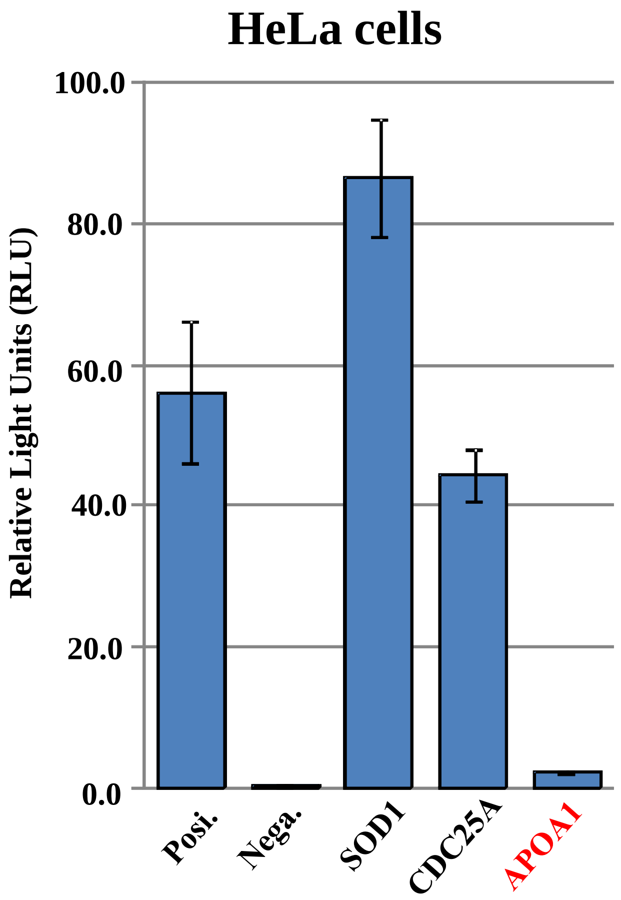
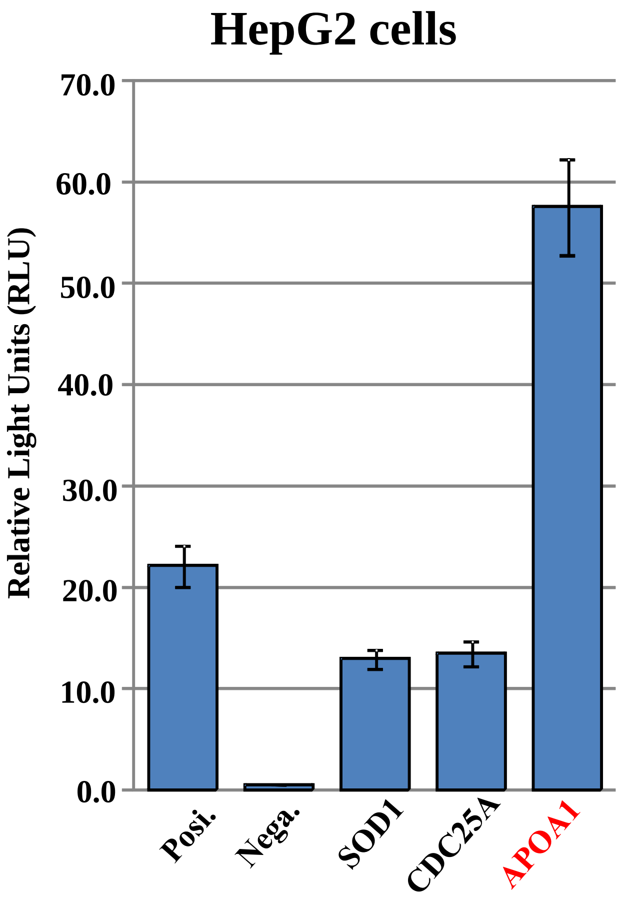
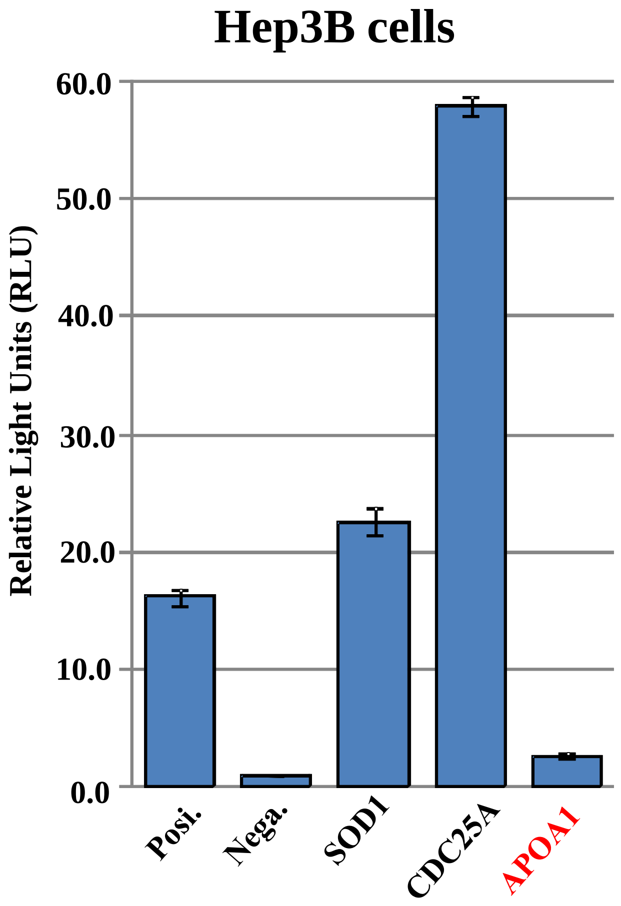
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

