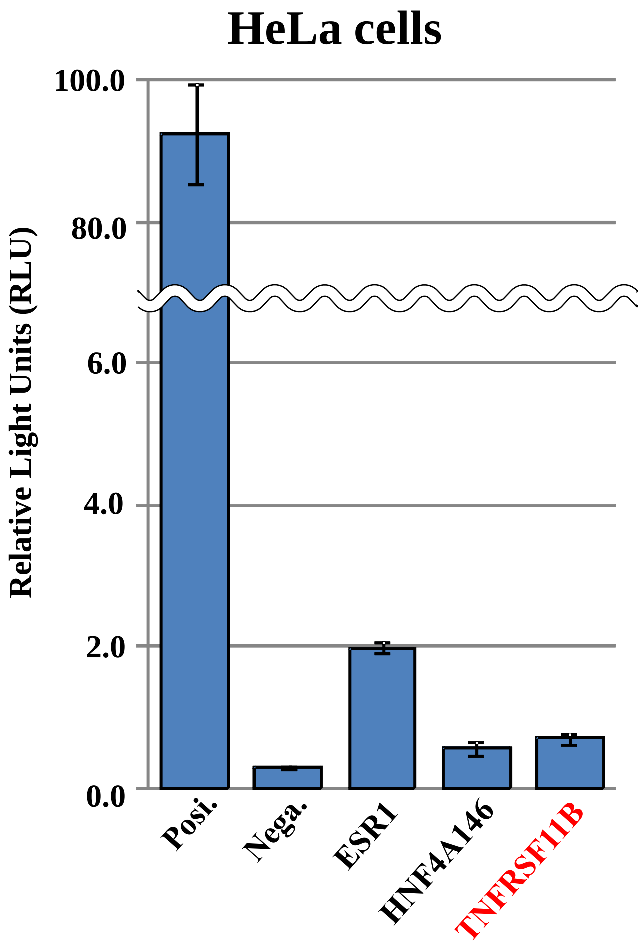
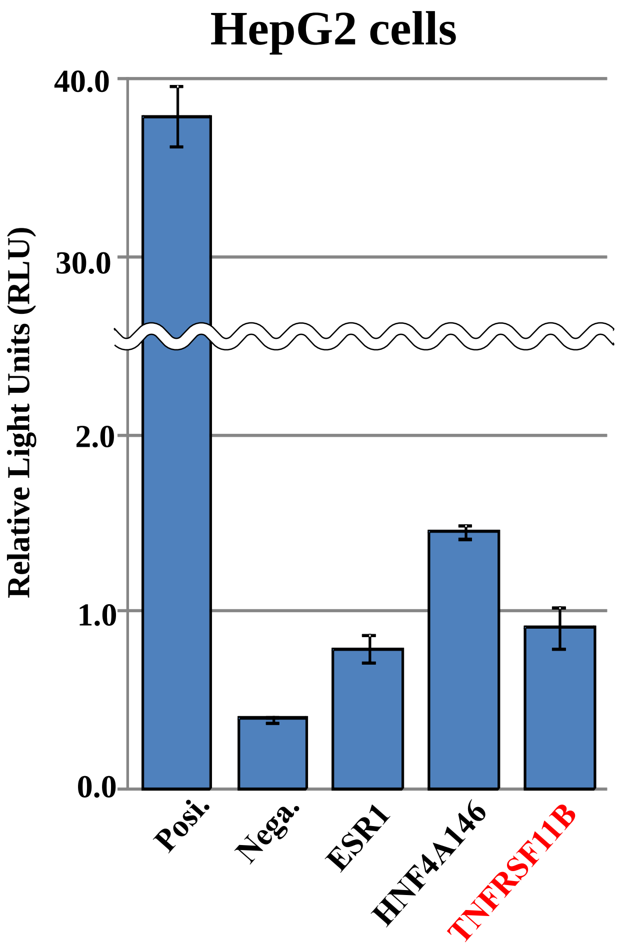
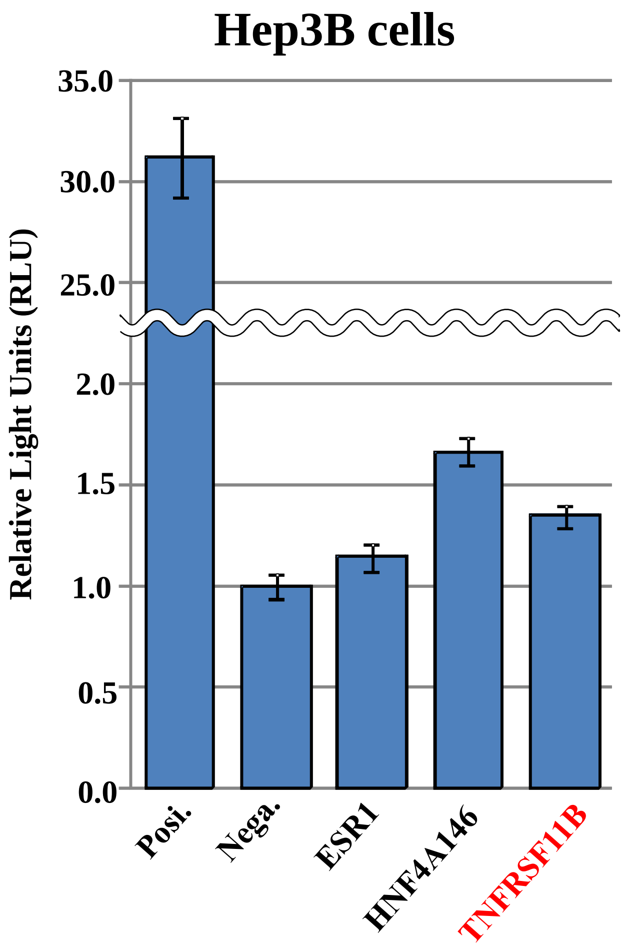
The Promoter Activities of Reporter Constructs







