NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe28G01

Lot# : 7672_B3Bd

Vector : pKA1U5

Gene	TIGD2	
RefSeq_mRNA	NM_145715.3	3186 bp

● Plasmid DNA purification

Date : 2023/03/09 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/03/10 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/03/10

DNA concentration (O.D.): 249 ng/ul

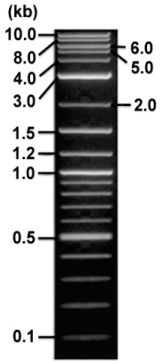
DNA	0.4	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.6	ul
Total	10	ul

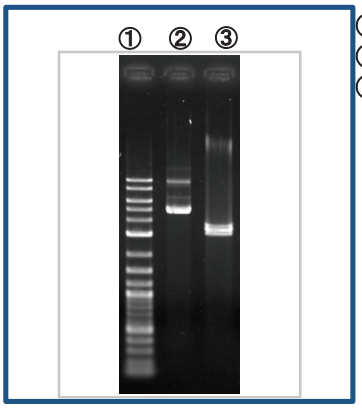
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 3.4 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 : 2026/06/17

full sequence	ARe28G01hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (249 ng/ul)	64	ul
10x TE	64	ul
dH_2O	510	ul
Total	637	ul

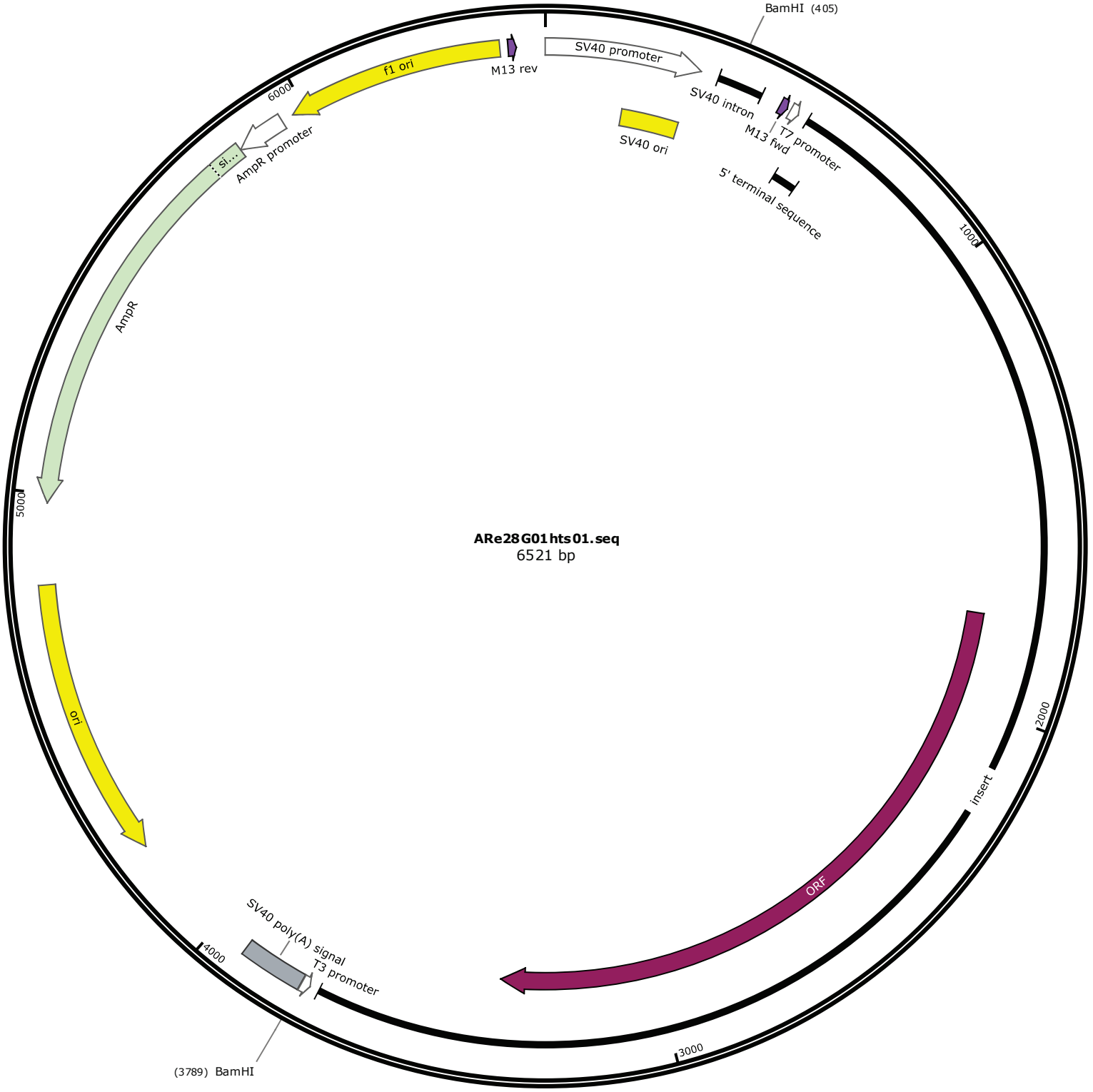
● Shipping

☑ 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)
SV40 promoter
f1 ori
M13 rev
6000
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
1000
AmpR promoter
si...
AmpR
5000
ARe28G01hts01.seq
6521 bp
ori
2000
insert
ORF
SV40 poly(A) signal
T3 promoter
4000
3000
(3789) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_145715:Homo sapiens tigger transposable...

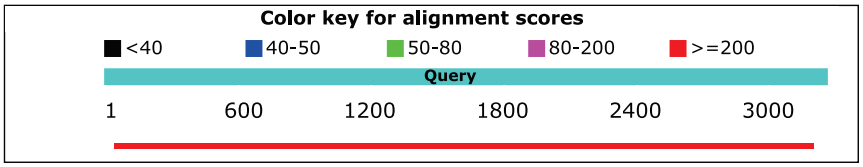
RID 33ZSJW2M114 (Expires on 06-18 09:57 am)

Query ID	NM_145715.3	**Subject ID**	lcl|Query_4682815
Description	Homo sapiens tigger transposable element derived 2 (TIGD2), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3186	**Subject Length**	6521
		Program	BLASTN 2.17.0+

ARe28G01hts01.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	5781	5781	99%	0.0	99.87%	Query_4682815

