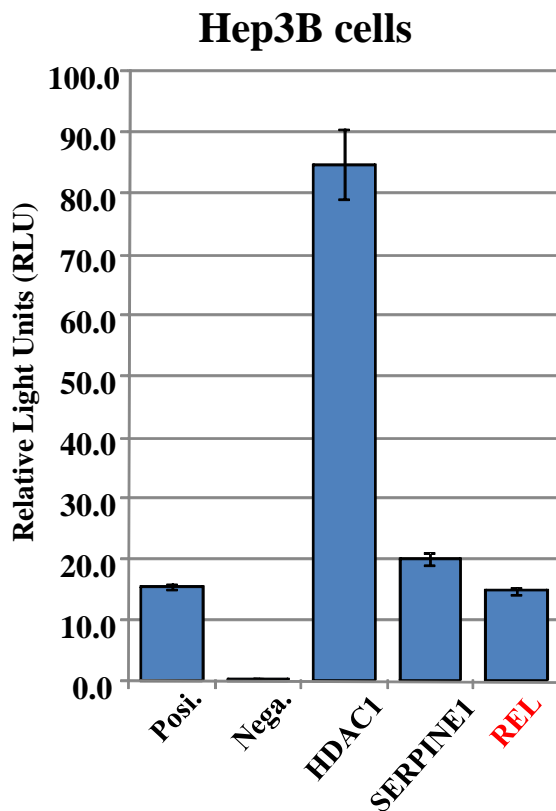
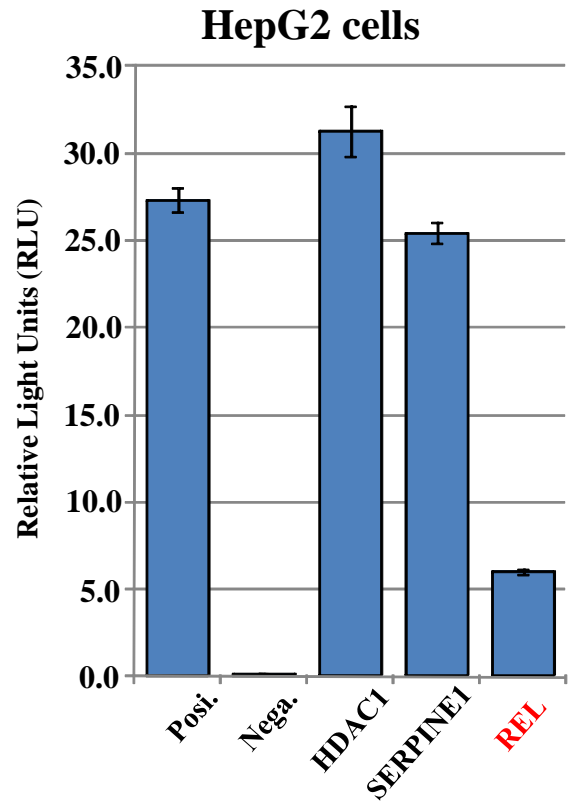
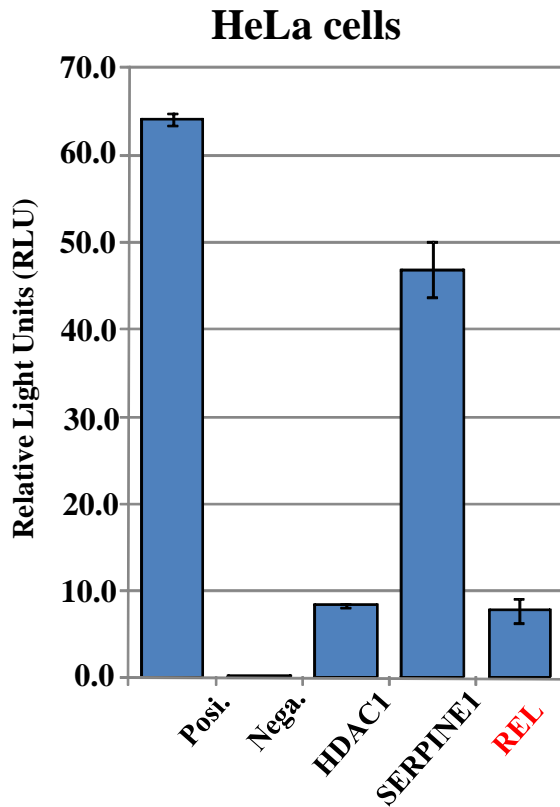


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

HDAC1: pGL4-phHDAC1 (RDB# 7484)

SERPINE1: pGL4-phSERPINE1 (RDB# 7461)

REL: pGL4-phREL (RDB# 7481)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.08.12

