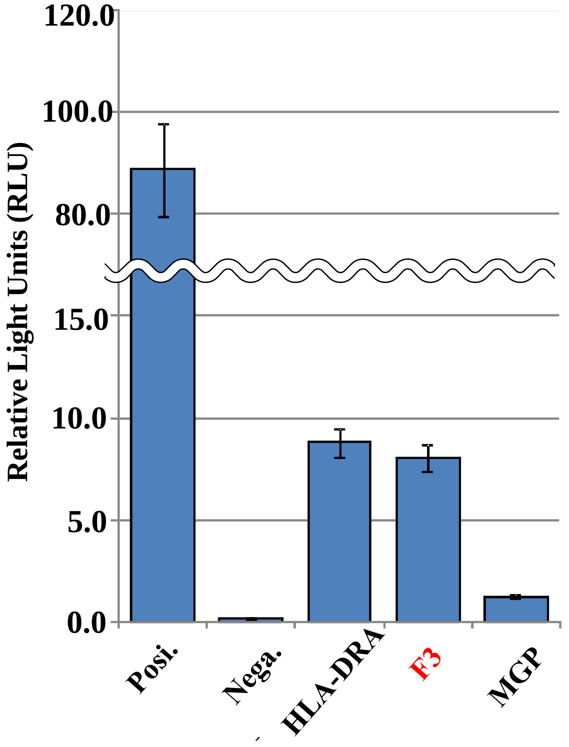
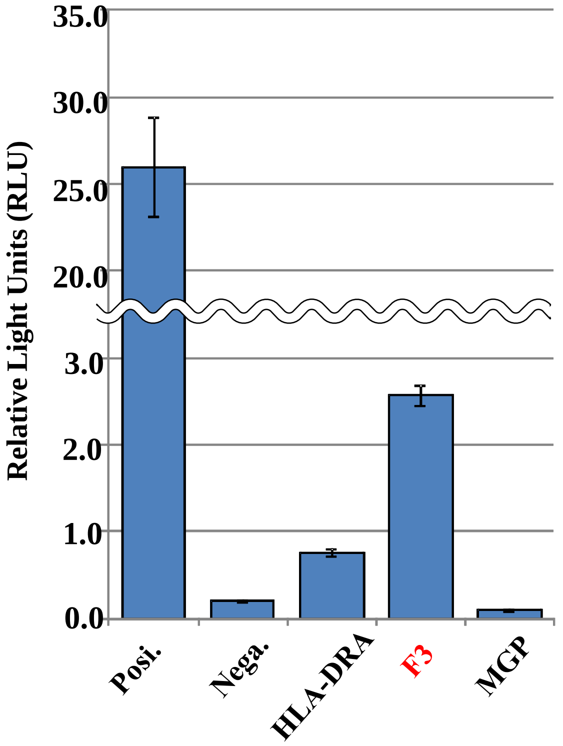
The Promoter Activities of Reporter Constructs

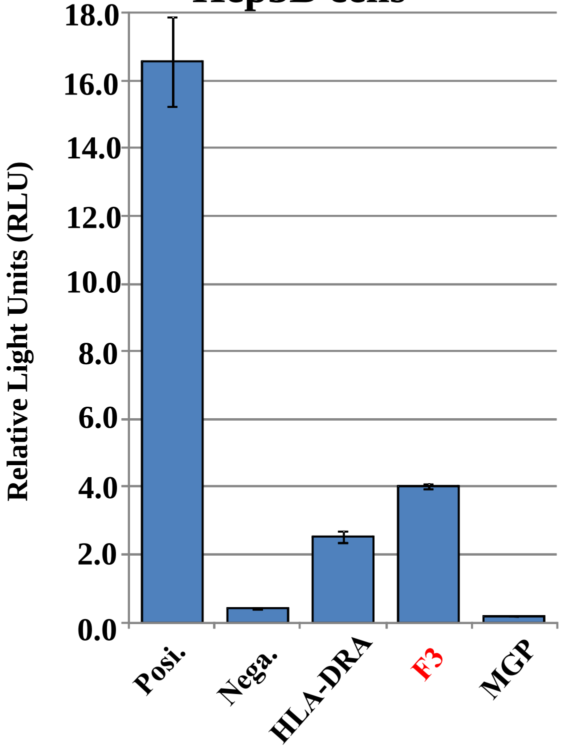
HeLa cells



HepG2 cells



Hep3B cells



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

HLA-DRA: pGL4-phHLA-DRA(RDB# 7389)
F3: pGL4-phF3 (RDB# 7458)
MGP: pGL4-phMGP (RDB# 7394)

