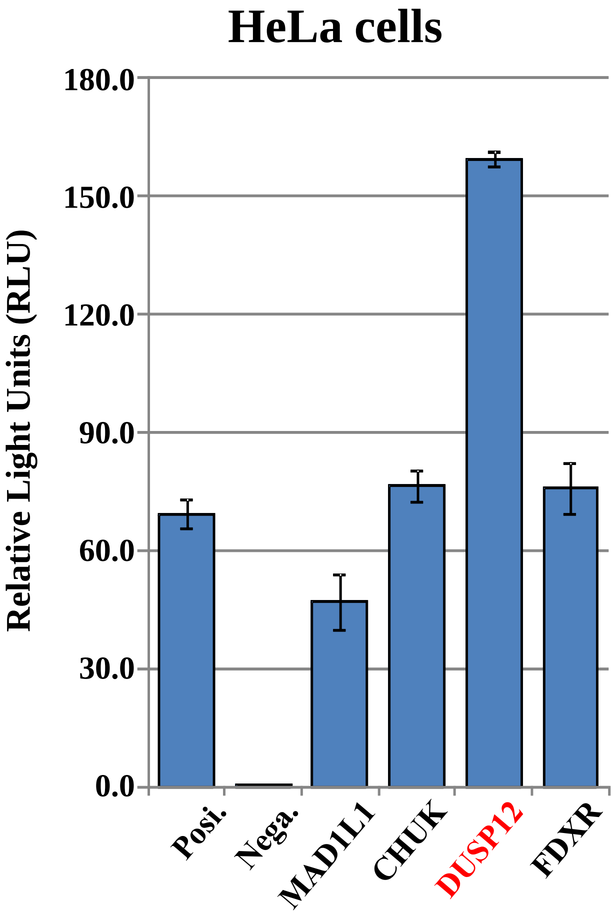
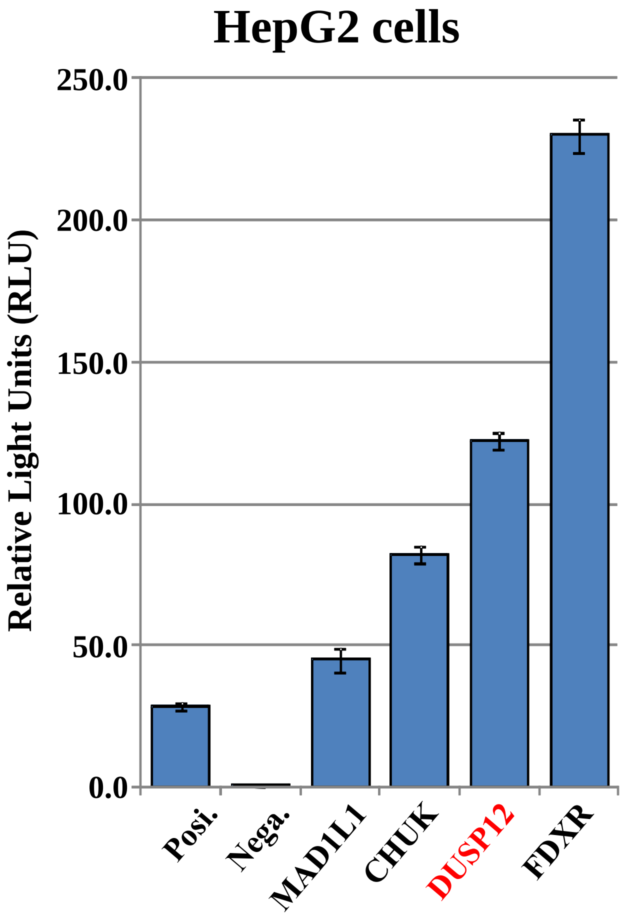
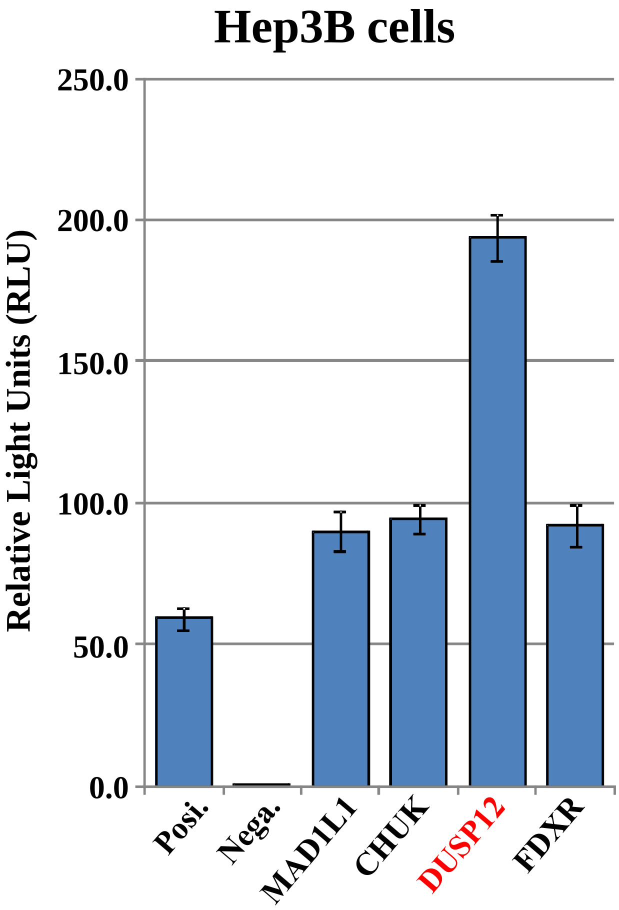
The Promoter Activities of Reporter Constructs







