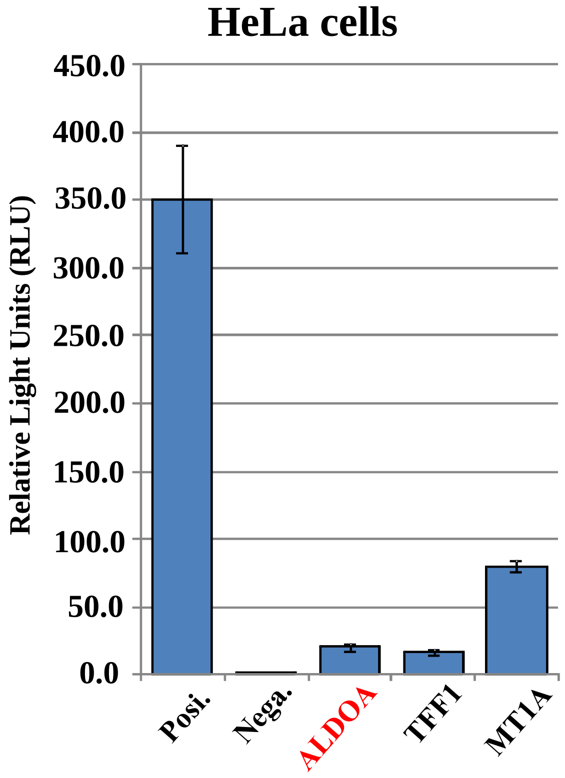
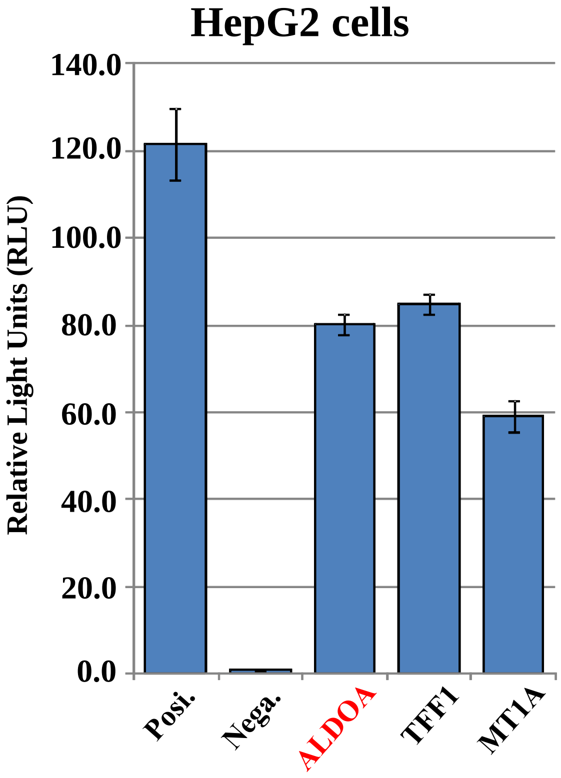
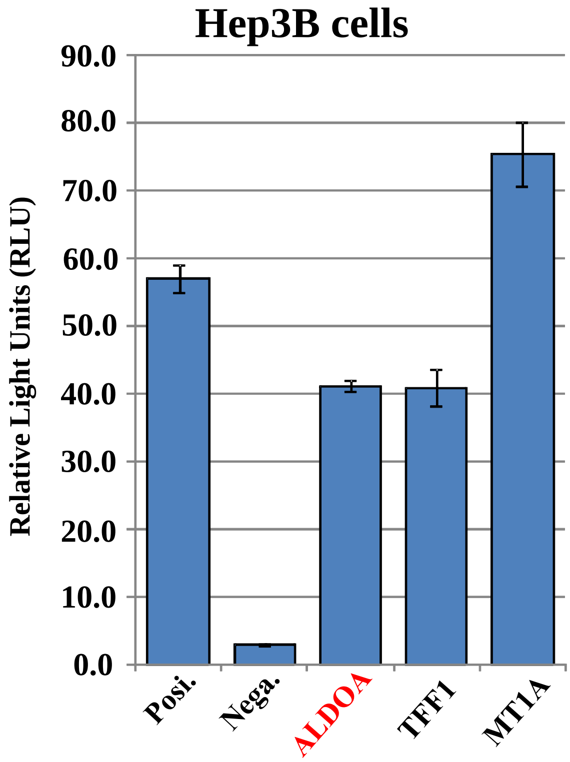
The Promoter Activities of Reporter Constructs







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

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.09.09

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5498

2nd Nucleotide Sequence
  File Name         : RDB7512F.fasta
  Sequence Size     : 468

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.249% / 457 bp]     INT/OPT.Score : <    328/  1700 >

