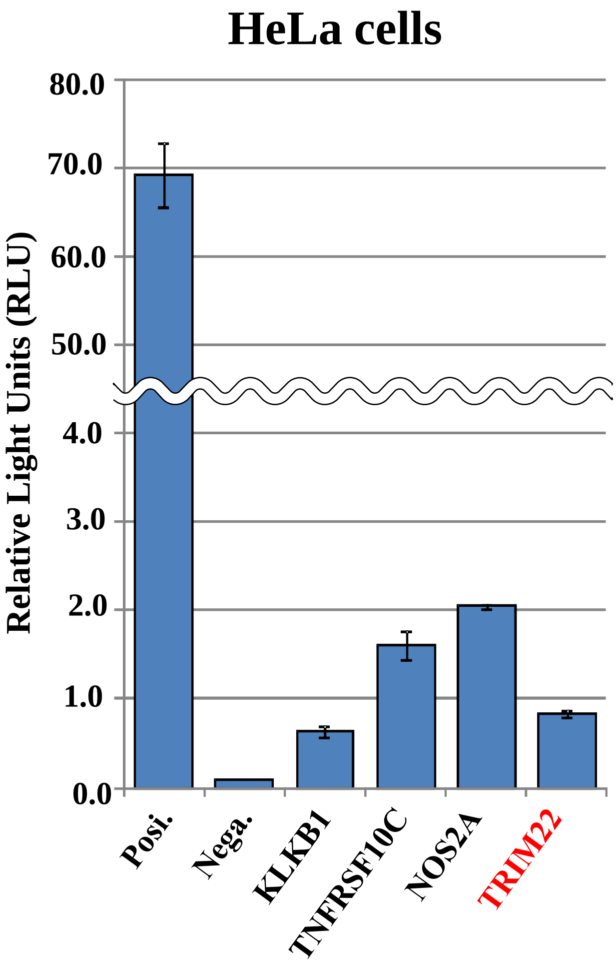
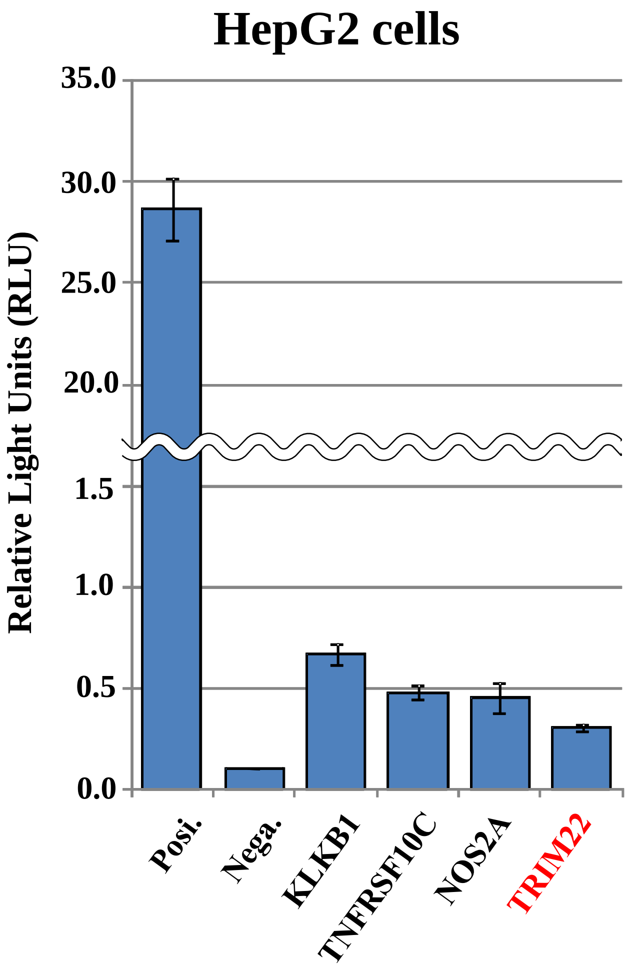
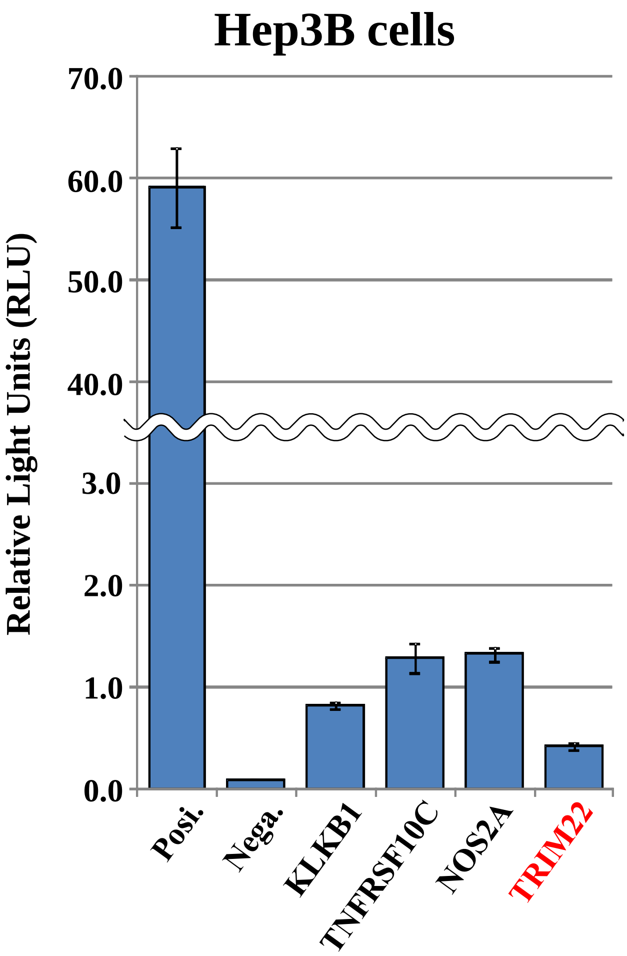
The Promoter Activities of Reporter Constructs







