

AC ID Score Loc. Str. Consensus Sequence Signal Sequence

M00184 V\$MYOD_Q6 0.802283 1 (-) NNCANCTGNY AGCAGACGCT
M00178 V\$CREB_Q4 0.745583 2 (+) NSTGACGTMANN GCAGACGCTCCC
M00253 V\$CAP_01 0.903401 2 (+) NCANNNNN GCAGACGC
M00255 V\$GC_01 0.848114 3 (-) NRGGGGCGGGGCK CAGACGCTCCCTCA
M00035 V\$VMAF_01 0.785452 4 (+) NNNTGCTGACTCAGCANN AGACGCTCCCTCAGCAAGG
M00147 V\$HSF2_01 0.809612 4 (-) NGAANNWTCK AGACGCTCCC
M00008 V\$SP1_01 0.801812 6 (-) GRGGCRGGGW ACGCTCCCTC
M00085 V\$ZID_01 0.783505 6 (+) NGGCTCYATCAYC ACGCTCCCTCAGC
M00243 V\$EGR1_01 0.743121 6 (-) WTGCGTGGGCGK ACGCTCCCTCAG
M00174 V\$AP1_Q6 0.781873 8 (-) NNTGACTCANN GCTCCCTCAGC
M00189 V\$AP2_Q6 0.793658 9 (+) MKCCSCNNGGCG CTCCCTCAGCAA
M00141 V\$LYF1_01 0.847176 10 (-) TTTGGGAGR TCCCTCAGC
M00256 V\$NRSF_01 0.764397 10 (+) TTCAGCACCACGGACAGMGSC TCCCTCAGCAAGGACAGCAGA
M00057 V\$COMP1_01 0.791018 12 (+) NNTNWKGATTGRCNRSRANMRRNN CCTCAGCAAGGACAGCAGAGGACC
M00175 V\$AP4_Q5 0.829978 13 (+) NNCAGCTGNN CTCAGCAAGG
M00176 V\$AP4_Q6 0.762716 13 (+) CWCAGCTGGN CTCAGCAAGG
M00253 V\$CAP_01 0.873829 14 (+) NCANNNNN TCAGCAAG
M00214 V\$SEF1_C 0.726940 16 (+) AACACGGATATCTGTGGTY AGCAAGGACAGCAGAGGAC
M00192 V\$GR_Q6 0.788504 18 (-) NNNNNNCNNTNTGTNCTNN CAAGGACAGCAGAGGACCA
M00005 V\$AP4_01 0.763833 19 (+) WGARYCAGCTGYGGNCK AAGGACAGCAGAGGACCA
M00205 V\$GRE_C 0.815494 19 (-) GGTACAANNTGTYCTK AAGGACAGCAGAGGAC
M00056 V\$MYOGNF1_01 0.743167 21 (-) CRSCTGTNNNTTTGGCACNSNGCCARN
GGACAGCAGAGGACCTAGCTAAGAGGGAGA
M00175 V\$AP4_Q5 0.896083 22 (+) NNCAGCTGNN GACAGCAGAG
M00175 V\$AP4_Q5 0.834603 22 (-) NNCAGCTGNN GACAGCAGAG
M00176 V\$AP4_Q6 0.840641 22 (-) CWCAGCTGGN GACAGCAGAG
M00122 V\$USF_02 0.756992 23 (+) NNRNCACGTGNYNN ACAGCAGAGGACCA
M00122 V\$USF_02 0.756992 23 (-) NNRNCACGTGNYNN ACAGCAGAGGACCA
M00001 V\$MYOD_01 0.821654 24 (-) SRACAGGTGKYG CAGCAGAGGACC
M00023 V\$HOX13_01 0.773075 26 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GCAGAGGACCAGCTAAGAGGGAGAGAAGCA
M00143 V\$PAX5_01 0.771781 27 (+) NCNNNRNKCANNNGNWNRKRGRCSRSNN
CAGAGGACCAGCTAAGAGGGAGAGAAGC
M00059 V\$YY1_01 0.787680 29 (+) NNNNNCCATNTWNNWN GAGGACCAGCTAAGAGG
M00079 V\$EVII_02 0.774269 31 (+) AGAYAAGATAA GGACCAGCTAA
M00272 V\$P53_02 0.821219 31 (+) NGRCWTGYCY GGACCAGCTA
M00272 V\$P53_02 0.825322 31 (-) NGRCWTGYCY GGACCAGCTA
M00057 V\$COMP1_01 0.773533 32 (+) NNTNWKGATTGRCNRSRANMRRNN GACCAGCTAAGAGGGAGAGAAGCA
M00127 V\$GATA1_03 0.820676 32 (+) RNSNNGATAANNNGN GACCAGCTAAGAGG
M00011 V\$EVII_06 0.777076 33 (+) ACAAGATAA ACCAGCTAA
M00128 V\$GATA1_04 0.837010 33 (+) NNCWGATARNNNN ACCAGCTAAGAGG
M00175 V\$AP4_Q5 0.874320 33 (-) NNCAGCTGNN ACCAGCTAAG
M00176 V\$AP4_Q6 0.884240 33 (-) CWCAGCTGGN ACCAGCTAAG
M00059 V\$YY1_01 0.809961 35 (-) NNNNNCCATNTWNNWN CAGCTAAGAGGGAGAGA
