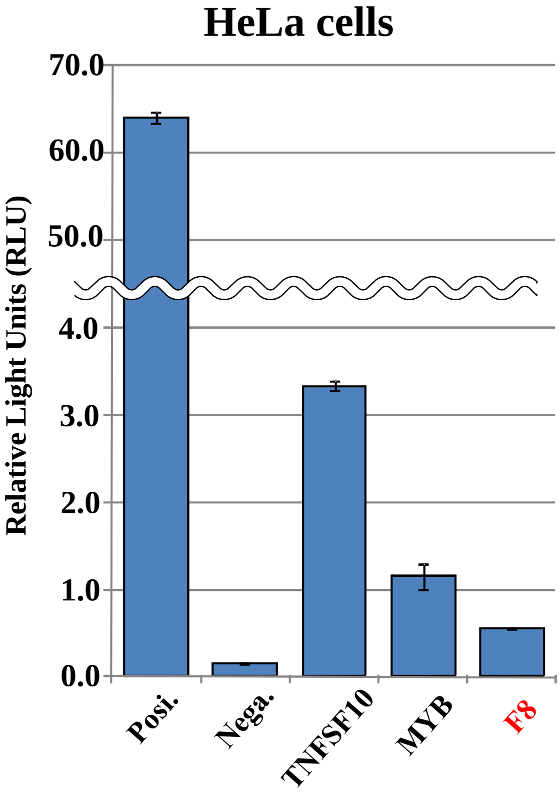
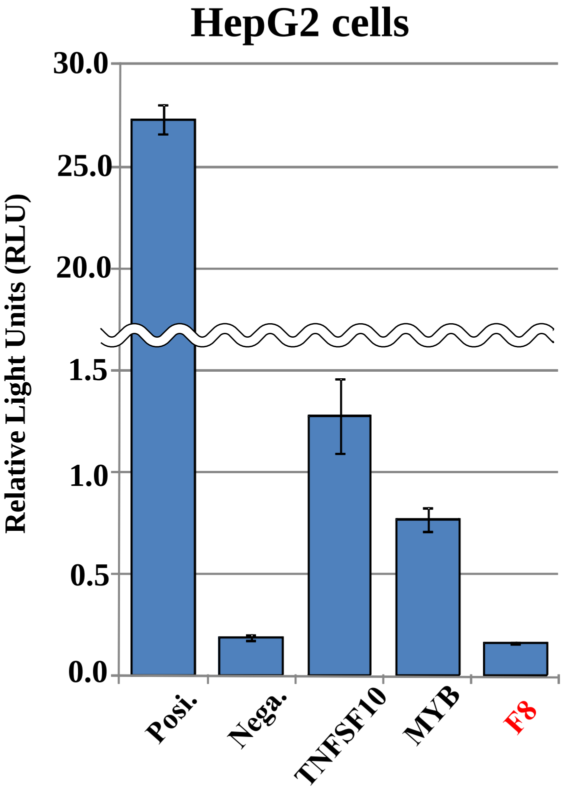
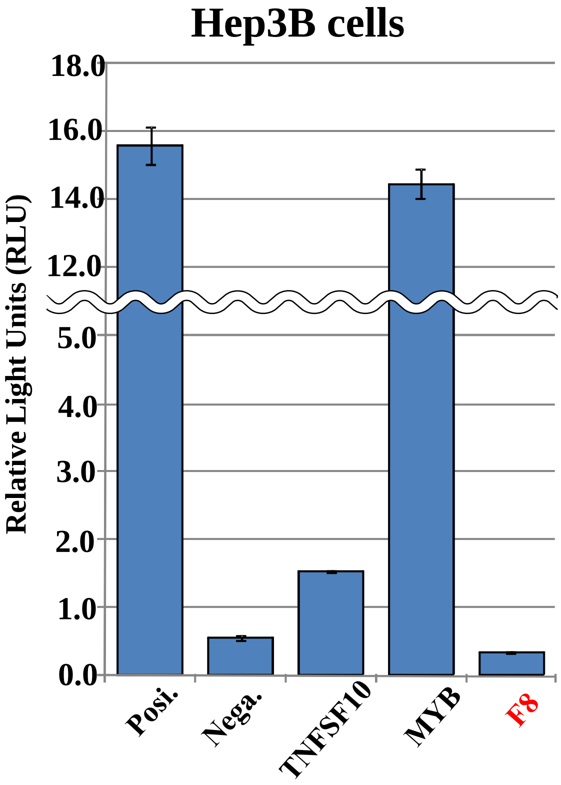
The Promoter Activities of Reporter Constructs







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

TNFSF10: pGL4-phTNFSF10 (RDB# 7526)
MYB: pGL4-phMYB (RDB# 7480)
F8: pGL4-phF8 (RDB# 7519)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.09.25

