6-19

NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARe66B12
Vector : pKA1U5

Lot# : 7672_B3Bd

Gene	ZNF792	
RefSeq_mRNA	NM_175872.5	4068 bp

● **Plasmid DNA purification**

Date : 23.03.22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.24 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● **Digestion by restriction enzyme/Concentrarion calibration**

Date : 23.03.24

DNA concentration (O.D.): 293 ng/ul

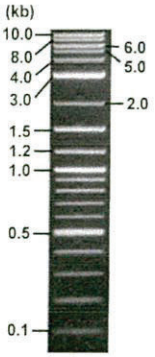
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 4.4 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 : 2026/06/17

full sequence : ARe66B12hts01.seq

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2026/07/23

DNA (293 ng/ul)	76 ul
10x TE	89 ul
dH_2O	726 ul
Total	891 ul

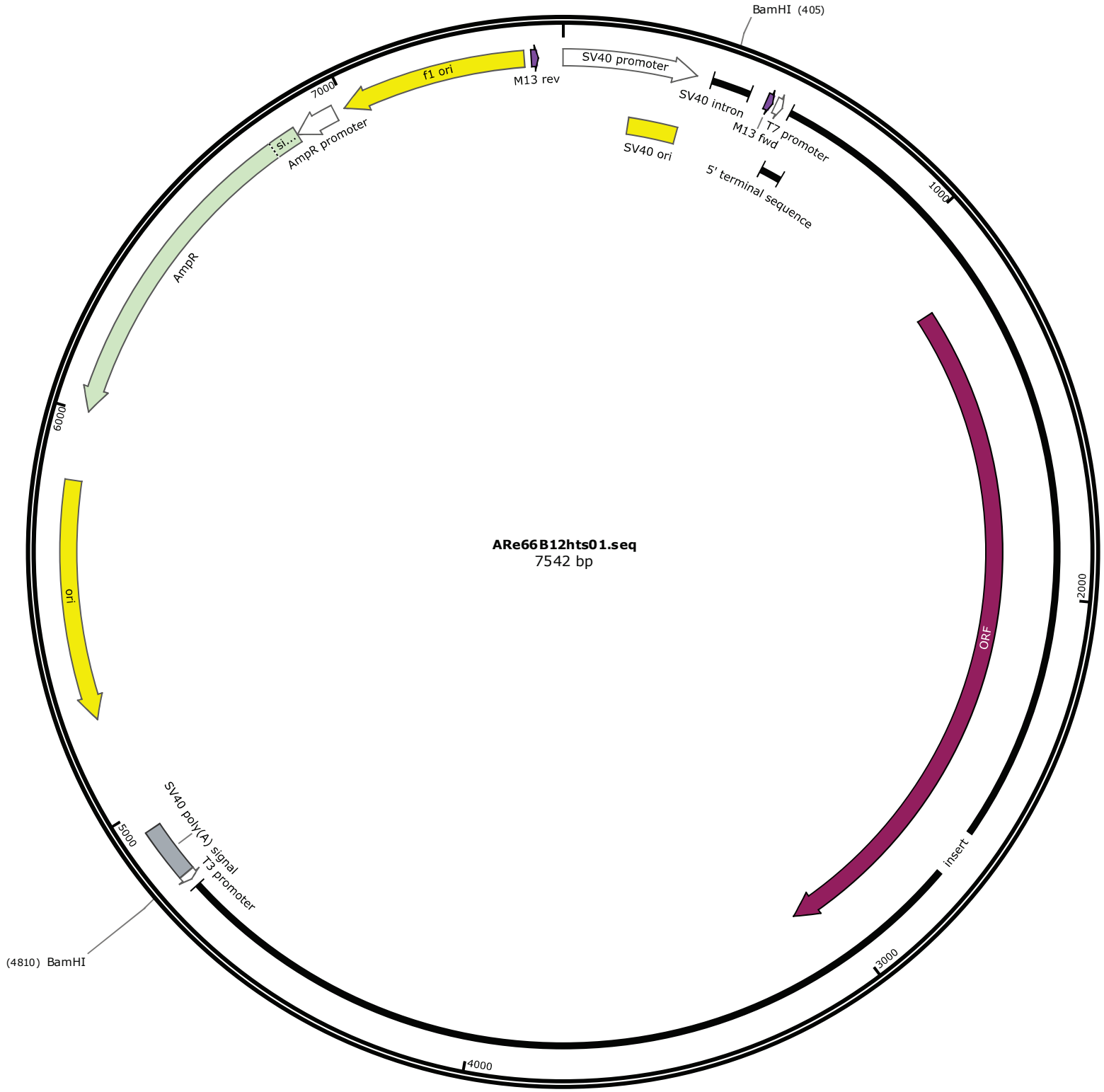
● **Shipping**

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '26.07.23 笹沼

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


BamHI (405)
SV40 promoter
f1 ori
M13 rev
7000
SV40 intron
T7 promoter
M13 fwd
AmpR promoter
SV40 ori
5' terminal sequence
1000
AmpR
6000
ori
ORF
2000
SV40 poly(A) signal
T3 promoter
5000
insert
(4810) BamHI
3000
4000
ARe66B12hts01.seq
7542 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001145115:Homo sapiens protein phosphatase...

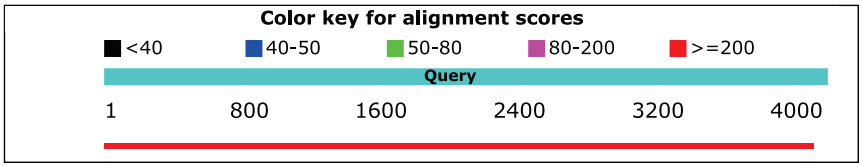
RID 34J9XPH1114 (Expires on 06-18 15:14 pm)

Query ID	NM_175872.5	**Subject ID**	lcl|Query_5731889
Description	Homo sapiens zinc finger protein 792 (ZNF792), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	4068	**Molecule type**	dna
		Subject Length	7542
		Program	BLASTN 2.17.0+