M00141 V\$LYF1_01 0.842576 37 (+) TTTGGGAGR GCTAAGAGG
M00085 V\$ZID_01 0.778456 39 (-) NGGCTCYATCAYC TAAGAGGGAGAGA
M00033 V\$P300_01 0.818678 41 (+) NNRGGAGTNNNS AGAGGGAGAGAAGC
M00108 V\$NRF2_01 0.808140 41 (+) ACCGGAAGNS AGAGGGAGAG
M00127 V\$GATA1_03 0.781970 41 (+) RNSNNGATAANNNGN AGAGGGAGAGAAGC
M00008 V\$SP1_01 0.848528 42 (+) GRGGCRGGGW GAGGGAGAGA
M00057 V\$COMP1_01 0.780599 42 (+) NNTNWKGATTGRCNRSRANMRRNN GAGGGAGAGAAGCAACTACAGACC
M00281 V\$RFX1_02 0.762212 42 (+) NNGTNRCNATRGYAACNNN GAGGGAGAGAAGCAACTAC
M00127 V\$GATA1_03 0.850318 43 (+) RNSNNGATAANNNGN AGGGAGAGAAGCAA
M00280 V\$RFX1_01 0.861415 43 (+) NNGTNRCNWRGYAACNN AGGGAGAGAAGCAACTA
M00258 V\$ISRE_01 0.750600 45 (-) CAGTTTCWCTTTYCC GGAGAGAAGCAACTA
M00179 V\$CREBP1_Q2 0.767375 47 (+) NSTGACGTMASN AGAGAAGCAACT
M00147 V\$HSF2_01 0.892052 49 (+) NGAANNWTCK AGAAGCAACT
M00222 V\$THIE47_01 0.828211 55 (-) NNNNGNRTCTGGMWTT AACTACAGACCCCCC
M00115 V\$TAXCREB_02 0.685850 56 (+) RTGACGCATAYCCCC ACTACAGACCCCCC

M00144 V\$PAX5_02 0.755190 56 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
ACTACAGACCCCCCTGAAAACAACCCT
M00257 V\$RREB1_01 0.800068 57 (+) CCCCCAACMMCCCC CTACAGACCCCCC
M00008 V\$SP1_01 0.841166 59 (-) GRGGCRGGGW ACAGACCCCC
M00253 V\$CAP_01 0.888615 59 (+) NCANNNNN ACAGACCC
M00255 V\$GC_01 0.818226 60 (-) NRGGGCGGGGCKN CAGACCCCCCTGA
M00008 V\$SP1_01 0.889298 61 (-) GRGGCRGGGW AGACCCCCC
M00008 V\$SP1_01 0.849377 62 (-) GRGGCRGGGW GACCCCCCT
M00084 V\$MZF1_02 0.811297 62 (-) KNNKAGGGGNA GACCCCCCTGAA
M00008 V\$SP1_01 0.894677 63 (-) GRGGCRGGGW ACCCCCCCTG
M00073 V\$DELTAEF1_01 0.818713 64 (+) NNNCACCTNAN CCCCCCTGAA
M00083 V\$MZF1_01 0.875708 64 (-) NGNGGGGA CCCCCCT
M00141 V\$LYF1_01 0.879888 65 (-) TTTGGGAGR CCCCCCTGA
M00141 V\$LYF1_01 0.867110 66 (-) TTTGGGAGR CCCCCTGAA
M00217 V\$USF_C 0.863469 66 (+) NCACGTGN CCCCCTGA
M00006 V\$MEF2_01 0.804348 68 (+) CTCTAAAAATAACYCY CCCTGAAAACAACCCT
M00216 V\$TATA_C 0.786639 68 (+) NCTATAAAAR CCCTGAAAAC
M00143 V\$PAX5_01 0.764622 69 (+) NCNNNRNKCANNNGNWNRKRGRCSRSNNN
CCTGAAAACAACCCTCAGACGCCACATC
M00257 V\$RREB1_01 0.805664 69 (+) CCCCCAACMMCCCC CCTGAAAACAACCC
M00053 V\$CREL_01 0.815628 72 (-) SGRNWTTC GAAAACAACC
M00160 V\$SRY_02 0.786553 72 (+) NWWAACA AWANN GAAAACAACCCT
M00004 V\$CMYB_01 0.763711 73 (-) NCNRNNGRCNGTTGGKGG AAAACAACCCTCAGACGC
M00008 V\$SP1_01 0.793035 74 (-) GRGGCRGGGW AAACAACCCT
M00148 V\$SRY_01 0.984496 74 (+) AACWAM AAACAAC
M00272 V\$P53_02 0.817409 74 (-) NGRCWTGYCY AAACAACCCT
M00008 V\$SP1_01 0.837203 75 (-) GRGGCRGGGW AACAACCCTC
M00200 V\$CAAT_C 0.717140 75 (+) ACCAATCANCNNGCYYSNCNCWNNT AACAACCCTCAGACGCCACATCCCC
M00189 V\$AP2_Q6 0.848116 78 (+) MKCCCSCNGGCG AACCCCTCAGACG
M00244 V\$NGFIC_01 0.740451 81 (-) WTGCGTGGGYGG CCTCAGACGCCA
