



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 : 2009.06.25

1st Nucleotide Sequence

File Name : Reference Seq. GNU

Sequence Size : 5519

2nd Nucleotide Sequence

File Name : RDB7300F.fasta

Sequence Size : 671

Unit Size to Compare = 1

Pick up Location = 1

[97.583% / 662 bp] INT/OPT. Score : < 343/ 2415 >

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1'          GG CCTAACTGGC CGGTACCTGA G-CTCGCTAG CCTCGAGGAT
          ** *****
1'' GTGCCAGAAC ATGTCTCTGG CCTAACTGGC CGGTACCTGA GACTCGCTAG CCTCGAGGAT

42' -AACTGTCAA AATCTCCCTT CCATCTAAT- TAATTCCTCA TCCAACATG NTTCCAAAAC
          *****
61'' GAAGTGTCAA AATCTCCCTT CCATCTAATG TAATTCCTCA TCCAACATG TGTCCAAAAC

100' GAGAATAGAA AATTAGCCCC AATAAGCCCA GGCAACTGAA ANAGTAAATG CTATGTTGTA
          *****
121'' GAGAATAGAA AATTAGCCCC AATAAGCCCA GGCAACTGAA A-AGTAAATG CTATGTTGTA

160' CTTTGATCCA TGGTCACAAC TCATAATCTT GGNAAGAGTG GACAGAAAAG ACAAAGAGT
          *****
180'' CTTTGATCCA TGGTCACAAC TCATAATCTT GG-AAAAGTG GACAGAAAAG ACAAAGAGT

220' GAACHTTAAA ACTCGAATTT ATTNTTACCA GTATCTCCTA TGAAGGGCTA GTAACCAAAA
          *****
239'' GAACHTTAAA ACTCGAATTT ATT-TTACCA GTATCTCCTA TGAAGGGCTA GTAACCAAAA

280' TAATCCACGC ATCANGGGAG AGAAATGCCT TAAGGCATAC GTTTTGGACA TTTAGCGTCC
          *****
298'' TAATCCACGC ATCA-GGGAG AGAAATGCCT TAAGGCATAC GTTTTGGACA TTTAGCGTCC
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340' CTGCANAATT CTGGCCATCG CCGCTTCCTT TGTCCATCAG AAGGCAGGAA ACTTTANTAT
***** *** ***** ***** ***** ***** *****
357" CTGCA-AATT CTGGCCATCG CCGCTTCCTT TGTCCATCAG AAGGCAGGAA ACTTTA-TAT

400' TGGTGACCCG TGGAGCTCAC ATTA ACTATT TACAGGGTAA CTGCTTANGG ACCAGTATTA
***** ***** ***** ***** ***** ** *****
415" TGGTGACCCG TGGAGCTCAC ATTA ACTATT TACAGGGTAA CTGCTTA-GG ACCAGTATTA

460' TGAGGAGAAT TTACCTTTCC CGCCTCTCTT TCCAAGAANA CAAGGAGGGG GTGAAGGTAC
***** ***** ***** ***** * ***** *****
474" TGAGGAGAAT TTACCTTTCC CGCCTCTCTT TCCAAGAA-A CAAGGAGGGG GTGAAGGTAC

520' GGAGAACAGT ATTTCTTCTG TTGAAAGCAN ACTTAGCTAC AAAGATAAAT TACAGCTATG
***** ***** ***** ***** ***** *****
533" GGAGAACAGT ATTTCTTCTG TTGAAAGCA- ACTTAGCTAC AAAGATAAAT TACAGCTATG

580' TACTGTAAG GTAGCTATTT NCATTCCACA AAATAAGAGT TTTTAAAAA GCTATGTATG
***** ***** ***** ***** ***** *****
592" TACTGTAAG GTAGCTATTT -CATTCCACA AAATAAGAGT TTTTAAAAA GCTATGTATG

