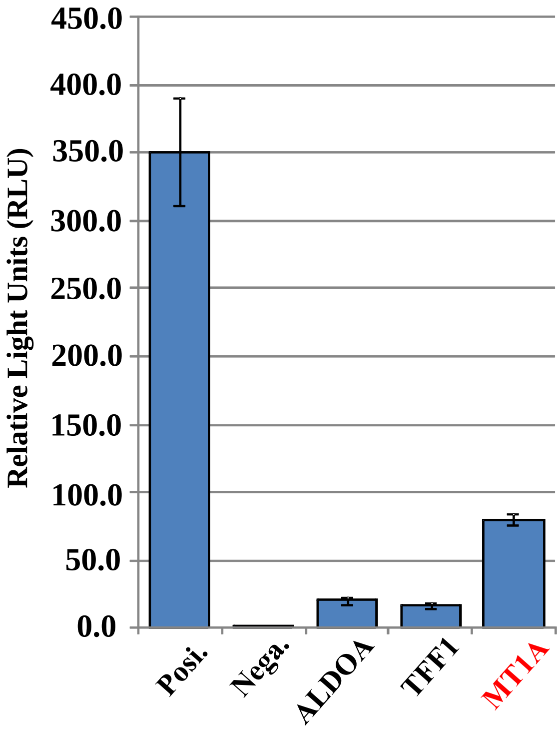
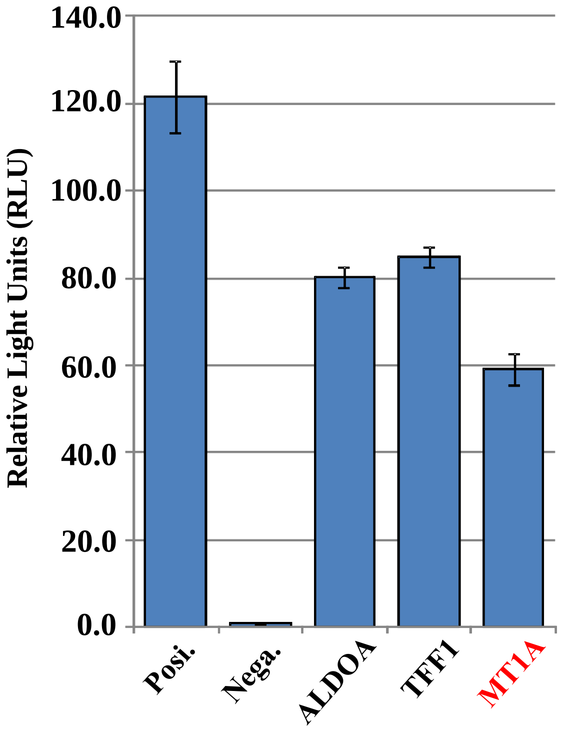
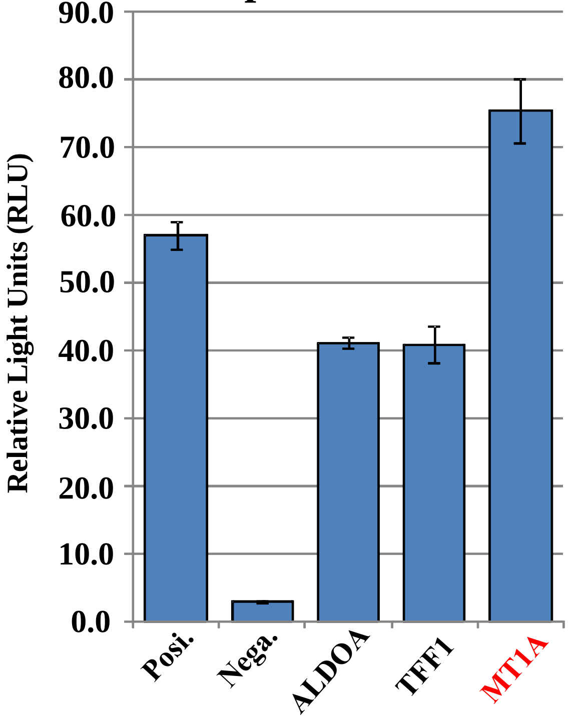
The Promoter Activities of Reporter Constructs