M00017 V\$ATF_01 0.741673 82 (+) CNSTGACGTNNNYC CTCAGACGCCACAT
M00017 V\$ATF_01 0.767375 82 (-) CNSTGACGTNNNYC CTCAGACGCCACAT
M00177 V\$CREB_Q2 0.779415 83 (+) NSTGACGTAANN TCAGACGCCACA
M00177 V\$CREB_Q2 0.777724 83 (-) NSTGACGTAANN TCAGACGCCACA
M00178 V\$CREB_Q4 0.806411 83 (+) NSTGACGTMANN TCAGACGCCACA
M00178 V\$CREB_Q4 0.780666 83 (-) NSTGACGTMANN TCAGACGCCACA
M00179 V\$CREBP1_Q2 0.751226 83 (+) NSTGACGTMASN TCAGACGCCACA
M00179 V\$CREBP1_Q2 0.754906 83 (-) NSTGACGTMASN TCAGACGCCACA
M00253 V\$CAP_01 0.940365 83 (+) NCANNNNN TCAGACGC
M00039 V\$CREB_01 0.775797 85 (+) TGACGTMA AGACGCCA
M00039 V\$CREB_01 0.839813 85 (-) TGACGTMA AGACGCCA
M00041 V\$CREBP1CJUN_01 0.793611 85 (-) TGACGTYA AGACGCCA
M00115 V\$TAXCREB_02 0.631415 85 (+) RTGACGCATAYCCCC AGACGCCACATCCCC
M00211 V\$PADS_C 0.852823 86 (-) NGTGGTCTC GACGCCACA
M00222 V\$TH1E47_01 0.822016 86 (-) NNNNGNRTCTGGMWTT GACGCCACATCCCCTG
M00273 V\$R_01 0.736465 86 (-) NNGKCCNCSNRNYGTGGTGYN GACGCCACATCCCCTGACAAG
M00050 V\$E2F_02 0.745904 87 (-) TTTSGCGC ACGCCACA
M00115 V\$TAXCREB_02 0.689113 87 (+) RTGACGCATAYCCCC ACGCCACATCCCCTG
M00122 V\$USF_02 0.767868 87 (+) NNRNCACGTGNYNN ACGCCACATCCCCT
M00122 V\$USF_02 0.767868 87 (-) NNRNCACGTGNYNN ACGCCACATCCCCT
M00255 V\$GC_01 0.839294 87 (-) NRGGGCGGGGCKN ACGCCACATCCCCT
M00001 V\$MYOD_01 0.853543 88 (-) SRACAGGTGKYG CGCCACATCCCC
M00196 V\$SP1_Q6 0.753551 88 (-) NGGGGCGGGGYN CGCCACATCCCCT
M00098 V\$PAX2_01 0.768846 89 (-) NNNNGTCANGNRTKANNNN GCCACATCCCCTGACAAGC
M00187 V\$USF_Q6 0.847358 89 (+) GYCACGTGNC GCCACATCCC
M00196 V\$SP1_Q6 0.750395 89 (-) NGGGGCGGGGYN GCCACATCCCCTG
M00261 V\$OLF1_01 0.769903 89 (+) NNCNANTCCCYNGRGARNNKGN GCCACATCCCCTGACAAGCTGC
M00271 V\$AML1_01 0.897865 89 (-) TGTGGT GCCACA
M00075 V\$GATA1_01 0.923495 90 (-) SNNGATNNNN CCACATCCCC
M00076 V\$GATA2_01 0.922418 90 (-) NNNGATRNNN CCACATCCCC
M00077 V\$GATA3_01 0.840939 90 (-) NNGATARNNG CCACATCCC

M00261 V\$OLF1_01 0.796006 90 (-) NNCNANTCCCYNGRGARNNKGN CCACATCCCCTGACAAGCTGCC
M00056 V\$MYOGNF1_01 0.743838 91 (+) CRSCTGTNNNTTTGGCACNSNGCCARNN
CACATCCCCTGACAAGCTGCCAGGCAGGT
M00122 V\$USF_02 0.823804 92 (+) NNRNCACGTGNYNN ACATCCCCTGACAA
M00122 V\$USF_02 0.823804 92 (-) NNRNCACGTGNYNN ACATCCCCTGACAA
M00253 V\$CAP_01 0.884179 92 (+) NCANNNNN ACATCCCC
M00189 V\$AP2_Q6 0.829044 93 (+) MKCCCSCNGGCG CATCCCCTGACA
M00220 V\$REBP1_01 0.851529 93 (+) NATCACGTGAY CATCCCCTGAC
M00175 V\$AP4_Q5 0.792165 94 (-) NNCAGCTGNN ATCCCCTGAC
M00184 V\$MYOD_Q6 0.778223 94 (+) NNCANCTGNY ATCCCCTGAC
M00187 V\$USF_Q6 0.810456 94 (-) GYCACGTGNC ATCCCCTGAC
M00083 V\$MZF1_01 0.863241 95 (-) NGNGGGGA TCCCCTGA
M00141 V\$LYF1_01 0.837209 95 (-) TTTGGGAGR TCCCCTGAC
M00217 V\$USF_C 0.848708 95 (+) NCACGTGN TCCCCTGA
M00072 V\$CP2_01 0.848199 96 (+) GCNMNAMCMAG CCCCTGACAAG
