NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe64G10

Lot# : 7672_B5H6

Vector : pKA1U5

Gene	DHRS3	
RefSeq_mRNA	NM_004753.7	2201 bp

● Plasmid DNA purification

Date : 2025/08/06 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/08/07 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/07

DNA concentration (O.D.): 394 ng/ul

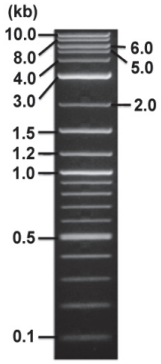
< Size of fragment expected from this clone >

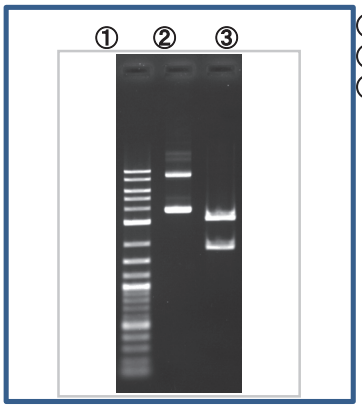
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

BamHI 3.1kb (vector), 1.8 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 : 2025/08/18

full sequence	ARe64G10hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/08/19

DNA (394 ng/ul)	82 ul
10x TE	129 ul
dH_2O	1,081 ul
Total	1,292 ul

● Shipping

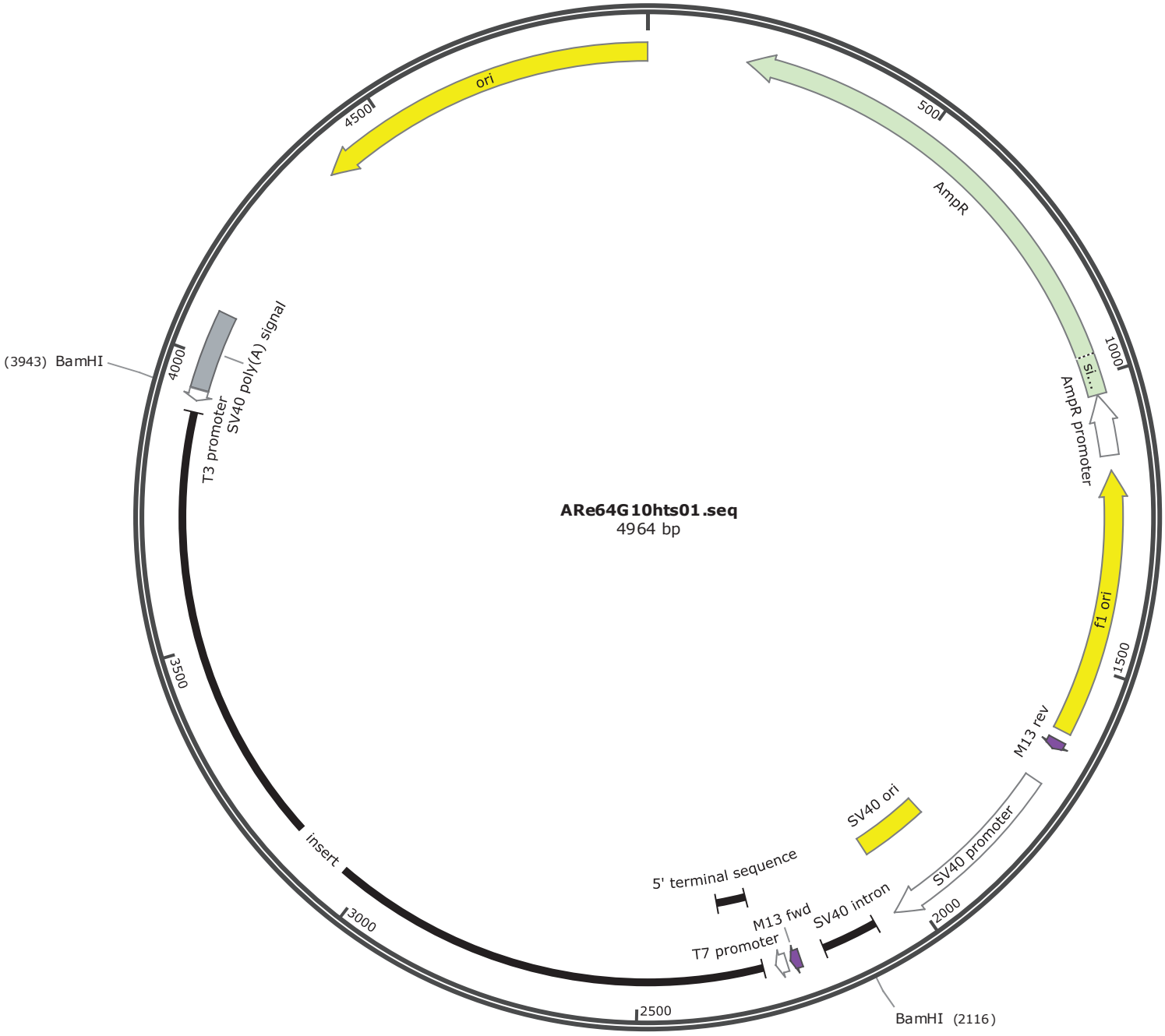
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

