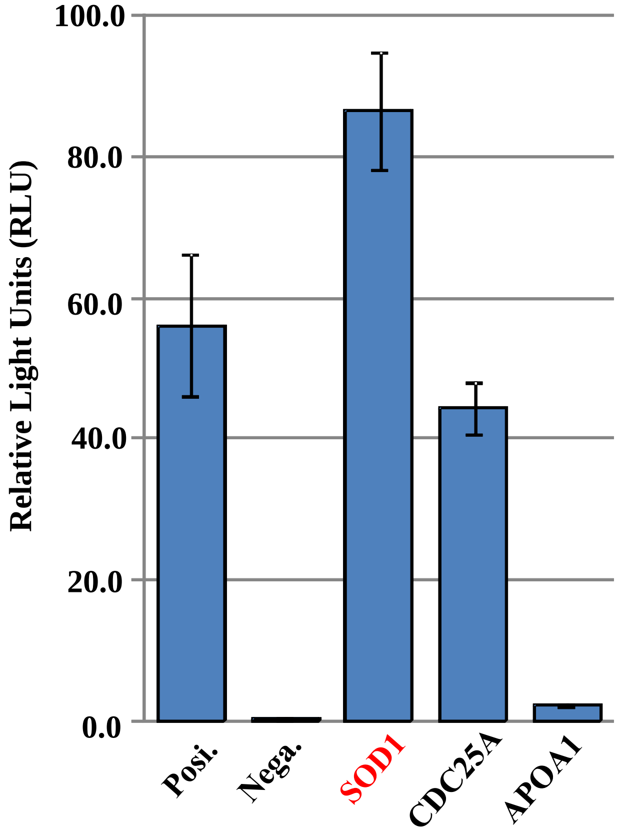
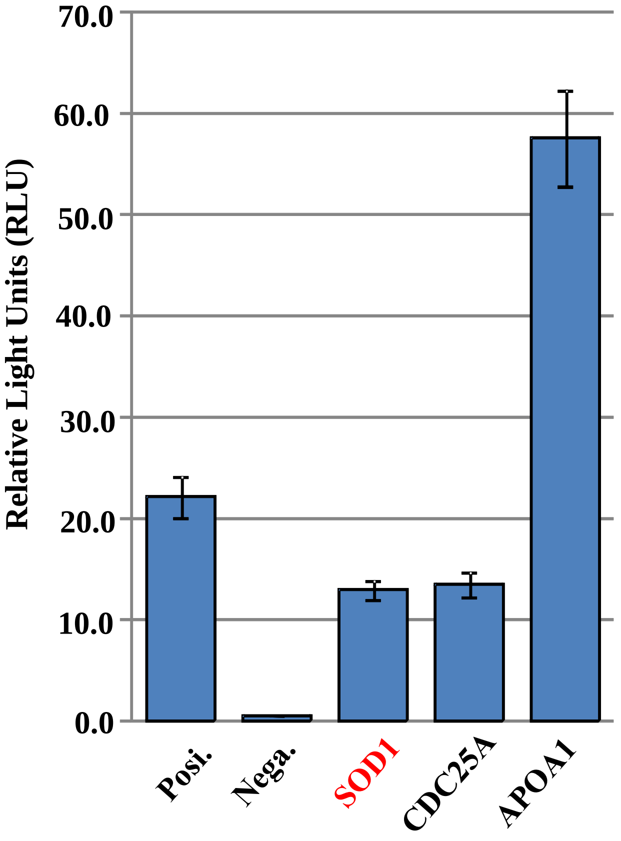
The Promoter Activities of Reporter Constructs

