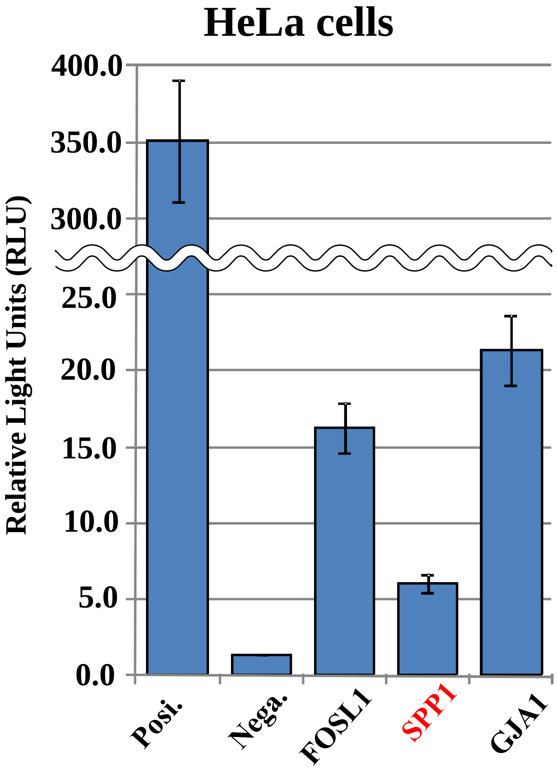
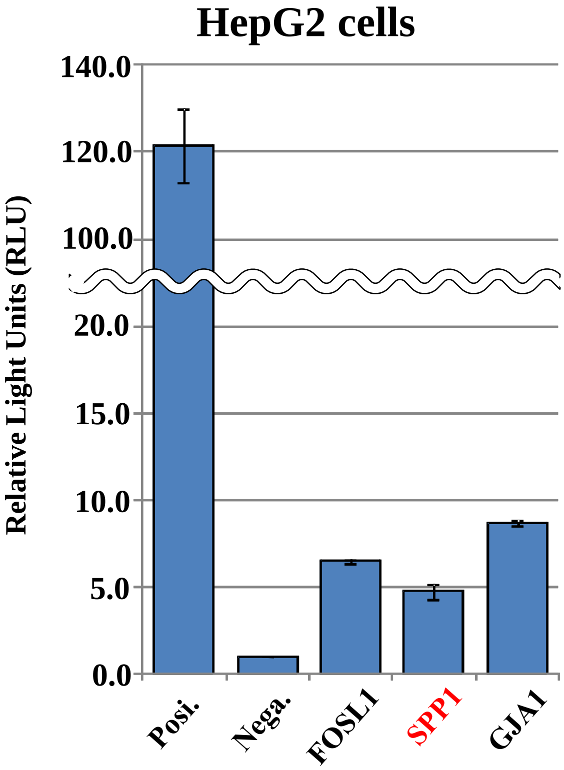
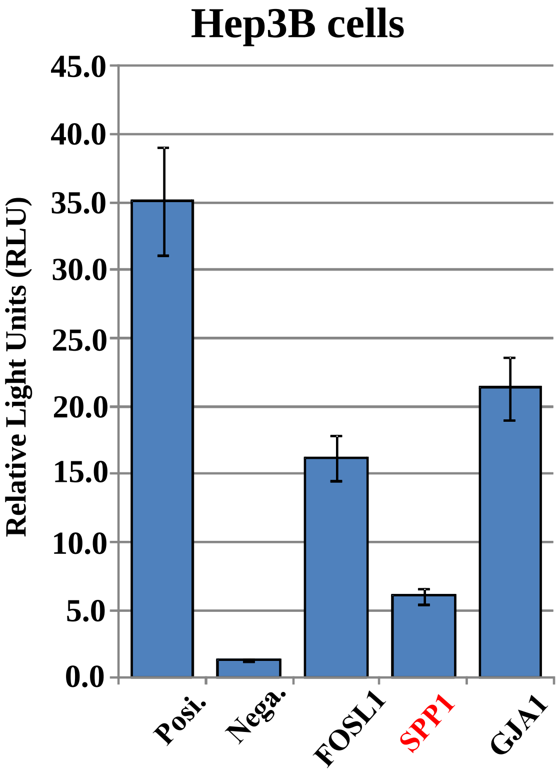
The Promoter Activities of Reporter Constructs