Alignments

Sequence ID: Query_4682815 Length: 6521 Number of Matches: 1
Range 1: 575 to 3716

Score	Expect	Identities	Gaps	Strand	Frame
5781 bits(3130)	0.0()	3138/3142(99%)	0/3142(0%)	Plus/Plus	

Features:

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Query  45   GCTCGTCCCTCGCCGCTGCCGGGCCACCAGTGCCAGCCTGCCTCAGGAGACTCCATTTGC  104
Sbjct  575  ............................................................  634

Query  105  GCTTAGTGTGGTCTGGGCGCCGCGCAGGCGGTCCCAGGGCGATGCCCGGGGCCGGCGGAC  164
Sbjct  635  ............................................................  694

Query  165  TGGCGTTCCCTGTGCCAAGCGGCCGCCCGCTGGCTGGCTGGCTGCAGCAGTGACATCCTG  224
Sbjct  695  ............................................................  754

Query  225  GTCGCCGGCGTCCAGGCGGAATCCGGGCTCCCTCCGCGGGAGGAAAGACGTCCCGCGCTC  284
Sbjct  755  ............................................................  814

Query  285  TGAAGCTCGCCCAGCGGGGAGAGGCCCTCGCTAACACGGCTTCTCCCTGACCTCTTAATT  344
Sbjct  815  ............................................................  874

Query  345  TCAGGAGGTTTCGGAGCCTCCGAGTATCTCTACAGCCCCCACAGGAACTGCTTCTGTTGG  404
Sbjct  875  ...........................A................................  934

Query  405  TCCATCGAGGATCGTCTTTCACCAGGATTATTGTAACATCATCTTCACCGAGCCTGCCAC  464
Sbjct  935  ............................................................  994
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Query                465   CCCATAGCCTCTACCTTGGGTCCTCATTTCCACCGATGCAGttttttttGATGCTTTCTTT  524
Sbjct                995   ............................................................  1054

