NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARi09B12

Lot# : 7675_B5B4

Vector : pGCAP10

Gene	TMEM37	
RefSeq_mRNA	NM_183240.3	1687 bp

● Plasmid DNA purification

Date : 2026/02/04

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

Date : 2026/02/05

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/02/05

DNA concentration (O.D.): 111 ng/ul

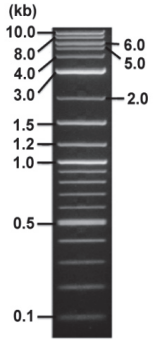
< Size of fragment expected from this clone >

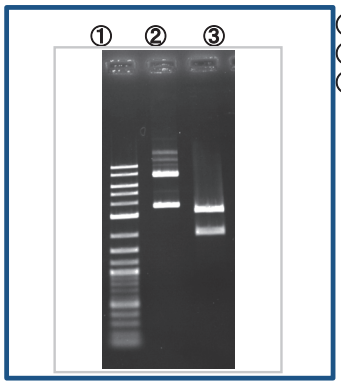
DNA	0.9	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.1	ul
Total	10	ul

BamHI 3.1kb (vector), 1.9 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the sequence

Date : 2026/02/09

full sequence	ARi09B12hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/02/10

DNA (111 ng/ul)	82	ul
10x TE	36	ul
dH_2O	246	ul
Total	364	ul

● Shipping

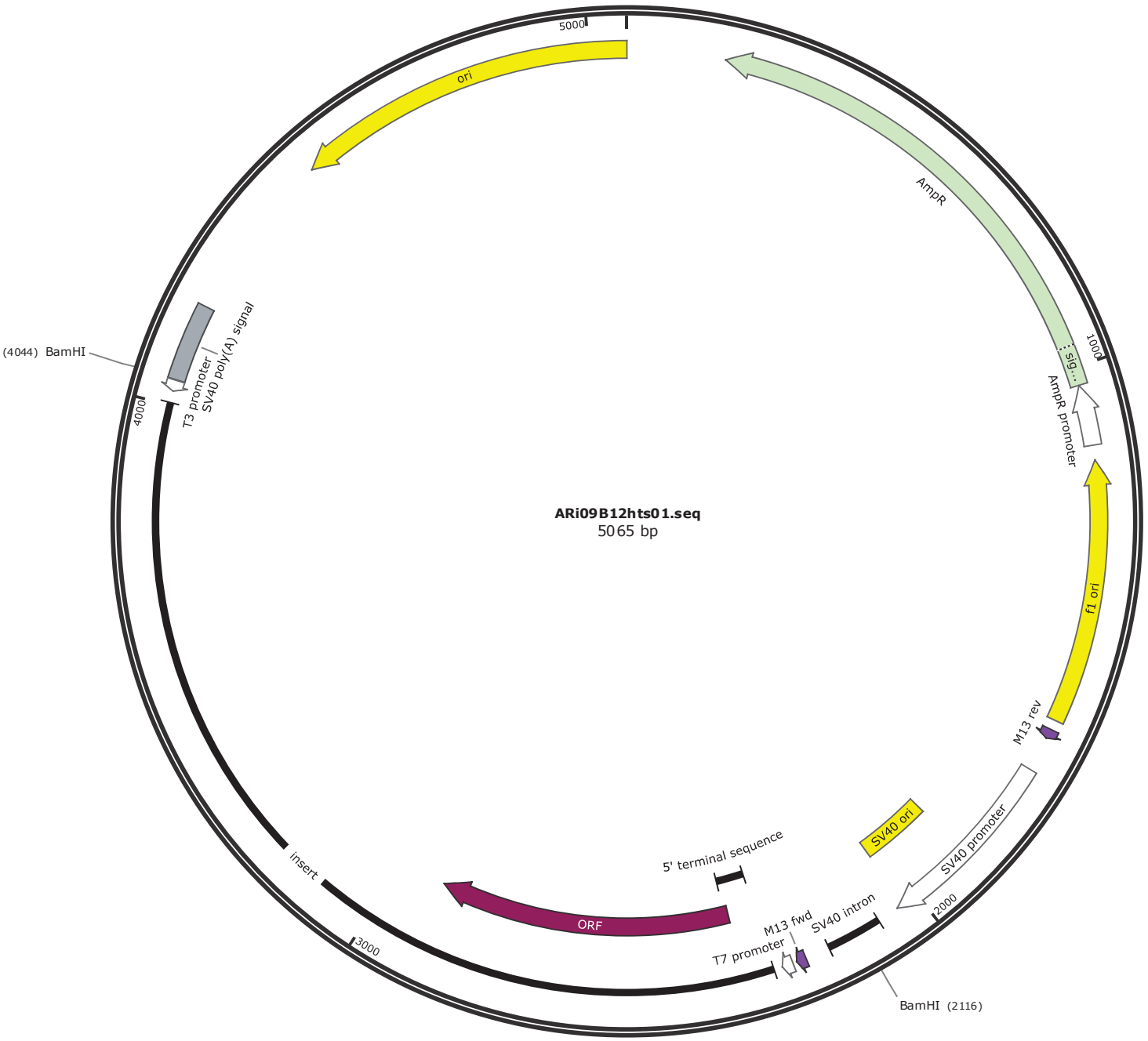
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.02.10
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http://dna.brc.riken.jp/index.html


