NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd65F09

Lot# : 7677_B5Jk

Vector : pGCAP10

Gene	GNPAT	
RefSeq_mRNA	NM_014236.4	2641 bp

● Plasmid DNA purification

Date : 2026/10/21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/10/22 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/10/22

DNA concentration (O.D.): 366 ng/ul

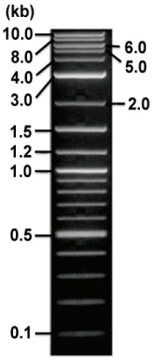
< Size of fragment expected from this clone >

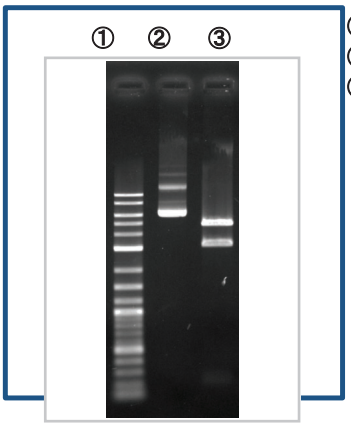
DNA	0.28	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.72	ul
Total	10	ul

BamHI 3.1kb (vector), 4.8, 0.1 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 : 2026/10/27

full sequence	RBd65F09hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/11/10

DNA (366 ng/ul)	84	ul
10x TE	123	ul
dH_2O	1,023	ul
Total	1,230	ul

● Shipping

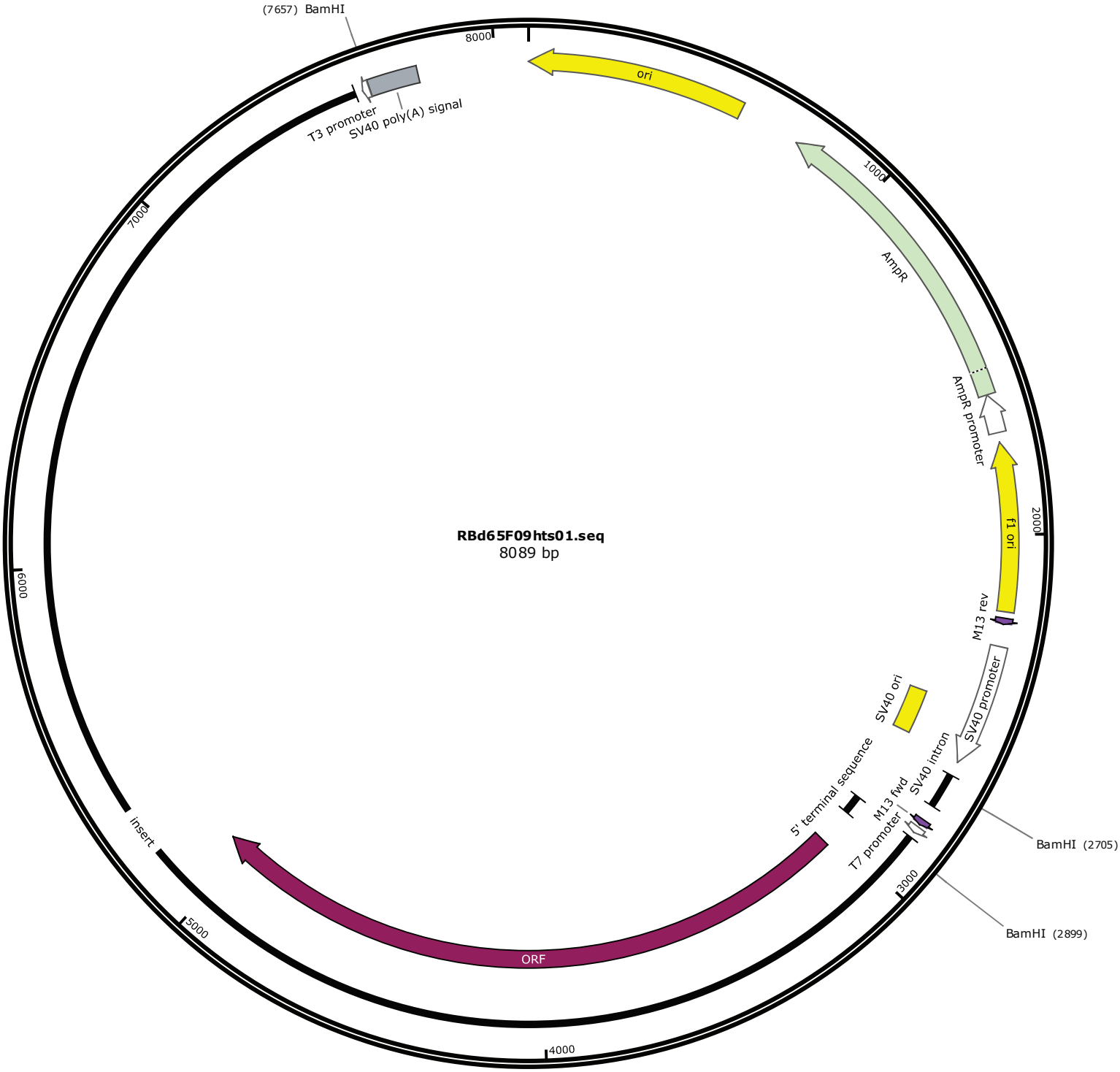
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.11.10
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http://dna.brc.riken.jp/index.html