M00173 V\$AP1_Q2 0.793558 98 (+) RSTGACTNMNW CCTGACAAGCT
M00174 V\$AP1_Q6 0.776608 98 (+) NNTGACTCANN CCTGACAAGCT
M00193 V\$NF1_Q6 0.840220 98 (-) NNTTGGCNNNNNNCCNNN CCTGACAAGCTGCCAGGC
M00139 V\$AHR_01 0.728305 100 (-) CYYCNRRSTNGCGTGASW TGACAAGCTGCCAGGCAG
M00272 V\$P53_02 0.839097 100 (+) NGRCWTGYCY TGACAAGCTG
M00272 V\$P53_02 0.868406 100 (-) NGRCWTGYCY TGACAAGCTG
M00175 V\$AP4_Q5 0.861534 102 (-) NNCAGCTGNN ACAAGCTGCC
M00176 V\$AP4_Q6 0.846154 102 (-) CWCAGCTGGN ACAAGCTGCC
M00184 V\$MYOD_Q6 0.819864 102 (+) NNCANCTGNY ACAAGCTGCC
M00280 V\$RFX1_01 0.773934 104 (-) NNGTNRCNWRGYAACNN AAGCTGCCAGGCAGGTT
M00209 V\$NFY_C 0.775454 105 (-) NCTGATTGGYTASY AGCTGCCAGGCAGG
M00223 V\$STAT_01 0.795059 108 (-) TTCCCRKAA TGCCAGGCA
M00189 V\$AP2_Q6 0.800781 109 (-) MKCCCSCNGGCG GCCAGGCAGGTT
M00255 V\$GC_01 0.808182 109 (+) NRGGGGCGGGGCKN GCCAGGCAGGTTCT
M00236 V\$ARNT_01 0.782048 110 (-) NNNNNCACGTGNNNNN CCAGGCAGGTTCTCTT
M00002 V\$E47_01 0.781037 111 (+) NSNGCAGGTGKNCNN CAGGCAGGTTCTCTT
M00008 V\$SP1_01 0.861552 111 (+) GRGGCRGGGW CAGGCAGGTT
M00272 V\$P53_02 0.869578 112 (+) NGRCWTGYCY AGGCAGGTTC
M00272 V\$P53_02 0.895955 112 (-) NGRCWTGYCY AGGCAGGTTC
M00277 V\$LMO2COM_01 0.812921 112 (+) SNNCAGGTGNNN AGGCAGGTTCTC
M00146 V\$HSF1_01 0.800315 113 (+) RGAANRTTCN GGCAGGTTCT
M00146 V\$HSF1_01 0.801103 113 (-) RGAANRTTCN GGCAGGTTCT
M00147 V\$HSF2_01 0.863586 113 (+) NGAANNWTCK GGCAGGTTCT
M00147 V\$HSF2_01 0.857301 113 (-) NGAANNWTCK GGCAGGTTCT
M00184 V\$MYOD_Q6 0.845157 113 (-) NNCANCTGNY GGCAGGTTCT
M00183 V\$MYB_Q6 0.831950 114 (-) NNNAACKGNC GCAGGTTCTC
M00127 V\$GATA1_03 0.841499 115 (-) RNSNNGATAANNNGN CAGGTTCTCTTCCT
M00258 V\$ISRE_01 0.860521 115 (+) CAGTTTCWCTTTYCC CAGGTTCTCTTCCTC
M00007 V\$ELK1_01 0.846025 118 (-) NNNACMGGAAAGTNCNN GTTCTCTTCCTCTCAC
M00074 V\$CETSIP54_02 0.855366 120 (-) NNAMMGGAWRWNN TCTCTTCCTCTCA
M00108 V\$NRF2_01 0.920058 121 (-) ACCGGAAGNS CTCTTCCTCT
M00223 V\$STAT_01 0.870683 124 (+) TTCCCRKAA TTCCTCTCA
M00141 V\$LYF1_01 0.828776 126 (-) TTTGGGAGR CCTCTCACA
M00191 V\$ER_Q6 0.756179 127 (+) NNARGNNANNTGACCYN CTCTCACATACTGACCCAC
M00262 V\$STAF_01 0.738873 127 (+) NTTWCCCANMATGCAYYRCGY CTCTCACATACTGACCCACGGC
M00007 V\$ELK1_01 0.780227 128 (-) NNNACMGGAAAGTNCNN TCTCACATACTGACCC
M00045 V\$E4BP4_01 0.771260 128 (-) NRTTAYGTAAYN TCTCACATACTG
M00076 V\$GATA2_01 0.819125 130 (+) NNNGATRNNN TCACATACTG
M00253 V\$CAP_01 0.876294 130 (+) NCANNNNN TCACATAC
M00032 V\$CETSIP54_01 0.818305 131 (-) NCMGGAWGYN CACATACTGA
M00037 V\$NFE2_01 0.867522 135 (+) TGCTGASTCAY TACTGACCCAC
M00172 V\$AP1FJ_Q2 0.844479 136 (+) RSTGACTNMNW ACTGACCCACG
M00173 V\$AP1_Q2 0.844510 136 (+) RSTGACTNMNW ACTGACCCACG
M00174 V\$AP1_Q6 0.867619 136 (+) NNTGACTCANN ACTGACCCACG
