NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARi16D12
Vector : pGCAP10

Lot# : 7675_B3Bd

Gene ZNF772
RefSeq_mRNA NM_001144068.2 : 5292 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.): 299 ng/ul

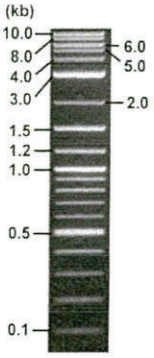
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

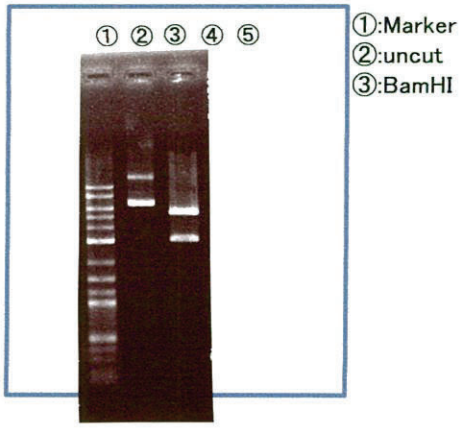
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 5.5 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 : 2026/06/19

full sequence : ARi16D12hts01.seq

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2026/07/23

DNA (299 ng/ul)	76 ul
10x TE	91 ul
dH_2O	742 ul
Total	909 ul

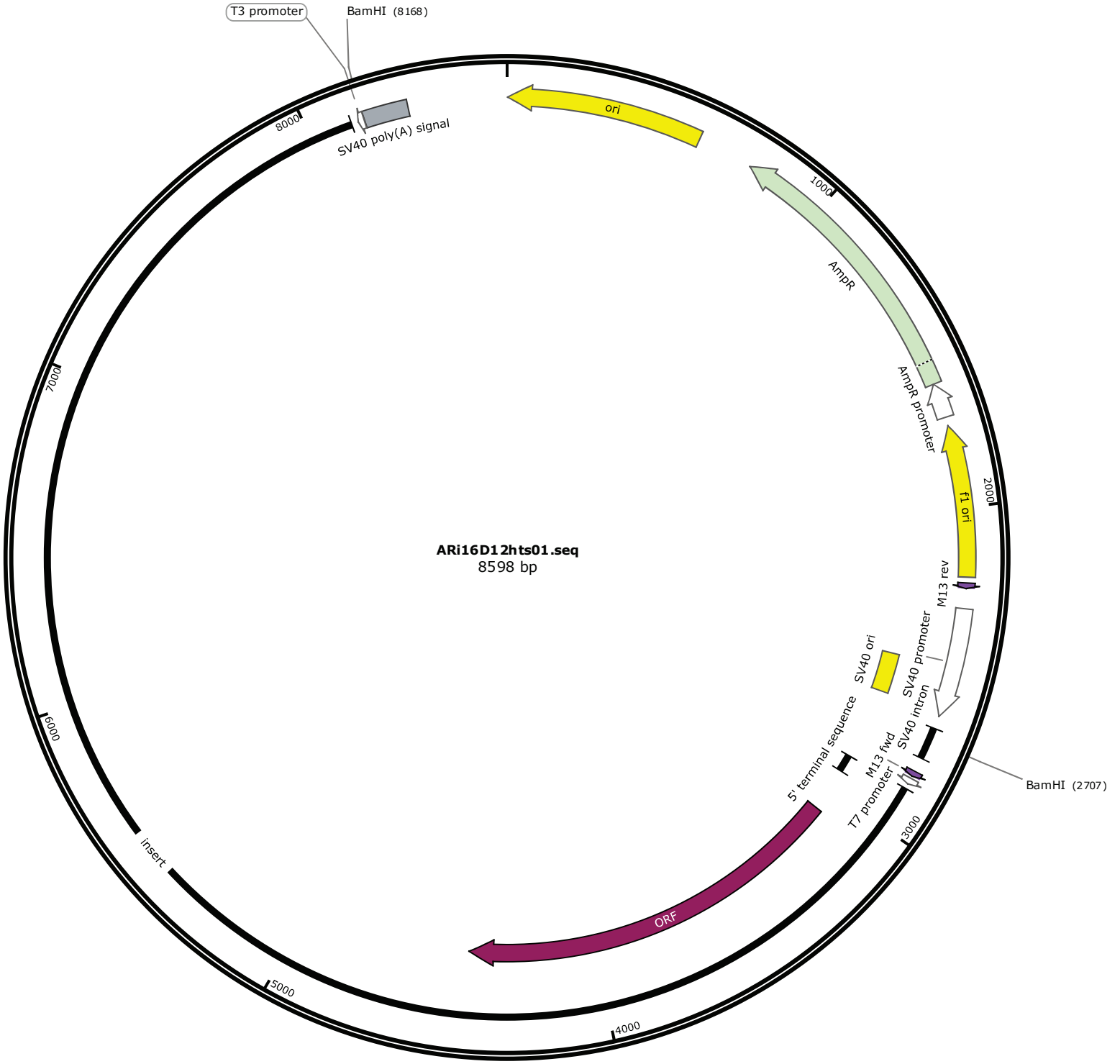
● **Shipping**

☑ 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


T3 promoter
BamHI (8168)
SV40 poly(A) signal
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 ori
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
BamHI (2707)
1000
2000
3000
4000
5000
6000
7000
8000
ARi16D12hts01.seq
8598 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001144068:Homo sapiens zinc finger protein...

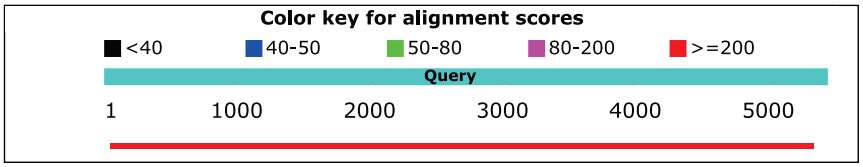
RID 39GFXHDX114 (Expires on 06-20 12:13 pm)

Query ID	NM_001144068.2	**Subject ID**	lcl|Query_6846547
Description	Homo sapiens zinc finger protein 772 (ZNF772), transcript variant 2, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	5292	**Subject Length**	8598
		Program	BLASTN 2.17.0+

ARi16D12hts01.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	9524	9524	99%	0.0	99.45%	Query_6846547

Alignments

Sequence ID: Query_6846547 Length: 8598 Number of Matches: 1