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5645

2nd Nucleotide Sequence
  File Name        : RDB7519F.fasta
  Sequence Size    : 729

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.507% / 722 bp]     INT/OPT.Score : <    394/  2649 >

     1’                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                            * ********** ********** ********** **********
     1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

    42’ TCCGTGCTTC AGTTTCATCA CCCATAAAAT GAAGGTAAGA ATAGTACCNT GTATTTAAAA
        ********** ********** ********** ********** ******** * **********
    61″ TCCGTGCTTC AGTTTCATCA CCCATAAAAT GAAGGTAAGA ATAGTACC-T GTATTTAAAA

   102’ GCACCTAGAA CAGTTCCTGG CATATAGTGT CAGCTGTCAN TCTCTGCATC CTTGTACCTG
        ********** ********** ********** *********  ********** **********
   120″ GCACCTAGAA CAGTTCCTGG CATATAGTGT CAGCTGTCA- TCTCTGCATC CTTGTACCTG

   162’ TCAGAGAGGA GTGTTTATCA AAGGGGCTTC NTTGCTGCCT GTTTCCAAAC CAGTCGACAA
        ********** ********** **********  ********* ********** **********
   179″ TCAGAGAGGA GTGTTTATCA AAGGGGCTTC -TTGCTGCCT GTTTCCAAAC CAGTCGACAA

   222’ TATACCAATT GCTCCCTAAC ANCATTCTTG TTTGTGCAGA ACTGAGCTCA ATGATAACAT
        ********** ********** * ******** ********** ********** **********
   238″ TATACCAATT GCTCCCTAAC A-CATTCTTG TTTGTGCAGA ACTGAGCTCA ATGATAACAT
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282’ TTTTATAGCA ACNCCTGATC AAGTTTCTTC TCATAATCTC TTACACTTTG AGGCCCCTGC
     ********** ** ******* ********** ********** ********** **********
297″ TTTTATAGCA AC-CCTGATC AAGTTTCTTC TCATAATCTC TTACACTTTG AGGCCCCTGC

342’ AGGNGGCCCT CACTCTCCCT AATAAACATT AACCTGAGTA GGGTGTTTGA GCTCNACCAT
     *** ****** ********** ********** ********** ********** **** *****
356″ AGG-GGCCCT CACTCTCCCT AATAAACATT AACCTGAGTA GGGTGTTTGA GCTC-ACCAT

402’ GGCTACATTC TGATGTAAAG AGATATATCC TATACCTGGG CCAAANTGTA AACAGCCTGG
     ********** ********** ********** ********** ***** **** **********
414″ GGCTACATTC TGATGTAAAG AGATATATCC TATACCTGGG CCAAA-TGTA AACAGCCTGG

462’ CAAAAGTGTT AGGTTAAAAA CAAAACAAAA TAAATANAAT GAATAAATGC CAGGTGGTTA
      ********* ********** ********** ****** *** ********** **********
473″ -AAAAGTGTT AGGTTAAAAA CAAAACAAAA TAAATA-AAT GAATAAATGC CAGGTGGTTA

522’ TGAGTGCTAT TGAGAAAAAT GAAGCCANAG AGGGATATCA GTGATGCAGG TGGGGGTAAA
     ********** ********** ******* ** ********** ********** ******** *
531″ TGAGTGCTAT TGAGAAAAAT GAAGCCA-AG AGGGATATCA GTGATGCAGG TGGGGGTAGA

582’ GAGCTTACAA CATAAATGNT GGTGTTCCAT ATTTAAACCT CATTCAACAG GGAAGATTGG
     ********** ******** * ********** ********** ********** **********
590″ GAGCTTACAA CATAAATG-T GGTGTTCCAT ATTTAAACCT CATTCAACAG GGAAGATTGG

642’ AGCTGAAATN GTGAAGGAGT TGTGGGAG-T GGAACTACGT GGAAATCTGG GGGAAAGGTG
     *********  ********** ******** * ********** ********** **********
649″ AGCTGAAAT- GTGAAGGAGT TGTGGGAGTT GGAACTACGT GGAAATCTGG GGGAAAGGTG

701’ TNTTTGGGTA AAAGAAATAG CAAGTGTTGA GGTCCAGGGG CATGAGTGTG CTNTGATATT
     *.******** ***.*****. *
708″ TTTTTGGGTA AAANAAATAN CC
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1st Nucleotide Sequence

File Name : Reference Seq.GNU

Sequence Size : 5645

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2nd Nucleotide Sequence
  File Name        : RDB7519R.fasta (Complementary)
  Sequence Size    : 764