M00177 V\$CREB_Q2 0.767335 136 (+) NSTGACGTAANN ACTGACCCACGG
M00178 V\$CREB_Q4 0.745835 136 (+) NSTGACGTMANN ACTGACCCACGG

M00188 V\$AP1_Q4 0.866728 136 (+) RSTGACTMANN ACTGACCCACG
M00115 V\$TAXCREB_02 0.655443 137 (+) RTGACGCATAYCCCC CTGACCCACGGCTCC
M00199 V\$AP1_C 0.793003 137 (+) NTGASTCAG CTGACCCAC
M00199 V\$AP1_C 0.854810 137 (-) NTGASTCAG CTGACCCAC
M00251 V\$XBP1_01 0.747650 137 (-) NNGNTGACGTGKNNNWT CTGACCCACGGCTCCAC
M00264 V\$STAF_02 0.758053 137 (+) MNTTCCCAKMATKCMWNGCRN CTGACCCACGGCTCCACCCTC
M00189 V\$AP2_Q6 0.780331 139 (+) MKCCSCNNGGCG GACCCACGGCTC
M00196 V\$SP1_Q6 0.752762 140 (-) NGGGGGCGGGGYN ACCCAGGCTCCA
M00227 V\$VMYB_02 0.817990 140 (+) NSYAACGGN ACCCAGGCG
M00187 V\$USF_Q6 0.866928 141 (+) GYCACGTGNC CCCACGGCTC
M00175 V\$AP4_Q5 0.781284 143 (+) NNCAGCTGNN CACGGCTCCA
M00176 V\$AP4_Q6 0.806815 143 (+) CWCAGCTGGN CACGGCTCCA
M00085 V\$ZID_01 0.868294 145 (+) NGGCTCYATCAYC CGGCTCCACCCTC
M00255 V\$GC_01 0.936306 145 (-) NRGGGGCGGGGCKN CGGCTCCACCCTCT
M00196 V\$SP1_Q6 0.871383 146 (-) NGGGGGCGGGGYN GGCTCCACCCTCT
M00237 V\$AHRARNT_02 0.730372 146 (-) GRGKATYGCGTGMSWNSCC GGCTCCACCCTCTCTCCCC
M00008 V\$SP1_01 0.827293 147 (-) GRGGCRGGGW GCTCCACCCT
M00083 V\$MZF1_01 0.875708 149 (-) NGNGGGGA TCCACCCT
M00084 V\$MZF1_02 0.867283 149 (-) KNNNKAGGGGNAA TCCACCCTCTCTC
M00244 V\$NGFIC_01 0.781195 150 (-) WTGCGTGGGYGG CCACCCTCTCTC
M00246 V\$EGR2_01 0.749526 150 (-) NTGCGTRGGCGK CCACCCTCTCTC
M00253 V\$CAP_01 0.891572 150 (+) NCANNNNN CCACCCTC
M00127 V\$GATA1_03 0.794463 151 (-) RNSNNGATAANNNGN CACCCTCTCTCCCC
M00008 V\$SP1_01 0.793035 152 (-) GRGGCRGGGW ACCCTCTCTC
M00033 V\$P300_01 0.822768 153 (-) NNNRGGAGTNNNNS CCCTCTCTCCCCTG
M00075 V\$GATA1_01 0.802073 153 (-) SNGATNNNN CCCTCTCTCC
M00077 V\$GATA3_01 0.875942 153 (-) NNGATARNG CCCTCTCTC
M00278 V\$LMO2COM_02 0.816712 153 (-) NMGATANS G CCTCTCTC
M00008 V\$SP1_01 0.837486 156 (-) GRGGCRGGGW TCTCTCCCCT
M00073 V\$DELTAEF1_01 0.822612 158 (+) NNNCACCTNAN TCTCCCCTGGA
M00189 V\$AP2_Q6 0.782169 159 (-) MKCCSCNNGGCG CTCCCCTGGAAA
M00215 V\$SRF_C 0.788826 159 (-) NCCWTATATGGNCWN CTCCCCTGGAAAGGA
M00025 V\$ELK1_02 0.790940 160 (+) NNNNCCGGAARYNN TCCCCTGGAAAGGA
M00083 V\$MZF1_01 0.863241 160 (-) NGNGGGGA TCCCCTGG
M00141 V\$LYF1_01 0.847176 160 (-) TTTGGGAGR TCCCCTGGA
M00217 V\$USF_C 0.820530 160 (+) NCACGTGN TCCCCTGG
M00050 V\$E2F_02 0.764788 163 (-) TTTSGCGC CCTGGAAA
M00258 V\$ISRE_01 0.735452 164 (-) CAGTTTCWCTTTYCC CTGGAAAGGACACCA
M00053 V\$CREL_01 0.847330 166 (-) SGRNWTTC GGAAAGGACA
M00146 V\$HSF1_01 0.768807 166 (+) RGAANRTTCN GGAAAGGACA
M00032 V\$CETSIP54_01 0.842477 168 (+) NCMGGAWGYN AAAGGACACC
M00191 V\$ER_Q6 0.767348 168 (+) NNARGNNANNNTGACCYN AAAGGACACCATGAGCACT
M00192 V\$GR_Q6 0.858538 168 (-) NNNNNNCNNTNTGTNCTNN AAAGGACACCATGAGCACT