ARi09B12hts01.seq
5065 bp
5000
ori
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 ori
SV40 intron
2000
BamHI (2116)
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
3000
4000
T3 promoter
SV40 poly(A) signal
(4044) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_183240|

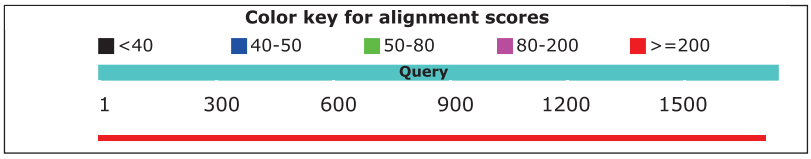
RID SK4XAF4X114 (Expires on 02-10 14:58 pm)

Query ID	NM_183240.3	**Subject ID**	lcl|Query_1072835
Description	Homo sapiens transmembrane protein 37 (TMEM37), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1687	**Subject Length**	5065
		Program	BLASTN 2.17.0+

ARi09B12hts01.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	3040	3040	100%	0.0	99.17%	Query_1072835

Alignments

Sequence ID: Query_1072835 Length: 5065 Number of Matches: 1
Range 1: 2281 to 3969

Score	Expect	Identities	Gaps	Strand	Frame
3040 bits(1646)	0.0()	1680/1694(99%)	12/1694(0%)	Plus/Plus	

