NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBb27H05

Lot# : 7676_B5KI

Vector : pGCAP1

Gene	ABHD11	
RefSeq_mRNA	NM_148912.4	1418 bp

● Plasmid DNA purification

Date : 2025/11/25

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

Date : 2025/11/26

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/11/26

DNA concentration (O.D.): 201 ng/ul

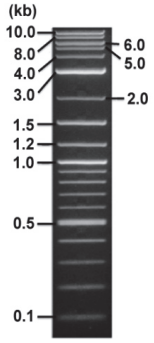
DNA	0.5	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.5	ul
Total	10	ul

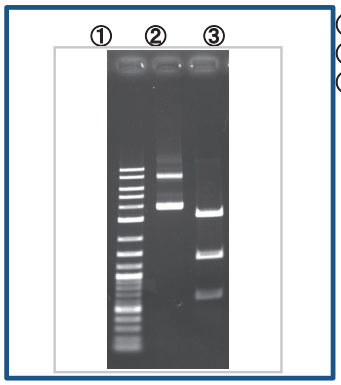
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.3, 0.6 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 : 2025/11/27

full sequence	RBb27H05hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/12/02

DNA (201 ng/ul)	84	ul
10x TE	68	ul
dH_2O	524	ul
Total	675	ul

● Shipping

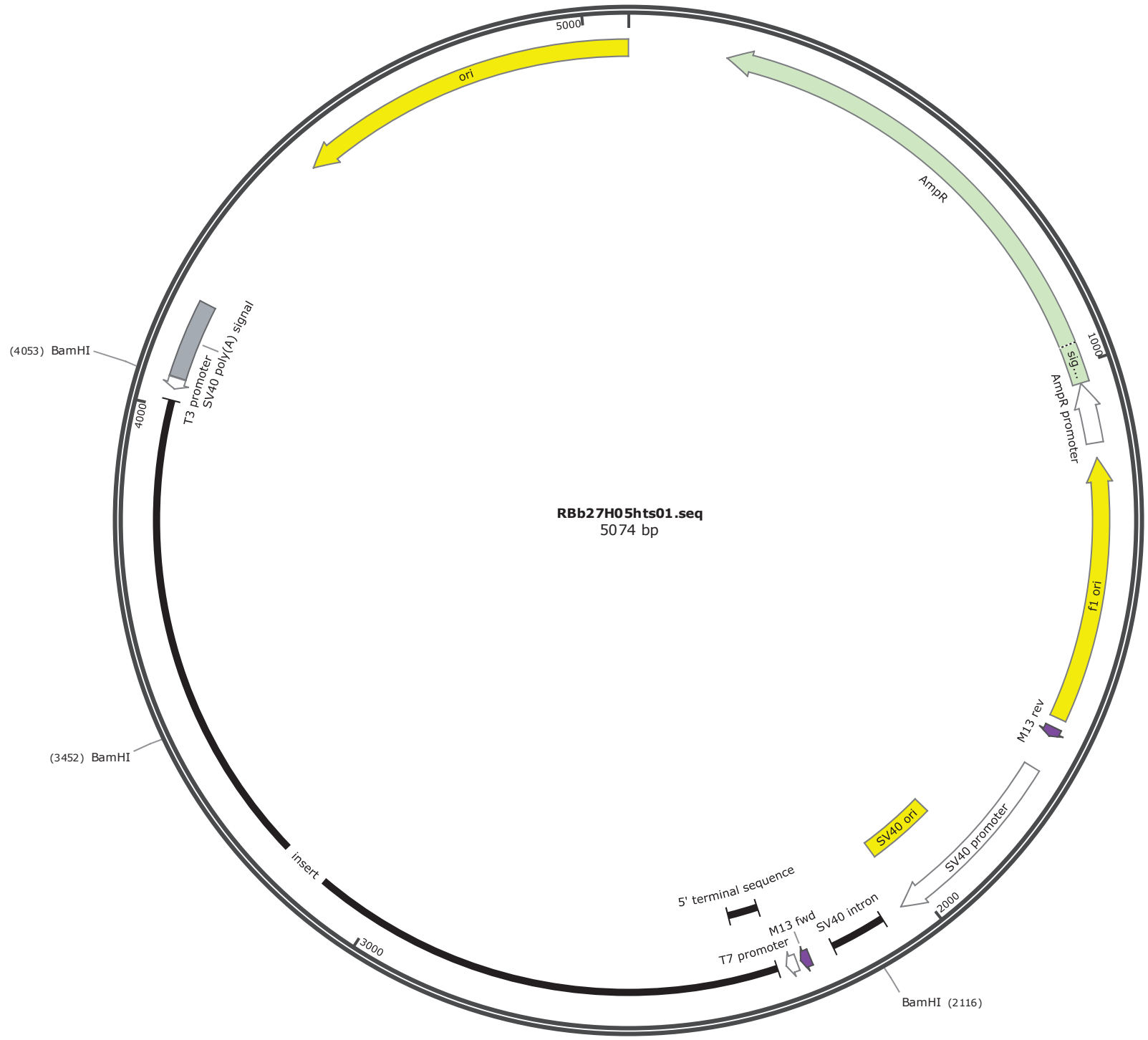
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'25.12.02
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http://dna.brc.riken.jp/index.html