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 : 2009.04.24

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5552

2nd Nucleotide Sequence
  File Name        : RDB7384F.fasta
  Sequence Size    : 634

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 615 bp]     INT/OPT.Score : <   2460/  2460 >

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

    43’ TGGGCTGGTG ACATGGGTGG TAGGAAGAAT TTACCAACAC AGTTGTAGGT AAAGAAAGGC
        ********** ********** ********** ********** ********** **********
    61″ TGGGCTGGTG ACATGGGTGG TAGGAAGAAT TTACCAACAC AGTTGTAGGT AAAGAAAGGC

   103’ AGGTTTATTA GATAAAGTAT GAAAATACAT TGCAAGGGTG CAACAGGCAG GTCAGCAAGA
        ********** ********** ********** ********** ********** **********
   121″ AGGTTTATTA GATAAAGTAT GAAAATACAT TGCAAGGGTG CAACAGGCAG GTCAGCAAGA

   163’ GAGAAGCTGA CTGCTAGGAA ACAAAGGCTT GCTGGGGATT TTGTAGAATG GTGCTTATGT
        ********** ********** ********** ********** ********** **********
   181″ GAGAAGCTGA CTGCTAGGAA ACAAAGGCTT GCTGGGGATT TTGTAGAATG GTGCTTATGT

   223’ TGTGGGTGGA AGAGGGCTTT GTGCAGTACT AATAATGCCA GGGTTGCAGT GAACTAACTT
        ********** ********** ********** ********** ********** **********
   241″ TGTGGGTGGA AGAGGGCTTT GTGCAGTACT AATAATGCCA GGGTTGCAGT GAACTAACTT
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283’ CCATTTTTCT ATCAGCTGAG GGTCTGGTGA TGGCTGGGCA CAGGCAGATT GTGAGTTATT
     ********** ********** ********** ********** ********** **********
301″ CCATTTTTCT ATCAGCTGAG GGTCTGGTGA TGGCTGGGCA CAGGCAGATT GTGAGTTATT

343’ TGCACAGCAG GGCTATGTGT CCTGGACCAC GAAGAAAGGC AGACTTATGG CTTGTCTGCT
     ********** ********** ********** ********** ********** **********
361″ TGCACAGCAG GGCTATGTGT CCTGGACCAC GAAGAAAGGC AGACTTATGG CTTGTCTGCT

403’ TTCTCCTTTT GCTTCCCTTC GTCCAGCCAG CCTGACTCCT TTTCCCTAAT TAGGACTCCA
     ********** ********** ********** ********** ********** **********
421″ TTCTCCTTTT GCTTCCCTTC GTCCAGCCAG CCTGACTCCT TTTCCCTAAT TAGGACTCCA

463’ CACGCAAGGG TTTGTTCTGT TCCAGAATAG AGACACGTCG ATGTATCTAT CTTTATACCA
     ********** ********** ********** ********** ********** **********
481″ CACGCAAGGG TTTGTTCTGT TCCAGAATAG AGACACGTCG ATGTATCTAT CTTTATACCA

