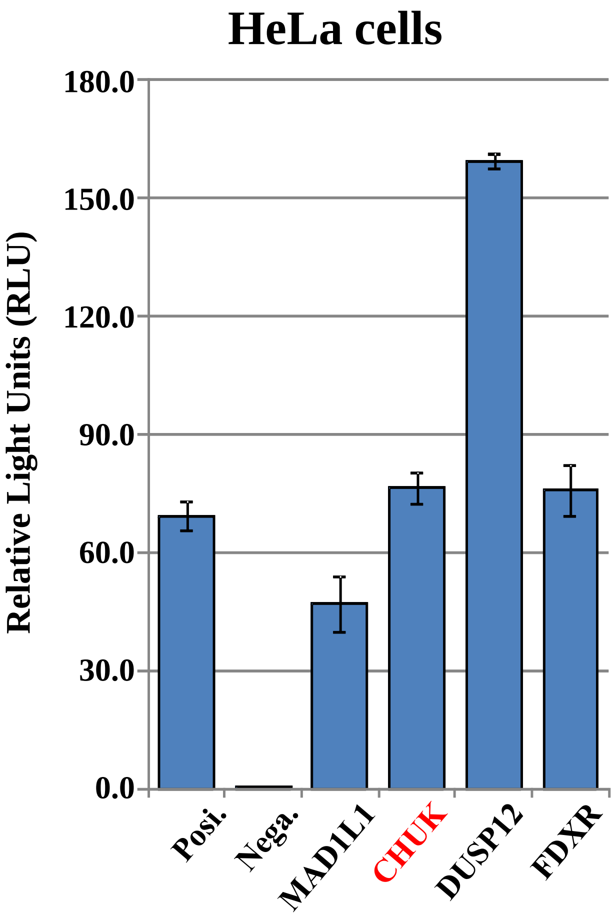
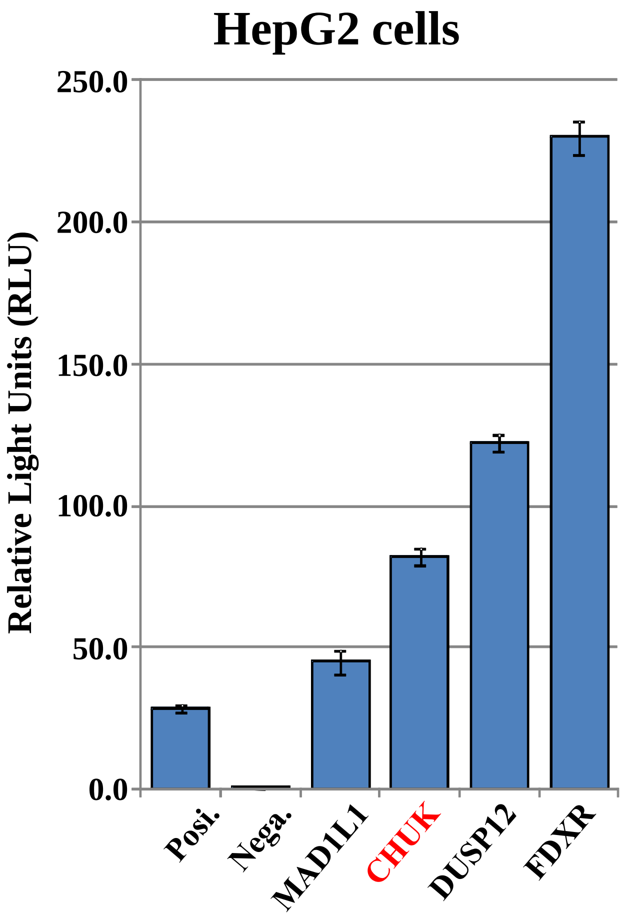
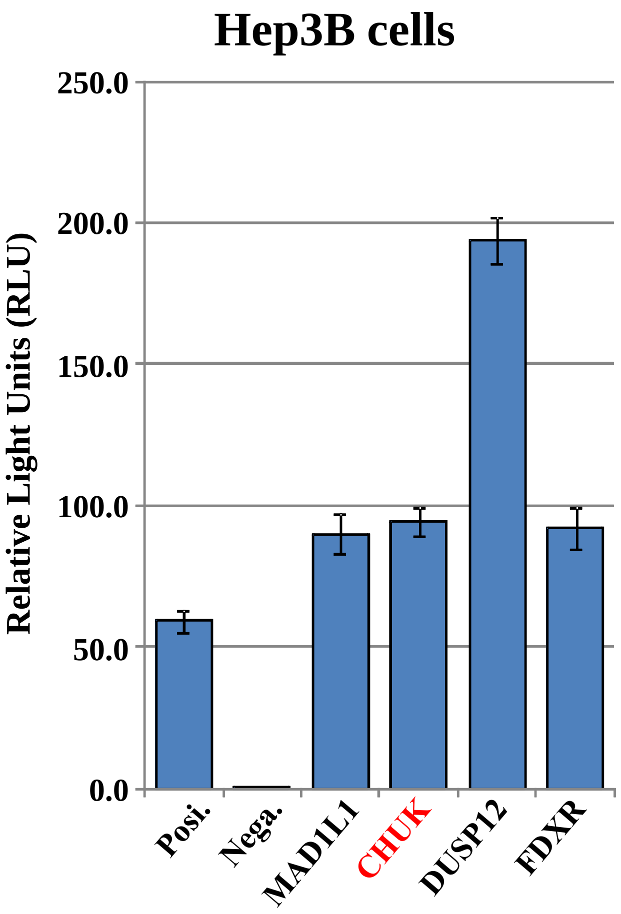
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

