



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 : 2010.01.25

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5441

2nd Nucleotide Sequence

File Name : RDB7310F.fasta
Sequence Size : 531

Unit Size to Compare = 1
Pick up Location = 1

[89.038% / 520 bp] INT/OPT.Score : < 340/ 1556 >

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1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAG----
          *  * * * *  ** *****  * ****.* * *  **
1'' CNTTTTGTAG GGCAAGCCGN TCAATCTAAT CGCTACCTTC GATCGCNAAC CCATAGCCCA

39' -----GATC TGTGGGGAGA ACAAAGGAT AAGGG-CTCA GAGAGCTTCA GGGNATATGT
          *  ***** ** ***** ***** *. *  **** **  **.*****
61'' ATCCAGTAT CGTGGGGAGA AC-AAAGGAT AAGGGACNCT TAGAGACTC- -GGGATATGT

92' GATGACTCA CCAGGTGAGG CCGCCAGACT GCTGCAGGGG AAGCNAAGG AGAAGCTGAG
          ***** ***** ***** ***** *** . **** *****
118'' GATGACTCA CCAGGTGAGG CCGCCAGACT GCTGCAGGGG AAG-ACAAGG AGAAGCTGAG

152' AAGATGAAGG AAAAGTCAGG GTCTGGAGGG GCGGGNGGTC AGGGAGCTCC TGGGAGATAT
          ***** ***** ***** ***** **** ***** *****
177'' AAGATGAAGG AAAAGTCAGG GTCTGGAGGG GCGGG-GGTC AGGGAGCTCC TGGGAGATAT

212' GGCCACATGT AGCGGCTCTG AGGAATNGGG TTACAGGAGA CCTCTGGGGA GATGTGACCA
          ***** ***** ***** ** ***** ***** *****
236'' GGCCACATGT AGCGGCTCTG AGGAAT-GGG TTACAGGAGA CCTCTGGGGA GATGTGACCA
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272' CAGCAATGGG TAGGAGANAT GTCCAGGGCT ATGGAAGTCG AGTATGGGA CCCCCCTTA
 ***** ** ***** ***** ***** *****
 295" CAGCAATGGG TAGGAGA-AT GTCCAGGGCT ATGGAAGTCG AGTATGGGA CCCCCCTTA

 332' ACGAAGACNA GGGCCATGTA GAGGGCCCA GGGAGTAAA GAGCCTCCAG GACCTCCAGN
 ***** * ***** ***** ***** ***** *****
 354" ACGAAGAC-A GGGCCATGTA GAGGGCCCA GGGAGTAAA GAGCCTCCAG GACCTCCAG-

 392' GTATGGAATA CAGGGGACGT TT-AAGAAGA TATGGCCACA CACTGGGGCC CNTGAGAAGT
 ***** ***** ** ***** ***** ***** * *****
 412" GTATGGAATA CAGGGGACGT TAAAGAAGA TATGGCCACA CACTGGGGCC C-TGAGAAGT

 451' GAGAGCTTCA TG-AAAAAAA T-CAGGGA-C CCCAGAGTT- CCTT-GNAA G-CCAAGACT
 ***** ** ***** * ***** * ***** ***** ** ** * *****
 471" GAGAGCTTCA TGAAAAAAA TCCAGGGACC CCCAGAGTTC CCTTGGGAAA GCCCAAGAAC

 505' GAAACCAGCA TTATGAGTCT CCGGGTCAGA ATGAAAGAAN GAAGGCCTGC CCCAGTGGGG

 531" T

1st Nucleotide Sequence

File Name : Reference Seq. gnu
 Sequence Size : 5441

2nd Nucleotide Sequence

File Name : RDB7310R. fasta (Complementary)
 Sequence Size : 690

Unit Size to Compare = 1

Pick up Location = 1

[91.311% / 679 bp] INT/OPT. Score : < 254/ 2176 >



601' GCTGTCCCAG GCTTGTCCCT GCTACCCCCA CCCAGCCTTT CCTGANGGCC TCAAGCCTGC
*** ** ***** ** * ***** .
1" AAACC CAAGGCCCTT CCTG--GGCT TC-AGCCT-N

