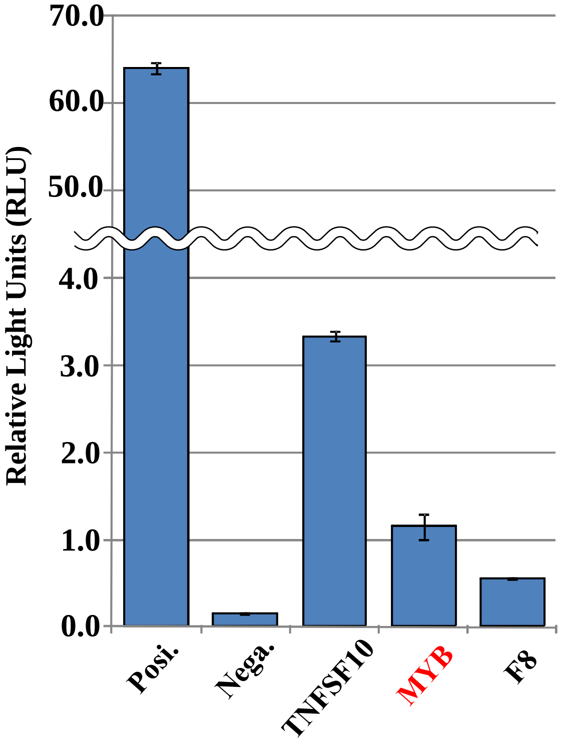
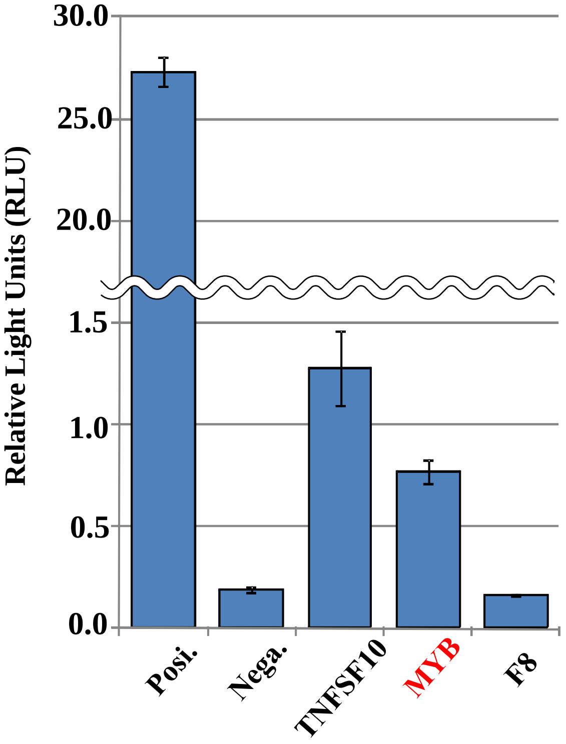
# The Promoter Activities of Reporter Constructs

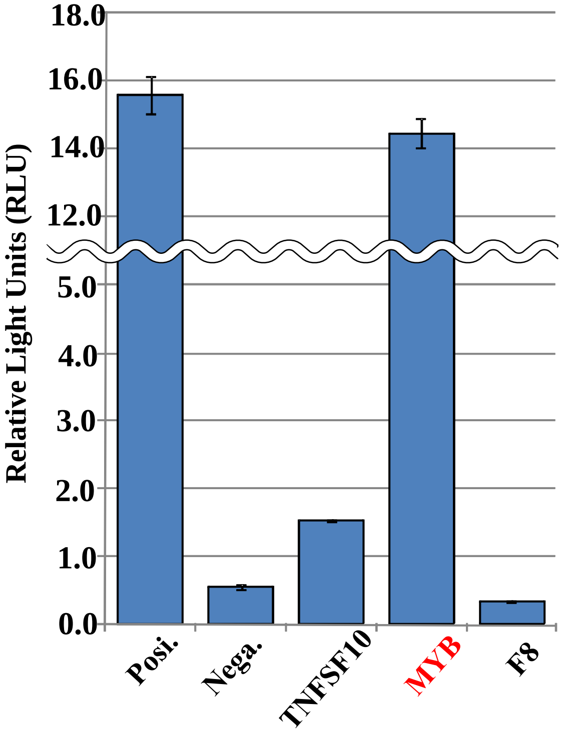
HeLa cells



HepG2 cells



Hep3B cells



**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 : 2009.08.12

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5705

2nd Nucleotide Sequence
  File Name        : RDB7480F.fasta
  Sequence Size    : 669