640' TATGTGCTGC ANTATAGAGC AGATATACAG CCTATTAAGC GTCGTCACTA AACATAAAA
***** * *****
651" TATGTGCTGC A-TATAGAGC CC

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5519

2nd Nucleotide Sequence

File Name : RDB7300R.fasta (Complementary)
Sequence Size : 628

Unit Size to Compare = 1
Pick up Location = 1



[94.505% / 637 bp] INT/OPT. Score : < 430/ 2191 >

721' TTACTCGCCC CAGTCTGTCC CGACGTGACT TCNCTCGACC CTCTAAAGAC GTACAGACCA
** * * * * *
1" AAACC CCAGAAACAA

781' -GACACGGCG GCGGCGGCGG GAGANGGGGA TT-CCCTGCG -CCCCCGGAC CTCAGGGCCG
* **** * * * ** ****, ***** ** ***** ***** ** *****
16" CGGCGGGGCG GCGGCGGCGG GAGAGGGGGA TTCCCTGCG CCCCCGAAC CTCAGGGCCG

838' CTCAGATTCC TGGAGAGNGA AGCCAAGTGT CTTCTGCC TCCCCGGTA TCCCATCAA
***** ** ***** ***** ***** *****
76" CTCAGATTCC TGGAGAG-GA AGCCAAGTGT CTTCTGCC TCCCCGGTA TCCCATCAA

898' GCGGATCANG TCCAGAACTG GCTCTCGGAA GCGCTCGGC AAAGACTGCG AAGAAGAAAN
***** * ***** ***** ***** ***** *****
135" GCGGATCA-G TCCAGAACTG GCTCTCGGAA GCGCTCGGC AAAGACTGCG AAGAAGAAA-

958' AGACATCTGG CGGAAACCTG TGGCCTGGG GCGGTGGAAC TCGGGAGGA NGAGGGAGGG
***** ***** ***** ***** ***** *****
193" AGACATCTGG CGGAAACCTG TGGCCTGGG GCGGTGGAAC TCGGGAGGA -GAGGGAGGG

1018' ATCAGACAGG AGAGTGGGGA CTACCCCTC TGCTCCCAA TNTGGGCAG CTTCTGGGT
***** ***** ***** ***** * ***** *****
252" ATCAGACAGG AGAGTGGGGA CTACCCCTC TGCTCCCAA T-TGGGCAG CTTCTGGGT

1078' TTCCGATTTT CTCATTTCG TGGTAAAAA ACNCTGCC CCACCGGCT TACGCAATT
***** ***** ***** ** ***** ***** *****
311" TTCCGATTTT CTCATTTCG TGGTAAAAA AC-CCTGCC CCACCGGCT TACGCAATT

1138' TTTAAGGGG AGAGGAGGGA AAANATTTGT GGGGGTACG AAAAGCGGA AAGAAACAGT
***** ***** ** ***** ***** ***** *****
370" TTTAAGGGG AGAGGAGGGA AAA-ATTTGT GGGGGTACG AAAAGCGGA AAGAAACAGT

1198' CATTTCGTC CATGNGGCTT GGTTTTAGT CTTATAAAA GGAAGTTCT CTCGGTTAGC
***** **** ***** ***** ***** ***** *****



429" CATTTCGTCA CATG-GGCTT GGTTTTTCAGT CTTATAAAAA GGAAGGTTCT CTCGGTTAGC

1258' GACCANATTG TCATACGACT TGCAGTGAG- CGTCAGGAGC ACGTCCAGGA -ACTCCTCAG

***** **

488" GACCA-ATTG TCATACGACT TGCAGTGAGT CGTCAGGAGC ACGTCCAGGA CACTCCTCAG

1316' CAGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCA-ATC CGGTACTGTT GGTAAGCCA

***** **

547" CAGATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCACATC CGGTACTGTT GGTAAGCCA

1375' CCATGGAAGA TGCCAAAAC ATTAAGAAGG GCCCAGCGCC ATTCTACCCA CTCGAAGACG

***** * **

607" CCATGGAACA TGCCAAAC AT