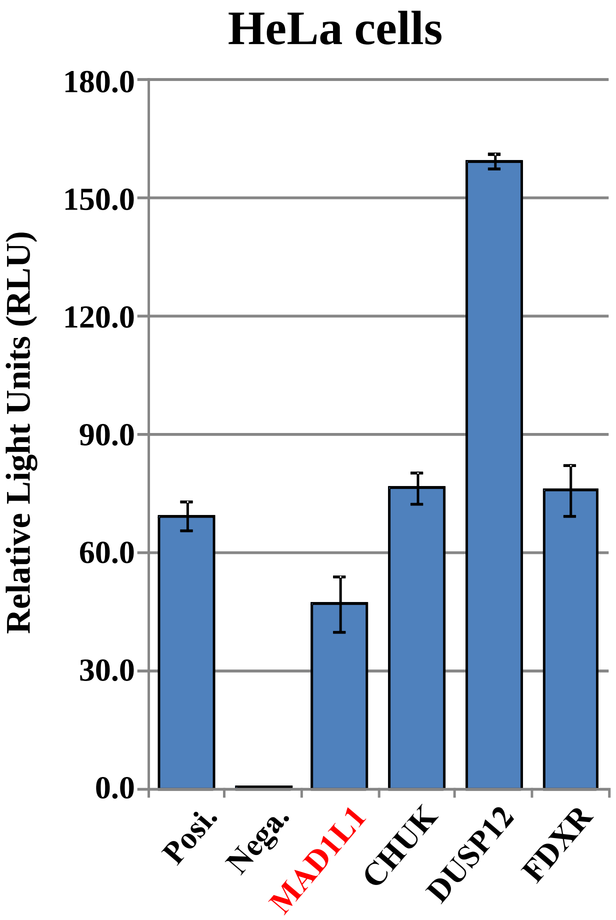
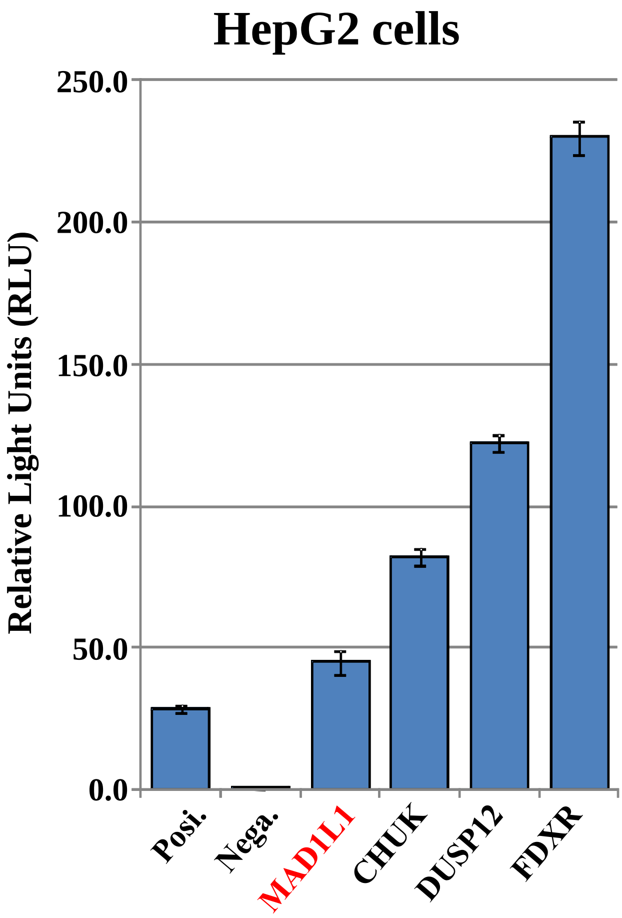
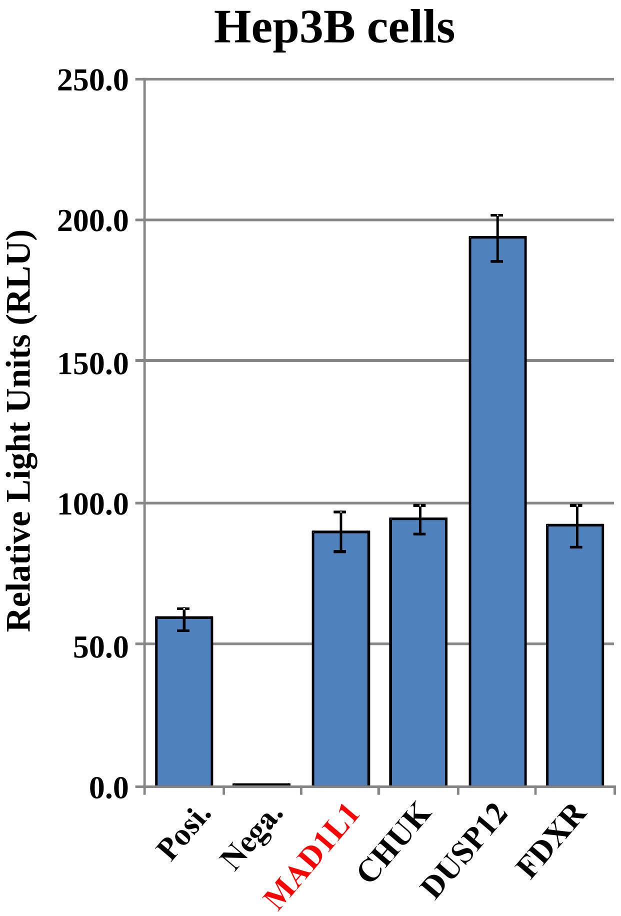
The Promoter Activities of Reporter Constructs