Range 1: 2870 to 8112

Score	Expect	Identities	Gaps	Strand	Frame
9524 bits(5157)	0.0()	5221/5250(99%)	11/5250(0%)	Plus/Plus	

Features:

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Query          47    ATTAATCCACTGGTTTAGTTTCCAGAACGCAATGTCAGACCTGAGGTGACAGAAAAGGGA  106
Sbjct          2870  ..............................................................  2929

Query          107   AAACGTGAGAGAGTGTCTTCTTCCCTGAAGAGAGGTGGGCCTGAGGCTTGACAGTGGCGC  166
Sbjct          2930  ..............................................................  2989

Query          167   TGCCTGAGTGACCTAGCCGCTGGGCTGGGCCCTGGACAGCTGATCCCAGGTTCCTGCACT  226
Sbjct          2990  ..............................................................  3049

CDS:zinc finger prot  1                                    M  G  A  A  A  E  P  M  G  P
Query          227   TGTCGCCACCCTTCCGTAGTCCACAGGCCTGAT---GGCGGCGGCTGAGCCGATGGGCCC  283
Sbjct          3050  ..............................GGC.....................  3109

CDS:zinc finger prot  10    A  Q  V  P  M  N  S  E  V  I  V  D  P  I  Q  G  Q  V  N  F
Query          284   GGCACAGGTTCCCATGAACTCAGAAGTAATTGTGGACCCTATACAGGGGCAGGTGAACTT  343
Sbjct          3110  ..............................................................  3169

CDS:zinc finger prot  30    E  D  V  F  V  Y  F  S  Q  E  E  W  V  L  L  D  E  A  Q  R
Query          344   TGAGGACGTGTTCGTGTACTTCTCCCAGGAGGAGTGGGTGCTCCTTGATGAGGCTCAGAG  403
Sbjct          3170  ..............................................................  3229
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60_61 ins"GCG"

