NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS154C04

Lot# : 6608_B4F4

Vector : pGCAP10

Gene	TMBIM6	
RefSeq_mRNA	NM_003217.3	2837 bp

● Plasmid DNA purification

Date : 2024/06/04 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/06/05 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/06/05

DNA concentration (O.D.): 357 ng/ul

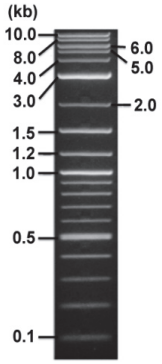
DNA	0.3 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

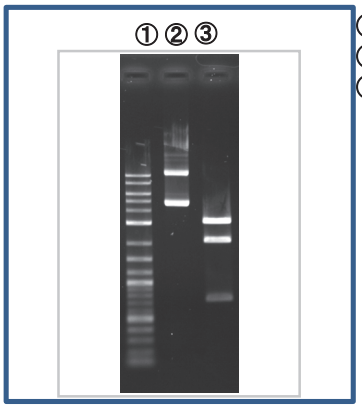
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.1, 0.7 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 : 2024/06/10

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 : 2024/06/11

DNA (357 ng/ul)	84 ul
10x TE	120 ul
dH_2O	996 ul
Total	1,200 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.06.11 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_000117:Homo sapiens emerin (EMD), mRNA

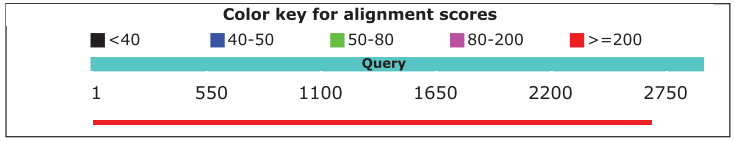
RID 64WA4E03114 (Expires on 06-08 10:32 am)

Query ID	NM_003217.3	**Subject ID**	lcl|Query_3605887
Description	Homo sapiens transmembrane BAX inhibitor motif containing 6 (TMBIM6), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2837	**Subject Length**	2632
		Program	BLASTN 2.15.0+

RBdS154C04hts.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



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'24.06.07
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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	4844	4844	92%	0.0	99.92%	Query_3605887

Alignments

Sequence ID: Query_3605887 Length: 2632 Number of Matches: 1
Range 1: 2 to 2630

Score	Expect	Identities	Gaps	Strand	Frame
4844 bits(2623)	0.0()	2627/2629(99%)	0/2629(0%)	Plus/Plus	

