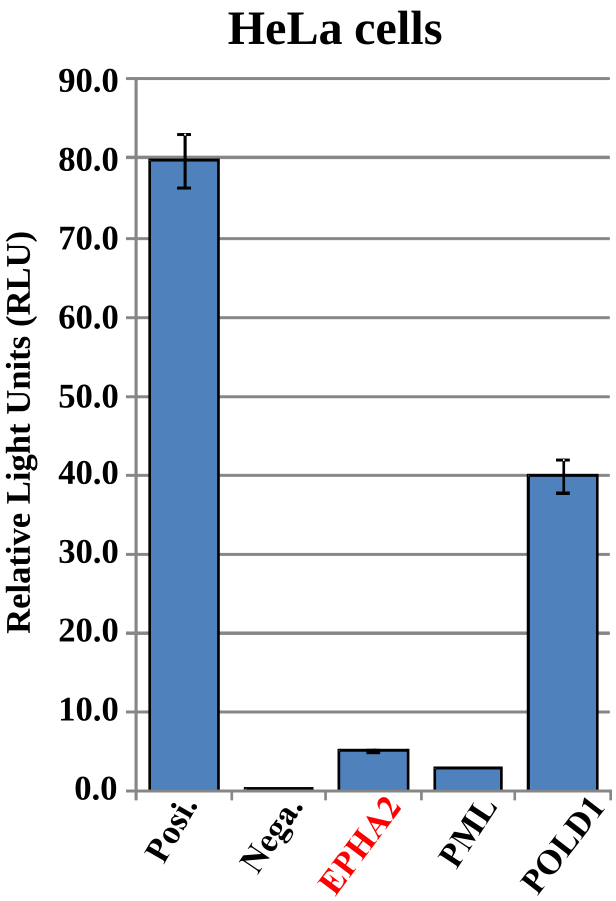
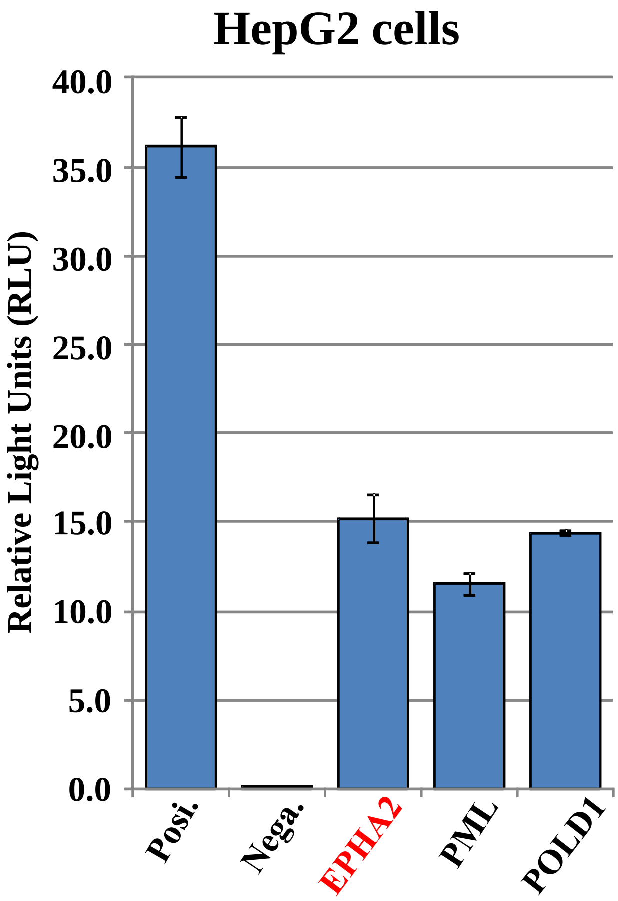
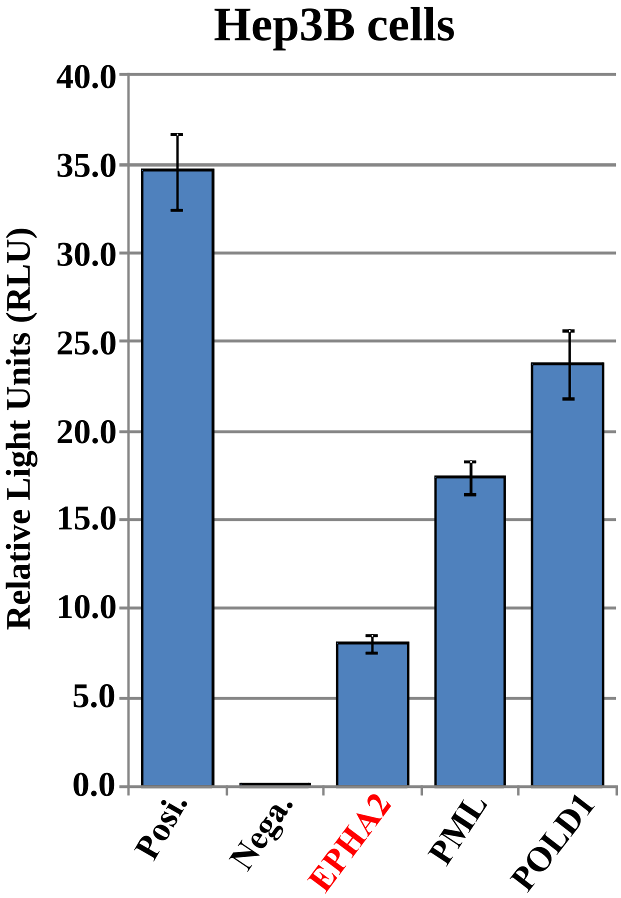

