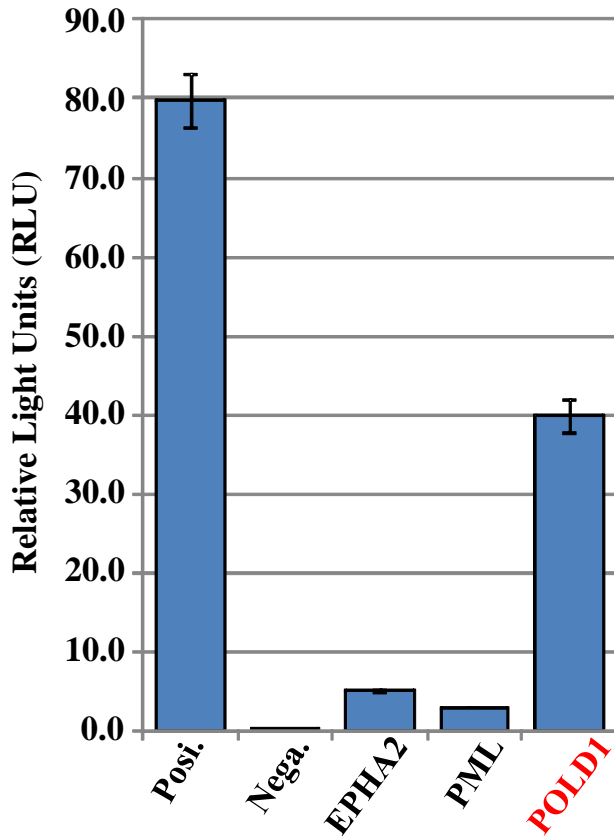
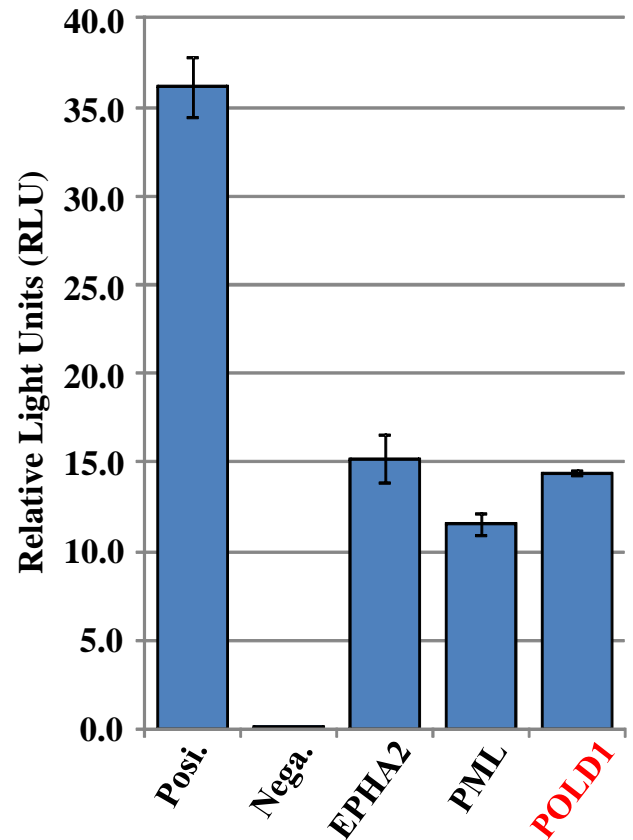


