NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARe70F04
Vector : pKA1U5

Lot# : 7672_B3Bd

Gene	ZNRF2	
RefSeq_mRNA	NM_147128.4	3167 bp

● Plasmid DNA purification

Date : 23.03.22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.24 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.24

DNA concentration (O.D.): 288 ng/ul

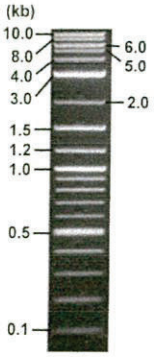
< Size of fragment expected from this clone >

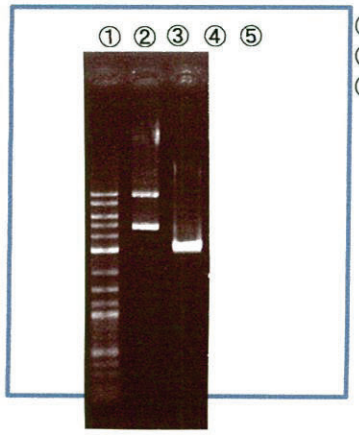
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

BamHI 3.1kb (vector), 3.0 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 : 2026/06/18

full sequence : ARe70F04hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (288 ng/ul)	72 ul
10x TE	83 ul
dH_2O	674 ul
Total	829 ul

● Shipping

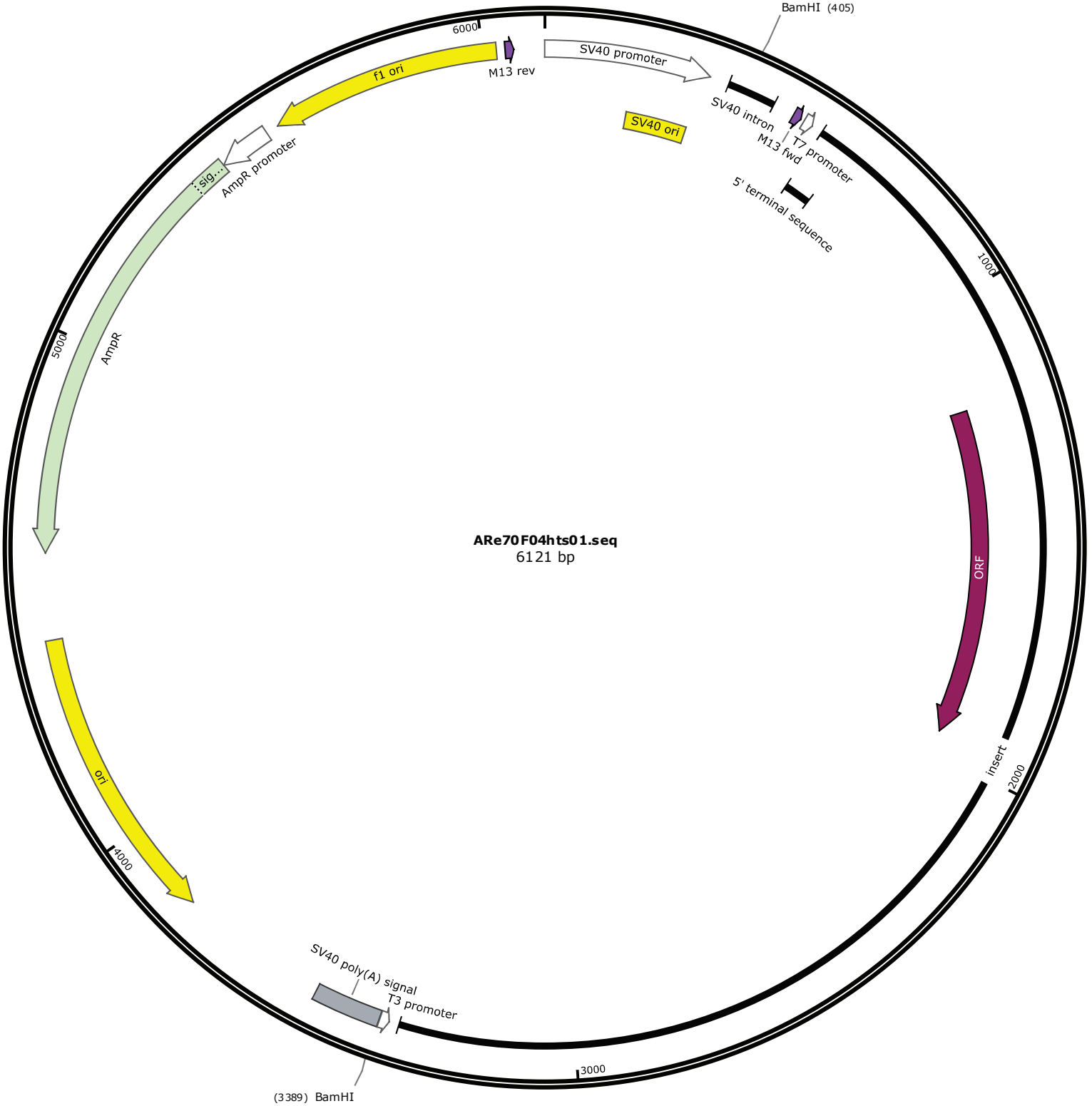
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

