

SuppTable 5. DREs identified in promoter sequences (-1500 to +1500 of the transcriptional start site) for genes listed in Table 3

| refseq    | locuslink | gene_abbr | gene_name   | match_ind | mat_score | dre_seq               | match_str |
|-----------|-----------|-----------|---|-----------|-----------|-----------------------|-----------|
| NM_025341 | 66082     | Abhd6     | abhydrolase domain containing 6                       | 709       | 0.8379    | gagatctGCGTGccctgt    | +         |
| NM_025341 | 66082     | Abhd6     | abhydrolase domain containing 6                       | 1187      | 0.8009    | tggctgaGCGTGatttgaa   | +         |
| NM_009692 | 11806     | Apoa1     | apolipoprotein A-I                                    | 310       | 0.8291    | ttgacctGCGTGggactac   | +         |
| NM_009692 | 11806     | Apoa1     | apolipoprotein A-I                                    | 577       | 0.8056    | agactaGCGTGgggcctg    | +         |
| NM_009811 | 12368     | Casp6     | caspase 6   | -132      | 0.8105    | aaaaaacGCGTGcccttgc   | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 1185      | 0.9357    | gcgcctGCGTGagagcca    | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | -650      | 0.907     | tctgattGCGTGcccacat   | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 686       | 0.8608    | ccttcgtGCGTGggacaga   | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 487       | 0.8507    | gcgcctGCGTGggcgatg    | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 749       | 0.8444    | tgcgtcGCGTGaaaacaag   | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 148       | 0.8412    | CGATCACGCGTGACCTGTG   | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 27        | 0.8295    | TGACCAACGCGTGACCCGCT  | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 145       | 0.7873    | aggtaacGCGTGatcgcaa   | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 252       | 0.7829    | ggtgaaGCGTGggctcag    | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 1496      | 0.7594    | gacatgaGCGTGgtctatg   | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 24        | 0.7573    | gggtcacGCGTGgtcaaaa   | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | -633      | 0.7503    | attccagGCGTGtctaataat | -         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 99        | 0.7415    | TGCAGCCGCGTGGCCCTGG   | +         |
| NM_173047 | 109857    | Cbr3      | carbonyl reductase 3                                  | 654       | 0.7406    | tgacaagGCGTGgtccct    | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -984      | 0.9805    | cggattGCGTGagaagag    | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1206     | 0.973     | cgggttGCGTGgtatgt     | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -871      | 0.9499    | ccttgtGCGGTGccaagca   | +         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -491      | 0.9394    | caagtcGCGTGagaagcg    | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1059     | 0.9133    | ccagctGCGTGacacac     | +         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -895      | 0.8585    | gaggctGCGTGgttaa      | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1294     | 0.8377    | caggtagGCGTGccgggt    | +         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1277     | 0.8354    | tggtgtGCGTGtccgtcc    | +         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1382     | 0.8002    | gaacttgGCGTGtctaact   | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -822      | 0.7996    | ctgtctcGCGTGgtatctt   | +         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -1249     | 0.7825    | ctgaacaGCGTGgtccac    | -         |
| NM_009992 | 13076     | Cyp1a1    | cytochrome P450, family 1, subfamily a, polypeptide 1 | -52       | 0.7609    | taaggagGCGTGggccaaca  | +         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | 684       | 0.904     | cctccctGCGTGccagagt   | -         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | -719      | 0.8574    | ccttaggcGCGTGcccccc   | +         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | 600       | 0.773     | TGCCAGAGCGCTGGCGCCAG  | +         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | -566      | 0.7619    | agctcgGCGTGggaccgaa   | -         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | 623       | 0.7488    | gtacacGCGTGggggcg     | +         |