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.241% / 665 bp]     INT/OPT.Score : <    295/  2384 >

   1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT
                         ** ********** ********** ********** **********
   1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT

  43' CTTGAAACCT CGCATGCTTC ACCGTNTTAA TAAAATTATG ACTCATTTTA GTAAGAACAT
      ********** ********** ***** **** ********** ********** **********
  61" CTTGAAACCT CGCATGCTTC ACCGT-TTAA TAAAATTATG ACTCATTTTA GTAAGAACAT

 103' GCTTTTTTAG TAAGAANAAA ATGCTTTCTG AGCTAAGTTT GAACTGCTGG GGCACATGGG
      ********** ****** *** ********** ********** ********** **********
 120" GCTTTTTTAG TAAGAA-AAA ATGCTTTCTG AGCTAAGTTT GAACTGCTGG GGCACATGGG

 163' ACACCCANCA AACCCAGTCA GCAGAAGTCT CAAACTCCTA AAAGATTAAA GGAAAAATNA
      ******* ** ********** ********** ********** ********** ******** *
 179" ACACCCA-CA AACCCAGTCA GCAGAAGTCT CAAACTCCTA AAAGATTAAA GGAAAAAT-A

 223' CATTAGTGTG TACAGAGAAT GAAAAAAAAA TCCCCAATGG TTCTAATCTN ATAAACGGAA
      ********** ********** ********** ********** *********  **********
 237" CATTAGTGTG TACAGAGAAT GAAAAAAAAA TCCCCAATGG TTCTAATCT- ATAAACGGAA
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283’ GTAAAACTAA AACTCCCCTA AAATCCCCCC AGTCATCAAT NCCTTATAAA TTCAGCACTT
     ********** ********** ********** **********  ********* **********
296″ GTAAAACTAA AACTCCCCTA AAATCCCCCC AGTCATCAAT -CCTTATAAA TTCAGCACTT

343’ ATCTTCTTCC TTTACTTCTG GAGACCCTCA TNTAAACAAC ACGAAAGCCT TTGCTGACTT
     ********** ********** ********** * ******** ********** **********
355″ ATCTTCTTCC TTTACTTCTG GAGACCCTCA T-TAAACAAC ACGAAAGCCT TTGCTGACTT

403’ TTATCTCGTA AAATAGAGCC CTNCAAATGA CACTAAGCAG GGATACCGAC CTCCAAAATC
     ********** ********** ** ******* ********** ********** **********
414″ TTATCTCGTA AAATAGAGCC CT-CAAATGA CACTAAGCAG GGATACCGAC CTCCAAAATC

463’ ACAAACTGTT TTANCTTCTA AAACCATGCA TGCAAACGTG GGGTTTCCTG AGTTCTGCTA
     ********** *** ****** ********** ********** ********** **********
473″ ACAAACTGTT TTA-CTTCTA AAACCATGCA TGCAAACGTG GGGTTTCCTG AGTTCTGCTA

523’ GGGGNCGGGC TGTCTGGACC CCCGTGTATT TTTTTTTTTT TTTTTTTTTT TTTTTNTTTT
     **** ***** ********** ********** *********      ****** *****    *
532″ GGGG-CGGGC TGTCTGGACC CCCGTGTATT TTTTTTTTTC CCACTTTTTT TTTTT----T

583’ TTTGCAGGTG TGCAATCCAG GGTGCGCGCT CTGTGCAGGG AGGGGANGCA AAGGTGTGCG
     ********** ********** ********** ********** ****** ***  * *******
587″ TTTGCAGGTG TGCAATCCAG GGTGCGCGCT CTGTGCAGGG AGGGGA-GCA GAAGTGTGCG