検
'26.07.23
笹沼

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


BamHI (405)
6000
f1 ori
M13 rev
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
1000
sig...
AmpR promoter
5000
AmpR
ORF
ARe70F04hts01.seq
6121 bp
insert
2000
ori
4000
SV40 poly(A) signal
T3 promoter
3000
(3389) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: AB371497:AB371497 pKA1U5/ARPE-19 vector-capped...

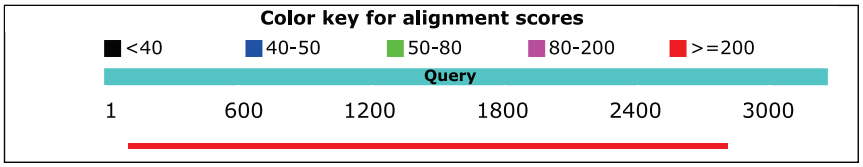
RID 36KA8WEX114 (Expires on 06-19 09:43 am)

Query ID	NM_147128.4	**Subject ID**	lcl|Query_7878245
Description	Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	3167	**Molecule type**	dna
		Subject Length	6121
		Program	BLASTN 2.17.0+

ARe70F04hts01.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	4931	4931	84%	0.0	99.96%	Query_7878245

Alignments

Sequence ID: Query_7878245 Length: 6121 Number of Matches: 1
Range 1: 571 to 3243

Score	Expect	Identities	Gaps	Strand	Frame
4931 bits(2670)	0.0()	2672/2673(99%)	0/2673(0%)	Plus/Plus	