| NM_011303 | 20148     | Dhrs3     | dehydrogenase/reductase (SDR family) member 3         | -839      | 0.7398    | ggttgcGCGTGttcgagt    | +         |
| NM_010145 | 13849     | Ephx1     | epoxide hydrolase 1, microsomal                       | 71        | 0.8456    | cactccaGCGTGagagt     | +         |
| NM_010145 | 13849     | Ephx1     | epoxide hydrolase 1, microsomal                       | 720       | 0.8227    | tggctgtGCGTGgtctqac   | +         |
| NM_010145 | 13849     | Ephx1     | epoxide hydrolase 1, microsomal                       | 144       | 0.8088    | gtatccGCGTGcaatagg    | +         |
| NM_010145 | 13849     | Ephx1     | epoxide hydrolase 1, microsomal                       | -377      | 0.7988    | gtgttctGCGTGggcaagg   | -         |
| NM_010145 | 13849     | Ephx1     | epoxide hydrolase 1, microsomal                       | 790       | 0.7778    | aacgttgGCGTGttcagca   | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | 341       | 0.9138    | cacaggGCGTGccaggcg    | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | 462       | 0.8376    | tccctctGCGTGccagcac   | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | -1306     | 0.8366    | caggccGCGTGactgcag    | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | 559       | 0.7979    | ggacaccGCGTGgttaggc   | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | -118      | 0.7931    | agtccggGCGTGggcagg    | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | 669       | 0.7596    | tggcttagGCGTGggcccg   | +         |
| NM_010634 | 16592     | Fabp5     | fatty acid binding protein 5, epidermal               | 569       | 0.7268    | tggtaggGCGTGgtttctg   | +         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -1443     | 0.8991    | ggaaactGCGTGggccagag  | +         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -1394     | 0.8858    | gtccctGCGTGgagggcg    | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -207      | 0.8055    | ggggaggGCGTGaaaccca   | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | 512       | 0.7884    | ggaggcGCGTGcatcaga    | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -1208     | 0.7882    | tagaccGCGTGggatct     | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -1059     | 0.778     | ttccacGCGTGtcatitta   | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -66       | 0.7753    | gggtggagGCGTGccactg   | -         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | 486       | 0.7725    | ttctccGCGTGgttgggg    | +         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | -1056     | 0.7706    | atgacacGCGTGggagaag   | +         |
| NM_008655 | 17873     | Gadd45b   | growth arrest and DNA-damage-inducible 45 beta        | 951       | 0.7529    | CCCGACAGCGCTGGTCTTGT  | +         |
| NM_008086 | 14451     | Gas1      | growth arrest specific 1                              | 1201      | 0.8011    | AACGACTGCGTGTCGATG    | +         |
| NM_008086 | 14451     | Gas1      | growth arrest specific 1                              | 994       | 0.7725    | ACCAGCAGCGCTGGGCCCG   | +         |
| NM_008086 | 14451     | Gas1      | growth arrest specific 1                              | 893       | 0.7667    | ccggccGCGTGgttgtga    | -         |
| NM_010292 | 103988    | Gck       | glucokinase   | -1259     | 0.7337    | tccctaggGCGTGgtctct   | -         |
| NM_010302 | 14673     | Gna12     | guanine nucleotide binding protein, alpha 12          | 1197      | 0.8856    | acttcatGCGTGtctggga   | +         |
| NM_010302 | 14673     | Gna12     | guanine nucleotide binding protein, alpha 12          | -131      | 0.8211    | tggccaaGCGTGcttgg     | -         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | -930      | 0.8429    | ccaaacaGCGTGttaaag    | +         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | -769      | 0.8319    | acacgacGCGTGggggaaa   | +         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | 360       | 0.8308    | ctgttctGCGTGaccctga   | -         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | -772      | 0.8025    | ctccacGCGTGgtctgtat   | -         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | 165       | 0.8018    | AACCTCGGCGTGGGAGGta   | +         |