Query                525   AGTAATGTGACATCACATGTCCACTATCCTCCTTTCCAGCTGCCAAATCTAGTAGGTTTA  584
Sbjct                1055  ............................................................  1114

Query                585   AGTCGCTTTTAAAGTAGAGTTTTCTGCCTGTTCCACTTTCACCTTATTTGCACTGTTCAC  644
Sbjct                1115  ............................................................  1174

Query                645   TTCTGTCCGGGTCATCTTCTCTTGCGTATGATTTCCACAAGCACTCACTTGCGCAACCTA  704
Sbjct                1175  ............................................................  1234

Query                705   TAGCAGAGTCCGTGCCTAGAGAGACAGCATTCCATACAATCCACTGCTTGACAAAGACCA  764
Sbjct                1235  ............................................................  1294

Query                765   CATAGTCAGAGGGTGAGTTTTCCCATTGTATTTTCCTGTATGTCAAGTTTGCAAGTCCTC  824
Sbjct                1295  ............................................................  1354

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Sbjct                1355  ............................................................  1414

Query                885   GTGGCTATTCTGGCAAAGAACATTACCTGCAAGGATGGCAAGAATTGAGTATGCAATAGT  944
Sbjct                1415  ............................................................  1474

Query                945   ACTGTTTTAGAAGCCTTACCAGTACAGTTTCTAGCCTCTAGTGTGATTGCACTTCATGAA  1004
Sbjct                1475  ............................................................  1534

Query                1005  AGACCCTGAACCCTGAGGAGGAAGAAAGATAGAAGATAAGAGTTAATTGGCGCTAGGCTT  1064
Sbjct                1535  ............................................................  1594

Query                1065  TGTTGTAGGAAGTTTGTAAGTTTTAAAATAGCAAGTAGATTCACGTAGACCTTGTCAGGA  1124
Sbjct                1595  ............................................................  1654

Query                1125  AATTGGTCACTATCCATCTAGGCCCTAGAAGTGAGAGGAGGAATCTTACGAACTCATTTT  1184
Sbjct                1655  ..........................................A.................  1714

Query                1185  CTAGTTGCTTTGTATTCAAATCTTAGTTGTTAATTATCTTGTTCTAGTAATCACCTAAAA  1244
Sbjct                1715  ............................................................  1774

CDS:tigger transposa 1                       M  L  G  K  R  K  R  V  V  L  T  I  K  D  K
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Sbjct                1775  ............................................................  1834

CDS:tigger transposa 16    L  D  I  I  K  K  L  E  E  G  I  S  F  K  K  L  S  V  V  Y
Query                1305  CTTGACATTATTAAGAAACTTGAGGAAGGCATCTCTTTCAAAAAACTTTCCGTGGTGTAC  1364
Sbjct                1835  ............................................................  1894

CDS:tigger transposa 36    G  I  G  E  S  T  V  R  D  I  K  K  N  K  E  R  I  I  N  Y
Query                1365  GGAATTGGTGAATCCACAGTTCGTGATATTAAAAAGAACAAAGAAAGGATTATAAACTAT  1424
Sbjct                1895  ............................................................  1954

CDS:tigger transposa 56    A  N  S  S  D  P  T  S  G  V  S  K  R  K  S  M  K  S  S  T
Query                1425  GCAAACAGTTCAGATCCTACCAGTGGAGTATCCAAACGTAAATCTATGAAGTCATCAACA  1484
Sbjct                1955  ............................................................  2014

CDS:tigger transposa 76    Y  E  E  L  D  R  V  M  I  E  W  F  N  Q  Q  K  T  D  G  I
Query                1485  TACGAGGAGCTTGATAGAGTTATGATAGAGTGGTTTAACCAACAGAAAACAGATGGGATT  1544
Sbjct                2015  ............................................................  2074

CDS:tigger transposa 96    P  V  S  G  T  I  C  A  K  Q  A  K  F  F  F  D  A  L  G  M
Query                1545  CCAGTGTCCGGAACGATTTGTGCAAAACAAGCCAAGTTCTTTTTTGATGCTTTGGGAATG  1604
Sbjct                2075  ............................................................  2134

