



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

**BRCA2:** pGL4-phBRCA2(RDB# 7691)

**HIF1A:** pGL4-phHIF1A(RDB# 7693)

**ATF3:** pGL4-phATF3 (RDB# 7710)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.07

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5716

2nd Nucleotide Sequence

File Name : RDB7691F.fasta  
Sequence Size : 683

Unit Size to Compare = 1

Pick up Location = 1

[98.519% / 675 bp] INT/OPT. Score : < 2360/ 2553 >

```
1'          GGC CTAAGTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC
          *** *****
1" GTGCCAGAAC TTTCTCTGGC CTAAGTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC

44' CAAAGCAGAA TGCCTAACTC ATAAAATGTT TGGTAAGTGG CAGCTGTTAT TAGTAAGGAT
          *****
61" CAAAGCAGAA TGCCTAACTC ATAAAATGTT TGGTAAGTGG CAGCTGTTAT TAGTAAGGAT

104' CACAGACGTA TTTCTTTGCG AATTAGACTT AGAGCAAAG CTTTAGAATC TATCTGCATT
          *****
121" CACAGACGTA TTTCTTTGCG AATTAGACTT AGAGCAAAG CTTTAGAATC TATCTGCATT

164' AGTAAGGCCT CTTTCTACAA CTAAGGATTA CTGATTATCA AACTAAAATG GTCCTAAGG
          *****
181" AGTAAGGCCT CTTTCTACAA CTAAGGATTA CTGATTATCA AACTAAAATG GTCCTAAGG

224' AACCAAGCGG AGCCACCCT TTTCTAATC CAAGGTTGCT TCTGTTTACT GCTCAAGCAC
          *****
241" AACCAAGCGG AGCCACCCT TTTCTAATC CAAGGTTGCT TCTGTTTACT GCTCAAGCAC

284' CTTCTGGAAG CAGCAAGGCC CCCATGGGAG CAACTCTCAC TGAATCCATT TGAAGGTTTT
          *****
301" CTTCTGGAAG CAGCAAGGCC CCCATGGGAG CAACTCTCAC TGAATCCATT TGAAGGTTTT
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344' GTAGGTCTTA CAACAAACCC TATTCAGCCT TGTATTAGGC ATGTTACAGA ACCAACGAAT
*****
361" GTAGGTCTTA CAACAAACCC TATTCAGCCT TGTATTAGGC ATGTTACAGA ACCAACGAAT

404' TCGGAGATGA AGTCAGGTCT TCCAGTTCAG CCTGCGAGGA AGACAGGTGA TCCGAATCCT
*****
421" TCGGAGATGA AGTCAGGTCT TCCAGTTCAG CCTGCGAGGA AGACAGGTGA TCCGAATCCT

464' AAGAATGCAA AAGATGGGCC GGGTGTGGTG GCTCATGCCT GTAATCCCAG CGCTTTGGGA
*****
481" AAGAATGCAA AAGATGGGCC GGGTGTGGTG GCTCATGCCT GTAATCCCAG CGCTTTGGGA

524' GGCCGAGGCA GGCAGATCAC CTGAGGTCCG GAGGTTGAGA CCAGACTGAC CAACAACGGA
*****
541" GGCCGAGGCA GGCAGATCAC CTGAGGTCCG GAGGTTGAGA CCAGACTGAC CAACAACGGA

584' GAAACCCCGT CTCTACTTAA AAATGCAAAG TTAGCCGTGC GTGGTGGCCC ATGCCTGTAT
**** ***** * ***** * ***** ***** ** *** *****
601" GAAA-CCCGT CTCTACTT-A AAATGCAAAG -TNGCCGTGC GTGGTGG-CC ATG-CTGTA-

644' TCCCAGCTAC TCGGGAGGCT GAGGCAGGAG AACCACTGA TCCCTGGAGG CGGAAGTTGC
***** ** ***** ** *** ** **
655" TCCCAGCTAC TC-GGAGGCT GA-GCA-GAG AA

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1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5716

2nd Nucleotide Sequence

File Name : RDB7691R. fasta (Complementary)  
Sequence Size : 681

Unit Size to Compare = 1  
Pick up Location = 1



[99.707% / 682 bp] INT/OPT. Score : < 2707/ 2709 >

901' AGAACAGCTA CTGGAAGTAA AATCCTCTGA TTTCAAATAA CAGCCCCGCC CACTACCACT  
\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
1" CTAA AATCCTCTGA TTTCANATAA CAGCCCCGCC CACTACCACT

961' AAGTGAAGTC ATCCACAACC ACACACCGAC CACTCTAAGC TTTTGTAA GA TCGGCTCGCT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
45" AAGTGAAGTC ATCCACAACC ACACACCGAC CACTCTAAGC TTTTGTAA GA TCGGCTCGCT

1021' TTGGGGAACA GGTCTTGAGA GAACATCCCT TTTAAGGTCA GAACAAAGGT ATTCATAGG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
105" TTGGGGAACA GGTCTTGAGA GAACATCCCT TTTAAGGTCA GAACAAAGGT ATTCATAGG

1081' TCCAGGTCG TGTCCCGAGG GCGCCACCC AAACATGAGC TGGAGCAAAA AGAAAGGGAT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
165" TCCAGGTCG TGTCCCGAGG GCGCCACCC AAACATGAGC TGGAGCAAAA AGAAAGGGAT

1141' GGGGACTTG GAGTAGGCAT AGGGGCGGCC CCTCCAAGCA GGGTGGCCTG GGA CTCTTAA  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
225" GGGGACTTG GAGTAGGCAT AGGGGCGGCC CCTCCAAGCA GGGTGGCCTG GGA CTCTTAA

1201' GGGTCAGCGA GAAGAGAACA CACTCTCCAG CTCCCGCTTT ATTCGGTCAG ATACTGACGG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
285" GGGTCAGCGA GAAGAGAACA CACTCTCCAG CTCCCGCTTT ATTCGGTCAG ATACTGACGG

1261' TTGGGATGCC TGACAAGGAA TTTCTTTTCG CCACACTGAG AAATACCCGC AGCGGCCAC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
345" TTGGGATGCC TGACAAGGAA TTTCTTTTCG CCACACTGAG AAATACCCGC AGCGGCCAC

1321' CCAGGCCTGA CTTCCGGGTG GTGCGTGTGC TGC GTGTCGC GTCACGGCGT CACGTGGCCA  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
405" CCAGGCCTGA CTTCCGGGTG GTGCGTGTGC TGC GTGTCGC GTCACGGCGT CACGTGGCCA

1381' GCGCGGGCTT GTGGCGGAG CTTCTGAAAC TAGGCGGCAG AGGCGGAGCC GCTGTGGCAC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*



465" GCGCGGGCTT GTGGCGCGAG CTTCTGAAAC TAGGCGGCAG AGGCGGAGCC GCTGTGGCAC

1441' TGCTGCGCCT CTGCTGCGCC TCGGGTGTCT TTTGCGGCGG TGGGTCGCCG CCGGGAGAAG

\*\*\*\*\*

525" TGCTGCGCCT CTGCTGCGCC TCGGGTGTCT TTTGCGGCGG TGGGTCGCCG CCGGGAGAAG

1501' CGTGAGGGGA CAGATATCAA GATCTGGCCT CGGCGGCCAA GCTTGGAAT CCGGTACTGT

\*\*\*\*\*

585" CGTGAGGGGA CAGATATCAA GATCTGGCCT CGGCGGCCAA GCTTGGAAT CCGGTACTGT

1561' TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATTAAAGAAG GGCCAGCGC CATTCTACCC

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

645" TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CA-TAAGA