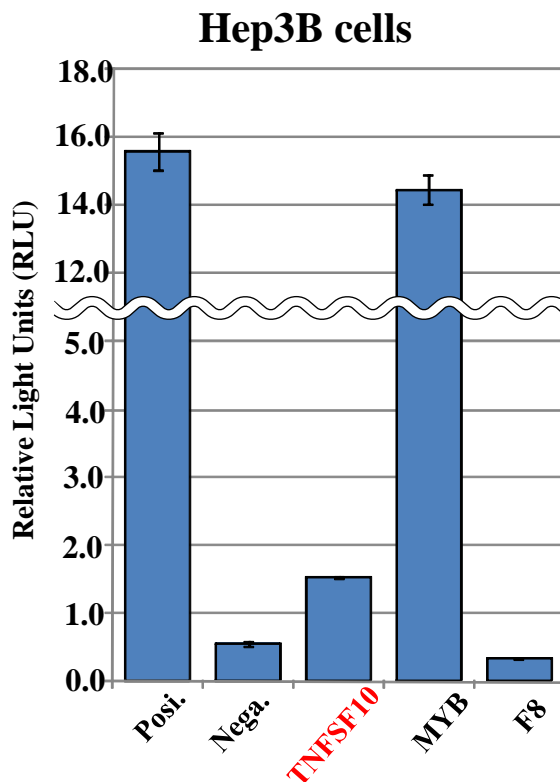
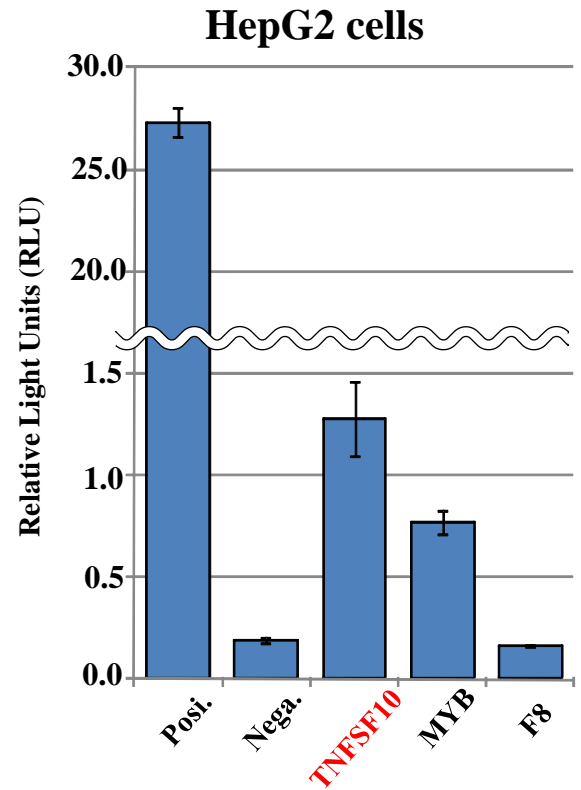
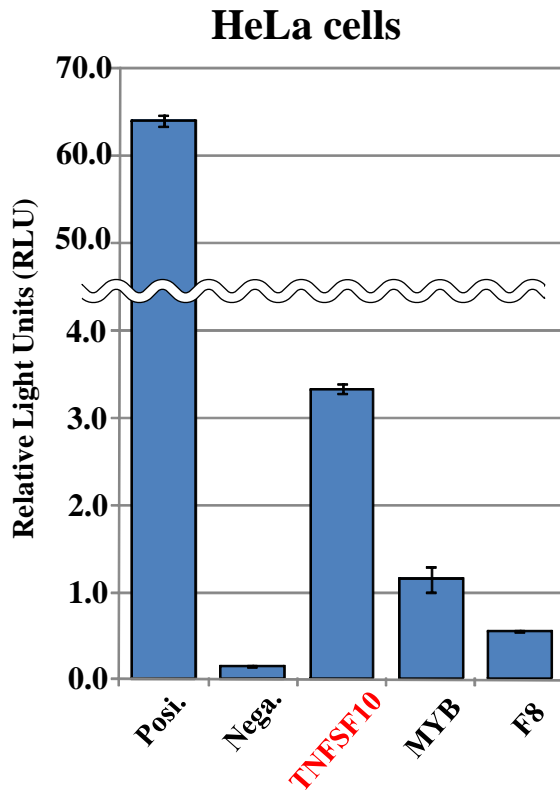


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

TNFSF10: pGL4-phTNFSF10 (RDB# 7526)

MYB: pGL4-phMYB (RDB# 7480)

F8: pGL4-phF8 (RDB# 7519)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.10.20

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5738

2nd Nucleotide Sequence

File Name : RDB7526F.fasta
Sequence Size : 745

Unit Size to Compare = 1
Pick up Location = 1

[95.289% / 743 bp] INT/OPT. Score : < 385/ 2592 >

```
1'          GGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATGGGTC
          *****
1" CAGAACATTT CTCTGGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATGGGTC

47' CCAAACITTA GGTTTCAAAG GATCTCTTGG AGTACTTGCT GAANAAATGT AGGTTCTTAA
          *****
61" CCAAACITTA GGTTTCAAAG GATCTCTTGG AGTACTTGCT GAA-AAATGT AGGTTCTTAA

107' GTCCACTGCC AGAAACTCTG ACTCAGTGGG TCAANGAATG GAATAACTAA ACAATGGCCC
          *****
120" GTCCACTGCC AGAAACTCTG ACTCAGTGGG TCAA-GAATG GAATAACTAA ACAATGGCCC

167' CATGCAGTGG TTCATGCCTG TAATCNCCAG CACGTTGGGA GGTTGAAGCA AGAGGATCAC
          *****
179" CATGCAGTGG TTCATGCCTG TAATC-CCAG CACGTTGGGA GGTTGAAGCA AGAGGATCAC

227' TTGAGGTCAG GAGTTCNGAG ACCAGCCTGG CCTACATGGT AAAACCCCAT CTCTACTAAA
          *****
238" TTGAGGTCAG GAGTTC-GAG ACCAGCCTGG CCTACATGGT AAAACCCCAT CTCTACTAAA
```

