NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd17H08

Lot# : 7677_B4F4

Vector : pGCAP10

Gene	C3orf39	
RefSeq_mRNA	NM_032806.6	2547 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.): 293 ng/ul

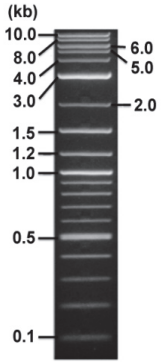
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

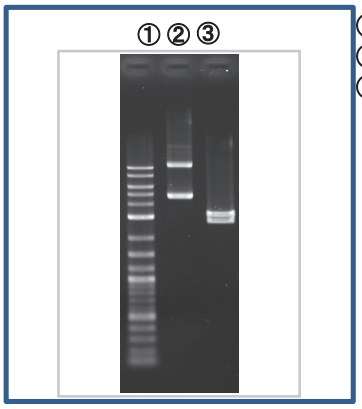
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.7 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/vecter junction sequence

Date : 2024/06/07

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 : 2024/06/11

DNA (293 ng/ul)	86 ul
10x TE	101 ul
dH_2O	821 ul
Total	1,008 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_003217:Homo sapiens transmembrane BAX inhibitor...

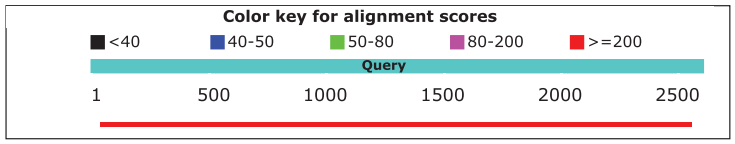
RID 64MXJTU9114 (Expires on 06-08 08:26 am)

Query ID	NM_032806.6	**Subject ID**	lcl|Query_1866773
Description	Homo sapiens protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-) (POMGNT2), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2547	**Subject Length**	2541
		Program	BLASTN 2.15.0+

RBd17H08hts.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	4626	4626	98%	0.0	99.96%	Query_1866773

Alignments

Sequence ID: Query_1866773 Length: 2541 Number of Matches: 1
Range 1: 2 to 2509

Score	Expect	Identities	Gaps	Strand	Frame
4626 bits(2505)	0.0()	2507/2508(99%)	0/2508(0%)	Plus/Plus	

Features:

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Sbjct           2   ACGGCGGGCACCTGCGAGCCTGGAGGTGGCGGTCGCTGCGAACCCGGCGGCGCGGCCAAA  61

Query         100   CCTGTGCTGGCTGCCTGGGCCTTCTGGGCCTCCTGGGCCAGAAGCTGGCGCTGGGGGCGG  159
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct          62   CCTGTGCTGGCTGCCTGGGCCTTCTGGGCCTCCTGGGCCAGAAGCTGGCGCTGGGGGCGG  121

Query         160   CGGCGGGGGTGGGAAAGCGGCGCCGCCGTGGGGCCTCCTGGACGCGTCGGCGGAGGTGGCT  219
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Sbjct          122  CGGCGGGGGTGGGAAAGCGGCGCCGCCGTGGGGCCTCCTGGACGCGTCGGCGGAGGTGGCT  181

Query         220   TCGTCCCGCGGAGTCCAGGCTTCAGGCTTTCACCAGTTCTCAGGATGCCCATAGGGATGG  279
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct          182  TCGTCCCGCGGAGTCCAGGCTTCAGGCTTTCACCAGTTCTCAGGATGCCCATAGGGATGG  241

Query         280   GTGAAGCCTGCCTGGCCTGTGGTGCTTCCCAGTGGCCGTCATCTCATTAGGGCCCCACAG  339
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Sbjct          242  GTGAAGCCTGCCTGGCCTGTGGTGCTTCCCAGTGGCCGTCATCTCATTAGGGCCCCACAG  301

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Sbjct          302  TGGCATTAGGATGCACCTCTCGGCGGTGTTCAACGCCCTCCTGGTGTCGGTGCTGGCAGC  361

CDS:protein O-linked  18     V  L  W  K  H  V  R  L  R  E  H  A  A  T  L  E  E  E  L  A
Query         400   GGTCCTGTGGAAGCATGTGCGGCTGCGTGAGCATGCAGCCACACTGGAGGAGGAGCTGGC  459
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Sbjct          422  CCTCAGCCGACAGGCCACAGAGCCAGCCCCAGCACTGAGGATCGACTACCCGAAGGCACT  481

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CDS:protein O-linked  118    D  L  S  T  V  E  D  H  N  T  Q  Y  F  N  F  V  E  L  P  A
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Sbjct          782  CCGCTTCAACCCCGACAACCTCATGCACGTCTTTCATGACGACCTGCTGCCACTCTTCTA  841
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Sbjct                 842    CACCCTGCGGCAGTTTCCCGGCCTGGCCCACGAGGCACGGCTCTTCTTCATGGAGGGCTG  901