Posi.: pGL3 Control Vector
(SV40 promoter)
Nega.: Empty Vector

ESR1: pGL4-phESR1(RDB# 7528)
HNF4A146: pGL4-phHNF4A 146(RDB# 7534)
TNFRSF11B: pGL4-phTNFRSF11B(RDB# 7533)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]
Date : 2009.11.06
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5746
2nd Nucleotide Sequence
  File Name        : RDB7533F.fasta
  Sequence Size    : 776
  Unit Size to Compare = 1
  Pick up Location     = 1
[95.361% / 776 bp]     INT/OPT.Score : <    545/  2654 >

    1’                     G GCCTAACTGG CCGGTACCTG AG-CTCG-CT AGCCTCGAGG
                           * ********** ********** ** **** ** ** *   ***
    1″ CGGTGCCGAA CTTTACTCTG GCCTAACTGG CCGGTACCTG AGACTCGACT AGACCTCAGG

   40’ ATAGATGAGG CTCAGGGAGA CGTAAACCTT TCCCAGGGTT AAC-ACTGAA GNGACTCAGT
       ********** ********** ********** ********** *** ****** * ********
   61″ ATAGATGAGG CTCAGGGAGA CGTAAACCTT TCCCAGGGTT AACAACTGAA G-GACTCAGT

   99’ TATTGATTAG TTTTCTCCAA GGTCTGACAC CCACATATTG GCNATCATTT TATGTT-CTG
       ********** ********** ********** ********** ** ******* ****** ***
  120″ TATTGATTAG TTTTCTCCAA GGTCTGACAC CCACATATTG GC-ATCATTT TATGTTACTG

  158’ AGAAAAACAC CTTCAAATAA TATCCTAGAC AAACNATTAC TCTAACAAAA ACAATAATAC
       ********** ********** ********** **** ***** ********** **********
  179″ AGAAAAACAC CTTCAAATAA TATCCTAGAC AAAC-ATTAC TCTAACAAAA ACAATAATAC

  218’ TGCTATTTAT ATTGTGTTTC ACTACNTAAC ACTTGGATTG ACTTGAGTCC CATGGCAAGT
       ********** ********** ***** **** ********** ********** **********
  238″ TGCTATTTAT ATTGTGTTTC ACTAC-TAAC ACTTGGATTG ACTTGAGTCC CATGGCAAGT

