NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe32F05
Vector : pKA1U5

SUPT20H
Lot# : 7672_B3Bd

Gene	FAM48A	
RefSeq_mRNA	NM_017569.4	2901 bp

Plasmid DNA purification

Date : 23.03.08 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.09 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.09

DNA concentration (O.D.): 242 ng/ul

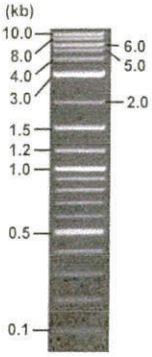
DNA	0.4 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.6 ul
Total	10 ul

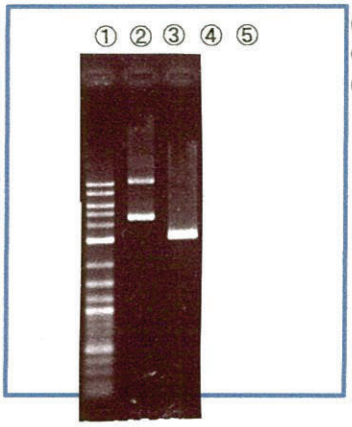
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 3.1 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: ARe32F05hts01.seq

Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (242 ng/ul)	74 ul
10x TE	72 ul
dH_2O	571 ul
Total	716 ul

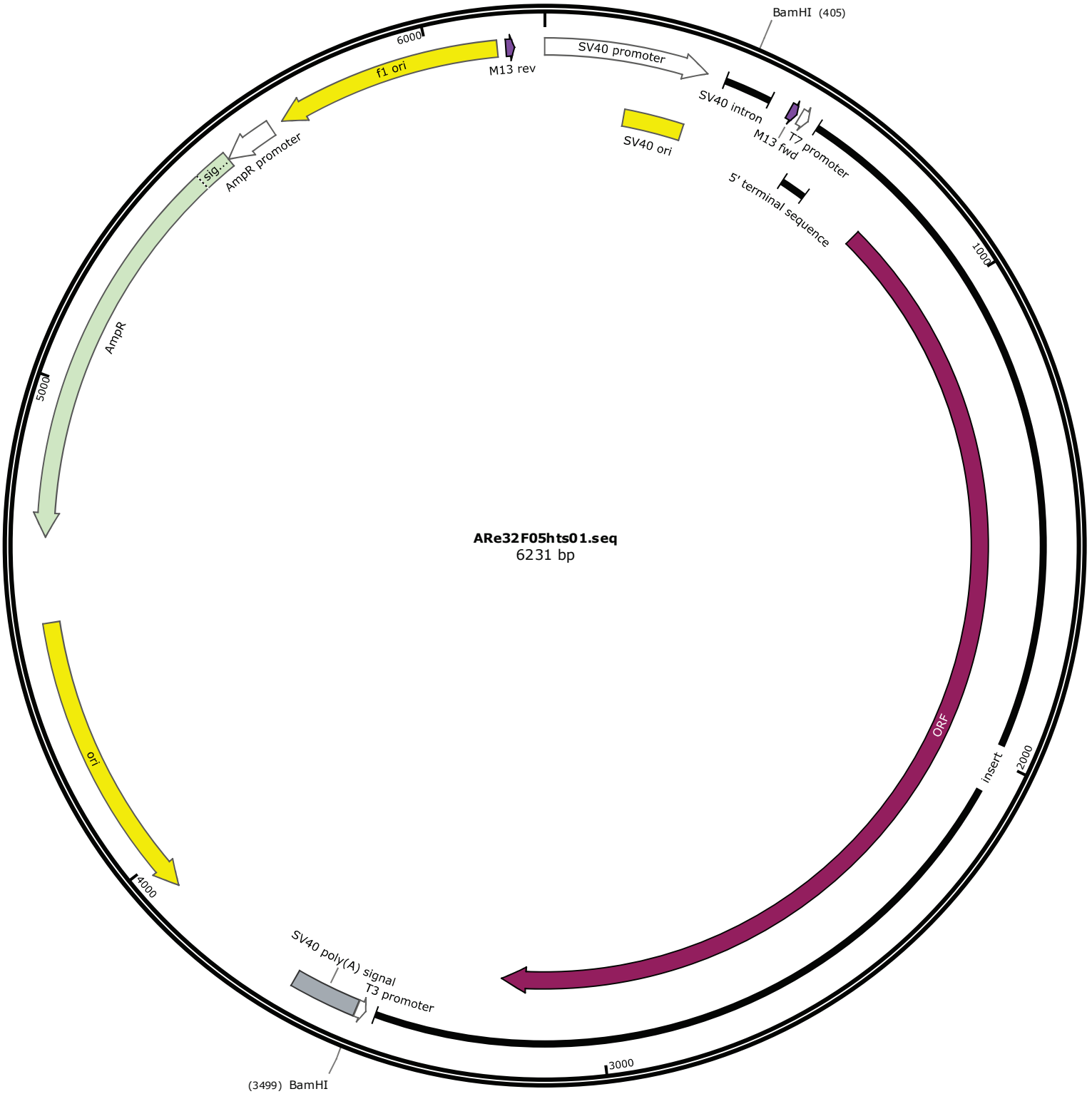
Shipping

☑ 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
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
1000
2000
3000
SV40 poly(A) signal
T3 promoter
(3499) BamHI
4000
ori
5000
AmpR
sig...
AmpR promoter
6000
f1 ori
M13 rev
SV40 ori
ARe32F05hts01.seq
6231 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001278480:Homo sapiens SPT20 homolog, SAGA...

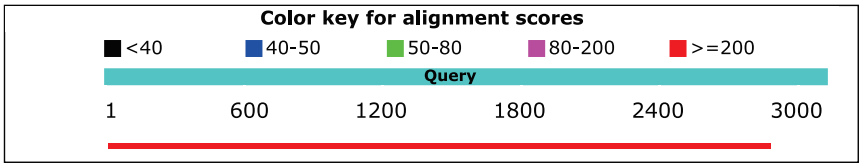
RID 348HA67R114 (Expires on 06-18 12:27 pm)

Query ID	NM_001278480.2	**Subject ID**	lcl|Query_834201
Description	Homo sapiens SPT20 homolog, SAGA complex component (SUPT20H), transcript variant 3, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3056	**Subject Length**	6231
		Program	BLASTN 2.17.0+

ARe32F05hts01.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	5269	5269	93%	0.0	99.96%	Query_834201

Alignments

Sequence ID: Query_834201 Length: 6231 Number of Matches: 1
Range 1: 575 to 3430

Score	Expect	Identities	Gaps	Strand	Frame
5269 bits(2853)	0.0()	2855/2856(99%)	0/2856(0%)	Plus/Plus	

Features:

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Query              20   GGAACTGGCTGTTGGTGGGGGTGCAGCACTGAGCCGCCGACGGGGCGGGTGGGCTTTGCT  79
Sbjct              575  ............................................................  634

Query              80   GCCGAGCAGGCGGCGCCGTCTTGGGGCCTAGCGGCGAGGCGACCCGCACAGTACTGTAAG  139
Sbjct              635  ............................................................  694

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Sbjct              695  ............................................................  754

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Sbjct              755  ............................................................  814

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Query              260  GAGTATGTCATTGAAAGTGCCCGACAGAGACCTCCTAAAAGGAAATACCTATCAAGTGGA  319
Sbjct              815  ............................................................  874

CDS:transcription fa 33   R  K  S  V  F  Q  K  L  Y  D  L  Y  I  E  E  C  E  K  E  P
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Sbjct              875  ............................................................  934
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Sbjct                 935   ..............................................................  994

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Sbjct                 1055  ..............................................................  1114

CDS:transcription fa  113   E  Y  L  D  A  E  E  L  P  P  I  L  V  D  L  L  E  K  S  Q
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Sbjct                 1115  ..............................................................  1174

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Sbjct                 1175  ..............................................................  1234

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Sbjct                 1295  ..............................................................  1354

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

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Sbjct                 1415  ..............................................................  1474

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Sbjct                 1475  ..............................................................  1534

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Sbjct                 1535  ..............................................................  1594

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Sbjct                 1595  ..............................................................  1654

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Sbjct                 1715  ..............................................................  1774

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Sbjct                 1775  ..............................................................  1834
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Sbjct                 1835  ..............................................................  1894

CDS:transcription fa  373   D  E  E  S  D  S  Q  M  S  P  S  H  S  S  T  D  D  H  S  N
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Sbjct                 1895  ..............................................................  1954

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Sbjct                 1955  ..............................................................  2014

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Sbjct                 2015  ..............................................................  2074

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Sbjct                 2075  ..............................................................  2134

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Sbjct                 2135  ..............................................................  2194

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

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Sbjct                 2435  ..............................................................  2494

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

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Sbjct                 2555  ..............................................................  2614

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Sbjct                 2735  ..................................................  2794

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Sbjct                 3395  ....................................  3430
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