ARe66B12hts01.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	7474	7474	100%	0.0	99.83%	Query_5731889

Alignments

Sequence ID: Query_5731889 Length: 7542 Number of Matches: 1
Range 1: 629 to 4696

Score	Expect	Identities	Gaps	Strand	Frame
7474 bits(4047)	0.0()	4061/4068(99%)	0/4068(0%)	Plus/Plus	

Features:

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Query  1    CTTCCCGCCCTGGACCCTCAGCCTGACGAGAGGCTGGGCAGAAACTCGCGATCCCCAGGC  60
Sbjct  629  ...T........................................................  688

Query  61   CCTGCCTGTGCACCAGCGGCTGGCGCCAGGCCAATGACAGTACGGGAGAGGGCAACTCTC  120
Sbjct  689  ............................................................  748

Query  121  CCGGCCGCCACGGTGGGGGCCGGAACTTCCTGCACTGCAGCCTCGCAGGTCATTTCCCGG  180
Sbjct  749  ............................................................  808

Query  181  CGGGGAGGCTGAGTCCCCAGGAGCTGGGGACCCCGAGTTGGGGGCGGGGCGGCTGGGGCT  240
Sbjct  809  ............................................................  868

Query  241  ACGCCCGTGAAGCTGCCCCGCCGGCTTTCCCGGACCGCGAGGGGGACAGTGAGGCCGGGA  300
Sbjct  869  ............................................................  928

Query  301  CCCCCTCCGCGCCTTTGCACCAGCCGTGACCCCTTGCAACGGGGGTACCCAGCGGAGCTG  360
Sbjct  929  ............................................................  988

Query  361  CGCGCTCTCGGCGCCCCCGGAGCCTGCGCCCCGGGCCCCTTGCGCATTTTGCACGGGGGA  420
Sbjct  989  ............................................................  1048
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Query                 421   GACTGAGGCTAGGAGTGCGACCCTCAGCCCGGGGTCACACCTCGTCTGGGGCACGGCCAG  480
Sbjct                 1049  ............................................................  1108