643’ GTGGGCACCG CCTGGGCCGG GCGGGGCGGG GTGGGTGNGG GCCCGGGTGT GTGCTGGGGT
     ********** ****** * * * *
646″ GTGGGCACCG CCTGGGGCCG GGGC
```

1st Nucleotide Sequence
File Name : Reference Seq.GNU
Sequence Size : 5705

2nd Nucleotide Sequence
File Name : RDB7480R.fasta (Complementary)
Sequence Size : 563

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Unit Size to Compare = 1
Pick up Location     = 1



[94.552% / 569 bp]     INT/OPT.Score : <    450/  1949 >

 1021' CACCGCTTGC CGCCCCNCGC GACAGTGAGT GG-GAG-CTG G-AGGA-GCT CTGGTCCCGC
               ** * *** .**   *  * ***  ** *** *** * **** *** .*********
    1″        CGC CCCCCGGCGA CAGGGGGAGA GGAGAGCCTG GAAGGAGGCT NTGGTCCCGC

 1077' TGCCC-GGGA GCNACGCGGA GCCGGGCGAC CGCGGTGCGG CAGCCAGGGA GGAGGGGAGG
       ***** **** **.  ***** ********** ********** ********** **********
   54″ TGCCCGGGGA GCACGGCGGA GCCGGGCGAC CGCGGTGCGG CAGCCAGGGA GGAGGGGAGG

 1136' CGGNCGGGAC TGGGCGCGGG TCGG-CGC-C GCCGCGACCC GGGAGCGGGG TTTGCTNCAG
       *** ****** ********** * **  **   ********** ********** ****** ***
  114″ CGG-CGGGAC TGGGCGCGGG TTGGTTGCGT GCCGCGACCC GGGAGCGGGG TTTGCT-CAG

 1194' GAAAAGGCGC CGTCGCGGCC CCCGGCCACC CCTCCCTGGC CCCGGGCNTC CCTGCCCGCG
       ********** ********** ********** ********** ******* ** **********
  172″ GAAAAGGCGC CGTCGCGGCC CCCGGCCACC CCTCCCTGGC CCCGGGC-TC CCTGCCCGCG

 1254' CGCCTCCCGG GCCTCGCGGC GCGCTAGGCG CACCGCGGNC GGCGCGAGCG CCGAATGGGA
       ********** ********** ********** ******** * ********** **********
  231″ CGCCTCCCGG GCCTCGCGGC GCGCTAGGCG CACCGCGG-C GGCGCGAGCG CCGAATGGGA

 1314' GCGGCGACCC GGCCAGCCCG GCAGCCCCGN CGGGCGGCAG CCAGGGCGAC CGCGGAGGCG
       ********** ********** *********  ********** ********** **********
  290″ GCGGCGACCC GGCCAGCCCG GCAGCCCCG- CGGGCGGCAG CCAGGGCGAC CGCGGAGGCG

 1374' GCGGGCAGGG CGCGTGCGCA NCTGCAGGGG CGCCAGATTT GGCGGGAGGG GGAGTGTCCA
       ********** **********  ********* ********** ********** **********
  349″ GCGGGCAGGG CGCGTGCGCA -CTGCAGGGG CGCCAGATTT GGCGGGAGGG GGAGTGTCCA

 1434' AAGCTCTTTG TNTTGATGGC ATCTCTGTTT ACAGAGTTTA CACTTTAATA TCAACCTGTT
       ********** * ******** ********** ********** ********** **********
  408″ AAGCTCTTTG T-TTGATGGC ATCTCTGTTT ACAGAGTTTA CACTTTAATA TCAACCTGTT
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1494' TCCTCCTCCT CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT
      ********** ********** ********** ********** ********** **********
 467" TCCTCCTCCT CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT

1554' AAAG-CCACC ATGGAAGATG CCAAAAACAT TAAGAAGGGC CCAGCGCCAT TCTACCCACT
      **** ***** ********** ********** *******
 527" AAAGACCACC ATGGAAGATG CCAAAAACAT TAAGAAG
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