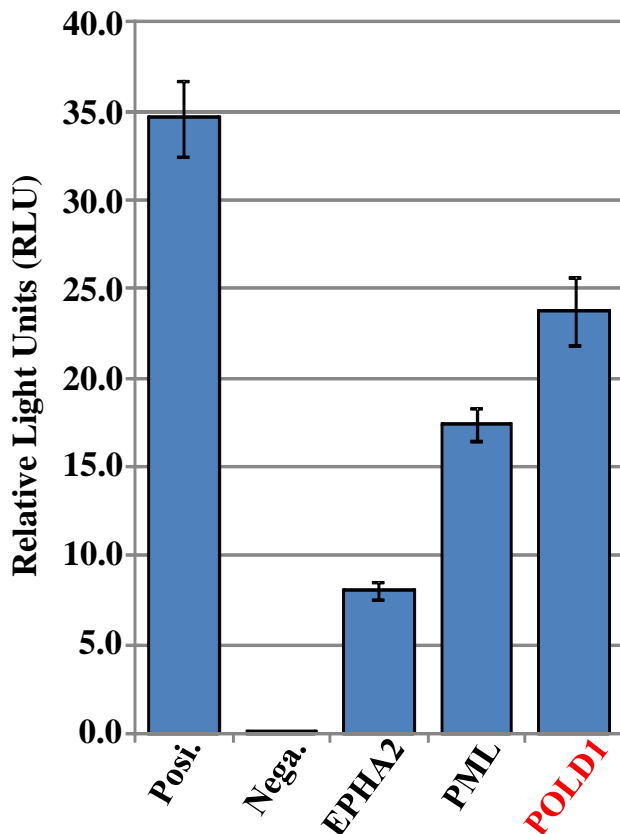
HeLa cells



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 : 5550

2nd Nucleotide Sequence

File Name : RDB7344F.fasta
Sequence Size : 651

Unit Size to Compare = 1
Pick up Location = 1

[99.512% / 615 bp] INT/OPT. Score : < 2306/ 2432 >

```
1' GGCCTAA CTGGCCGGTA CCTGAGCTCG
*****
1" AGAATGCAAT TTCAAGTGCC AGAACATTAC TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG

28' CTAGCCTC-G AGGATCTGAT TGAGCAGGTG GGA CTGGGTG TCCCAGGCT GTTGGGAAAA
*****
61" CTAGCCTCAA AGGATCTGAT TGAGCAGGTG GGA CTGGGTG TCCCAGGCT GTTGGGAAAA

87' GGGTGGCACA TAGGGTCCCA GTGTTGGGTG GTGTGTCGCC TGCTGTGAAA GTTCAGGACA
*****
121" GGGTGGCACA TAGGGTCCCA GTGTTGGGTG GTGTGTCGCC TGCTGTGAAA GTTCAGGACA

147' GAGGCCTCAG CCTCAGGGTC ACCTCCCTGG ACAAGGTGAA TCAGAACTCA CCCTTGAAGG
*****
181" GAGGCCTCAG CCTCAGGGTC ACCTCCCTGG ACAAGGTGAA TCAGAACTCA CCCTTGAAGG

207' ATAAACAGGA TTTAAGTGAA TGAGGGGACC TGGACTTCTG TCCGAACAAC AAGTGTTTGC
*****
241" ATAAACAGGA TTTAAGTGAA TGAGGGGACC TGGACTTCTG TCCGAACAAC AAGTGTTTGC
```



```

267' TGAGGCCTCC TGTGGGCCAG GCACTGGGTT GGCCATTCTA GAGATGGAGA CATTACCCA
*****
301" TGAGGCCTCC TGTGGGCCAG GCACTGGGTT GGCCATTCTA GAGATGGAGA CATTACCCA

327' ATAAATGTTT CCAGAGCATT AACTACAGTT AGGCACAATT CTAGGCACTG GAAACATCTG
*****
361" ATAAATGTTT CCAGAGCATT AACTACAGTT AGGCACAATT CTAGGCACTG GAAACATCTG

387' TGAACAAGAT AACCATCCTC CTACCAAGAC TCGGGGATA GGGACTTTAA TGAGCGTGGC
*****
421" TGAACAAGAT AACCATCCTC CTACCAAGAC TCGGGGATA GGGACTTTAA TGAGCGTGGC

447' ACTGTGGTGG GGCTAGAGGA AATCAGGGAA GGTATCACAA CAGAGGCAAT CGCTGGGACC
*****
481" ACTGTGGTGG GGCTAGAGGA AATCAGGGAA GGTATCACAA CAGAGGCAAT CGCTGGGACC

507' TAAACAAGA GCCTGGGGC TGGCCTCCA AGTTGAGGGA ACAGCACGTG CAAAGTTTGA
*****
541" TAAACAAGA GCCTGGGGC TGGCCTCCA AGTTGAGGGA ACAGCACGTG CAAAGTTTGA

567' AAGGAGAGAC GCCAGGAGTT CGGAGCGAAG CGACGAAGTT CCTCCAATCC TTCCTGCCCC
*****
601" AAGGAGAGAC GCCAAGAGTT CGGAGCGAAG CGACGAAGTT CCTCCAATTT T

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5550

2nd Nucleotide Sequence

File Name : RDB7344R. fasta (Complementary)
Sequence Size : 677

Unit Size to Compare = 1
Pick up Location = 1



[98.964% / 676 bp] INT/OPT. Score : < 1884/ 2645 >

