NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARa24B03
Vector : pKA1U5

Lot# : 7671_B3Bd

Gene	VMA21	
RefSeq_mRNA	NM_001017980.4	4715 bp

● Plasmid DNA purification

Date : 23.03.14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.15

DNA concentration (O.D.): 224 ng/ul

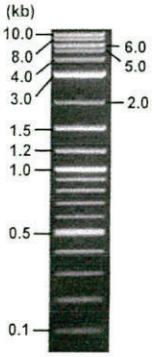
DNA	0.45 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.55 ul
Total	10 ul

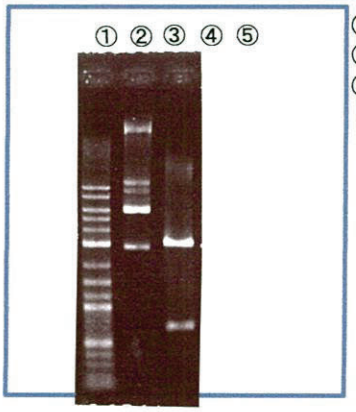
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 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 sequence

Date : 2026/06/16

full sequence: ARa24B03hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (224 ng/ul)	72 ul
10x TE	65 ul
dH_2O	509 ul
Total	645 ul

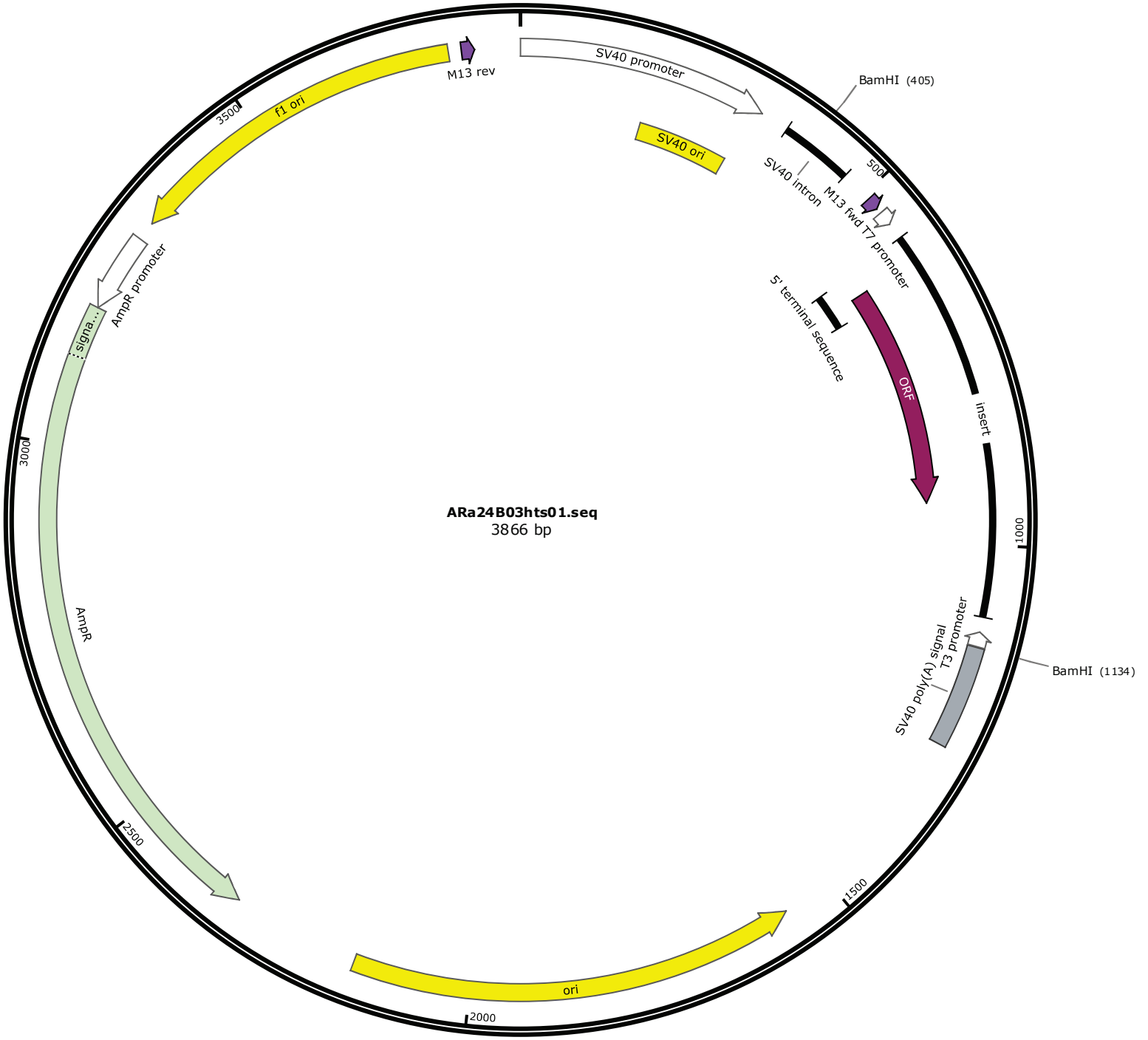
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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


