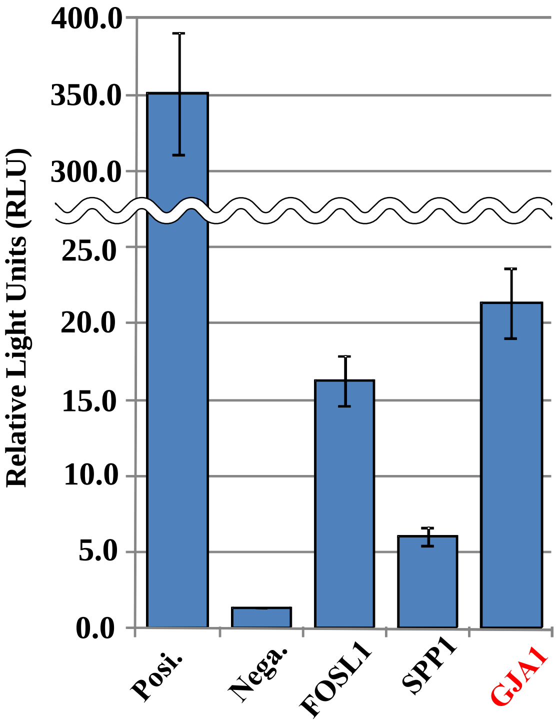
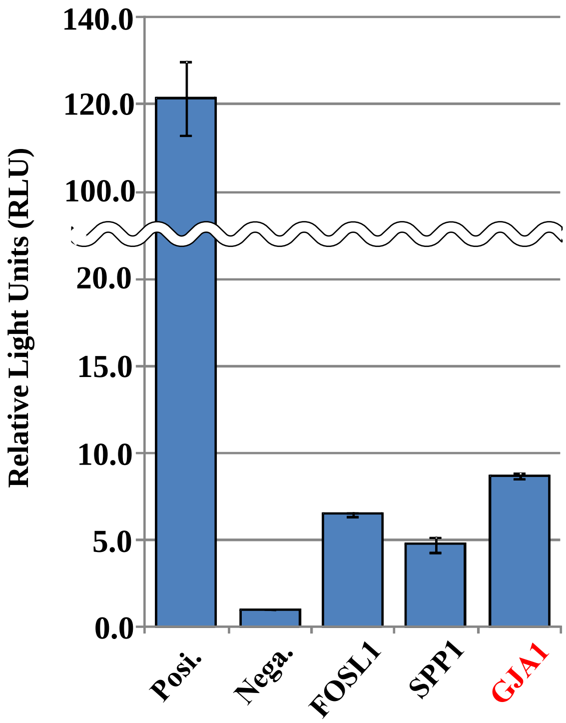
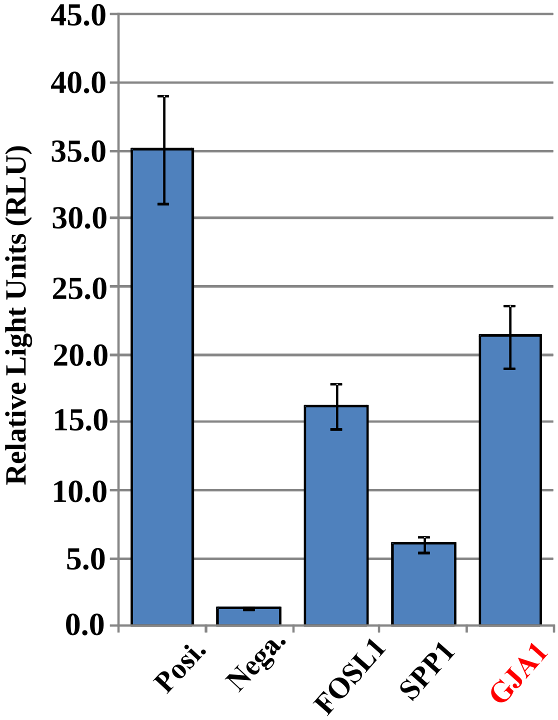
The Promoter Activities of Reporter Constructs


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 : 2009.11.16

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5498

2nd Nucleotide Sequence
  File Name         : RDB7538F.fasta
  Sequence Size     : 733

  Unit Size to Compare = 1
  Pick up Location     = 1
[97.368% / 722 bp]     INT/OPT.Score : <    2488/   2692 >

      1'            GGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG ATGGGAACGG
                    ********* ********** ********** ********** **********
      1" GAACTTTCTC TGGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG ATGGGAACGG