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 : 2009.09.30

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5569

2nd Nucleotide Sequence
  File Name        : RDB7513F.fasta
  Sequence Size    : 642

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.476% / 634 bp]     INT/OPT.Score : <    268/  2333 >

   1’                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
                         ** ********** ********** ********** **********
   1″ GGTGCCGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

  43’ AAGTGGCTAT AGTGCTGGAA CCCAANCTTC TTAGTTTCTT GAATCCTACA TGTGTGCTAT
      ********** ********** ***** **** ********** ********** **********
  61″ AAGTGGCTAT AGTGCTGGAA CCCAA-CTTC TTAGTTTCTT GAATCCTACA TGTGTGCTAT

 103’ GATTTAGATA TTTTGTNCAC TGCCAAATCT CATGTTGAAA TGTGTCCTCC ACTATTGCAG
      ********** ****** *** ********** ********** ********** **********
 120″ GATTTAGATA TTTTGT-CAC TGCCAAATCT CATGTTGAAA TGTGTCCTCC ACTATTGCAG

 163’ GTGGGGCNCT AGAGGGAGCT TTTGGGGTCA TGAGGACACA TCCCTAAAGA ATGACTTGNG
      ******* ** ********** ********** ********** ********** ******** *
 179″ GTGGGGC-CT AGAGGGAGCT TTTGGGGTCA TGAGGACACA TCCCTAAAGA ATGACTTG-G

 223’ TGCCATCCCA TGGTAAAGAG TGTGTTCATC CTCTGGTAGG TCACTCCAGN TGGTGGCTGT
      ********** ********** ********** ********** *********  **********
 237″ TGCCATCCCA TGGTAAAGAG TGTGTTCATC CTCTGGTAGG TCACTCCAG- TGGTGGCTGT
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283’ GAATGAAAGT GATTAGAAAG GGACTGGTAT AGACTCAATG NTTATGCCTT AGTCAGGTGT
     ********** ********** ********** **********  ********* **********
296″ GAATGAAAGT GATTAGAAAG GGACTGGTAT AGACTCAATG -TTATGCCTT AGTCAGGTGT

343’ ACTTTAGGGA AATAACTGGA TGTCTTGCTT TNTTAATTTT ATTTTTTTAG AGAAGTTGAC
     ********** ********** ********** * ******** ********** **********
355″ ACTTTAGGGA AATAACTGGA TGTCTTGCTT T-TTAATTTT ATTTTTTTAG AGAAGTTGAC

403’ TTGCTATGTG GACTAGGCAG GANCTGGAAG TCCTGGGCTT AAGTGATGCT CCCGCCTCAG
     ********** ********** ** ******* *********  ********** **********
414″ TTGCTATGTG GACTAGGCAG GA-CTGGAAG TCCTGGGCTC AAGTGATGCT CCCGCCTCAG

463’ CCTCCTAAGT AGCNTTGGAC TACAGCTTCC CGCCACCTCC CCCATCTTGC TTTTTAGTTT
     ********** *** ****** ********** ********** ********** **********
473″ CCTCCTAAGT AGC-TTGGAC TACAGCTTCC CGCCACCTCC CCCATCTTGC TTTTTAGTTT

523’ AAAGNCAGGG TCAGCACATC ACATGAAGTC ATCTCCTTTT TGGGGATATC CCACANTGTC
     **** ***** ********** ********** ********** ********** ***** ****
532″ AAAG-CAGGG TCAGCACATC ACATGAAGTC ATCTCCTTTT TGGGGATATC CCACA-TGTC

583’ CAGAACTGCC AGACGGTAGT GGGGTGGCCG GCTAGGCTGT GGGGAGNCAC GGAGATTTAT
     ******* ** ********** ********** ********** ****  .*** **
590″ CAGAACTACC AGACGGTAGT GGGGTGGCCG GCTAGGCTGT GGGGGAGCAC GGG
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5569