Features:

```
Query  107  GATCCTCCCGCCAGCCCGGCCCCTCCTTCGCAGGGGGAGCGAGGCGACGGTTGCCGGGAA  166
Sbjct  571  ...G.............................................................  630

Query  167  GCGCGCGCCACCTCTCCCTCCCATTTTTCGTTCTCCCCTCGCGCGCCACCCGTTTTTCCT  226
Sbjct  631  ...............................................................  690

Query  227  CTTTCTCCGTTAATAACAGCTGGGTGGCTGGGGGAGGAGGGAAGGTGGCCCCGGCGGAGT  286
Sbjct  691  ...............................................................  750

Query  287  CTGGGCGGGCGCCTCCCACTCAGCCGCCAGCCGCCGTGGGAGCCGGAGGATGGCGGCGGT  346
Sbjct  751  ...............................................................  810

Query  347  AGCAGCGGCCGCCCGAGAGGAGGCGGTGCCGAGATCGGGGGCGCCGAGCGCGGCAGCAGA  406
Sbjct  811  ...............................................................  870

Query  407  GAGCGGTAGCGGCCCGTCGTGGCGCACCAGAACCGAAACCAGCGGCAGCCGCACGGCCAC  466
Sbjct  871  ...............................................................  930

Query  467  TTGAGCCGCCCCTTCCTGCTGGAGCCAGCGAGGGGTGCCTGCAGCCGGGACCCCTTCCTC  526
Sbjct  931  ...............................................................  990
```

```
Query                 527   TCCGCGTCTCCTCGTCTCCCGCGCCCGCGTCAGGCCGTCGGCCTCGCCCGCCGCCCCAAG  586
Sbjct                 991   ............................................................  1050

Query                 587   AAGAGCGCGCCGGGCGCCGACTGCCCCTCTGGACGCCGGGCGGCGGCCCTGGACGTGCGG  646
Sbjct                 1051  ............................................................  1110

Query                 647   GGGCCTCTCTGGGCCGGCCGCGGCGCCTGGGCCCTGCCCTCTAGCTCCCGCGCTCGCTCC  706
Sbjct                 1111  ............................................................  1170

CDS:E3 ubiquitin-pro  1                                                          M  G
Query                 707   CGCCCTCCCGGCTCTCGGGGCGCAGCGCGCGGGCCCGGCCCGGGGCAGGGCGGACATGGG  766
Sbjct                 1171  ............................................................  1230

CDS:E3 ubiquitin-pro  3       A  K  Q  S  G  P  A  A  A  N  G  R  T  R  A  Y  S  G  S  D
Query                 767   CGCCAAACAGAGCGGCCCGGCCGCCGCTAACGGCCGCACGCGCGCGTACTCGGGCTCGGA  826
Sbjct                 1231  ............................................................  1290

CDS:E3 ubiquitin-pro  23      L  P  S  S  S  S  G  G  A  N  G  T  A  G  G  G  G  G  A  R
Query                 827   TCTACCTTCCAGTAGCAgcggaggcgccaatgggaccgcgggcggcggcgggggcgctcg  886
Sbjct                 1291  ............................................................  1350

CDS:E3 ubiquitin-pro  43      A  A  A  A  G  R  F  P  A  Q  V  P  S  A  H  Q  P  S  A  S
Query                 887   ggccgccgccgcggggAGGTTCCCGGCTCAGGTgcccagcgcgcaccagcccagcgcctc  946
Sbjct                 1351  ............................................................  1410

CDS:E3 ubiquitin-pro  63      G  G  A  A  A  A  A  A  A  P  A  A  P  A  A  P  R  S  R  S
Query                 947   cggcggcgccgcggcggccgcggcggccccggcagccccggcggccccgcgcagccgctc  1006
Sbjct                 1411  ............................................................  1470

CDS:E3 ubiquitin-pro  83      I  G  G  A  V  G  S  V  A  S  G  A  R  A  A  Q  S  P  F  S
Query                 1007  cctcggcggggccgTGGGGAGCGTGGCGTCGGGGGCCCGCGCGGCGCAGTCCCCCTTCAG  1066
Sbjct                 1471  ............................................................  1530

CDS:E3 ubiquitin-pro  103     I  P  N  S  S  S  G  P  Y  G  S  Q  D  S  V  H  S  S  P  E
Query                 1067  CATCCCGAACAGCAGCAGCGGCCCGTACGGCTCGCAGGACTCGGTGCACAGCAGCCCTGA  1126
Sbjct                 1531  ............................................................  1590

CDS:E3 ubiquitin-pro  123     D  G  G  G  G  R  D  R  P  V  G  G  S  P  G  G  P  R  L  V
Query                 1127  GGAcggcggcggcggccgggaccggccggtgggcgggagccccggcgggccgcgccTGGT  1186
Sbjct                 1591  ............................................................  1650

CDS:E3 ubiquitin-pro  143     I  G  S  L  P  A  H  L  S  P  H  M  F  G  G  F  K  C  P  V
Query                 1187  GATCGGCTCCTTACCAGCTCACCTCTCGCCGCACATGTTTGGAGGATTTAAGTGCCCTGT  1246
Sbjct                 1651  ............................................................  1710

CDS:E3 ubiquitin-pro  163     C  S  K  F  V  S  S  D  E  M  D  L  H  L  V  M  C  L  T  K
Query                 1247  ATGCTCAAAATTTGTATCCTCAGATGAAATGGATTTGCATCTTGTAATGTGTTTAACAAA  1306
Sbjct                 1711  ............................................................  1770

CDS:E3 ubiquitin-pro  183     P  R  I  T  Y  N  E  D  V  L  S  K  D  A  G  E  C  A  I  C
Query                 1307  GCCACGAATAACCTATAATGAGGATGTACTGAGTAAAGATGCTGGGGAATGTGCAATATG  1366
Sbjct                 1771  ............................................................  1830

