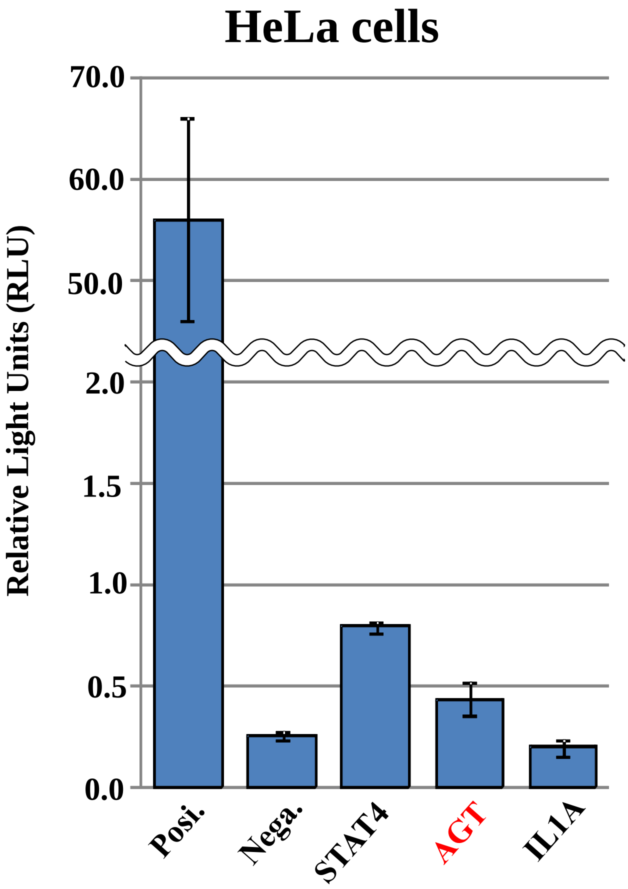
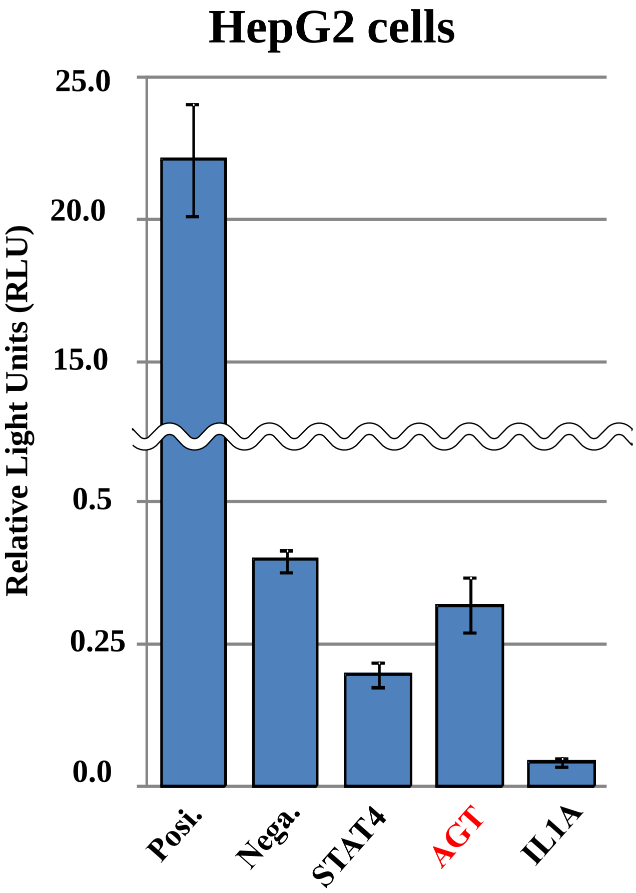
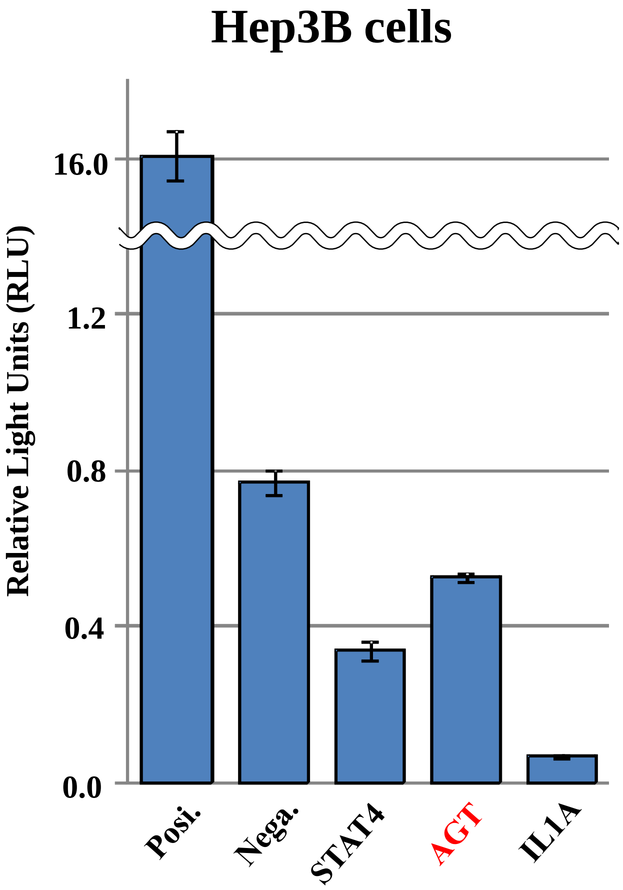
The Promoter Activities of Reporter Constructs







