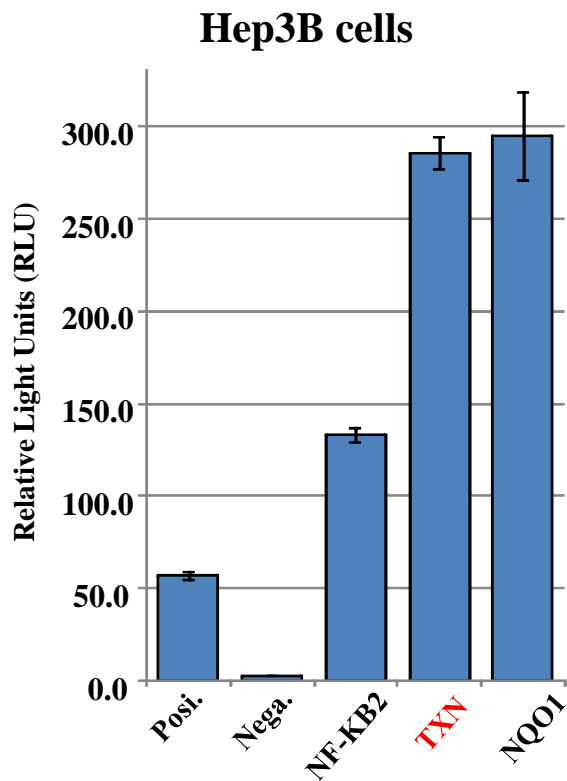
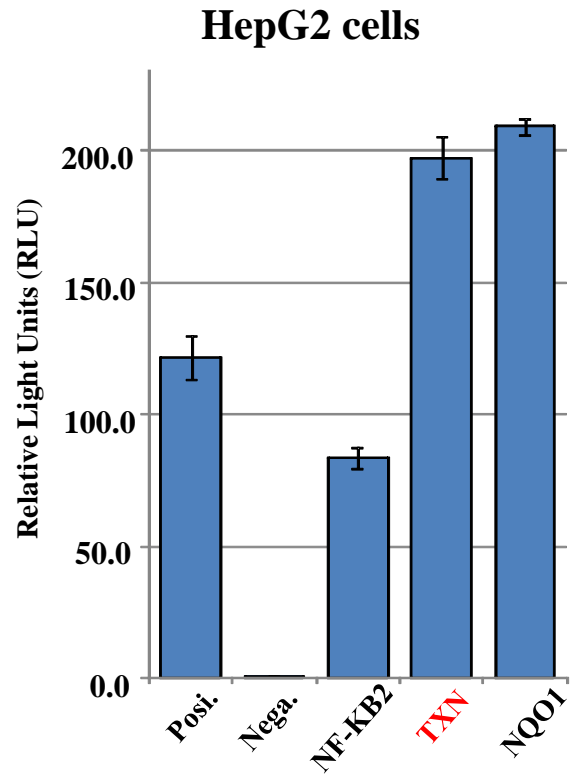
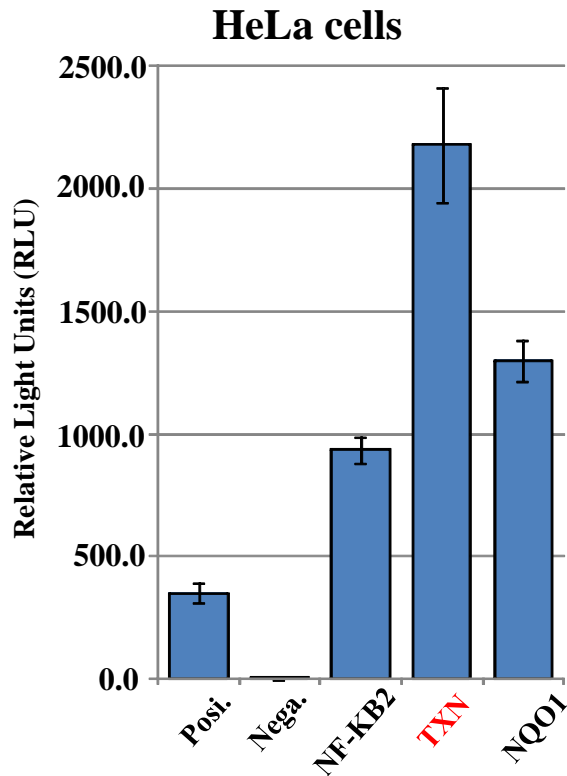


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

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

****TXN:**** pGL4-ph**TXN** (RDB# 7518)

NQO1: pGL4-phNQO1 (RDB# 7570)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.09.30

