NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe91G02

Lot# : 7672_B5Gt

Vector : pKA1U5

Gene	TRIM47	
RefSeq_mRNA	NM_033452.3	2269 bp

● Plasmid DNA purification

Date : 2025/07/29 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/07/30 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/07/23

DNA concentration (O.D.): 371 ng/ul

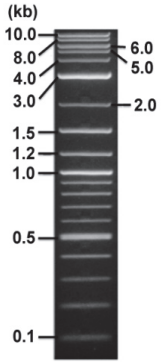
< Size of fragment expected from this clone >

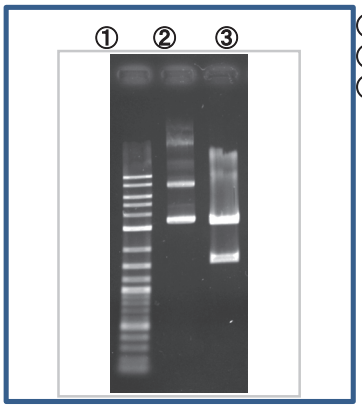
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

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 sequence

Date : 2025/08/01

full sequence	ARe91G02hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/08/05

DNA (371 ng/ul)	80 ul
10x TE	119 ul
dH_2O	988 ul
Total	1,187 ul

● Shipping

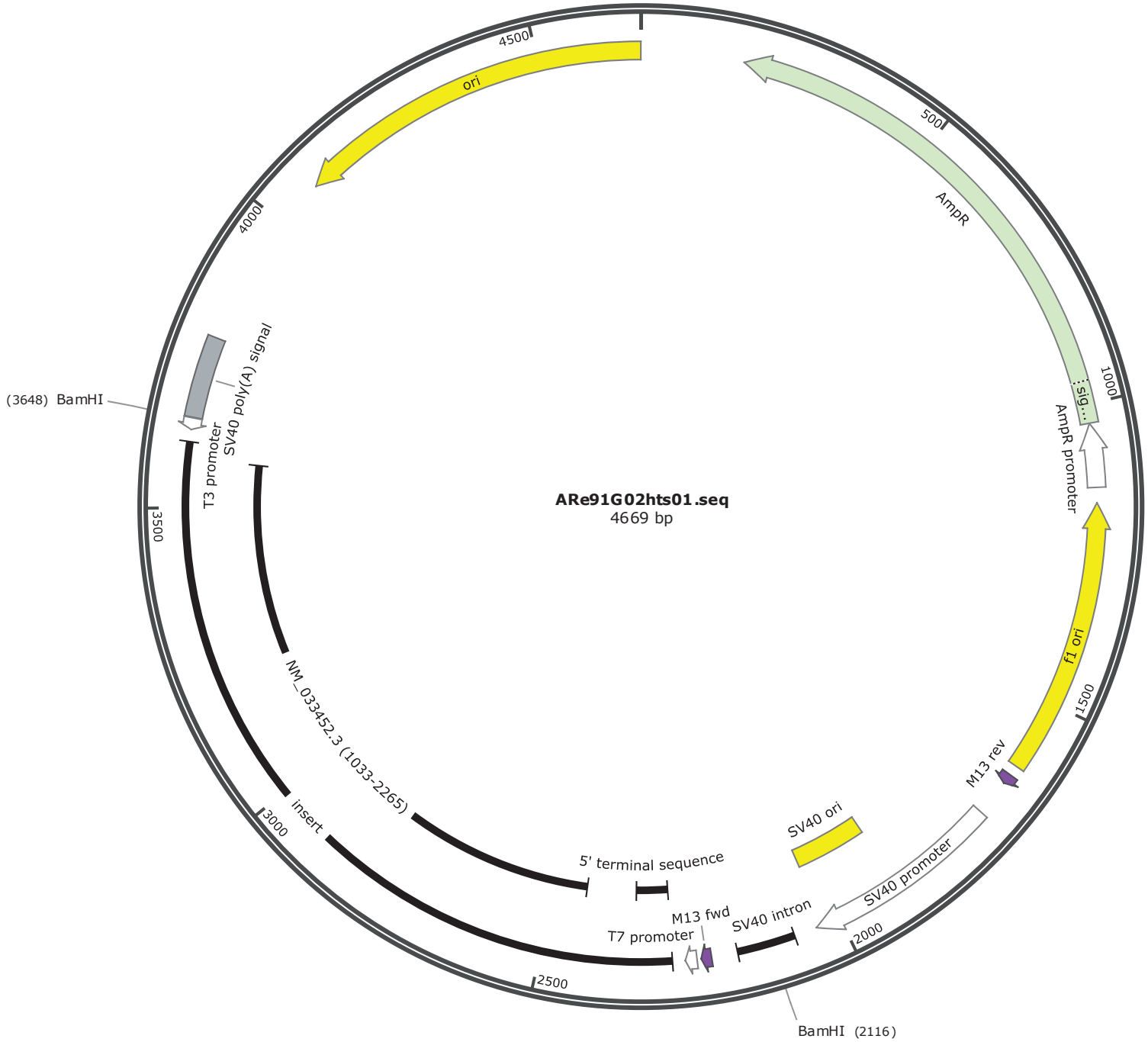
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