| NM_010324 | 14718     | Got1      | glutamate oxaloacetate transaminase 1, soluble        | -255      | 0.7756    | tggctgaGCGTGttccaaat  | -         |
| NM_010274 | 14571     | Gpd2      | glycerol phosphate dehydrogenase 2, mitochondrial     | 105       | 0.8427    | CCCTTGCCTGACGACCG     | +         |
| NM_010274 | 14571     | Gpd2      | glycerol phosphate dehydrogenase 2, mitochondrial     | -385      | 0.7998    | gtggcccGCGTGggggagg   | +         |
| NM_010274 | 14571     | Gpd2      | glycerol phosphate dehydrogenase 2, mitochondrial     | -1139     | 0.7992    | aaatttGCGTGttcaagg    | +         |
| NM_010274 | 14571     | Gpd2      | glycerol phosphate dehydrogenase 2, mitochondrial     | -602      | 0.7685    | taccccaGCGTGttctgt    | -         |
| NM_010357 | 14860     | Gsta4     | glutathione S-transferase, alpha 4                    | -1081     | 0.8753    | ctggatGCGTGtcttgt     | +         |
| NM_010357 | 14860     | Gsta4     | glutathione S-transferase, alpha 4                    | -466      | 0.8425    | aaaccaGCGTGcaacatg    | +         |
| NM_010357 | 14860     | Gsta4     | glutathione S-transferase, alpha 4                    | -127      | 0.8073    | ctccataGCGTGtcttgt    | +         |
| NM_010357 | 14860     | Gsta4     | glutathione S-transferase, alpha 4                    | -294      | 0.7174    | attaaagGCGTGgaccaact  | +         |
| NM_013541 | 14870     | Gstp1     | glutathione S-transferase, pi 1                       | -559      | 0.8275    | tctgtatGCGTGctlgacc   | +         |

|           |        |         |  |       |        |                      |   |
|-----------|--------|---------|--|-------|--------|----------------------|---|
| NM_013541 | 14870  | Gstp1   | glutathione S-transferase, pi 1                | -11   | 0.8056 | ggcctacGCGTGcgccctc  | + |
| NM_013541 | 14870  | Gstp1   | glutathione S-transferase, pi 1                | 163   | 0.7831 | gcctggGCGTGgggtggg   | + |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | 595   | 0.8414 | cacatgaGCGTGtccttgtt | - |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | 921   | 0.8372 | TGCCGCTGCGTGAGGGTAG  | + |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | -99   | 0.8281 | tggcttgCCTGgtggag    | - |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | 513   | 0.8205 | gtggcagGCGTGccccgc   | - |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | 439   | 0.8145 | GTGAGGCAGCTGCAGGGCG  | + |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | -868  | 0.7999 | gaggtaaGCGTGgagaggg  | + |
| NM_019479 | 55927  | Hes6    | hairy and enhancer of split 6 (Drosophila)     | -1119 | 0.7866 | gacacagGCGTGtccttgt  | + |
| NM_146001 | 215114 | Hip1    | huntingtin interacting protein 1               | 826   | 0.9005 | gaggttGCGTGccggcat   | + |
| NM_146001 | 215114 | Hip1    | huntingtin interacting protein 1               | -1173 | 0.732  | attataGCGTGggccctt   | - |
| NM_022882 | 64898  | Lpin2   | lipin 2  | -165  | 0.8024 | tgcctcGCGTGggccacg   | + |
| NM_022882 | 64898  | Lpin2   | lipin 2  | -432  | 0.7811 | ggggggGCGTGgtggcag   | + |
| NM_022882 | 64898  | Lpin2   | lipin 2  | -1323 | 0.7643 | cactcaGCGTGgttcttc   | - |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | 480   | 0.8657 | ccggctgaGCGTGatgggg  | - |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | 686   | 0.8135 | ttggcccGCGTGcctgtca  | - |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | -441  | 0.7948 | cttggcGCGTGggggacct  | + |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | 584   | 0.7779 | ggctggGCGTGgggttgt   | + |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | 875   | 0.7624 | cgggaaGCGTGgcgcaga   | + |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | 156   | 0.7546 | ctacggGCGTGggggcagt  | - |
| NM_008509 | 16956  | Lpl     | lipoprotein lipase                             | -330  | 0.721  | ttaacaGCGTGtacctaa   | - |