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5641

2nd Nucleotide Sequence

File Name : RDB7518F.fasta
Sequence Size : 751

Unit Size to Compare = 1
Pick up Location = 1

[96.779% / 745 bp] INT/OPT.Score : < 390/ 2678 >

```
1'          GGCCTAAC TGGCCGGTAC CTGAGCTCGC TAGCCTCGAG
          *****
1'' CGAGGTGCCA GAACATGTCT CTGGCCTAAC TGGCCGGTAC CTGAGCTCGC TAGCCTCGAG

39' GAT-TCCTCA GCCCCTAGA AACTTTGCAC AATAGATTCA AAACCTCNTG GTTTCCTCCC
    *** *****
61'' GATGTCCTCA GCCCCTAGA AACTTTGCAC AATAGATTCA AAACCTCTGG TGTTCTCCCT

98' TTCCTCTGTC TGAAGAGTG AAAGAAGGAA GCCAGGGANT TTCAGGGGGC AGCCAGGCAG
    *****
121'' TTCCTCTGTC TGAAGAGTG AAAGAAGGAA GCCAGGGA-T TTCAGGGGGC AGCCAGGCAG

158' CAGTATCACC ACCCCTAGGC AATCACACCN TAGTTGCAGC TTCATCGGGA ACAGCTCAGC
    *****
180'' CAGTATCACC ACCCCTAGGC AATCACACCC- TAGTTGCAGC TTCATCGGGA ACAGCTCAGC

218' TCTGAAAACA CAGACCTGGG NACTCTCCCT CCCAGCCTTC TAGCTCTCGT TCCTGTGAGC
    *****
239'' TCTGAAAACA CAGACCTGGG -ACTCTCCCT CCCAGCCTTC TAGCTCTCGT TCCTGTGAGC

278' AGCTTTTCAA CNCTCCACTT CCAGCCGCTG ACAGGCCCTC CTGGCTCCAC AAGGCCAGCT
    ***** * *****
```



298" AGCTTTTCAA C-CTCCACTT CCAGCCGCTG ACAGGCCCTC CTGGCTCCAC AAGGCCAGCT

338' AANCATACCC ACCTTCCACA ATCCCAGCC CTGCCAGACA TAACCTGCAA CAGNGCATTG
 ** ***** ***** ***** ***** ***** ***** *****

357" AA-CATACCC ACCTTCCACA ATCCCAGCC CTGCCAGACA TAACCTGCAA CAG-GCATTG

398' CTGGATCAAT GCAAACCTCG ACTTCTGTTC CAGGAGTCTG CCTCNTGTTA GAAGAATCTC
 ***** ***** ***** ***** ***** ***** *****

415" CTGGATCAAT GCAAACCTCG ACTTCTGTTC CAGGAGTCTG CCTC-TGTTA GAAGAATCTC

458' ACACAAGTGT GCGTGCTGTG CCATTGTAAA TGCTGNTATA AGGTGGCCAG GCCCAATCAG
 ***** ***** ***** ***** ***** ***** *****

474" ACACAAGTGT GCGTGCTGTG CCATTGTAAA TGCTG-TATA AGGTGGCCAG GCCCAATCAG

518' TCCCTGCAAG ACACCGAACA GTAAGANACT ATCTATGGAG TGTTTACTAT GTGCCAAGCA
 ***** ***** ***** ** ***** ***** ***** *****

533" TCCCTGCAAG ACACCGAACA GTAAGA-ACT ATCTATGGAG TGTTTACTAT GTGCCAAGCA

578' CCGTCCTTTG CAAGCACNTA TTAACCCTCA AAATACCACC ACCGTGAGAT TGAGACCATC
 ***** ***** ** ***** ***** ***** ***** *****

592" CCGTCCTTTG CAAGCAC-TA TTAACCCTCA AAATACCACC ACCGTGAGAT TGAGACCATC

638' ATGATTCCNC GTTCTACAGA AGGAAACACT GAGACTTCAG GAGGTCAGGA CCTTTCCAGN
 ***** * ***** ***** ***** *. * ***** ***** **

651" ATGATTCC-C GTTCTACAGA AGGAAACACT GAGAC-TNAN GAGGTCAGGA CCTTT-CAG-

698' GGTCACAACT GCGTAACTAA GTTGCAGAGC TCAACCCAGT GGCACCTCCA NTCTCACAGG
 ***** ***** * *. ***** ***** *****

707" GGTCACAACT GCGTAACTAA G-TNCAGAGC TCAACCCAGT -GCACTT

1st Nucleotide Sequence

File Name : Reference Seq. gnu
 Sequence Size : 5641

2nd Nucleotide Sequence



File Name : RDB7518R.fasta (Complementary)