検 '25.08.05 笹沼

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


ARe91G02hts01.seq
4669 bp
4500
ori
500
AmpR
1000
AmpR promoter
1500
f1 ori
M13 rev
2000
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
2500
BamHI (2116)
5' terminal sequence
SV40 ori
insert
NM_033452.3 (1033-2265)
3000
3500
T3 promoter
SV40 poly(A) signal
(3648) BamHI
4000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_173547:Homo sapiens tripartite motif containing...

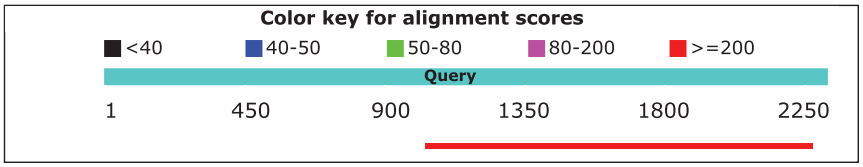
RID 8SGG74HU114 (Expires on 08-02 12:26 pm)

Query ID	NM_033452.3	**Subject ID**	lcl|Query_6002615
Description	Homo sapiens tripartite motif containing 47 (TRIM47), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2269	**Subject Length**	4669
		Program	BLASTN 2.17.0+

ARe91G02hts01.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	2278	2278	54%	0.0	100.00%	Query_6002615

Alignments

Sequence ID: Query_6002615 Length: 4669 Number of Matches: 1
Range 1: 2349 to 3581

Score	Expect	Identities	Gaps	Strand	Frame
2278 bits(1233)	0.0()	1233/1233(100%)	0/1233(0%)	Plus/Plus	

