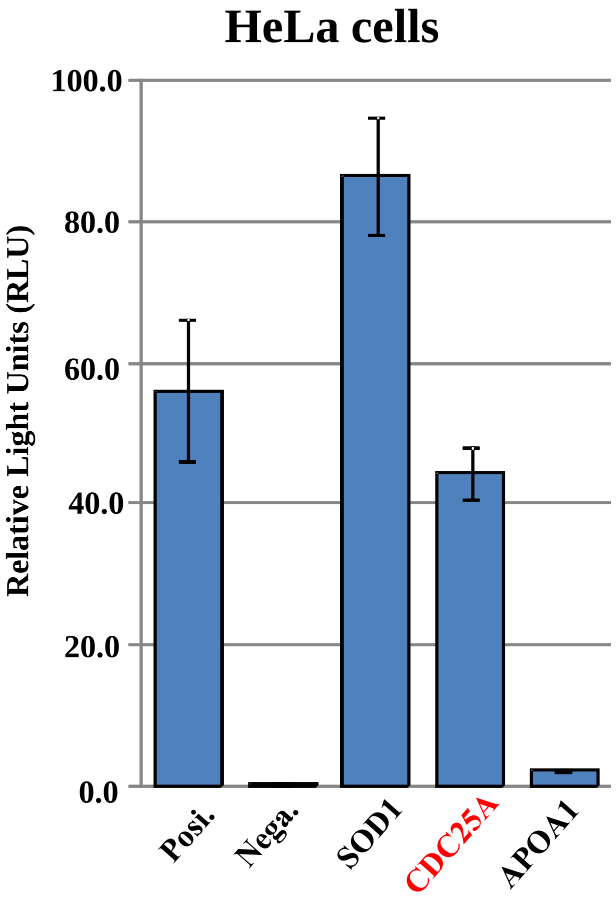
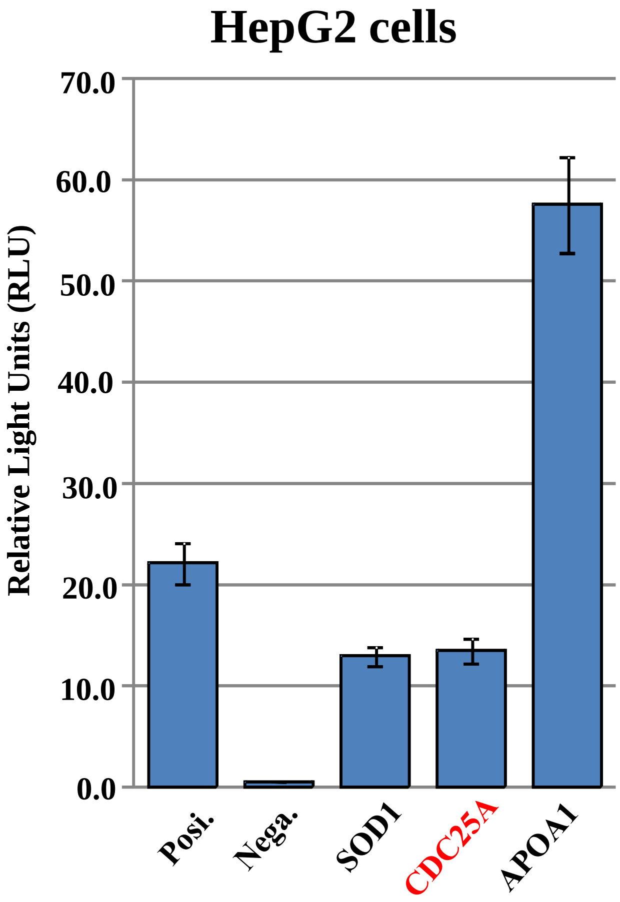
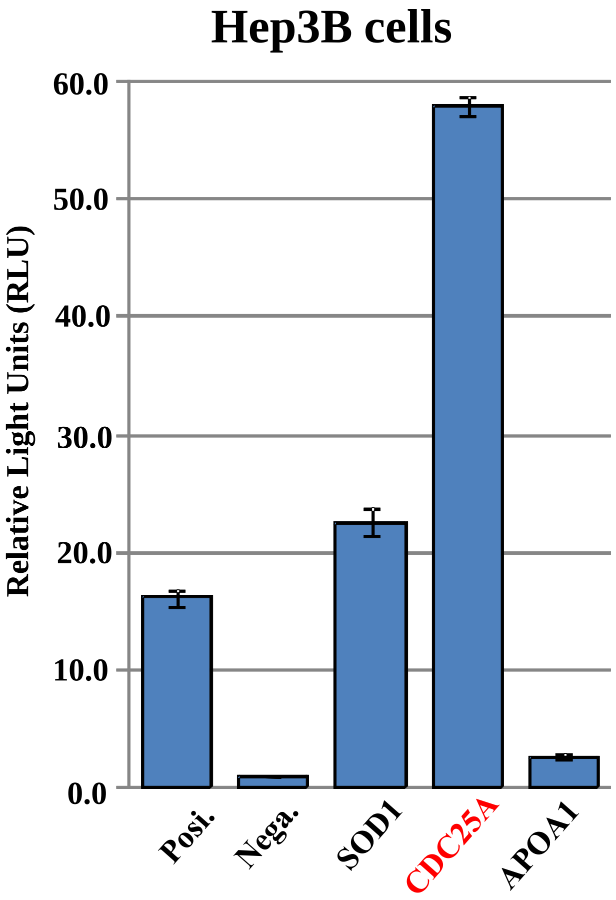
The Promoter Activities of Reporter Constructs