(7657) BamHI
8000
ori
1000
AmpR
AmpR promoter
f1 ori
2000
M13 rev
SV40 promoter
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
BamHI (2705)
3000
BamHI (2899)
4000
ORF
5000
insert
6000
7000
T3 promoter
SV40 poly(A) signal
RBd65F09hts01.seq
8089 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_014236:Homo sapiens glyceronephosphate...

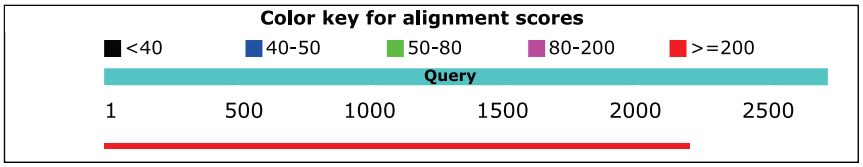
RID E0D8A6B3114 (Expires on 10-28 13:22 pm)

Query ID	NM_014236.4	**Subject ID**	lcl|Query_8269417
Description	Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2641	**Subject Length**	8089
		Program	BLASTN 2.17.0+

RBd65F09hts01.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	3989	3989	82%	0.0	99.77%	Query_8269417

Alignments

Sequence ID: Query_8269417 Length: 8089 Number of Matches: 1
Range 1: 2872 to 5047

Score	Expect	Identities	Gaps	Strand	Frame
3989 bits(2160)	0.0()	2171/2176(99%)	1/2176(0%)	Plus/Plus	

