NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBd95E02

Lot# : 7677_B5KI

Vector : pGCAP10

Gene	ABHD4	
RefSeq_mRNA	NM_022060.3	3051 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.): 165 ng/ul

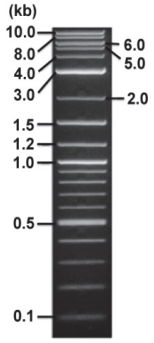
DNA	0.6	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.4	ul
Total	10	ul

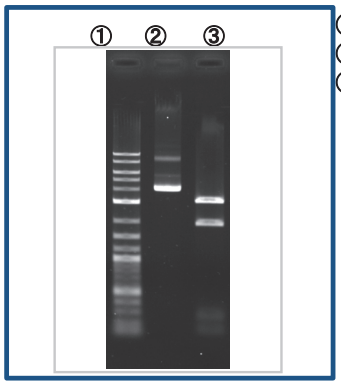
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.0, 0.3, 0.2, 0.2 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 : 2025/11/28

full sequence	RBd95E02hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/12/02

DNA (165 ng/ul)	84	ul
10x TE	55	ul
dH_2O	415	ul
Total	554	ul

● Shipping

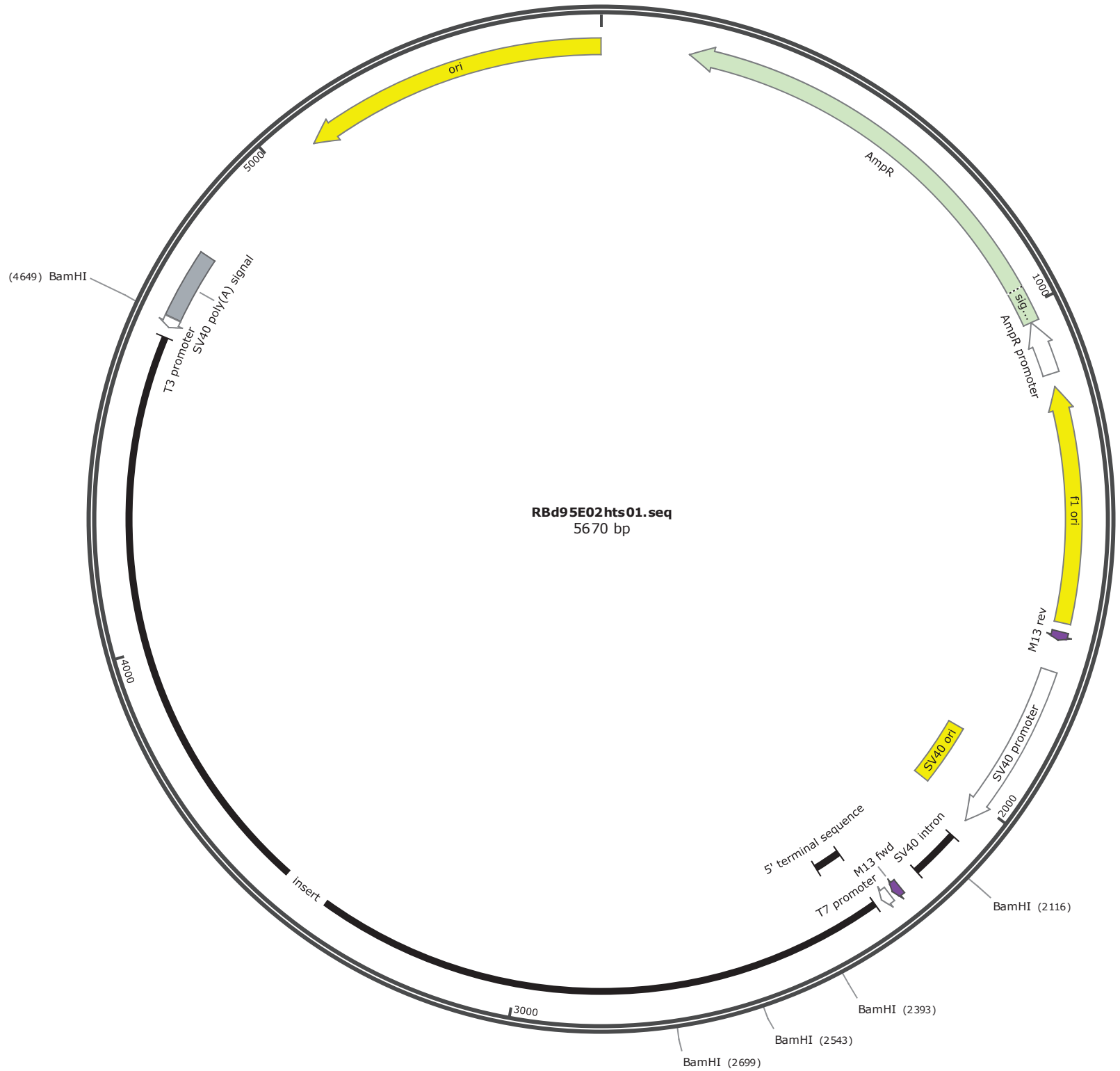
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ 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


