NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS022J14

Lot# : 6608_B4F4

Vector : pGCAP10

Gene	EMD	
RefSeq_mRNA	NM_000117.3	1281 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.): 289 ng/ul

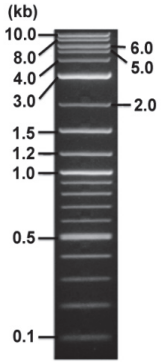
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

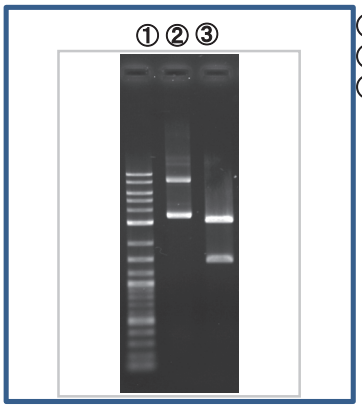
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.5 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 sequence

Date : 2024/06/10

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 : 2024/06/11

DNA (289 ng/ul)	86 ul
10x TE	99 ul
dH_2O	809 ul
Total	994 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

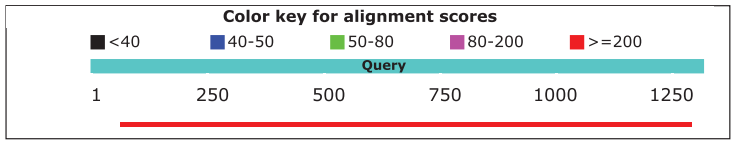
RID 64VXJW3D114 (Expires on 06-08 10:25 am)

Query ID	NM_000117.3	**Subject ID**	lcl|Query_3074727
Description	Homo sapiens emerin (EMD), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	1281	**Molecule type**	dna
		Subject Length	1260
		Program	BLASTN 2.15.0+

RBdS022J14hts.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	2248	2248	95%	0.0	100.00%	Query_3074727

Alignments

Sequence ID: Query_3074727 Length: 1260 Number of Matches: 1
Range 1: 2 to 1218

Score	Expect	Identities	Gaps	Strand	Frame
2248 bits(1217)	0.0()	1217/1217(100%)	0/1217(0%)	Plus/Plus	

Features:

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Query                65   GTGACGCGAGCGCGGCCGCTCCCGATGCGCTCGTGCCGCCCCCGCCGTGCTCCTCGGCAG  124
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2    GTGACGCGAGCGCGGCCGCTCCCGATGCGCTCGTGCCGCCCCCGCCGTGCTCCTCGGCAG  61

Query                125  CCGTTGCTCGGCCGGTTTTGGTAGGCCCGGGCCGCCGCCAGGCCTCCGCCTGAGCCCGCA  184
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                62   CCGTTGCTCGGCCGGTTTTGGTAGGCCCGGGCCGCCGCCAGGCCTCCGCCTGAGCCCGCA  121

CDS:emerin [Homo sap 1                 M  D  N  Y  A  D  L  S  D  T  E  L  T  T  L  L  R  R
Query                185  CCCGCCATGGACAACTACGCAGATCTTTCGGATACCGAGCTGACCACCTTGCTGCGCCGG  244
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                122  CCCGCCATGGACAACTACGCAGATCTTTCGGATACCGAGCTGACCACCTTGCTGCGCCGG  181

CDS:emerin [Homo sap 19    Y  N  I  P  H  G  P  V  V  G  S  T  R  R  L  Y  E  K  K  I
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Sbjct                182  TACAACATCCCGCACGGGCCTGTAGTAGGATCAACTCGTAGGCTTTACGAGAAGAAGATC  241

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                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                242  TTCGAGTACGAGACCCAGAGGCGGCGGCTCTCGCCCCCCAGCTCGTCCGCCGGCCTCCTCT  301

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Sbjct                362  AAAGAGGACGCTTTACTCTACCAGAGCAAGGGCTACAATGACGACTACTATGAAGAGAGC  421

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Query                485  TACTTCACCACCAGGACTTATGGGGAGCCCGAGTCTGCCGGCCCGTCCAGGGCTGTCCGC  544
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Sbjct                422  TACTTCACCACCAGGACTTATGGGGAGCCCGAGTCTGCCGGCCCGTCCAGGGCTGTCCGC  481

CDS:emerin [Homo sap 119   Q  S  V  T  S  F  P  D  A  D  A  F  H  H  Q  V  H  D  D  D
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Sbjct                542  CTTTTGTCTTCTTCTGAAGAGGAGTGCAAGGATAGGGAACGCCCCATGTACGGCCGGGAC  601

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Sbjct                602  AGTGCCTACCAGAGCATCACGCACTACCGCCCTGTTTCAGCCTCCAGGAGCTCCCTGGAC  661

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                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CDS:emerin [Homo sap 199   S  W  L  T  R  R  A  I  R  P  E  N  R  A  P  G  A  G  L  G
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Sbjct              782   CAGGATCGCCAGGTCCCGCTCTGGGGCCAGCTGCTGCTTTTCCTGGTCTTTGTGATCGTC  841