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 : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5621

2nd Nucleotide Sequence
  File Name        : RDB7374F.fasta
  Sequence Size    : 517

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.004% / 502 bp]     INT/OPT.Score : <   1012/  1938 >

   1’                   GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCA
                        *** ********** ********** ********** *********
   1″ GTGCCGAACT TGTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATC-

  44’ AAGCAAGCAG TGATGTGGTG TGTTTATTTT CTTTTACTCA TCTAGGAACT TGACGCAGCT
      **** ***** ********** ********** ********** ********** **********
  60″ AAGC-AGCAG TGATGTGGTG TGTTTATTTT CTTTTACTCA TCTAGGAACT TGACGCAGCT

 104’ TTATA-TTTA ATAAAATAAT AGAGATTGCA TTATTTTAAG GTACTTTCAT GCTTTGAAGT
      ***** **** ********** ********** ********** ********** **********
 119″ TTATATTTTA ATAAAATAAT AGAGATTGCA TTATTTTAAG GTACTTTCAT GCTTTGAAGT

 163’ TTTGTTTTTT TTAAACTGGC TTCCTCAAAG CCATTTCCTG GAGGTGTACT CATCCCTCAA
      ********** ********** ********** ********** ********** **********
 179″ TTTGTTTTTT TTAAACTGGC TTCCTCAAAG CCATTTCCTG GAGGTGTACT CATCCCTCAA

 223’ GAAGAGTTTG TTGACTATGA TTAAATTCCA AGGACCAGTG GGGGAAGTCT GGAAACCCAG
      ********** ********** ********** ********** ********** **********
 239″ GAAGAGTTTG TTGACTATGA TTAAATTCCA AGGACCAGTG GGGGAAGTCT GGAAACCCAG
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283’ GAATCTCCAT CAGGAATCTG GGGCTCTGTC CAGCTCCCCG AAGGAAACTG CGGGTCAGAT
     ********** ********** ********** ********** ********** **********
299″ GAATCTCCAT CAGGAATCTG GGGCTCTGTC CAGCTCCCCG AAGGAAACTG CGGGTCAGAT

343’ GTTTTGA-TT TTTTTTTTTC TTTGAGAAAC AGAATCTCAC TCTGTCACCC AGGCTGGAGT
     ******* ** ********** ********** ********** ********** **********
359″ GTTTTGATTT TTTTTTTTTC TTTGAGAAAC AGAATCTCAC TCTGTCACCC AGGCTGGAGT

402’ GCAGTGAAGT GATCTTGGCT CACTGTAAGC TCCACTTCCC GGGTTCACGC CATTCGGCCT
     ********** ********** ********** ********** *********  **********
419″ GCAGTGAAGT GATCTTGGCT CACTGTAAGC TCCACTTCCC GGGTTCACGA CATTCGGCCT

462’ CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCCATCACCA CGCCCGGCTA TTTTTTTTTT
     ********** ********** ********** *********
479″ CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCCATCACC




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5621

2nd Nucleotide Sequence
  File Name        : RDB7374R.fasta (Complementary)
  Sequence Size    : 815

  Unit Size to Compare = 1
  Pick up Location     = 1



[95.314% / 811 bp]     INT/OPT.Score : <   2632/  2792 >

661’ ATGTTTTGAC TTTTCATTTT ATTTCTGGTT GCAGTCAGGT TGTTAAGTCC AGGGACTCTT
                                                                 ** *
  1″                                                         TATTCTTTG
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 721' GCCCT-ACTC CA--CCTC-- GTTCTC--TT ATT--CCATT TC-ATTCCC- --GGGGCAC-
      ***** **** **  ****     *****  * ***  * *** ** ******     *******
  10″ GCCCTAACTC CACCCCTCGG TTTCTCTTTA ATTCCCAATT TCAATTCCCG GGGGGGCACA

