



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

GADD45B: pGL4-ph GADD45B (RDB# 7529)

CYP1A1: pGL4-ph CYP1A1 (RDB# 7541)

Sp1: pGL4-ph Sp1 (RDB# 7531)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.10.29

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5778

2nd Nucleotide Sequence

File Name : RDB7529F.fasta
Sequence Size : 800

Unit Size to Compare = 1
Pick up Location = 1

[94.492% / 817 bp] INT/OPT. Score : < 424/ 2690 >

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1'          GGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATCCCGT
          *****
1'' CCAGAACTTT CTCTGGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATCCCGT

47' CCGTCCCTCT CTTCCGGCGC TGNAGGGCGC AGAAACTC-G GCGCGGCCAC CAGATGGCGC
          ***** ** ***** * *****
61'' CCGTCCCTCT CTTCCGGCGC TG-AGGGCGC AGAAACTCGG GCGCGGCCAC CAGATGGCGC

106' CACCGCGCCT CGCANGCCCC GGGACATTTC GTGCCCCAGC GGTGGGCGGC GCGGAGGAGG
          ***** **** ***** ***** *****
120'' CACCGCGCCT CGCA-GCCCC GGGACATTTC GTGCCCCAGC GGTGGGCGGC GCGGAGGAGG

166' TGGGANTGCG TCAGCCGGAC CCGCGGGCCG GGGAGCCGGG CAACTGGGGA AAGTGANGCC
          ***** ***** ***** ***** *****
179'' TGGGA-TGCG TCAGCCGGAC CCGCGGGCCG GGGAGCCGGG CAACTGGGGA AAGTGA-GCC

226' GCCGGGCGGA GGCCAGACCC CAGGCTGGCG GGGGAGGGGA CTCAGATNGT GAGTCACCCG
          ***** ***** ***** ***** ***** ** *****
237'' GCCGGGCGGA GGCCAGACCC CAGGCTGGCG GGGGAGGGGA CTCAGAT-GT GAGTCACCCG
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286' GGAGCCCCA GTCGACCGTG GGAGACGTTG TCATGCGGNG GCCTGCCAGC CTCGCTCCTG

 296'' GGAGCCCCA GTCGACCGTG GGAGACGTTG TCATGCGG-G GCCTGCCAGC CTCGCTCCTG

 346' AACAGCCTTC CCGGGGCGGC GGAGTCCTGN CAGGCGGCCG TGCCTGGCGC ACACGCGTGG

 355'' AACAGCCTTC CCGGGGCGGC GGAGTCCTG- CAGGCGGCCG TGCCTGGCGC ACACGCGTGG

 406' CTCCAACAG AACTAGCCTA NTGGCCTCAC CAAGCCTCAG TTTCCCTTT TGCATAATGC

 414'' CTCCAACAG AACTAGCCTA -TGGCCTCAC CAAGCCTCAG TTTCCCTTT TGCATAATGC

 466' ACATAAGCAT CNCCCCTGC TTCCAGGTC TTGGATTAA TCATCCATGA ATCCGGAGGG

 473'' ACATAAGCAT C-CCCCCTGC TTCCAGGTC TTGGATTAA TCATCCATGA ATCCGGAGGG

 526' GTNGGGGGT ACCAGGTCCG CACCAGCAC TCAATGCAGG TCAGCGCCA CCCNCGGAGT
 ** *****
 532'' GT-GGGGGT ACCAGGTCCG CACCAGCAC TCAATGCAGG TCAGCGCCA CCC-CGGAGT

 586' GAGAAATAA AGTAGCCGTC ATCCTTGAC GTGGGCCCTG GGTGNGCGC GTGCAGCGG

 590'' GAGAAATAA AGTAGCCGTC ATCCTTGAC GTGGGCCCTG GGTG-GCGC GTGCAGCGG

 646' AGCCTGCACC ATTCCCCTCA ACAATGGCT TCTCCNAGG CCTGGAGGCC TCCGCACGGG

 649'' AGCCTGCACC ATTCCCCTCA ACAATGGCT TCTCC-GGG CCTGNAGGCC T-CGCACGGG

 706' CAAAGGCTGG AACGCCAGG AGCCGGNCGG GGGCGGGCC GCGCCACCTG CACCTCCAC
 * *****
 707'' C-AAGGCTGG -ACGCCA-GC AG-CGG-CG GGGCGGGG-C GCG-CACCTG CA-CT-CCA-

