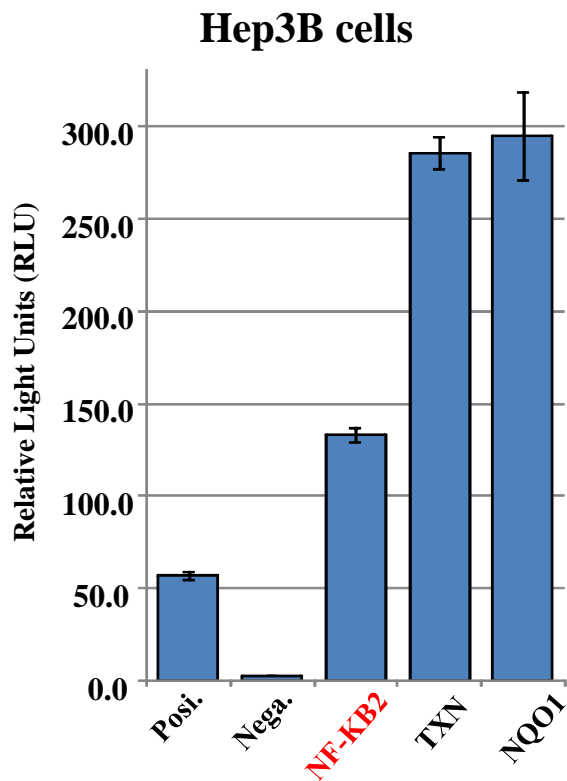
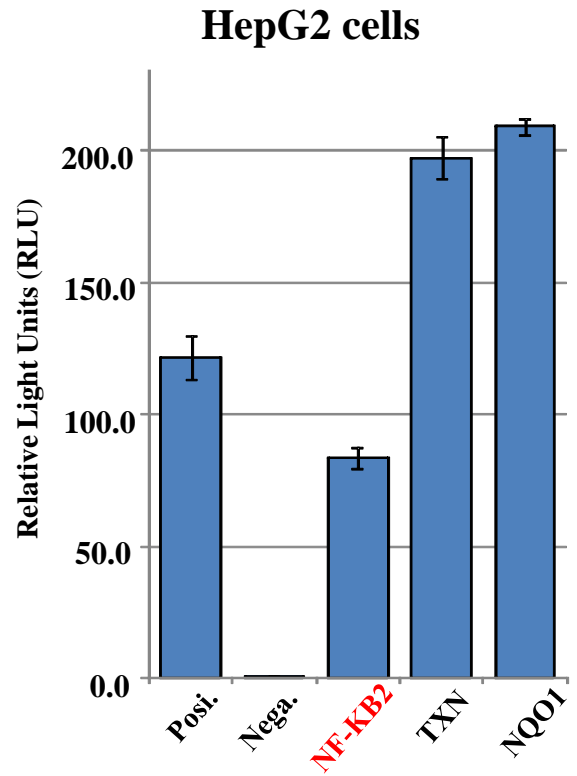
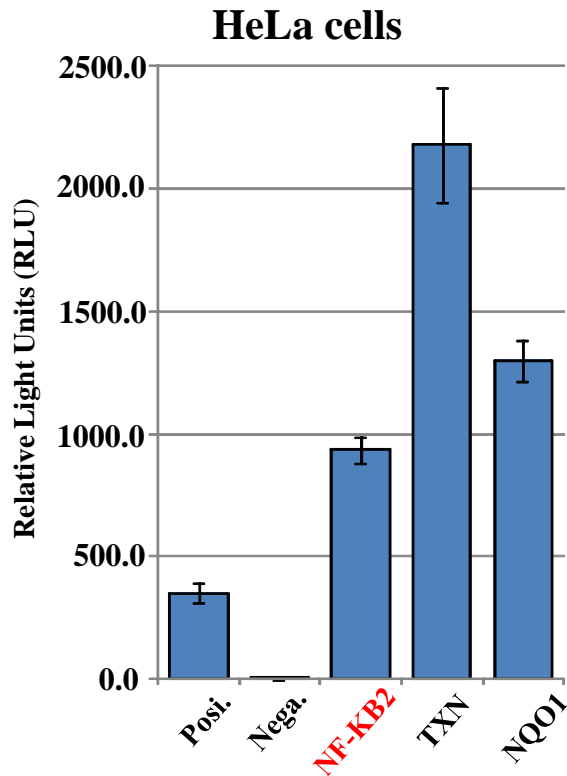