     50' TGTCTACCAG AATATATTTG GCATCCTTCT TTTTTCTGGT ATTTGCCTGA GTGAGAAAAG
         ********** ********** ********** ********** ********** **********
     61" TGTCTACCAG AATATATTTG GCATCCTTCT TTTTTCTGGT ATTTGCCTGA GTGAGAAAAG

    110' TGTTAGGAAT AGGAAGGCCA GATGAGTTTG CTTTCCCTCC AGAGAATACT GGCCAAGAAA
         ********** ********** ********** ********** ********** **********
    121" TGTTAGGAAT AGGAAGGCCA GATGAGTTTG CTTTCCCTCC AGAGAATACT GGCCAAGAAA

    170' TTTCCTGTCC AACCTCAGGA GCATCACTGA AGCCTGTTTA TGAGGAATTG TCCTACCACA
         ********** ********** ********** ********** ********** **********
    181" TTTCCTGTCC AACCTCAGGA GCATCACTGA AGCCTGTTTA TGAGGAATTG TCCTACCACA

    230' ACACTGTGTT ATGGCATTTG GGAAGCCCTC AGAGGAGCTG CCTGCTCTAA GATTGAGGCC
         ********** ********** ********** ********** ********** **********
    241" ACACTGTGTT ATGGCATTTG GGAAGCCCTC AGAGGAGCTG CCTGCTCTAA GATTGAGGCC

    290' ACATGACTCA GGCCATTATA AACCCTAATG CAGAGCCCTG AAGAGGGAGA GCATTTGGAA
         ********** ********** ********** ********** ********** **********
    301" ACATGACTCA GGCCATTATA AACCCTAATG CAGAGCCCTG AAGAGGGAGA GCATTTGGAA
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350' GGGGATAGGG AAGCACATAA AGATGATATG CTCAGCTTTA CTGTCGTTGG GCAGAAAACT
     ********** ********** ********** ********** ********** **********
361″ GGGGATAGGG AAGCACATAA AGATGATATG CTCAGCTTTA CTGTCGTTGG GCAGAAAACT

410' CTCTAGTGGG CTTGAGAGGG GGAACTGATT TTAAGGAGGG CTGAATAGTT TGGGAACCTA
     ********** ********** ********** ********** ********** **********
421″ CTCTAGTGGG CTTGAGAGGG GGAACTGATT TTAAGGAGGG CTGAATAGTT TGGGAACCTA

470' CTTAATGCAA CCATAGTCTG TATTTTTAAA ATCCTCACAT TTCACTACAG ATTTGGGTTT
     ********** ********** ********** ********** ********** **********
481″ CTTAATGCAA CCATAGTCTG TATTTTTAAA ATCCTCACAT TTCACTACAG ATTTGGGTTT

530' TAGTGTCTTG GCATAAATAG GGCCTTAATA TAAATTCTTA GTTTTCTGGA GACATGGTAG
     ********** ********** ********** ********** ********** **********
541″ TAGTGTCTTG GCATAAATAG GGCCTTAATA TAAATTCTTA GTTTTCTGGA GACATGGTAG

590' AGGTCAGATA TCAAGATTTC ATAGGCAAAC AAAACATGCT ATATATGTAA AAAATGTATA
     ********** ********** **********  ********* ******** * **********
601″ AGGTCAGATA TCAAGATTTC ATAGGCAAAC -AAACATGCT ATATATGT-A AAAATGTATA

650' TACACACACA GCCTTTTGCT AAACTGAAAG AAAGTAAAAA TTCAAAGCAG TCAAGGGGTT
     ********** *** ******  ***** ***  ****  ***  ** ****** *** ***
659″ TACACACACA GCC-TTTGCT -AACTG-AAG -AAGT--AAA ATC-AAGCAG TCAGGGGTGA

710' GAAAGATGGA TTGGGTATGG ACTTTTCTTC ATCTATGTCA ATTTTTGAAA TCTCTCTCCC
       * *****   **
712″ AGATGATGGG ATGACTTCTC AA
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Date : 2009.11.06

1st Nucleotide Sequence

File Name : Reference Seq 0.gnu

Sequence Size : 5498

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2nd Nucleotide Sequence
  File Name        : RDB7538R.fasta (Complementary)
  Sequence Size    : 803

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.328% / 817 bp]     INT/OPT.Score : <   2772/  2932 >