  278’ CTAAGTGTTG ATATCTNCAG GTTGCAGATG TCAAAACTAC GATTCAAAAT ACAAGGAGTG
       ********** ****** *** ********** ********** ********** ******* **
  297″ CTAAGTGTTG ATATCT-CAG GTTGCAGATG TCAAAACTAC GATTCAAAAT ACAAGGAATG

  338’ ATTTGGANGT CATACAATTT TGTCCACACT CACTGAGCTA CATTTATTCA CTAGTTCANC
       ******* ** ********** ********** ********** ********** ******** *
  356″ ATTTGGA-GT CATACAATTT TGTCCACACT CACTGAGCTA CATTTATTCA CTAGTTCA-C
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398' TTAAGAAACC AGCATGCTGT TACATTCTGG CCCTTGAGGG ACAAAGCTGN AATGACACCC
     ********** ********** ********** ********** *********  **********
414″ TTAAGAAACC AGCATGCTGT TACATTCTGG CCCTTGAGGG ACAAAGCTG- AATGACACCC

458' CGTCTTCTGT AATTTGCAGG ATGGAACAGT CTGTGGATCC NACTTTGAAC TCGTGGTGGA
     ********** ********** ********** **********  ********* **********
473″ CGTCTTCTGT AATTTGCAGG ATGGAACAGT CTGTGGATCC -ACTTTGAAC TCGTGGTGGA

518' AGGATGTCCC TTGGAAGGGG CAGATGCTCT GNATCCTGGT AAGCCATCCT TGCTCCCCAG
     ********** ********** ********** * ******** ********** **********
532″ AGGATGTCCC TTGGAAGGGG CAGATGCTCT G-ATCCTGGT AAGCCATCCT TGCTCCCCAG

578' GGGTCCCCTC TCCTGATTCT TCNACCTTCC TTCCCTTGAA TCTGGTGAAA GGCAGTATTT
     ********** ********** ** ******* ** ******* ********** **********
591″ GGGTCCCCTC TCCTGATTCT TC-ACCTTCC TT-CCTTGAA TCTGGTGAAA GGCAGTATTT

638' GCCCTTCTCT GGANGACATA TAACTTGAAC ACTTGGCCCT GATGGGGAAG CAG-CTCTGC
     ********** *** ****** * ** ***** ** ******* ********** *** ******
649″ GCCCTTCTCT GGA-GACATA TTACCTGAAC ACCTGGCCCT GATGGGGAAG CAGCCTCTGC

697' AGGGANCTTT TTCAGCCATC TGTAAACAAT TTCAGTGGCA ACCCGCGAAC TGTAATNCCA
     ***** **** ** .****** *** ****** *********  ******** * *** **. **
708″ AGGGA-CTTT TT-NGCCATC TGTTAACAAT TTCAGTGGC- ACCCGCGACC TGT-ATT-CA