M00205 V\$GRE_C 0.889644 169 (-) GGTACAANNTGTCTK AAGGACACCATGAGCA
M00069 V\$YY1_02 0.770796 170 (+) NNNCGGCCATCTTGNCSTNW AGGACACCATGAGCACTGAA
M00211 V\$PADS_C 0.842238 172 (-) NGTGGTCTC GACACCATG
M00076 V\$GATA2_01 0.819125 174 (-) NNGATRN NN CACCATGAGC
M00277 V\$LMO2COM_01 0.794078 174 (+) SNNCAGGTGNNN CACCATGAGCAC
M00062 V\$IRF1_01 0.793866 180 (+) SAAAAGYGAAACC GAGCACTGAAAGC
M00063 V\$IRF2_01 0.798724 180 (+) GAAAAGYGAAASY GAGCACTGAAAGC
M00032 V\$CETSIP54_01 0.810429 184 (+) NCMGGAWGYN ACTGAAAGCA
M00238 V\$BARBIE_01 0.786953 184 (+) ATNNAAGCNGRNGG ACTGAAAGCATGATC
M00059 V\$YY1_01 0.780472 185 (-) NNNNNCCATNTWNNNWN CTGAAAGCATGATCCGG
M00272 V\$P53_02 0.807151 189 (+) NGRCWTGYCY AAGCATGATC
M00272 V\$P53_02 0.806272 189 (-) NGRCWTGYCY AAGCATGATC
M00098 V\$PAX2_01 0.826400 190 (-) NNNNGTCANGNRTKANN NN AGCATGATCCGGGACGTGG
M00127 V\$GATA1_03 0.788829 190 (+) RNSNNGATAANNNGN AGCATGATCCGGGA
M00146 V\$HSF1_01 0.769200 190 (+) RGAANRTTCN AGCATGATCC
M00146 V\$HSF1_01 0.790469 190 (-) RGAANRTTCN AGCATGATCC
M00147 V\$HSF2_01 0.829575 190 (+) NGAANNWTCK AGCATGATCC
M00147 V\$HSF2_01 0.828835 190 (-) NGAANNWTCK AGCATGATCC

M00224 V\$STAT1_01 0.738021 190 (+) NNNSANTTCCGGGAANTGNSN AGCATGATCCGGGACGTGGAG
M00074 V\$CETS1P54_02 0.858966 192 (-) NNAMMGGAWRWNN CATGATCCGGGAC
M00075 V\$GATA1_01 0.894373 192 (+) SNNGATNNNN CATGATCCGG
M00075 V\$GATA1_01 0.838105 192 (-) SNNGATNNNN CATGATCCGG
M00076 V\$GATA2_01 0.858367 192 (+) NNNGATRNNN CATGATCCGG
M00076 V\$GATA2_01 0.859720 192 (-) NNNGATRNNN CATGATCCGG
M00032 V\$CETS1P54_01 0.818848 193 (-) NCMGGAWGYN ATGATCCGGG
M00189 V\$AP2_Q6 0.794807 193 (-) MKCCSCNNGGCG ATGATCCGGGAC
M00144 V\$PAX5_02 0.749354 195 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
GATCCGGGACGTGGAGCTGGCCGAGGAG
M00113 V\$CREB_02 0.776229 197 (+) NNGNTGACGYNN TCCGGGACGTGG
M00251 V\$XBP1_01 0.766026 197 (+) NNGNTGACGTGKNNNWT TCCGGGACGTGGAGCTG
M00017 V\$ATF_01 0.799895 198 (+) CNSTGACGTNNNYC CCGGGACGTGGAGC
M00032 V\$CETS1P54_01 0.813688 198 (+) NCMGGAWGYN CCGGGACGTG
M00055 V\$NMYC_01 0.795620 199 (+) NNNCACGTGNNN CGGGACGTGGAG
M00055 V\$NMYC_01 0.823601 199 (-) NNNCACGTGNNN CGGGACGTGGAG
M00008 V\$SP1_01 0.827010 200 (+) GRGGCRGGGW GGGACGTGGA
M00187 V\$USF_Q6 0.833100 200 (-) GYCACGTGNC GGGACGTGGA
M00255 V\$GC_01 0.828270 200 (+) NRGGGGCGGGGCK GGGACGTGGAGCTG
M00085 V\$ZID_01 0.843046 201 (-) NGGCTCYATCAYC GGACGTGGAGCTG
M00217 V\$USF_C 0.845018 201 (-) NCACGTGN GGACGTGG
M00002 V\$E47_01 0.825030 204 (+) NSNGCAGGTGKNCNN CGTGGAGCTGGCCGA
M00277 V\$LMO2COM_01 0.817227 205 (-) SNNCAGGTGNNN GTGGAGCTGGCC
M00175 V\$AP4_Q5 0.803863 206 (-) NNCAGCTGNN TGGAGCTGGC
M00176 V\$AP4_Q6 0.802556 206 (-) CWCAGCTGGN TGGAGCTGGC
M00184 V\$MYOD_Q6 0.792721 206 (+) NNCANCTGNY TGGAGCTGGC