523’ GTACTATAGC TGCTACTTCT TGACCAATTA CAGCTTTAGT ATCTCTCTCA CCTGTCCTCC
     ********** ********** ********** ********** ********** **********
541″ GTACTATAGC TGCTACTTCT TGACCAATTA CAGCTTTAGT ATCTCTCTCA CCTGTCCTCC

583’ CTATACAAAA GATATATAAA ATATACTCAC TGTACTGAGT ATCTTCCTGC AGCATTCAGT
     ********** ********** ********** ***
601″ CTATACAAAA GATATATAAA ATATACTCAC TGTT
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5552

2nd Nucleotide Sequence
  File Name        : RDB7384R.fasta (Complementary)
  Sequence Size    : 638

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[97.806% / 638 bp]     INT/OPT.Score : <   2134/  2396 >

  781' CTTGCTTAAT TAAAGTTGGT TTCTTGTAGT CCTGG--CCG GAGG-ACA-T TGACTTAC-A
                           * **  *    * *****  *** **** *** * ******** *
    1″                     T TTTGTAGGTT CCTGGCCCCG GAGGAACATT TGACTTACAA

  836' AAAATATAGG ATTAGTATCT TC-AAAATAA ATAGACAGTA AACATC-AAC AAGGATTCAC
       ********** ********** ** ******* ********** ****** *** **********
   42″ AAAATATAGG ATTAGTATCT TCAAAAATAA ATAGACAGTA AACATCAAAC AAGGATTCAC

  894' ACCCC-AATA ATGAAATTGG GCAGAAAAAG GAAAAATAAT CATGAAATGC ACAGTAAAGA
       ***** **** ********** ********** ********** ********** **********
  102″ ACCCCAAATA ATGAAATTGG GCAGAAAAAG GAAAAATAAT CATGAAATGC ACAGTAAAGA

  953' TGGCTCCATA ATATTGAAAA AAATTTTACT TCAAATGCAT AAAATGATGC TTCTGATTCA
       ********** ********** ********** ********** ********** **********
  162″ TGGCTCCATA ATATTGAAAA AAATTTTACT TCAAATGCAT AAAATGATGC TTCTGATTCA

 1013' GCTGGTGCGA CATTTATTTC ACATTTGAGT TCAGCTGCTC CTGATGTCTC TTTCCTGAAA
       ********** ********** ********** ********** ********** **********
  222″ GCTGGTGCGA CATTTATTTC ACATTTGAGT TCAGCTGCTC CTGATGTCTC TTTCCTGAAA

 1073' ATTTCAATAC TAAGAGCTCG AGAAACCCTG TATTTGGGGA AGCTTATCCT TCACCATCAA
       ********** ********** ********** ********** ********** **********
  282″ ATTTCAATAC TAAGAGCTCG AGAAACCCTG TATTTGGGGA AGCTTATCCT TCACCATCAA

 1133' CTTTGGGGGT AGGGGTCAGA GGGAACAAGG GTGGAAAGGC CGCGCTGAAT GGGGCCGAAG
       ********** ********** ********** ********** ********** **********
  342″ CTTTGGGGGT AGGGGTCAGA GGGAACAAGG GTGGAAAGGC CGCGCTGAAT GGGGCCGAAG

 1193' CTCCGCCCCT CAGCGATAAG TCCAGATTCC TGCGGCCGAC GTGGTCCTCC GAGGGAGCAG
       ********** ********** ********** ********** ********** **********
  402″ CTCCGCCCCT CAGCGATAAG TCCAGATTCC TGCGGCCGAC GTGGTCCTCC GAGGGAGCAG

 1253' CAGAGCCGCC GAGGCTGGCG AGTCCCAGGG GAAGGATGTT CTAGCCGGAG TCTACTCGAT
       ********** ********** ********** ********** ********** **********
  462″ CAGAGCCGCC GAGGCTGGCG AGTCCCAGGG GAAGGATGTT CTAGCCGGAG TCTACTCGAT
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1313' GGTAGGGCAG GAAGCCGCCT TGTCTCTGGG CGCGGCCATA TCAAGATCTG GCCTCGGCGG
      ********** ********** ********** ********** ********** **********
 522″ GGTAGGGCAG GAAGCCGCCT TGTCTCTGGG CGCGGCCATA TCAAGATCTG GCCTCGGCGG

1373' CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA
      ********** ********** ********** ********** ********** *******
 582″ CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACAT
```