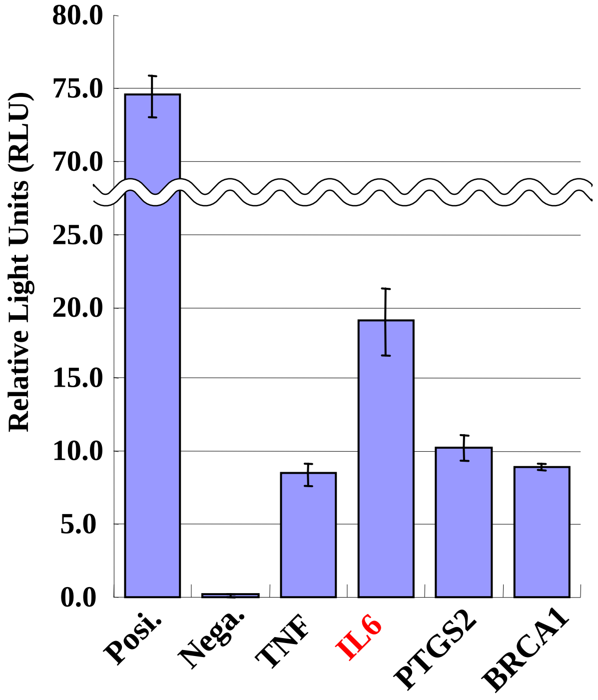
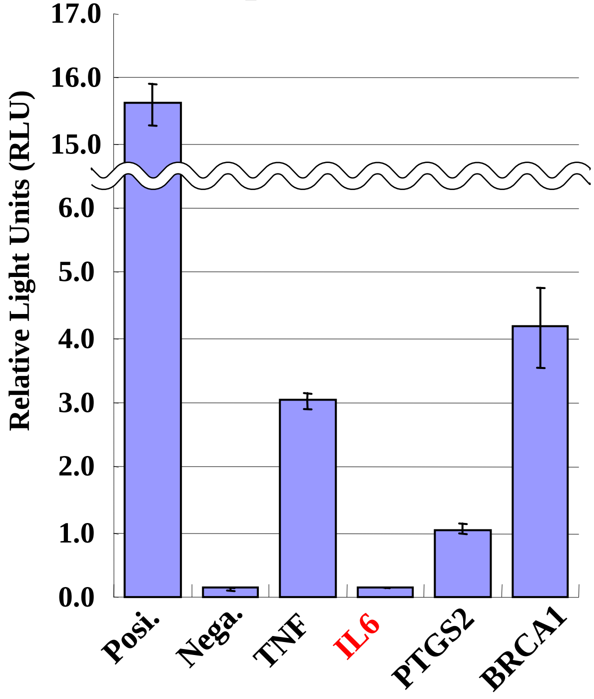
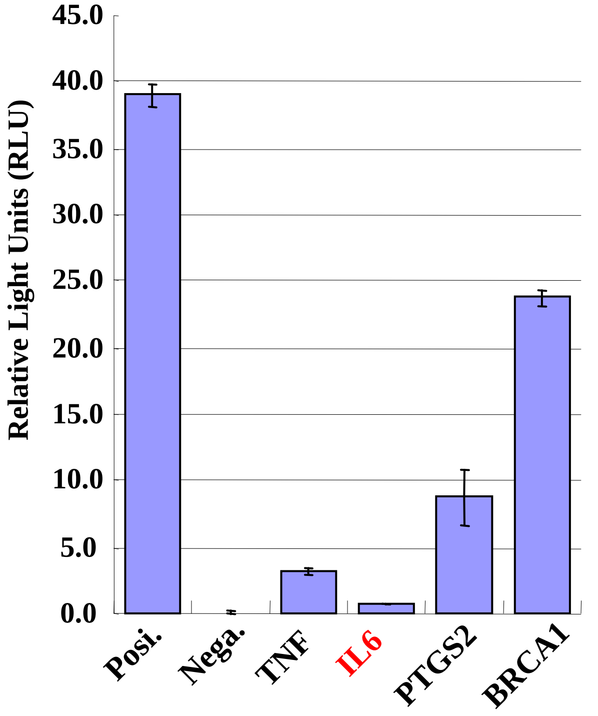
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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)