M00272 V\$P53_02 0.826202 208 (-) NGRCWTGYCY GAGCTGGCCG
M00189 V\$AP2_Q6 0.790671 211 (-) MKCCSCNNGGCG CTGGCCGAGGAG
M00243 V\$EGR1_01 0.762000 212 (+) WTGCGTGGGCGK TGGCCGAGGAGG
M00244 V\$NGFIC_01 0.761019 212 (+) WTGCGTGGGYGG TGGCCGAGGAGG
M00237 V\$AHRARNT_02 0.747639 213 (-) GRGKATYGCGTGMSWNSCC GGCCGAGGAGGCGCTCCCC
M00189 V\$AP2_Q6 0.786535 214 (-) MKCCSCNNGGCG GCCGAGGAGGCG
M00196 V\$SP1_Q6 0.805366 215 (+) NGGGGGCGGGGYN CCGAGGAGGCGCT
M00255 V\$GC_01 0.792259 215 (+) NRGGGGCGGGGCK CCGAGGAGGCGCTC
M00115 V\$TAXCREB_02 0.653960 217 (-) RTGACGCATAYCCCC GAGGAGGCGCTCCCC
M00115 V\$TAXCREB_02 0.689113 218 (+) RTGACGCATAYCCCC AGGAGGCGCTCCCCA
M00255 V\$GC_01 0.786134 218 (+) NRGGGGCGGGGCK AGGAGGCGCTCCCC
M00008 V\$SP1_01 0.826161 220 (+) GRGGCRGGGW GAGGCGCTCC
M00051 V\$NFKAPPAB50_01 0.752554 220 (+) GGGGATYCCC GAGGCGCTCC
M00255 V\$GC_01 0.790544 220 (-) NRGGGGCGGGGCK GAGGCGCTCCCCAA
M00208 V\$NFKB_C 0.758368 221 (+) NGGGACTTTCCA AGGCGCTCCCCA
M00051 V\$NFKAPPAB50_01 0.831630 222 (+) GGGGATYCCC GCGCTCCCC
M00051 V\$NFKAPPAB50_01 0.857619 222 (-) GGGGATYCCC GCGCTCCCC
M00054 V\$NFKAPPAB_01 0.786267 222 (+) GGGAMTTYCC GCGCTCCCC
M00072 V\$CP2_01 0.791595 223 (+) GCNMNAMCMAG GCGCTCCCCAA
M00141 V\$LYF1_01 0.886277 226 (-) TTTGGGAGR CTCCCCAAG
M00189 V\$AP2_Q6 0.892693 226 (+) MKCCSCNNGGCG CTCCCCAAGAAG
M00083 V\$MZF1_01 0.917265 227 (-) NGNGGGGA TCCCCAAG
M00141 V\$LYF1_01 0.825198 227 (-) TTTGGGAGR TCCCCAAGA
M00108 V\$NRF2_01 0.791667 230 (+) ACCGGAAGNS CCAAGAAGAC
M00068 V\$HEN1_01 0.741064 231 (-) NNNGNCNCAGCTGCGNCCCN CAAGAAGACAGGGGGGGCCCCAG
M00192 V\$GR_Q6 0.799665 231 (-) NNNNNNCNNTNTGTNCTNN CAAGAAGACAGGGGGGGCC
M00126 V\$GATA1_02 0.782813 232 (+) NNNNNGATANKGN AAGAAGACAGGGGG
M00127 V\$GATA1_03 0.830475 232 (+) RNSNNGATAANN GN AAGAAGACAGGGGG
M00128 V\$GATA1_04 0.811581 233 (+) NNCWGATARNNNN AGAAGACAGGGGG
M00075 V\$GATA1_01 0.773445 234 (+) SNNGATNNNN GAAGACAGGG
M00076 V\$GATA2_01 0.805142 234 (+) NNNGATRNNN GAAGACAGGG
M00002 V\$E47_01 0.843712 235 (+) NSNGCAGGTGKNCNN AAGACAGGGGGGGCCC
M00122 V\$USF_02 0.764139 235 (+) NNRNCACGTGNYNN AAGACAGGGGGGGCC
M00122 V\$USF_02 0.764139 235 (-) NNRNCACGTGNYNN AAGACAGGGGGGGCC
M00278 V\$LMO2COM_02 0.810984 235 (+) NMGATANSG AAGACAGGG

M00139 V\$AHR_01 0.714221 236 (-) CYYCNRRSTNGCGTGASW AGACAGGGGGGCCCCAGG
M00175 V\$AP4_Q5 0.799238 237 (+) NNCAGCTGNN GACAGGGGGG
M00176 V\$AP4_Q6 0.806815 237 (+) CWCAGCTGGN GACAGGGGGG
M00184 V\$MYOD_Q6 0.830352 237 (-) NNCANCTGNY GACAGGGGGG
M00189 V\$AP2_Q6 0.810432 237 (-) MKCCSCNNGGCG GACAGGGGGGCC
M00217 V\$USF_C 0.864810 238 (-) NCACGTGN ACAGGGGG
M00008 V\$SP1_01 0.830408 239 (+) GRGGCRGGGW CAGGGGGGCC
M00083 V\$MZF1_01 0.875708 240 (+) NGNGGGGA AGGGGGGC
M00051 V\$NFKAPPAB50_01 0.857619 241 (+) GGGGATYCCC GGGGGGCCCC
