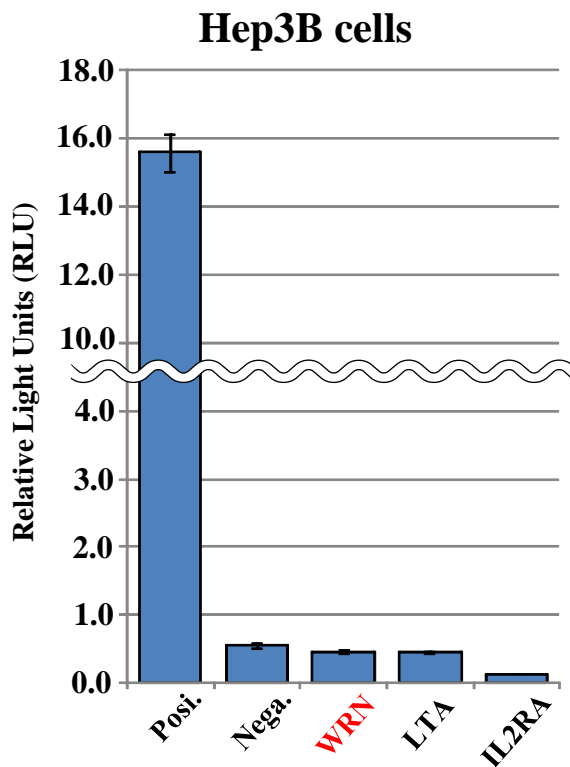
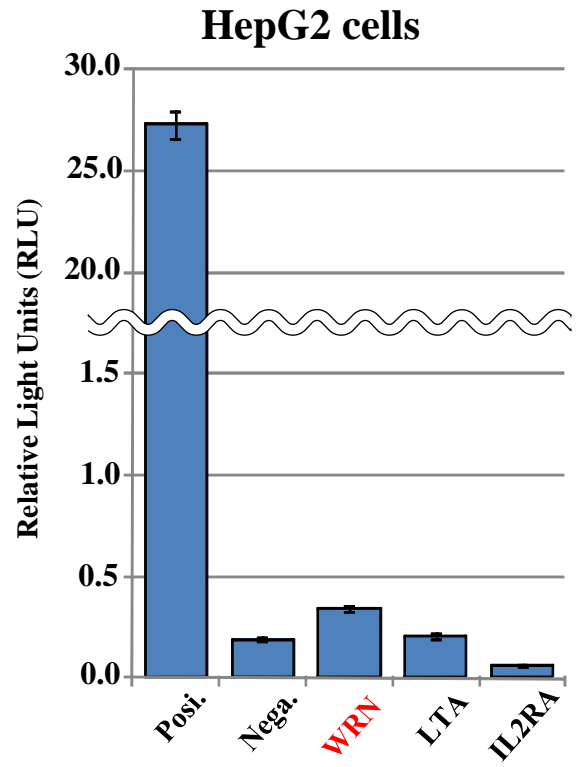
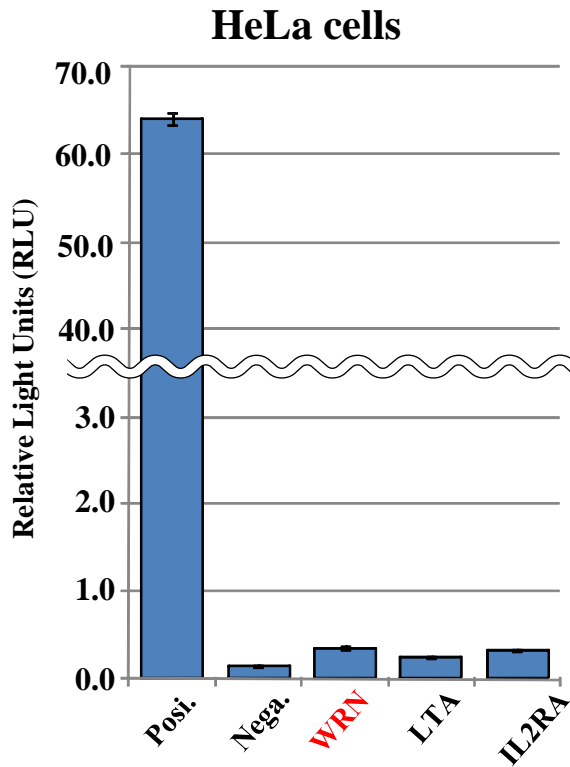


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

WRN: pGL4-phWRN (RDB# 7569)

LTA: pGL4-phLTA (RDB# 7486)

IL2RA: pGL4-phIL2RA (RDB# 7525)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5562

2nd Nucleotide Sequence

File Name : RDB7569F.fasta
Sequence Size : 642

Unit Size to Compare = 1
Pick up Location = 1

[99.679% / 623 bp] INT/OPT.Score : < 2480/ 2480 >

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

43' TGTTCCTGGC CCAAAGTGT GCCAAAATAA CCTATCATGC CAGTCCCCCG CATCATGGTT
          *****
61" TGTTCCTGGC CCAAAGTGT GCCAAAATAA CCTATCATGC CAGTCCCCCG CATCATGGTT

103' TGTCTAATCC GTAGGAAGCG ACCCCGCTGA TTTTCCTTTA GGTCTAGGTA ATATTTCTTA
          *****
121" TGTCTAATCC GTAGGAAGCG ACCCCGCTGA TTTTCCTTTA GGTCTAGGTA ATATTTCTTA

163' TTGTCCCTCT CGATATAGTC TGTTTTCAGG AACTGTGAG GATGCTCTTC GGACCCACC
          *****
181" TTGTCCCTCT CGATATAGTC TGTTTTCAGG AACTGTGAG GATGCTCTTC GGACCCACC

