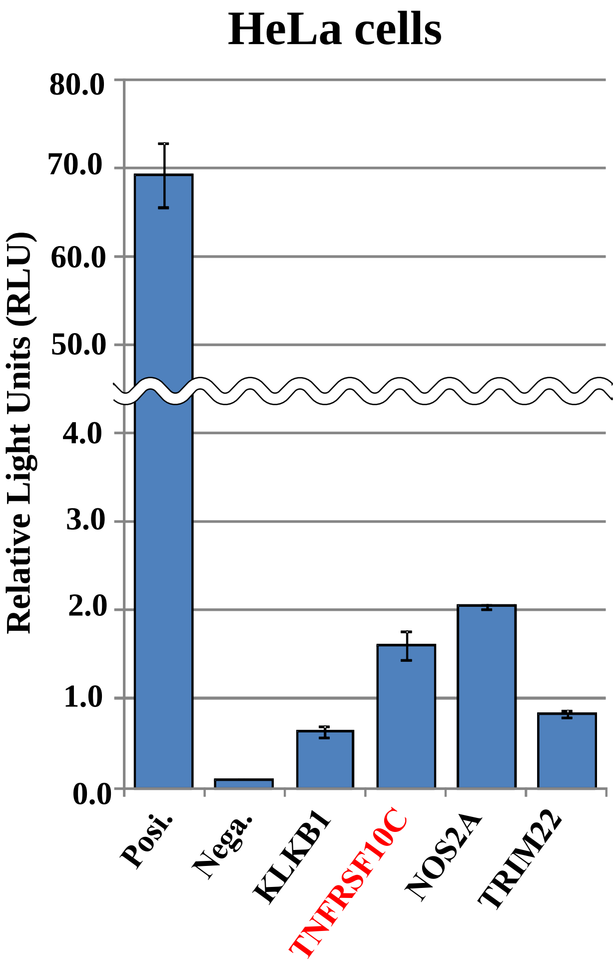
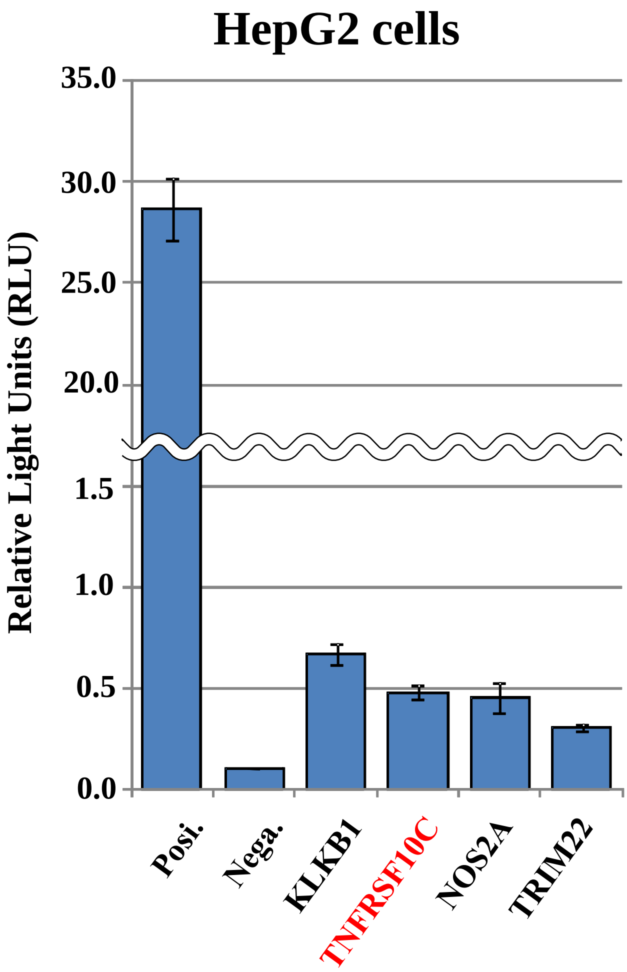
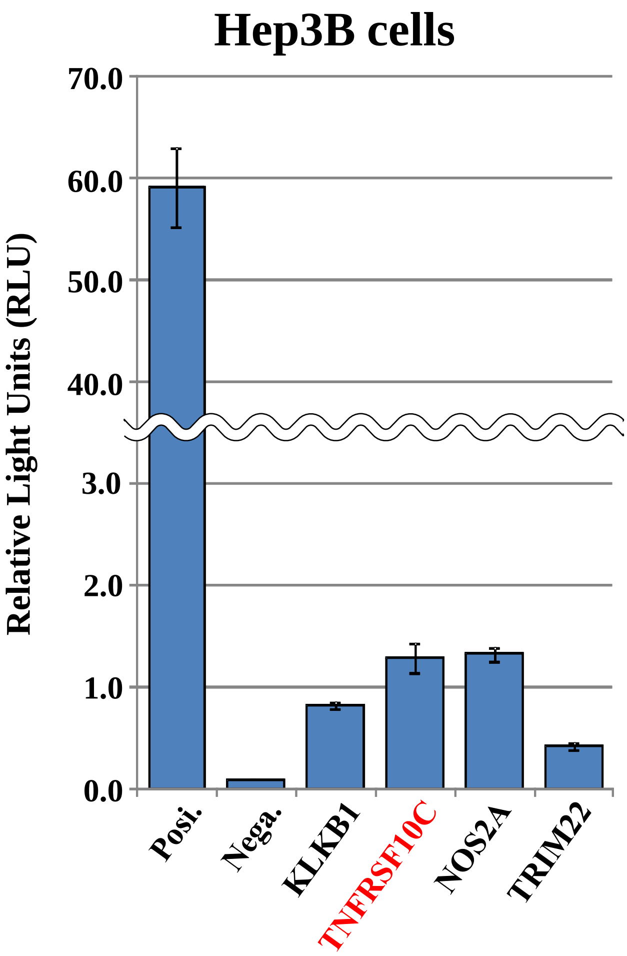
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