HeLa cells


HepG2 cells


Hep3B cells

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

EPHA2: pGL4-phEPHA2 (RDB# 7342)
PML: pGL4-phPML (RDB# 7343)
POLD1: pGL4-phPOLD1 (RDB# 7344)

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    : 5405

2nd Nucleotide Sequence
  File Name        : RDB7342F.fasta
  Sequence Size    : 510

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.797% / 492 bp]     INT/OPT.Score : <   1768/  1952 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT
                           ** ********** ********** ********** **********
     1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT

    43' GTCCACA-TC CGGCAGAGAA GACCCACGTA CCTGGGTAGC AGGTCCCGGG CATCAAAGCG
        ******* ** ********** ********** ********** ********** **********
    61" GTCCACATTC CGGCAGAGAA GACCCACGTA CCTGGGTAGC AGGTCCCGGG CATCAAAGCG

   102' AGGATGGGGT CAGAGAGGAA GAGGTAGGCA AAGGGAGTCT GGGGCCTCCC AGGAAATCAG
        ********** ********** ********** ********** ********** **********
   121" AGGATGGGGT CAGAGAGGAA GAGGTAGGCA AAGGGAGTCT GGGGCCTCCC AGGAAATCAG

   162' GCCTGCCACA GTTGCTCTTC CTGGACTGGT CAAATGGTGA TTGGCCAACA GGCAGCCGTG
        ********** ********** ********** ********** ********** **********
   181" GCCTGCCACA GTTGCTCTTC CTGGACTGGT CAAATGGTGA TTGGCCAACA GGCAGCCGTG

   222' GGTGGCTGGG CAGGCGGGCC AGAGCAAATT TCCCGTTTGT TTCACTCACA CTAGCCGCTT
        ********** ********** ********** ********** ********** **********
   241" GGTGGCTGGG CAGGCGGGCC AGAGCAAATT TCCCGTTTGT TTCACTCACA CTAGCCGCTT
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    282' CTGTCAGGAA GGGAGATGAG CTCATGTCTG AGGAAGTTTT GTGAAGAGGC CTTATCAAGG
         ********** ********** ********** ********** ********** **********
    301″ CTGTCAGGAA GGGAGATGAG CTCATGTCTG AGGAAGTTTT GTGAAGAGGC CTTATCAAGG

    342' GGCAGGTGGT AGGCAGGTGT CCTCCAAACT GTCAAAACCT ATCAACCCAT GCCAGGGTCG
         ********** ********** ********** ********** ********** **********
    361″ GGCAGGTGGT AGGCAGGTGT CCTCCAAACT GTCAAAACCT ATCAACCCAT GCCAGGGTCG

    402' GGGGCCAGGG GTGCCCCTTG CCCCCTTCCC CAAAAAGAAG CAGTGGTTCA AGCAGAGACC
         ********** ********** ********** ********** ********** **********
    421″ GGGGCCAGGG GTGCCCCTTG CCCCCTTCCC CAAAAAGAAG CAGTGGTTCA AGCAGAGACC