223' GAGACTGGTG GGGAGGGTGC CGAGTGCTTC TGCCTCCTTC TGGAGCCTTG CTCTTTGCTG
          *****
241" GAGACTGGTG GGGAGGGTGC CGAGTGCTTC TGCCTCCTTC TGGAGCCTTG CTCTTTGCTG
```

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283' TGGCCATGCT CTTGCCGGTG GCCTTTCAGG CCCAGGTGGG CATAGTGCTC GATGAAGTCC
*****
301" TGGCCATGCT CTTGCCGGTG GCCTTTCAGG CCCAGGTGGG CATAGTGCTC GATGAAGTCC

343' CCTAGACAGT CTTTCAGCTC CGCTGCCACA GACAGGGAGA GGGTCAGTTT ACTCTTTCTG
*****
361" CCTAGACAGT CTTTCAGCTC CGCTGCCACA GACAGGGAGA GGGTCAGTTT ACTCTTTCTG

403' ATGTTGTCCT GCCGGCCTCT CCCTATCCAG ACTTCGGCTA TCTTTAGGAA GCGGCCCGG
*****
421" ATGTTGTCCT GCCGGCCTCT CCCTATCCAG ACTTCGGCTA TCTTTAGGAA GCGGCCCGG

463' GAGCTTTGCT TCACGTCTAG GTAAAACCTC TTTTCTGGA TGTCCACTCG TTTGGAGGCC
*****
481" GAGCTTTGCT TCACGTCTAG GTAAAACCTC TTTTCTGGA TGTCCACTCG TTTGGAGGCC

523' AGCTCCTGGA TTTCGGCTGC GCCCCCGGCC TGATTAGGGG TGGCTGAGGC CGCGTAGTGG
*****
541" AGCTCCTGGA TTTCGGCTGC GCCCCCGGCC TGATCCGGGG TGGCTGAGGC CGCGTAGTGG

583' GGGTAGTGGG AGTGCTGGGC CTGGGGATAG AGTCTACTCT TGCTTAGGCC AGAGCCCCT
*****
601" GGGTAGTGGG AGTGCTGGGC CTGGGGATAG AGTCTACTCT TT

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5562

2nd Nucleotide Sequence

File Name : RDB7569R. fasta (Complementary)
Sequence Size : 538

Unit Size to Compare = 1

Pick up Location = 1



[94.403% / 536 bp] INT/OPT. Score : < 1628/ 1950 >

901' CCCGCATCCC TCCGCCGCC CCGGGGCCG -TCCGCACG CCGCCGCCG CCGTCCCGC
* . * . ** ****. *. *. *** *. *. * * *. * * ****. * *

1" CCNTNCNGCC CCGGNCCNGN TTCCAGNANG CAGCNCGGCC CAGTCCNGGG

960' CTCCGCGGCC CCAGGTCTCC AGCCGGCGGG CACTC-ACAT CATCTCT-GC C-ATCACCGC
. *** **** *****. *** ***** ***** ***** ** * *****

51" NTCCCGGGCC CCAGGTNTCC AGCCGGCGGG CACTCAACAT CATCTCTGGC CAATCACCGC

1017' CGCCGCCGAT GCCCTTAC- GACCACCGCC GCCGCCACCG CCAGCTCTCG GCCCTCTGC
***** ***** ***** ***** ***** *****

111" CGCCGCCGAT GCCCTTACG GACCACCGCC GCCGCCACCG CCAGCTCTCG GCCCTCTGC

1076' TGCAGCCGCC GCAGCCGCC CCCCCGCCT CCTCCCCGC CGCCGCCGT CGCACTGCC
***** ***** ***** ***** ***** *****

171" TGCAGCCGCC GCAGCCGCC CCCCCGCCT CCTCCCCGC CGCCGCCGT CGCACTGCC

1136' CCCGCCGAG CAGCCGGCA GGGGCATCG CCGCGGGCC CACCGAGCC GCCCTCCTG
***** ***** ***** ***** ***** *****

231" CCCGCCGAG CAGCCGGCA GGGGCATCG CCGCGGGCC CACCGAGCC GCCCTCCTG

1196' CGGCCGCTGC GGGGCCGCC GCCTGACTTC GGACACCGC CCCGCACCG CCAGGAGGG
***** ***** ***** ***** ***** *****

291" CGGCCGCTGC GGGGCCGCC GCCTGACTTC GGACACCGC CCCGCACCG CCAGGAGGG

1256' AGGGAAGGG AGGCGGGAG AGCGACGGC GGGGGCGGC GGTGGACCC GCCTCCCCG
***** ***** ***** ***** ***** *****

351" AGGGAAGGG AGGCGGGAG AGCGACGGC GGGGGCGGC GGTGGACCC GCCTCCCCG

1316' GCACAGCCTG CTGAGGGAA GAGGGGTCT CCGCTTCC TCAGTGATCA AGATCTGGC
***** ***** ***** ***** ***** *****

411" GCACAGCCTG CTGAGGGAA GAGGGGTCT CCGCTTCC TCAGTGATCA AGATCTGGC

1376' TCGCGGCCA AGCTTGCAA TCCGGTACTG TTGGTAAAG CACCATGGAA GATGCCAAA
***** ***** ***** ***** ***** *****

471" TCGCGGCCA AGCTTGCAA TCCGGTACTG TTGGTAAAG CACCATGGAA GATGCCAAA



1436' ACATTAAGAA GGGCCCAGCG CCATTCTACC CACTCGAAGA CGGGACCGCC GGCGAGCAGC

531" ACATTAAT