NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBb35C07

Lot# : 7676_B6Hk

Vector : pGCAP1

Gene	BASP1	
RefSeq_mRNA	NM_006317.5	1807 bp

● Plasmid DNA purification

Date : 2026/08/24 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/08/25 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/08/25

DNA concentration (O.D.): 66 ng/ul

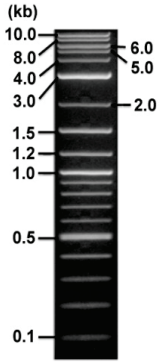
< Size of fragment expected from this clone >

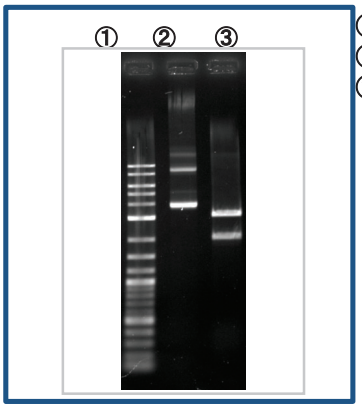
DNA	1.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.5 ul
Total	10 ul

BamHI 3.1kb (vector), 2.1 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 : 2026/08/28

full sequence	RBb35C07hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/09/01

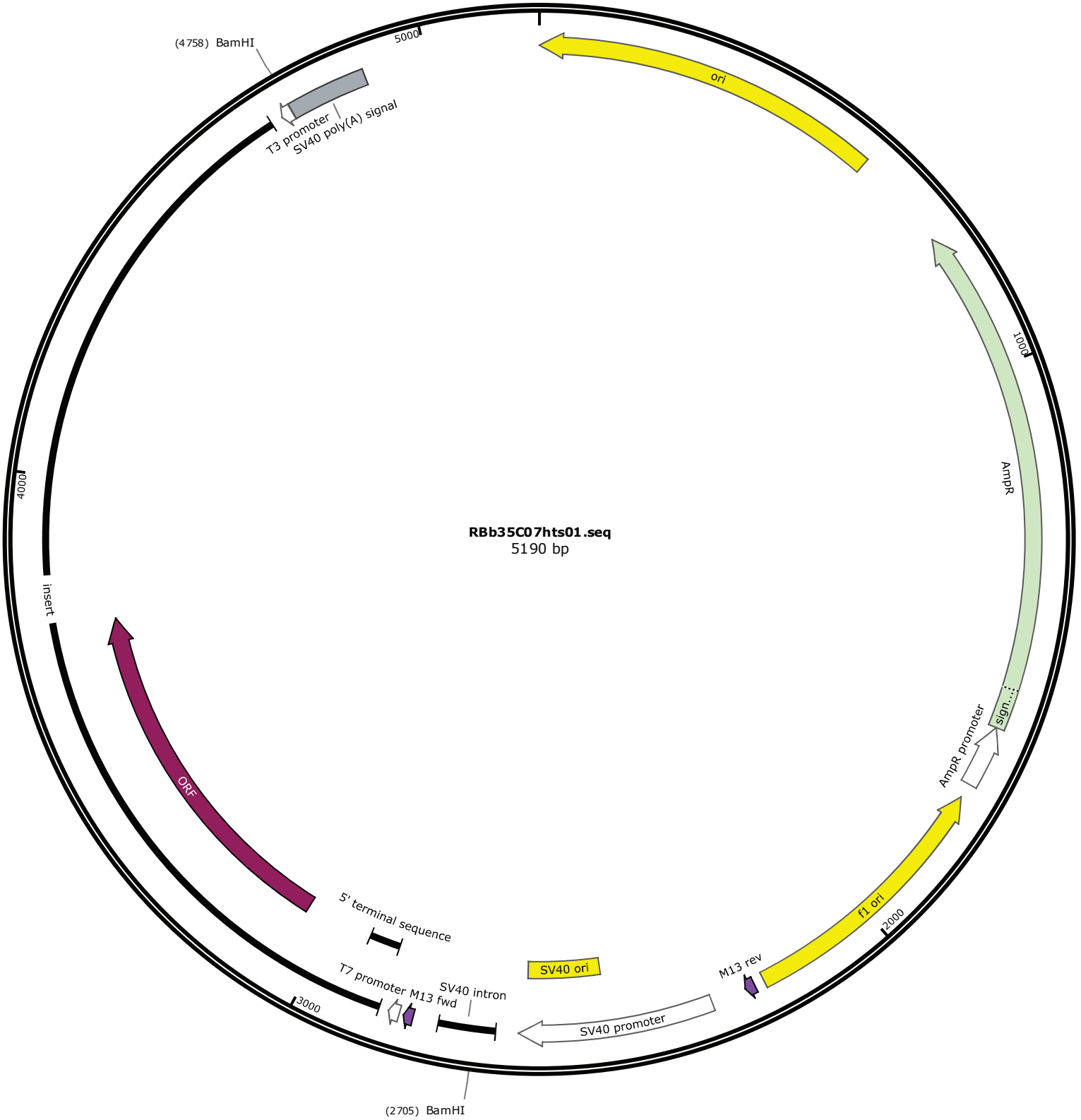
DNA (66 ng/ul)	84 ul
10x TE	22 ul
dH_2O	116 ul
Total	222 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '26.09.01 笹沼