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      : 5500

2nd Nucleotide Sequence
  File Name          : RDB7458F.fasta
  Sequence Size      : 633

  Unit Size to Compare = 1
  Pick up Location     = 1

[99.514% / 617 bp]     INT/OPT.Score : <   2164/   2440 >

    1'                    GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATAA
                          *** ********** ********** ********** **********
    1" GGTGCCGAAC TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATAA

   44' TTCTCCAGTC GTGTCTTGCA GGCAATATAG AGTAATAATA ATAAAAATGA CAGGAGATAC
       ********** ********** ********** ********** ********** **********
   61" TTCTCCAGTC GTGTCTTGCA GGCAATATAG AGTAATAATA ATAAAAATGA CAGGAGATAC

  104' TTTGACAGGA TGGCTTAAAA TGCCACTCAA TAGATGAAGA GTTGTTCTCA TGCTTGGCAA
       ********** ********** ********** ********** ********** **********
  121" TTTGACAGGA TGGCTTAAAA TGCCACTCAA TAGATGAAGA GTTGTTCTCA TGCTTGGCAA

  164' GTTTACAGCA AAGCCCAGAA GGAGAAGCCA GAAAATAATT TAGAAAAACC AAAGCTTAAA
       ********** ********** ********** ********** ********** **********
  181" GTTTACAGCA AAGCCCAGAA GGAGAAGCCA GAAAATAATT TAGAAAAACC AAAGCTTAAA

  224' ACTAGTGGCA CACAACTCTG GTTACATTTT TCATTTTCAT TTTTGGTTCC TCTGCATTTC
       ********** ********** ********** ********** ********** **********
  241" ACTAGTGGCA CACAACTCTG GTTACATTTT TCATTTTCAT TTTTGGTTCC TCTGCATTTC

  284' GGTGGAACTC AGTCCCACAG ATGTCTTCTT CAATGTGGGA ACCATCCTTT CTGGAACCAC
       ********** ********** ********** ********** ********** **********
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   301″ GGTGGAACTC AGTCCCACAG ATGTCTTCTT CAATGTGGGA ACCATCCTTT CTGGAACCAC

   344’ AGAGCTGCAG ATGTCACGCT GGAATTCTCC CAGAGGCAAA CTGCCAGATG TGAGGCTGCT
        ********** ********** ********** ********** ********** **********
   361″ AGAGCTGCAG ATGTCACGCT GGAATTCTCC CAGAGGCAAA CTGCCAGATG TGAGGCTGCT

   404’ CTTCCTCAGT CACTATCTCT GGTCGTACCG GGCGATGCCT GAGCCAACTG ACCCTCAGAC
        ********** ********** ********** ********** ********** **********
   421″ CTTCCTCAGT CACTATCTCT GGTCGTACCG GGCGATGCCT GAGCCAACTG ACCCTCAGAC

   464’ CTGTGAGCCG AGCCGGTCAC ACCGTGGCTG ACACCGGCAT TCCCACCGCC TTTCTCCTGT
        ********** ********** ********** ********** ********** **********
   481″ CTGTGAGCCG AGCCGGTCAC ACCGTGGCTG ACACCGGCAT TCCCACCGCC TTTCTCCTGT

   524’ GCGACCCGCT AAGGGCCCCG CGAGGTGGGC AGGCCAGGTA TTCTTGACCT TCGTGGGGTA
        ********** ***** **** ********** ********** ********** **********
   541″ GCGACCCGCT AAGGG-CCCG CGAGGTGGGC AGGCCAGGTA TTCTTGACCT TCGTGGGGTA

   584’ GAAGAAGCCA CCGTGGCTGG GAGAGGGCCC TGCTCACAGC CACACGTTTA CTTCGCTGCA
        ********** ********** **** ** ** ****
   600″ GAAGAAGCCA CCGTGGCTGG GAGAAGGGCC TGCT
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5500

2nd Nucleotide Sequence
  File Name         : RDB7458R.fasta (Complementary)
  Sequence Size     : 680

