



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

TF: pGL4-phTF (RDB# 7540)

APOB : pGL4-ph APOB (**RDB# 7527**)

APP : pGL4-ph APP(RDB# 7692)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.11.05

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5706

2nd Nucleotide Sequence

File Name : RDB7527F.fasta
Sequence Size : 700

Unit Size to Compare = 1
Pick up Location = 1

[96.132% / 698 bp] INT/OPT. Score : < 366/ 2516 >

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1'          GGCCTAAC TGGCCGGTAC CTGAGCTCGC TAGCCTCGAG GATGCAGGCG
          *****
1'' CGAACTTTCT CTGGCCTAAC TGGCCGGTAC CTGAGCTCGC TAGACCTCAG GATGCAGGCG

49' AAGGTCTTTC TGTGAGTCTC CTCTGAGGGA ACTGGGTCTN TTATACATAG TTA CTGTTTC
          *****
61'' AAGGTCTTTC TGTGAGTCTC CTCTGAGGGA ACTGGGTCT- TTATACATAG TTA CTGTTTC

109' AGAATTGATC CTTCTGGAAT CATCAGTCTT NCACCAGTAG CTTGTTACAT CTGGGGTTAT
          *****
120'' AGAATTGATC CTTCTGGAAT CATCAGTCTT -CACCAGTAG CTTGTTACAT CTGGGGTTAT

169' CTCATAATTC AAACAAAGCT GNACAAGTTG TAACAATGAG CACACACTGA CTTCTGCAAC
          *****
179'' CTCATAATTC AAACAAAGCT G-ACAAGTTG TAACAATGAG CACACACTGA CTTCTGCAAC

229' AGGCGCTGTC CANCTTCCCA TCCGCACTCT ACCGGCTTGC TCCTGGCCGC CTCCCACTCG
          *****
238'' AGGCGCTGTC CA-CTTCCCA TCCGCACTCT ACCGGCTTGC TCCTGGCCGC CTCCCACTCG
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289' CCTNTCCTGG GTGGTCCCC AGCAGTTATA CCTACCTGGT TGTCGCCCC TCTANTCCTA
    *** ***** ***** ***** ***** ***** ***** *****
297" CCT-TCCTGG GTGGTCCCC AGCAGTTATA CCTACCTGGT TGTCGCCCC TCTA-TCCTA

349' CCACAATTGC TCACTAGCGG TTCCTGCGT ACACAGCTTG TCTCCNCTAA CCAGAGTGGA
    ***** ***** ***** ***** ***** ***** *****
355" CCACAATTGC TCACTAGCGG TTCCTGCGT ACACAGCTTG TCTCC-CTAA CCAGAGTGGA

409' GGTGCCTTGG GGACACAGCC AGGCTCAGAC ATTACNTCA GCTCATCATA GTGCCATCCC
    ***** ***** ***** ***** ** ***** ***** *****
414" GGTGCCTTGG GGACACAGCC AGGCTCAGAC ATTAC-TCA GCTCATCATA GTGCCATCCC

469' ATCAATAACC CTTTCTGAGT GATCCTGNGG TTAGTAAACC GAGTGTCCCT GAAATTCCAC
    ***** ***** ***** ** ***** ***** ***** *****
473" ATCAATAACC CTTTCTGAGT GATCCTG-GG TTAGTAAACC GAGTGTCCCT GAAATCCCAC

529' TACCGCTGAT TCCCTCCANG CTGGGCAGAG GCAGCGAGCG CTGGCTGAAG CTTCCGGTGG
    ***** ***** . * ***** ***** ***** *****
532" TACCGCTGAT TCCCTACAG CTGGGCAGAG GCAGCGAGCG CTGGCTGAAG TTTCCGGTGG

589' GAAATGGGCN AGTGCCTAGA AGAGAAGGAA ACGATGCATG AGAAGTTCC AGATGTCTAT
    ***** ***** * ***** ***** ***** ***** *****
592" GAAATGGGC- AGTGCCTAGA AAGGAAGGAA ACGATGCATG AGAAGTTCC AGATGTCTAT

649' NGAGGAACAT GACGTGTCCT GTCCACTACT CTGCTTTTCC TCG-TCCGCC TCNCCCACCA
    **, ***** ***** ***** ***** ***** *****
651" -GANGAACAT GACGTGTCCT GTCCACTACT CTGCTTTTCC TCGTTCCGCC C