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 : 2010.03.09

1st Nucleotide Sequence
  File Name        : Reference Seq (insert)
  Sequence Size    : 1460

2nd Nucleotide Sequence
  File Name        : RDB7709F.fasta
  Sequence Size    : 666

Unit Size to Compare : 6

Percent Similarity   : 100.0
Percent Identity     : 100.0


     1’ AAACAGTGGG ACCACAGACC ATGTGAACTG TGCAGAGAGG CCTAAATAGC CTGGGGTTTC
        ********** ********** ********** ********** ********** **********
    60″ AAACAGTGGG ACCACAGACC ATGTGAACTG TGCAGAGAGG CCTAAATAGC CTGGGGTTTC

    61’ TGGAGGGAAG GGAGGTTCCT GGGTGGTGGA GCACTGGTGC ACAGAAAAGG AGATGAATCC
        ********** ********** ********** ********** ********** **********
   120″ TGGAGGGAAG GGAGGTTCCT GGGTGGTGGA GCACTGGTGC ACAGAAAAGG AGATGAATCC

   121’ TGAGAGAGAG GTTCCTCACT GTGAAGGGTC TGGTGTTGGG GCCAAAGGTT TGGGGTTTCC
        ********** ********** ********** ********** ********** **********
   180″ TGAGAGAGAG GTTCCTCACT GTGAAGGGTC TGGTGTTGGG GCCAAAGGTT TGGGGTTTCC

   181’ ACCTGTCCAG CATGGCTTTT CAAACTGTAG GGTTTTTTTT TTTTGAGTGG GGGGCAGGGG
        ********** ********** ********** ********** ********** **********
   240″ ACCTGTCCAG CATGGCTTTT CAAACTGTAG GGTTTTTTTT TTTTGAGTGG GGGGCAGGGG

   241’ GTGTCTCACT TTGTTGCCCA GGCTGGTCTC AAATTCGTGG GCTCAGGCAA TCCTCCCACC
        ********** ********** ********** ********** ********** **********
   300″ GTGTCTCACT TTGTTGCCCA GGCTGGTCTC AAATTCGTGG GCTCAGGCAA TCCTCCCACC
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301' TCGCCCTCCC AAAGTGCTGG GATGATAGGC GTGAGCCACT AAGCCCAGCA GTAGGTTGCA
     ********** ********** ********** ********** ********** **********
360″ TCGCCCTCCC AAAGTGCTGG GATGATAGGC GTGAGCCACT AAGCCCAGCA GTAGGTTGCA

361' ATTAAATCAT GCACTTATGG CCCTCAAAAT CCGTCTAGGA GCTGCCACAG GTTCGGCGCT
     ********** ********** ********** ********** ********** **********
420″ ATTAAATCAT GCACTTATGG CCCTCAAAAT CCGTCTAGGA GCTGCCACAG GTTCGGCGCT

421' GTAAAAGTAA ATATGCCCAC TTAGAAAATG GGGATAATTC CTATGTCACA GAGTTGTAAA
     ********** ********** ********** ********** ********** **********
480″ GTAAAAGTAA ATATGCCCAC TTAGAAAATG GGGATAATTC CTATGTCACA GAGTTGTAAA

481' GATTAAATGA ATTAATACAG ATTAACACAC TGGGAACAGT GTCAAGTGCA TAAGCATTAT
     ********** ********** ********** ********** ********** **********
540″ GATTAAATGA ATTAATACAG ATTAACACAC TGGGAACAGT GTCAAGTGCA TAAGCATTAT

