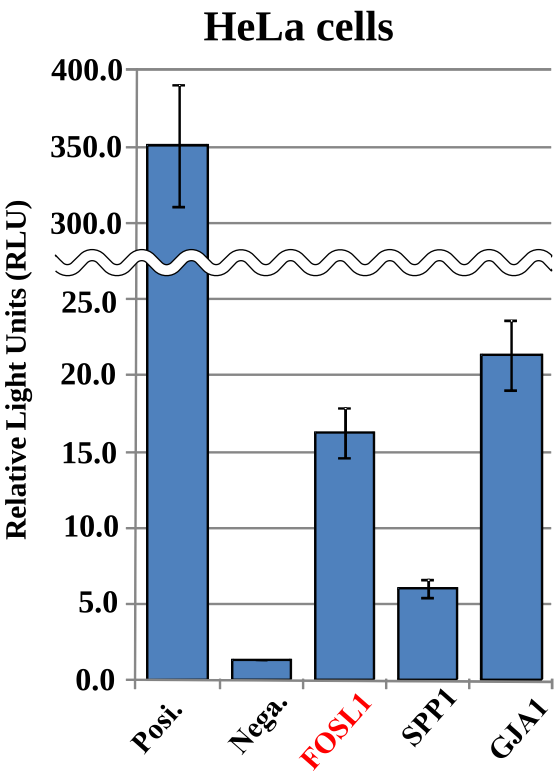
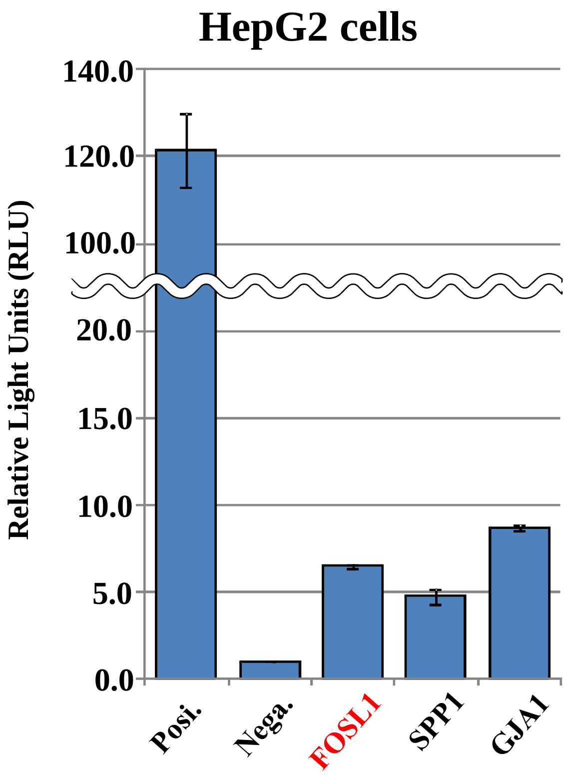
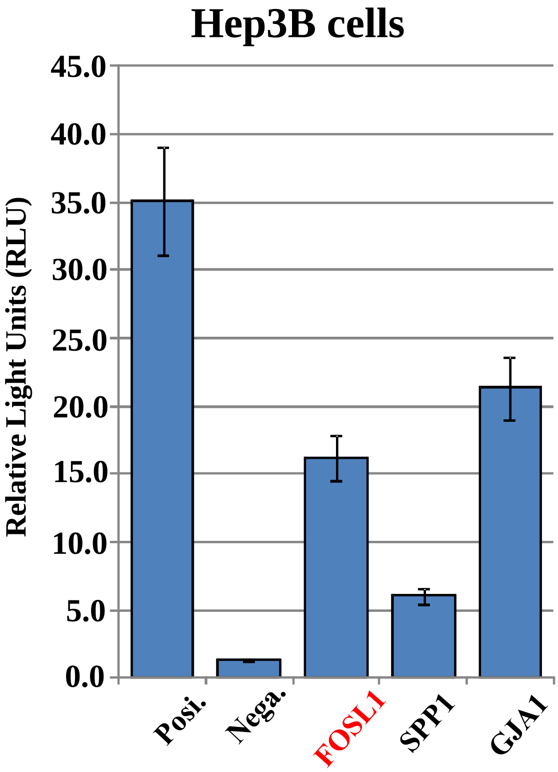
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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 : 2009.08.28