Sequence Size : 756

Unit Size to Compare = 1

Pick up Location = 1

[94.531% / 768 bp] INT/OPT.Score : < 427/ 2672 >

721' GCAGAGCTCA ACCCA-GTGG CA-CTTCCAN TCTCACACGC AGCTGTCTGA TGGTCAAGAG

* *** * *** ** * ** *.****. ***** ***** *****

1" GGTCA AACCACGTCG CANCNTCCAT TCTCACACG- AGCTGTCTGA TGGTCAAGAG

779' --CCCAACCA GTCCCCGGT CGNTTCTAC CGCACTAAC CGCTGTGTCA AGCTGGAGCA

** ***** ***** * **, ** * **, ***** ***** **** **.

55" CCCCAAACCA GTCCCCGTT CGTTTCTACC CGCNCTAAC CGCTGTGTCA GGCTGAGGCN

837' GCGGGCTCAG CAGNTGAAAA TGAAGAACA GAAGGAGGTT ACAGAGAAGA GAA-CGGTCA

*****. * *** ***** ***** ** ***** ***** ** ** **.

115" GCGGGCTCNG CAG-TGAAAA TGAAGAACA GAGGGAGGTT ACAGAGAAGA GAACCGTTCN

896' CGGTANAATT CCGGAGAGGA -GGCAAGGAC GTACACACCG AGATACTTCC CGGTCACNCG

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

174" CGGTA-AATT CCGGAGAGGA GGGCAAGGAC GTACACACCG AGATACTTCC CGGTCAC-CG

955' TTA CT CAGCA CTTTGTGGG TTCACGTGGC TGGGGGGGCC GGGGCGTGNG CGGCCCTTTT

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

232" TTA CT CAGCA CTTTGTGGG TTCACGTGGC TGGGGGGGCC GGGGCGTG-G CGGCCCTTTT

1015' CGAGGAATCC AGCCCTGCCT GGGCGGTCCC CATCTCGAGN CGTGGGCGTG TTCGATTCAG

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

291" CGAGGAATCC AGCCCTGCCT GGGCGGTCCC CATCTCGAG- CGTGGGCGTG TTCGATTCAG

1075' GCCCGGCGGA CGCATCCCCA GGTGACCCGG NGAGGGACCT TGTGTCTCTG GGGGTGACTG

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

350" GCTCGGCGGA CGCATCCCCA GGTGACCCGG -GAGGGACCT TGTGTCTCTG GGGGTGACTG

1135' TCCGTCTCCC CGCCTCCAC CNGTCACGCG CAGTGCTGAT CCCCACTTCC AGCTGGAGTG

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

409" TCCGTCTCCC CGCCTCCAC C-GTCACGCG CAGTGCTGAT CCCCACTTCC AGCTGGAGTG



1195' CGAGCTGGGC TTNGGGGTTA CAGGAGCCGA AGCCCTGGAG CTCCGCCCA CGCTTGC GCC
 ***** ** ***** ***** ***** ***** *****
 468" CGAGCTGGGC TT-GGGGTTA CAGGAGCCGA AGCCCTGGAG CTCCGCCCA CGCTTGC GCC

 1255' AGCNCCCGCC CCGATCCCGG CTCGCAGGCT CCAGGGGCGG GCGTGGCCG GGGCNGCAGC
 *** ***** ***** ***** ***** ***** *****
 527" AGC-CCCGCC CCGATCCCGG CTCGCAGGCT CCAGGGGCGG GCGTGGCCG GGGC-GCAGC

 1315' GACGGGCGCG GAGGTCCGGC CGGGCGCGCG CGCCCCGCC ACACGNCAGC CCGGGCGTGC
 ***** ***** ***** ***** ***** . *****
 585" GACGGGCGCG GAGGTCCGGC CGGGCGCGCG CGCCCCGCC ACACGNCAGC CCGGGCGTGC

 1375' CAGTTTATAA AGGGAGAGAG CAAGCAGCGA GTCTTGNAAG CTCTGTTTGG TGCTTTGGAT
 ***** ***** ***** ***** ** ***** *****
 645" CAGTTTATAA AGGGAGAGAG CAAGCAGCGA GTCTTG-AAG CTCTGTTTGG TGCTTTGGAT

 1435' CCATTTATCA AGATCTGGCC TCGGCGGCCA AGCTTGCAA TCCGGTACTG TTGGTAAAGC
 ***** ***** ***** ***** ***** ***
 704" CCATTTATCA AGATCTGGCC TCGGCGGCCA AGCTTGCAA TCCGGTACTG TTG