 766' GCGCACCCA CCCTGATNAC TCGCGGGGTC GCGGAGGAG GCGCCACTTT CTCTCCAGA

 756'' GCGCA-CCA -CCTGAT--C T-GC-GGGT -GCAAGAGCG CCACTTCTCT CC

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5778

2nd Nucleotide Sequence

File Name : RDB7529R.fasta (Complementary)
Sequence Size : 798

Unit Size to Compare = 1
Pick up Location = 1

[96.560% / 814 bp] INT/OPT. Score : < 424/ 2907 >

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841' GCAACCTCCC ACTTTCGGGG CCCTCGAGGA GGCCTCCCGC GACCNACCAG GTGACAGCTG
      *****
1'' AAACCTCCA CTTTTCGGGC CCCTCG-NGA GGCCTCCCGC GACC-ACCAG GTGACAGCTG

901' ATGTGTATTG GGCTCTTACT GTCAGCCGTA TTTTANTGCC ATGCTCTGCA AACCAGCGAG
      ***** **
58'' ATGTGTA-TG GGCTCTTACT GTCAGCCGT- NTTTA-TGCC ATGCTCTGCA NACCAGGCAG

961' GCCGGCGCTG CAGACCCATT ACTCAGNACG GGAACAGAGA -GGCCGGGAG AAGCGAAATC
      *****
115'' GCCGGCGCTG CAGACCCATT ACTCAG-ACG GGAACAGAGA GGGCCGGGAG AAGCGAAATC

1020' ACCCAGGGGC TGGGGTCGNT CGCAGCCAGG AGAGACTCCG GCCCTCACCA CCACCTGGGC
      *****
174'' ACCCAGGGGC TGGGGTCG-T CGCAGCCAGG AGAGACTCCG GCCCTCACCA CCACCTGGGC

1080' GAGATCACGN CTGCAAACGG GGCCCTTCC CGGTGCAG-C CCCTCCACCC CCAGCAGAAC
      *****
233'' GAGATCACG- CTGCAAACGG GGCCCTTCC CGGTGCAGCC CCCTCCACCC CCAGCAGAAC

1139' TNTGGGAAAG GCGCGGTCCG GGA CTCTCCG CGGATCGGGA GGGGATTCCA GGNCCCCC
      *
292'' T-TGGGAAAG GCGCGGTCCG GGA CTCTCCG CGGATCGGGA GGGGATTCCA GG-CCCCC
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1199' GAAAGTCCGG GCCGCCTCGC GCGCTGGAAA TCCCGCGCGC GCCNCCGAAC CGCGGCTCGG

 350" GAAAGTCCGG GCCGCCTCGC GCGCTGGAAA TCCCGCGCGC GCC-CCGAAC CGCGGCTCGG

1259' CTGCCGGGAA ATCAGGAGAA AAAAATTCT GCTTNTTTTT TCTTTTCTGG CATTGCGGT

 409" CTGCCGGGAA ATCAGGAGAA AAAAATTCT GCTT-TTTTT TCTTTTCTGG CATTGCGGT

1319' CACCTACCGG GCCCCGCGC GCCCTNCCTC CCGGTTCTCG CCCCACGTG GGGGCCCCC

 468" CACCTACCGG GCCCCGCGC GCCCT-CCTC CCGGTTCTCG CCCCACGTG GGGGCCCCC

1379' GCACGCCGCT CCTCCNCCT CCCCTCCGTC GGCCAACCGC AGAGCTAGCT GCACTCGCC

 527" GCACGCCGCT CCTCCC-CCT CCCCTCCGTC GGCCAACCGC AGAGCTAGCT GCACTCGCC

1439' TTGTCTTNC CACCAATAGG AGGGGCGAAT GACTCCACTG AGGCCACGCC CAATGTTCA
 ***** *
 586" TTGTCTT-TC CACCAATAGG AGGGGCGAAT GACTCCACTG AGGCCACGCC CAATGTTCA

1499' AGTCTATAAA AGTCGGTGCC GGAGGCTCCC AGCTCAGATC GCCGAAGCGN TCGGACTACC

 644" AGTCTATAAA AGTCGGTGCC GGAGGCTCCC AGCTCAGATC GCCGAAGCG- TCGGACTACC

1559' GTTGGTTTCC GCAACTTCCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA

 703" GTTGGTTTCC GCAACTTCCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA

1619' CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA GAAGGGCCA GCGCCATTCT

 763" CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACA