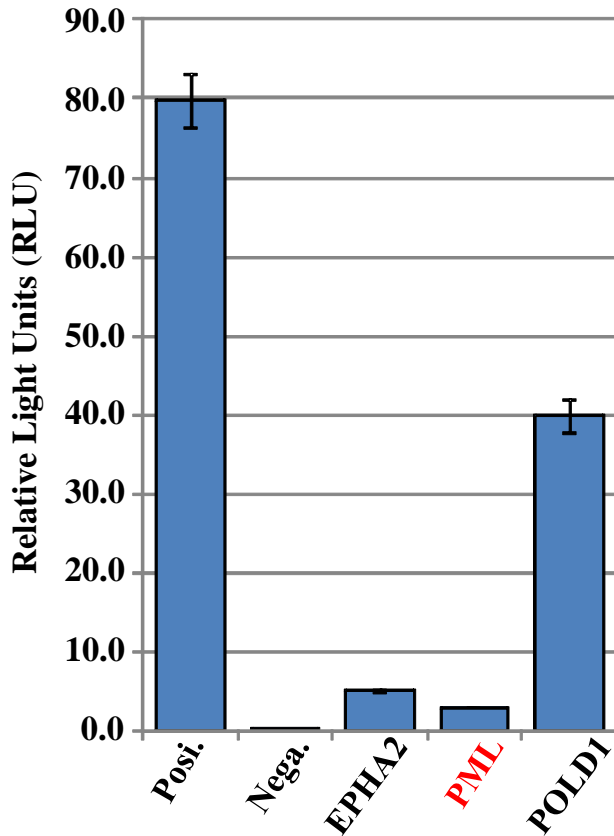
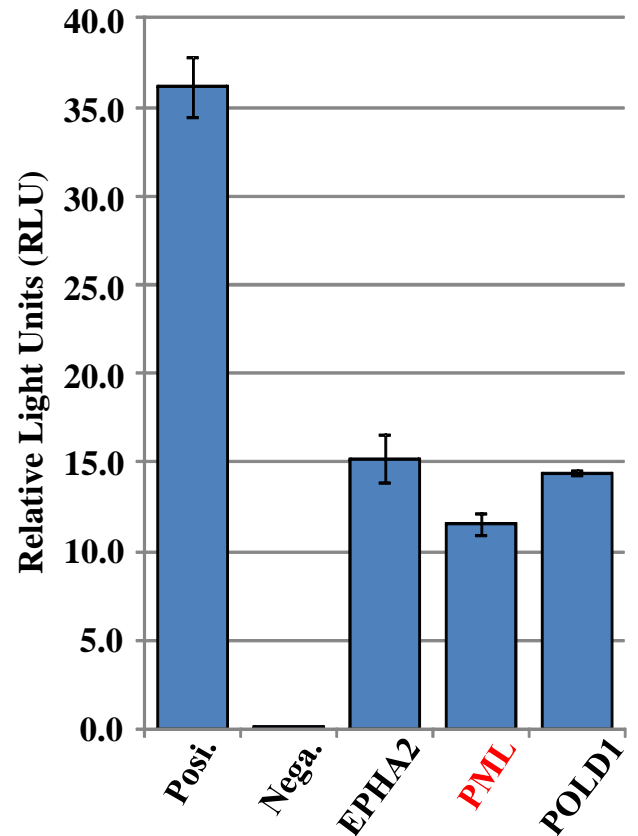


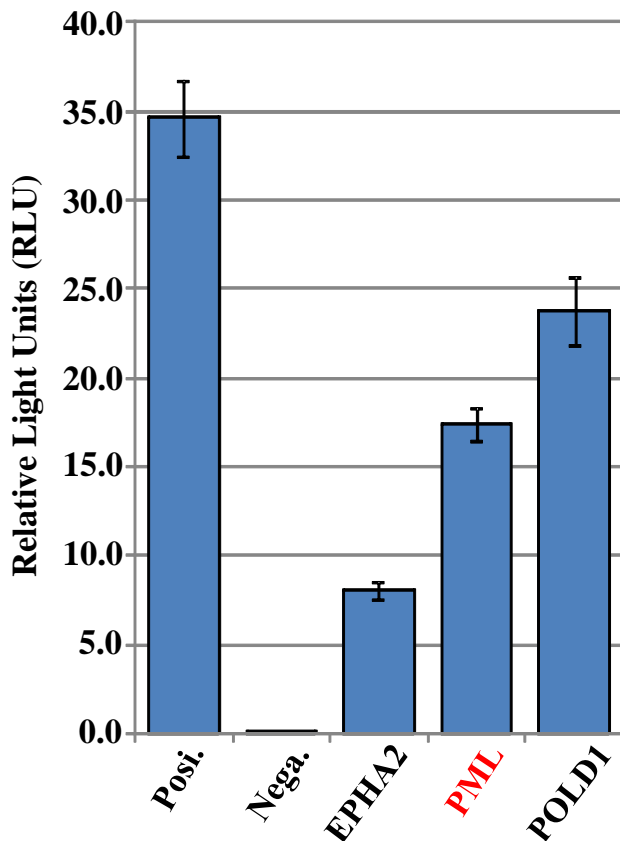
### HeLa cells



### 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)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5547

2nd Nucleotide Sequence

File Name : RDB7343F.fasta  
Sequence Size : 502

Unit Size to Compare = 1  
Pick up Location = 1

[95.148% / 474 bp] INT/OPT. Score : < 1150/ 1642 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC
          ** *****
1'' AGTTGCAGGT GCCAGAACAT TATACTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC

33' CTCGAGGATA TCCTGCCATA GCCCACTTCC AGGTCCCTTG TGCAGATGGC TGCCACCAT
          *****
61'' CTCGAGGATA TCCTGCCATA GCCCACTTCC AGGTCCCTTG TGCAGATGGC TGCCACCAT

93' ATTTGGCTTT CATGGA CTGACTGA TTCTCTAAAG GCCTGGGAGT ACTGACCAGG CTGGAGGGAA
          *****
121'' ATTTGGCTTT CATGGA CTGACTGA TTCTCTAAAG GCCTGGGAGT ACTGACCAGG CTGGAGGGAA

153' GGCAGGCTC CTGAGGCCTT ACAGTCCTA GGAAGTTGCG TATCTGCCA ACCCCTGCTC
          *****
181'' GGCAGGCTC CTGAGGCCTT ACAGTCCTA GGAAGTTGCG TATCTGCCA ACCCCTGCTC

213' TCCACCCTGC AGACTGTAAG GTTTACAAGA GCCAGGCCCT ATCATCATCC TTTCTAGTCT
          ****
241'' TCCACCCTGC AGACTGTAAG GTTTACAAGA GCCAGGCCCT ATCATCATCC TTTCTAGTCT
```



```

273' GTTTCTAAGT TGGAAC-AGA GTACGGAATG GGTACACAGG AGCCAGCACA GTGGTTGCGA
***** **
301" GTTTCTAAGT TGGAACAAGA GTACGGAATG GGTACACAGG AGCCAGCACA GTGGTTGCGA

332' -TGGTTTAAAG TTTGAAGCCG GGGCGCTGAC CCAGTGAGGT CACCTGGAAC TGTGCCCC-T
***** **
361" TTGGTTTAAAG TTTGAAGCCG GGGCGCTGAC CCAGTGAGGT CACCTGGAAC TGTGCCCCCTT

390' TTCCCCTTAC CAGCTGGG-A GTCTG-ACAT GC--TTTTCC A--TTGGCG- -AAG-ACCT-
***** **
421" TTCCCCTTAC CAGCTGGGAA GTCTGAACAT GCTTTTTCCC ATTTGGGCGA AAAGAACCTA

440' AG-CTGGCTC TCCCCTCACC CTCTTCATAC CCGCTCTCCA GCTCTCCCCC TCCCTCCTGC
** **
481" AGCCTGGGCC TCCTCCCCC TT

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5547

2nd Nucleotide Sequence

File Name : RDB7343R. fasta (Complementary)  
Sequence Size : 524

Unit Size to Compare = 1

Pick up Location = 1

[96.935% / 522 bp] INT/OPT. Score : < 1368/ 1852 >

```

901' TACAACCCTA AATCCCTGGT GAATTTCCAC -TGC-TTTTG CA-GGT-CCC AGCTGTGGGC
** **
1" TTTTCCAC TTGCTTTTTG CAGGGTCCCC AGCTGTGGGC

```



957' TCTCCTTTCC -AGAATGTCT CCG-TTTGCA GGCTTGCTCT T-CCATTACA -TC-TACGGC  
 \*\*\*\*\*  
 40" TCTCCTTTCC AAGAATGTCT CCGTTTTGCA GGCTTGCTCT TCCATTACA TTCTTACGGC

1012' TCTTAGAAAG CA-GGGGCTG C-GTGT-GGC TCATCTTTGT ACGCCAGCT CCCGGCAGGA  
 \*\*\*\*\*  
 100" TCTTAGAAAG CAGGGGCTG CCGTGTGGC TCATCTTTGT ACGCCAGCT CCCGGCAGGA

1069' CGTGGCAC-G AAGCAGTGCC AGTGTGAACG GATGAATGGA TCAAAGCCGG GAGCAGGGCT  
 \*\*\*\*\*  
 160" CGTGGCACGG AAGCAGTGCC AGTGTGAACG GATGAATGGA TCAAAGCCGG GAGCAGGGCT

1128' GCCCCCTGC AGCTCTGCC TACCTCTCCC GCTTTACCGT AAGTCAGCGG TAGGTCTGCA  
 \*\*\*\*\*  
 220" GCCCCCTGC AGCTCTGCC TACCTCTCCC GCTTTACCGT AAGTCAGCGG TAGGTCTGCA

1188' GCTCTCGCC TCTACCTCCT CCCGCTCTG GCGGTGTCTT TAAAACCCAC AGTCGGCCTC  
 \*\*\*\*\*  
 280" GCTCTCGCC TCTACCTCCT CCCGCTCTG GCGGTGTCTT TAAAACCCAC AGTCGGCCTC

1248' TCTGCCCCCT AGAACCGCCC CCAGCTTCTG TCTCACTTCC TCTCCAGAGG CGGGCCCTGA  
 \*\*\*\*\*  
 340" TCTGCCCCCT AGAACCGCCC CCAGCTTCTG TCTCACTTCC TCTCCAGAGG CGGGCCCTGA

1308' GCCGGCACCT CCCCTTTCGG ACAGCTCAAG GGA CTGCA TCAAGATCTG GCCTCGGCGG  
 \*\*\*\*\*  
 400" GCCGGCACCT CCCCTTTCGG ACAGCTCAAG GGA CTGCA TCAAGATCTG GCCTCGGCGG

1368' CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATG-CC AAAACATTA  
 \*\*\*\*\*  
 460" CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGTC AAAACACTA

1427' AGAAGGGCCC AGCGCCATTC TACCACTCG AAGACGGGAC CGCCGGCGAG CAGCTGCACA  
 \*\*\*\*\*  
 520" AGAAG