



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

APAF1: pGL4-phAPAF1 (RDB# 7316)

**GADD45A**: pGL4-phGADD45A (**RDB# 7320**)

MKI67: pGL4-phMKI67 (RDB# 7323)

TP53: pGL4-phTP53 (RDB#7330)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.01

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5467

2nd Nucleotide Sequence

File Name : RDB7320F.fasta  
Sequence Size : 720

Unit Size to Compare = 1  
Pick up Location = 1

[98.138% / 698 bp] INT/OPT.Score : < 2392/ 2617 >

```
1'          GG CCTAACTG-G CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
          ** ***** * ***** ***** *****
1'' GTGCCAGAAC ATTTCTCTGG CCTAACTGTG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

42' CAAAGGAAGG GACTTTTGAA CTA CTCAGTG AGAGTCTATA TATTAAAGTT TGTTTTCAA
          ***** ***** ***** ***** ***** *****
61'' CAAAGGAAGG GACTTTTGAA CTA CTCAGTG AGAGTCTATA TATTAAAGTT TGTTTTCAA

102' AAATGTGTAA CTACCATTG CAGTTTTAAA GGTCTGCTTT CCACCTACAA GTTGCCATTA
          ***** ***** ***** ***** ***** *****
121'' AAATGTGTAA CTACCATTG CAGTTTTAAA GGTCTGCTTT CCACCTACAA GTTGCCATTA

162' TCTCAAAGGT GAAATTTTAG CATATGACTA AAAACTTCCT ATAGTTACAG CTTCATGATT
          ***** ***** ***** ***** ***** *****
181'' TCTCAAAGGT GAAATTTTAG CATATGACTA AAAACTTCCT ATAGTTACAG CTTCATGATT

222' CAGCATCTAA CATCAATAAT TCACAGTGAG ATCATAGGAG GCTCTCTGTG GAAGGTAACG
          ***** ***** ***** ***** ***** *****
241'' CAGCATCTAA CATCAATAAT TCACAGTGAG ATCATAGGAG GCTCTCTGTG GAAGGTAACG
```



```

282' ACATACATAC GTTAGGAAAG GAAGCTTAGG GCATATCGAG AGCATTTTGA ATTAGACTT
*****
301" ACATACATAC GTTAGGAAAG GAAGCTTAGG GCATATCGAG AGCATTTTGA ATTAGACTT

342' GTGGGCTGTG TGGGTGTCAG ATGTTGTCT CTCAGCTGGT GGGCGTCCAG AAGGATCCTT
*****
361" GTGGGCTGTG TGGGTGTCAG ATGTTGTCT CTCAGCTGGT GGGCGTCCAG AAGGATCCTT

402' GTTTGGGCAA GGCTCTTTGA GAAAGGAGAA TCTGGGTTGC CAGGGATTCC CACATGTGGT
*****
421" GTTTGGGCAA GGCTCTTTGA GAAAGGAGAA TCTGGGTTGC CAGGGATTCC CACATGTGGT

462' CACCAGCTCC CCACGCAGAC CAGCTCACGA TTTCCAGTT ACACCGGGCA GGTGGGAAAC
*****
481" CACCAGCTCC CCACGCAGAC CAGCTCACGA TTTCCAGTT ACACCGGGCA GGTGGGAAAC

522' CGTTCTGCTT TCTGTGAAA AGATTCTAAC TTGGTTCCT GCCATCCCTG AATACAAACG
****
541" CGTTATGCTT TCTGTGAAA AGATTCTAAC TTGGTTCCT GCCATCCCTG AATACAAACG

582' GGTTGGTTTT TCTTTTTTCA GCTTCC-AAC CCTTGCAG-C TTTCAAAAA TAAATCAA-
*****
601" GGTTGGTTTT TCTTTTTTCA GCCTCAAAC CCTTGCAGCC TTTCAAAAA TAAATCAAAC

639' CCAG-CCATC A-GGGACCG -AAATAATAC TAC-TGCTAA -TAAGCAGC- TTCGCCTAGA
****
661" CCAGCCCATC AGGGGACCG AAAATAATAC TACTTGCNAA TTAAGCAGCT TTCGCCTAA

