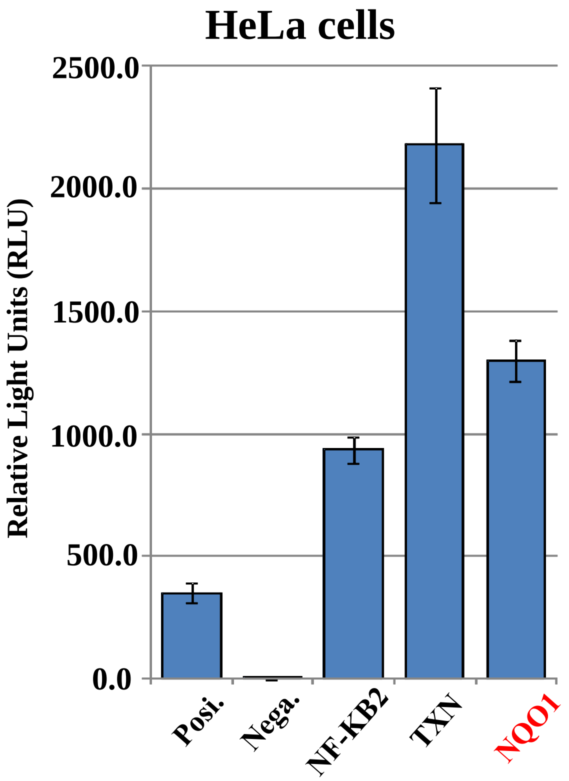
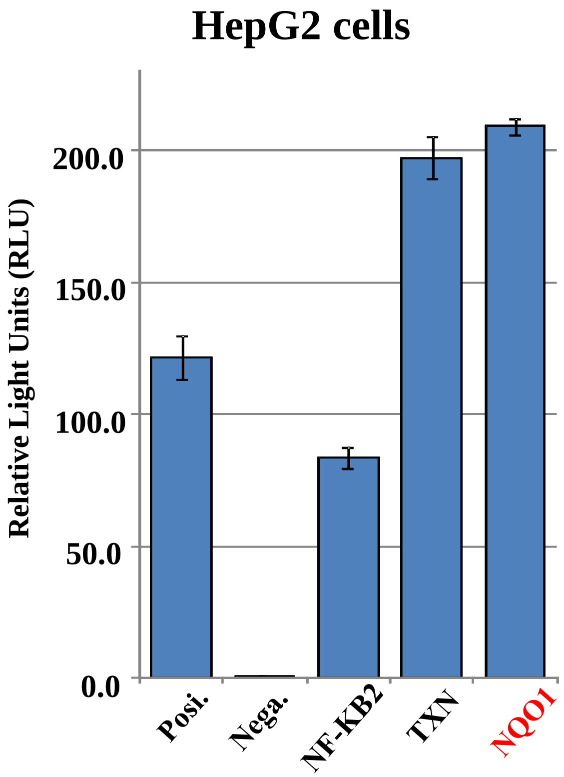
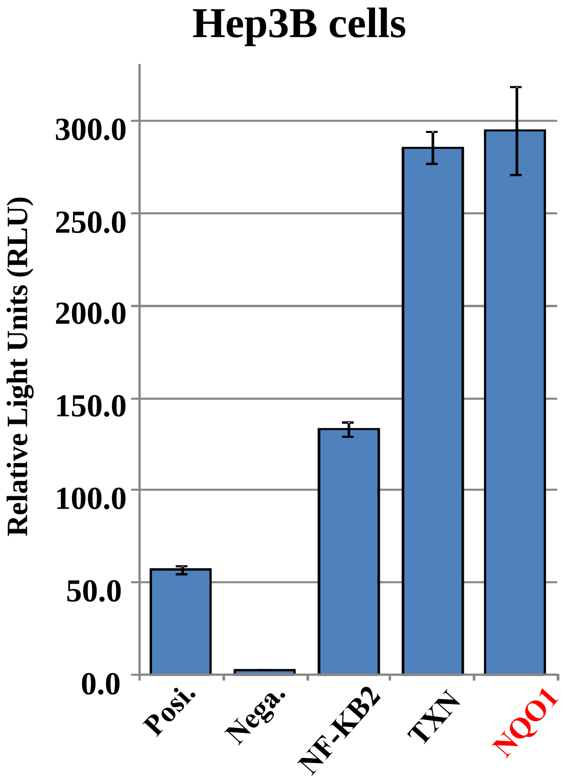
The Promoter Activities of Reporter Constructs