RBd95E02hts01.seq
5670 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
insert
T3 promoter
SV40 poly(A) signal
(4649) BamHI
BamHI (2116)
BamHI (2393)
BamHI (2543)
BamHI (2699)
1000
2000
3000
4000
5000

BLAST ® » blastn suite-2sequences » RID-JHUZMC73114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NR_171625:Homo sapiens abhydrolase domain...

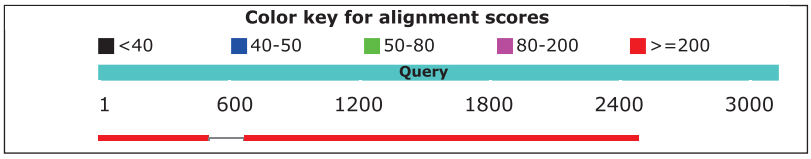
RID JHUZMC73114 (Expires on 11-29 07:25 am)

Query ID	NM_022060.3	**Subject ID**	lcl|Query_7097591
Description	Homo sapiens abhydrolase domain containing 4, N-acyl phospholipase B (ABHD4), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3051	**Subject Length**	5670
		Program	BLASTN 2.17.0+

RBd95E02hts01.seq

Graphic Summary

Distribution of the top 2 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	3315	4225	75%	0.0	99.89%	Query_7097591

Alignments

Sequence ID: Query_7097591 Length: 5670 Number of Matches: 2
Range 1: 2777 to 4577

Score	Expect	Identities	Gaps	Strand	Frame
3315 bits(1795)	0.0()	1799/1801(99%)	0/1801(0%)	Plus/Plus	