287' AATACAANAA AAATTAGCTG GGCATGGTGG CATGCACCTG TAATCCCAGC TACTTGGGNA
 ***** ** *****
 297" AATACAA-AA AAATTAGCTG GGCATGGTGG CATGCACCTG TAATCCCAGC TACTTGGG-A

 347' GGCTGAGGCA GGAGAATTGC TTGAATCTGG GAGGTGGAGG TTGTAGTGGN GCCGAGATTG

 355" GGCTGAGGCA GGAGAATTGC TTGAATCTGG GAGGTGGAGG TTGTAGTGG- GCCGAGATTG

 407' TGCCATTGCA CCACTGCACT CCAGCCTGGG CGATAAAGTG NAGATTCTGT CAAAAAATA

 414" TGCCATTGCA CCACTGCACT CCAGCCTGGG CGATAAAGTG -AGATTCTGT CAAAAAATA

 467' AATAAATACA TGAAGAGAG AAAGAAAGAA A---NGAAAG AAAGAAAGAA AGAAAGAAAG

 473" AATAAATACA TGAAGAGAG AAAGGAAGAA AGAAAGAAAG AAAGAAAGAA AGAAAGAAAG

 524' AAAGAAAGAA AGAAAGAAGG AAAGANAG--- -GAAAGAA--- -TAGAAAAGA AAAG-AAAGA

 533" AAAGAAAGAA AGAAAGAAAG AAAGAAAGAA GGAAAGAAGG AAAGAATAGA AAAGAAAAGA

 577' AAGAAAGAAA GGAAGAAAAG GAANAGAAAG AAATGCTGAA TAAGATATAG AGACAACATA

 593" AAGAAAGGAA GGAAGAAAAG GAA-AGAAAG AAATGCTGAA TAAGATATAG AGACCACATA

 637' CAGCTGGGCC AGCTNTATGA CATCTGATAG TGGGGAGATT TGGGGCTGGG TCCTGAATCT

 652" CAGCTGGGCC AGCT-TATGA CATCTGATAG TGGGGAGATT TGGGGCTGGG TCCTGAATCT

 697' GAGGGNTAAT TAACTCCCTG TAACTTCTTT TCCTAATCTG TAAAAGGATA GTGACANGCG

 711" GAGGG-TANT TAACT-CCNG T-ACCTCTTT TCCTATTT

1st Nucleotide Sequence

File Name : Reference Seq. GNU
 Sequence Size : 5738



2nd Nucleotide Sequence

File Name : RDB7526R.fasta (Complementary)

Sequence Size : 482

Unit Size to Compare = 1

Pick up Location = 1

[98.361% / 488 bp] INT/OPT.Score : < 632/ 1837 >

1081' TATGGAAGTT TCAGGTCATA AAAATTATCN TTATAATTTA GAAAACAGGC CTTGTGCCTA

1"

TTGCCTA

1141' TGACAGCCAG GCCATGAGGC NTTAGAGCTC TGTGGTAGAA TGAGGATATG TTAGGAAAA

8" TGACAGCCAG GCCATGAGGC -TTAGAGCTC TGTGGTAGAA TGAGGATATG TTAGGAAAA

1201' GCAAAGAAAA TNCCCTCCCC TCTTTGGCTG AGGACATTAT CAAAAGGAGA GCAAGAAAGA

67" GCAAAGAAAA T-CCCTCCCC TCTTTGGCTG AGGACATTAT CAAAAGGAGA GCAAGAAAGA

1261' GANAGAGAGA AATGGGCTTG AGGTGAGTGC AGATAAGGGG TGCATGGATC CTGNAGGGCA

** *****

126" GA-AGAGAGA AATGGGCTTG AGGTGAGTGC AGATAAGGGG TGCATGGATC CTG-AGGGCA

1321' AGGAGAGGAG CTTCTTTCAG TTTCCCTCCT TTCCAACGAC TACTNTTGAG ACAAGAGCTG

184" AGGAGAGGAG CTTCTTTCAG TTTCCCTCCT TTCCAACGAC TACT-TTGAG ACAAGAGCTG

1381' TCCCTGGGCA GTAGGAAAGG GGAGGGACAG TTGCANGGTT CAATAGATGT GGGTGGGGCC

243" TCCCTGGGCA GTAGGAAAGG GGAGGGACAG TTGCA-GGTT CAATAGATGT GGGTGGGGCC

1441' AAGGCCACAG AACCAGAAA AACAACNTCA TTCGCTTCA TTTCTCACT GACTATAAAA

302" AAGGCCACAG AACCAGAAA AACAAC-TCA TTCGCTTCA TTTCTCACT GACTATAAAA



1501' GAATAGAGAA GGAAGGNCT TCAGTGACCG GCTGCCTATC AAGATCTGGC CTCGGCGGCC

***** ** ***** ***** ***** *****

361" GAATAGAGAA GGAAGGGCT TCAGTGACCG GCTGCCTATC AAGATCTGGC CTCGGCGGCC

1561' AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA

***** ***** ***** ***** ***** *****

421" AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA

1621' AGGCCAGC GCCATTCTAC CCACTCGAAG ACGGACCGC CGGCGAGCAG CTGCACAAAG

**

481" AG