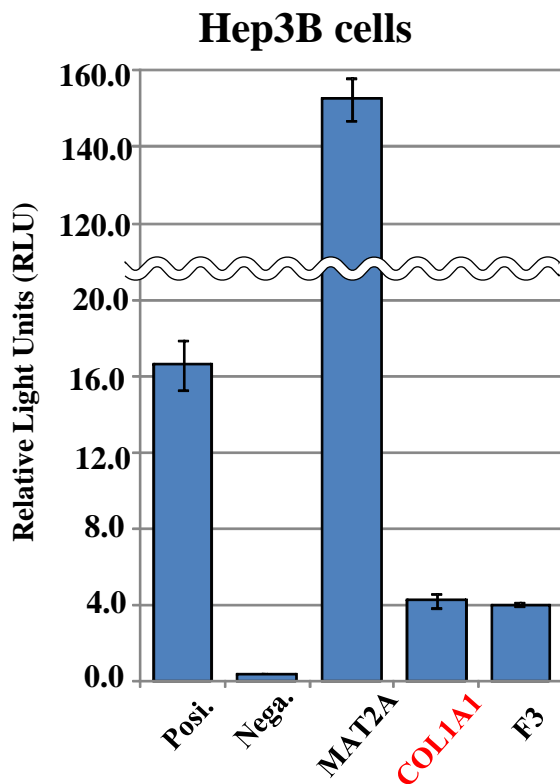
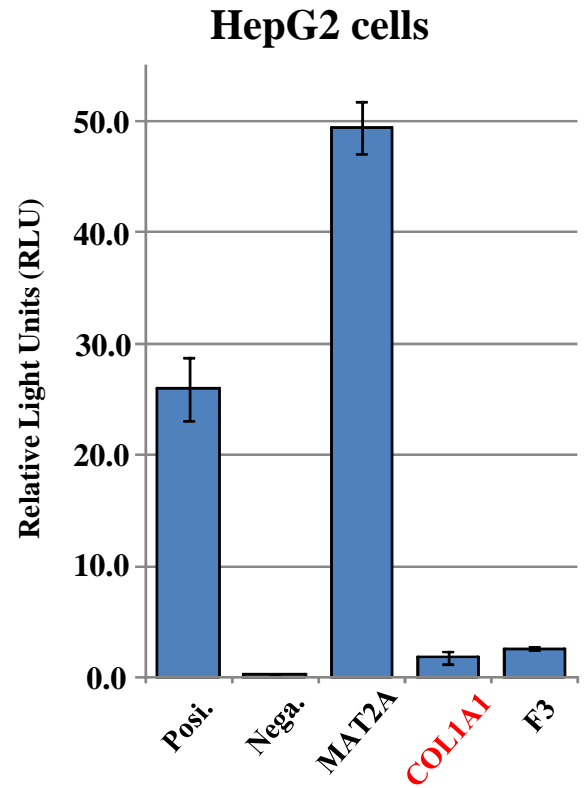
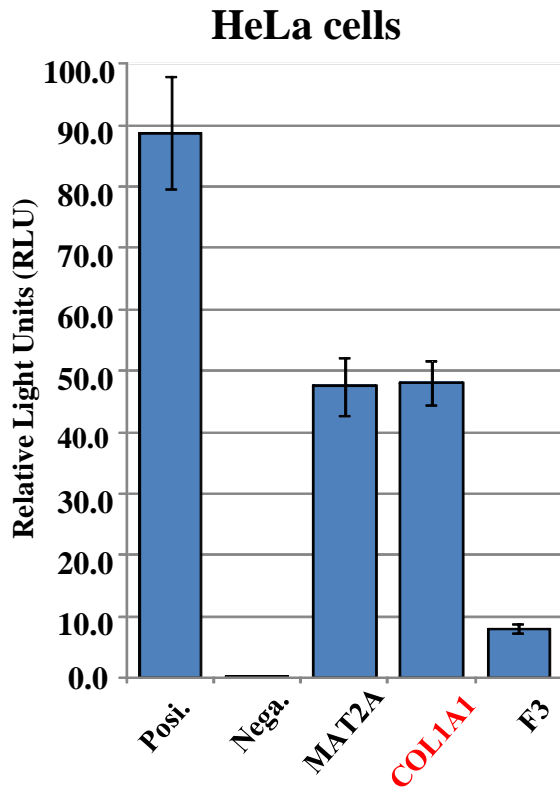