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

STAT4: pGL4-phSTAT4 (RDB# 7711)
AGT: pGL4-phAGT(RDB# 7683)
IL1A: pGL4-phIL1A (RDB# 7682)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.07

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5738

2nd Nucleotide Sequence
  File Name        : RDB7683F.fasta
  Sequence Size    : 735

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.961% / 724 bp]     INT/OPT.Score : <   2609/  2716 >

      1'                   GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATTG
                           *** ********** ********** ********** **********
      1″ GTGCCAGAAC TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATTG

     44' GGTCCAATCT AACCAAAATT ATTTTCTTAT GTTCTCCCCA GTAACGTGTC ATTATTAAGA
         ********** ********** ********** ********** ********** **********
     61″ GGTCCAATCT AACCAAAATT ATTTTCTTAT GTTCTCCCCA GTAACGTGTC ATTATTAAGA

    104' GAAGTTTGGC TTGCTTAGAG GCCAAATTTA GAGGGTCCTG AAATTTTATT TTCTTTTACA
         ********** ********** ********** ********** ********** **********
    121″ GAAGTTTGGC TTGCTTAGAG GCCAAATTTA GAGGGTCCTG AAATTTTATT TTCTTTTACA

    164' CCACTTTCCA GCATGTTACC TGATCAGTTG TTTATTATCT TTGCTGTTGA ATGGAGTGAT
         ********** ********** ********** ********** ********** **********
    181″ CCACTTTCCA GCATGTTACC TGATCAGTTG TTTATTATCT TTGCTGTTGA ATGGAGTGAT

    224' CATTCCAAGG GCCCGAGGCA GGAGGCCCAG GCACAGTGGA AACTCTCCCA AAGACCAGGA
         ********** ********** ********** ********** ********** **********
    241″ CATTCCAAGG GCCCGAGGCA GGAGGCCCAG GCACAGTGGA AACTCTCCCA AAGACCAGGA
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284' TCTTTGTTTT GTTCCCTGAC ATATGCTGAG CACCAGGAAT AGTGAGTGAA TGAAACAAAT
     ********** ********** ********** ********** ********** **********
301″ TCTTTGTTTT GTTCCCTGAC ATATGCTGAG CACCAGGAAT AGTGAGTGAA TGAAACAAAT

344' TGTGAGGCTT TAAAGAGCCG AAATATTTAA ACACTGGGCA CAAGGTTGTT GCTTAATCAG
     ********** ********** ********** ********** ********** **********
361″ TGTGAGGCTT TAAAGAGCCG AAATATTTAA ACACTGGGCA CAAGGTTGTT GCTTAATCAG

404' TGCTAGATCC TTACCTCCCC CTTGTGTCCA GGTGGACTTG TTACTGCAGT TAAACCACTT
     ********** ********** ********** ********** ********** **********
421″ TGCTAGATCC TTACCTCCCC CTTGTGTCCA GGTGGACTTG TTACTGCAGT TAAACCACTT

464' GCTGATCCTC AAACAACTAG TTAGTGGCAC AGCCAGGCCT AGGACCCCAG TCTCTACTGT
     ********** ********** ********** ********** ********** **********
481″ GCTGATCCTC AAACAACTAG TTAGTGGCAC AGCCAGGCCT AGGACCCCAG TCTCTACTGT

524' TCCAACTAAC CCATTCGCAG GCAGGAGCAC TTTGAATGGT CTCTTATTTT AAAAAAATTA
     ********** ********** ********** ********** ********** **********
541″ TCCAACTAAC CCATTCGCAG GCAGGAGCAC TTTGAATGGT CTCTTATTTT AAAAAAATTA

584' AATTAAAATT GTCTATTTAT TTAGAGACAG AGTCTTACTC TGTAGCCCAG GCTCGAGTGC
     ********** ********** ********** ********** ********** **********
601″ AATTAAAATT GTCTATTTAT TTAGAGACAG AGTCTTACTC TGTAGCCCAG GCTCGAGTGC

