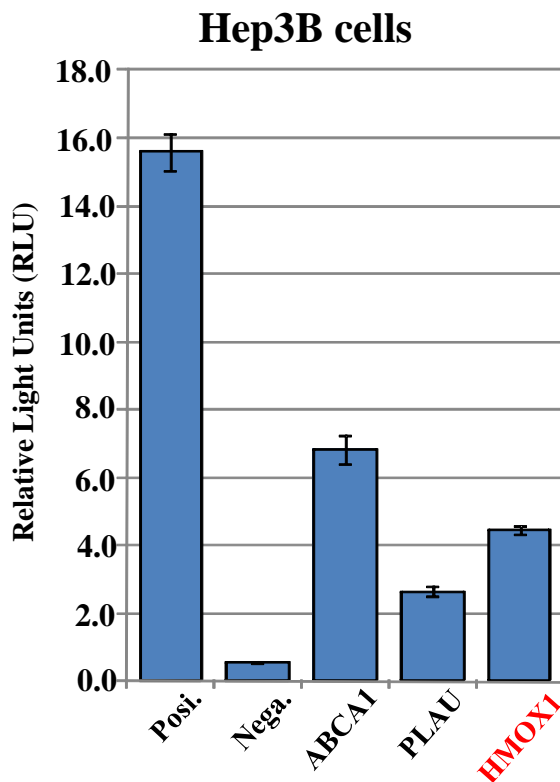
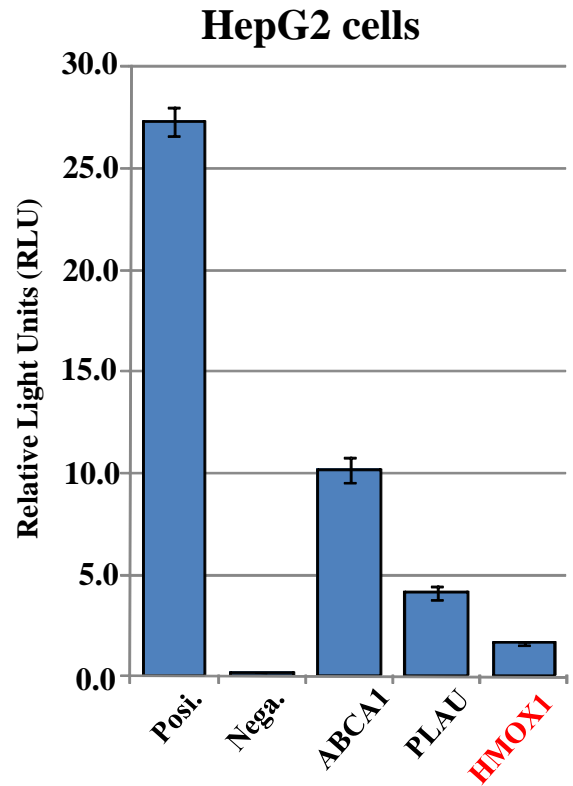
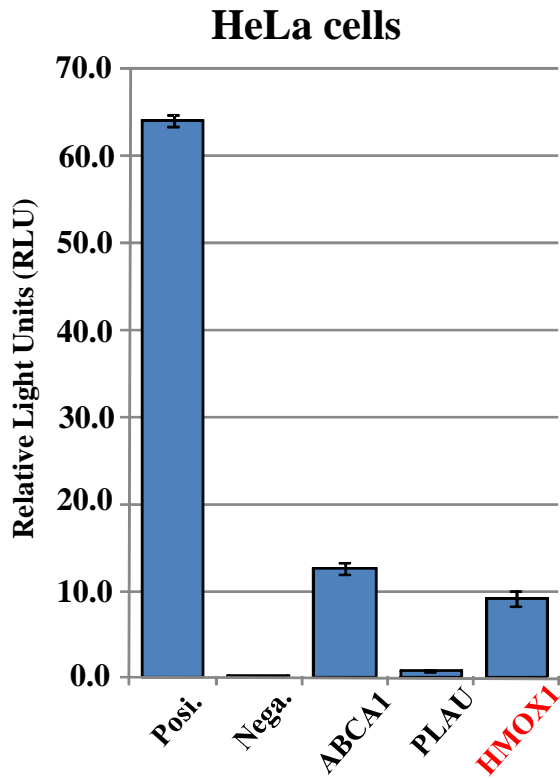