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)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.20

1st Nucleotide Sequence
  File Name         : Reference Seq (NQ01)-insert
  Sequence Size     : 1399

2nd Nucleotide Sequence
  File Name         : RDB7570F.fasta
  Sequence Size     : 721

Unit Size to Compare : 6

Percent Similarity    : 99.2
Percent Identity      : 99.2


     1’ ATTTTGT-CA GATGGGG--- TCTCACTTTG TTGCTCAG-G CTTTTCTCAA ACTCTTGGGC
        ** **** ** *******     ********* ******** * ********** **********
    59″ ATGTTGTGCA GATGGGGGGT GCTCACTTTG TTGCTCAGTG CTTTTCTCAA ACTCTTGGGC

    56’ TCAAG-TGAT CCTCCTGCCT CAGCCTCCCA AAGTAATTTG TAAATACGTG TAAATAATAT
        ***** **** ********** ********** ********** ********** **********
   119″ TCAAGTTGAT CCTCCTGCCT CAGCCTCCCA AAGTAATTTG TAAATACGTG TAAATAATAT

   115’ AGTCCTCTCT TG-TTGCA-T CAAAATGAAT GCAAAAATGT CACGATGGGG CC-GGGCGCG
        ********** ** ***** * ********** ********** ********** ** *******
   179″ AGTCCTCTCT TGTTTGCAGT CAAAATGAAT GCAAAAATGT CACGATGGGG CCGGGGCGCG

   172’ GTGGCTCATG CCTGTAATCC CAGCACTTCG GGAGGCCGAG GCGGTAGGAT CACCTGAGGT
        ********** ********** ********** ********** ********** **********
   239″ GTGGCTCATG CCTGTAATCC CAGCACTTCG GGAGGCCGAG GCGGTAGGAT CACCTGAGGT

   232’ CGGGAGTTGG AAACCAGTTT TCTGGTGCCT CCTTAACTTT TGCACTGGAG GGACAACGGA
        ********** ********** ********** ********** ********** **********
   299″ CGGGAGTTGG AAACCAGTTT TCTGGTGCCT CCTTAACTTT TGCACTGGAG GGACAACGGA
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292’ AGGGCCCTGT GTCATCCTCA CCTCCCCCAT CTGTGATTCT TCTGATGGTT AATTACCACT
     ********** ********** ********** ********** ********** **********
359″ AGGGCCCTGT GTCATCCTCA CCTCCCCCAT CTGTGATTCT TCTGATGGTT AATTACCACT

352’ TTAAAGCTCT AGTTCTTTTT CCTTCACCTA CTGAGAGTAT ATCTCCTTCT TTACAGTAAC
     ********** ********** ********** ********** ********** **********
419″ TTAAAGCTCT AGTTCTTTTT CCTTCACCTA CTGAGAGTAT ATCTCCTTCT TTACAGTAAC

412’ TTTTACTTTA TAGAGTTTTT TTTGAGACGG AGTCTCACTT CGTCACCCAG GCGGGAGTGC
     ********** ********** ********** ********** ********** **********
479″ TTTTACTTTA TAGAGTTTTT TTTGAGACGG AGTCTCACTT CGTCACCCAG GCGGGAGTGC

472’ AGTGGCACGA TCTCGACCCA CTGCAACCTC CGCCTTCCGG GTTCAAGCGA TTCTCCTGCC
     ********** ********** ********** ********** ********** **********
539″ AGTGGCACGA TCTCGACCCA CTGCAACCTC CGCCTTCCGG GTTCAAGCGA TTCTCCTGCC

532’ TCAGCCTCCC GAGTAGCTGG GACTTACAGG CGCCCGCCAT CACGCCCAGC TAATTTTTCA
     *******    ********** ********** ********** ********** **********
599″ TCAGCCT-AA GAGTAGCTGG GACTTACAGG CGCCCGCCAT CACGCCCAGC TAATTTTTCA

592’ GTACAGAC-G GGGCTTCACC AGGTT--GGC CAGGCT-GGT CTCGAA--CT -CCTGA-CCT
     ******** * ********** *****  * * ****** *** ******  **  ***** ***
658″ GTACAGACGG GGGCTTCACC AGGTTTGGCC CAGGCTGGGT CTCGAAACCT CCCTGACCCT