Features:

```
Query          15   GTTAGAAGCGCTGGTAGGCCTTGGAGAGGCGGGGTTAGGAAGAGTGGAGACTGCTGCACGG  74
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           2   GTTAGAAGCGCTGGTAGGCCTTGGAGAGGCGGGGTTAGGAAGAGTGGAGACTGCTGCACGG  61

CDS:bax inhibitor 1  1                M  N  I  F  D  R  K  I  N  F  D  A  L  L  K  F
Query          75   ACTCTGGAACCATGAACATATTTGATCGAAAGATCAACTTTGATGCGCTTTTAAAATTTT  134
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           62   ACTCTGGAACCATGAACATATTTGATCGAAAGATCAACTTTGATGCGCTTTTAAAATTTT  121

CDS:bax inhibitor 1  17   S  H  I  T  P  S  T  Q  H  L  K  K  V  Y  A  S  F  A  L
Query          135  CTCATATAACCCCGTCAACGCAGCAGCACCTGAAGAAGGTCTATGCAAGTTTTGCCCTTT  194
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           122  CTCATATAACCCCGTCAACGCAGCAGCACCTGAAGAAGGTCTATGCAAGTTTTGCCCTTT  181

CDS:bax inhibitor 1  37   C  M  F  V  A  A  A  G  A  Y  V  H  M  V  T  H  F  I  Q  A
Query          195  GTATGTTTGTGGCGGCTGCAGGGGCCTATGTCCATATGGTCACTCATTTCATTCAGGCTG  254
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           182  GTATGTTTGTGGCGGCTGCAGGGGCCTATGTCCATATGGTCACTCATTTCATTCAGGCTG  241

CDS:bax inhibitor 1  57   G  L  L  S  A  L  G  S  L  I  L  M  I  W  L  M  A  T  P  H
Query          255  GCCTGCTGTCTGCCTTGGGCTCCCTGATATTGATGATTTGGCTGATGGCAACACCTCATA  314
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           242  GCCTGCTGTCTGCCTTGGGCTCCCTGATATTGATGATTTGGCTGATGGCAACACCTCATA  301

CDS:bax inhibitor 1  77   S  H  E  T  E  Q  K  R  L  G  L  L  A  G  F  A  F  L  T  G
