**Table S5.** Results of CLOVER analysis of the enhancer region with sequence information for human and mouse *CPS1*. Results were filtered to exclude motifs for transcription factors that are not expressed in the liver.

|  |
| --- |
| Sequence file: CPS1\_enhancer\_element.txt (5 sequences, 2875 bp, 40.4% C+G) |
| Motif file: transfac\_pro\_n (588 motifs) |  |  |  |
|  |  |  |  |  |
| Motif  | Raw score  | P-value from randomizing |  |
| M00447|AR  | 10.8 | 0 |  |  |
| M00724|HNF3alpha  | 10.1 | 0 |  |  |
| M00912|C/EBP  | 6.34 | 0 |  |  |
| M00117|C/EBPbeta  | 6.07 | 0.001 |  |  |
| M00109|C/EBPbeta  | 5.83 | 0.002 |  |  |
| M00123|c-Myc:Max  | 4.52 | 0 |  |  |
| M00921|GR  | 4.09 | 0.002 |  |  |
| M00967|HNF4, COUP  | 3.64 | 0.004 |  |  |
| M00116|C/EBPalpha  | 3.44 | 0.006 |  |  |
| M00707|TFIIA  | 3.26 | 0.003 |  |  |
| M00981|CREB, ATF  | 2.52 | 0 |  |  |
| M00801|CREB  | 1.01 | 0 |  |  |
|  |  |  |  |  |
| Motif  | Location  | Strand  | Sequence  | Score |
| **>humanCPS1\_enhancer** |  |  |  |  |
| M00921|GR  | 256 - 263  | +  | cctgttct  | 6.99 |
| M00981|CREB, ATF  | 264 - 272  | -  | ctacgtcat  | 8.05 |
| M00109|C/EBPbeta  | 325 - 338  | -  | atgttgcaccacat  | 7.08 |
| M00123|c-Myc:Max  | 331 - 342  | +  | caccacatgctt  | 7.87 |
| M00707|TFIIA  | 349 - 360  | -  | gatcctcaaata  | 6.31 |
| M00967|HNF4, COUP  | 375 - 383  | +  | agggtccag  | 7.47 |
| M00921|GR  | 385 - 392  | +  | agtgtcct  | 6.49 |
| M00109|C/EBPbeta  | 454 - 467  | -  | atcttgcaaaatca  | 7.41 |
| M00724|HNF3alpha  | 470 - 480  | +  | tgtttactctt  | 8.11 |
| M00724|HNF3alpha  | 489 - 499  | -  | ttaagaaaaca  | 6.11 |
| M00447|AR  | 508 - 522  | +  | agagttgtttgttct  | 6.57 |
| M00724|HNF3alpha  | 513 - 523  | +  | tgtttgttctg  | 9.29 |
| M00921|GR  | 515 - 522  | +  | tttgttct  | 6.65 |
| M00117|C/EBPbeta  | 560 - 573  | -  | tcgttgtgcaaaga  | 6.17 |
|  |  |  |  |  |
| **>mouseCPS1\_enhancer** |  |  |  |  |
| M00109|C/EBPbeta  | 117 - 130  | +  | agtttgtgaaagca  | 6.03 |
| M00981|CREB, ATF  | 284 - 292  | -  | caacgtcat  | 6.98 |
| M00117|C/EBPbeta  | 311 - 324  | +  | ctcttgcttcacta  | 6.35 |
| M00967|HNF4, COUP  | 337 - 345  | +  | caagtccat  | 6.3 |
| M00109|C/EBPbeta  | 342 - 355  | -  |  ccattacacaacat  | 8.34 |
| M00123|c-Myc:Max  | 372 - 383  | +  | catcacacgtgt  | 6.82 |
| M00967|HNF4, COUP  | 394 - 402  | +  | agggtccag  | 7.72 |
| M00921|GR  | 404 - 411  | +  | agtgtcct  | 6.49 |
| M00001|MyoD  | 428 - 439  | -  | taccacctctct  | 6.18 |
| M00189|AP-2  | 440 - 451  | +  | ctcctcatggcg  | 6.06 |
| M00912|C/EBP  | 470 - 481  | +  | cttgcaaaatca  | 7.28 |
| M00724|HNF3alpha  | 486 - 496  | +  | tgtttactctt  | 7.9 |
| M00447|AR  | 522 - 536  | +  | agagcagtttgttct  | 11 |
| M00724|HNF3alpha  | 527 - 537  | +  | agtttgttctg  | 6.71 |
| M00921|GR  | 529 - 536  | +  | tttgttct  | 6.54 |
| M00921|GR  | 534 - 541  | +  | tctgttca  | 6.31 |
| M00707|TFIIA  | 548 - 559  | +  | tataagaggggg  | 8.67 |
| M00912|C/EBP  | 562 - 573  | -  | ggttttggcaat  | 6.11 |