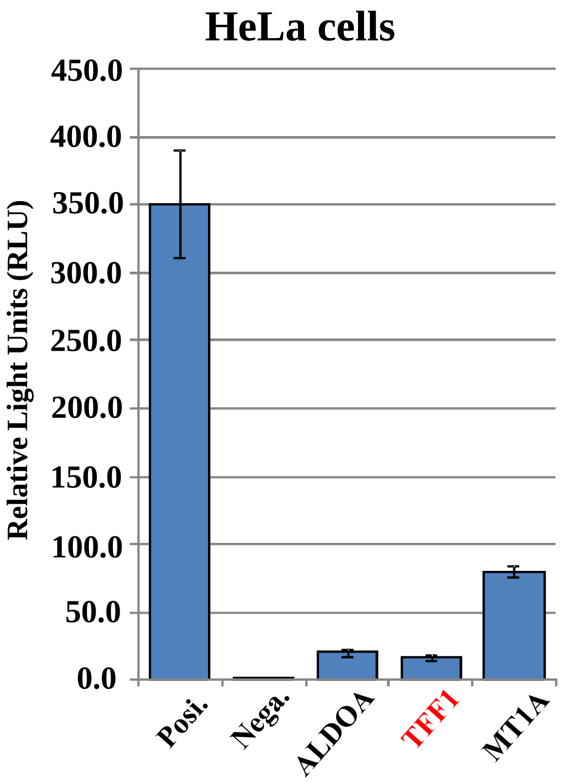
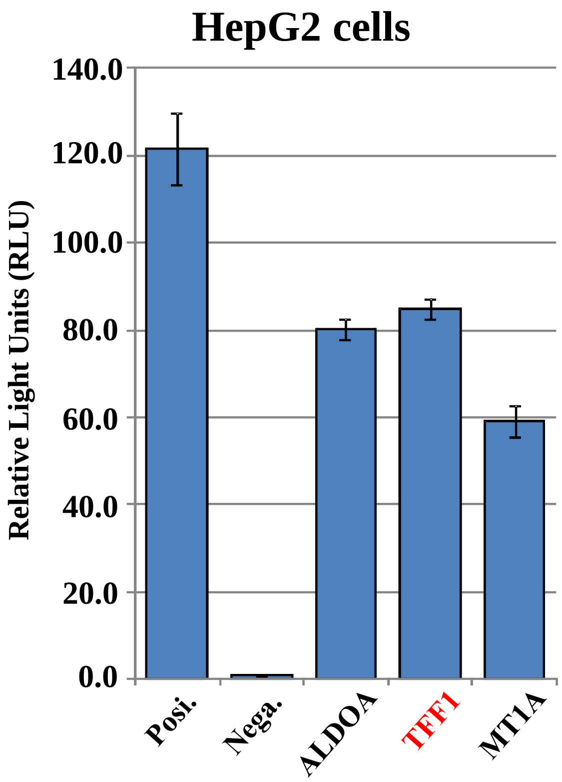
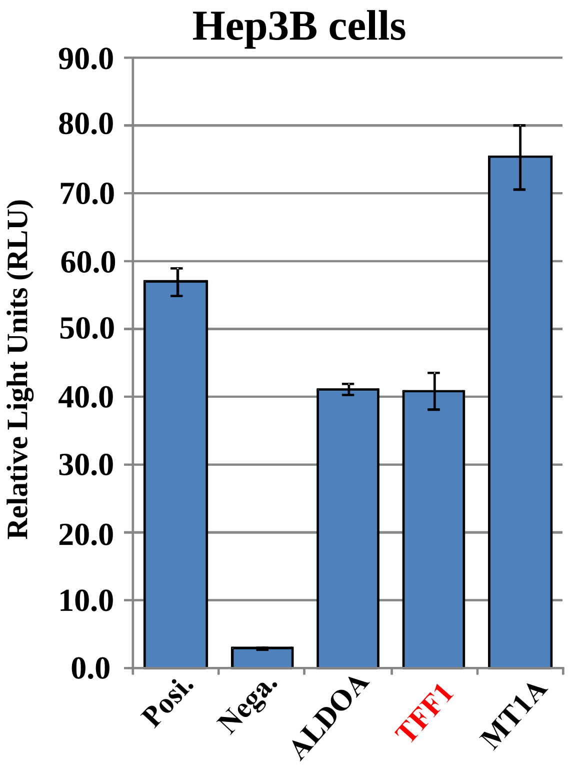
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