661' CACCAAGCCC CCAGCTCCTT CTCCCCGCAG GGACCCNAAA CACAGGCCTC AGGACTCAAC
***** ***** ***** ***** . ***** ** ***** *****
32" CACC-AGCCC CCAGCTCCTT CTCCCCGC-N GGACCC-AAA CACAGGCCTC AGGACTCAAC

721' ACAGCTTTTC CCTCCAACCC CGTTTTNCNTC TCCCTCAAGG ACTCAGCTTT CTGAAGCCCC
***** ***** ***** ** ***** ***** *****
89" ACAGCTTTTC CCTCCAACCC CGTTTT-C TCCCTCAAGG ACTCAGCTTT CTGAAGCCCC

781' TCCAGTTCT AGTTCTATNC TTTTCTCTGC ATCCTGTCTG GAAGTTAGAA GGAACAGAC
***** ***** * ***** ***** ***** *****
148" TCCAGTTCT AGTTCTAT-C TTTTCTCTGC ATCCTGTCTG GAAGTTAGAA GGAACAGAC

841' CACAGACCTN GGTCCCCAAA AGAAATGGAG GCAATAGGTT TTGAGGGGCA TGGGGACGGG
***** ***** ***** ***** ***** *****
207" CACAGACCT- GGTCCCCAAA AGAAATGGAG GCAATAGGTT TTGAGGGGCA TGGGGACGGG

901' NGTTCAGCCT CCAGGGTCTT ACACACAAAT CAGTCAGTGG CCCAGAAGAC CNCCCTCGG
***** ***** ***** ***** ***** * *****
266" -GTTTCAGCCT CCAGGGTCTT ACACACAAAT CAGTCAGTGG CCCAGAAGAC C-CCCCTCGG

961' AATCGGAGCA GGGAGGATGG GGAGTGTGAG GGGTATCCTT GANTGCTTGT GTGTCCCAA
***** ***** ***** ***** ** ***** *****
324" AATCGGAGCA GGGAGGATGG GGAGTGTGAG GGGTATCCTT GA-TGCTTGT GTGTCCCAA

1021' CTTTCAAAT CCCC GCCCCC GCGATGGAGA AGANAACCGA GACAGAAGGT GCAGGGCCCA
***** ***** ***** ** ***** ***** *****
383" CTTTCAAAT CCCC GCCCCC GCGATGGAGA AGA-AACCGA GACAGAAGGT GCAGGGCCCA

1081' CTACCGCTTC CTCCAGATGA GTCNATGGG TTTCTCCACC AAGGAAGTTT TCCGCTGTT
***** ***** ** ***** ***** ***** *****
442" CTACCGCTTC CTCCAGATGA GTC-ATGGG TTTCTCCACC AAGGAAGTTT TCCGCTGTT

1141' GAATGATTCT TTCCNCGCC CTCCTCTCGC CCCAGGGACA TATAAAGGCA GTTGTGGCA
***** ***** ***** ***** ***** ***** * *****
501" GAATGATTCT TTCC-CGCC CTCCTCTCGC CCCAGGGACA TATAAAGGCA G-TGTTGGCA

1201' CACCCANGCC AGCAGACGCT CCCTCAGCAA GGACAGCAGA ATCAAGATCT GGCCTGGCG
 ***** ** ***** ** ***** * ***** ** ***** *.** * *
 559" CACCCA-GCC AGCAGA-GCT CCCTCAGTCA AAACAGCAGA ATC-AGATCG GNCCT--GGG

 1261' GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA
 *. * ** * ***** * . * ***** * ** ** ** * * . * *
 614" GNCCGTCTGG TCAATCGCGC TNAGGTGGTT GTCCAACGAT TGAGTTTCCN ATACTGGGGG

 1321' AGAAGGGCCC AGCGCCATTC TACCCACTCG AAGACGGGAC CGCCGGCGAG CAGCTGCACA

 674" TTAGCCGCTT CAAACCC