



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

TP53: pGL4-phTP53 (RDB# 7330)

TBXAS1: pGL4-phTBXAS1 (RDB# 7347)

PCNA: pGL4-phPCNA (RDB# 7365)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5563

2nd Nucleotide Sequence

File Name : RDB7347F.fasta
Sequence Size : 611

Unit Size to Compare = 1
Pick up Location = 1

[99.659% / 587 bp] INT/OPT. Score : < 2220/ 2316 >

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1'          GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA
          *****
1" TGCAGGTGCC AGAACATTTT TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA

38' GGATATGGCT GCAGAAGTTT TCCTTGATTG TTCCCCAAA TATGTTTTCC AAGCTTTTAG
          *****
61" GGATATGGCT GCAGAAGTTT TCCTTGATTG TTCCCCAAA TATGTTTTCC AAGCTTTTAG

98' AATTCTCTTC TTCCTCAGGA ACACCAATTA TTCTTAGGTT TGGTCATTTA ACATAATCCC
          *****
121" AATTCTCTTC TTCCTCAGGA ACACCAATTA TTCTTAGGTT TGGTCATTTA ACATAATCCC

158' AGACTTCTTG GAGGCTTTGT TCATATTTTC TTATTCTTTT TTCTTTGTCT TTGTTGAATT
          *****
181" AGACTTCTTG GAGGCTTTGT TCATATTTTC TTATTCTTTT TTCTTTGTCT TTGTTGAATT

218' GGGTTAATTT GAAGACCTTG TCTTTGAGCT CTGATTTTCT TTCTTCTACT TGTTC AATTC
          *****
241" GGGTTAATTT GAAGACCTTG TCTTTGAGCT CTGATTTTCT TTCTTCTACT TGTTC AATTC
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278' TATTGCTGAG ACTTCCAGA GCATTCACA TTTCTAAAAG TGTGTCCAAA GTTCCTGAA
*****
301" TATTGCTGAG ACTTCCAGA GCATTCACA TTTCTAAAAG TGTGTCCAAA GTTCCTGAA

338' TTTTCAATTA TTTTTCTTT AAGCTATTTT ATTGAATATT TCTCCATTG AATATTGGGG
*****
361" TTTTCAATTA TTTTTCTTT AAGCTATTTT ATTGAATATT TCTCCATTG AATATTGGGG

398' GATTGTGTTG GGAGAGGAGG GTCTCCCTTT CCCACTTCCG CAAATGGGGC ACTCACAGTA
*****
421" GATTGTGTTG GGAGAGGAGG GTCTCCCTTT CCCACTTCCG CAAATGGGGC ACTCACAGTA

458' TTTGGAGTGT CTTCTGGGTC CTGCAGGAGC AGTCTGGTTC CTTCAGAGAG TCTGTGGGTC
*****
481" TTTGGAGTGT CTTCTGGGTC CTGCAGGAGC AGTCTGGTTC CTTCAGAGAG TCTGTGGGTC

518' CTTTTGGGAT TGCTGGTTTT TTCTTGCAGT TGATCT-GGA GCTAAAATTC ACCAT-GGAA
*****
541" CTTTTGGGAT TGCTGGTTTT TTCTTGCAGT TGATCTGGGA GCTAAAATTC ACCATGGGAA

576' GCCTCCAGAT GCTGCTCTGT CTGAAGCTGC AATCTAGTCC TGCCACCCAG CCACTATGAT
*****
601" GCCTCCAGAT T

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5563

2nd Nucleotide Sequence

File Name : RDB7347R. fasta (Complementary)
Sequence Size : 402

Unit Size to Compare = 1

Pick up Location = 1



[99.751% / 402 bp] INT/OPT. Score : < 1602/ 1602 >

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1021' GGAGAAGAGT CTCTCTTTGA AGACTTCCTC TCAGAGTACA AGTCCGTGGT TACAACCATT
      ***** ***** ***** *****
1''      AGACTTCCTC TCAGAGTACA AGTCCGTGGT TACAACCATT

1081' TTGTTTCTCA GCAAACATGG GGAAGTTTGC TTTTCTTCTC TGAGGAAGTT AATATAAATG
      ***** ***** ***** ***** ***** *****
41'' TTGTTTCTCA GCAAACATGG GGAAGTTTGC TTTTCTTCTC TGAGGAAGTT AATATAAATG

1141' TTTATTGACA GTGCAGTCAT CAAGGAATAA AGTTGCTGAT TCATTCCTTT AACTGAAAC
      ***** ***** ***** ***** ***** *****
101'' TTTATTGACA GTGCAGTCAT CAAGGAATAA AGTTGCTGAT TCATTCCTTT AACTGAAAC

1201' CCTTTGTTGT GCCCTCCTCT TCCTCCTCT TTATAGGGAG AACTCTGAG AAAGAGCACA
      ***** ***** ***** ***** ***** *****
161'' CCTTTGTTGT GCCCTCCTCT TCCTCCTCT TTATAGGGAG AACTCTGAG AAAGAGCACA

1261' TTGTGGGGGC CCACTCCATG TGATGTTTGC TTGGTTCCT GTTCCCTTTT CTACCTGCAG
      ***** ***** ***** ***** ***** *****
221'' TTGTGGGGGC CCACTCCATG TGATGTTTGC TTGGTTCCT GTTCCCTTTT CTACCTGCAG

1321' AGCACGGTTC CCATAAGGGC GCGGAGATCA GCCTCCTGTC TCATCAAGAT CTGGCCTCGG
      ***** ***** ***** ***** ***** *****
281'' AGCACGGTTC CCATAAGGGC GCGGAGATCA GCCTCCTGTC TCATCAAGAT CTGGCCTCGG

1381' CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT
      ***** ***** ***** ***** ***** *****
341'' CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT

1441' TAAGAAGGGC CCAGCGCCAT TCTACCCACT CGAAGACGGG ACCGCCGGCG AGCAGCTGCA
      *
401'' AA
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