# The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

**NF-KB2:** pGL4-phNF-KB2 (RDB# 7478)

TXN: pGL4-phTXN (RDB# 7518)

NQO1: pGL4-phNQO1 (RDB# 7570)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.08.28

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5568

2nd Nucleotide Sequence

File Name : RDB7478F.fasta  
Sequence Size : 716

Unit Size to Compare = 1

Pick up Location = 1

[98.714% / 700 bp] INT/OPT.Score : < 1870/ 2706 >

```
1'          G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
           * *****
1'' GGTGCCAGAA CATTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

42' CTGCGCCAGT CCAGAGTTAA ACTTTCAGCC NAATGAAAAA GGGCGCGAGG CGTGACGCAC
     *****
61'' CTGCGCCAGT CCAGAGTTAA ACTTTCAGCC -AATGAAAAA GGGCGCGAGG CGTGACGCAC

102' GGAAACGTCA TGGGAATTCC CNCCCTCCGG GGGGCCGAGA AGGGGCTTTC CCGGCCCTGA
     *****
120'' GGAAACGTCA TGGGAATTCC C-CCCTCCGG GGGGCCGAGA AGGGGCTTTC CCGGCCCTGA

162' GCCCTGCTGG CANGGCGAGG TGTGCGGACC GGTCCCAGGT GGGTCGGGCG CGGAGAGAAG
     *****
179'' GCCCTGCTGG CA-GGCGAGG TGTGCGGACC GGTCCCAGGT GGGTCGGGCG CGGAGAGAAG

222' CCGNCAACCA GAGCCGCCGC CACGGTGAGT GGCTGGATTC AGACCCTGG GTGGCCGGGA
     ***
238'' CCG-CAACCA GAGCCGCCGC CACGGTGAGT GGCTGGATTC AGACCCTGG GTGGCCGGGA

282' CAAGAGAAAA GAGGGAGGAG GGCCTTTAGC GGACAGCGCC TGGGGCTGGA GAGCAGCAGC
     *****
297'' CAAGAGAAAA GAGGGAGGAG GGCCTTTAGC GGACAGCGCC TGGGGCTGGA GAGCAGCAGC
```



```

342' TGCACACAGC CGGAAAGGGC GCGCAGGCGA CGACACTCGG ATCCACGTGG ACACCGTTGT
*****
357" TGCACACAGC CGGAAAGGGC GCGCAGGCGA CGACACTCGG ATCCACGTGG ACACCGTTGT

402' ACAAAGATAC GCGGACCCGT ACGTACACCT GTACCTGTGC TGGCGCACAC ACGGCAGCGT
*****
417" ACAAAGATAC GCGGACCCGT ACGTACACCT GTACCTGTGC TGGCGCACAC ACGGCAGCGT

462' CCGTGCAGTC GCACTCGCAC ACACATGCAC ACGGAGACGT GCCCACCAGT GCACTGGTGC
*****
477" CCGTGCAGTC GCACTCGCAC ACACATGCAC ACGGAGACGT GCCCACCAGT GCACTGGTGC

522' CTGCACCCAC ACCCTTCACG CACAAACTCA AGATACGCTC ACCCGTGTCC GTACATCAAG
*****
537" CTGCACCCAC ACCCTTCACG CACAAACTCA AGATACGCTC ACCCGTGTCT GTACATCAAG

582' ACAGGCGCTG ACACACACCC ACACTGAGAA GCTCGGGATT CACCTATCTA CACACATGCT
*****
597" ACAGGCGCTG ACACACACCA ACACTGAGAA GCTCGGGATA CACCTATCTA CACACATGCT

642' CGTTGCACA CTCATGTTGA CGCCATGGAC ACACAACATG CAACCAAGCA CTACAGCCGA
*****
657" CGTTGCACA CTCATGTCGA CGCCATGGAC ACACAAAATG CAACCAAGCA CTACAGCCGG

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5568

2nd Nucleotide Sequence

File Name : RDB7478R. fasta (Complementary)  
Sequence Size : 748

Unit Size to Compare = 1  
