CDS:MICOS complex su  254   I A G E K K S A Q W R T V E G A L K E R
Query                 841   TTGCAGGCGAGAAGAAATCTGCTCAGTGGCGCACAGTGGAGGGTGCATTGAAGGAACGCA  900
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Sbjct                 842   TTGCAGGCGAGAAGAAATCTGCTCAGTGGCGCACAGTGGAGGGTGCATTGAAGGAACGCA  901

CDS:MICOS complex su  274   R K A V D E A A D A L L K A K E E L E K
Query                 901   GAAAGGCAGTAGATGAAGCTGCCGATGCCCTTCTCaaagccaaagaagagttagagaaga  960
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 902   GAAAGGCAGTAGATGAAGCTGCCGATGCCCTTCTCAAAGCCAAAGAAGAGTTAGAGAAGA  961

CDS:MICOS complex su  294   M K S V I E N A K K K E V A G A K P H I
Query                 961   tgaaaagtgtgattgaaaatgcaaagaaaaaaagaGGTTGCTGGGGCCAAGCCTCATATAA  1020
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Sbjct                 962   TGAAAAGTGTGATTGAAAATGCAAAGAAAAAAGAGGTTGCTGGGGCCAAGCCTCATATAA  1021

CDS:MICOS complex su  314   T A A E G K L H N M I V D L D N V V K K
Query                 1021  CTGCTGCAGAGGGTAAACTTCACAACATGATAGTTGATCTGGATAATGTGGTCAAAAAGG  1080
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CDS:MICOS complex su  354   A R D D F K R E L D S I T P E V L P G W
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Sbjct                 1142  CTCGGGATGACTTTAAACGAGAGCTGGACAGTATTACTCCAGAAGTCCTTCCTGGGTGGA  1201

CDS:MICOS complex su  374   K G M S V S D L A D K L S T D D L N S L
Query                 1201  AAGGAATGAGTGTTTCAGACTTAGCTGACAAGCTCTCTACTGATGATCTGAACTCCCTCA  1260
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Sbjct                 1202  AAGGAATGAGTGTTTCAGACTTAGCTGACAAGCTCTCTACTGATGATCTGAACTCCCTCA  1261

CDS:MICOS complex su  394   I A H A H R R I D Q L N R E L A E Q K A
Query                 1261  TTGCTCATGCACATCGTCGTATTGATCAGCTGAACAGAGAGCTGGCAGAACAGAAGGCCA  1320
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Sbjct                 1262  TTGCTCATGCACATCGTCGTATTGATCAGCTGAACAGAGAGCTGGCAGAACAGAAGGCCA  1321

CDS:MICOS complex su  414   T E K Q H I T L A L E K Q K L E E K R A
Query                 1321  CCGAAAAGCAGCACATCACGTTAGCCTTGGAGAAACAAAAGCTGGAAGAAAAGCGGGCAT  1380
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Sbjct                 1322  CCGAAAAGCAGCACATCACGTTAGCCTTGGAGAAACAAAAGCTGGAAGAAAAGCGGGCAT  1381

CDS:MICOS complex su  434   F D S A V A K A L E H H R S E I Q A E Q
Query                 1381  TTGACTCTGCAGTAGCAAAAGCATTAGAACATCACAGAAGTGAAATACAGGCTGAACAGG  1440
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CDS:MICOS complex su  454   D R K I E E V R D A M E N E M R T Q L R
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Sbjct                 1442  ACAGAAAGATAGAAGAAGTCAGAGATGCCATGGAAAATGAAATGAGAACCCAGCTTCGCC  1501

CDS:MICOS complex su  474   R Q A A A H T D H L R D V L R V Q E Q E
Query                 1501  GACAGGCAGCTGCCCACACTGATCACTTGCGAGATGTCCTTAGGGTACAAGAACAGGAAT  1560
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Sbjct                 1502  GACAGGCAGCTGCCCACACTGATCACTTGCGAGATGTCCTTAGGGTACAAGAACAGGAAT  1561

CDS:MICOS complex su  494   L K S E F E Q N L S E K L S E Q E L Q F
Query                 1561  TGAAGTCTGAATTTGAGCAGAACCTGTCTGAGAAACTCTCTGAACAAGAATTACAATTTC  1620
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CDS:MICOS complex su  514   R R L S Q E Q V D N F T L D I N T A Y A
Query                 1621  GTCGTCTCAGTCAAGAGCAAGTTGACAACTTTACTCTGGATATAAATACTGCCTATGCCA  1680
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CDS:MICOS complex su  534   R L R G I E Q A V Q S H A V A E E E A R
Query                 1681  GACTCAGAGGAATCGAACAGGCTGTTCAGAGCCATGCAGTTGCTGAAGAGGAAGCCAGAA  1740
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Sbjct                 1682  GACTCAGAGGAATCGAACAGGCTGTTCAGAGCCATGCAGTTGCTGAAGAGGAAGCCAGAA  1741