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'25.08.19
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http://dna.brc.riken.jp/index.html


ARe64G10hts01.seq
4964 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 ori
SV40 promoter
SV40 intron
M13 fwd
5' terminal sequence
T7 promoter
insert
T3 promoter
SV40 poly(A) signal
(3943) BamHI
BamHI (2116)
500
1000
1500
2000
2500
3000
3500
4000
4500

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001319225:Homo sapiens dehydrogenase/reductase...

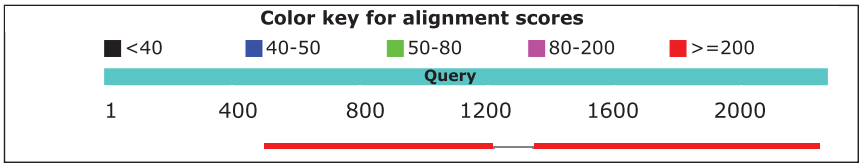
RID A5B1MEDV114 (Expires on 08-19 12:29 pm)

Query ID	NM_004753.7	**Subject ID**	lcl|Query_6409125
Description	Homo sapiens dehydrogenase/reductase 3 (DHRS3), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2201	**Subject Length**	4964
		Program	BLASTN 2.17.0+

ARe64G10hts01.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	1628	2925	72%	0.0	100.00%	Query_6409125

Alignments

Sequence ID: Query_6409125 Length: 4964 Number of Matches: 2
Range 1: 2992 to 3872

Score	Expect	Identities	Gaps	Strand	Frame
1628 bits(881)	0.0()	881/881(100%)	0/881(0%)	Plus/Plus	

Features:

```
CDS:short-chain dehy  154    T  T  K  A  F  L  P  R  M  L  E  L  Q  N  G  H  I  V  C  L
Query                 1321   GACCACCAAGGCCTTCCTGCCGCGTATGCTGGAGCTGCAGAATGGCCACATCGTGTGCCT  1380
Sbjct                 2992   ............................................................  3051

CDS:short-chain dehy  174    N  S  V  L  A  L  S  A  I  P  G  A  I  D  Y  C  T  S  K  A
Query                 1381   CAACTCCGTGCTGGCACTGTCTGCCATCCCCGGTGCCATCGACTACTGCACATCCAAAGC  1440
Sbjct                 3052   ............................................................  3111

CDS:short-chain dehy  194    S  A  F  A  F  M  E  S  L  T  L  G  L  L  D  C  P  G  V  S
Query                 1441   GTCAGCCTTCGCCTTCATGGAGAGCCTGACCCTGGGGCTGCTGGACTGTCCGGGAGTCAG  1500
Sbjct                 3112   ............................................................  3171

CDS:short-chain dehy  214    A  T  T  V  L  P  F  H  T  S  T  E  M  F  Q  G  M  R  V  R
Query                 1501   CGCCACCACAGTGCTGCCCTTCCACACCAGCACCGAGATGTTCCAGGGCATGAGAGTCAG  1560
Sbjct                 3172   ............................................................  3231

CDS:short-chain dehy  234    F  P  N  L  F  P  P  L  K  P  E  T  V  A  R  R  T  V  E  A
Query                 1561   GTTTCCCAACCTCTTTCCCCCACTGAAGCCGGAGACGGTGGCCCGGAGGACAGTGGAAGC  1620
Sbjct                 3232   ............................................................  3291

CDS:short-chain dehy  254    V  Q  L  N  Q  A  L  L  L  L  P  W  T  M  H  A  L  V  I  L
Query                 1621   TGTGCAGCTCAACCAGGCCCTCCTCCTCCTCCCATGGACAATGCATGCCCTCGTTATCTT  1680
Sbjct                 3292   ............................................................  3351
```

```
CDS:short-chain dehy  274    K  S  I  L  P  Q  A  A  L  E  E  I  H  K  F  S  G  T  Y  T
Query                 1681   GAAAAGCATACTTCCACAGGCTGCACTCGAGGAGATCCACAAATTCTCAGGAACCTACAC  1740
Sbjct                 3352   ............................................................  3411

CDS:short-chain dehy  294    C  M  N  T  F  K  G  R  T
Query                 1741   CTGCATGAACACTTTCAAAGGGCGGACATAGAGACAGGATGAAGACATGCTTGAGGAGCC  1800
Sbjct                 3412   ............................................................  3471

Query                 1801   ACGGAGTTTGGGGGCCACAGCACCTGGGCACACACCCGAGCACCTGTCCATTGGCATGCT  1860
Sbjct                 3472   ............................................................  3531

Query                 1861   TCTGCTGGGTGAGCAGGACAGCTCCTGTCCCCAGCGAAGAATCCGGCTGCCCCTGGGCCA  1920
Sbjct                 3532   ............................................................  3591

Query                 1921   GTCCCAGGACCTTTGCACAGGACTGATGGGTATAACTGACCCCCACAGGGAGGCAGGAAA  1980
Sbjct                 3592   ............................................................  3651

Query                 1981   ACAGCCAGAAGCCACCTTGACACTTTTGAACATTTCCAGTTCTGTAGAGTTTATTGTCAA  2040
Sbjct                 3652   ............................................................  3711

Query                 2041   TTGCTTCTCAAGTCTAACCAGCCTCAGCAGTGTGCATAGACCATTTCCAGGAGGGTCTGT  2100
Sbjct                 3712   ............................................................  3771

Query                 2101   CCCCAGATGCTCTGCCTCCCGTTCCAAAACCCACTCATCCTCAGCTTGCACAAACTGGTT  2160
Sbjct                 3772   ............................................................  3831

Query                 2161   GAACGGCAGGAATGAAAAATAAAGAGAGATGGCTTTTGTGA  2201
Sbjct                 3832   ........................................  3872
```