Features:

```
CDS:E3 ubiquitin-pro  334   Q  E  L  L  A  L  R  L  A  L  E  D  G  C  G  P  G  P  G  P
Query                 1033  CAGGAGCTGCTGGCACTAAGGCTGGCCCTGGAGGATGGGTGTGGCCCTGGGCCTGGACCC  1092
Sbjct                 2349  ............................................................  2408

CDS:E3 ubiquitin-pro  354   P  R  E  L  S  F  T  K  S  S  Q  A  V  R  A  V  R  D  M  L
Query                 1093  CCGAGGGAGCTCAGCTTCACCAAATCATCCCAAGCTGTCCGTGCAGTGAGAGACATGCTG  1152
Sbjct                 2409  ............................................................  2468

CDS:E3 ubiquitin-pro  374   A  V  A  C  V  N  Q  W  E  Q  L  R  G  P  G  G  N  E  D  G
Query                 1153  GCCGTGGCCTGCGTCAACCAGTGGGAGCAGCTGAGGGGGCCGGGTGGCAACGAGGATGGG  1212
Sbjct                 2469  ............................................................  2528

CDS:E3 ubiquitin-pro  394   P  Q  K  L  D  S  E  A  D  A  E  P  Q  D  L  E  S  T  N  L
Query                 1213  CCACAGAAGCTGGACTCGGAAGCTGATGCTGAGCCCCAAGACCTCGAGAGTACGAACCTC  1272
Sbjct                 2529  ............................................................  2588

CDS:E3 ubiquitin-pro  414   L  E  S  E  A  P  R  D  Y  F  L  K  F  A  Y  I  V  D  L  D
Query                 1273  TTGGAGAGTGAAGCTCCCAGGGACTATTTCCTCAAGTTTGCCTATATTGTGGATTTGGAC  1332
Sbjct                 2589  ............................................................  2648

CDS:E3 ubiquitin-pro  434   S  D  T  A  D  K  F  L  Q  L  F  G  T  K  G  V  K  R  V  L
Query                 1333  AGCGACACAGCAGACAAGTTCCTGCAGCTGTTTGGAACCAAAGGTGTCAAGAGGGTGCTG  1392
Sbjct                 2649  ............................................................  2708
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CDS:E3 ubiquitin-pro  454   C  P  I  N  Y  P  L  S  P  T  R  F  T  H  C  E  Q  V  L  G
Query                 1393  TGTCCTATCAACTACCCCTTGTCGCCCACCCGCTTCACCCATTGTGAGCAGGTGCTGGGC  1452
Sbjct                 2709  ............................................................  2768

CDS:E3 ubiquitin-pro  474   E  G  A  L  D  R  G  T  Y  Y  W  E  V  E  I  I  E  G  W  V
Query                 1453  GAGGGTGCCCTGGACCGAGGCACCTACTACTGGGAGGTGGAGATTATCGAGGGCTGGGTC  1512
Sbjct                 2769  ............................................................  2828

CDS:E3 ubiquitin-pro  494   S  M  G  V  M  A  E  D  F  S  P  Q  E  P  Y  D  R  G  R  L
Query                 1513  AGCATGGGGGTCATGGCCGAAGACTTCTCCCCACAAGAGCCCTACGACCGCGGCCGGCTG  1572
Sbjct                 2829  ............................................................  2888

CDS:E3 ubiquitin-pro  514   G  R  N  A  H  S  C  C  L  Q  W  N  G  R  S  F  S  V  W  F
Query                 1573  GGCCGCAACGCCCACTCCTGCTGCCTGCAGTGGAATGGACGCAGCTTCTCCGTCTGGTTT  1632
Sbjct                 2889  ............................................................  2948

CDS:E3 ubiquitin-pro  534   H  G  L  E  A  P  L  P  H  P  F  S  P  T  V  G  V  C  L  E
Query                 1633  CATGGGCTGGAGGCTCCCCTGCCCCACCCCTTCTCTCGCCCACGGTTGGGGTCTGCCTGGAA  1692
Sbjct                 2949  ............................................................  3008

CDS:E3 ubiquitin-pro  554   Y  A  D  R  A  L  A  F  Y  A  V  R  D  G  K  M  S  L  L  R
Query                 1693  TACGCTGACCGTGCCTTGGCCTTCTATGCTGTACGGGACGGCAAGATGAGCCTCCTGCGG  1752
Sbjct                 3009  ............................................................  3068

CDS:E3 ubiquitin-pro  574   R  L  K  A  S  R  P  R  R  G  G  I  P  A  S  P  I  D  P  F
Query                 1753  AGGCTGAAGGCCTCCGGCCCCGCCGGGGTGGCATCCCGGCCTCCCCCATTGACCCCTTC  1812
Sbjct                 3069  ............................................................  3128

CDS:E3 ubiquitin-pro  594   Q  S  R  L  D  S  H  F  A  G  L  F  T  H  R  L  K  P  A  F
Query                 1813  CAGAGCCGCCTGGACAGTCACTTTGCGGGGCTCTTCACCCACAGACTCAAGCCTGCCTTC  1872
Sbjct                 3129  ............................................................  3188

CDS:E3 ubiquitin-pro  614   F  L  E  S  V  D  A  H  L  Q  I  G  P  L  K  K  S  C  I  S
Query                 1873  TTCCTGGAGAGTGTGGACGCCCACTTGCAGATCGGGCCCCTCAAGAAGTCCTGCATATCC  1932
Sbjct                 3189  ............................................................  3248

CDS:E3 ubiquitin-pro  634   V  L  K  R  R
Query                 1933  GTGCTGAAGAGGAGGTGATGCCGGGCACGGGCGCTCCTGCTGCCGTCTCTGCTCCAGGAA  1992
Sbjct                 3249  ............................................................  3308

Query                 1993  GCTGCCTCCTCTGGGCCCTCTCCTTCGTCTGGGAAGGCACCAGCATGAGTCCCACACACC  2052
Sbjct                 3309  ............................................................  3368

Query                 2053  CAGCCTTCTCATTTCTAGAGGCTTCCACCTTTTTATACACTCAGCCTTCCCTCTCCCAGG  2112
Sbjct                 3369  ............................................................  3428

Query                 2113  CAGGAGGACCCCCAGACCCTGTTCCCCTGCAGACCTCACTTCTGGGAGACAGAGCTACAG  2172
Sbjct                 3429  ............................................................  3488

Query                 2173  CTGGGACAGCTCCAAGCTACCCTAACCCCTCCTTTCCCAGGTTTCTAGAATAGTGTCTGG  2232
Sbjct                 3489  ............................................................  3548

Query                 2233  CATGTAGTAGATGCTCAATAAACACTTGTTGAA  2265
Sbjct                 3549  .................................  3581
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