CDS:tigger transposa 116   E  G  D  F  N  A  S  S  G  W  L  T  R  F  K  Q  R  H  G  I
Query                1605  GAAGGTGATTTTAATGCATCGTCAGGCTGGCTAACTCGATTTAAGCAGCGCCATGGTATT  1664
Sbjct                2135  ............................................................  2194

CDS:tigger transposa 136   P  K  A  A  G  K  G  T  K  L  K  G  D  E  T  A  A  R  E  F
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Sbjct                2195  ............................................................  2254

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Sbjct                2255  ............................................................  2314

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Sbjct                2315  ............................................................  2374

CDS:tigger transposa 196   D  Q  S  T  S  G  C  R  S  S  R  E  R  I  I  I  M  C  C  A
Query                1845  GACCAAAGTACTTCTGGGTGTAGGTCAAGCAGAGAGAGAATCATCATTATGTGTTGCGCA  1904
Sbjct                2375  ............................................................  2434

CDS:tigger transposa 216   N  A  T  G  L  H  K  L  N  L  C  V  V  G  K  A  K  K  P  R
Query                1905  AATGCCACAGGTTTACACAAACTTAATCTTTGTGTTGTGGGGAAGGCCAAAAAGCCCCGA  1964
Sbjct                2435  ............................................................  2494

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Sbjct                2495  ............................................................  2554

CDS:tigger transposa 256   W  I  E  Q  S  V  F  R  Q  W  F  E  K  Y  F  V  P  Q  V  Q
Query                2025  TGGATAGAACAGTCTGTTTTCAGACAGTGGTTTGAAAAGTACTTTGTGCCACAGGTACAG  2084
Sbjct                2555  ............................................................  2614

CDS:tigger transposa 276   K  H  L  K  S  K  G  L  L  E  K  A  V  L  L  L  D  F  P  P
Query                2085  AAGCATTTGAAATCCAAGGGACTTTTAGAAAAAGCAGTGCTTCTTTTAGATTTCCCCCCA  2144
Sbjct                2615  ............................................................  2674

CDS:tigger transposa 296   A  R  P  N  E  E  M  L  S  S  D  D  G  R  I  I  V  K  Y  L
Query                2145  GCACGTCCAAATGAAGAAATGTTGAGTTCAGATGATGGCAGAATAATTGTGAAGTATTTG  2204
Sbjct                2675  ............................................................  2734

CDS:tigger transposa 316   P  P  N  V  T  S  L  I  Q  P  M  S  Q  G  V  L  A  T  V  K
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Sbjct                2735  ............................................................  2794

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Sbjct                2795  ............................................................  2854

CDS:tigger transposa 356   F  W  K  N  L  T  V  L  D  A  I  Y  E  V  S  R  A  W  N  M
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Sbjct                2855  ............................................................  2914

CDS:tigger transposa 376   V  K  S  S  T  I  T  K  A  W  K  K  L  F  P  G  N  E  E  N
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Sbjct                2915  ............................................................  2974
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CDS:tigger transposa  396   S  G  M  N  I  D  E  G  A  I  L  A  A  N  L  A  T  V  L  Q
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Sbjct                 2975  ............................................................  3034

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Sbjct                 3035  ............................................................  3094

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Sbjct                 3095  ............................................................  3154

CDS:tigger transposa  456   A  A  E  Q  K  P  S  S  K  S  R  K  T  E  L  N  P  E  K  H
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Sbjct                 3155  ............................................................  3214

CDS:tigger transposa  476   I  S  H  K  A  A  L  E  W  T  E  N  L  L  D  Y  L  E  Q  Q
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Sbjct                 3215  ............................................................  3274

CDS:tigger transposa  496   D  D  M  L  L  S  D  K  L  V  L  R  R  L  R  T  I  I  R  K
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Sbjct                 3275  ............................................................  3334

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Sbjct                 3335  ............................................................  3394

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Sbjct                 3395  ............................................................  3454

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Sbjct                 3515  ............................................................  3574

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Sbjct                 3635  ............................................................  3694

Query                 3165  ATTTTTATGATTTTTCTTTGAA  3186
Sbjct                 3695  .......................  3716
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2683 A>G (H475R)

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