Posi.: pGL3 Control Vector
(SV40 promoter)
Nega.: Empty Vector

ALDOA: pGL4-phALDOA(RDB# 7512)
TFF1: pGL4-phTFF1 (RDB# 7511)
MT1A: pGL4-phMT1A (RDB# 7513)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.09.09

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5645

2nd Nucleotide Sequence
  File Name         : RDB7511F.fasta
  Sequence Size     : 684

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.189% / 676 bp]     INT/OPT.Score : <    563/  2466 >

     1’                      G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
     1″ GTGCCAGAAC ATTGTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

    42’ GAGGGGCTGC AGAAATG-TA CTGACTAGGT CACCCAAGAA NAAGATAGTA CCTTTGTTAG
        ********** ******* ** ********** **********  ********* **********
    61″ GAGGGGCTGC AGAAATGTTA CTGACTAGGT CACCCAAGAA -AAGATAGTA CCTTTGTTAG

   101’ GCTAGCATGC AT-TTTCCTC AGGGCCTAAT TTNCTCACTG AAGAAGAAAA GATTTCTCCT
        ********** **  .****** ********** ** ******* ********** **********
   120″ GCTAGCATGC ATGNTTCCTC AGGGCCTAAT TT-CTCACTG AAGAAGAAAA GATTTCTCCT

   160’ GTTGTCCATT TCTTCATGCA GCTNCTTCAA CAGCTGTTTC TCGAATGCCA ATCAAAGCCA
        ********** ********** *** ****** ********** ********** **********
   179″ GTTGTCCATT TCTTCATGCA GCT-CTTCAA CAGCTGTTTC TCGAATGCCA ATCAAAGCCA

   220’ CTGTTCTAGG GTCTNGGGGC CACCTCAAGG CACTAGGAGA TGAGGACTTC TGCTCCCATG
        ********** **** ***** ********** ********** ********** **********
   238″ CTGTTCTAGG GTCT-GGGGC CACCTCAAGG CACTAGGAGA TGAGGACTTC TGCTCCCATG
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280’ CGCCCNTCCC GTCTGCTGCA GGGAGGAGTG CAATGAATAA ATAACCAACA TAATGTNGTC
     ***** **** ********** ********** ********** ********** ****** ***
297″ CGCCC-TCCC GTCTGCTGCA GGGAGGAGTG CAATGAATAA ATAACCAACA TAATGT-GTC

340’ AGTCACTTGT TTTATCCACC AGGAGGTAAT AAGAGCTATG AAAGAGANAA GCTCCGAGCA
     ********** ********** ********** ********** ******* ** **********
355″ AGTCACTTGT TTTATCCACC AGGAGGTAAT AAGAGCTATG AAAGAGA-AA GCTCCGAGCA

400’ GGGGAGGGGA GTGAGGCATG GTACAGGAGA GCAGGAGGNC TGTCCTCTAA AATACAGGAG
     ********** ********** ********** ******** * ********** **********
414″ GGGGAGGGGA GTGAGGCATG GTACAGGAGA GCAGGAGG-C TGTCCTCTAA AATACAGGAG

460’ TCCAGGGGAC CAACTGGGAA GGTGTGGGAN GGGGGAGGGA GGGAGCCCCA TAGACACAGG
     ********** ********** *********. ****  ** * ********** **********
473″ TCCAGGGGAC CAACTGGGAA GGTGTGGGAG GGGGAGGGAA GGGAGCCCCA TAGACACAGG

520’ GGAGTGAACC ACGTTCACTT NTGTCAGTTT TTGATGGCAG CTCGTATATA CTATTTTTTT
     ********** ** *******  ********* ********** ********** **********
533″ GGAGTGAACC ACATTCACTT -TGTCAGTTT TTGATGGCAG CTCGTATATA CTATTTTTTT

580’ CTCCCTCCTG CNCCCCAGCC CCTCCCAGAA GGAGACTTAA TCTGTCGCTC AGGCTGGAGT
     ********** * ******** ********** ********** ********** **********
592″ CTCCCTCCTG C-CCCCAGCC CCTCCCAGAA GGAGACTTAA TCTGTCGCTC AGGCTGGAGT