RBb27H05hts01.seq
5074 bp
5000
ori
AmpR
1000
...sig...
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 ori
2000
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
BamHI (2116)
3000
insert
(3452) BamHI
4000
T3 promoter
SV40 poly(A) signal
(4053) BamHI

BLAST ® » blastn suite-2sequences » RID-JG08U9TP114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC075793:Homo sapiens hypothetical protein...

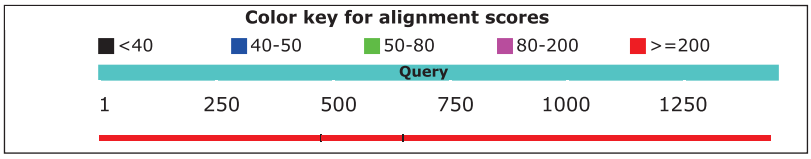
RID JG08U9TP114 (Expires on 11-28 14:43 pm)

Query ID	NM_148912.4	**Subject ID**	lcl|Query_8123875
Description	Homo sapiens abhydrolase domain containing 11 (ABHD11), transcript variant 1, also known as A, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1418	**Subject Length**	5074
		Program	BLASTN 2.17.0+

RBb27H05hts01.seq

Graphic Summary

Distribution of the top 3 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	2621	100%	0.0	99.87%	Query_8123875

Alignments

Sequence ID: Query_8123875 Length: 5074 Number of Matches: 3
Range 1: 3193 to 3975

Score	Expect	Identities	Gaps	Strand	Frame
1441 bits(780)	0.0()	782/783(99%)	0/783(0%)	Plus/Plus	

Features:

```
CDS:sn-1-specific di  202   Q  D  M  A  V  R  Q  H  L  L  T  N  L  V  E  V  D  G  R  F
Query                 636   CAGGACATGGCCGTGCGGCAGCACCTGCTCACTAACCTGGTAGAGGTAGACGGGCGCTTC  695
Sbjct                 3193  ............................................................  3252

CDS:sn-1-specific di  222   V  W  R  V  N  L  D  A  L  T  Q  H  L  D  K  I  L  A  F  P
Query                 696   GTGTGGAGGGTGAACTTGGATGCCCTGACCCAGCACCTAGACAAGATCTTGGCTTTCCCA  755
Sbjct                 3253  ............................................................  3312

CDS:sn-1-specific di  242   Q  R  Q  E  S  Y  L  G  P  T  L  F  L  L  G  G  N  S  Q  F
Query                 756   CAGAGGCAGGAGTCCTACCTCGGGCCAACACTCTTTCTCCTTGGTGGAAACTCCCAGTTC  815
Sbjct                 3313  ............................................................  3372

CDS:sn-1-specific di  262   V  H  P  S  H  H  P  E  I  M  R  L  F  P  R  A  Q  M  Q  T
Query                 816   GTGCATCCCAGCCACCACCCTGAGATTATGCGGCTCTTCCCTCGGGCCCAGATGCAGACG  875
Sbjct                 3373  ............................................................  3432

CDS:sn-1-specific di  282   V  P  N  A  G  H  W  I  H  A  D  R  P  Q  D  F  I  A  A  I
Query                 876   GTGCCGAACGCTGGCCACTGGATCCACGCTGACCGCCCACAGGACTTCATAGCTGCCATC  935
Sbjct                 3433  ............................................................  3492

CDS:sn-1-specific di  302   R  G  F  L  V
Query                 936   CGAGGCTTCCTGGTCTAAGAGTTGCTGGCAAGAAGATGGCCGGGCGTGGTGGCTCATGCC  995
Sbjct                 3493  ............................................................  3552
```

```
Query  996   TGTAATTCCAGCACTTTGGGAGGCTAAGGCGGGAGGATGACTTGAGGCCAGGAGTTGGAG  1055
Sbjct  3553  ............................................................  3612

Query  1056  ACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCTGGC  1115
Sbjct  3613  ...........................................................T  3672

Query  1116  GTGGTGGTGCACACCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGAATCACTTGA  1175
Sbjct  3673  ............................................................  3732

Query  1176  ACCCTGGAGGCAGAGGTTGCAATGAGCCGAGATCACACCACTACACTCCAGCCTAGGCAA  1235
Sbjct  3733  ............................................................  3792

Query  1236  CAGAGCAAGACTCTGTCTCaaaaaaaacaaaacaaaaaGGAGGCACAAAACCCCAGGCTT  1295
Sbjct  3793  ............................................................  3852

Query  1296  CAAGTCTCTGCAGCCTGCTCCACATTTGGGCACAGAAGGACTCAGACAGGCACTGTGTGG  1355
Sbjct  3853  ............................................................  3912

Query  1356  GCACGAGGTTTTACAGGGGTGGTCAGACCTCAGGCTTTAATGAATAAAGACACTACTCCC  1415
Sbjct  3913  ............................................................  3972

Query  1416  AAA  1418
Sbjct  3973  ...  3975
```