  Unit Size to Compare = 1
  Pick up Location     = 1


[96.684% / 784 bp]     INT/OPT.Score : <    436/  2789 >

   721' CAAGTGTTGA GGTCCAGGGG CATGAGTGTG CTNTGATATT TTAGGGAAGA GTAAGGAGAC
                            * ******* ** ***** * ***.****** ** *******
     1"                      AGGAGTGTG CT-TGATA-T TTANGGAAGA GT-AGGAGAC

   781' CAGTATAACC AGAGTGAGAT GAGNACTACA GAGGTCAGGA GAAAGGGCAT GCAGACCATG
        ******* ** **********  ** ****** * .*** .** **** ***** **********
    37" CAGTATACCC AGAGTGAGAT -AG-ACTACA G-NGTC-NGA GAAA-GGCAT GCAGACCATG

   841' TGGGATGCTC TAGGNACCTA GGCCATGGTA AAGATGTAGG GTTTTACCCT GATGGAGGTC
        ********** **** ***** ********** ********** ********** **********
    92" TGGGATGCTC TAGG-ACCTA GGCCATGGTA AAGATGTAGG GTTTTACCCT GATGGAGGTC

   901' AGAAGNCCAT TGAAGGATTC TGAGAAGAGG AGTGACAGGA CTCGCTTTAT AGTTTTNAAA
        ***** **** ** ******* ********** ********** ********** ****** ***
   151" AGAAG-CCAT TGGAGGATTC TGAGAAGAGG AGTGACAGGA CTCGCTTTAT AGTTTT-AAA

   961' TTATAACTAT AAATTATAGT TTTTAAAACA ATAGTTGCCT AACCTCANTG TTATATGTAA
        ********** ********** ********** ********** ******* ** **********
   209" TTATAACTAT AAATTATAGT TTTTAAAACA ATAGTTGCCT AACCTCA-TG TTATATGTAA

  1021' AACTACAGTT TTAAAAACTA TAAATTCCTC ATACTGGCNA GCAGTGTGAG GGGCAAGGGC
        ********** ********** ********** ******** * ********** **********
   268" AACTACAGTT TTAAAAACTA TAAATTCCTC ATACTGGC-A GCAGTGTGAG GGGCAAGGGC

  1081' AAAAGCAGAG AGACTAACAG GTTGCTGGTN TACTCTTGCT AGTGCAAGTG AATTCTAGAA
        ********** ********** *********  ********** ********** **********
   327" AAAAGCAGAG AGACTAACAG GTTGCTGGT- TACTCTTGCT AGTGCAAGTG AATTCTAGAA
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1141’ TCTTCGACAA CATCCAGAAC NTTCTCTTGC TGCTGCCACT CAGGAAGAGG GTTGGAGTAG
      ********** **********  ********* ********** ********** **********
 386″ TCTTCGACAA CATCCAGAAC -TTCTCTTGC TGCTGCCACT CAGGAAGAGG GTTGGAGTAG

1201’ GCTAGGAATA GNGAGCACAA ATTAAAGCTC CTGTTCACTT TGACTTCTCC ATCCCTCTCC
      ********** * ******** ********** ********** ********** **********
 445″ GCTAGGAATA G-GAGCACAA ATTAAAGCTC CTGTTCACTT TGACTTCTCC ATCCCTCTCC

1261’ TCNCTTTCCT TAAAGGTTCT GATTAAAGCA GACTTATGCC CCTACTGCTC TCANGAAGTG
      ** ******* ********** ********** ********** ********** *** ******
 504″ TC-CTTTCCT TAAAGGTTCT GATTAAAGCA GACTTATGCC CCTACTGCTC TCA-GAAGTG

1321’ AATGGGTTAA GTTTAGCAGC CTCCCTTTTG CTACTTCAGT TCTTNCCTGT GGCTGCTTCC
      ********** ********** ********** ********** **** ***** **********
 562″ AATGGGTTAA GTTTAGCAGC CTCCCTTTTG CTACTTCAGT TCTT-CCTGT GGCTGCTTCC

1381’ CACTGATAAA AAGGAAGCAA TCCTATCGGT TACTGNCTTA GTGCTGAGCA CATCCAGTGG
      ********** ********** ********** ***** **** ********** **********
 621″ CACTGATAAA AAGGAAGCAA TCCTATCGGT TACTG-CTTA GTGCTGAGCA CATCCAGTGG

1441’ GTAAATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA
      ********** ********** ********** ********** ********** **********
 680″ GTAAATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA

1501’ CCATGGAAGA TGCCAAAAAC ATTAAGAAGG GCCCAGCGCC ATTCTACCCA CTCGAAGACG
      ********** ********** *****
 740″ CCATGGAAGA TGCCAAAAAC ATTAA
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