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

ABCA1: pGL4-phABCA1 (RDB# 7680)

PLAU: pGL4-phPLAU (RDB# 7487)

HMOX1: pGL4-phHMOX1 (RDB# 7485)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.08.17

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5712

2nd Nucleotide Sequence

File Name : RDB7485F.fasta
Sequence Size : 728

Unit Size to Compare = 1

Pick up Location = 1

[98.876% / 712 bp] INT/OPT. Score : < 2612/ 2773 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG
          ** *****
1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATG

43' CTGTAGTGGC CCTAGGCTGA ATTCCAGGAA GTTTTTTTTT TTTTTTTTGT TTTTTTTTTT
          ***** ***** ***** ***** *****
61" CTGTAGTGGC CCTAGGCTGA ATTCCAGGAA GTTTTTTTTT TTTTTTTTGT TTTTTTTTTT

103' TTTTGTAGGG ACAGCGTCTT GTTCTGTTGC CCAGGTTAGA ATACAGTAGC GTGGTCACAG
          ***** ***** ***** ***** *****
121" TTTTGTAGGG ACAGCGTCTT GTTCTGTTGC CCAGGTTAGA ATACAGTAGC GTGGTCACAG

163' CTCACTCCAG CCTCTACATC CCAGGCTCAA GTGAACCTCC AGCCTCAGCC TCCCAAGTAG
          ***** ***** ***** ***** *****
181" CTCACTCCAG CCTCTACATC CCAGGCTCAA GTGAACCTCC AGCCTCAGCC TCCCAAGTAG

223' CTGGGACCAC AGGCATGTGC CACCATGCCC AGCTAATTTA TTTTATATTT TGTAGAGACA
          ***** ***** ***** ***** *****
241" CTGGGACCAC AGGCATGTGC CACCATGCCC AGCTAATTTA TTTTATATTT TGTAGAGACG

283' GGGTCTCCCT ATGTTGCCA GGCCAGTCTC GAACTCAAAG CAATCTTCCC ACCTCGACTG
          ***** ***** ***** ***** *****
301" GGGTCTCCCT ATGTTGCCA GGCCAGTCTC GAACTCAAAG CAATCTTCCC ACCTCGACTG
```

```

343' GGCTCAAAGC GCTCTTCCCA CCTCAACCTC CCAAAGTACT GGGACTACAG GTGTGAGCTA
*****
361" GGCTCAAAGC GCTCTTCCCA CCTCAACCTC CCAAAGTACT GGGACTACAG GTGTGAGCTA

403' CCATGCCAGG CCTGAAAGCC ATCTTAAAAA AAAAATCTTA GAATGAGAAT CACAGTATTG
*****
421" CCATGCCAGG CCTGAAAGCC ATCTTAAAAA AAAAATCTTA GAATGAGAAT CACAGTATTG

463' GGAAAGGACT GTATGAATCA TCTGGTCCAT TCGTTTTGTC CTCTGGGTTC ACCCAGTGAC
*****
481" GGAAAGGACT GTATGAATCA TCTGGTCCAT TCGTTTTGTC CTCTGGGTTC ACCCAGTGAC

523' CCTATTTCCC CCGAGTTCTA AGGAGTCCAC CTCATGCAGA ATTGATTCAA TAGGCGATCA
*****
541" CCTATTTCCC CCGAGTTCTA AGGAGTCCAC CTCATGCAGA ATTGATTCAA TAGGCGATCA

583' GCAAGGGCCA GCTCTGCTCT GGGCCCTGAG CAGGCACTGA GTATAAGTCA GACCTGAATG
*****
601" GCAAGGGCCA GCTCTGCTCT GGGCCCTGAG CAGGCACTGA GTATAAGTCA GACCTGAATG