2009, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.25

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5563

2nd Nucleotide Sequence
  File Name         : RDB7313F.fasta
  Sequence Size     : 667

  Unit Size to Compare = 1
  Pick up Location     = 1



[90.657% / 578 bp]     INT/OPT.Score : <    591/  1729 >

      1’ GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TGAGCTGTCT GGGTCTCTGG
                                                                       ***
      1″     GCTCGC CGCCTAGATC TACACGATTN GGCCGACAAC ATCGCACAGA TAACAGTTGG

     61’ AGACTGGAGG GNACAACCTA GTCTAGAGCC CATTTGCATG AGACCAAGGA TCCTCCTGCA
            *****   *.*   *  *   ***      * *******   ** ****** * ********
     57″ GTTCTGGACA GGAGTTCACA --CTATCTAA CCTTTGCAT- -GAACAAGGA T-CTCCTGCA

    121’ AGNAGACACC ATCCTGAGGG AAGAGGGCTT CTGAACCAGC TTGACCCAAT AAGNAAATTC
         *   ** *** ** **** ** **** *** * *** ****** **** ***** *** ******
    112″ A---GAGACC AT-CTGA-GG AAGA-GGC-T CTG-ACCAGC TTGA-CCAAT AAG-AAATTC

    181’ TTGGGTGCCG ACGCGGAAGC AGATTCAGAG CCTAG-AGCC GTGCCNTGCG TCCGTAGTTT
         ********** ********** ********** ***** **** ***** **** **********
    162″ TTGGGTGCCG ACGCGGAAGC AGATTCAGAG CCTAGCAGCC GTGCC-TGCG TCCGTAGTTT

    240’ CCTTCTAGCT TCTTTTGATT TCAAATCAAG ACTTACNAGG GAGAGGGAGC -GATAAAC-A
         ********** ********** ********** ****** *** **********  ******* *
    221″ CCTTCTAGCT TCTTTTGATT TCAAATCAAG ACTTAC-AGG GAGAGGGAGC AGATAAACAA
```

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298’ CAAACTCTGC -AAGATGCCA CAAGGTCCTC NCTTTGACAT CCCCAACAAA GAGGTGAGTA
     **********  ********* **********  ********* ********** **********
280″ CAAACTCTGC AAAGATGCCA CAAGGTCCTC -CTTTGACAT CCCCAACAAA GAGGTGAGTA

357’ GTATTCTCCC CCTTTCTGCC CNTGAACCAA GTGGGCTTCA GTAATTTCAG GGCTCCAGGA
     ********** ********** * ******** ********** ********** **********
339″ GTATTCTCCC CCTTTCTGCC C-TGAACCAA GTGGGCTTCA GTAATTTCAG GGCTCCAGGA

417’ GACCTGGGGC CCNATGCAGG TGCCCCAGTG AAACAGTGGT GAAGAGACTC AGTGGCAATG
     ********** ** ******* ********** ********** ********** **********
398″ GACCTGGGGC CC-ATGCAGG TGCCCCAGTG AAACAGTGGT GAAGAGACTC AGTGGCAATG

477’ GGGNAGAGCA CTGGCAGCAC AAGGCAAACC TCTGGCACAG AGAGCAAAGT CCTCNACTGG
     *** ****** ********** ********** ********** ********** **** *****
457″ GGG-AGAGCA CTGGCAGCAC AAGGCAAACC TCTGGCACAG AGAGCAAAGT CCTC-ACTGG

537’ GAGGATTCCC AAGGGGTCAC TTGGGAGAGG GCAGGGCAGC AGCCANACCT CCTCTAAGTG
     ********** ********** ********** ********** *****. *** **********
515″ GAGGATTCCC AAGGGGTCAC TTGGGAGAGG GCAGGGCAGC AGCCAC-CCT CCTCTAAGTG

597’ GGCTGAAGCA GGTGAAGAAA GTGGCAGAAG CCACGCNGGT GGCAAAAAGG AGTCACACAC
     ******* ** ******* ** ** *****   .* **
574″ GGCTGAA-CA GGTGAAG-AA GT-GCAGAGC NCGCGTGCAA AAGATCCCCT CCCCTGAACT

657’ TCCACCTGGA GACGCCTTGA AGTAACTNGC ACGAAATTTG AGGATGGCCA GGCAGTTCTA

631″ GAAGTACTGC CGATGAGTGC AGAGTCTACG CCTCAGA
```