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

FOSL1: pGL4-phFOSL1 (RDB# 7476)
SPP1: pGL4-phSPP1 (RDB# 7552)
GJA1: pGL4-phGJA1 (RDB# 7538)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.11.19

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5692

2nd Nucleotide Sequence
  File Name         : RDB7552F.fasta
  Sequence Size     : 645

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.795% / 635 bp]     INT/OPT.Score : <    307/  2349 >

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

    43' TTGGCAAAAG GAAGCTGACA CTTTAGGACT ANATAAAAAC CACAATTACT TTTGCAGCAA
        ********** ********** ********** * ******** ********** **********
    61" TTGGCAAAAG GAAGCTGACA CTTTAGGACT A-ATAAAAAC CACAATTACT TTTGCAGCAA

   103' CCTAATAATA AATAGGACCA TTNTATTTTT CATCTCAATT ACACACAAGT CTTAACAATA
        ********** ********** ** ******* ********** ********** **********
   120" CCTAATAATA AATAGGACCA TT-TATTTTT CATCTCAATT ACACACAAGT CTTAACAATA

   163' AAGGTGTAAG GTANAATAAA TAGTGCAATC TGCATTTCAC AACTGAGAAA GCAAATGAAG
        ********** *** ****** ********** ********** ********** **********
   179" AAGGTGTAAG GTA-AATAAA TAGTGCAATC TGCATTTCAC AACTGAGAAA GCAAATGAAG

   223' ATAANGTAAT CTCAAGGCAA TATTAAATAT TTTAAAAGGA CCCAGAGCTC TGCTANTCCC
        **** ***** ********** ********** ********** ********** ***** ****
   238" ATAA-GTAAT CTCAAGGCAA TATTAAATAT TTTAAAAGGA CCCAGAGCTC TGCTA-TCCC
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283’ TGAATTCTGC TCTAATATTC GGACTTTCCC TGTAATTTTC TTTCATNTCA GACACCTTTT
     ********** ********** ********** ********** ****** *** **********
296″ TGAATTCTGC TCTAATATTC GGACTTTCCC TGTAATTTTC TTTCAT-TCA GACACCTTTT

343’ AAATACCTAG TAAAGTGTTT TTTAATACAG AAATTTTNTA AAAATGTTTT TCTTTTTAAG
     ********** ********** ********** ******* ** ********** **********
355″ AAATACCTAG TAAAGTGTTT TTTAATACAG AAATTTT-TA AAAATGTTTT TCTTTTTAAG

403’ TGGCCTACTT TACATACCTT GGGAGAAANA ACTAGAAAAA AAGATGATTC CAAAATCGAA
     ********** ********** ******** * ********** ********** **********
414″ TGGCCTACTT TACATACCTT GGGAGAAA-A ACTAGAAAAA AAGATGATTC CAAAATCGAA

463’ TCTGTTCCTT TAGAAATGTN GCAAAATTTC CTTATTGATG CATACAATTT AAAGATCTTA
     ********** *********  ********** ********** ********** **********
473″ TCTGTTCCTT TAGAAATGT- GCAAAATTTC CTTATTGATG CATACAATTT AAAGATCTTA

523’ CGTCTACTCT NCATTTTAAT AACCTGTTCT TTTAAAGGAC ATTACAATTC GTGACTGCCT
     **********  ********* ******* ** ********** ********** **********
532″ CGTCTACTCT -CATTTTAAT AACCTGTCCT TTTAAAGGAC ATTACAATTC GTGACTGCCT