Features:

```
CDS:(Lyso)-N-acylpho  214   G  P  G  L  V  Q  R  F  R  P  D  F  K  R  K  F  A  D  F  F
Query                 647   GGGCCTGGTCTGGTGCAGCGATTCCGGCCGGACTTCAAACGCAAGTTTGCAGACTTCTTT  706
Sbjct                 2777  ............................................................  2836

CDS:(Lyso)-N-acylpho  234   E  D  D  T  I  S  E  Y  I  Y  H  C  N  A  Q  N  P  S  G  E
Query                 707   GAAGATGATACCATATCAGAGTATATTTACCACTGCAACGCACAGAATCCCAGTGGTGAG  766
Sbjct                 2837  ............................................................  2896

CDS:(Lyso)-N-acylpho  254   T  A  F  K  A  M  M  E  S  F  G  W  A  R  R  P  M  L  E  R
Query                 767   ACAGCATTCAAAGCCATGATGGAGTCCTTTGGCTGGGCCCGGCGCCCTATGCTGGAGCGA  826
Sbjct                 2897  ............................................................  2956

CDS:(Lyso)-N-acylpho  274   I  H  L  I  R  K  D  V  P  I  T  M  I  Y  G  S  D  T  W  I
Query                 827   ATTCACTTGATTCGAAAAGATGTGCCTATCACTATGATCTACGGGTCCGACACCTGGATA  886
Sbjct                 2957  ............................................................  3016

CDS:(Lyso)-N-acylpho  294   D  T  S  T  G  K  K  V  K  M  Q  R  P  D  S  Y  V  R  D  M
Query                 887   GATACCAGTACGGGAAAAAAGGTGAAGATGCAGCGGCCGGATTCCTATGTCCGAGACATG  946
Sbjct                 3017  ............................................................  3076

CDS:(Lyso)-N-acylpho  314   E  I  K  G  A  S  H  H  V  Y  A  D  Q  P  H  I  F  N  A  V
Query                 947   GAGATTAAGGGTGCCTCCCACCATGTCTATGCTGACCAGCCACACATCTTCAATGCTGTG  1006
Sbjct                 3077  ............................................................  3136
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CDS:(Lyso)-N-acylpho  334   V  E  E  I  C  D  S  V  D
Query                 1007  GTGGAGGAGATCTGCGACTCAGTTGATTGAGCTGCTCTCTGAAGAGGAAGAGGAGAAAGC  1066
Sbjct                 3137  ............................................................  3196

Query                 1067  CAGAGAGTCACTCTTACCTCCCTGTCTGCTTACTCACCCACTCTGTCCTTTCCTCACCAA  1126
Sbjct                 3197  ............................................................  3256

Query                 1127  CTAACATGTGCCAGCCAGGCAGAGTCTTGTGCTGTTCCCAGAACAGGACGACAGTGAAAA  1186
Sbjct                 3257  ............................................................  3316

Query                 1187  GAACACTCTTGACCCTACACTGAAGGCTGAAGGCAGAAGCCACAAGAGGCCTTGAGTGCC  1246
Sbjct                 3317  ............................................................  3376

Query                 1247  ACCCCCAGGGAAGAACATAAAGGGTTGCACAATGCCACCCATCCACTCCTTGCCAAGTGT  1306
Sbjct                 3377  ............................................................  3436

Query                 1307  TACCCAGATGGTGGAGGATGTGAAGGGATTGCACCAAGCCACATTCACTCTCTCTGTGGC  1366
Sbjct                 3437  ............................................................  3496

Query                 1367  CTTTCTTCCTCTGGGCAAAGAAGGGCTTCCAGTGGCCTTTCCTCACTCTGTAGTGTTTGT  1426
Sbjct                 3497  ............................................................  3556

Query                 1427  GGGGATAGGTTCCATGCAAGAACACCTTCCTCCTCCATCCCCCACTTCACCCCATCCCAT  1486
Sbjct                 3557  ............................................................  3616

Query                 1487  ACCAGTTCCATCCAGGGTCTGCTTAACTGCCAAGAGCAGGTCCTGGAGTTCCCTTCACCT  1546
Sbjct                 3617  ............................................................  3676

Query                 1547  GCAGAGTCCTTTTCATGACCTAGGAGGTCTTATTCAAAGCCCTCATTGACAGAGGAGGAA  1606
Sbjct                 3677  ............................................................  3736

Query                 1607  ACAGGCCAAGGCAGGACATGGCTGGACCATGGTGATACAGCTCTGTGTGATTCAAGTTCT  1666
Sbjct                 3737  ............................................................  3796

Query                 1667  GGCAGAGCTTGTAAGGCTAGAGCCCAGGTCTGCCGACACCCTGTGCTTGTTGCACACTTG  1726
Sbjct                 3797  ............................................................  3856

Query                 1727  ATTTGCTAAGGCTGGAGACAGGCACCATTGCCATGGGGCTGGTCCTAGTCACTGGCCGAG  1786
Sbjct                 3857  ............................................................  3916

Query                 1787  GATAAGCCCGTCCCTGTCCCACATTCTAGCCCCACTATGCGGGGGTGCTGTTGTCCTGCC  1846
Sbjct                 3917  ............................................................  3976

Query                 1847  TGTGTCTCATCCCCGGCTGCCTAAGCTAGGGACACTCAAGTGCTTCCTTCCTTGCCCCAT  1906
Sbjct                 3977  ............A...............................................  4036

Query                 1907  CTTCCTCCCAACTGGAGGCCTCTGAGCCTCCCCTGTGCCTTGGGCCCTGAAGCCCCATAT  1966
Sbjct                 4037  ............................................................  4096

Query                 1967  GTAGTATAGAGCAAAGGTGGCTCCTGGTGAAGAGAGGGTGGAAAGGCCCTTCAGCCCCAG  2026
Sbjct                 4097  ............................................................  4156

Query                 2027  GGCCATGTCTGGGTTCTCCATGCCCATCAGTCTCTGCAGTTTCTCTACCTGCCCCCAGAG  2086
Sbjct                 4157  ............................................................  4216

Query                 2087  CTGAGGCCATCTGCAAGCCCCTGCCCATGGCCCAATGGGGAGCCTCCAGCCACAAGTTCC  2146
Sbjct                 4217  ............................................................  4276
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Query                 2147  CTGTCCTTATCAGCCACTGGGTGGTTCCCACTGCATGACCCTCTATCCCTGCCATCTGTC  2206
Sbjct                 4277  ............................................................  4336

Query                 2207  CCCATGGTTTCCAGCTCAATCCACCCCTGACCCATCTGTCAGCTTTTTCCCAGGGAGCCG  2266
Sbjct                 4337  ............................................................  4396

Query                 2267  TTTCAGGGGTTCTGGGCAGTAGGCTGGGCCTGGCCTCAGAACCTGGTGGCTCCTGCCTGC  2326
Sbjct                 4397  ............................................................  4456

Query                 2327  TCCTTCACTTTTGTAAAACCATCCCCTTCACCAGAATGGTATTAACTCCTGGTGCTTTGT  2386
Sbjct                 4457  ............................................................  4516

Query                 2387  ACTACTGGTCCAGCTGCCCTGGGCTCCTTTTCTATATTAATAAAGAAACGAGTAAAAATT  2446
Sbjct                 4517  ..............T.............................................  4576

Query                 2447  A  2447
Sbjct                 4577  .  4577
```