   1'                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                          * ********** ********** ********** **********
   1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

  42' TGCCTGTAAT CCCAGCTACC TGGGAGGCTG AGGCTGGAGG ANCTGCTTGA GCCCAGGAGT
      ********** ********** ********** ********** * ******** **********
  61″ TGCCTGTAAT CCCAGCTACC TGGGAGGCTG AGGCTGGAGG A-CTGCTTGA GCCCAGGAGT

 102' TCAAGACCAG CCTTAACAAC ATAGCAAGAC CANCATCTCT AAAAATTCAG AAAAAAAGGC
      ********** ********** ********** ** ******* ********** **********
 120″ TCAAGACCAG CCTTAACAAC ATAGCAAGAC CA-CATCTCT AAAAATTCAG AAAAAAAGGC

 162' TGGGCACAGT GGCTCATGCC AGTNAATCCT AGCACTTTGG GAGGCCAAGG CGGGCGGGAT
      ********** ********** *** ****** ********** ********** **********
 179″ TGGGCACAGT GGCTCATGCC AGT-AATCCT AGCACTTTGG GAGGCCAAGG CGGGCGGGAT

 222' TGCCTGAGGT TAGGNAGTTC GAGACCAGCC TGGCCAACAT GGTGAAACCC CGTCTCTACT
      ********** **** ***** ********** ********** ********** **********
 238″ TGCCTGAGGT TAGG-AGTTC GAGACCAGCC TGGCCAACAT GGTGAAACCC CGTCTCTACT
```

```
 282' AAAAANTACA AAAATTAGGT GTGCGTGGTG GCAGTCGCCT GTAATCTCAG CTACTCNGGG
      ***** **** ********** ********** ********** ********** ****** ***
 297″ AAAAA-TACA AAAATTAGGT GTGCGTGGTG GCAGTCGCCT GTAATCTCAG CTACTC-GGG

 342' AGGCTGAGGC GGGAGAATCG CTTGAACCCA GGAGACATAG GTTGTAGNTG AGCCAAGATC
      ********** ********** ********** ********** ******* ** **********
 355″ AGGCTGAGGC GGGAGAATCG CTTGAACCCA GGAGACATAG GTTGTAG-TG AGCCAAGATC

 402' ACACCATTGC ACTCCAGCCT GGGAGATGAG CGAAAATCNT GTCTCCAAAA AATAAATAAA
      ********** ********** ********** ******** * ********** ******
 414″ ACACCATTGC ACTCCAGCCT GGGAGATGAG CGAAAATC-T GTCTCCAAAA AATAAA




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5498

2nd Nucleotide Sequence
  File Name        : RDB7512R.fasta (Complementary)
  Sequence Size    : 316

  Unit Size to Compare = 1
  Pick up Location     = 1



[94.969% / 318 bp]     INT/OPT.Score : <    511/  1102 >

1021' GACCCAGGCG GGCGGCGGCG GGATTCGCTC TNTCCCCTTC GCTCCCCGCG AGAAAGCCCC
                                                                  *****
   1″                                                             GCCCC

1081' GAGGGCCGCG GCGGCGCAGA GCNC-GGTGA CAGTTGAAGC TTAGGC-GGG AA-GAGGG-A
      ********** ********** **.* ***** ********** ****** *** ** ***** *
   6″ GAGGGCCGCG GCGGCGCAGA GCCCGGGTGA CAGTTGAAGC TTAGGCGGGG AAGGAGGGAA
```

```
1137’ GGCGCGA-GG CGGGAAGANG GGAGTTTGGG CCTCGGCAGC CGCCGTACAA ACACCGCTCT
      ******* ** ********.* *   ** *** ********** ********** **********
  66” GGCGCGAGGG CGGGAAGAGG GAGTTTGGGG CCTCGGCAGC CGCCGTACAA ACACCGCTCT

1196’ GGTCACCATN GGCAACAGCG GGATGCCGCG AACGGCTTCT GGGCGGGGCC GGTCCCTCGG
      *********  ********** ********** ********** ********** **********
 126” GGTCACCAT- GGCAACAGCG GGATGCCGCG AACGGCTTCT GGGCGGGGCC GGTCCCTCGG

1256’ NACGATTGGA CCTAGCTTGG CGCGGAATCC GTGAATTGCC CGATCAAGAT CTGGCCTCGG
       ********* ********** ********** ********** ********** **********
 185” -ACGATTGGA CCTAGCTTGG CGCGGAATCC GTGAATTGCC CGATCAAGAT CTGGCCTCGG

1316’ CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACA-
      ********** ********** ********** ********** ********** ***** ***
 244” CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAACACAT

1375’ TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC GAGCAGCTGC
      *********  ***
 304” TTAAGAAGGA CCC
```