644' AGTGGTGCAA TCATAGCTCA CTGTAACCTC CATCTCCTGG CCTCAAAAAG TGTTTGAATT
     ******** * .********* **** ***** ***** ****    * ***** ** ******
661″ AGTGGTGC-A NCATAGCTCA CTGT-ACCTC CATCT-CTGG ---CTAAAAG TG-TTGAATA

704' ACAGATGCGA GGCACTGTAC CTGGCCCGAA TGTTCTGTTC AGACAAAGCC ACCTCTAAGT
     * *         * ****. * *
714″ AGATCGAGCC TGTACTGNCC CC
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1st Nucleotide Sequence
  File Name   : Reference Seq.GNU
  Sequence Size   : 5738

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2nd Nucleotide Sequence
  File Name        : RDB7683R.fasta (Complementary)
  Sequence Size    : 709

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.294% / 708 bp]     INT/OPT.Score : <   2216/  2795 >

    901' AAAAAGAGGT ATTTGTGTGT TTGTTGATTG TTCAGTCAGT GAATGTACAG CTTCTGCCTC
                    *** ****** ******** * ********** ********** **********
      1″         AA ATTGGTGTGT TTGTTGATGG TTCAGTCAGT GAATGTACAG CTTCTGCCTC

    961' ATATCCAGGC ACCATCTCTT CCTGCTCTTT GTTGTTAAAT GTTCCATTCC TGGGTAATTT
         **** ***** ********** ********** ********** ********** **********
     53″ ATATTCAGGC ACCATCTCTT CCTGCTCTTT GTTGTTAAAT GTTCCATTCC TGGGTAATTT

   1021' CATGTCTGCC ATCGTGGATA TGCCGTGGCT CCTTGAACCT GCTNTGTGTT GAAGCAGGAT
         ********** ********** ********** *****.**** *** ****** **********
    113″ CATGTCTGCC ATCGTGGATA TGCCGTGGCT CCTTGNACCT GCT-TGTGTT GAAGCAGGAT

   1081' CTTCCTTCCT GTCCCTTCAG TGCCCTAATA CCATGTATTT AAGGCTGGAC ACATCACCAC
         ********** ********** ********** ********** ********** **********
    172″ CTTCCTTCCT GTCCCTTCAG TGCCCTAATA CCATGTATTT AAGGCTGGAC ACATCACCAC

   1141' TCCCAACCTG CCTCACCCAC TGCGTCACTT GTGATCACTG GCTTCTGGCG ACTCTCACCA
         ********** ********** ********** ********** ********** **********
    232″ TCCCAACCTG CCTCACCCAC TGCGTCACTT GTGATCACTG GCTTCTGGCG ACTCTCACCA

   1201' AGGTCTCTGT CATGCCCTGT TATAATGACT ACAAAAGCAA GTCTTACCTA TAGGAAAATA
         ********** ********** ********** ********** ********** **********
    292″ AGGTCTCTGT CATGCCCTGT TATAATGACT ACAAAAGCAA GTCTTACCTA TAGGAAAATA

   1261' AGAATTATAA CCCTTTTACT GGTCATGTGA AACTTACCAT TTGCAATTTG TACAGCATAA
         ********** ********** ********** ********** ********** **********
    352″ AGAATTATAA CCCTTTTACT GGTCATGTGA AACTTACCAT TTGCAATTTG TACAGCATAA
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1321’ ACACAGAACA GCACATCTTT CAATGCCTGC ATCCTGAAGG CATTTTGTTT GTGTCTTTCA
      ********** ********** ********** ********** ********** **********
 412″ ACACAGAACA GCACATCTTT CAATGCCTGC ATCCTGAAGG CATTTTGTTT GTGTCTTTCA

1381’ ATCTGGCTGT GCTATTGTTG GTGTTTAACA GTCTCCCCAG CTACACTGGA AACTTCCAGA
      ********** ********** ********** ********** ********** **********
 472″ ATCTGGCTGT GCTATTGTTG GTGTTTAACA GTCTCCCCAG CTACACTGGA AACTTCCAGA

1441’ AGGCACTTTT CACTTGCTTG TGTGTTTTCC CCAGTGTCTA TTAGAGGCCT TTGCACAGGG
      ********** ********** ********** ********** ********** **********
 532″ AGGCACTTTT CACTTGCTTG TGTGTTTTCC CCAGTGTCTA TTAGAGGCCT TTGCACAGGG

1501’ TAGGCTCTTT GGAGCAGCTG AAGGTCACAC ATCCCATATC AAGATCTGGC CTCGGCGGCC
      ********** ********** ********** ********** ********** **********
 592″ TAGGCTCTTT GGAGCAGCTG AAGGTCACAC ATCCCATATC AAGATCTGGC CTCGGCGGCC

1561’ AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA
      ********** ********** ********** ********** ********** ********
 652″ AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAA
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