Features:

```
Query          1     CCGTCCTGGCTGAGATGGCGGCGCCCGGGATCCTGTGTAGCGGCTGCAGAGGGTGCCGCC  60
Sbjct          2872  ............................................................  2931

Query          61    GCCCTAGGCGAAGTAGGGCCGTCCTGAGCGAAAGAACCGCCCCCAGCAGGAGCACCACCA  120
Sbjct          2932  ............................................................  2991

CDS:dihydroxyacetone  1                                                  M  E  S  S
Query          121   CGGCTTAGCAAAGAATCCCAGACCCCGCCCGGGAAGGCAGCCGCACCATGGAGTCTTCCA  180
Sbjct          2992  ...T........................................................  3051

CDS:dihydroxyacetone  5     S  S  S  N  S  Y  F  S  V  G  P  T  S  P  S  A  V  V  L  L
Query          181   GTTCATCTAACTCTTATTTCTCCGTTGGCCCAACCAGTCCCAGCGCTGTCGTGCTCCTCT  240
Sbjct          3052  ............................................................  3111

CDS:dihydroxyacetone  25    Y  S  K  E  L  K  K  W  D  E  F  E  D  I  L  E  E  R  R  H
Query          241   ACTCGAAGGAGCTCAAAAAGTGGGATGAGTTTGAAGATATTTTAGAAGAGAGGAGGCATG  300
Sbjct          3112  ............................................................  3171

CDS:dihydroxyacetone  45    V  S  D  L  K  F  A  M  K  C  Y  T  P  L  V  Y  K  G  I  T
Query          301   TCAGTGACTTGAAATTTGCAATGAAATGCTACACACCTCTTGTCTATAAGGGAATTACTC  360
Sbjct          3172  ............................................................  3231
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CDS:dihydroxyacetone  65    P  C  K  P  I  D  I  K  C  S  V  L  N  S  E  E  I  H  Y  V
Query                 361   CATGTAAACCAATTGATATTAAATGTAGTGTTCTCAATTCTGAGGAGATTCATTATGTCA  420
Sbjct                 3232  ............................................................  3291

CDS:dihydroxyacetone  85    I  K  Q  L  S  K  E  S  L  Q  S  V  D  V  L  R  E  E  V  S
Query                 421   TTAAACAGCTTTCCAAGGAATCCCTTCAATCTGTGGATGTCCTCCGAGAGGAAGTGAGTG  480
Sbjct                 3292  ............................................................  3351

CDS:dihydroxyacetone  105   E  I  L  D  E  M  S  H  K  L  R  L  G  A  I  R  F  C  A  F
Query                 481   AGATCTTAGATGAAATGAGTCACAAACTGCGTCTTGGAGCCATTCGGTTTTGTGCCTTCA  540
Sbjct                 3352  ............................................................  3411

CDS:dihydroxyacetone  125   T  L  S  K  V  F  K  Q  I  F  S  K  V  C  V  N  E  E  G  I
Query                 541   CCCTGAGCAAAGTATTTAAACAAATTTTCTCGAAGGTGTGTGTAAATGAAGAAGGTATTC  600
Sbjct                 3412  ............................................................  3471

CDS:dihydroxyacetone  145   Q  K  L  Q  R  A  I  Q  E  H  P  V  V  V  L  L  P  S  H  R  S
Query                 601   AGAAACTACAAAGAGCCATCCAGGAGCATCCTGTTGTTCTGCTGCCTAGTCATCGAAGTT  660
Sbjct                 3472  ............................................................  3531

CDS:dihydroxyacetone  165   Y  I  D  F  L  M  L  S  F  L  L  Y  N  Y  D  L  P  V  P  V
Query                 661   ACATTGACTTCCTCATGTTGTCTTTTCTTCTATACAATTATGATTTGCCTGTGCCAGTTA  720
Sbjct                 3532  ............................................................  3591

CDS:dihydroxyacetone  185   I  A  A  G  M  D  F  L  G  M  K  M  V  G  E  L  L  R  M  S
Query                 721   TAGCAGCAGGAATGGACTTCCTGGGAATGAAAATGGTTGGTGAGCTGCTACGAATGTCGG  780
Sbjct                 3592  ............................................................  3651