    541' CATAAATAGG GCCTTAATAT AAATTCTTAG TTTTCTGGAG ACATGGTAGA GGTCAGATAT
                                **** **     **    **  **    ****  **** ** **
      1"                    CC TAATTATTCT AGTTTCTGAA AC--TGTAG- GGTC-GA-AT

    601' CAAGATTTCA TAGGCAAACA AAACATGCTA TATATGTAAA AAATGTATAT ACACACACAG
         * ** .**** ** ** .**  ******** * ******* ** ***** ** * **********
     38" C-AG-NTTCA TA-GC-NACC AAACATGC-A TATATGT-AA AAATG-AT-T ACACACACAG

    661' CCTTTTGCTA AACTGAAAGA AAGTAAAAAT TCAAAGCAGT CAAGGGGTTG AAAGATGGAT
         ** ******  ***** **** **** ***** ********** ********** **********
     90" CC-TTTGCT- AACTG-AAGA AAGT-AAAAT TCAAAGCAGT CAAGGGGTTG AAAGATGGAT

    721' TGGGTATGGA CTTTTCTTCA TCTATGTCAA TTTTTGAAAT CTCTCTCCCA TCTCCACCAT
         ********** ********** ********** ********** ********** **********
    146" TGGGTATGGA CTTTTCTTCA TCTATGTCAA TTTTTGAAAT CTCTCTCCCA TCTCCACCAT

    781' TCCCTTTGTT AATTGTCCTT GCTTACATTT AAAGGAAGGG AATTAGATCA TCAAACAGGT
         ********** ********** ********** ********** ********** **********
    206" TCCCTTTGTT AATTGTCCTT GCTTACATTT AAAGGAAGGG AATTAGATCA TCAAACAGGT

    841' CACTCACACC TACCTCTAAC TTCACACACC TTGGTCAATG TGAAACAAGC TTGAACTGGT
         ********** ********** ********** ********** ********** **********
    266" CACTCACACC TACCTCTAAC TTCACACACC TTGGTCAATG TGAAACAAGC TTGAACTGGT

    901' TATATGCTTC CCCACCATTT TTATTTATTG TAAGCTACTT TAAAAATTTT AGACAATGTT
         ********** ********** ********** ********** ********** **********
    326" TATATGCTTC CCCACCATTT TTATTTATTG TAAGCTACTT TAAAAATTTT AGACAATGTT
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 961’ GTAATAAAAA TATACACCTT TTTCCCCCAT TATCCCTGGT CTTCTGGTGA AGCAAGCAGT
      ********** ********** ********** ********** ********** **********
 386″ GTAATAAAAA TATACACCTT TTTCCCCCAT TATCCCTGGT CTTCTGGTGA AGCAAGCAGT

1021’ GTAATCAATG ATTCTTATGT GTGAGGAGCA ACTCCAAGTA GAGGCGTTCA TGTCCCTAAT
      ********** ********** ********** ********** ********** **********
 446″ GTAATCAATG ATTCTTATGT GTGAGGAGCA ACTCCAAGTA GAGGCGTTCA TGTCCCTAAT

1081’ GCTTTTTTAT TTTTCCTCAT CAGCAAATTT AAACTACAAC TTTATCCTGA TCCCACTGCT
      ********** ********** ********** ********** ********** **********
 506″ GCTTTTTTAT TTTTCCTCAT CAGCAAATTT AAACTACAAC TTTATCCTGA TCCCACTGCT

1141’ GCTCTTTGCC TCTTCTCCCC CCAGCCCTTC CACATTTACC AGCCTCCTCC CTACCTCCTC
      ********** ********** ********** ********** ********** **********
 566″ GCTCTTTGCC TCTTCTCCCC CCAGCCCTTC CACATTTACC AGCCTCCTCC CTACCTCCTC

1201’ CCAGCCTTTC CCTTTGCCCT CCCCTTTCTT CTAGCCCCTC CTCCCAGTTG AGTCAGTGGC
      ********** ********** ********** ********** ********** **********
 626″ CCAGCCTTTC CCTTTGCCCT CCCCTTTCTT CTAGCCCCTC CTCCCAGTTG AGTCAGTGGC

1261’ TTGAAACTTT TAAAAGCTCT GTGCTCCAAG TTACAAAATC AAGATCTGGC CTCGGCGGCC
      ********** ********** ********** ********** ********** **********
 686″ TTGAAACTTT TAAAAGCTCT GTGCTCCAAG TTACAAAATC AAGATCTGGC CTCGGCGGCC

1321’ AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA
      ********** ********** ********** ********** ********** ********
 746″ AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAA
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