Query                 481   GTGGGTGGTAGCCTCAGCCTGCGAGACCCCCTACCCCCGCCCCGTGGTTTCCCGCACCGT  540
Sbjct                 1109  ..............................................CG............  1168

CDS:zinc finger prot  1                                   M  A  A  A  A  L  R  D  P  A  Q
Query                 541   GGGGCCCTGCTCTGACCACAGACTCCGATGGCAGCGGCGGCGCTGCGGGACCCCGCGCAG  600
Sbjct                 1169  ............................................................  1228

CDS:zinc finger prot  12    G  C  V  T  F  E  D  V  T  I  Y  F  S  Q  E  E  W  V  L  L
Query                 601   GGCTGCGTGACCTTTGAGGACGTGACCATTTACTTCTCCCAGGAGGAGTGGGTGCTCCTC  660
Sbjct                 1229  ............................................................  1288

CDS:zinc finger prot  32    D  E  A  Q  R  L  L  Y  C  D  V  M  L  E  N  F  A  L  I  A
Query                 661   GATGAGGCTCAGAGACTCCTGTACTGCGATGTGATGCTGGAAAACTTTGCACTTATAGCC  720
Sbjct                 1289  ............................................................  1348

CDS:zinc finger prot  52    S  L  G  L  I  S  F  R  S  H  I  V  S  Q  L  E  M  G  K  E
Query                 721   TCGCTGGGACTTATATCTTTCAGGTCCCACATCGTTTCCCAGTTGGAGATGGGGAAAGAG  780
Sbjct                 1349  ............................................................  1408

CDS:zinc finger prot  72    P  W  V  P  D  S  V  D  M  T  S  A  M  A  R  G  A  Y  G  R
Query                 781   CCCTGGGTGCCTGACAGTGTGGATATGACATCAGCCATGGCCAGAGGGGCTTATGGCAGG  840
Sbjct                 1409  ............................................................  1468

CDS:zinc finger prot  92    P  G  S  D  F  C  H  G  T  E  G  K  D  L  P  S  F  H  N  V
Query                 841   CCTGGCTCTGATTTTTGCCATGGAACAGAGGGCAAGGACTTACCTTCTGAGCATAACGTT  900
Sbjct                 1469  ............................................................  1528

CDS:zinc finger prot  112   S  V  E  G  V  A  Q  D  R  S  P  E  A  T  L  C  P  Q  K  T
Query                 901   TCTGTAGAAGGAGTGGCACAGGACAGGAGTCCCGAGGCAACTCTGTGCCCCCAGAAGACC  960
Sbjct                 1529  ............................................................  1588

CDS:zinc finger prot  132   C  P  C  D  I  C  G  L  R  L  K  D  I  L  H  L  A  E  H  Q
Query                 961   TGCCCCTGTGACATATGTGGCCTACGTTTGAAAGACATTTTGCATTTGGCTGAACACCAG  1020
Sbjct                 1589  ............................................................  1648

CDS:zinc finger prot  152   T  T  H  P  R  Q  K  P  F  V  C  E  A  Y  V  K  G  S  E  F
Query                 1021  ACAACACATCCCAGGCAGAAACCATTTGTGTGTGAGGCATATGTGAAAGGCTCTGAGTTC  1080
Sbjct                 1649  ............................................................  1708

CDS:zinc finger prot  172   S  A  N  L  P  R  K  Q  V  Q  Q  N  V  H  N  P  I  R  T  E
Query                 1081  AGTGCAAACCTTCCCCGGAAACAGGTGCAGCAGAACGTACACAACCCTATCAGAACGGAG  1140
Sbjct                 1709  ..............A.............................................  1768

CDS:zinc finger prot  192   E  G  Q  A  S  P  V  K  T  C  R  D  H  T  S  D  Q  L  S  T
Query                 1141  GAGGGCCAGGCTTCCCCTGTAAAGACCTGCAGAGACCACACATCAGATCAGCTTTCCACC  1200
Sbjct                 1769  ............................................................  1828