1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5563

2nd Nucleotide Sequence
  File Name          : RDB7476F.fasta
  Sequence Size      : 676

  Unit Size to Compare = 1
  Pick up Location     = 1

[97.252% / 655 bp]     INT/OPT.Score : <   1282/  2472 >

    1'                       GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTC-GAGG
                             ********** ********** ********** ***** ****
    1" GGTGCCAGAA CATATTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCAGAGG

   40' ATCTTGGCCT TCCAAAGTGC TAGGATTACA AGCATGAGCC ACCACACCTG GCCCCAGCCC
       **** ***** ********** ********** ********** ********** **********
   61" ATCTAGGCCT TCCAAAGTGC TAGGATTACA AGCATGAGCC ACCACACCTG GCCCCAGCCC

  100' TC-TTTCTGT AGTCGTGTGA CAACTGACAG CTCAGTACTC CATCTGGGCC TCAGTTTCCT
       ** * ***** ********** ********** ********** ********** **********
  121" TCATATCTGT AGTCGTGTGA CAACTGACAG CTCAGTACTC CATCTGGGCC TCAGTTTCCT

  159' CATCTATGAT GGAAGTAATC AGAGAGAAGC TTTGGGATGG TGCCCAGCAC TAACATTCTG
       ********** ********** ********** ********** ********** **********
  181" CATCTATGAT GGAAGTAATC AGAGAGAAGC TTTGGGATGG TGCCCAGCAC TAACATTCTG

  219' GATGTGCGAC AAGGTGTCTG TGAAGGTGTA AGGGCTTTGA AAATCTTGGC TGAGCCTGGG
       ********** ********** ********** ********** ****** *** **********
  241" GATGTGCGAC AAGGTGTCTG TGAAGGTGTA AGGGCTTTGA AAATCTAGGC TGAGCCTGGG

  279' CTTGGAGTGC CCACGGCTGT GACTTGGCAA CCTGTGCCAG CTACTCACTT AGCGACTTCA
       ********** ********** ********** ********** *********  **********
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301″ CTTGGAGTGC CCACGGCTGT GACTTGGCAA CCTGTGCCAG CTACTCACTA AGCGACTTCA

339’ AGCAATTCAT TTCAGCATCT CCCAGCCTCA GTTTCCCCAT CTGTAAAACA GGGATGAGGA
     ********** ********** ********** ********** ********** **********
361″ AGCAATTCAT TTCAGCATCT CCCAGCCTCA GTTTCCCCAT CTGTAAAACA GGGATGAGGA

399’ TGATACCTGC CTCACATTCA CTCACCTT-T GACATACTCT -CCAAACAAG TCTGGTGGCC
     ********** ********** ******** * **********  ********* **********
421″ TGATACCTGC CTCACATTCA CTCACCTTAT GACATACTCT ACCAAACAAG TCTGGTGGCC

457’ ACAAGCCTCC GAAAGGCACT GACCGTAATG AAGATGGCGT TTATCAGACC TCAGGACACC
     ********** ********** ********** **********   ******** **********
481″ ACAAGCCTCC GAAAGGCACT GACCGTAATG AAGATGGCGT AAATCAGACC TCAGGACACC

517’ TGTAGTGGCC CTGAATTAAA ACTCGTTATA GCTCCTGAAA TTATCCTGAG TAATACTATT
     ********** ********** ********** ********** ********** *********
541″ TGTAGTGGCC CTGAATTAAA ACTCGTTATA GCTCCTGAAA TTATCCTGAG TAATACTATA

577’ ATATTGCATT TTATGTGGGG TTAGTTCAAA GCATTACCTT ATCGCAAACA TTTAAAATAT
     **** ****  ********** * ******** ***  ***** **********  * *******
601″ ATATAGCATA TTATGTGGGG TCAGTTCAAA GCACAACCTT ATCGCAAACA CTAAAAATAT