| NM_010766 | 17167  | Marco   | macrophage receptor with collagenous structure | 1311  | 0.8766 | cgcgcgtGCGTGtgcacac  | - |
| NM_010766 | 17167  | Marco   | macrophage receptor with collagenous structure | 1328  | 0.83   | cgccatGCGTGtgcagt    | + |
| NM_010766 | 17167  | Marco   | macrophage receptor with collagenous structure | 1315  | 0.797  | tgtggccGCGTGcgctgtc  | - |
| NM_010849 | 17869  | Myc     | myelocytomatosis oncogene                      | -387  | 0.8807 | gggacgtGCGTGacgcgg   | + |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | 289   | 0.8558 | tgccttgCCTGtgtggag   | + |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | 964   | 0.8439 | taagatGCGTGgggggg    | + |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | 202   | 0.8414 | acccaaaGCGTGgcgcagg  | - |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | -152  | 0.804  | cgccgggGCGTGggggca   | + |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | -703  | 0.7885 | ccgttgcGCGTGtgcctgtc | - |
| NM_008714 | 18128  | Notch1  | Notch gene homolog 1 (Drosophila)              | 719   | 0.7718 | agggtggGCGTGggactga  | + |
| NM_008706 | 18104  | Nqo1    | NAD(P)H dehydrogenase, quinone 1               | -326  | 0.9009 | tccctaGCGTGcaaagt    | + |
| NM_008706 | 18104  | Nqo1    | NAD(P)H dehydrogenase, quinone 1               | 588   | 0.7416 | aatcagGCGTGgtatat    | - |
| NM_011044 | 18534  | Pck1    | phosphoenolpyruvate carboxykinase 1, cytosolic | 800   | 0.8016 | ggacactGCGTGggcaaga  | + |
| NM_011044 | 18534  | Pck1    | phosphoenolpyruvate carboxykinase 1, cytosolic | 1124  | 0.7684 | ctgcaaaGCGTGccacacg  | + |
| NM_009396 | 21928  | Tnfaip2 | tumor necrosis factor, alpha-induced protein 2 | -1078 | 0.7983 | tgacctgGCGTGatccagg  | - |
| NM_009396 | 21928  | Tnfaip2 | tumor necrosis factor, alpha-induced protein 2 | 848   | 0.7917 | cgccggcGCGTGgcctcca  | - |
| NM_009396 | 21928  | Tnfaip2 | tumor necrosis factor, alpha-induced protein 2 | 72    | 0.7244 | atgtagaGCGTGgttttg   | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -300  | 0.9092 | cgtggctGCGTGgcgcgt   | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -426  | 0.8757 | ggttgcGCGTGccaaqtg   | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | 571   | 0.8212 | atgaactGCGTGgaccaca  | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -876  | 0.8179 | ttaatttGCGTGtgttgt   | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -761  | 0.8021 | cctccagGCGTGggccccc  | + |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -292  | 0.7691 | gggttgtGCGTGgtctgt   | - |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -1093 | 0.7512 | agatagaGCGTGgtctct   | + |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -214  | 0.7471 | tcaaggGCGTGgtcatac   | + |
| NM_009466 | 22235  | Ugdh    | UDP-glucose dehydrogenase                      | -1317 | 0.7446 | aaagtggGCGTGggcgtaa  | + |
| NM_011723 | 22436  | Xdh     | xanthine dehydrogenase                         | 1051  | 0.8774 | aaatgttGCGTGctatgtt  | - |
| NM_011723 | 22436  | Xdh     | xanthine dehydrogenase                         | -620  | 0.7874 | cttcggGCGTGgcctata   | - |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -278  | 0.9023 | ggccgtGCGTGgtggct    | - |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -282  | 0.8487 | cgtgcgtGCGTGgtgcgg   | - |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -274  | 0.8408 | ccggggcGCGTGgtgttgt  | - |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -234  | 0.8345 | ccagccctGCGTGgtgtccg | + |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -191  | 0.8292 | ccggccGCGTGgtgttgt   | + |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -911  | 0.7972 | ttgtttaGCGTGgtccccac | + |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | 315   | 0.7679 | ccgggaaGCGTGggagccgg | - |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | -472  | 0.759  | tggcacGCGTGctgttagg  | + |
| NM_133348 | 70025  |         | brain acyl-CoA hydrolase                       | 182   | 0.7565 | ccggccGCGTGgtctgtgg  | - |

**RefSeq** RefSeq (mRNA)  
**Match\_Ind** Location relative to TSS  
**Mat\_Score** Matrix similarity score based on 13 bona fide DREs (19 nucleotides in matrix)  
**DRE\_Seq** Actual 19 bp sequence  
**Match\_Str** Plus or minus strand