CDS:zinc finger prot  212   C  R  E  G  G  K  D  F  V  A  T  A  G  F  L  Q  C  E  V  T
Query                 1201  TGCAGGGAGGGTGGGAAGGACTTTGTGGCCACAGCAGGGTTTCTGCAGTGTGAGGTCACT  1260
Sbjct                 1829  ............................................................  1888

CDS:zinc finger prot  232   P  S  D  G  E  P  H  E  A  T  E  G  V  V  D  F  H  I  A  L
Query                 1261  CCCAGCGATGGGGAGCCGCACGAGGCCACCGAAGGTGTGGTGGATTTTCACATTGCACTA  1320
Sbjct                 1889  ............................................................  1948

CDS:zinc finger prot  252   R  H  N  K  C  C  E  S  G  D  A  F  N  N  K  S  T  L  V  Q
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1097 G>A (R177Q)

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Query                 1321  AGGCATAACAAGTGCTGTGAATCTGGGGATGCCTTCAATAACAAATCCACTCTTGTTCAG  1380
Sbjct                 1949  ............................................................  2008

CDS:zinc finger prot  272   H  Q  R  I  H  S  R  E  R  P  Y  E  C  S  K  C  G  I  F  F
Query                 1381  CACCAGAGAATCCACAGCAGAGAAAGGCCTTATGAATGCAGCAAATGTGGAATCTTCTTC  1440
Sbjct                 2009  ............................................................  2068

CDS:zinc finger prot  292   T  Y  A  A  D  L  T  Q  H  Q  K  V  H  N  R  G  K  P  Y  E
Query                 1441  ACTTACGCCGCTGACCTCACTCAACACCAGAAAGTTCACAATAGAGGAAAACCGTATGAG  1500
Sbjct                 2069  ............................................................  2128

CDS:zinc finger prot  312   C  C  E  C  G  K  F  F  S  Q  H  S  S  L  V  K  H  R  R  V
Query                 1501  TGCTGTGAATGTGGAAAATTCTTCAGCCAGCACTCCAGCCTTGTTAAACATCGCAGGGTT  1560
Sbjct                 2129  ............................................................  2188

CDS:zinc finger prot  332   H  T  G  E  S  P  H  V  C  G  D  C  G  K  F  F  S  R  S  S
Query                 1561  CACACCGGTGAAAGCCCTCACGTGTGTGGTGACTGTGGGAAATTCTTCAGCCGAAGCTCC  1620
Sbjct                 2189  ............................................................  2248

CDS:zinc finger prot  352   N  L  I  Q  H  K  R  V  H  T  G  E  K  P  Y  E  C  S  D  C
Query                 1621  AACCTCATTCAGCATAAGAGGGTTCACACTGGTGAAAAGCCATATGAGTGCAGCGACTGT  1680
Sbjct                 2249  ............................................................  2308

CDS:zinc finger prot  372   G  K  F  F  S  Q  R  S  N  L  I  H  H  K  R  V  H  T  G  R
Query                 1681  GGGAAGTTCTTCAGCCAGCGTTCCAACCTCATTCATCATAAGAGGGTTCATACGGGCAGA  1740
Sbjct                 2309  ............................................................  2368

CDS:zinc finger prot  392   S  A  H  E  C  S  E  C  G  K  S  F  N  C  N  S  S  L  I  K
Query                 1741  AGTGCCCATGAGTGCAGTGAATGTGGGAAATCTTTCAACTGCAACTCCAGCCTAATTAAA  1800
Sbjct                 2369  ............................................................  2428

CDS:zinc finger prot  412   H  W  R  V  H  T  G  E  R  P  Y  K  C  N  E  C  G  K  F  F
Query                 1801  CATTGGAGAGTTCACACTGGAGAAAGACCTTACAAGTGTAACGAATGTGGGAAATTCTTC  1860
Sbjct                 2429  ............................................................  2488

CDS:zinc finger prot  432   S  H  I  A  S  L  I  Q  H  Q  I  V  H  T  G  E  R  P  H  G
Query                 1861  AGCCACATTGCCAGCCTCATTCAACATCAGATAGTTCACACTGGCGAGCGGCCTCACGGG  1920
Sbjct                 2489  ............................................................  2548