Query          315  GCCATGAAACTGAACAGAAAAGACTGGGACTTCTTGCTGGATTTGCATTCCTTACAGGAG  374
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           302  GCCATGAAACTGAACAGAAAAGACTGGGACTTCTTGCTGGATTTGCATTCCTTACAGGAG  361

CDS:bax inhibitor 1  97   V  G  L  G  P  A  L  E  F  C  I  A  V  N  P  S  I  L  P  T
Query          375  TTGGCCTGGGCCCTGCCCTGGAGTTTTGTATTGCTGTCAACCCCAGCATCCTTCCCACTG  434
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           362  TTGGCCTGGGCCCTGCCCTGGAGTTTTGTATTGCTGTCAACCCCAGCATCCTTCCCACTG  421

CDS:bax inhibitor 1  117  A  F  M  G  T  A  M  I  F  T  C  F  T  L  S  A  L  Y  A  R
Query          435  CTTTCATGGGCACGGCAATGATCTTTACCTGCTTCACCCTCAGTGCACTCTATGCCAGGC  494
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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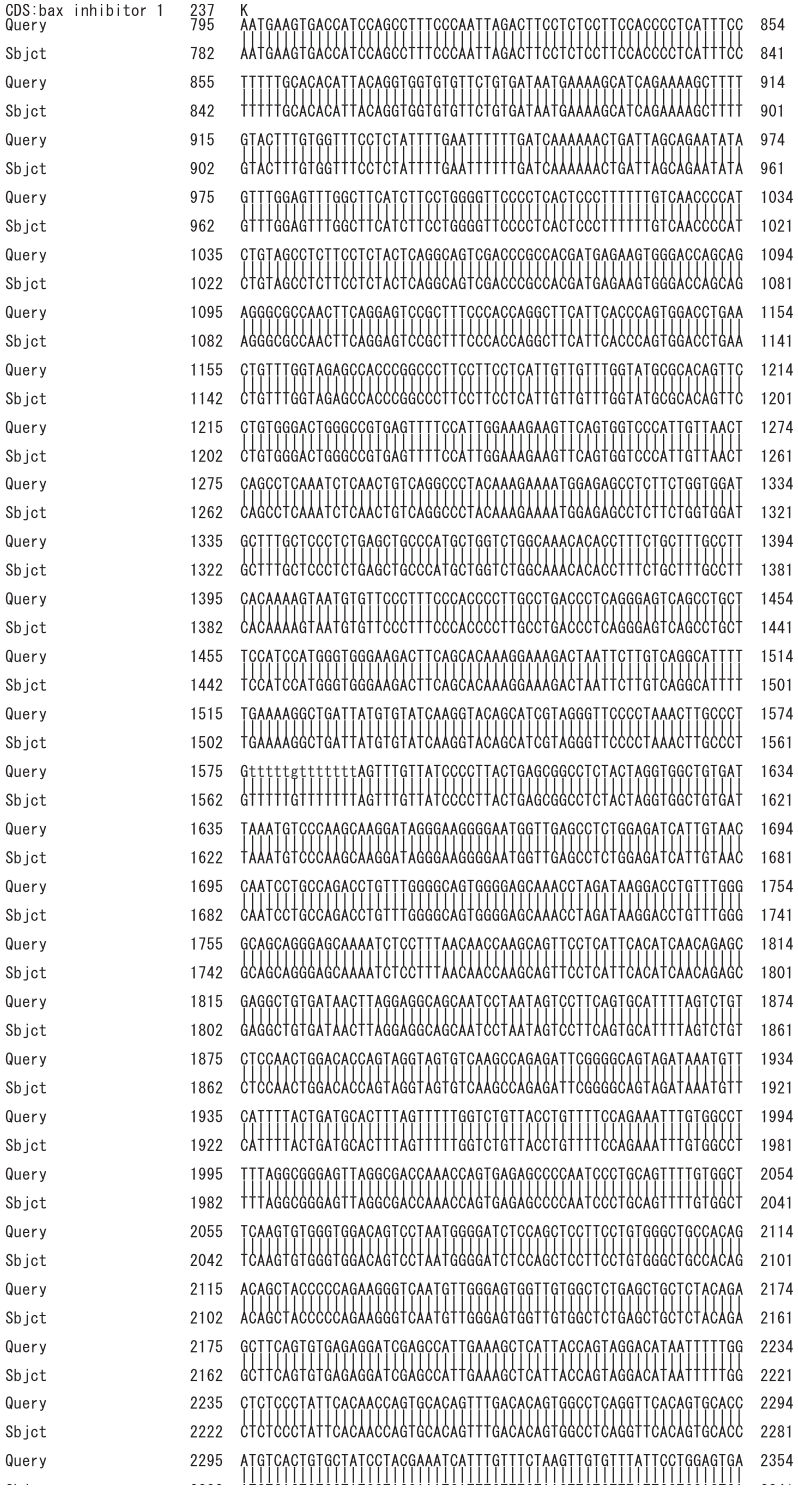
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Sbjct           482  GCCGTAGCTACCTCTTTCTGGGAGGTATCTTGATGTCAGCCCTGAGCTTGTTGCTTTTGT  541

CDS:bax inhibitor 1  157  S  S  L  G  N  V  F  F  G  S  I  W  L  F  Q  A  N  L  Y  V
Query          555  CTTCCCTGGGGAATGTTTTCTTTGGATCCATTTGGCTTTTCCAGGCAAACCTGTATGTGG  614
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           542  CTTCCCTGGGGAATGTTTTCTTTGGATCCATTTGGCTTTTCCAGGCAAACCTGTATGTGG  601

CDS:bax inhibitor 1  177  G  L  V  V  M  C  G  F  V  L  F  D  T  Q  L  I  I  E  K  A
Query          615  GACTGGTGGTCATGTGTGGCTTCGTCCTTTTTGATACTCAACTCATTATTGAAAAGGCCG  674
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           602  GACTGGTGGTCATGTGTGGCTTCGTCCTTTTTGATACTCAACTCATTATTGAAAAGGCCG  661