Range 2: 2291 to 2992

Score	Expect	Identities	Gaps	Strand	Frame
1297 bits(702)	0.0()	702/702(100%)	0/702(0%)	Plus/Plus	

Features:

```
Query                 500    TCCCTAAACTCCTCTGTCAGTCTGTAAACATTACCTGAGAATTCCCCAGCCGAAACGGCT  559
Sbjct                 2291   ............................................................  2350

Query                 560    GCTGGGGCAAGAAACTTCTTGTTAGAACTTTCCACCTCCGGCTTCCCCCTCCACCTCTTT  619
Sbjct                 2351   ............................................................  2410

Query                 620    TACCGTCCCAACCTTAGGAGACGCTTTTTCTCCCCCAGAGGAGAATTTATCttttttttt  679
Sbjct                 2411   ............................................................  2470

Query                 680    ttttttttttttcttttCTCACCCGGTGCTTTGCATTTGGGAAGAGGTGATTTCAAGAGT  739
Sbjct                 2471   ............................................................  2530

Query                 740    GGCCAGGTGGGACGCCTCTCTCCTCCTTATTCGGTTTACTATTTATTGTTCGGGGTGTTT  799
Sbjct                 2531   ............................................................  2590

Query                 800    TTTAATTCCTGTATTGCTCGGCCCGGGGAGTTTCGCCCCCTGCCCGGCTCCGCGGCGCGG  859
Sbjct                 2591   ............................................................  2650

CDS:short-chain dehy  1        M  V  W  K  R  L  G  A  L  V  M  F  P  L  Q  M  I  Y  L
Query                 860    AGGATGGTGTGGAAACGGCTGGGCGCGCTGGTGATGTTCCCTCTACAGATGATCTATCTG  919
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Sbjct                 2651   ............................................................  2710

CDS:short-chain dehy  20     V  V  K  A  A  V  G  L  V  L  P  A  K  L  R  D  L  S  R  F
Query                 920    GTGGTGAAAGCAGCCGTCGGACTGGTGCTGCCCGCCAAGCTGCGGGACCTGTCGCGGGAG  979
Sbjct                 2711   ............................................................  2770

CDS:short-chain dehy  40     N  V  L  I  T  G  G  G  R  G  I  G  R  Q  L  A  R  E  F  A
Query                 980    AACGTCCTCATCACCGGCGGCGGGAGAGGCATCGGGCGTCAGCTCGCCCGCGAGTTCGCG  1039
Sbjct                 2771   ............................................................  2830

CDS:short-chain dehy  60     E  R  G  A  R  K  I  V  L  W  G  R  T  E  K  C  L  K  E  T
Query                 1040   GAGCGCGGCGCCAGAAAGATTGTTCTCTGGGGCCGGACTGAGAAATGCCTGAAGGAGACG  1099
Sbjct                 2831   ............................................................  2890

CDS:short-chain dehy  80     T  E  E  I  R  Q  M  G  T  E  C  H  Y  F  I  C  D  V  G  N
Query                 1100   ACGGAGGAGATCCGGCAGATGGGCACTGAGTGCCATTACTTCATCTGTGATGTGGGCAAC  1159
Sbjct                 2891   ............................................................  2950

CDS:short-chain dehy  100    R  E  E  V  Y  Q  T  A  K  A  V  R  E  K
Query                 1160   CGGGAGGAGGTGTACCAGACGGCCAAGGCCGTCCGGGAGAAG  1201
Sbjct                 2951   ........................................  2992
```

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