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Sbjct                 1742  AAGCCCACCAACTCTGGCTTTCAGTGGAGGCATTAAAGTACAGCATGAAGACCTCATCTG  1801

CDS:MICOS complex su  574   A E T P T I P L G S A V E A I K A N C S
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Sbjct                 1802  CAGAAACACCTACTATCCCGCTGGGTAGTGCAGTTGAGGCCATCAAAGCCAACTGTTCTG  1861

CDS:MICOS complex su  594   D N E F T Q A L T A A I P P E S L T R G
Query                 1861  ATAATGAATTCACCCAAGCTTTAACCGCAGCTATCCCTCCAGAGTCCCTGACCCGTGGGG  1920
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Sbjct                 1862  ATAATGAATTCACCCAAGCTTTAACCGCAGCTATCCCTCCAGAGTCCCTGACCCGTGGGG  1921

CDS:MICOS complex su  614   V Y S E E T L R A R F Y A V Q K L A R R
Query                 1921  TGTACAGTGAAGAGACCCTTAGAGCCCGTTTCTATGCTGTTCAAAAACTGGCCCGAAGGG  1980
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Sbjct                 1922  TGTACAGTGAAGAGACCCTTAGAGCCCGTTTCTATGCTGTTCAAAAACTGGCCCGAAGGG  1981

CDS:MICOS complex su  634   V A M I D E T R N S L Y Q Y F L S Y L Q
Query                 1981  TAGCAATGATTGATGAAACCAGAAATAGCTTGTACCAGTACTTCCTCTCCTACCTACAGT  2040
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Sbjct                 1982  TAGCAATGATTGATGAAACCAGAAATAGCTTGTACCAGTACTTCCTCTCCTACCTACAGT  2041

CDS:MICOS complex su  654   S L L L F P P Q Q L K P P P E L C P E D
Query                 2041  CCCTGCTCCTATTCCCACCTCAGCAACTGAAGCCGCCCCCAGAGCTCTGCCCTGAGGATA  2100
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Sbjct                 2042  CCCTGCTCCTATTCCCACCTCAGCAACTGAAGCCGCCCCCAGAGCTCTGCCCTGAGGATA  2101

CDS:MICOS complex su  674   I N T F K L L S Y A S Y C I E H G D L E
Query                 2101  TAAACACATTTAAATTACTGTCATATGCTTCCTATTGCATTGAGCATGGTGATCTGGAGC  2160
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CDS:MICOS complex su  694   L A A K F V N Q L K G E S R R V A Q D W
Query                 2161  TAGCAGCAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAGTGGCACAGGACTGGC  2220
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Sbjct                 2162  TAGCAGCAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAGACGAGTGGCACAGGACTGGC  2221

CDS:MICOS complex su  714   L K E A R M T L E T K Q I V E I L T A Y
Query                 2221  TGAAGGAAGCCCGAATGACCCTAGAAACGAAACAGATAGTGGAAATCCTGACAGCATATG  2280
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2222  TGAAGGAAGCCCGAATGACCCTAGAAACGAAACAGATAGTGGAAATCCTGACAGCATATG  2281

CDS:MICOS complex su  734   A S A V G I G T T Q V Q P E
Query                 2281  CCAGCGCCGTAGGAATAGGAACCACTCAGGTGCAGCCAGAGTGAGGTTTAGGAAGATTTT  2340
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Sbjct                 2462  TGTTGCATTTATATTCTTTCCATTTGCTATCATGTCAGTGAACGCCAGGAGTGCTTTCTT  2521

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                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query                 2641  AGCAACAAGATGAAAA  2656
                            ||||||||||||||||
Sbjct                 2642  AGCAACAAGATGAAAA  2657
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HHS Vulnerability Disclosure