MAD1L1: pGL4-phMAD1L1 (RDB# 7374)
CHUK: pGL4-phCHUK (RDB# 7383)
DUSP12: pGL4-phDUSP2 (RDB# 7384)
FDXR: pGL4-phFDXR (RDB#7385)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.04.24

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5557

2nd Nucleotide Sequence
  File Name        : RDB7383F.fasta
  Sequence Size    : 591

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.127% / 573 bp]     INT/OPT.Score : <   1910/  2222 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                           ** ********** ********** ********** **********
     1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

    43' CATGGAAACC ATGCACTTAC AGAAACCAGA ACCTCCCATA CCACATGTTA CTAATGACCT
        ********** ********** ********** ********** ********** **********
    61″ CATGGAAACC ATGCACTTAC AGAAACCAGA ACCTCCCATA CCACATGTTA CTAATGACCT

   103' ACAACATCGA CTTCGTCTGT ATCATGCAGT GCTCAACATT CTGGTTGCAG CATCACATTT
        ********** ********** ********** ********** ********** **********
   121″ ACAACATCGA CTTCGTCTGT ATCATGCAGT GCTCAACATT CTGGTTGCAG CATCACATTT

   163' ATCAATAATT TGATTCCATG CTGATTCCTT TACTTGGAGT ATTGAGATCC CCCAGGTACA
        ********** ********** ********** ********** ********** **********
   181″ ATCAATAATT TGATTCCATG CTGATTCCTT TACTTGGAGT ATTGAGATCC CCCAGGTACA

   223' GTGAAGGTAT GACCCTCTTA AATGGAAGAC CAGGAGTTGT TTCCCCTATG CTATGGCAAT
        ********** ********** ********** ********** ********** **********
   241″ GTGAAGGTAT GACCCTCTTA AATGGAAGAC CAGGAGTTGT TTCCCCTATG CTATGGCAAT
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    283' CCGCCACCCG GAAGCACTTG CTGCACCAAC AGCATTCCCA AAGCTTGCCT CTGCAGCCCT
         ********** ********** ********** ********** ********** **********
    301″ CCGCCACCCG GAAGCACTTG CTGCACCAAC AGCATTCCCA AAGCTTGCCT CTGCAGCCCT

    343' GTAGCACCCA TTAGAAACAC TTCTCACAAT GAACTACTGT GCTGGCAAAC CCATAACTGG
         ********** ********** ********** ********** ********** **********
    361″ GTAGCACCCA TTAGAAACAC TTCTCACAAT GAACTACTGT GCTGGCAAAC CCATAACTGG

    403' ACTGCCGGAC AGCAAGCTCT GTGAGGCATC TAGGAAAAAA GCTCGCGAAA TCCCGAGAAA
         ********** ********** ********** ********** ********** **********
    421″ ACTGCCGGAC AGCAAGCTCT GTGAGGCATC TAGGAAAAAA GCTCGCGAAA TCCCGAGAAA

    463' CACTCTTCAC TCC-GGAATA GCGTCACATT CTTGAGTCAT TTGGGATGAC AGGGGATATC
         ********** *** ****** ********** ********** ********** **********
    481″ CACTCTTCAC TCCGGGAATA GCGTCACATT CTTGAGTCAT TTGGGATGAC AGGGGATATC