1st Nucleotide Sequence

File Name : Reference Seq.gnu

Sequence Size : 5563

2nd Nucleotide Sequence

File Name : RDB7313R.fasta (Complementary)

Sequence Size : 622

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Unit Size to Compare = 1
Pick up Location     = 1



[87.745% / 612 bp]     INT/OPT.Score : <    583/  1866 >

  781' CTTCANTAAT CCCAGGCTTG GGGGGCTGCG ATGGAGTCAG AGGAAACTCA GTTCAGNAAC

    1"                                                                A

  841' ATCTTT-GGT TTTTAC-AAA TACAAA-TTA ACT-GGAACG C-TAAATTCT AGNCCTG-TT
       ****** *** ****** *** ****** *** *** ****** * ******** **.**** **
    2" ATCTTTGGGT TTTTACAAAA TACAAATTTA ACTGGGAACG CTTAAATTCT AGCCCTGTTT

  895' AATCTGG-TC ACT-GAAAAA AAA-TTTTTT TTTTTTCAAA AAACATANGC TTTAGCTTAT
       ******* ** *** ****** *** ****** ********** ******* ** **********
   62" AATCTGGTTC ACTGGAAAAA AAATTTTTTT TTTTTTCAAA AAACATA-GC TTTAGCTTAT

  952' TTTTTTTCTC TTTGTAAAAC TTCGTGCATG ACTTCAGCNT TTACTCTTTG TCAAGACATG
       ********** ********** ********** ****    .* ********** **********
  121" TTTTTTTCTC TTTGTAAAAC TTCGTGCATG ACTTTCAGCT TTACTCTTTG TCAAGACATG

 1012' CCAAAGTGCT GAGTCACTAA TAAAAGAAAN AAAAGAAAGT AAAGGAAGAG TGGTTCTGCT
       ********** ********** *********  ********** ********** **********
  181" CCAAAGTGCT GAGTCACTAA TAAAAGAAA- AAAAGAAAGT AAAGGAAGAG TGGTTCTGCT

 1072' TCTTAGCGCT AGCCTCAATG NACGACCTAA GCTGCACTTT TCCCCCTAGT TGTGTCTTGC
       ********** ********** .  ******* ********** ********** **********
  240" TCTTAGCGCT AGCCTCAATG ACAGACCTAA GCTGCACTTT TCCCCCTAGT TGTGTCTTGC

 1132' CATGCTAAAG GNACGTCACA TTGCACAATC TTAATAAGGT TTCCAATCAG CCCCACCCGC
       ********** * ******** ********** ********** ********** **********
  300" CATGCTAAAG G-ACGTCACA TTGCACAATC TTAATAAGGT TTCCAATCAG CCCCACCCGC

 1192' TCNTGGCCCC ACCCTCACCC TCCAACAAAG ATTTATCAAA TGTGGGATTT TCCCATGAGT
       ** ******* ********** ********** ********** ********** **********
  359" TC-TGGCCCC ACCCTCACCC TCCAACAAAG ATTTATCAAA TGTGGGATTT TCCCATGAGT
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1252’ CTCAATATTA GAGTCTCAAC CCCCAATAAA TATAGGACTG GAGATGTCTG AGGCTCATTC
      ********** ********** ********** ********** ********** **********
 418″ CTCAATATTA GAGTCTCAAC CCCCAATAAA TATAGGACTG GAGATGTCTG AGGCTCATTC

1312’ TGCCCTCGAG CCCACCGGGA ACGAAAGAGA -AG-CTCTAT CTCCCCTCCA GGAATCAAGA
      ********** ********** * ********  ** ****   **** *  *  ****  * **
 478″ TGCCCTCGAG CCCACCGGGA AAGAAAGAGA NAGACTCTTA CTCCACATCC GGAAATACGA

1370’ TCTGGCCTCG GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT
         ** ** *    * *  .  ****  **     *. *   * **    ***    *  **.
 538″ ATAGGTCTGG AGCGACCGNA TTGGACATGA CCTNGTTGAG GTGGTCCCAA AAGAGANTCC

1430’ GCCAAAAACA TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC
      *  ** *  * **
 598″ GATAACAGGA TTGCGCTGAA NACNA
```