KLKB1: pGL4-phKLKB1 (RDB# 7373)
TNFRSF10C: pGL4-ph TNFRSF10C (RDB# 7375)
NOS2A: pGL4-phNOS2A (RDB# 7377)
TRIM22: pGL4-phTRIM22 (RDB#7382)

20010 DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5568

2nd Nucleotide Sequence
  File Name        : RDB7375F.fasta
  Sequence Size    : 711

  Unit Size to Compare = 1
  Pick up Location     = 1



[95.441% / 680 bp]     INT/OPT.Score : <   2106/  2428 >

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

    43' CCTGTCCTCT CACCTCCTGC CTAGATCTGC CCCCAGCACA CATTCCTGAC TCCACACATT
        ********** ********** ********** ********** ********** **********
    61″ CCTGTCCTCT CACCTCCTGC CTAGATCTGC CCCCAGCACA CATTCCTGAC TCCACACATT

   103' TCTCAGTGCC TGCGACCTGG CACACATTTC TGATCCGAAC TCAGTGCCTG GGGCCTGGCA
        ********** ********** ********** ********** ********** **********
   121″ TCTCAGTGCC TGCGACCTGG CACACATTTC TGATCCGAAC TCAGTGCCTG GGGCCTGGCA

   163' GGTGCCCAGG GCACTCCATT GCTCAAATCC AAGCCTGTGG AGAGGATGAC ATATCATTCC
        ********** ********** ********** ********** ********** **********
   181″ GGTGCCCAGG GCACTCCATT GCTCAAATCC AAGCCTGTGG AGAGGATGAC ATATCATTCC

   223' CAGGTTTCTG ATGAGCAGAA AAAAAAATCT TTGTTTCTAT AGTGCTATCC TCTTTTATCC
        ********** ********** ********** ********** ********** **********
   241″ CAGGTTTCTG ATGAGCAGAA AAAAAAATCT TTGTTTCTAT AGTGCTATCC TCTTTTATCC
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283' ACCATGTGAG AGGTCAGGAG CCGACTCACC CCAAGGGTCT AGGAGTTGTG CCATTGACCT
     ********** ********** ********** ********** ********** **********
301″ ACCATGTGAG AGGTCAGGAG CCGACTCACC CCAAGGGTCT AGGAGTTGTG CCATTGACCT

343' TACTGCCTAG GGTCACAGGC TGGCACCCTT CAGTACCACA CATTGGATCT CTCCACACAG
     ********** ********** ********** ********** ********** **********
361″ TACTGCCTAG GGTCACAGGC TGGCACCCTT CAGTACCACA CATTGGATCT CTCCACACAG