CDS:E3 ubiquitin-pro  203     L  E  E  L  Q  Q  G  D  T  I  A  R  L  P  C  L  C  I  Y  H
Query                 1367  CCTTGAAGAATTGCAGCAGGGAGATACTATAGCACGACTGCCTTGTCTATGCATATATCA  1426
Sbjct                 1831  ............................................................  1890

CDS:E3 ubiquitin-pro  223     K  G  C  I  D  E  W  F  E  V  N  R  S  C  P  E  H  P  S  D
Query                 1427  TAAAGGCTGCATAGATGAATGGTTTGAAGTAAATAGATCTTGCCCTGAGCACCCTTCAGA  1486
```

```
Sbjct                 1891  ............................................................  1950

Query                 1487  TTAAGCGTCAGCTTCCTGTTTTATAGGTTTTCTTGTCTTGACAAGATGCTTGAAAAACCA  1546
Sbjct                 1951  ............................................................  2010

Query                 1547  AGAGGATATGAAAATCTGTCTCTGGAGAAACAAAGACGCAGGCATACTCAGCCAGAAATC  1606
Sbjct                 2011  ............................................................  2070

Query                 1607  TGAGTTTTGTGAGACTTGGTAATACAGAGATGGACAATCGTACTGGGGTaaaaaaaCCCT  1666
Sbjct                 2071  ............................................................  2130

Query                 1667  GCTGAAGAGAGGACAGTGACCACAGAACTCAGTGTACCAAACATGCATACAAAGGACACA  1726
Sbjct                 2131  ............................................................  2190

Query                 1727  CAGGGATTTTGAAAATGCTGCACATCCCTTAATAGTCATCTACATAGGTAATACTGATAA  1786
Sbjct                 2191  ............................................................  2250

Query                 1787  ACATTTTGTATTCAGACGCCAAAGTTAACTGATTTAAAAGTTGATTTACTTTTTATTAAG  1846
Sbjct                 2251  ............................................................  2310

Query                 1847  TTCTCCAGAGCTGCACAACTAGTTAtgttttgatttgttttgttttttaatttggggtct  1906
Sbjct                 2311  ............................................................  2370

Query                 1907  ctttgttttCCCCAACATAATGTTCATAATGTTTCTGCATTCATCTGTTCTTAAATTGAA  1966
Sbjct                 2371  ............................................................  2430

Query                 1967  AAACATATAATTTACTTCTTATAAATTGAAGTCTTAAATGTGAAACCAAGAAATGTAATC  2026
Sbjct                 2431  ............................................................  2490

Query                 2027  AAGCAGTAAAAACATCTGAATGTAGACCATGATCTCAAGTTCTTCCATTTTCTCCCCCAC  2086
Sbjct                 2491  ............................................................  2550

Query                 2087  GAGTGGAAAATAGACTTCTACATAGGAAAGCTAAAATATGTTAATATTTTTAAATTAAAG  2146
Sbjct                 2551  ............................................................  2610

Query                 2147  GTTTAATATCAGAATGCAGTCCAAAGAGCAAATCATATTACATAATTACATTTTAATTAA  2206
Sbjct                 2611  ............................................................  2670

Query                 2207  ATATAGAATATTCTACTGAATTGCAATTTATTAAATATTCTTATCCTCTTAAATAAAACT  2266
Sbjct                 2671  ............................................................  2730

Query                 2267  GCTCAACAGTTAATCAGCAGTGAATCATCTTGCAGCTATGCAATTTaaaaaaaaTACAGA  2326
Sbjct                 2731  ............................................................  2790

Query                 2327  TTACCAATTTCAAGTGCTGCCAGCTAAAATAACTGTTTTAACGGGTATCTTTTGTTTGTT  2386
Sbjct                 2791  ............................................................  2850

Query                 2387  CTTTTCACTTAATTATTTTATTGTGCTTTGCATCTCCAGGCAGTTCTCTCACATTTGGGT  2446
Sbjct                 2851  ............................................................  2910

Query                 2447  AAAATGTTTAGCAGGCTGTAAACTTAAGAAAAGGGTAAAATAAAATTTTCTGGAGAGGAA  2506
Sbjct                 2911  ............................................................  2970

Query                 2507  CTTGGAATTTGAGGGAGATTTTATATACCTTTAAAAACTGTAATTTAATTGGGATGCCAG  2566
Sbjct                 2971  ............................................................  3030

Query                 2567  GTTTATAGCAATTTGCAACTTTAATTTTCCAGATAATCTGGAGGTTAGCATTTGATAAAT  2626
Sbjct                 3031  ............................................................  3090
```

```
Query  2627  GATTTTTTAAAGTAGATATGAAGATTTTGTTAATTTATAATTTATTCATGTGTTATTACT  2686
Sbjct  3091  ............................................................  3150

Query  2687  GTAATTGAAAATGTTATAGACACTTTTAAATTCAGTTTGTGTAGAAAGAAATGTGTTAAA  2746
Sbjct  3151  ............................................................  3210

Query  2747  CAAAATTATGTTAATAAATATTCCCACATAATA  2779
Sbjct  3211  .................................  3243
```



BLAST is a registered trademark of the National Library of Medicine