



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

TNF: pGL4-phTNF (RDB#7310)

IL6: pGL4-phIL6(RDB#7313)

PTGS2:pGL4-phPTGS2 (RDB#7300)

BRCA1: pGL4-phBRCA1 (RDB#7296)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.23

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5394

2nd Nucleotide Sequence

File Name : RDB7296F.fasta
Sequence Size : 597

Unit Size to Compare = 1
Pick up Location = 1

[97.104% / 587 bp] INT/OPT. Score : < 384/ 2099 >

```
1'          G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
              * *****
1'' GTGCCAGAAC ATTGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

42' -TCCTCCCTT GAACTTCTCC AAACCTCTT AGTGTGACNG TGACCCACCC CCTAGCTAAC
      *****
61'' GTCCTCCCTT GAACTTCTCC AAACCTCTT AGTGTGACGT TGACCCACCC CCTAGCTAAC

101' CCAGGCTGCT TCCTTACCAG CTTCCCGCCN CCCTGGGGAG GCGGCAATGC AAAGACCGTC
      *****
121'' CCAGGCTGCT TCCTTACCAG CTTCCCGCC- CCCTGGGGAG GCGGCAATGC AAAGACCGTC

161' CGCTGCCAGC TCTGCCGCTA NTCTCTGTGG GGTGAATCTA ACATGGCGGA CAAAGACAGT
      *****
180'' CGCTGCCAGC TCTGCCGCTA -TCTCTGTGG GGTGAATCTA ACATGGCGGA CAAAGACAGT

221' AACTAGTCCC GNTTCTCCG CGTTTTCGCC AAGAAGATTG GCTCTTACCA CTTGTCCCTC
      ***** * *****
239'' AACTAGTCCC G-TTCTCCG CGTTTTCGCC AAGAAGATTG GCTCTTACCA CTTGTCCCTC
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281' AANAACGACC ACCCCATTGA CTGGTGGCGA TTGCGTCGAC GGAGACGGGG CAANAAGCAA
    ** ***** ***** ***** ***** ***** ***** *****
298'' AA-AACGACC ACCCCATTGA CTGGTGGCGA TTGCGTCGAC GGAGACGGGG CAA-AAGCAA

341' GCTGAACCCG AAAAATAACA AACACTGGGG CTGAGGGGTG GAACNTACGA GTGCGCAGAC
    ***** ***** ***** ***** ***** ***** *****
356'' GCTGAACCCG AAAAATAACA AACACTGGGG CTGAGGGGTG GAAC-TACGA GTGCGCAGAC

401' ATGGGCCAGA GCGCATTTC CCTGCCCCAG GCAAANTTCG GCGCTACTG CGTCCCGCA
    ***** ***** ***** ***** ***** ***** *****
415'' ATGGGCCAGA GCGCATTTC CCTGCCCCAG GCAAA-TTCG GCGCTACTG CGTCCCGCA

461' GGCCACTGAC CTTACAAGAC TACTTGNCCT CAGACTCCTG GGGCTGGATG GGAATTGTAG
    ***** ***** ***** ** ***** ***** ***** *****
474'' GGCCACTGAC CTTACAAGAC TACTTG-CCC CAGACTCCTG GGGCTGGATG GGAATTGTAG

521' TCTCCCTAAA GAGTTGTNAC GTATCTTTTT AA-GGCCTAG -TTTCTG-CT TTC-AAAAT-
    ***** ***** ** ***** ** ***** ** ** *****
533'' TCTCCCTAAA GAGTTGT-AC GTATCTTTTT AAGGGCCTAG TTTTCTGCCT TTCAAAAATA

576' ACGAAAACAT AACNACTCCA GTCCATAACT GTTGACAAGT ACAAGCGCGC ACAGGTCTCC
    *****
592'' ACGAAA

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5394

2nd Nucleotide Sequence

File Name : RDB7296R.fasta (Complementary)
Sequence Size : 661

Unit Size to Compare = 1

Pick up Location = 1



[97.633% / 676 bp] INT/OPT. Score : < 332/ 2458 >

```
601' TAACTGTTGA CAAGTACAAG CGCGCACAGG TCTCCAATCN TATCCACTGG ATTTCCGTGA
      ***** **
1''  AACTG-TGA CAAGTACAGG CGCGCACAGG TCTCC-ATC- TATCCACT-G ATTTCCGTGA

661' GAATTGTGCC CGCTCTGGTA TTGGATGTTT NCTCTCCATA AGACTACAGT TTCTAAGGAA
      *****
56'' GAATTGTGCC CGCTCTGGTA TTGGATGTTT -CTCTCCATA AGACTACAGT TTCTAAGGAA

721' CACTGTGGCG AAGACCTTTC ANTTCCGCAA CGCATGCTGG AAATAATTAT TTCCCTCCAC
      *****
115'' CACTGTGGCG AAGACCTTTC A-TTCCGCAA CGCATGCTGG AAATAATTAT TTCCCTCCAC

781' CCCCCAACA ATNCCTTATT ACTTATATTT ACCGAAACTG GAGACCTCCA TTAGGGCGGA
      *****
174'' CCCCCAACA AT-CCTTATT ACTTATATTT ACCGAAACTG GAGACCTCCA TTAGGGCGGA

841' AAGNAGTGGG GGATTGGGAC CTCTTCTTAC GACTGCTTTG GACAATAGGT AGCGNATTCT
      ***
233'' AAG-AGTGGG GGATTGGGAC CTCTTCTTAC GACTGCTTTG GACAATAGGT AGCG-ATTCT

901' GACCTTCGTA CAGCAATTAC TGTGATGCAA TAAGCCGCAA CTGGANAGAG TAGAGGCTAG
      *****
291'' GACCTTCGTA CAGCAATTAC TGTGATGCAA TAAGCCGCAA CTGGA-AGAG TAGAGGCTAG

961' AGGGCAGGCA CTTTATGGCA AACTCAGGTA GAATTCNTTC CTCTTCGGTC TCTTTCCTTT
      *****
350'' AGGGCAGGCA CTTTATGGCA AACTCAGGTA GAATTC-TTC CTCTTCGGTC TCTTTCCTTT

1021' TACGTCATCC GGGGGCAGAC TGGGTGNCC AATCCAGAGC CCCGAGAGAC GCTTGCTCT
      *****
409'' TACGTCATCC GGGGGCAGAC TGGGTGG-CC AATCCAGAGC CCCGAGAGAC GCTTGCTCT

1081' TTCTGTCCCT CCCATCCTNC TGATTGTACC TTGATTCGT ATTCTGAGAG GCTGCTGCTT
      *****
468'' TTCTGTCCCT CCCATCCT-C TGATTGTACC TTGATTCGT ATTCTGAGAG GCTGCTGCTT
```

1141' AGCGGTAGCN CCCTTGTTT CCGTGGCAAC GGAAAAGCGC GGGAATTACA GATATCAAGA

527" AGCGGTAGC- CCCTTGTTT CCGTGGCAAC GGAAAAGCGC GGGAATTACA GAT-TCAAGA

1201' TCTGGCCTCG GCGGCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT

585" TCTGGCCTCG GCGGCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT

1261' GCCAAAACA TTAAGAAGG CCCAGCGCA TTCTACCCAC TCGAAGACGG GACCGCCGGC

645" GCCAAAACA TTAAGAA