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5706

2nd Nucleotide Sequence

File Name : RDB7481F.fasta
Sequence Size : 612

Unit Size to Compare = 1
Pick up Location = 1

[97.342% / 602 bp] INT/OPT. Score : < 383/ 2175 >

```
1'          G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGA-
          * *****
1'' GGTGCCAGAA CATGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

41' TACG-TGCCT GACCATATGA AAAGGTGAGA TTTCTTTTT TTTGGTCTNT TGCACTCTCT
     **** *****
61'' TACGTTGCCT GACCATATGA AAAGGTGAGA TTTCTTTTT TTTGGTCT-T TCACTCTCT

100' TCAGTGGATT GCCTGTGATG TGCA-TCATG GTACGTTTTA NGTACATATC CAATAATAAA
     *****
120'' TCAGTGGATT GCCTGTGATG TGCATTCATG GTACGTTTTA -GTACATATC CAATAATAAA

159' ACTGTTTCAT TCTTTTGTG TACATTGCGC ANTTTCGTGG AAAGAACAGT TTGGGGTTGG
     *****
179'' ACTGTTTCAT TCTTTTGTG TACATTGCGC A-TTTCGTGG AAAGAACAGT TTGGGGTTGG

219' CAGGATATTT TAAATTATTT GCNCCATATG GGTCCCCCAG TTTTGGGCAC TTGTATGGCA
     *****
238'' CAGGATATTT TAAATTATTT GC-CCATATG GGTCCCCCAG TTTTGGGCAC TTGTATGGCA
```



```

279' GGCTGATATT CCCNCATTAC CTCTCCGTAC TAATTTTAAAC TAGTAAGGGA CAGGGGCAAG
***** ** ** ***** ***** ***** ***** *****
297" GGCTGATATT CCC-CATTAC CTCTCCGTAC TAATTTTAAAC TAGTAAGGGA CAGGGGCAAG

339' GGCANTGGAG CTTTGGAGTC AGACAACCCT GGCTTTAAAC TGTGCCTTTT ATCAGNCATT
**** ***** ***** ***** ***** ***** ***** ****
356" GGCA-TGGAG CTTTGGAGTC AGACAACCCT GGCTTTAAAC TGTGCCTTTT ATCAG-CATT

399' CTGAAGTACT GTATGTTGAA GTAACCTTCTC TGAACCCCGA ATACTTNCAT CTATAAAGTT
***** ***** ***** ***** ***** ** *****
414" CTGAAGTACT GTATGTTGAA GTAACCTTCTC TGAACCCCGA ATACTT-CAT CTATAAAGTT

459' AGGAATAATA AATACGTCAT AGATTAAGTA TGGACATNTA TCTGATGCAT AGCAGGTACT
***** ***** ***** ***** ** ***** *****
473" AGGAATAATA AATACGTCAT AGATTAAGTA TGGACAT-TA TCTGATGCAT AGCAGGTACT

519' ATTCAAATGA AGGAAACGAA GTTATCCTNA GGTCTTTTAA TGCACTAAAT GTGTGCTCCA
***** ***** ***** * ***** ***** *****
532" ATTCAAATGA AGGAAACGAA GTTATCCT-A GGTCTTTTAA TGCACTAAAT GTGTGCTCCA

579' TTTCCG-CCT TTCTGGCAT NCTGTGTGAA ATCTCAGGAT ATAGTGTCCA CTAAACTTCA
***** ** **** *****
591" TTTCCGCCCT TTCTGGCAT TT

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5706

2nd Nucleotide Sequence

File Name : RDB7481R.fasta (Complementary)
Sequence Size : 619

Unit Size to Compare = 1
Pick up Location = 1



[98.400% / 625 bp] INT/OPT. Score : < 880/ 2340 >

901' GGANAGAGGG GGAACCACCT CTCGAAAACC CCGGCCGTCG CCCTCCCAGG CCGNGAGAG

1" TT

961' TGG-CCCCG CGCGCCCC- AAAAGCTCCC CAGCGGCCGG CCCTTCNTA CGTCATCCGC

**** **

3" TCGGCCCCCG CGCGCCCCA AAAAGCTCCC CAGCGGCCGG CCCTTC-TA CGTCATCCGC

1019' ACCCTCCCGC CCGTCTCTGA ACTTTAAACC AACTCGGNA AGAACAACT GGAGGAGGGG

62" ACCCTCCCGC CCGTCTCTGA ACTTTAAACC AACTCGG-A AGAACAACT GGAGGAGGGG

1079' GATTTCTCAG GAGCCAGCGG CTTTCTCACN GCTGCTAGCC GTCACCTCCC GGCTCCGCC

121" GATTTCTCAG GAGCCAGCGG CTTTCTCAC- GCTGCTAGCC GTCACCTCCC GGCTCCGCC

1139' GTTCCCTGCG CTCCGAAGC NCCACCCAA GCTCCGCTC CCTCGACCC CTCCAAGCC

180" GTTCCCTGCG CTCCGAAGC -CCACCCAA GCTCCGCTC CCTCGACCC CTCCAAGCC

1199' AGCCGCCGA GNCAGCGCG GGGCGTATG CGTGGGGCC GCGGGGAGC GTGCGGGGG

239" AGCCGCCGA G-CAGCGCG GGGCGTATG CGTGGGGCC GCGGGGAGC GTGCGGGGG

1259' ACNAGGCAGG GCGGGGCGC TGGGGCGGT CGCGCGCGC GCGGCCGGA GGTNCGCCC

** *****

298" AC-AGGCAGG GCGGGGCGC TGGGGCGGT CGCGCGCGC GCGGCCGGA GGT-CGCCC

1319' GCCACGCCT CCGGTGAGG GTTGTGCGT CGGGCTACG TCAGNCCGG GAAATTCCC

356" GCCACGCCT CCGGTGAGG GTTGTGCGT CGGGCTACG TCAG-CGCG GAAATTCCC

1379' CTCCGCCAG GCTGCTCGC TCTGGCTGG GCCAGACTC GGCTCTCCC GCTCCGCC

415" CTCCGCCAG GCTGCTCGC TCTGGCTGG GCCAGACTC GGCTCTCCC GCTCCGCC



1439' CTGCCCTGG CTCCGTACG GTGGACGGCG ACGCTGGGTG ACCCGGGGTG CAAGAATTCA

475" CTGCCCTGG CTCCGTACG GTGGACGGCG ACGCTGGGTG ACCCGGGGTG CAAGAATTCA

1499' GGGTTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGTACT GTTGGTAAAG

535" GGGTTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGTACT GTTGGTAAAG

1559' CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCAGC GCCATTCTAC CCACTCGAAG

595" CCACCATGGA AGATGCCAAA AACAT