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5706

2nd Nucleotide Sequence

File Name : RDB7527R.fasta (Complementary)
Sequence Size : 750



Unit Size to Compare = 1

Pick up Location = 1

[97.375% / 762 bp] INT/OPT. Score : < 473/ 2791 >

781' TGC GCCCTCG GAGGTTGCTC TNTCCCAGA GGCCTCTCCT CGCTGGGGTT TCTGAAGAC

1"

C TGCTGGGGTT TCTGAAGAC

841' AGATACTTGG ACNTCCTGCT GGGACCAGGC AGGCCACCCA TCCTCAGGGG CAGTGAAGG

****.***** ** ***** ***** ** ***** *****

22" AGATNCTTGG AC-TCCTGCT -GGACCAGGC AGGGCACCCA TCCTCAGGGG CAGTGAAGG

901' TCANCTCACC AGACCTCCCT GCATCCCCT TCTCTCCT CCCCAGCAC GGGCNTGAAC

*** ***** ***** * * * ***** ***** ***** **** *****

80" TCA-CTCACC AGACCTGCGT GGATCCCCT TCTCTCCT CCCCAGCAC GGGC-TGAAC

961' CCCGCAGCCA CAGATTCTGA TCAGGATTAG GGTGTGGTG CAAATNCAA GGTCCACCAA

***** ***** ***** ***** ***** ***** *****

138" CCCGCAGCCA CAGATTCTGA TCAGGATTAG GGTGTGGTG CAAAT-CCAA GGTCCACCAA

1021' AATGAAAAG AAGTAACCGA TGGGAACACG TCTCCANCCA AGACAGCGCT CAGGACTGGT

***** ***** ***** ***** ** ***** *****

197" AATGAAAAG AAGTAACCGA TGGGAACACG TCTCCA-CCA AGACAGCGCT CAGGACTGGT

1081' TCTCCTCGTG GCTCCCAATT CAGTCCANGG AGAAGCAGAG ATTTTGTCCC CATGGTGGGT

***** ***** ***** ** ***** ***** *****

256" TCTCCTCGTG GCTCCCAATT CAGTCCA-GG AGAAGCAGAG ATTTTGTCCC CATGGTGGGT

1141' CATCTGAAGA AGGCACCCNC TGGTCAGGGC AGGCTTCTCA GACCCTGAGG CGCTGGCCAT

***** ***** * ***** ***** ***** *****

315" CATCTGAAGA AGGCACCC-C TGGTCAGGGC AGGCTTCTCA GACCCTGAGG CGCCGGCCAT

1201' GGCCCCACTN GAGACACAGG AAGGGCCGCG CCAGAGCACT GAAGACGCTT GGGGAAGGGA

***** ***** ***** ***** ***** *****

374" GGCCCCACT- GAGACACAGG AAGGGCCGCG CCAGAGCACT GAAGACGCTT GGGGAAGGGA



1261' NACCCACCTG GGACCCAGCC CCTGGTGGCT GCGGCTGCAT CCCAGGTGGG CNCCCCTCCC

 433" -ACCCACCTG GGACCCAGCC CCTGGTGGCT GCGGCTGCAT CCCAGGTGGG C-CCCCTCCC

1321' CGAGGCTCTT CAAGGCTCAA AGAGAAGCCA GTGTAGAAAA GCNAAACAGG TCAGGCCCGG

 491" CGAGGCTCTT CAAGGCTCAA AGAGAAGCCA GTGTAGAAAA GC-AAACAGG TCAGGCCCGG

1381' GAGGCGCCCT TTGGACCTTT TGCAATCCTG GCGNCTCTTG CAGCCTGGGC TTCCTATAAA

 550" GAGGCGCCCT TTGGACCTTT TGCAATCCTG GCG-CTCTTG CAGCCTGGGC TTCCTATAAA

1441' TGGGGTGCGG GCGCCGCGG CGCANTTCCC ACCGGGACCT GCGGGGCTGA GTGCCCTTCT

 609" TGGGGTGCGG GCGCCGCGG CGCA-TTCCC ACCGGGACCT GCGGGGCTGA GTGCCCTTCT

1501' CGGTTATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC

 668" CGGTTATCAA GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC

1561' ACCATGGAAG ATGCCAAAAA CATTAAGAAG GGCCAGCGC CATTCTACCC ACTCGAAGAC

 728" ACCATGGAAG ATGCCAAAAA CAT