  Unit Size to Compare = 1
  Pick up Location     = 1

[98.824% / 680 bp]     INT/OPT.Score : <   2156/  2632 >
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  661' CCAGGTGGGC AAAGCATCCG GGAAATGCCC TCCGCTGCCC GAGGGGAGCC CAGAG-CCCG
                                                     **** ***** ****
    1″                                               AGCC CAGAGCCCCG

  720' TGCTTTCTAT T-AAATGTTG TAAATGCCGC CTC-TCCCAC TTTATCACCA AATGGAAGGG
       ********** * ******** ********** *** ****** ********** **********
   15″ TGCTTTCTAT TAAAATGTTG TAAATGCCGC CTCTTCCCAC TTTATCACCA AATGGAAGGG

  778' AAGAATTCTT CCAAGGCGCC CTCCCTTTCC TGCCATAGAC CTGCAACCCA CCTAAGCTGC
       ********** **********  ********* ********** ********** **********
   75″ AAGAATTCTT CCAAGGCGCC TTCCCTTTCC TGCCATAGAC CTGCAACCCA CCTAAGCTGC

  838' ACGTCGGAGT CGCGGGCCTG GGTGAATCCG GGGGCCTTGG GGGACCCGGG CAACTAGACC
       ********** ********** ********** ********** ********** * ********
  135″ ACGTCGGAGT CGCGGGCCTG GGTGAATCCG GGGGCCTTGG GGGACCCGGG CCACTAGACC

  898' CGCCTGCGTC CTCCAGGGCA GCTCCGCGCT CGGTGGCGCG GTTGAATCAC TGGGGTGAGT
       ********** ********** ********** ********** ********** **********
  195″ CGCCTGCGTC CTCCAGGGCA GCTCCGCGCT CGGTGGCGCG GTTGAATCAC TGGGGTGAGT

  958' CATCCCTTGC AGGGTCCCGG AGTTTCCTAC CGGGAGGAGG CGGGGCAGGG GTGTGGACTC
       ********** ********** ********** ********** ********** **********
  255″ CATCCCTTGC AGGGTCCCGG AGTTTCCTAC CGGGAGGAGG CGGGGCAGGG GTGTGGACTC

 1018' GCCGGGGGCC GCCCACCGCG ACGGCAAGTG ACCCGGGCCG GGGGCGGGGA GTCGGGAGGA
       ********** ********** ********** ********** ********** **********
  315″ GCCGGGGGCC GCCCACCGCG ACGGCAAGTG ACCCGGGCCG GGGGCGGGGA GTCGGGAGGA

 1078' GCGGCGGGGG CGGGCGCCGG GGGCGGGCAG AGGCGCGGGA GAGCGCGCCG CCGGCCCTTT
       ********** ********** ********** ********** ********** **********
  375″ GCGGCGGGGG CGGGCGCCGG GGGCGGGCAG AGGCGCGGGA GAGCGCGCCG CCGGCCCTTT

 1138' ATAGCGCGCG GGGCACCGGC TCCCCAAGAC TGCGAGCTCC CCGCACCCCC TCGCACTCCC
       ********** ********** ********** ********** ********** **********
  435″ ATAGCGCGCG GGGCACCGGC TCCCCAAGAC TGCGAGCTCC CCGCACCCCC TCGCACTCCC

 1198' TCTGGCCGGC CCAGGGCGCC TTCAGCCCAA CCTCCCCAGC CCCACGGGCG CCACGGAACC
       ********** ********** ********** ********** ********** **********
  495″ TCTGGCCGGC CCAGGGCGCC TTCAGCCCAA CCTCCCCAGC CCCACGGGCG CCACGGAACC
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1258’ CGCTCGATCT CGCCGCCAAC TGGTAGACAT GGAG-ACCCC TGCATCAAGA TCTGGCCTCG
      ********** ********** ********** **** ***** ********** **********
 555″ CGCTCGATCT CGCCGCCAAC TGGTAGACAT GGAGCACCCC TGCATCAAGA TCTGGCCTCG

1317’ GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAAAACA
      ********** ********** ********** ********** ******* ** ****** ***
 615″ GCGGCCAAGC TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAACAT GCCAAACACA

1377’ TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC GAGCAGCTGC
      ******
 675″ TTAAGA
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