583’ GNCCCCTCTT AAAAATTTCA TAATAGTTAA CACACATATA GTCCTTAAGA TANCGCAGAG
     * ******** ********** ********** ********** **** ***** **.
591″ G-CCCCTCTT AAAAATTTCA TAATAGTTAA CACACATATA GTCCCTAAGA TACGCC
```

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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5692

2nd Nucleotide Sequence
  File Name        : RDB7552R.fasta (Complementary)
  Sequence Size    : 738

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[97.333% / 750 bp]     INT/OPT.Score : <    501/  2756 >

  781' GCCCAAGNGT TGCACAGGTC AGCAGTGACA CAGCGGAATT CAGAACCACG GTCTGGCTNC
                                                        * ** ******** *
    1"                                                  CCCG GTCTGGCT-C

  841' CTGAAGCAGC CCTCTCAAGC AGTCATCCTG CTCTCAGTCA G-AAACTGCT NTTACTTCTG
       **** **.** ******* ** ********** ********** * ********  *********
   14" CTGAGGCNGC CCTCTCAGGC AGTCATCCTG CTCTCAGTCA GAAAACTGCT -TTACTTCTG

  900' CAACATCTAG AATAAATTAC CATTCTTCTA TTTCATATAG ANATTTTATA TTTTAATGTC
       ********** ********** ********** ********** * ******** **********
   73" CAACATCTAG AATAAATTAC CATTCTTCTA TTTCATATAG A-ATTTTATA TTTTAATGTC

  960' ACTAGTGCCA TTTGTCTAAG TAACAAGCTA CTNGCATACT CGAAATCACA AAGCTAAGCT
       ********** ********** ********** ** ******* ********** **********
  132" ACTAGTGCCA TTTGTCTAAG TAACAAGCTA CT-GCATACT CGAAATCACA AAGCTAAGCT

 1020' TGAGTAGTAA AGGACAGAGG CAANGTTTTC TGAACTCCTT GCAGGCTTGA ACAATAGCCT
       ********** ********** *** ****** ********** ********** **********
  191" TGAGTAGTAA AGGACAGAGG CAA-GTTTTC TGAACTCCTT GCAGGCTTGA ACAATAGCCT

 1080' TCTGGCTCTT CAATNAAGTA CAATCATACA GGCAAGAGTG GTTGCAGATA TTACCTTTAT
       ********** **** ***** ********** ********** ********** **********
  250" TCTGGCTCTT CAAT-AAGTA CAATCATACA GGCAAGAGTG GTTGCAGATA TTACCTTTAT

 1140' GTTACNTTAA ACCGAAAGAA ACAAAAATCC ATTCTATTTA ATTTTACATT AATGTTNTTT
       ***** **** ********** ********** ********** ********** ****** ***
  309" GTTAC-TTAA ACCGAAAGAA ACAAAAATCC ATTCTATTTA ATTTTACATT AATGTT-TTT

 1200' CCCTACTTTC TCCCTTTTTC ATGGGATCCC TAAGTGCTCT TCCTGGANTG CTGAATGCCC
       ********** ********** ********** ********** ******* ** **********
  367" CCCTACTTTC TCCCTTTTTC ATGGGATCCC TAAGTGCTCT TCCTGGA-TG CTGAATGCCC

 1260' ATCCCGTAAA TGAAAAAGCT AGTTAATGAT ATTGTACANT AAGTAATGTT TTAACTGTAG
       ********** ********** ********** ******** * ********** **********
  426" ATCCCGTAAA TGAAAAAGCT AGTTAATGAT ATTGTACA-T AAGTAATGTT TTAACTGTAG
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1320’ ATTGTGTGTG TGCGTTTTTG TTTTTTTTTN GTTTTAACCA CAAAACCAGA GGGGGAAGTG
      ********** **********  ********. ********** ********** **********
 485″ ATTGTGTGTG TGCGTTTTTG GTTTTTTTTT GTTTTAACCA CAAAACCAGA GGGGGAAGTG

1380’ TGGGAGCAGG TGGGCTGGGC NAGTGGCAGA AAACCTCATG ACACAATCTC TCCGCCTCCC
      ********** **********  ********* ********** **********  *********
 545″ TGGGAGCAGG TGGGCTGGGC -AGTGGCAGA AAACCTCATG ACACAATCTC GCCGCCTCCC

1440’ TGTGTTGGTG GNAGGATGTC TGCAGCAGCA TTTAAATTCT GGGAGGGCTT GGATCAAGAT
      ********** * ******** ********** ********** ********** **********
 604″ TGTGTTGGTG G-AGGATGTC TGCAGCAGCA TTTAAATTCT GGGAGGGCTT GGATCAAGAT

1500’ CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG
      ********** ********** ********** ********** ********** **********
 663″ CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG

1560’ CCAAAAACAT TAAGAAGGGC CCAGCGCCAT TCTACCCACT CGAAGACGGG ACCGCCGGCG
      ********** ******
 723″ CCAAAAACAT TAAGAA
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