Applied Biosystems

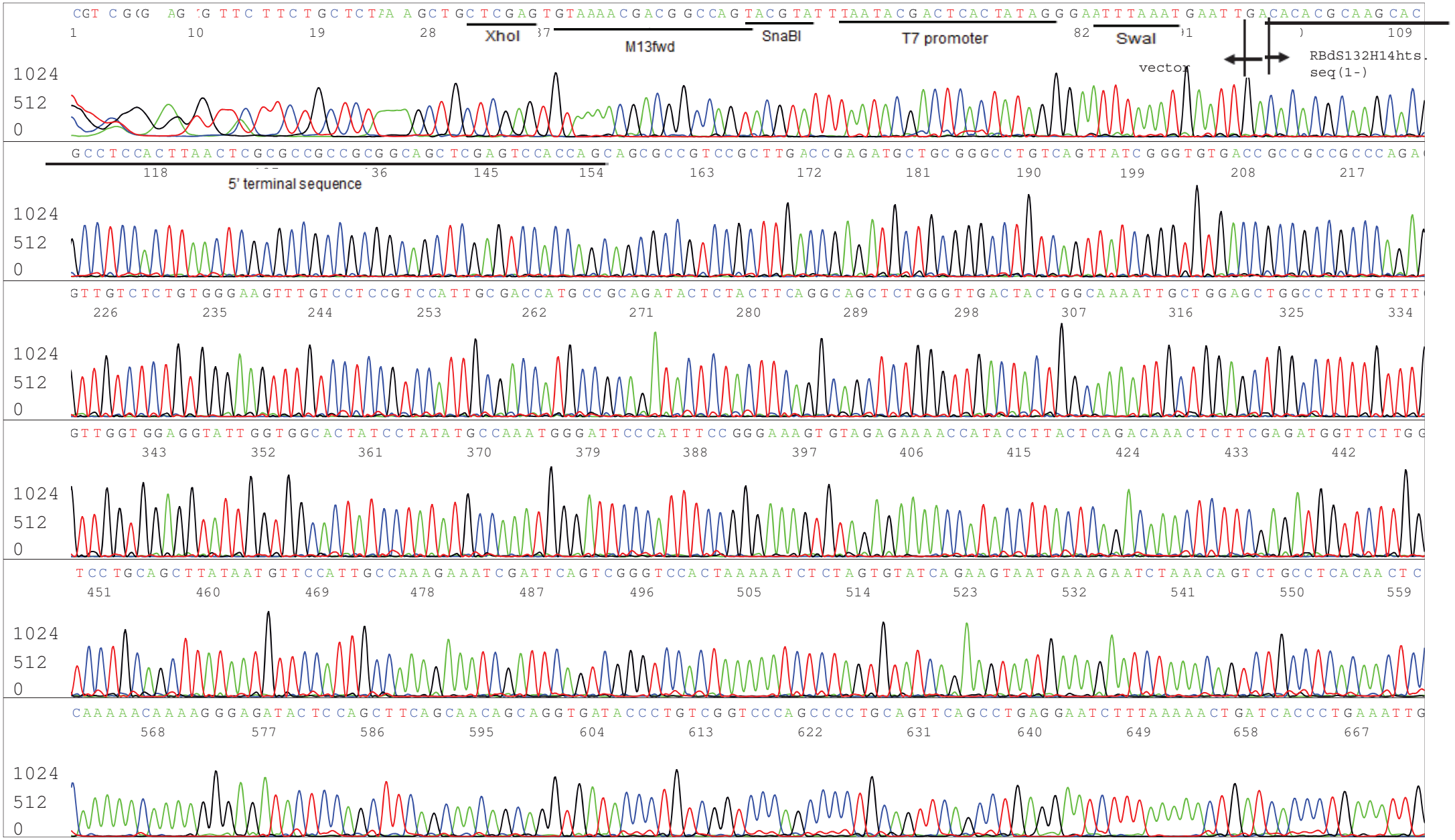
S/N G:390 A:749 T:397 C:604
KB.bcp
KB 1.4.1.8 Cap:1

Primer A : pGCAP-F

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KB_3500_POP7_BDTv3.mob
Pts 1432 to 13672 Pk1 Loc:1409
Version 6.0 HiSQV Bases: 912

Inst Model/Name 3500/3500 Instrument
Apr 24,2024 03:16PM, JST
Apr 24,2024 03:43PM, JST
Spacing:12.17 Pts/Panel1350
Plate Name: 20240424_GNP



Applied Biosystems

S/N G:99 A:147 T:152 C:128
KB.bcp
KB 1.4.1.8 Cap:4

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1417 to 13669 Pk1 Loc:1394
Version 6.0 HiSQV Bases: 136

Inst Model/Name 3500/3500 Instrument
Apr 24,2024 03:16PM, JST
Apr 24,2024 03:43PM, JST
Spacing:12.54 Pts/Panel1350
Plate Name: 20240424_GNP