Range 2: 2286 to 2777

Score	Expect	Identities	Gaps	Strand	Frame
909 bits(492)	0.0()	492/492(100%)	0/492(0%)	Plus/Plus	

Features:

```
CDS:(Lyso)-N-acylpho  1           M  A  D  D  L  E  Q  Q  S  Q  G  W  L  S  S  W  L  P
Query                 1     GTTTACTATGGCCGATGATCTGGAGCAGCAGTCTCAAGGCTGGCTGAGTAGCTGGCTGCC  60
Sbjct                 2286  ............................................................  2345

CDS:(Lyso)-N-acylpho  19    T  W  R  P  T  S  M  S  Q  L  K  N  V  E  A  R  I  L  Q  C
Query                 61    CACGTGGCGCCCCACTTCCATGTCTCAGCTGAAGAATGTGGAAGCCAGGATCCTCCAGTG  120
Sbjct                 2346  ............................................................  2405

CDS:(Lyso)-N-acylpho  39    L  Q  N  K  F  L  A  R  Y  V  S  L  P  N  Q  N  K  I  W  T
Query                 121   TCTCCAGAATAAGTTCCTGGCCAGATATGTATCCCTCCCAAACCAGAATAAGATCTGGAC  180
Sbjct                 2406  ............................................................  2465

CDS:(Lyso)-N-acylpho  59    V  T  V  S  P  E  Q  N  D  R  T  P  L  V  M  V  H  G  F  G
Query                 181   GGTGACTGTGAGCCCCGAGCAAAACGACCGCACCCCCTTGGTGATGGTGCATGGTTTTGG  240
Sbjct                 2466  ............................................................  2525

CDS:(Lyso)-N-acylpho  79    G  G  V  G  L  W  I  L  N  M  D  S  L  S  A  R  R  T  L  H
Query                 241   GGGCGGCGTGGGTCTCTGGATCCTCAACATGGACTCACTGAGTGCCCGCCGCACACTGCA  300
Sbjct                 2526  ............................................................  2585

CDS:(Lyso)-N-acylpho  99    T  F  D  L  L  G  F  G  R  S  S  R  P  A  F  P  R  D  P  E
Query                 301   CACCTTCGATCTGCTTGGCTTCGGGCGAAGCTCAAGGCCAGCATTCCCAAGGGACCCGGA  360
Sbjct                 2586  ............................................................  2645

CDS:(Lyso)-N-acylpho  119   G  A  E  D  E  F  V  T  S  I  E  T  W  R  E  T  M  G  I  P
Query                 361   GGGGGCTGAGGATGAGTTTGTGACATCGATAGAGACATGGCGGGAGACCATGGGGATCCC  420
Sbjct                 2646  ............................................................  2705

CDS:(Lyso)-N-acylpho  139   S  M  I  L  L  G  H  S  L  G  G  F  L  A  T  S  Y  S  I  K
Query                 421   CAGCATGATCCTCCTGGGGCACAGTTTGGGAGGATTCCTGGCCACTTCTTACTCAATCAA  480
Sbjct                 2706  ............................................................  2765
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```
CDS:(Lyso)-N-acylpho  159    Y  P  D  R
Query                 481    GTACCCTGATAG  492
Sbjct                 2766   ............  2777
```



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