NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARe32F11
Vector : pKA1U5

SNHG15
Lot# : 7672_B3Bd

Gene	C7orf40	
Accession No.	AB371433	780 bp

● Plasmid DNA purification

Date : 23.02.28 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.01 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.01

DNA concentration (O.D.): 72 ng/ul

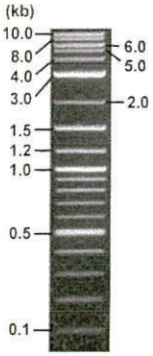
DNA	1.4 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.6 ul
Total	10 ul

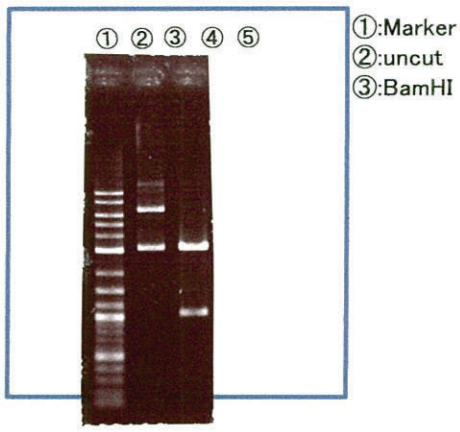
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.0 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 : 2026/06/17

full sequence : ARe32F11hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (72 ng/ul)	70 ul
10x TE	20 ul
dH_2O	111 ul
Total	202 ul