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CDS:zinc finger prot  50    L  L  Y  R  D  V  M  L  E  N  F  A  L  M  A  S  L  G  C  W
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Sbjct                 3230  ............................................................  3289

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Query                 464   GCATGGAATGGAGGATGAAGAGATACCTTTTGAGCAGAGCTTTTCTATAGGAATGTCACA  523
Sbjct                 3290  ............................................................  3349

CDS:zinc finger prot  90    I  R  I  P  K  G  G  P  S  T  Q  K  A  Y  P  C  G  T  C  G
Query                 524   GATCAGGATTCCCAAGGGAGGTCCTTCTACTCAGAAGGCTTACCCCTGTGGGACATGTGG  583
Sbjct                 3350  ............................................................  3409

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Query                 584   CCTGGTCTTAAAAGACATTTTGCACTTGGCTGAGCACCAGGAAACACACCCAGGGCAGAA  643
Sbjct                 3410  ............................................................  3469

CDS:zinc finger prot  130   P  Y  M  C  V  L  C  G  K  Q  F  C  F  S  A  N  L  H  Q  H
Query                 644   ACCATACATGTGTGTGCTGTGTGGGAAACAGTTCTGCTTCAGTGCAAACCTTCACCAGCA  703   680 C>G (C141W)
Sbjct                 3470  ..........................................G.................  3529

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Sbjct                 3530  ............................................................  3589

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Query                 764   GAACAACTGTGCTGTGCAATCAATGGAGATGTCTTTTGTGACAGGGGAGGCTTGTAAGGA  823   786 A>T (M177L)
Sbjct                 3590  ..........................T.................................  3649

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Sbjct                 3650  ............................................................  3709

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Sbjct                 3710  ............................................................  3769

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Query                 944   ATGTGGGAAAACCTTCAGCCGCAAAGACTCACTTGTTCAACACCAGAGAGTCCACACTGG  1003
Sbjct                 3770  ............................................................  3829

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Sbjct                 3830  ............................................................  3889

CDS:zinc finger prot  270   Q  H  Q  R  I  H  T  G  E  M  P  Y  E  C  G  I  C  G  K  V
Query                 1064  TCAGCACCAGAGAATCCACACTGGAGAAATGCCTTATGAGTGTGGCATATGTGGGAAAGT  1123
Sbjct                 3890  ............................................................  3949

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Sbjct                 3950  ............................................................  4009

CDS:zinc finger prot  310   K  C  S  E  C  G  K  A  Y  S  H  K  S  T  L  V  Q  H  E  S
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Sbjct                 4010  ............................................................  4069

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Query                 1244  TATCCATACTGGAGAAAGGCCATATGAGTGCAGCGAATGTGGAAAATACTTTGGTCACAA  1303
Sbjct                 4070  ............................................................  4129
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Sbjct                 4130  ..........................C.................................  4189   1328 T>C

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Sbjct                 4190  ............................................................  4249

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Sbjct                 4370  ............................................................  4429

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Sbjct                 4430  ............................................................  4489

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Sbjct                 4910  ............................................................  4969

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Sbjct                 4970  ......G.....................T.....................T..  5029

Query                 2204  CTGTTCGCTTTGTGGGTTGGGTTGAGAACAGAATTGAGCTAAGCCAGTATGAAGGGAAGA  2263
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Sbjct  6523  ..........................................................  6582

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Sbjct  6583  ..........................................................  6642

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Sbjct  6703  ........................T.................................  6762

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Sbjct  6763  ..........................................................  6822

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Sbjct  6823  ..........................................................  6882

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Sbjct  7363  ..........................................................  7422

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Sbjct  7483  ..........................................................  7542
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Sbjct  7903  ............................................................  7962

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Sbjct  7963  ..........T.................................................  8022

Query  5203  TTACTTCTCTGCAGTTCTGTCAGATTTTGCTTCACATATTTTAGTATGTTTTTATTAGGT  5262
Sbjct  8023  ........................................G...................  8082

Query  5263  GAATAATAAATATTTCCTATTTTATGTCCA  5292
Sbjct  8083  ..............................  8112
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