CDS:emerin [Homo sap  239    L  F  F  I  Y  H  F  M  Q  A  E  E  G  N  P  F
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Sbjct              842   CTCTTCTTCATTTACCACTTCATGCAGGCTGAAGAAGGCAACCCCTTCTAGAGGGAGCCA  901

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                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct              962   GGGGGTGGGGGTGGGGGCAGGGGCAGGGGCTTTATGTGTTTTGCTTGGGGGGCGCTGGG  1021

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Query              1265  GCCCCGTTTATTTGTAA  1281
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Sbjct              1202  GCCCCGTTTATTTGTAA  1218
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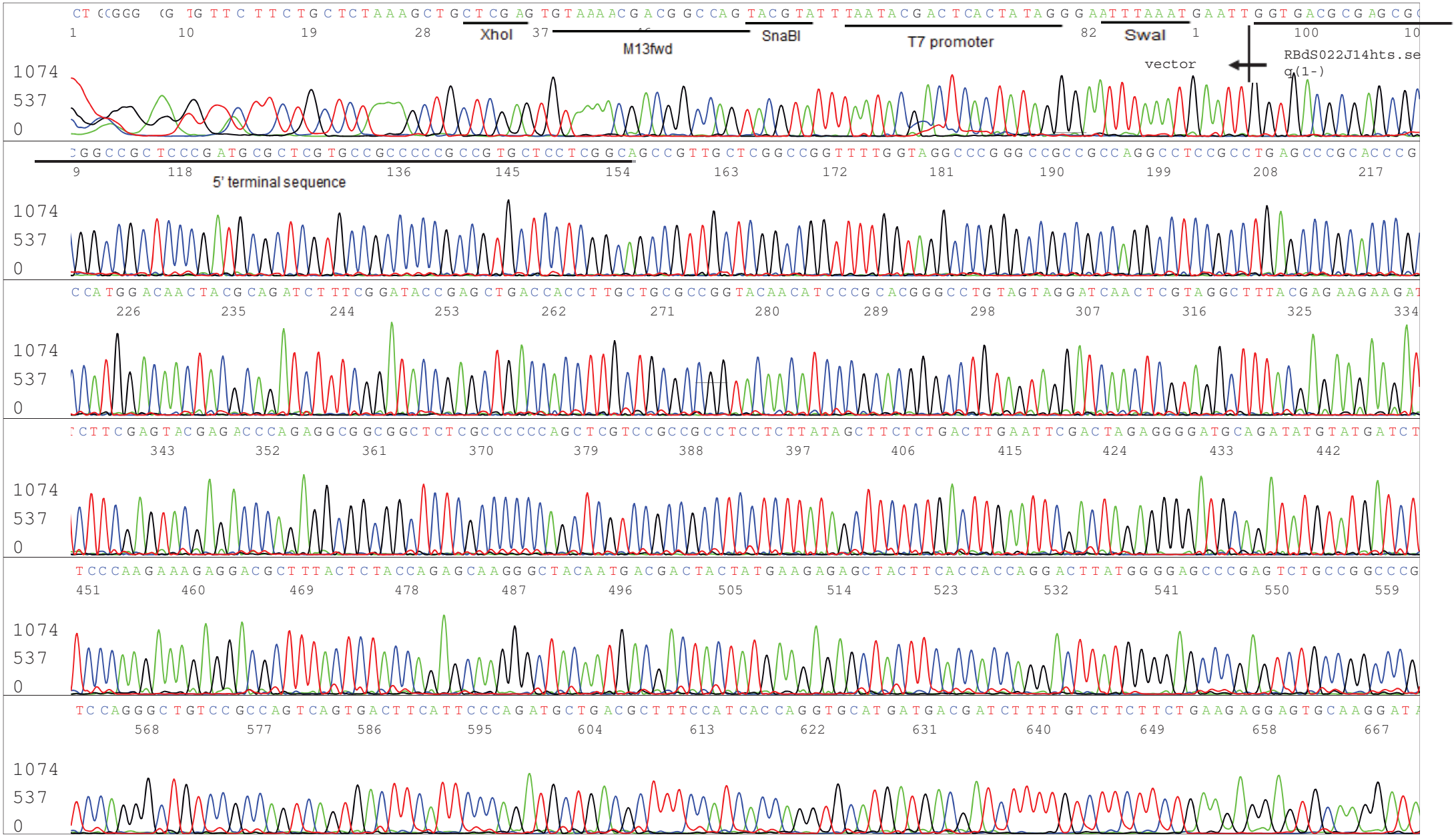
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KB 1.4.1.8 Cap:11

Primer A : pGCAP-F

5' CTCAGTGGATGTTGCCTTTAC 3'

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Pts 1568 to 12793 Pk1 Loc:1545
Version 6.0 HiSQV Bases: 853

Inst Model/Name 3500/3500 Instrument
Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:11.27 Pts/Panel1350
Plate Name: 20240605_GNP



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S/N G:73 A:110 T:94 C:131
KB.bcp
KB 1.4.1.8 Cap:14

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1563 to 12771 Pk1 Loc:1540
Version 6.0 HiSQV Bases: 84

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Jun 05,2024 03:16PM, JST
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Plate Name: 20240605_GNP