2nd Nucleotide Sequence
  File Name         : RDB7513R.fasta (Complementary)
  Sequence Size     : 624

  Unit Size to Compare = 1
  Pick up Location     = 1
```

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[97.950% / 634 bp]     INT/OPT.Score : <    436/  2338 >

 781' GNACAGGCAA GGCGACAGCG AGGAGAAACG AAAATCACAT CGGTGGCGGT TGNCTCTGCA
                                               * ********** ** *******
   1″                                         TT CGGTGGCGGT TG-CTCTGCA

 841' CACAACTCGC TCGCTACCGC ACGCTCCACG CTCTGCACTA CGCNCGATCC GGGGACAGGA
      ********** ********** ********** ********** *** ****** **********
  22″ CACAACTCGC TCGCTACCGC ACGCTCCACG CTCTGCACTA CGC-CGATCC GGGGACAGGA

 901' GCAGGAGGCT GTGGCTGCAC TCAGACTTCG GGACNAGGCC GAGCTGAAAA CCGTGAGAGG
      ********** ********** ********** **** ***** ********** **********
  81″ GCAGGAGGCT GTGGCTGCAC TCAGACTTCG GGAC-AGGCC GAGCTGAAAA CCGTGAGAGG

 961' GGTGGGGTGG AGGCGACCGA AACGCNCAAG GCTGGGTTCC CGGAACGCGC GGGGACTAGG
      ********** ********** ***** **** ********** ********** **********
 140″ GGTGGGGTGG AGGCGACCGA AACGC-CAAG GCTGGGTTCC CGGAACGCGC GGGGACTAGG

1021' GTGGAAGGCA ACTTCGNGGG AAACTGGGAA AGGCGACCGG GACCTCGGGG ACGCCCCGTA
      ********** ****** *** ********** ********** ********** **********
 199″ GTGGAAGGCA ACTTCG-GGG AAACTGGGAA AGGCGACCGG GACCTCGGGG ACGCCCCGTA

1081' CCCCGGGNCG TAAACTCACT CCCGCGTTAG C-GGCCCCAA AGCGGGGAGG GGGTGGTCCN
      ******* ** ********** ********** * *** **** ********** *********
 258″ CCCCGGG-CG TAAACTCACT CCCGCGTTAG CGGGCGCCAA AGCGGGGAGG GGGTGGTCC-

1140' CGTGGTCCGC ACCCAGGGGA GCTCAGTGGA CTGTGCGCCT TGCCTTTCTG NCTGCGCAAA
      ********** ********** ********** ********** **********  *********
 316″ CGTGGTCCGC ACCCAGGGGA GCTCAGTGGA CTGTGCGCCT TGCCTTTCTG -CTGCGCAAA

1200' GCCCAGTCCA GGTCATCACC TCGGGCGGGG CGGACTCGGC TNGGGCGGAC TCAGCGGGGC
      ********** ********** ********** ********** * ******** **********
 375″ GCCCAGTCCA GGTCATCACC TCGGGCGGGG CGGACTCGGC T-GGGCGGAC TCAGCGGGGC

1260' GGGCGCAGGC GCAGGGCGGG TCCTTTGCGT CCNGGCCCTC TTTCCCCTGA CCATAAAAGC
      ********** ********** ********** ** ******* ********** **********
 434″ GGGCGCAGGC GCAGGGCGGG TCCTTTGCGT CC-GGCCCTC TTTCCCCTGA CCATAAAAGC
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1320' AGCCGCTGGC TGCTGGGCCC TACNCAAGCC TTCCACGTGC GCCTTATAGA TCAAGATCTG
      ********** ********** *** ****** ********** ********** **********
 493″ AGCCGCTGGC TGCTGGGCCC TAC-CAAGCC TTCCACGTGC GCCTTATAGA TCAAGATCTG

1380' GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA
      ********** ********** ********** ********** ********** **********
 552″ GCCTCGGCGG CCAAGCTTGG CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA

1440' AAAACATTAA GAAGGGCCCA GCGCCATTCT ACCCACTCGA AGACGGGACC GCCGGCGAGC
      ********** ***
 612″ AAAACATTAA GAA
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