(4758) BamHI
5000
ori
T3 promoter
SV40 poly(A) signal
1000
AmpR
sign...
AmpR promoter
f1 ori
2000
M13 rev
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
3000
(2705) BamHI
SV40 ori
5' terminal sequence
ORF
insert
4000
RBb35C07hts01.seq
5190 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_006317.5|

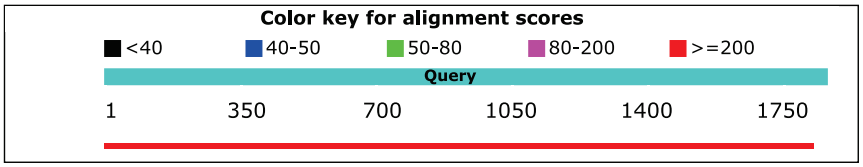
RID 91MSJ9SP114 (Expires on 08-29 08:15 am)

Query ID	NM_006317.5	**Subject ID**	lcl|Query_3170835
Description	Homo sapiens brain abundant membrane attached signal protein 1 (BASP1), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1807	**Subject Length**	5190
		Program	BLASTN 2.17.0+

RBb35C07hts01.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	3301	3301	100%	0.0	99.61%	Query_3170835

Alignments

Sequence ID: Query_3170835 Length: 5190 Number of Matches: 1
Range 1: 2869 to 4677

Score	Expect	Identities	Gaps	Strand	Frame
3301 bits(1787)	0.0()	1804/1811(99%)	6/1811(0%)	Plus/Plus	