    462' ACCAGGATTC AAATCCTGCT TCTACTACCC GTGAGCTGTG CACCCTTTGG GCATGTTGTT
         ********** ********** **********
    481″ ACCAGGATTC AAATCCTGCT TCTACTACCC




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5405

2nd Nucleotide Sequence
  File Name        : RDB7342R.fasta (Complementary)
  Sequence Size    : 657

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.543% / 657 bp]     INT/OPT.Score : <   2552/  2600 >

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                                           ******** ********** **********
      1″                                   GGAAATGA ACCTATTCTC AGATCATAGT
```

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 661’ AGGCTTATAG GCTTCTGAAC AGAGATACTC TTTTTGACCA TCAGCAGCTT GATATACTCT
      ********** ********** ********** ********** ********** **********
  29″ AGGCTTATAG GCTTCTGAAC AGAGATACTC TTTTTGACCA TCAGCAGCTT GATATACTCT

 721’ TCAAGGGTTT TAGGAAGGAG GGCATCCAGG TCTATTTCTG GGCCACTCTC TCAGGCCTGC
      ********** ********** ********** ********** **********  *********
  89″ TCAAGGGTTT TAGGAAGGAG GGCATCCAGG TCTATTTCTG GGCCACTCTC CCAGGCCTGC

 781’ TGCTTAGGAG GCAACTGCTT ATTGGACCCC CAATCCATTT CAGCTCAGAC CTTCAGGCCA
      ********** ********** ********** ********** ********** **********
 149″ TGCTTAGGAG GCAACTGCTT ATTGGACCCC CAATCCATTT CAGCTCAGAC CTTCAGGCCA

 841’ GCGTTGAGCT CAGTCGCATT GAGCTCAGTC TCAGAGGTGA AGGGCAGAAT GGGTATGGCT
      ********** ********** ********** ********** ********** **********
 209″ GCGTTGAGCT CAGTCGCATT GAGCTCAGTC TCAGAGGTGA AGGGCAGAAT GGGTATGGCT

 901’ CAGCGCAAAA CCATTAAACG TTTCCACCGA GGATACCAGG CTCAGAGATC CCTGGGGGCT
      ********** ********** ********** ********** ********** **********
 269″ CAGCGCAAAA CCATTAAACG TTTCCACCGA GGATACCAGG CTCAGAGATC CCTGGGGGCT

 961’ AATCCGTAGG GGCGCTGGCG CTTTGAGACG CTCAAACTTT GGAAGGCCTG CGGGGAGCCC
      ********** ********** ********** ********** ********** **********
 329″ AATCCGTAGG GGCGCTGGCG CTTTGAGACG CTCAAACTTT GGAAGGCCTG CGGGGAGCCC

1021’ GCGAGTCCAG AGGGCCCCAA GGTCCTCCTC CAAACCCCTC CGGACTTCCC CTCCCTCTCC
      ********** ********** ********** ********** ********** **********
 389″ GCGAGTCCAG AGGGCCCCAA GGTCCTCCTC CAAACCCCTC CGGACTTCCC CTCCCTCTCC

1081’ TCCGGGTGCC AGCCCGGCCC CTTTAAAGAC ATTCCTGAGG GCGGGCGTTG GTGACGTCAC
      ********** ********** ********** ********** ********** **********
 449″ TCCGGGTGCC AGCCCGGCCC CTTTAAAGAC ATTCCTGAGG GCGGGCGTTG GTGACGTCAC

1141’ GCAGGGCATG AATGAACAGG AGTCGGTTCT CACCCAACTT CCATTAAGGA CTCGGGGCAG
      ********** ********** ********** ********** ********** **********
 509″ GCAGGGCATG AATGAACAGG AGTCGGTTCT CACCCAACTT CCATTAAGGA CTCGGGGCAG

1201’ GAGGATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA
      ********** ********** ********** ********** ********** **********
 569″ GAGGATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA
```

```
1261’ CCATGGAA-G ATGCCAAAAA CATTAAGAAG GGCCCAGCGC CATTCTACCC ACTCGAAGAC
      ********   ********** *********
 629″ CCATGGAACA ATGCCAAAAA CATTAAGAA
```