SOD1: pGL4-phSOD1 (RDB# 7686)
CDC25A: pGL4-phCDC25A(RDB# 7709)
APOA1: pGL4-phAPOA1(RDB# 7684)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.26


1st Nucleotide Sequence
  File Name        : Reference Seq.prj
  Sequence Size    : 5727

2nd Nucleotide Sequence
  File Name        : RDB7684F.fasta (Complementary)
  Sequence Size    : 491

  Unit Size to Compare = 1
  Pick up Location     = 1



[94.969% / 477 bp]     INT/OPT.Score : <    968/  1594 >

   1081’ GGGGGAGGGG AGTGAAGTAG TCTCCCTGGA ATGCTGGTGG TGGGGGAGGC AGTCTCCTTG

      1″                                                             CCNT

   1141’ GTGGAGGAGT CCCAGCGTCC CT-CCCCTCC CCTCCTC-TG CCAACACAA- TGGACAATGG
                    ***  * ***  * ******* ******* ** *********  **********
      5″ NCCCCCTTTC CCCCCCTTCC TTCCCCCTCC CCTCCTCTTG CCAACACAAT TGGACAATGG

   1198’ CAAC-TGCCC ACACACTCCC ATGGAGGGGA AGGGGA-TGA GTGCAGGGAA CCCCGACCCC
         **** ***** ********** ********** ****** *** ********** **********
     65″ CAACTTGCCC ACACACTCCC ATGGAGGGGA AGGGGATTGA GTGCAGGGAA CCCCGACCCC

   1256’ ACCCGGGAGA CC-TGCAA-G CC-TGCAGAC ACTCCCCTCC C-GCCCCCAC TGAACCCTTG
         ********** ** ***** * ** ******* ********** * ******** **********
    125″ ACCCGGGAGA CCTTGCAATG CCTTGCAGAC ACTCCCCTCC CTGCCCCCAC TGAACCCTTG

   1312’ ACCCC-TGCC C-TGCA-GCC CCCGCA-GC- TTGCTGTTTG CCCACTCTA- TTTGCCCA-G
         ***** **** * **** *** ****** **  ********** *********  ******** *
    185″ ACCCCTTGCC CTTGCATGCC CCCGCATGCT TTGCTGTTTG CCCACTCTAT TTTGCCCATG
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 1365' CCCCAGGGAC AGAGCTGATC CTTGAACTCT TAAGTTCCAC ATTGCCAGGA CCAGTGAGCA
       ********** ********** ********** ********** ********** **********
  245″ CCCCAGGGAC AGAGCTGATC CTTGAACTCT TAAGTTCCAC ATTGCCAGGA CCAGTGAGCA

 1425' GCAACAGGGC CGGGGCTGGG CTTATCAGCC TCCCAGCCCA GACCCTGGCT GCAGACATAA
       ********** * ******** ********** ********** ********** **********
  305″ GCAACAGGGC CAGGGCTGGG CTTATCAGCC TCCCAGCCCA GACCCTGGCT GCAGACATAA

 1485' ATAGGCCCTG CAAGAGCTGG CTGCTTAGAG ACTGCGAGAA GGATCAAGAT CTGGCCTCGG
       ********** ********** ********** ********** ********** **********
  365″ ATAGGCCCTG CAAGAGCTGG CTGCTTAGAG ACTGCGAGAA GGATCAAGAT CTGGCCTCGG

 1545' CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACA-
       ********** ********** ********** ********** ********** ***** ***
  425″ CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC ATGGAAGATG CCAAACACAC

 1604' TTAAGAAGGG CCCAGCGCCA TTCTACCCAC TCGAAGACGG GACCGCCGGC GAGCAGCTGC
        ******
  485″ ATAAGAA



1st Nucleotide Sequence
  File Name        : Reference Seq.prj
  Sequence Size    : 5727