    522' CT-GGAGCAG GTGTATT-GG GAAGTCAGTG AACAAGAAGG CT-AATTCAT TAGTGGGCCT
         ** ******  ******* ** ********** ********** ** ******* *
    541″ CTGGGAGCAA GTGTATTGGG GAAGTCAGTG AACAAGAAGG CTAAATTCAT T




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5557

2nd Nucleotide Sequence
  File Name        : RDB7383R.fasta (Complementary)
  Sequence Size    : 689

  Unit Size to Compare = 1
  Pick up Location     = 1

[97.281% / 662 bp]     INT/OPT.Score : <   2286/  2416 >

    721' AAGTTTAGAA AAGACTAATT GCTGGACGCG GTGGCTCATG TCTATAATCC CAGCACTCTG
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   1″                                          CC CCCAGGCAAC TTCTTGGGAA

 781' GGATGCCAAG GT-GGGAGG- AC-TAC-TTG AG-ACCAGGA -GTTC-GGGA CCA-GCCT-G
           * * * ** ******  ** *** *** ** *******  **** **** *** **.* *
  23″ ATGCCCAAGG GTGGGGAGGA ACTTACTTTG AGAACCAGGA GGTTCGGGGA CCAGGCNTGG

 832' GGC-AACGTA GCAAGA-CCA TGTCTCTA-C AAAAAAT-AA AAAATTAGCC AAGCGAGGTG
      *** *****. ****** *** ******** * ******* ** **** ***** **********
  83″ GGCAAACGTN GCAAGACCCA TGTCTCTACC AAAAAATAAA AAAAATAGCC AAGCGAGGTG

 888' GTGCGCGCCT GCAATCCCAG CTACTCGGGA GGTGAGAAGA TCGCTTAATT CCGGGAGGTC
      ********** ********** ********** ********** ********** **********
 143″ GTGCGCGCCT GCAATCCCAG CTACTCGGGA GGTGAGAAGA TCGCTTAATT CCGGGAGGTC

 948' GAGGCTGCAG TGAGCCGTGA TCGTGCCATT GCACTCCAGC CTGGGCAACG GAGCGAGACC
      ********** ********** ********** ********** ********** **********
 203″ GAGGCTGCAG TGAGCCGTGA TCGTGCCATT GCACTCCAGC CTGGGCAACG GAGCGAGACC

1008' CCATCTTAAT TAAAAAGAAA AAAATACAGG AGAGACTGGG CTGCTTTGAA AAGTGGATTT
      ********** ********** ********** ********** ********** **********
 263″ CCATCTTAAT TAAAAAGAAA AAAATACAGG AGAGACTGGG CTGCTTTGAA AAGTGGATTT

1068' GACGGGAATG TGGGGTTTGG AGAGATCTTA TGTTTTCCAA GACTAGAAAA ACATTGTGGT
      ********** ********** ********** ********** ********** **********
 323″ GACGGGAATG TGGGGTTTGG AGAGATCTTA TGTTTTCCAA GACTAGAAAA ACATTGTGGT

1128' TCCGTTCAGC CCTCCCGGAA AATACGTAGG GGACTTAAAG AGCGGACCGA GTACCTGTTT
      ********** ********** ********** ********** ********** **********
 383″ TCCGTTCAGC CCTCCCGGAA AATACGTAGG GGACTTAAAG AGCGGACCGA GTACCTGTTT

1188' GTTTCCCCAT CCCTTAGCCG GCAGGGCTCT GGCAGCGCCC TGGGAGAACT TAGGGAAGGG
      ********** ********** ********** ********** ********** **********
 443″ GTTTCCCCAT CCCTTAGCCG GCAGGGCTCT GGCAGCGCCC TGGGAGAACT TAGGGAAGGG

1248' CCTTCTCGCA GCGGTTACCG GAAGTGACGC ATTCATTCTC GCGAGAACAA AGACGCGCGA
      ********** ********** ********** ********** ********** **********
 503″ CCTTCTCGCA GCGGTTACCG GAAGTGACGC ATTCATTCTC GCGAGAACAA AGACGCGCGA

1308' GCATCGGCGG CCCGGAACCG GCCTTGGAAC AACTGTGGAA CCTGAGGCCA TCAAGATCTG
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      ********** ********** ********** ********** ********** **********
 563″ GCATCGGCGG CCCGGAACCG GCCTTGGAAC AACTGTGGAA CCTGAGGCCA TCAAGATCTG

1368’ GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA
      ********** ********** ********** ********** ********** **********
 623″ GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA

1428’ AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC GCCGGCGAGC
      *******
 683″ AAAACAT
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