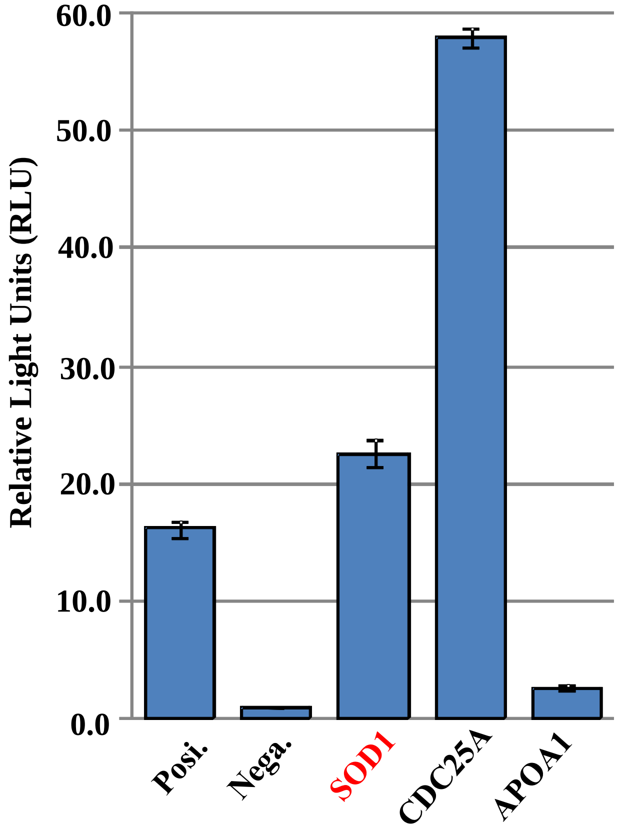
HeLa cells



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 : 2010.01.07

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5713

2nd Nucleotide Sequence
  File Name        : RDB7686F.fasta
  Sequence Size    : 642

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 623 bp]     INT/OPT.Score : <   2492/  2492 >

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

     42' GAAATCTGCC GAACTTCCTG GAACCCAAAG AAACTTTAGC CTTGGGCAAA GGCCCTTTGG
         ********** ********** ********** ********** ********** **********
     61" GAAATCTGCC GAACTTCCTG GAACCCAAAG AAACTTTAGC CTTGGGCAAA GGCCCTTTGG

    102' CCAGCATTTG CACTGTTTAT GCAACCGTTT AGAATATACG AATTATCTGG AGACTACTAC
         ********** ********** ********** ********** ********** **********
    121" CCAGCATTTG CACTGTTTAT GCAACCGTTT AGAATATACG AATTATCTGG AGACTACTAC

    162' CAAATACAAC AGGCAAAACT GCAAATATGT ATACTTCCTA GAGGATGATA AAAAAATGTG
         ********** ********** ********** ********** ********** **********
    181" CAAATACAAC AGGCAAAACT GCAAATATGT ATACTTCCTA GAGGATGATA AAAAAATGTG

    222' AATTGTATTT CTCTGATAGA GGATGCATTA GAGTCTGAGG GTCTAAATAG CGTAAATAAT
         ********** ********** ********** ********** ********** **********
    241" AATTGTATTT CTCTGATAGA GGATGCATTA GAGTCTGAGG GTCTAAATAG CGTAAATAAT
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282’ AAATAAGTAA ATAAATCGAT AGTAGTGTAC TCCAAACGAG GCTGGAATAG CTTCTATTGT
     ********** ********** ********** ********** ********** **********
301″ AAATAAGTAA ATAAATCGAT AGTAGTGTAC TCCAAACGAG GCTGGAATAG CTTCTATTGT

342’ TGTTTCACAC TGGACTTCAA TTAAGTCTCA GTATTTTGCC ATACTCAATA TTAAGTACTA
     ********** ********** ********** ********** ********** **********
361″ TGTTTCACAC TGGACTTCAA TTAAGTCTCA GTATTTTGCC ATACTCAATA TTAAGTACTA

402’ GGCTGGACGT GGTGGCTCAT GTCTGTAATC CCAGCACTTT GGGAGGCCGA GGTGGGTAGA
     ********** ********** ********** ********** ********** **********
421″ GGCTGGACGT GGTGGCTCAT GTCTGTAATC CCAGCACTTT GGGAGGCCGA GGTGGGTAGA

462’ TGGCTGGCTT GAGCTCAGGA GTTTGAAACC AGCCTGGGCA ACATGGTAAA ACCCCATCTG
     ********** ********** ********** ********** ********** **********
481″ TGGCTGGCTT GAGCTCAGGA GTTTGAAACC AGCCTGGGCA ACATGGTAAA ACCCCATCTG

522’ TACCCAAAAT ACAAAAATCA GCCAGGTGTG GTGGCACATG CCTGTGGTCC CAGGTACTTG
     ********** ********** ********** ********** ********** **********
541″ TACCCAAAAT ACAAAAATCA GCCAGGTGTG GTGGCACATG CCTGTGGTCC CAGGTACTTG

582’ GGAGGCTGAG GCAGGAGGAT GGCTTGAACC CAGGAGGTGG AGGCTGCAGT GAGCTATGAT
     ********** ********** ********** ********** **
601″ GGAGGCTGAG GCAGGAGGAT GGCTTGAACC CAGGAGGTGG AG