CDS:bax inhibitor 1  197  E  H  G  D  Q  D  Y  I  W  H  C  I  D  L  F  L  D  F  I  T
Query          675  AACATGGAGATCAAGATTATATCTGGCACTGCATTGATCTCTTCTTAGATTTCATTACTG  734
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           662  AACATGGAGATCAAGATTATATCTGGCACTGCATTGATCTCTTCTTAGATTTCATTACTG  721

CDS:bax inhibitor 1  217  V  F  R  K  L  M  M  I  L  A  M  N  E  K  D  K  K  K  E  K
Query          735  TCTTCAGAAAACTCATGATGATCCTGGCCATGAATGAAAAGGATAAGAAGAAAAGAGAAGA  794
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct           722  TCTTCAGAAAACTCATGATGATCCTGGCCATGAATGAAAAGGATAAGAAGAAAAGAGAAGA  781
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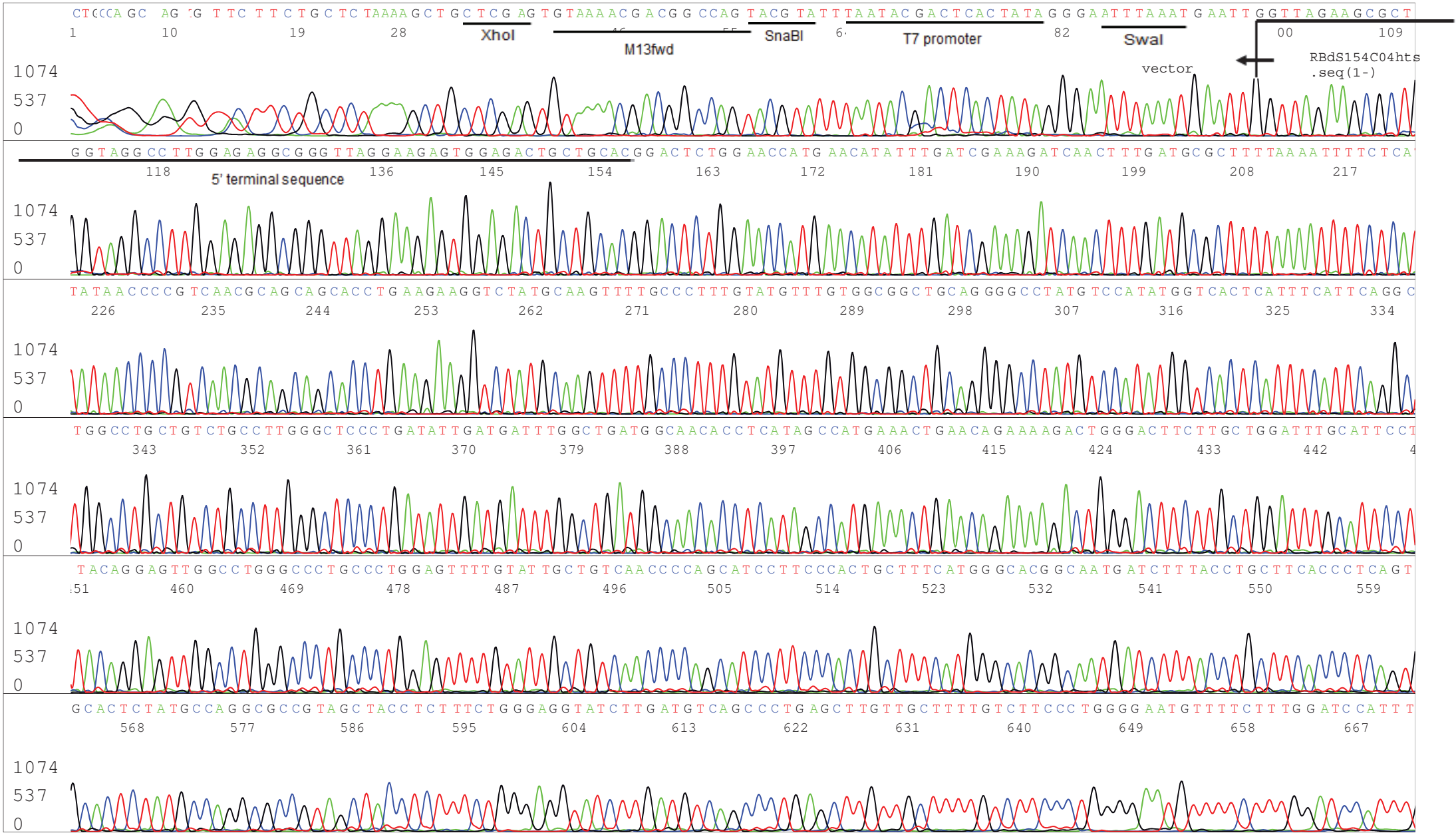
Applied Biosystems

S/N G:383 A:551 T:574 C:567
KB.bcp
KB 1.4.1.8 Cap:3

Primer A : pGCAP-F
5' CTCAGTGGATGTTGCCTTTAC 3'

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6608_RBdS154C04_B4F4_pGCAP_F
KB_3500_POP7_BDTv3.mob
Pts 1596 to 13107 Pk1 Loc:1573
Version 6.0 HiSQV Bases: 840

Inst Model/Name 3500/3500 Instrument
Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:11.49 Pts/Panel1350
Plate Name: 20240605_GNP



Applied Biosystems

S/N G:72 A:116 T:104 C:104
KB.bcp
KB 1.4.1.8 Cap:6

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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6608_RBdS154C04_B4F4_pGCAP_R
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Pts 1586 to 12803 Pk1 Loc:1563
Version 6.0 HiSQV Bases: 109

Inst Model/Name 3500/3500 Instrument
Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:11.28 Pts/Panel1350
Plate Name: 20240605_GNP