ARa24B03hts01.seq
3866 bp
M13 rev
SV40 promoter
BamHI (405)
f1 ori
SV40 ori
SV40 intron
M13 fwd
T7 promoter
AmpR promoter
5' terminal sequence
ORF
insert
signa...
AmpR
SV40 poly(A) signal
T3 promoter
BamHI (1134)
ori
500
1000
1500
2000
2500
3000
3500

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_001017980.4|

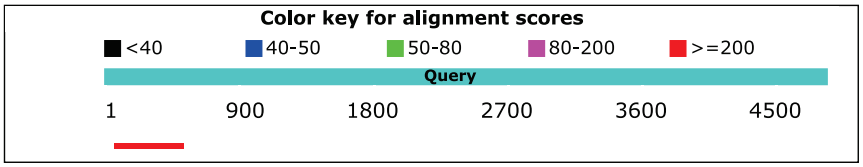
RID 31S7KDF4114 (Expires on 06-17 13:36 pm)

Query ID	NM_001017980.4	**Subject ID**	lcl|Query_6144515
Description	Homo sapiens vacuolar ATPase assembly factor VMA21 (VMA21), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	4715	**Subject Length**	3866
		Program	BLASTN 2.17.0+

ARa24B03hts01.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	817	817	9%	0.0	100.00%	Query_6144515

Alignments

Sequence ID: Query_6144515 Length: 3866 Number of Matches: 1
Range 1: 575 to 1016

Score	Expect	Identities	Gaps	Strand	Frame
817 bits(442)	0.0()	442/442(100%)	0/442(0%)	Plus/Plus	

Features:

```
CDS:vacuolar ATPase   1                                       M  E  R  P  D  K  A  A  L
Query                 71    GCCGCCGAGCGCCTGTGCCGGCACGGCTACACCATGGAGCGCCCGGATAAGGCGGCGCTG  130
Sbjct                 575   ............................................................  634

CDS:vacuolar ATPase   10     N  A  L  Q  P  P  E  F  R  N  E  S  S  L  A  S  T  L  K  T
Query                 131   AACGCACTGCAGCCTCCTGAGTTCAGAAATGAAAGCTCATTAGCATCTACACTGAAGACG  190
Sbjct                 635   ............................................................  694

CDS:vacuolar ATPase   30     L  L  F  F  T  A  L  M  I  T  V  P  I  G  L  Y  F  T  T  K
Query                 191   CTCCTGTTCTTCACAGCTTTAATGATCACTGTTCCTATTGGGTTATATTTCACAACTAAA  250
Sbjct                 695   ............................................................  754

CDS:vacuolar ATPase   50     S  Y  I  F  E  G  A  L  G  M  S  N  R  D  S  Y  F  Y  A  A
Query                 251   TCTTACATATTTGAAGGCGCCCTTGGGATGTCCAATAGGGACAGCTATTTTTACGCTGCT  310
Sbjct                 755   ............................................................  814

CDS:vacuolar ATPase   70     I  V  A  V  V  A  V  H  V  V  L  A  L  F  V  Y  V  A  W  N
Query                 311   ATTGTTGCAGTGGTCGCCGTCCATGTGGTGCTGGCCCTCTTTGTGTATGTGGCCTGGAAT  370
Sbjct                 815   ............................................................  874

CDS:vacuolar ATPase   90     E  G  S  R  Q  W  R  E  G  K  Q  D
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```
Query  371   GAAGGCTCACGACAGTGGCGTGAAGGCAAACAGGATTAAAGTGAACATCACCTTTTTATA  430
Sbjct  875   ............................................................  934

Query  431   GCATTAAATTCATTTTTTAAAATGATAAATGCTGGAGGGGGCCATCTGATTTGAATAAAG  490
Sbjct  935   ............................................................  994

Query  491   TTGAAAGAACATGTTAAAGTCA  512
Sbjct  995   .......................  1016
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