```

#### 1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5467

#### 2nd Nucleotide Sequence

File Name : RDB7320R.fasta (Complementary)  
Sequence Size : 695



Unit Size to Compare = 1  
Pick up Location = 1

[97.986% / 695 bp] INT/OPT. Score : < 1986/ 2616 >

661' AATACTA-CT GCTAAT-AAG CAGCTTC-GC CTAGACTTA- GATAACAAC ACTTCTGAGG

\*\*\*\* \*\* \* \*\*\*\* \*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\*

1" ACTACCT GGTAATAAAG CAGCTTCGGC CTAGACCTAG GATAACAAC ACTTCTGAGG

717' TAAACTTTGC CCCGGAGGTC TGGAGACACT TTTTAAATGT AACCTGCTTA CTAATAATTA

\* \*\*\*\*\* \*\*\*\*\* \*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\*

58" TAAACTTTGC CCCGGAGGTC TGGAAACACT TTTTAAAGGT AACCTGCTTA CTAATAATTA

777' CTAGACTTCA GTGCA-TTAA CCCT-GGAAA TAGATTTTAA TAGCCACCCC -TAAAACAA

\*\*\*\*\* \*\*\*\*\* \*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

118" CTAGACTTCA GTGCATTTAA CCCTGGGAAA TAGATTTTAA TAGCCACCCC TTTAAAACAA

834' AAGACATGAA AAGATAATAA GAAAAAAGTG CCGCAACTAT TATAGAAAAA CACTTGGCAG

\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

178" AAGACATGAA AAGATAATAA GAAAAAAGTG CCGCAACTAT TATAGAAAAA CACTTGGCAG

894' CCTGCTTCAG CCCAAGCTGA GGCCACCTCT AGCCTCTGCT AAAGCCCCC ACTCCAATG

\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

238" CCTGCTTCAG CCCAAGCTGA GGCCACCTCT AGCCTCTGCT AAAGCCCCC ACTCCAATG

954' GTCCCCGCCA ACCGGATAAG AGTGCGCGCG GGACCCGCCT TCCCCTCTCG GCACCGCCCC

\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\*

298" GTCCCCGCCA ACCGGATAAG AGTGCGCGCG GGACCCGCCT TCCCCTCTAG GCACCGCCCC

1014' CGCCCCGCC CCCTCGGCTC GCCTCCCGCG TGGCTCCTCC CTTTCCGCT CCTCTCAACC

\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

358" CGCCCCGCC CCCTCGGCTC GCCTCCCGCG TGGCTCCTCC CTTTCCGCT CCTCTCAACC

1074' TGACTIONCAGG AGCTGGGGTC AAATTGCTGG AGCAGGCTGA TTTGCATAGC CCAATGGCCA

\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

418" TGACTIONCAGG AGCTGGGGTC AAATTGCTGG AGCAGGCTGA TTTGCATAGC CCAATGGCCA



1134' AGCTGCATGC AAATGAGGCG GAAGGTGGTT GGCTGAGGGT TGGCAGGATA ACCCCGGAGA  
 \*\*\*\*\*  
 478" AGCTGCATGC AAATGAGGCG GAAGGTGGTT GGCTGAGGGT TGGCAGGATA ACCCCGGAGA  
  
 1194' GCGGGGCCCT TTGCCTCCA GTGGCTGGTA GGCAGTGGCT GGGAGGCAGC GGCCCAATTA  
 \*\*\*\*\*  
 538" GCGGGGCCCT TTGCCTCCA GTGGCTGGTA GGCAGTGGCT GGGAGGCAGC GGCCCAATTA  
  
 1254' GTGTCGTGCG GCCATCAAGA TCTGGCCTCG GCGGCAAGC TTGGCAATCC GGTACTGTTG  
 \*\*\*\*\*  
 598" GTGTCGTGCG GCCATCAAGA TCTGGCCTCG GCGGCAAGC TTGGCAATCC GGTACTGTTG  
  
 1314' GTAAAG-CCA CCATGGAAGA TGCCAAAAAC ATTAAGAAG GCCCAGCGCC ATTCTACCCA  
 \*\*\*\*\*  
 658" GTAAAGACCA CCATGGAAGA TGCCAAAAAC ATTAAGAA