640’ GCNAGTAGGG TGATCTCGAC TCACTGCAAC CTCCGCCTCC CAGGTTCAAG TGANTTCTCC
     ** ******* ********** ********** *****
651″ GC-AGTAGGG TGATCTCGAC TCACTGCAAC CTCCG
```

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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5645

2nd Nucleotide Sequence
  File Name         : RDB7511.fasta (Complementary)
  Sequence Size     : 648
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  Unit Size to Compare = 1
  Pick up Location     = 1



[98.024% / 658 bp]     INT/OPT.Score : <    425/  2434 >

  841' CCTGCNTTTG GCCTCCCAAA GTGTTGGGAT TACAGGCGTG AGCCACTGCG CCAGGCNCTA
                                         ********* ********** ****** ***
    1″                                  AACAGGCGTG AGCCACTGCG CCAGGC-CTA

  901' CAATTTCATT ATTAAAACAA TTCCACTGTA AAAGAATTAG CTTAGGCNCT AGACGGAATG
       ********** ********** ********** ********** ******* ** **********
   30″ CAATTTCATT ATTAAAACAA TTCCACTGTA AAAGAATTAG CTTAGGC-CT AGACGGAATG

  961' GGCTTCATGA GCTCCTTCCC TTCCCCCTGC AAGGTCACNG GTGGCCACCC CGTGAGCCAC
       ********** ********** ********** ******** * **** ***** **********
   89″ GGCTTCATGA GCTCCTTCCC TTCCCCCTGC AAGGTCAC-G GTGGTCACCC CGTGAGCCAC

 1021' TGTTGTCACG GCCAAGCCTT TTTCCGGCCN ATCTCTCACT ATGAATCACT TCTGCAGTGA
       ********** ********** *********  ********** ********** **********
  148″ TGTTGTCACG GCCAAGCCTT TTTCCGGCC- ATCTCTCACT ATGAATCACT TCTGCAGTGA

 1081' GTACAGTATT TACCCTGGCG NGGAGGGCCT CTCAGATATG AGTAGGACCT GGATTAAGGT
       ********** **********  ********* ********** ********** **********
  207″ GTACAGTATT TACCCTGGCG -GGAGGGCCT CTCAGATATG AGTAGGACCT GGATTAAGGT

 1141' CAGGTTGGAG GNAGACTCCC ATGGGAAAGA GGGACTTTCT GAATCTCAGA TCCCTCAGCC
       ********** * ******** ********** ********** ********** **********
  266″ CAGGTTGGAG G-AGACTCCC ATGGGAAAGA GGGACTTTCT GAATCTCAGA TCCCTCAGCC

 1201' AANGATGACC TCACCACATG TCGTCTCTGT CTATCAGCAA ATCCTTCCAT GTANGCTTGA
       ** ******* ********** ********** ********** ********** *** ******
  325″ AA-GATGACC TCACCACATG TCGTCTCTGT CTATCAGCAA ATCCTTCCAT GTA-GCTTGA

 1261' CCATGTCTAG GAAACACCTT TGATAAAAAT CAGTGGAGAT TATTNGTCTC AGAGGATCCC
       ********** ********** ********** ********** **** ***** **********
  383″ CCATGTCTAG GAAACACCTT TGATAAAAAT CAGTGGAGAT TATT-GTCTC AGAGGATCCC
```

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1321’ CGGGCCTCCT TAGGCAAATG TTATCTAACG CTCTTNTAAG CAAACAGAGC CTGCCCTATA
      ********** ********** ********** ***** **** ********** **********
 442″ CGGGCCTCCT TAGGCAAATG TTATCTAACG CTCTT-TAAG CAAACAGAGC CTGCCCTATA

1381’ AAATCCGGGG CTCGGGCGGC CTCTCANTCC CTGACTCGGG GTCGCCTTTG GAGCAGAGAG
      ********** ********** ****** *** ********** ********** **********
 501″ AAATCCGGGG CTCGGGCGGC CTCTCA-TCC CTGACTCGGG GTCGCCTTTG GAGCAGAGAG

1441’ GAGGATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA
      ********** ********** ********** ********** ********** **********
 560″ GAGGATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC CGGTACTGTT GGTAAAGCCA

1501’ CCATGGAAG- ATGCCAAAAA CATTAAGAAG GGCCCAGCGC CATTCTACCC ACTCGAAGAC
      *********  ********** *********
 620″ CCATGGAAGA ATGCCAAAAA CATTAAGAA
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