Features:

```
CDS:voltage-dependen  1                                                   M  T  A
Query                 1     AGCGGAGCAGCTGGAGCGATCGAGGCTGCAGCGCGGCCGCCGGGCGCAGCATGACTGCCG  60
Sbjct                 2281  ...C.........................................................  2340

CDS:voltage-dependen  4     V  G  V  Q  A  Q  R  P  L  G  Q  R  Q  P  R  R  S  F  F  E
Query                 61    TCGGCGTGCAGGCCCAGAGGCCTTTGGGCCAAAGGCAGCCCCGCCGGTCCTTCTTTGAAT  120
Sbjct                 2341  ...........................................................  2400

CDS:voltage-dependen  24    S  F  I  R  T  L  I  I  T  C  V  A  L  A  V  V  L  S  S  V
Query                 121   CCTTCATCCGGACCCTCATCATCACGTGTGTGGCCCTGGCTGTGGTCCTGTCCTCGGTCT  180
Sbjct                 2401  ...........................................................  2460

CDS:voltage-dependen  44    S  I  C  D  G  H  W  L  L  A  E  D  R  L  F  G  L  W  H  F
Query                 181   CCATTTGTGATGGGCACTGGCTCCTGGCTGAGGACCGCCTCTTCGGGCTCTGGCACTTCT  240
Sbjct                 2461  ...........................................................  2520

CDS:voltage-dependen  64    C  T  T  T  N  Q        T  I  C  F  R  D  L  G  Q  A  H  V
Query                 241   GCACCACCACCAACCAGA------CGATCTGCTTCAGAGACCTGGGCCAGGCCCATGTGC  294
Sbjct                 2521  ..................GTGTGC..................................  2580

CDS:voltage-dependen  82    P  G  L  A  V  G  M  G  L  V  R  S  V  G  A  L  A  V  V  A
Query                 295   CCGGGCTGGCCGTGGGCATGGGCCTGGTACGCAGCGTGGGCGCCTTGGCCGTGGTGGCCG  354
Sbjct                 2581  ...........................................................  2640
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258_259 ins 6nt

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CDS:voltage-dependen  102   A  I  F  G  L  E  F  L  M  V  S  Q  L  C  E  D  K  H  S  Q
Query                 355   CCATTTTTGGCCTGGAGTTCCTCATGGTGTCCCAGTTGTGCGAGGACAAACACTCACAGT  414
Sbjct                 2641  ............................................................  2700

CDS:voltage-dependen  122   C  K  W  V  M  G  S  I  L  L  L  V  S  F  V  L  S  S  G  G
Query                 415   GCAAGTGGGTCATGGGTTCCATCCTCCTCCTGGTGTCTTTCGTCCTCTCCTCCGGCGGGC  474
Sbjct                 2701  ............................................................  2760

CDS:voltage-dependen  142   L  L  G  F  V  I  L  L  R  N  Q  V  T  L  I  G  F  T  L  M
Query                 475   TCCTGGGTTTTGTGATCCTCCTCAGGAACCAAGTCACACTCATCGGCTTCACCCTAATGT  534
Sbjct                 2761  ............................................................  2820

CDS:voltage-dependen  162   F  W  C  E  F  T  A  S  F  L  L  F  L  N  A  I  S  G  L  H
Query                 535   TTTGGTGCGAATTCACTGCCTCCTTCCTCCTCTTCCTGAACGCCATCAGCGGCCTTCACA  594
Sbjct                 2821  ............................................................  2880

CDS:voltage-dependen  182   I  N  S  I  T  H  P  W  E
Query                 595   TCAACAGCATCACCCATCCCTGGGAATGACCGTGGAAATTTTAGGCCCCCTCCAGGGACA  654
Sbjct                 2881  ............................................................  2940

Query                 655   TCAGATTCCACAAGAAAATATGGTCAAAATGGGACTTTTCCAGCATGTGGCCTCTGGTGG  714
Sbjct                 2941  ............................................................  3000

Query                 715   GGCTGGGTTGGACAAGGGCCTTGAAACGGCTGCCTGTTTGCCGATAACTTGTGGGTGGTC  774
Sbjct                 3001  ............................................................  3060

Query                 775   AGCCAGAAATGGCCCGGGGGCCTCTGCACCTGGTCTGCAGGGCCAGAGGCCAGGAGGGTG  834
Sbjct                 3061  ............................................................  3120

Query                 835   CCTCAGTGCCACCAACTGCACAGGCTTAGCCAGATGTTGATTTTAGAGGAAGaaaaaaaC  894
Sbjct                 3121  ............................................................  3180

Query                 895   ATTTTAAAACTCCTTCTTGAATTTTCTTCCCTGGACTGGAATACAGTTGGAAGCACAGGG  954
Sbjct                 3181  ............................................................  3240

Query                 955   GTAACTGGTACCTGAGCTAGCTGCACAGCCAAGGATAGTTCATGCCTGTTTCATTGACAC  1014
Sbjct                 3241  ............................................................  3300

Query                 1015  GTGCTGGGATAGGGGCTGCAGAATCCCTGGGGCTCCCAGGGTTGTTAAGAATGGATCATT  1074
Sbjct                 3301  ............................................................  3360

Query                 1075  CTTCCAGCTAAGGGTCCAATCAGTGCCTAGGACTTTCTTCCACCAGCTCAAAGGGCCTTC  1134
Sbjct                 3361  ..........-----..........................................  3415

Query                 1135  GTATGTATGTCCCTGGCTTCAGCTTTGGTCATGCCAAAGAGGCAGAGTTCAGGATTCCCT  1194
Sbjct                 3416  ............................................................  3475

Query                 1195  CAGAATGCCCTGCACACAGTAGGTTTCCAAACCATTTGACTCGGTTTGCCTCCCTGCCCG  1254
Sbjct                 3476  ............................................................  3535

Query                 1255  TTGTTTAAACCTTACAAACCCTGGATAACCCCATCTTCTAGCAGCTGGCTGTG-CCTCTG  1313
Sbjct                 3536  ..................................................CC......  3595

Query                 1314  GGAGCTCTGCCTATCAGAACCCTACCTTAAGGTGGGTTTCCTTCCGAGAAGAGTTCTTGA  1373
Sbjct                 3596  ............................................................  3655

Query                 1374  GCAAGCTCTCCCAGGAGGGCCCACCTGACTGCTAATACACAGCCCTCCCCAAGGCCCGTG  1433
Sbjct                 3656  ............................................................  3715

Query                 1434  TGTGCATGTGTCTGTCTTTTGTGAGGGTTAGACAGCCTCAGGGCACCATTTTTAATCCCA  1493
Sbjct                 3716  ............................................................  3775

Query                 1494  GAACACATTTCAAAGAGCACGTATCTAGACCTGCTGGACTCTGCAGGGGGTGAGGGGGAA  1553
Sbjct                 3776  ............................................................  3835

Query                 1554  CAGCGAGAGCTTGGGTAATGATTAACACCCATGCTGGGGATGCATGGAGGTGAAGGGGGC  1613
Sbjct                 3836  ............................................................  3895

Query                 1614  CAGGAACCAGTGGAGATTTCCATCCTTGCCAGCACGTCTGTACTTCTGTTCATTAAAGTG  1673
Sbjct                 3896  ............................................................  3955

Query                 1674  CTCCCTTTCTAGTC  1687
Sbjct                 3956  ..............  3969
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