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)

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5559

2nd Nucleotide Sequence
  File Name        : RDB7382F.fasta
  Sequence Size    : 594

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.785% / 576 bp]     INT/OPT.Score : <    934/  2210 >

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

     43' AGATGGCCAT GCTCCATAGT GTCAGTCAGG GATCCATGTT ATGGAAGCTC CATGAGTTGC
         ********** ********** ********** ********** ********** **********
     61" AGATGGCCAT GCTCCATAGT GTCAGTCAGG GATCCATGTT ATGGAAGCTC CATGAGTTGC

    103' CTTTTTTTTT CTTTTTTTTT GGG--TGTGT GTGTGTATGT GTTGTGTGGT GTTTGTTTGT
         ********** ********** ***  ***** ********** ********** **********
    121" CTTTTTTTTT CTTTTTTTTT GGGTGTGTGT GTGTGTATGT GTTGTGTGGT GTTTGTTTGT

    161' TTGTTTTTTG TAGAGACAGG GTCTTACTAT GTCACCCAGG CTGCAGTGCT ATGGTGCAAT
         ********** ********** ********** ********** ********** **********
    181" TTGTTTTTTG TAGAGACAGG GTCTTACTAT GTCACCCAGG CTGCAGTGCT ATGGTGCAAT

    221' GACGCAATCT TGGCTCAATG CAACCTCCAC CTCCTGGGCT CAAGCCATCC TCCCATCTCA
         ********** ********** ********** ********** ********** **********
    241" GACGCAATCT TGGCTCAATG CAACCTCCAC CTCCTGGGCT CAAGCCATCC TCCCATCTCA
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    281’ GTTTCCTGAG TAGCTGGGAC TACAGGTGCA CATCACCACA CCCAGCTATT TTTTTTTTTT
         ********** ********** ********** ********** ******** * **********
    301″ GTTTCCTGAG TAGCTGGGAC TACAGGTGCA CATCACCACA CCCAGCTA-T TTTTTTTTTT