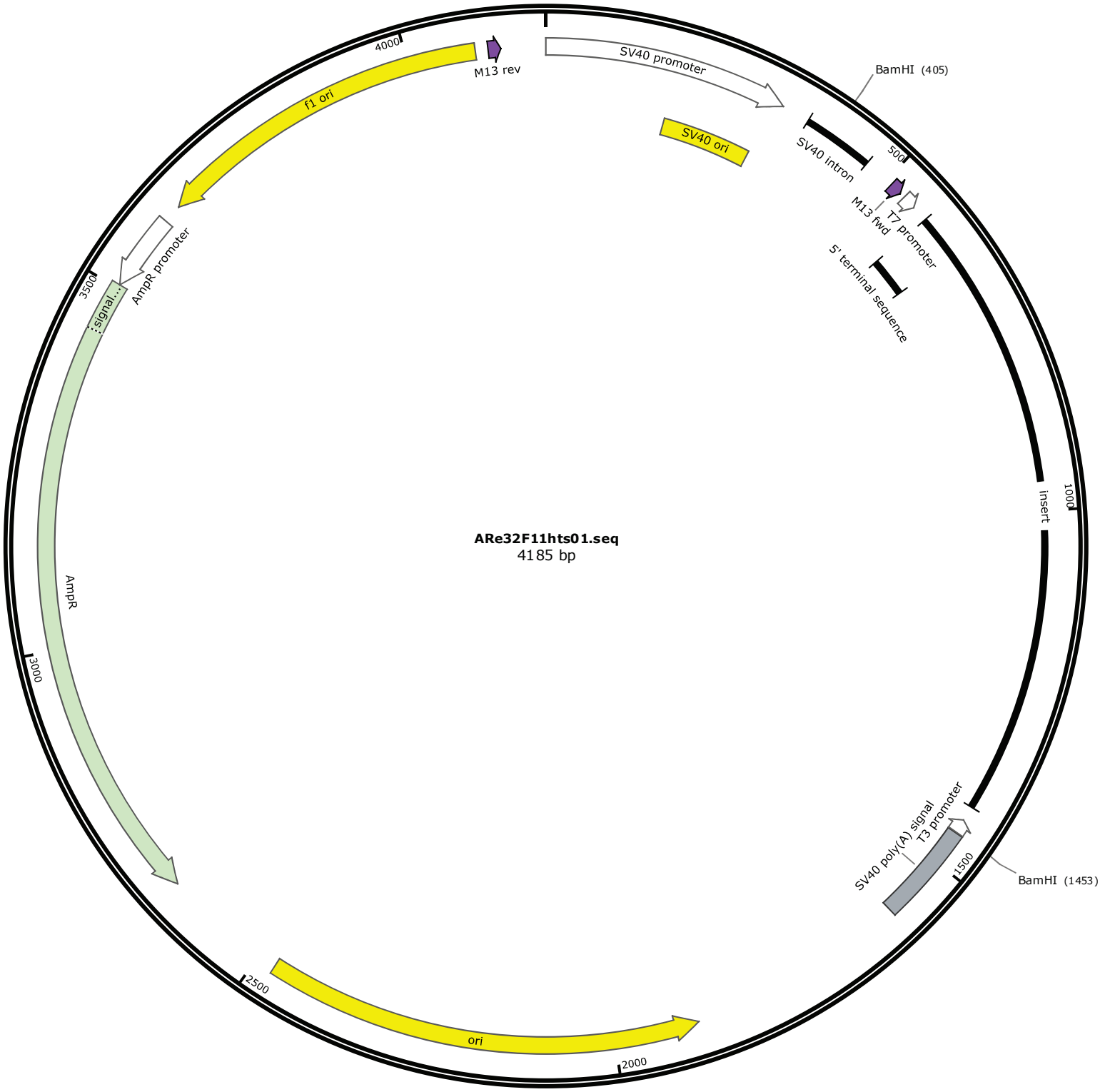
● Shipping

☑ 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


ARe32F11hts01.seq
4185 bp
4000
M13 rev
f1 ori
SV40 promoter
BamHI (405)
SV40 ori
SV40 intron
500
M13 fwd
T7 promoter
5' terminal sequence
insert
1000
3500
signal...
AmpR promoter
AmpR
3000
2500
ori
2000
SV40 poly(A) signal
T3 promoter
1500
BamHI (1453)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NR_003697:Homo sapiens small nucleolar RNA...

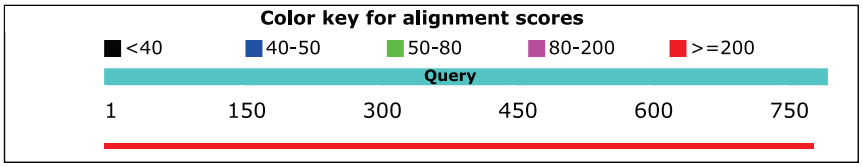
RID 34A46E7P114 (Expires on 06-18 12:54 pm)

Query ID	AB371433.1	**Subject ID**	lcl|Query_2155343
Description	AB371433 pKA1U5/ARPE-19 vector-capped full-length cDNA Homo sapiens cDNA clone HP05071-ARe32F11 5'.	**Description**	None See details
Molecule type	rna	**Molecule type**	dna
Query Length	780	**Subject Length**	4185
		Program	BLASTN 2.17.0+

ARe32F11hts01.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	1441	1441	100%	0.0	100.00%	Query_2155343

Alignments

Sequence ID: Query_2155343 Length: 4185 Number of Matches: 1
Range 1: 574 to 1353

Score	Expect	Identities	Gaps	Strand	Frame
1441 bits(780)	0.0()	780/780(100%)	0/780(0%)	Plus/Plus	