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

MAT2A: pGL4-phMAT2A (RDB# 7393)

COL1A1: pGL4-phCOL1A1 (RDB# 7459)

F3: pGL4-phF3 (RDB# 7458)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.07.13

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5502

2nd Nucleotide Sequence

File Name : RDB7459F.prj
Sequence Size : 400

Unit Size to Compare = 1
Pick up Location = 1

[100.000% / 400 bp] INT/OPT.Score : < 1600/ 1600 >

```
1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCAGTGGGAA GTAGCCCTA
                                     ***** *****
1"                                     CAGTGGGAA GTAGCCCTA

61' AAACAAAGTC AATCATCCTC TGCAGCCCAT CCCACACCCC CAAAGGAAAG TTCACCCAG
    ***** ***** ***** ***** ***** *****
20" AAACAAAGTC AATCATCCTC TGCAGCCCAT CCCACACCCC CAAAGGAAAG TTCACCCAG

121' ACACCCAAAA TATCCCATAC ATCCCAACA CTGAGTCCAG GTACAACTGG AGAAGGGGCT
    ***** ***** ***** ***** ***** *****
80" ACACCCAAAA TATCCCATAC ATCCCAACA CTGAGTCCAG GTACAACTGG AGAAGGGGCT

181' TTATGCAGCT CCCAGAAAGA CACCCCTTTA GCTAAGTGCC CTCCCTCCAC CCAGGTTCTC
    ***** ***** ***** ***** ***** *****
140" TTATGCAGCT CCCAGAAAGA CACCCCTTTA GCTAAGTGCC CTCCCTCCAC CCAGGTTCTC

241' TCTGGTTTGA CTGTGCTGGG AAGGAGGGTC TCTAAGCAGC CCCTGGCCAC AGCCATGGCA
    ***** ***** ***** ***** ***** *****
200" TCTGGTTTGA CTGTGCTGGG AAGGAGGGTC TCTAAGCAGC CCCTGGCCAC AGCCATGGCA
```



```

301' AACAAACTC TTCTCTAAGT CACCAATGAT CACAGGCCTC CCACTAAAAA TACTTCCCAA
*****
260'' AACAAACTC TTCTCTAAGT CACCAATGAT CACAGGCCTC CCACTAAAAA TACTTCCCAA

361' CTCTGGGGTG GAAGAGTTTG GGGGATGAAT TTTTAGGGGA TTGCAAGCCC CAATCCCCAC
*****
320'' CTCTGGGGTG GAAGAGTTTG GGGGATGAAT TTTTAGGGGA TTGCAAGCCC CAATCCCCAC

421' CTCTGTGTCC CTAGAATCCC CCACCCCTAC CTTGGCTGCT CCATCACCCA ACCACCAAAG
*****
380'' CTCTGTGTCC CTAGAATCCC C

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5502

2nd Nucleotide Sequence

File Name : RDB7459R.prj (Complementary)
Sequence Size : 187

Unit Size to Compare = 1
Pick up Location = 1

[100.000% / 185 bp] INT/OPT. Score : < 740/ 740 >

```

1081' GCAGAGCTGC GAAGAGGGGA GATGTGGGGT GGA CTCCCTT CCCTCCTCT CCCCCTCTCC
*****
1'' ATCCTT CCCTCCTCT CCCCCTCTCC

1141' ATTCCAATC CCAAATTGGG GGCCGGGCCA GGCAGCTCTG ATTGGCTGGG GCACGGGCGG
*****
27'' ATTCCAATC CCAAATTGGG GGCCGGGCCA GGCAGCTCTG ATTGGCTGGG GCACGGGCGG

```



1201' CCGGCTCCCC CTCTCCGAGG GGCAGGGTTC CTCCTGCTC TCCATCAGGA CAGTATAAAA

87" CCGGCTCCCC CTCTCCGAGG GGCAGGGTTC CTCCTGCTC TCCATCAGGA CAGTATAAAA

1261' GGGGCCCGGG CCAGTCGTCG GAGCAGACGG GAGTTTCTCC TATCAAGATC TGGCCTCGGC

147" GGGGCCCGGG CCAGTCGTCG GAGCAGACGG GAGTTTCTCC T