Features:

```
Query          1     AGTAGCGGCAGCGGCGACGACGGCGGCGGCAGCGCTCCAACTGGCTCCTCGCTCCGGGCT  60
Sbjct          2869  ............................................................  2928

Query          61    CCGCCGTCGAGCCGGGAGAGAGCCTCCGCCAGCGGCCAGGCACCAGCCAGACGACGCCAG  120
Sbjct          2929  ............................................................  2988

Query          121   CGACCCCGGCCTCTCGGCGGCACCGCGCTAACTCAGGGGCTGCATAGGCACCCAGAGCCG  180
Sbjct          2989  ...........................................T................  3048

CDS:brain acid solub  1              M  G  G  K  L  S  K  K  K  K  G  Y  N  V  N  D  E
Query          181   AACTCCAAGATGGGAGGCAAGCTCAGCAAGAAGAAGAAGGGCTACAATGTGAACGACGAG  240
Sbjct          3049  ............................................................  3108

CDS:brain acid solub  18    K  A  K  E  K  D  K  K  A  E  G  A  A  T  E  E  E  G  T  P
Query          241   AAAGCCAAGGAGAAAGACAAGAAGGCCGAGGGCGCGGCGACGGAAGAGGAGGGGACCCCG  300
Sbjct          3109  ............................................................  3168

CDS:brain acid solub  38    K  E  S  E  P  Q  A  A  A  E  P  A  E  A  K  E  G  K  E  K
Query          301   AAGGAGAGTGAGCCCCAGGCGGCCGCAGAGCCCGCCGAGGCCAAGGAGGGCAAGGAGAAG  360
Sbjct          3169  ............................................................  3228
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CDS:brain acid solub  58    P  D  Q  D  A  E  G  K  A  E  E  K  E  G  E  K  D  A  A  A
Query                 361   CCCGACCAGGACGCCGAGGGCAAGGCCGAGGAGAAGGAGGGCGAGAAGGACGCGGCGGCT  420
Sbjct                 3229  ............................................................  3288

CDS:brain acid solub  78    A  K  E  E  A  P  K  A  E  P  E  K  T  E  G  A  A  E  A  K
Query                 421   GCCAAGGAGGAGGCCCCGAAGGCGGAGCCCGAGAAGACGGAGGGCGCGGCAGAGGCCAAG  480
Sbjct                 3289  ............................................................  3348

CDS:brain acid solub  98    A  E  P  P  K  A  P  E  Q  E  Q  A  A  P  G  P  A  A  G  G
Query                 481   GCTGAgccccgaaggcgcccgagcaggagcaggcggcccccggccccgctgcgggcggc  540
Sbjct                 3349  ............................................................  3408

CDS:brain acid solub  118   E  A  P  K  A  A  E  A  A  A  A  P  A  E  S  A  A  P  A  A
Query                 541   gaggcccccaaagctgctgaggccgccgcggccccggccgAGAGCGCGGCCCCTGCCGCC  600
Sbjct                 3409  ............................................................  3468

CDS:brain acid solub  138   G  E  E  P  S  K  E  E  G  E  P  K  K  T  E  A  P  A  A  P
Query                 601   GGGGAGGAGCCCAGCAAGGAGGAAGGGGAACCCAAAAAGACTGAGGCGCCCGCAGCTCCT  660
Sbjct                 3469  ............................................................  3528

CDS:brain acid solub  158   A  A  Q  E  T  K  S  D  G  A  P  A  S  D  S  K  P  G  S  S
Query                 661   GCCGCCCAGGAGACCAAAAGTGACGGGGCCCCAGCTTCAGACTCAAAACCCGGCAGCTCG  720
Sbjct                 3529  ............................................................  3588

CDS:brain acid solub  178   E  A  A  P  S  S  K  E  T  P  A  A  T  E  A  P  S  S  T  P
Query                 721   GAGGCTGCCCCCTCTTCCAAGGAGACCCCCGCAGCCACGGAAGCGCCTAGTTCCACACCC  780
Sbjct                 3589  ............................................................  3648

CDS:brain acid solub  198   K  A  Q  G  P  A  A  S  A  E  E  P  K  P  V  E  A  P  A  A
Query                 781   AAGGCCCAGGGCCCCGCAGCCTCTGCAGAAGAGCCCAAGCCGGTGGAGGCCCCGGCAGCT  840
Sbjct                 3649  ............................................................  3708

CDS:brain acid solub  218   N  S  D  Q  T  V  T  V  K  E
Query                 841   AATTCCGACCAAACCGTAACCGTGAAAGAGTGACAAGGACAGCCTATAGGAAAAACAATA  900
Sbjct                 3709  ............................................................  3768

Query                 901   CCACTTAAAACAAtctcctctctctctctctctctctctctctatctctctctctatctc  960
Sbjct                 3769  ..............--............................................  3826

Query                 961   ctctctctctctcctctcctatctctcctctctctctctcCTATACTAACTTGTTTCAAA  1020
Sbjct                 3827  ............................................................  3886

Query                 1021  TTGGAAGTAATGATATGTATTGCCCAAGGAAAAATACAGGATGTTGTCCCATCAAGGGAG  1080
Sbjct                 3887  ............................................................  3946

Query                 1081  GGAGGGGGTGGGAGAATCCAAATAGTATTTTTGTGGGGAAATATCTAATATACCTTCAGT  1140
Sbjct                 3947  ............................................................  4006

Query                 1141  CAACTTTACCAAGAAGTCCTGGATTTCCAAGATCCGCGTCTGAAAGTGCAGTACATCGTT  1200
Sbjct                 4007  ............................................................  4066

Query                 1201  TGTACCTGAAACTGCCGCCACATGCACTCCTCCACCGCTGAGAGTTGAATAGCTTTTCTT  1260
Sbjct                 4067  ............................................................  4126

Query                 1261  CTGCAATGGGAGTTGGGAGTGATGCGTTTGATTCTGCCCACAGGGCCTGTGCCAAGGCAA  1320
Sbjct                 4127  ............................................................  4186

Query                 1321  TCAGATCTTTATGAGAGCAGTattttctgtgttttcttttaatttacagcctttcttat  1380
Sbjct                 4187  ............................................................  4246

Query                 1381  tttgatatttttttaATGTTGTGGATGAATGCCAGCTTTCAGACAGAGCCCACTTAGCTT  1440
Sbjct                 4247  ............................................................  4306

Query                 1441  GTCCACATGGATCTCAATGCCAATCCTCCATTCTTCCTCTCCAGATATTTTTGGGAGTGA  1500
Sbjct                 4307  ............................................................  4366

Query                 1501  CAAACATTCTCTCATCCTACTTAGCCTACCTAGATTTCTCATGACGAGTTAATGCATGTC  1560
Sbjct                 4367  ............................................................  4426

Query                 1561  CGTGGTTGGGTGCACCTGTAGTTCTGTTTATTGGTCAGTGGAAATG---aaaaaaaaaaa  1617
Sbjct                 4427  ..........................................AAA.............  4486

Query                 1618  aaaaaaaaGTCTGCGTTCATTGCAGTTCCAGTTTCTCTTCCATTCTGTGTCACAGACACC  1677
Sbjct                 4487  ............................................................  4546

Query                 1678  AACACACCACTCATTGGAAAATGGaaaaaaaaaac-aaaaaaaaaacaaaaaaaTGTACA  1736
Sbjct                 4547  ................................A...........................  4606

Query                 1737  ATGGATGCATTGAAATTATATGTAATTGTATAAATGGTGCAACAGTAATAAAGTTAAACA  1796
Sbjct                 4607  ............................................................  4666

Query                 1797  ATTAAAAAGAA  1807
Sbjct                 4667  ...........  4677
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