    341’ TAATTTTTCT TAGAGATGGG ATTTCACCAT GTTGCCCAGG CTGGTGTTGA AGTCCTGGAC
         ********** ********** ********** ********** ********** **********
    360″ TAATTTTTCT TAGAGATGGG ATTTCACCAT GTTGCCCAGG CTGGTGTTGA AGTCCTGGAC

    401’ TCAAGTGATC CACCCACCTG GGCCTCCCAG AGTGCTGGGA TTACAGGCAT GAGACACCAC
         ********** ********** ********** ********** ********** **********
    420″ TCAAGTGATC CACCCACCTG GGCCTCCCAG AGTGCTGGGA TTACAGGCAT GAGACACCAC

    461’ AGGCCTCCAT CAGTTTTTGA TGGCATTATC TGGCACATGC AGTTAAACAA GAATACAATA
         ********** ********** ********** ********** ********** ****** ***
    480″ AGGCCTCCAT CAGTTTTTGA TGGCATTATC TGGCACATGC AGTTAAACAA GAATACGATA

    521’ GACAACA-GG GTACAGAAGT ATGTGCATGA C-GTATAACA TGTTTC-AGT GCTGCTTTTT
         ******* ** ********** ********** * ******** ****** *** ****
    540″ GACAACAGGG GTACAGAAGT ATGTGCATGA CGGTATAACA TGTTTCAAGT GCTGG




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5559

2nd Nucleotide Sequence
  File Name        : RDB7382R.fasta (Complementary)
  Sequence Size    : 390

  Unit Size to Compare = 1
  Pick up Location     = 1


[98.718% / 390 bp]     INT/OPT.Score : <   1288/  1508 >
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1021’ GTCTCTGGAT CTTTATTTTC CTGGCTTAGG TCTTAAATAT AAGATAAATT CGACTAATAA
                                         * ** ********** **********
   1″                                    AAAT AAGATAAATT CGACTAATAA

1081’ TTATAGGACT GCATTGGAAT TCTAAGTATT CAGGCAAGCT GTATAACTGT AATTCACATT
      ********** ********** ********** ********** ********** **********
  25″ TTATAGGACT GCATTGGAAT TCTAAGTATT CAGGCAAGCT GTATAACTGT AATTCACATT

1141’ CTTTTTATTC AAATATTCTT GCTTGAGTAA ACCACAGTAA GAATAAGGAA GTAGTGACTG
      ********** ********** ********** ********** ********** **********
  85″ CTTTTTATTC AAATATTCTT GCTTGAGTAA ACCACAGTAA GAATAAGGAA GTAGTGACTG

1201’ AGTGCCTTGC CAGTACAGCA GATGCTAGAA CATAATGTAG CATTACTTTC CCCAGGGTTT
      ********** ********** ********** ********** ********** **********
 145″ AGTGCCTTGC CAGTACAGCA GATGCTAGAA CATAATGTAG CATTACTTTC CCCAGGGTTT

1261’ ATTGTTATGT AAGTTCTTGT TCAGCTTCCT TTGTTTTCTT TCACTTCTGA GAATTTAACT
      ********** ********** ********** ********** ********** **********
 205″ ATTGTTATGT AAGTTCTTGT TCAGCTTCCT TTGTTTTCTT TCACTTCTGA GAATTTAACT

1321’ TTCGTTTCTC ACTCAGCTCC TGTGGGGAAA CTCATTTGAT CAAGATCTGG CCTCGGC--G
      ********** ********** ********** ********** ********** *******  *
 265″ TTCGTTTCTC ACTCAGCTCC TGTGGGGAAA CTCATTTGAT CAAGATCTGG CCTCGGCGGG

1379’ GCCAA-GCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAGATGC CAAAAACATT
       **** **** ********** ********** ********** ********** **********
 325″ CCCAAGGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAGATGC CAAAAACATT

1438’ AAGAAGGGCC CAGCGCCATT CTACCCACTC GAAGACGGGA CCGCCGGCGA GCAGCTGCAC
      ******
 385″ AAGAAG
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