 767' AC--AACTTG GAA-GTC-TT TCTC-TG-AA AG-AAGG-AA AATTC-ATTG CAGA-CCCTT
      **  * ** * *** *** ** **** ** ** ** **** ** ***** ** * **** *****
  70″ ACNAACCTGG GAAGGTCTTT TCTCTTGAAA AGAAAGGAAA AATTCAATGG CAGACCCCTT

 817' AGG-AACAGC ATCTTC-TTA GA-GGGAAGC CA-GGGGCTG GGCAGAGACG GGAGGAGGAG
      *** ****** ****** *** ** ******* ** ******* ********** **********
 130″ AGGAAACAGC ATCTTCTTTA GAGGGGAAGC CAGGGGGCTG GGCAGAGACG GGAGGAGGAG

 873' AGGAAGAGAA TATGGAAACG AGTAAGGCAC ACTCTTCTCA GGAAGGCTCC AATTTGAAGG
      ********** **** ***** ********** ********** ********** **********
 190″ AGGAAGAGAA TATGTAAACG AGTAAGGCAC ACTCTTCTCA GGAAGGCTCC AATTTGAAGG

 933' ATAGACAAAG GTTACCATAA TAATGGTGGG GCCTGACCTC ACCCCATTGG ATGCTGTGCC
      ********** ********** ********** ********** ********** **********
 250″ ATAGACAAAG GTTACCATAA TAATGGTGGG GCCTGACCTC ACCCCATTGG ATGCTGTGCC

 993' CTGGCTTGCA GAGCACTGGG AAGGTAGCCT AGTAGCATAA ATTGCATTTC TAGTGGGCCC
      ********** ********** ********** ********** ****** *** **********
 310″ CTGGCTTGCA GAGCACTGGG AAGGTAGCCT AGTAGCATAA ATTGCACTTC TAGTGGGCCC

1053' AGAAAAAAGC AAAATAACGG ATTGATTCAA GCTGATACTG AGTAGCAAAA TTTTGGGAAG
      ********** ********** ********** ********** ********** **********
 370″ AGAAAAAAGC AAAATAACGG ATTGATTCAA GCTGATACTG AGTAGCAAAA TTTTGGGAAG

1113' AGTCAACGGT GCAAGTTTGT CCGAGGAGGC TGCCGTGGGC GCGGCTATTC CACACATTAC
      ********** ********** ********** ********** ********** **********
 430″ AGTCAACGGT GCAAGTTTGT CCGAGGAGGC TGCCGTGGGC GCGGCTATTC CACACATTAC

1173' GGCGCGAGGC GAAAGCCTTA GTGGAAGCGC GTCCTGCGCA AAGCCGGGGG GCCCCCGACT
      ********** ********** ********** ********** ********** **********
 490″ GGCGCGAGGC GAAAGCCTTA GTGGAAGCGC GTCCTGCGCA AAGCCGGGGG GCCCCCGACT

1233' GCGCCTTGGC TCAGCCTTCG GTTCCGAGTC CTTTCCGTGC GGAGTCTCCC AGGGGTGGCG
      ********** ********** ********** ********** ********** **********
 550″ GCGCCTTGGC TCAGCCTTCG GTTCCGAGTC CTTTCCGTGC GGAGTCTCCC AGGGGTGGCG
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1293’ GCTCCGGGTG CGGACGCGGA GTCCCCAGGA TCAGCCGGTG CGCAGACTCG GTTCTTTACG
      ********** ********** ********** ********** ********** **********
 610″ GCTCCGGGTG CGGACGCGGA GTCCCCAGGA TCAGCCGGTG CGCAGACTCG GTTCTTTACG

1353’ GCCCGATTGC CACGCAGGTC TCGCGAGAGC GCAGGCGCAA GTGTCGCGAT AAATGGGCGC
      ********** ********** ********** ********** ********** **********
 670″ GCCCGATTGC CACGCAGGTC TCGCGAGAGC GCAGGCGCAA GTGTCGCGAT AAATGGGCGC

1413’ CGGCGGAGAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA
      ********** ********** ********** ********** ********** **********
 730″ CGGCGGAGAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA

1473’ GCCACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA
      ********** ********** ******
 790″ GCCACCATGG AAGATGCCAA AAACAT
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