Range 2: 2280 to 2744

Score	Expect	Identities	Gaps	Strand	Frame
859 bits(465)	0.0()	465/465(100%)	0/465(0%)	Plus/Plus	

Features:

```
CDS:sn-1-specific di  1                                   M  L  R  W  T  R  A  W  R  L
Query                 3     GAGATGCGAGCCGGCCAACAGCTTGCAAGCATGCTCCGCTGGACCCGAGCCTGGAGGCTC  62
Sbjct                 2280  ............................................................  2339

CDS:sn-1-specific di  11     P  R  E  G  L  G  P  H  G  P  S  F  A  R  V  P  V  A  P  S
Query                 63    CCGCGTGAGGGACTCGGCCCCCACGGCCCTAGCTTCGCGAGGGTGCCTGTCGCACCCAGC  122
Sbjct                 2340  ............................................................  2399

CDS:sn-1-specific di  31     S  S  S  G  G  R  G  G  A  E  P  R  P  L  P  L  S  Y  R  L
Query                 123   AGCAGCAGCGGCGGCCGAGGGGGCGCCGAGCCGAGGCCGCTTCCGCTTTCCTACAGGCTT  182
Sbjct                 2400  ............................................................  2459

CDS:sn-1-specific di  51     L  D  G  E  A  A  L  P  A  V  V  F  L  H  G  L  F  G  S  K
Query                 183   CTGGACGGGGAGGCAGCCCTCCCGGCCGTCGTCTTTTTGCACGGGCTCTTCGGCAGCAAA  242
Sbjct                 2460  ............................................................  2519

CDS:sn-1-specific di  71     T  N  F  N  S  I  A  K  I  L  A  Q  Q  T  G  R  R  V  L  T
Query                 243   ACTAACTTCAACTCCATCGCCAAGATCTTGGCCCAGCAGACAGGCCGTAGGGTGCTGACG  302
Sbjct                 2520  ............................................................  2579

CDS:sn-1-specific di  91     V  D  A  R  N  H  G  D  S  P  H  S  P  D  M  S  Y  E  I  M
Query                 303   GTGGATGCTCGTAACCACGGTGACAGCCCCCACAGCCCAGACATGAGCTACGAGATCATG  362
Sbjct                 2580  ............................................................  2639
```



```
CDS:sn-1-specific di  111    S  Q  D  L  Q  D  L  L  P  Q  L  G  L  V  P  C  V  V  V  G
Query                 363   AGCCAGGACCTGCAGGACCTTCTGCCCCAGCTGGGCCTGGTGCCCTGCGTCGTCGTTGGC  422
Sbjct                 2640  ............................................................  2699

CDS:sn-1-specific di  131    H  S  M  G  G  K  T  A  M  L  L  A  L  Q  R
Query                 423   CACAGCATGGGAGGAAAGACAGCCATGCTGCTGGCACTACAGAGG  467
Sbjct                 2700  ............................................  2744
```

Range 3: 2914 to 3086

Score	Expect	Identities	Gaps	Strand	Frame
320 bits(173)	2e-90()	173/173(100%)	0/173(0%)	Plus/Plus	

Features:

```
CDS:sn-1-specific di  146    P  E  L  V  E  R  L  I  A  V  D  I  S  P  V  E  S  T  G  V
Query                 467   GCCAGAGCTGGTGGAACGTCTCATTGCTGTAGATATCAGCCCAGTGGAAAGCACAGGTGT  526
Sbjct                 2914  ............................................................  2973

CDS:sn-1-specific di  166    S  H  F  A  T  Y  V  A  A  M  R  A  I  N  I  A  D  E  L  P
Query                 527   CTCCCACTTTGCAACCTATGTGGCAGCCATGAGGGCCATCAACATCGCAGATGAGCTGCC  586
Sbjct                 2974  ............................................................  3033

CDS:sn-1-specific di  186    R  S  R  A  R  K  L  A  D  E  Q  L  S  S  V  I  Q
Query                 587   CCGCTCCCGTGCCCGAAAACTGGCGGATGAACAGCTCAGTTCTGTCATCCAGG  639
Sbjct                 3034  ......................................................  3086
```

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