644’ CAGG
     ****
718″ CAGG
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1st Nucleotide Sequence

File Name : Reference Seq (NQ01)-insert

Sequence Size : 1399

2nd Nucleotide Sequence

File Name : RDB7570R.fasta (Complementary)

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  Sequence Size     : 738

Unit Size to Compare : 6

Percent Similarity    : 100.0
Percent Identity      : 99.8


  742’ ATAACTGCTA TCTCCACACC AGCCTTGCCT TAGCTCATGG GAAACAAAAC CAATTAGTTC
       ***.****** ********** ********** ******** * ********** **********
  738” ATANCTGCTA TCTCCACACC AGCCTTGCCT TAGCTCAT-G GAAACAAAAC CAATTAGTTC

  802’ CCCCATTACC TGCCTTGAGG AGCAGGGGTG GTGCAGTGGC ATGCACCCAG GG-AAGTGTG
       ********** ********** ********** ********** ********** ** *******
  679” CCCCATTACC TGCCTTGAGG AGCAGGGGTG GTGCAGTGGC ATGCACCCAG GGAAAGTGTG

  861’ TTGTATGGGC CCCCAAGTGC AGAATCTGAA TCTTGCAAAG GAAGAAACAA ATTCGTCTCC
       ********** ********** ********** ********** ********** **********
  619” TTGTATGGGC CCCCAAGTGC AGAATCTGAA TCTTGCAAAG GAAGAAACAA ATTCGTCTCC

  921’ ACGGAGCATG TCTCCCCAGG ACTCTCAGCC TTCCAAATCC GCAGTCACAG TGACTCAGCA
       ********** ********** ********** ********** ********** **********
  559” ACGGAGCATG TCTCCCCAGG ACTCTCAGCC TTCCAAATCC GCAGTCACAG TGACTCAGCA

  981’ GAATCTGAGC CTAGGGCACC ACAGTAATCC GCATCCGGCT CTTTTTCTGC TCCATTTCGT
       ********** ********** ********** ********** ********** **********
  499” GAATCTGAGC CTAGGGCACC ACAGTAATCC GCATCCGGCT CTTTTTCTGC TCCATTTCGT

 1041’ GCCAAGGCTA AAAGGGCATG CCCACTTGAT CCCTGGACTC TCTTGGGACG ACTTCCACCC
       ********** ********** ********** ********** ********** **********
  439” GCCAAGGCTA AAAGGGCATG CCCACTTGAT CCCTGGACTC TCTTGGGACG ACTTCCACCC

 1101’ TGCATCCTCT TGCACCTCAG GGCACAGTGC GCAGATGGGC TTGCCTTAGC ACCCCCAGCC
       ********** ********** ********** ********** ********** **********
  379” TGCATCCTCT TGCACCTCAG GGCACAGTGC GCAGATGGGC TTGCCTTAGC ACCCCCAGCC

 1161’ AGATTTTTGA GGCCTCTGTC ACACACACCC CTACAATCCC CTCCCCCAGC CCCGAGAGAC
       ********** ********** ********** ********** ********** **********
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 319″ AGATTTTTGA GGCCTCTGTC ACACACACCC CTACAATCCC CTCCCCCAGC CCCGAGAGAC

1221’ TTTTCTTGAC TTCCACCAGT TGCTCCGGCG GGTGAGAGTG GAGAGGCCCC TCCTTCATCC
      ********** ********** ********** ********** ********** **********
 259″ TTTTCTTGAC TTCCACCAGT TGCTCCGGCG GGTGAGAGTG GAGAGGCCCC TCCTTCATCC

1281’ CCCAGGCTCC CTCCCTTCCT GGAGCTGCAG CCTCAGCATC CTCCGCCCAG CACCCCAGGA
      ********** ********** ********** ********** ********** **********
 199″ CCCAGGCTCC CTCCCTTCCT GGAGCTGCAG CCTCAGCATC CTCCGCCCAG CACCCCAGGA

1341’ TTCAGGCGTT GGGTCCCGCC CTTGTAGGCT GTCCACCTCA AACGGGCCGG ACAGG-ATAT
      ********** ********** ********** ********** ********** ***** ****
 139″ TTCAGGCGTT GGGTCCCGCC CTTGTAGGCT GTCCACCTCA AACGGGCCGG ACAGGCATAT
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