403' CAGCAGTGTG CTTAACTCAA TGGGGAGGTG AGTAGCCCAA GGTCAGATAG TTGGACCTGG
     ********** ********** ********** ********** ********** **********
421″ CAGCAGTGTG CTTAACTCAA TGGGGAGGTG AGTAGCCCAA GGTCAGATAG TTGGACCTGG

463' ATAGACACTT GACTGGGGGA CAGGCTTTGG AAGCCACTCC CCTGGGCCTC CTCTGTCCAT
     ********** ********** ********** ********** ********** **********
481″ ATAGACACTT GACTGGGGGA CAGGCTTTGG AAGCCACTCC CCTGGGCCTC CTCTGTCCAT

523' -GGGGCCTCA ATACTAGAGC CCACAAGGTC GGCCAGAGAG TGTCTGTG-C CTCGACCATG
      ********* ********** ********** ********** ******** * **********
541″ GGGGGCCTCA ATACTAGAGC CCACAAGGTC GGCCAGAGAG TGTCTGTGCC CTCGACCATG

581' C-AAAGGGTG CC-AGG-TTG T-GGCTAGGG -ATG---CCC CCGGGGTTCC TCTCCCTC-C
     * ******** ** *** *** * ********  ***   *** * ****** *  *** * * *
601″ CAAAAGGGTG CCAAGGTTTG TGGGCTAGGG AATGCCCCCC CGGGGGTTTC CCTCTCACAC

632' TACCTACTCC TCAGCCTCTG CATGTGCCCG TCATGGCCCC TGTGTCCTTC ATTCTGTCCA
     * ****  ** *    * **  **   ****   * *****
661″ TTCCTAACCC TACCTCCCTC CA--AGCCCT CCTTGGCCAA GGGTGCACCT TGT
```

1st Nucleotide Sequence
  File Name　　　　: Reference Seq.gnu
  Sequence Size　　: 5568

2nd Nucleotide Sequence
  File Name　　　　: RDB7375R.fasta (Complementary)
  Sequence Size　　: 464

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  Unit Size to Compare = 1
  Pick up Location     = 1



[99.784% / 464 bp]     INT/OPT.Score : <   1640/  1840 >

   961' CTCCAGTGCC TCCTCTGGAG CTCACTACCC AGACTACAGC AGCGCAGTGG GCAGCGCCTC
                                      ** ********** ********** **********
     1″                               CC AGACTACAGC AGCGCAGTGG GCAGCGCCTC

  1021' AGCTCCTTCC CCTTCTGCTG CCTACAGCCT GGACAGGACC CGGAATCAAA CCGCAGGCCC
        ********** ********** ********** ********** ********** **********
    33″ AGCTCCTTCC CCTTCTGCTG CCTACAGCCT GGACAGGACC CGGAATCAAA CCGCAGGCCC

  1081' TGGGTCACCG CTGCCGGAAA GAGCCAGTTC CTGTCCGTCC ATGCACCCAC CACCAAAACC
        ********** ********** ********** ********** ********** **********
    93″ TGGGTCACCG CTGCCGGAAA GAGCCAGTTC CTGTCCGTCC ATGCACCCAC CACCAAAACC

  1141' CAGGCCTTCC TGGAGGTGCT AGGGGAGGCC ATGCCCCTTT TCTGAGTGCT TGGAAGTGAC
        ********** ********** ********** ********** ********** **********
   153″ CAGGCCTTCC TGGAGGTGCT AGGGGAGGCC ATGCCCCTTT TCTGAGTGCT TGGAAGTGAC

  1201' TGCTGCAAGT GACAAGTGAC CACGCCTTTT CCCCCGCGGG TATAAATTCA GAGGCGCTGC
        ********** ********** ********** ********** ********** **********
   213″ TGCTGCAAGT GACAAGTGAC CACGCCTTTT CCCCCGCGGG TATAAATTCA GAGGCGCTGC

  1261' GCTCCGATTC TGGCAGTGCA GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA
        ********** ********** ********** ********** ********** **********
   273″ GCTCCGATTC TGGCAGTGCA GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA

  1321' TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGATC AAGATCTGGC
        ********** ********** ********** ********** ********** **********
   333″ TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGATC AAGATCTGGC

  1381' CTCGGCGGCC AAGCTT-GGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA
        ********** ****** *** ********** ********** ********** **********
   393″ CTCGGCGGCC AAGCTTGGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA
```

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1440' AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA
      ********** **
 453" AAACATTAAG AA
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