2nd Nucleotide Sequence
  File Name        : RDB7684R.fasta
  Sequence Size    : 770

  Unit Size to Compare = 1
  Pick up Location     = 1


[98.925% / 744 bp]     INT/OPT.Score : <   2768/  2914 >
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  1’                              GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC
                                  *** ********** ********** **********
  1″ ATGCATTGCG GTGCCGAACT TTACTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC

 34’ TCGAGGATTG AACCTGCCTG ACCCTTAGAT TTGAGGTTTT CTGGCTCCAG AATCTTCTCT
     ********** ********** ********** ********** ********** **********
 61″ TCGAGGATTG AACCTGCCTG ACCCTTAGAT TTGAGGTTTT CTGGCTCCAG AATCTTCTCT

 94’ GAAGTGAAAG GCATGAGGCC GACCACTCCC TGATCTGGTA AACAGAGATG TCAGCCTGGT
     ********** ********** ********** ********** ********** **********
121″ GAAGTGAAAG GCATGAGGCC GACCACTCCC TGATCTGGTA AACAGAGATG TCAGCCTGGT

154’ TTCTAGTGTT AGGGAGTTTC CTGGAGTGAT GGTACAGGGT ACATTTCTGC CCTGCATCCC
     ********** ********** ********** ********** ********** **********
181″ TTCTAGTGTT AGGGAGTTTC CTGGAGTGAT GGTACAGGGT ACATTTCTGC CCTGCATCCC

214’ AAGTCCAGAG ACTGGGTTCT AGGTCCAGCC TTTCTTCTAA CTCCCTGAGA GATGACAGCC
     ********** ********** ********** ********** ********** **********
241″ AAGTCCAGAG ACTGGGTTCT AGGTCCAGCC TTTCTTCTAA CTCCCTGAGA GATGACAGCC

274’ TCTGGGCAAA GTCCCTCTGT GCTCTTCAGT CTCTTCATCT GTGAGATGGT GGCATGGGGA
     ********** ********** ********** ********** ********** **********
301″ TCTGGGCAAA GTCCCTCTGT GCTCTTCAGT CTCTTCATCT GTGAGATGGT GGCATGGGGA

334’ GAGGCTGGAG TGATGTCACA GTTCCTCTCA GCCTGCATCA CAGGCTCTAG GACTCAGGTC
     ********** ********** ********** ********** ********** **********
361″ GAGGCTGGAG TGATGTCACA GTTCCTCTCA GCCTGCATCA CAGGCTCTAG GACTCAGGTC

394’ CTATCAGTAA CCTGCTGGGG GAGGTCTGGG CCTTCCAGGA GAAACCTGAC AAGATGGTGC
     ********** ******* ** ********** ********** ********** **********
421″ CTATCAGTAA CCTGCTGAGG GAGGTCTGGG CCTTCCAGGA GAAACCTGAC AAGATGGTGC

454’ TGCAAACACC AACGGACACA CAGCACTTTA CATTCACAGG CTGTCTCAGG GGCCTCCAAC
     ********** ********** ********** ********** ********** **********
481″ TGCAAACACC AACGGACACA CAGCACTTTA CATTCACAGG CTGTCTCAGG GGCCTCCAAC

514’ AACCCTGACC ATTCTTGCCC CATTTTGCAG ATAGAAAACC GAGGCTCAGA GAGATTATAT
     ********** ********** ********** ********** ********** **********
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541″ AACCCTGACC ATTCTTGCCC CATTTTGCAG ATAGAAAACC GAGGCTCAGA GAGATTATAT

574' AACTTGCCCA CGATCTTCCT CCAGCAAGAT GGAGGCCAAG TGAAATGAGA AAGCAGGTCT
     ********** ********** ********** ********** ********** ***** ****
601″ AACTTGCCCA CGATCTTCCT CCAGCAAGAT GGAGGCCAAG TGAAATGAGA AAGCAAGTCT

634' CCTGCCACTT CCTTTGCCCA GAGGTCTTCT CCCCACACCA GGGCTTCCCA AGGGCTGAGA
     ********** ********** ********** ********** ********** **********
661″ CCTGCCACTT CCTTTGCCCA GAGGTCTTCT CCCCACACCA GGGCTTCCCA AGGGCTGAGA

694' TCCAGTCACA CCTGTGCGTG ATCAAATATA AGTGTGAACA ATGCAAAGGG AGACGTCTTC
     * ******** ********** ***** **** *********  *.*****.*  *
721″ T-CAGTCACA CCTGTGCGTG ATCAATTATA AGTGTGAAC- ANGCAAANGA AA
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