637’ ACCACCCAGC CTGGGCAATA CGGCGAGACC CAATCCCTAC AAAAAACACA AAAATTACCT
     ********** *****
661″ ACCACCCAGC CTGGGG
```

1st Nucleotide Sequence

File Name : Reference Seq.gnu

Sequence Size : 5563

2nd Nucleotide Sequence

File Name : RDB7476R.fasta (Complementary)

Sequence Size : 690

Unit Size to Compare = 1

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  Pick up Location     = 1


[93.566% / 544 bp]     INT/OPT.Score : <    668/  1834 >

  721' TCCCACTTAC TTGGAGGGGG CGCTGAGGCA GGAGAATCCC TTTAGCTCAG GAAGTTGAGC

    1"                            AANTN ANNNNNGNGG GCCCGAAGTC CATAAACGAG

  781' CTGCAGTGCG CCGAGATCGA GCCACTGCAC TCCAGCCTGG GTGACAGAGA CCCGGTCTCA

   36" GAGGGGGAGC GAAGAAGAAA AATCCCGGGA GGGGAGGGAG GGGGGGCGGG AGGGCNAATG

  841' AAAATATAAA GTAAAATAAA ATATGCCACC ATTTTTGTAA CCCTGGTTTG TCATTTATTC

   96" AGCAGGATCA GNGGGNAAGA GACCCGGNAA AAAAAAGAAA AAAAGCCACC ANGAACGGGT

  901' ACTTTTCATA TACTCGAAGC CTTAAAACAA GGCCAGTGGA AAGA-CCTCA CTCCACGAAG
            ***.   *   ****    .******* ****** *** **** ***** ***** ****
  156" GCAAATCANC AAACTGAAG- -CNAAAACAA GGCCAG-GGA AAGACCCTCA CTCCA-GAAG

  960' CTTTGGGTGG CGGTTGGCGT GGCTCCTAGA GATGTGATTC TTTCGTGCTA TTTTGTGGGA
       *   .** ** *** *****  ********** **** *****  **** **.*    .*.****
  212" C---NGGGGG CGG-TGGCG- GGCTCCTAGA GATG-GATTC -TTCGGGCNA ---NGNGGGA

 1020' GCAGAAACGG AGGTTAGCCC AGGCCTCGAG AGGGCTGGGG CGGGGCGCGG GCTCTGGCAG
       ********** ********** ********** ********** ********** **********
  262" GCAGAAACGG AGGTTAGCCC AGGCCTCGAG AGGGCTGGGG CGGGGCGCGG GCTCTGGCAG

 1080' GTGCGTCAGT CCGCAGGGGA ACCCGGGGCT CCACCTGGGC GCGGCGAG-G AAGTTACACC
       ********** ********** ********** ********** ******** * **********
  322" GTGCGTCAGT CCGCAGGGGA ACCCGGGGCT CCACCTGGGC GCGGCGAGTG AAGTTACACC

 1139' ATGTATGGGC A-GCTACGTC AGGGGGGCGG GCCCGCAGCC GCCGGGGAAC GCCGAGCCGG
       ********** * ******** ********** ********** ********** **********
  382" ATGTATGGGC AGGCTACGTC AGGGGGGCGG GCCCGCAGCC GCCGGGGAAC GCCGAGCCGG

 1198' GCCCATCCCG GTGAAAAGGC TGCAGCCGGA CTTGGGGAGG CGTCGCCAAG TTCGGGACCG
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      ********** ********** ********** ********** ********** **********
 442″ GCCCATCCCG GTGAAAAGGC TGCAGCCGGA CTTGGGGAGG CGTCGCCAAG TTCGGGACCG

1258' ACGGGCCAAG GCGGCGCGTC TCGGGGGTGG AGCCTGGAGG TGACCGCGCC GC-TGCAACG
      ********** ********** ********** ********** ********** ** *******
 502″ ACGGGCCAAG GCGGCGCGTC TCGGGGGTGG AGCCTGGAGG TGACCGCGCC GCTTGCAACG

1317' CCCCCACCCC CCGCGGTCGC AGTGGTTCAG CCCGAGAACT TTTCATATCA AGATCTGGCC
      ********** ********** ********** ********** *********  **********
 562″ CCCCCACCCC CCGCGGTCGC AGTGGTTCAG CCCGAGAACT TTTCATATCT AGATCTGGCC

1377' TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGG-A AGATGCCAAA
      ********** ********** ********** ********** ******** * ******* **
 622″ TCGGCGGCCA AGCTTGGCAA TCCGGTACTG TTGGTAAAGC CACCATGGTA AGATGCCTAA

1436' AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG ACGGGACCGC CGGCGAGCAG
      *********
 682″ AACATTAAG
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