643' TGCCTGGAAG AGTGTCCAC GCATTCCAGC AGGGAAGCAG TTTGTATGAC AGGTGTCCCA
*****
661" TGCCTGGAAG AGTGT-CCAC GCATTCCAGC AGGGAAGCAG TTTGNATGAC AGGTGT-CCA

703' GTCCAGGCGG ATACCAGGTG CTGCCAGAGT GTGGAGGAGG CAGGCGGGGA CTTAGTCTCC
**
719" GT-CAGGCGG G

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5712

2nd Nucleotide Sequence

File Name : RDB7485R.fasta (Complementary)
Sequence Size : 592



Unit Size to Compare = 1

Pick up Location = 1

[100.000% / 591 bp] INT/OPT.Score : < 2364/ 2364 >

961' TGAGGAGGCA AGCAGTCAGC AGAGGATTCC AGCAGGTGAC ATTTTAGGGA GCTGGAGACA

***** *****

1"

TTTTTAGGGA GCTGGAGACA

1021' GCAGAGCCTG GGGTTGCTAA GTTCCTGATG TTGCCACCA GGCTATTGCT CTGAGCAGCG

***** ***** ***** ***** ***** *****

21" GCAGAGCCTG GGGTTGCTAA GTTCCTGATG TTGCCACCA GGCTATTGCT CTGAGCAGCG

1081' CTGCCTCCCA GCTTTCTGGA ACCTTCTGGG ACGCCTGGGG TGCATCAAGT CCCAAGGGGA

***** ***** ***** ***** ***** *****

81" CTGCCTCCCA GCTTTCTGGA ACCTTCTGGG ACGCCTGGGG TGCATCAAGT CCCAAGGGGA

1141' CAGGGAGCAG AAGGGGGGGC TCTGGAAGGA GCAAAATCAC ACCCAGAGCC TGCAGCTTCT

***** ***** ***** ***** ***** *****

141" CAGGGAGCAG AAGGGGGGGC TCTGGAAGGA GCAAAATCAC ACCCAGAGCC TGCAGCTTCT

1201' CAGATTTCTT TAAAGGTTTT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT ATGTGTGTGT

***** ***** ***** ***** ***** *****

201" CAGATTTCTT TAAAGGTTTT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT ATGTGTGTGT

1261' GTGTGTGTGT GTGTGTGTGT TTTCTCTAAA AGTCCTATGG CCAGACTTTG TTTCCAAGG

***** ***** ***** ***** ***** *****

261" GTGTGTGTGT GTGTGTGTGT TTTCTCTAAA AGTCCTATGG CCAGACTTTG TTTCCAAGG

1321' GTCATATGAC TGCTCCTCTC CACCCACAC TGGCCCGGGG CGGGCTGGGC GCGGGCCCT

***** ***** ***** ***** ***** *****

321" GTCATATGAC TGCTCCTCTC CACCCACAC TGGCCCGGGG CGGGCTGGGC GCGGGCCCT

1381' GCGGGTGTG CAACGCCCGG CCAGAAAGTG GGCATCAGCT GTTCCGCCTG GCCACGTGA

***** ***** ***** ***** ***** *****

381" GCGGGTGTG CAACGCCCGG CCAGAAAGTG GGCATCAGCT GTTCCGCCTG GCCACGTGA

1441' CCCGCCGAGC ATAAATGTGA CCGGCCCGG CTCCGGCAGT CAACGCCTGC CTCCTCTCGA



```
*****  
441" CCGCGGAGC ATAAATGTGA CCGGCGCGG CTCCGGCAGT CAACGCCTGC CTCCTCTCGA  
  
1501' GCGTCCTCAG CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT  
*****  
501" GCGTCCTCAG CATCAAGATC TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT  
  
1561' AAAGCCACCA TGGAAGATGC CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC  
***** **  
561" AAAGCCACCA TGGAAGATGC CAAAAACATT AA
```