1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5713

2nd Nucleotide Sequence
  File Name        : RDB7686R.fasta (Complementary)
  Sequence Size    : 694

  Unit Size to Compare = 1
  Pick up Location     = 1
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[99.856% / 694 bp]     INT/OPT.Score : <   2770/  2770 >

  841' CCCTCCTTGA GTGTTGTGGC CTTTAGGCCA GACAAAAACG CAGGTGATGC CTAGAAGCCA
                                                                  ****
    1″                                                            GCCA

  901' ACTAGTTGCC GTTTGGTTAT CTGTAGGGTT GTGGCCTTGC CAAACAGGAA AAATATAAAA
       ********** ********** ********** ********** ********** **********
    5″ ACTAGTTGCC GTTTGGTTAT CTGTAGGGTT GTGGCCTTGC CAAACAGGAA AAATATAAAA

  961' AGAATACCGA ATTCTGCCAA CCAAATAAGA AACTCTATAC TAAGGACTAA GAAAATTGCA
       ********** ********** ********** ** ******* ********** **********
   65″ AGAATACCGA ATTCTGCCAA CCAAATAAGA AAATCTATAC TAAGGACTAA GAAAATTGCA

 1021' GGGGAAGAAA AGGTAAGTCC CGGGATTGAG GTGTAGCGAC TTTCTATACC CTCAGAAAAC
       ********** ********** ********** ********** ********** **********
  125″ GGGGAAGAAA AGGTAAGTCC CGGGATTGAG GTGTAGCGAC TTTCTATACC CTCAGAAAAC

 1081' TAAAAAACAA GACAAAAAAA TGAAAACTAC AAAAGCATCC ATCTTGGGGC GTCCCAATTG
       ********** ********** ********** ********** ********** **********
  185″ TAAAAAACAA GACAAAAAAA TGAAAACTAC AAAAGCATCC ATCTTGGGGC GTCCCAATTG

 1141' CTGAGTAACA AATGAGACGC TGTGGCCAAA CTCAGTCATA ACTAATGACA TTTCTAGACA
       ********** ********** ********** ********** ********** **********
  245″ CTGAGTAACA AATGAGACGC TGTGGCCAAA CTCAGTCATA ACTAATGACA TTTCTAGACA

 1201' AAGTGACTTC AGATTTTCAA AGCGTACCCT GTTTACATCA TTTTGCCAAT TTCGCGTACT
       ********** ********** ********** ********** ********** **********
  305″ AAGTGACTTC AGATTTTCAA AGCGTACCCT GTTTACATCA TTTTGCCAAT TTCGCGTACT

 1261' GCAACCGGCG GGCCACGCCC CCGTGAAAAG AAGGTTGTTT TCTCCACATT TCGGGGTTCT
       ********** ********** ********** ********** ********** **********
  365″ GCAACCGGCG GGCCACGCCC CCGTGAAAAG AAGGTTGTTT TCTCCACATT TCGGGGTTCT

 1321' GGACGTTTCC CGGCTGCGGG GCGGGGGGAG TCTCCGGCGC ACGCGGCCCC TTGGCCCCGC
       ********** ********** ********** ********** ********** **********
  425″ GGACGTTTCC CGGCTGCGGG GCGGGGGGAG TCTCCGGCGC ACGCGGCCCC TTGGCCCCGC
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1381’ CCCCAGTCAT TCCCGGCCAC TCGCGACCCG AGGCTGCCGC AGGGGGCGGG CTGAGCGCGT
      ********** ********** ********** ********** ********** **********
 485″ CCCCAGTCAT TCCCGGCCAC TCGCGACCCG AGGCTGCCGC AGGGGGCGGG CTGAGCGCGT

1441’ GCGAGGCGAT TGGTTTGGGG CCAGAGTGGG CGAGGCGCGG AGGTCTGGCC TATAAAGTAG
      ********** ********** ********** ********** ********** **********
 545″ GCGAGGCGAT TGGTTTGGGG CCAGAGTGGG CGAGGCGCGG AGGTCTGGCC TATAAAGTAG

1501’ TCGCGGAGAC GGATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG
      ********** ********** ********** ********** ********** **********
 605″ TCGCGGAGAC GGATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG

1561’ TAAAGCCACC ATGGAAGATG CCAAAAACAT TAAGAAGGGC CCAGCGCCAT TCTACCCACT
      ********** ********** **********
 665″ TAAAGCCACC ATGGAAGATG CCAAAAACAT
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