CDS:zinc finger prot  452   C  G  E  C  G  K  A  F  S  R  S  S  D  L  M  K  H  Q  R  V
Query                 1921  TGTGGTGAGTGTGGGAAAGCCTTCAGCCGAAGCTCTGACCTCATGAAACATCAGCGAGTT  1980
Sbjct                 2549  ............................................................  2608

CDS:zinc finger prot  472   H  T  G  E  R  P  Y  E  C  N  E  C  G  K  L  F  S  Q  S  S
Query                 1981  CACACTGGTGAGCGGCCTTATGAATGCAATGAATGTGGGAAGTTATTTAGCCAGAGCTCC  2040
Sbjct                 2609  ............................................................  2668

CDS:zinc finger prot  492   S  L  N  S  H  R  R  L  H  T  G  E  R  P  Y  Q  C  S  E  C
Query                 2041  AGCCTCAATAGCCATCGGAGACTTCACACTGGTGAACGGCCTTACCAGTGCAGTGAATGT  2100
Sbjct                 2669  ............................................................  2728

CDS:zinc finger prot  512   G  K  F  F  N  Q  S  S  S  L  N  N  H  R  R  L  H  T  G  E
Query                 2101  GGGAAATTCTTTAACCAAAGCTCCAGCCTCAATAACCACCGGAGACTTCACACCGGCGAG  2160
Sbjct                 2729  ............................................................  2788

CDS:zinc finger prot  532   R  P  Y  E  C  S  E  C  G  K  T  F  R  Q  R  S  N  L  R  Q
Query                 2161  CGGCCTTATGAGTGCAGCGAATGTGGGAAAACCTTCAGGCAGAGGTCCAATCTGAGGCAG  2220
Sbjct                 2789  ............................................................  2848
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CDS:zinc finger prot  552   H  L  K  V  H  K  P  D  R  P  Y  E  C  S  E  C  G  K  A  F
Query                2221  CACCTGAAAGTTCACAAACCAGACAGGCCTTACGAATGCAGCGAATGTGGGAAAGCCTTC  2280
Sbjct                2849  ......................T.......................................  2908

CDS:zinc finger prot  572   N  Q  R  P  T  L  I  R  H  Q  K  I  H  I  R  E  R  S  M  E
Query                2281  AACCAAAGGCCTACCCTCATTCGGCATCAGAAGATTCACATCAGAGAAAGGAGCATGGAG  2340
Sbjct                2909  ........................................................  2968

CDS:zinc finger prot  592   N  V  L  L  P  C  S  Q  H  T  P  E  I  S  S  E  N  R  P  Y
Query                2341  AATGTGCTCCTTCCCTGTTCACAGCACACACCAGAGATAAGCTCTGAGAACAGACCTTAT  2400
Sbjct                2969  ........................................................  3028

CDS:zinc finger prot  612   Q  G  A  V  N  Y  K  L  K  L  V  H  P  S  T  H  P  G  E  V
Query                2401  CAGGGCGCTGTCAACTACAAGTTGAAACTTGTTCATCCAAGTACCCACCCTGGGGAGGTT  2460
Sbjct                3029  ........................................................  3088

CDS:zinc finger prot  632   P
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Sbjct                3089  ........................................................  3148

Query                2521  GAGTTTATCAGCGTTTTTTCACTGCTGGGGTTGTGATAGAAGCCATGTCAGCACCACACA  2580
Sbjct                3149  ..T.....................................................  3208

Query                2581  CTGCAGCTCTCCAAAGAGTGTGTCCACCACTCCACTGTGCTCAGGGAAGGCAGACCTCTC  2640
Sbjct                3209  ........................................................  3268

Query                2641  CTCTCTCTTTCCAATCCCTAAAGGGAATTAGGAGTAGTCTGAAGCCTTGGGAAGATGTCA  2700
Sbjct                3269  ........................................................  3328

Query                2701  TTCCCGCCCTGTATGGCTGGTTTAGCCATGGACATGACCAGCTTTTGGCTGTGAAGACCT  2760
Sbjct                3329  ........................................................  3388