CDS:protein O-linked  198    G  E  G  A  H  F  D  L  Y  K  L  L  S  P  K  Q  P  L  L  R
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HHS Vulnerability Disclosure

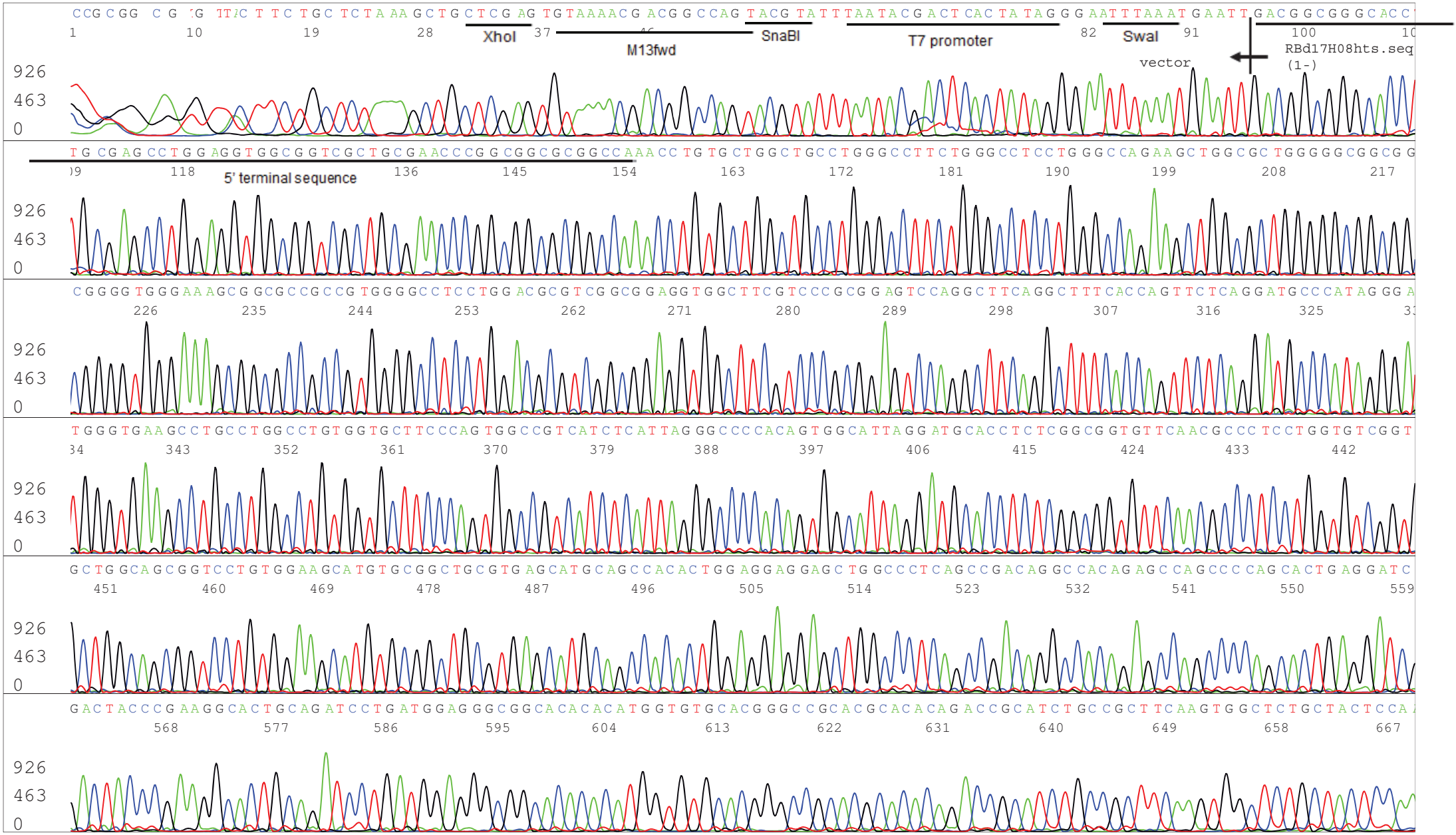
Applied Biosystems

S/N G:328 A:285 T:242 C:464
KB.bcp
KB 1.4.1.8 Cap:10

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KB_3500_POP7_BDTv3.mob
Pts 1573 to 12896 Pk1 Loc:1550
Version 6.0 HiSQV Bases: 835

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



Applied Biosystems

S/N G:41 A:62 T:63 C:72
KB.bcp
KB 1.4.1.8 Cap:13

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1583 to 12682 Pk1 Loc:1560
Version 6.0 HiSQV Bases: 75

Inst Model/Name 3500/3500 Instrument
Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:13.25 Pts/Panel1350
Plate Name: 20240605_GNP