Pick up Location = 1



[97.510% / 763 bp] INT/OPT. Score : < 2578/ 2821 >

661' ACGCCATGGA CACACAACAT GCAACCAAGC ACTACAGCCG AAACACACTT GTGGAGCTGT  
\*\*\*\* \* \*\*\* \*. \* \*\*\*\*\* \* \*\* \*\*\*\*\*  
1" AAGC A-TAC-GCNG --ACACAC-T GT-GAGCTG-

721' GATGGAGACA CACTCTTGTA TTAGGTGGGG GGGGGGGGGG GGGAGCGTGC AGAGATCTCC  
\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
28" GAT-GAGACA CACTC-TGTA -TAGGT---- -GGGGGGGGG GGGAGCGTGC AGAGATCTCC

781' CTGTGCCTG CGCGCCAGA A-CCGGTGCG GTGTGGACC AGCTGCTGTT GTGAGGTTTG  
\*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
80" CTGTGCCTG CGCGCCAGA ACCCGGTGCG GTGTGGACC AGCTGCTGTT GTGAGGTTTG

840' GGAGAGAGAG AAAAGAGCCC ACTCCGAGGA GGAGACACTT TTCCCGCAGC CCCAGAATCG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
140" GGAGAGAGAG AAAAGAGCCC ACTCCGAGGA GGAGACACTT TTCCCGCAGC CCCAGAATCG

900' CGTTCTCGGG GCAGAACCCC GGGGCTCCC ACAGGAAAGA GCCCCGCCT ACAGGCTGTT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
200" CGTTCTCGGG GCAGAACCCC GGGGCTCCC ACAGGAAAGA GCCCCGCCT ACAGGCTGTT

960' CGAAGGGGAG GCCGTCCGAC AGCAGGAATG TCCCCCAA AGCCCCGGG GTTATCAGC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
260" CGAAGGGGAG GCCGTCCGAC AGCAGGAATG TCCCCCAA AGCCCCGGG GTTATCAGC

1020' CGTGGCCTCC CTCCTGGCAG AAAATCCAA GGTTGCTCA GACCGGGGA GGGGAGCGGG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
320" CGTGGCCTCC CTCCTGGCAG AAAATCCAA GGTTGCTCA GACCGGGGA GGGGAGCGGG

1080' AGGCGGACTT GGCCCAGAC TGCCAGCCTC CTCCGGCCG TGAAGACCC TCCTGTTCCC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
380" AGGCGGACTT GGCCCAGAC TGCCAGCCTC CTCCGGCCG TGAAGACCC TCCTGTTCCC

1140' TGCCCTGGAG GGAGGAGGGG GCTTAACCCC CACCGGGGCT TCCGGATTC TCCTAGACCT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
440" TGCCCTGGAG GGAGGAGGGG GCTTAACCCC CACCGGGGCT TCCGGATTC TCCTAGACCT

1200' CTGCCCGCTG AAAAGCAGCG GGAGCCGTA GACTGTCGAG GGCCTCCGC CCCTCCGTC



```

*****
500' CTGCCCGCTG AAAAGCAGCG GGAGCCCGTA GACTGTGAG GGCCTCCGC CCCTCCGTC

1260' GCGAGGGCGG GGCCAGTGGC GTCATTTCCA GGCCCGCCCC CTCGGCCCC GCCTCCCTT
*****
560' GCGAGGGCGG GGCCAGTGGC GTCATTTCCA GGCCCGCCCC CTCGGCCCC GCCTCCCTT

1320' GGTATTTTCG GGACTTTCCT AAGCTGCTCT AACTTTCCTG CCCCTTCAT CAAGATCTGG
*****
620' GGTATTTTCG GGACTTTCCT AAGCTGCTCT AACTTTCCTG CCCCTTCAT CAAGATCTGG

1380' CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA
*****
680' CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

1440' AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA
*****
740' AAACATTA

```