757' TGAATGGGAC CACACTTTAC AAGTCATCAA GTCTAACTTC TAGACCANGG GAATTAATGG
     *********  *****
763″ TGAATGGGA- CACAC
```

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1st Nucleotide Sequence
  File Name       : Reference Seq.gnu
  Sequence Size   : 5746
2nd Nucleotide Sequence
  File Name       : RDB7533R.fasta (Complementary)
  Sequence Size   : 763
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```
  Unit Size to Compare = 1
  Pick up Location     = 1
[93.038% / 790 bp]     INT/OPT.Score : <    406/  2573 >

  781' CATCAAGTCT AACTTCTAGA CCANGGGAAT TAATGGGGGA GACAGCGAAC CCTAGAGCAA
                              *. *. .   ***  ****  ***  * *  ***** ** *
    1"                       AAAAAGNCNG GAATATGGGA AACA--GGA- CCTAG-GC-A

  841' AGTGCCAAAC TTCTNGTCGA TAGCTTGAGG CTAGTGGAAA GACCTCGAGG AGGCTACTCC
       **     *** **** ****  **** ** .* * *** **** ***.**   * **** *****
   36" AG---GCAAC TTCT-GTCG- TAGC-TG-NG C-AGT-GAAA GACNTC--AG AGGC-ACTCC

  901' AGAAGNTTCA GCGCGTAGGA AGCTCCGATA CCAATAGCCC TTTGATGATG GTGGGGNTTG
       ***** **** **********  ********. ** ******* ********** ****** ***
   84" AGAAG-TTCA GCGCGTAGGA TGCTCCGATN CC-ATAGCCC TTTGATGATG GTGGGG-TTG

  961' GTGAAGGGAA CAGTGCTCCG CAAGGTTATC CCTGCCCCAG GCAGTCCNAA TTTTCACTCT
       **** ***** ********** ** ******* ********** ******* ** **********
  141" GTGAGGGGAA CAGTGCTCCG CAGGGTTATC CCTGCCCCAG GCAGTCC-AA TTTTCACTCT

 1021' GCAGATTCTC TCTGGCTCTA ACTACCCCAG ATAACAAGNG AGTGAATGCA GAATAGCACG
       ********** ********** ********** ******** * ********** **********
  200" GCAGATTCTC TCTGGCTCTA ACTACCCCAG ATAACAAG-G AGTGAATGCA GAATAGCACG

 1081' GGCTTTAGGG CCAATCAGAC ATTAGTTAGN AAAAATTCCT ACTACATGGT TTATGTAAAC
        ********* ********** *********  ********** ********** **********
  259" TGCTTTAGGG CCAATCAGAC ATTAGTTAG- AAAAATTCCT ACTACATGGT TTATGTAAAC

 1141' TTGAAGATGA ATGATTGCGA NACTCCCCGA AAAGGGCTCA GACAATGCCA TGCATAAAGA
       ********** **********  ********* ********** ********** **********
  318" TTGAAGATGA ATGATTGCGA -ACTCCCCGA AAAGGGCTCA GACAATGCCA TGCATAAAGA

 1201' GGGGCCCTGT ANATTTGAGG TTTCAGAACC CGAAGTGAAG GGGTCAGGCA GCCGGGTACG
       ********** * ******** ********** ********** ** ******* **********
  377" GGGGCCCTGT A-ATTTGAGG TTTCAGAACC CGAAGTGAAG GGTTCAGGCA GCCGGGTACG

 1261' GC-NGGAAAC TCACAGCTTT CGCCCAGCGA GAGGACAAAG GTCTGGGACA CACTNCCAAC
       ** .* **** ********** ********** ********** ********** **** *****
  436" GCGTGTAAAC TCACAGCTTT CGCCCAGCGA GAGGACAAAG GTCTGGGACA CACT-CCAAC
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1320' TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACNACAA GCACAGCAGC
      ********** ********** ********** ********** ***** **** **********
 495″ TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGAC-ACAA GCACAGCAGC

1380' TGCCCAGCGT GTGCCCAGCC CTCCCACCGC TGGTCCNCGG CTGCCAGGAG GCTGGCCGCT
      ********** ********** ********** ****** *** ********** **********
 554″ TGCCCAGCGT GTGCCCAGCC CTCCCACCGC TGGTCC-CGG CTGCCAGGAG GCTGGCCGCT

1440' GGCGGGAAGG GGCCGGGAAA CCTCAGANGC CCCGCGGAGA CAGCAGCCGC CTTGTTCCTC
      ********** ********** ******* ** ********** ********** **********
 613″ GGCGGGAAGG GGCCGGGAAA CCTCAGA-GC CCCGCGGAGA CAGCAGCCGC CTTGTTCCTC

1500' AGCCCGGTGG CTTTTTTTNT CCCCTGCTCT CCCAGGGGCC AGACACATCA AGATCTGGCC
      ********** ******** * ********** ********** ********** **********
 672″ AGCCCGGTGG CTTTTTTT-T CCCCTGCTCT CCCAGGGGCC AGACACATCA AGATCTGGCC

1560' TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGAA GATGCCAAAA
      ********** ********** ********** **
 731″ TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTT
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