Features:

```
Query  1    GAGACCTGTACTCCGTACTCCGTACTTCGTAGTCGCAGCGGCGCGGTCTTCGGCAGTTTA  60
Sbjct  574  GAGACCTGTACTCCGTACTCCGTACTTCGTAGTCGCAGCGGCGCGGTCTTCGGCAGTTTA  633
Query  61   GTCATCCACCGCCATCCTGGGCCCCACGTGTTGCCTGACCATTCCTGAGCCCAGGTGGGA  120
Sbjct  634  GTCATCCACCGCCATCCTGGGCCCCACGTGTTGCCTGACCATTCCTGAGCCCAGGTGGGA  693
Query  121  GCCGTGGCTGAGGTGACGGTCTCAAAGTGGAAGAGCTTACTGTCACAGCAACTCCTTTGC  180
Sbjct  694  GCCGTGGCTGAGGTGACGGTCTCAAAGTGGAAGAGCTTACTGTCACAGCAACTCCTTTGC  753
Query  181  AAGATGCCCCGGCCAGGAATAGTTGCTGAACACCCCAGGCCTGCTGAGGTCCCTCCTTGA  240
Sbjct  754  AAGATGCCCCGGCCAGGAATAGTTGCTGAACACCCCAGGCCTGCTGAGGTCCCTCCTTGA  813
Query  241  GTCTCATGTTCAAGCAGTCTTTGTCCATGAAACTGGGAGGCGACCGTGTTAGCTGCCAGT  300
Sbjct  814  GTCTCATGTTCAAGCAGTCTTTGTCCATGAAACTGGGAGGCGACCGTGTTAGCTGCCAGT  873
Query  301  TCCTGACAGCCACCTCTCACCAGTGGCTTCACTCTGTGTCCCTGACCCAGCACATGGCAC  360
```

```
Sbjct  874   TCCTGACAGCCACCTCTCACCAGTGGCTTCACTCTGTGTCCCTGACCCAGCACATGGCAC  933
Query  361   AAGAGTGCCTGCCATCCGTCAGTGTTTCTACAGCAGCAATCCCAAGATGCTGGAGCTAGA  420
Sbjct  934   AAGAGTGCCTGCCATCCGTCAGTGTTTCTACAGCAGCAATCCCAAGATGCTGGAGCTAGA  993
Query  421   GGGGACCTGACCTGAGAGAAGATACCTTCAGTGGCTGCCAGGCTGTTCCTTGGAACCTGT  480
Sbjct  994   GGGGACCTGACCTGAGAGAAGATACCTTCAGTGGCTGCCAGGCTGTTCCTTGGAACCTGT  1053
Query  481   GCAGGGATGAGGCCTGCCTGTGTTAATACACCTAGTGAGGAGTGGAGCTGAATTTGAATG  540
Sbjct  1054  GCAGGGATGAGGCCTGCCTGTGTTAATACACCTAGTGAGGAGTGGAGCTGAATTTGAATG  1113
Query  541   CAAGCCTTGGCACCTTAATTGAGCAAGTTTGAAACCTCGCTTGTTGCCCTTCTGGAAGGA  600
Sbjct  1114  CAAGCCTTGGCACCTTAATTGAGCAAGTTTGAAACCTCGCTTGTTGCCCTTCTGGAAGGA  1173
Query  601   GTCAGGAATTTCCAGTTCTGGGCCTGGGCTGTGGGTCTGGCAGACAGACCTCTGGCCCTA  660
Sbjct  1174  GTCAGGAATTTCCAGTTCTGGGCCTGGGCTGTGGGTCTGGCAGACAGACCTCTGGCCCTA  1233
Query  661   GGTTTGGGTGCCAGGTTCTCTGCTTCCAGAATGAGAAGCTTTGCTGTGCACCAGGACCTG  720
Sbjct  1234  GGTTTGGGTGCCAGGTTCTCTGCTTCCAGAATGAGAAGCTTTGCTGTGCACCAGGACCTG  1293
Query  721   GGCCCTTCTGGTATCTCCTGAATGAAAAACAAGGGATATTTAATAAATATGGATTTAAAT  780
Sbjct  1294  GGCCCTTCTGGTATCTCCTGAATGAAAAACAAGGGATATTTAATAAATATGGATTTAAAT  1353
```

BLAST is a registered trademark of the National Library of Medicine



Support center Mailing list YouTube

- National Library Of Medicine
- National Institutes Of Health
- U.S. Department of Health & Human Services
- USA.gov

NCBI

National Center for Biotechnology Information, U.S. National Library of Medicine 8600 Rockville Pike, Bethesda MD, 20894 USA
Policies and Guidelines | Contact

HHS Vulnerability Disclosure