541' GTAAACTTTA GCTATTATTT GCTATTATTG TGTTTGCTGT TATTTCTCTC TAGGAGCTCC
     ********** ********** ********** ********** ********** **********
600″ GTAAACTTTA GCTATTATTT GCTATTATTG TGTTTGCTGT TATTTCTCTC TAGGAGCTCC

601' CAGGGGG
     *******
660″ CAGGGGG
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1st Nucleotide Sequence
  File Name         : Reference Seq (insert)
  Sequence Size     : 1460

2nd Nucleotide Sequence
  File Name         : RDB7709R.fasta (Complementary)
  Sequence Size     : 698

Unit Size to Compare : 6
```

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Percent Similarity   : 99.8
Percent Identity     : 99.8


  861’ CCACAATACT GCACGGTTAG AGGCCGAGCC AAGGCTGGAT CCGGCCAGAC CTCCACAGGT
       ********** ********** **********  ********* ********** **********
  698″ CCACAATACT GCACGGTTAG AGGCCGAGCC CAGGCTGGAT CCGGCCAGAC CTCCACAGGT

  921’ CTTCCTTAGC CTCCACATTG CCTCAGAGTG TGGGGCGCCC GGCTGGGGGC GAGGTAGCGG
       ********** ********** ********** ********** ********** **********
  638″ CTTCCTTAGC CTCCACATTG CCTCAGAGTG TGGGGCGCCC GGCTGGGGGC GAGGTAGCGG

  981’ AGGCCCAAAG GGGGCCGAAG CTAACTGGAC GGCAGCTCGC GATGGGAACT ACGCTTCCCA
       ********** ********** ********** ********** ********** **********
  578″ AGGCCCAAAG GGGGCCGAAG CTAACTGGAC GGCAGCTCGC GATGGGAACT ACGCTTCCCA

 1041’ GCATGCGACG GGGCAAAGGG GCCTTTCAGC CGCGAGCAGC GCCTCGCAGG TTCTGCTGGG
       ********** ********** ********** ********** ********** **********
  518″ GCATGCGACG GGGCAAAGGG GCCTTTCAGC CGCGAGCAGC GCCTCGCAGG TTCTGCTGGG

 1101’ AGTTTTCATT GACCTCTGCT CCCCCTCTCA TTTTGATCCC CGCTCTTCTG CTCTGGGCTC
       ********** ********** ********** ********** ********** **********
  458″ AGTTTTCATT GACCTCTGCT CCCCCTCTCA TTTTGATCCC CGCTCTTCTG CTCTGGGCTC

 1161’ CGCCCCCTTC TGAGAGCCGA TGACCTGGCA GAGTCCCGCG AGCCGCTTTC TTCTTCCCCT
       ********** ********** ********** ********** ********** **********
  398″ CGCCCCCTTC TGAGAGCCGA TGACCTGGCA GAGTCCCGCG AGCCGCTTTC TTCTTCCCCT

 1221’ CTCATTGGCC CAGCCTAGCT GCCATTCGGT TGAGAGGAGG AGAAGTTGCT TACTGATTGG
       ********** ********** ********** ********** ********** **********
  338″ CTCATTGGCC CAGCCTAGCT GCCATTCGGT TGAGAGGAGG AGAAGTTGCT TACTGATTGG

 1281’ TGGATTCCGT TTGGCGCCAA CTAGGAAAGG GGGGCGGGGC AGCAGCTGGC CCCACTGAGC
       ********** ********** ********** ********** ********** **********
  278″ TGGATTCCGT TTGGCGCCAA CTAGGAAAGG GGGGCGGGGC AGCAGCTGGC CCCACTGAGC

 1341’ CGCTATTACC GCGAAAGGCC GGCCTGGCTG CGACAGCCTG GGTAAGAGGT GTAGGTCGGC
       ********** ********** ********** ********** ********** **********
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 218″ CGCTATTACC GCGAAAGGCC GGCCTGGCTG CGACAGCCTG GGTAAGAGGT GTAGGTCGGC

1401’ TTGGTTTTCT GCTACCCGGA GCTGGGCAAG CGGGTGGGAG AACAGCGAAG ACAGCGTGAG
      ********** ********** ********** ********** ********** **********
 158″ TTGGTTTTCT GCTACCCGGA GCTGGGCAAG CGGGTGGGAG AACAGCGAAG ACAGCGTGAG
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