CDS:dihydroxyacetone  205   G  A  F  F  M  R  R  T  F  G  G  N  K  L  Y  W  A  V  F  S
Query                 781   GTGCCTTTTTCATGCGGCGTACCTTTGGTGGCAATAAACTCTACTGGGCTGTATTCTCTG  840
Sbjct                 3652  ............................................................  3711

CDS:dihydroxyacetone  225   E  Y  V  K  T  M  L  R  N  G  Y  A  P  V  E  F  F  L  E  G
Query                 841   AATATGTAAAAACTATGTTACGGAATGGTTATGCTCCTGTTGAATTTTTCCTCGAAGGGA  900
Sbjct                 3712  ............................................................  3771

CDS:dihydroxyacetone  245   T  R  S  R  S  A  K  T  L  T  P  K  F  G  L  L  N  I  V  M
Query                 901   CAAGAAGCCGCTCTGCCAAGACATTGACTCCTAAATTTGGTCTTCTGAATATTGTGATGG  960
Sbjct                 3772  ............................................................  3831

CDS:dihydroxyacetone  265   E  P  F  F  K  R  E  V  F  D  T  Y  L  V  P  I  S  I  S  Y
Query                 961   AGCCATTTTTTAAAAGAGAAGTTTTTGATACCTACCTTGTCCCAATTAGTATCAGTTATG  1020
Sbjct                 3832  ............................................................  3891

CDS:dihydroxyacetone  285   D  K  I  L  E  E  T  L  Y  V  Y  E  L  L  G  V  P  K  P  K
Query                 1021  ATAAGATCTTGGAAGAAACTCTTTATGTGTATGAGCTTCTAGGGGTTCCTAAACCAAAAG  1080
Sbjct                 3892  ............................................................  3951

CDS:dihydroxyacetone  305   E  S  T  T  G  L  L  K  A  R  K  I  L  S  E  N  F  G  S  I
Query                 1081  AGTCTACAACTGGGTTGCTGAAAGCCAGAAAGATTCTCTCTGAAAATTTTGGAAGCATCC  1140
Sbjct                 3952  .A............................................................  4011

CDS:dihydroxyacetone  325   H  V  Y  F  G  D  P  V  S  L  R  S  L  A  A  G  R  M  S  R
Query                 1141  ATGTGTACTTTGGAGATCCTGTGTCACTTCGATCTTTGGCAGCTGGGAGGATGAGTCGGA  1200
Sbjct                 4012  ............................................................  4071

CDS:dihydroxyacetone  345   S  S  Y  N  L  V  P  R  Y  I  P  Q  K  Q  S  E  D  M  H  A
Query                 1201  GCTCATATAACTTGGTTCCAAGATACATTCCTCAGAAACAGTCTGAGGACATGCATGCCT  1260
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Sbjct                 4072  ............................................................  4131

CDS:dihydroxyacetone  365   F  V  T  E  V  A  Y  K  M  E  L  L  Q  I  E  N  M  V  L  S
Query                 1261  TTGTCACTGAAGTTGCCTACAAAATGGAGCTTCTGCAAATTGAAAACATGGTTTTGAGCC  1320
Sbjct                 4132  ............................................................  4191

CDS:dihydroxyacetone  385   P  W  T  L  I  V  A  V  L  L  Q  N  R  P  S  M  D  F  D  A
Query                 1321  CCTGGACCCTAATAGTTGCTGTTCTGCTTCAGAACCGGCCATCCATGGACTTTGATGCTC  1380
Sbjct                 4192  ............................................................  4251

CDS:dihydroxyacetone  405   L  V  E  K  T  L  W  L  K  G  L  T  Q  A  F  G  G  F  L  I
Query                 1381  TGGTGGAAAAGACTTTATGGCTAAAAGGCTTAACCCAGGCATTTGGAGGGTTTCTCATTT  1440
Sbjct                 4252  ............................................................  4311

CDS:dihydroxyacetone  425   W  P  D  N  K  P  A  E  E  V  V  P  A  S  I  L  L  H  S  N
Query                 1441  GGCCTGATAATAAACCTGCTGAAGAAGTTGTCCCGGCCAGCATTCTTCTGCATTCCAACA  1500
Sbjct                 4312  ............................................................  4371