```
721' GCGGGGAAC AGCGGAAGTG AGAGTAGTTA CCAATGATCA CTTATCCTA AGAGTAGTGT
      * ***** *****
1'' ACC CTTATCCTA AGAGTAGTGT

781' ACCGGGCGCC CCACAAGTGT CCCTATCATG CGTTGTTGAG TCTAATTAC GTATAGGGAA
      ** ***** ** ***** ***** ** *****
24'' ACGGGGCGCC CCACAAGGT TCCTATCATG CGTTGTTGAG TCTAATNTAC GTATAGGGAA

841' ACTGAAGCTA GGATGAAGGA GAACAGATCA AGCCAGGACT CTACCGCTTA TCGGCCAGCC
      ***** ***** ***** ***** ***** *****
84'' ACTGAAGCTA GGATGAAGGA GAACAGATCA AGCCAGGACT CTACCGCTTA TCGGCCAGCC

901' TCTGCGGGA TCTTGGGCGT CAGGTCACCA GCTGGCTGCT GGCAGCGAC -GGGCAGCG
      ***** ***** ***** ***** ***** *****
144'' TCTGCGGGA TCTTGGGCGT CAGGTCACCA GCTGGCTGCT GGCAGCGAC GGGGCAGCG

960' CTCCCTACAC GGCCCCGGC GAGAGGCGG CGGGGGGACG CGGAGGATGC GCGGCAACA
      ***** ***** ***** ***** ***** *****
204'' CTCCCTACAC GGCCCCGGC GAGAGGCGG CGGGGGGACG CGGAGGATGC GCGGCAACA

1020' CCCGAGGTG GGAGGAGAGA GAACAGAACC GCGGCGGCC CAGACCGCAC GAGGTCGTGA
      ***** ***** ***** ***** ***** *****
264'' CCCGAGGTG GGAGGAGAGA GAACAGAACC GCGGCGGCC CAGACCGCAC GAGGTCGTGA

1080' AGGTAGCCGC GCGGAGGGC GTGGCTTCGG GCAGACAGGT CATGGGAGG CGGAGTTAAG
      ***** ***** ***** ***** ***** *****
324'' AGGTAGCCGC GCGGAGGGC GTGGCTTCGG GCAGACAGGT CATGGGAGG CGGAGTTAAG

1140' GGAATTTTC AGCAAGGGG CGAGGCCACT TCGGAAGCTG AGAGAGGGG CGGGCCTGC
      ***** ***** ***** ***** ***** *****
384'' GGAATTTTC AGCAAGGGG CGAGGCCACT TCGGAAGCTG AGAGAGGGG CGGGCCTGC

1200' CCTGCAGTCG AACAAGCGG GCGTGGCCTT GCCCGACTT GGCAGGCGG GGGCGTGGCC
      ***** ***** ***** ***** ***** *****
444'' CCTGCAGTCG AACAAGCGG GCGTGGCCTT GCCCGACTT GGCAGGCGG GGGCGTGGCC
```



1260' CGTCTCTGAG CGCCGCGGCT CTGGGCTTGC GCGCGCGGGA GTCAGGGGTC ACGGCGGCGT

504'' CGTCTCTGAG CGCCGCGGCT CTGGGCTTGC GCGCGCGGGA GTCAGGGGTC ACGGCGGCGT

1320' AGGCTGTGGC GGGAAACGCT GTTTGAAGCG ATCAAGATCT GGCCTCGGCG GCCAAGCTTG

564'' AGGCTGTGGC GGGAAACGCT GTTTGAAGCG ATCAAGATCT GGCCTCGGCG GCCAAGCTTG

1380' GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATG-C CAAAAACATT AAGAAGGGCC
***** *
624'' GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGTC CAAAAACATT AAGA