Query                2761  GAGCAGGGTTTTGCCAACAGCTTGTTCTAGAGAAGGTTTCCCTTTTTCTGGGACATTGTT  2820
Sbjct                3389  ........................................................  3448

Query                2821  GGTCTCATGTTATGCCTGTGAAGGATTTGTCCAGCCTTCATGTTACTCTACACAACAACT  2880
Sbjct                3449  ........................................................  3508

Query                2881  TATCTCCTGTGTATTGCCCTGGTTCATGTGATGATAATGGCCTTATGATAAAGCCGCCTT  2940
Sbjct                3509  ........................................................  3568

Query                2941  TAGTCTTCCATGTTCTGATCACTGTGTGGGGTGGTTCAAGAGCAGAGTTAAGATCTACCA  3000
Sbjct                3569  ........................................................  3628

Query                3001  AACTGAAGGGGTCTCCAGATTATCTTGGAGGGGACAGGAGGATGGCAGAGAAACAACTGT  3060
Sbjct                3629  ........................................................  3688

Query                3061  CAATCCAGATTTGACCTCATTTGCATTGCCACCAAGGCCTCCTAGGAAAAATTGTAGGAA  3120
Sbjct                3689  ........................................................  3748

Query                3121  TTTATGGGTATAATATTGTGGTCTGAATGGCGTGAATTTTTATCCCGAGGAGGGGGCAGT  3180
Sbjct                3749  ........................................................  3808

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Sbjct                3809  ........................................................  3868

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Sbjct                3869  ........................................................  3928
```

2244 C>T

```
Query                3301  GCCCTGAAGTTCAGCATTAGGCAGGTATCTCTTAACTGTAAGACATACCAGGCCCAGCTG  3360
Sbjct                3929  ..........................................C.............  3988

Query                3361  GGACCATAATTTGTACAGAAACACTGGATGTGATTAATAGGGAGTAGGCGAGATTATAGC  3420
Sbjct                3989  ........................................................  4048

Query                3421  AAACCAGCAGAAATGGAACTCTGCTAAATGTGCATCCGTGAATGCTCCCTTGAATGTGGC  3480
Sbjct                4049  ........................................................  4108

Query                3481  TGTGCAGGATTCAGGGTTTGCAGAAATTCTCAGGACCTCAGACCTCTGTCCTATGACTAA  3540
Sbjct                4109  ........................................................  4168

Query                3541  TGTTACTGGCAGAGCAAATAATCTAAAGGTTTTGGTTTTGTGGATTACCATCTCCGTGCT  3600
Sbjct                4169  ........................................................  4228

Query                3601  GTGCATCTGAAGGCCAGTGCTGTGCTGGCAGGAAAATAGGGACTGAGAAAAAGCAGATCC  3660
Sbjct                4229  ........................................................  4288

Query                3661  TATACTATAGGGACTGTAGTATCTATGACGTAGCCAGCCATTCTTTGCTCCCAAGGCAAG  3720
Sbjct                4289  ........................................................  4348

Query                3721  AAGAAAGAGATGACAGAGTCAATATAGGGTTGCCAAATCGGATTTTCTAAAATGAGTAGG  3780
Sbjct                4349  ........................................................  4408

Query                3781  AAGTTGGATTTTTATGTGCAACAGTTTCTTTTAATGCTTTGTTGATATGTGATTGTCATG  3840
Sbjct                4409  ........................................................  4468

Query                3841  CAATAATTATTCATATTTGGTAAGTTTTGTACATATATTATGTACACTCAGGGAACCAAT  3900
Sbjct                4469  ........................................................  4528

Query                3901  ACCATAATCATGATAATGAACGTATCCATCACCTGCAAAGCTACCTCATGCCCCTTTACA  3960
Sbjct                4529  ........................................................  4588

Query                3961  TTCCCTCCTTGCCTTCCCTAGGAAACCGTTGATTTACATTTTTTACTTTAGATTTGTTTG  4020
Sbjct                4589  ........................................................  4648

Query                4021  CCTTTTCTAGAATTAACACAATTGGAATCATAAAGTATTTATACTCTC  4068
Sbjct                4649  ................................................  4696
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