CDS:dihydroxyacetone  445   I  A  S  L  V  K  D  Q  V  I  L  K  V  D  S  G  D  S  E  V
Query                 1501  TTGCCAGCCTTGTCAAAGACCAGGTGATTCTGAAAGTGGACTCCGGAGACTCGGAAGTGG  1560
Sbjct                 4372  ............................................................  4431

CDS:dihydroxyacetone  465   V  D  G  L  M  L  Q  H  I  T  L  L  M  C  S  A  Y  R  N  Q
Query                 1561  TCGATGGGCTTATGCTCCAGCACATCACTCTCCTCATGTGCTCAGCTTATAGGAACCAGC  1620
Sbjct                 4432  ............................................................  4491

CDS:dihydroxyacetone  485   L  L  N  I  F  V  R  P  S  L  V  A  V  A  L  Q  M  T  P  G
Query                 1621  TGCTCAACATTTTTGTGCGCCCATCCTTAGTAGCAGTAGCATTGCAGATGACACCAGGGT  1680
Sbjct                 4492  ............................................................  4551

CDS:dihydroxyacetone  505   F  R  K  F  D  V  Y  S  C  F  R  F  L  R  D  V  F  A  D  E
Query                 1681  TCAGGAAAGAGGATGTCTACAGTTGCTTTCGCTTCCTACGTGATGTTTTTGCAGATGAGT  1740
Sbjct                 4552  ............................................................  4611

CDS:dihydroxyacetone  525   F  I  F  L  P  G  N  T  L  K  D  F  E  E  G  C  Y  L  L  C
Query                 1741  TCATCTTCCTTCCAGGAAACACACTAAAGGACTTTGAAGAAGGCTGTTACCTGCTTTGTA  1800
Sbjct                 4612  ............................................................  4671

CDS:dihydroxyacetone  545   K  S  E  A  I  Q  V  T  T  K  D  I  L  V  T  E  K  G  N  T
Query                 1801  AAAGTGAAGCCATACAAGTGACTACGAAAGACATCCTAGTTACAGAGAAAGGAAATACTG  1860
Sbjct                 4672  ............................................................  4731

CDS:dihydroxyacetone  565   V  L  E  F  L  V  G  L  F  K  P  F  V  E  S  Y  Q  I  I  C
Query                 1861  TGTTAGAATTTTTAGTAGGACTCTTTAAACCTTTTGTGGAAAGCTATCAGATAATTTGCA  1920
Sbjct                 4732  ............................................................  4791

CDS:dihydroxyacetone  585   K  Y  L  L  S  E  E  E  D  H  F  S  E  E  Q  Y  L  A  A  V
Query                 1921  AGTACCTTTTGAGTGAAGAAGAGGACCACTTCAGTGAGGAACAGTACTTGGCTGCAGTCA  1980
Sbjct                 4792  ............................................................  4851

CDS:dihydroxyacetone  605   R  K  F  T  S  Q  L  L  D  Q  G  T  S  Q  C  Y  D  V  L  S
Query                 1981  GAAAATTCACAAGTCAGCTTCTCGATCAAGGTACCTCTCAATGTTATGATGTATTATCTT  2040
Sbjct                 4852  ............................................................  4911

CDS:dihydroxyacetone  625   S  D  V  Q  K  N  A  L  A  A  C  V  R  L  G  V  V  E  K  K
Query                 2041  CTGATGTGCAGAAAAACGCCTTAGCAGCCTGTGTGAGGCTCGGAGTAGTGGAGAAGAAGA  2100
Sbjct                 4912  ............................................................  4971

CDS:dihydroxyacetone  645   K  I  N  N  N  C  I  F  N  V  N  E  P  A  T  T  K  L  E  E
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Query                2101  AGATAAATAATAACTGTATATTTAATGTGAATGAACCTGCCACAACCAAATTAGAAGAAA  2160
Sbjct                4972  ............................................................  5031

CDS:dihydroxyacetone  665   M  L   G  C  K
Query                2161  TGCTTG-GTTGTAAGA  2175
Sbjct                5032  ......T.A..G....  5047
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HHS Vulnerability Disclosure