M00051 V\$NFKAPPAB50_01 0.835629 241 (-) GGGGATYCCC GGGGGGCCCC
M00054 V\$NFKAPPAB_01 0.791261 241 (+) GGGAMTTYCC GGGGGGCCCC
M00054 V\$NFKAPPAB_01 0.825718 241 (-) GGGAMTTYCC GGGGGGCCCC
M00155 V\$ARP1_01 0.773593 243 (-) TGARCCYTTGAMCCYW GGGGCCCCAGGGCTCC
M00085 V\$ZID_01 0.775510 244 (+) NGGCTCYATCAYC GGGCCCCAGGGCT
M00189 V\$AP2_Q6 0.803309 244 (+) MKCCSCNNGGCG GGGCCCCAGGGC
M00264 V\$STAF_02 0.766436 244 (+) MNTTCCCAKMATKCMWNGCRN GGGCCCCAGGGCTCCAGGGCG
M00189 V\$AP2_Q6 0.893153 245 (+) MKCCSCNNGGCG GGCCCCAGGGCT
M00189 V\$AP2_Q6 0.847197 245 (-) MKCCSCNNGGCG GGCCCCAGGGCT
M00187 V\$USF_Q6 0.798994 246 (+) GYCACGTGNC GCCCCAGGGC
M00005 V\$AP4_01 0.801297 251 (-) WGARYCAGCTGYGGNCNK AGGGCTCCAGGCGGTGCT
M00189 V\$AP2_Q6 0.818704 252 (+) MKCCSCNNGGCG GGGCTCCAGGCG
M00189 V\$AP2_Q6 0.863281 252 (-) MKCCSCNNGGCG GGGCTCCAGGCG
M00055 V\$NMYC_01 0.746959 255 (-) NNNCACGTGNNN CTCCAGGCGGTG
M00189 V\$AP2_Q6 0.816866 255 (-) MKCCSCNNGGCG CTCCAGGCGGTG
M00277 V\$LMO2COM_01 0.845222 255 (+) SNNCAGGTGNNN CTCCAGGCGGTG
M00196 V\$SP1_Q6 0.798001 256 (+) NGGGGGCGGGGYN TCCAGGCGGTGCT
M00255 V\$GC_01 0.877266 256 (+) NRGGGGCGGGGCK TCCAGGCGGTGCTT
M00008 V\$SP1_01 0.864666 258 (+) GRGGCRGGGW CAGGCGGTGC
M00271 V\$AML1_01 0.835496 260 (+) TGTGGT GGCGGT
M00144 V\$PAX5_02 0.754807 261 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
GCGGTGCTTGTTCTCCTCAGCCTCTTCTCC
M00057 V\$COMP1_01 0.775569 262 (-) NNTNWKGATTGRCNRSRANMRRNN CGGTGCTTGTTCTCCTCAGCCTCTTC
M00075 V\$GATA1_01 0.775420 263 (+) SNGGATNNNN GTTGCTTGTT
M00272 V\$P53_02 0.853751 264 (+) NGRCWTGYCY GTGCTTGTTT
M00146 V\$HSF1_01 0.776290 265 (-) RGAANRTTCN TGCTTGTTCC
M00147 V\$HSF2_01 0.811460 265 (-) NGAANNWTCK TGCTTGTTCC
M00074 V\$CETSIP54_02 0.835079 267 (-) NNAMMGGAWRWNN CTTGTTCTCCTCAGC
M00084 V\$MZF1_02 0.814546 268 (-) KNNNKAGGGGNAA TTGTTCTCCTCAGCC
M00279 V\$MIF1_01 0.817293 268 (+) NNGTTGCWWGGYACNGS TTGTTCTCCTCAGCCTCTTC
M00280 V\$RFX1_01 0.765677 268 (-) NNGTNRNCRWGYAACNN TTGTTCTCCTCAGCCTCTT
M00114 V\$TAXCREB_01 0.710101 269 (-) GGGGGTTGACGYANA TGTTCTCCTCAGCCTCT
M00174 V\$AP1_Q6 0.792027 269 (-) NNTGACTCANN TGTTCTCCTCAGC
M00113 V\$CREB_02 0.790166 270 (-) NNGNTGACGYNN GTTCTCCTCAGCCT
M00199 V\$AP1_C 0.806414 270 (+) NTGASTCAG GTTCTCCTCAG
M00141 V\$LYF1_01 0.826220 271 (-) TTTGGGAGR TTCCTCAGC
M00255 V\$GC_01 0.807202 271 (-) NRGGGGCGGGGCK TTCCTCAGCCTCTT
M00008 V\$SP1_01 0.780861 273 (-) GRGGCRGGGW CCTCAGCCTC
M00143 V\$PAX5_01 0.812314 275 (-) NCNNNRNKCANNNGWGNRKRGCSSRNNN
TCAGCCTCTTCTCCTTCTGATCGTGCC
M00253 V\$CAP_01 0.968950 275 (+) NCANNNNN TCAGCCTC
M00057 V\$COMP1_01 0.777964 277 (-) NNTNWKGATTGRCNRSRANMRRNN AGCCTCTTCTCCTTCTGATCGTG
M00146 V\$HSF1_01 0.808586 277 (-) RGAANRTTCN AGCCTCTTCT
M00147 V\$HSF2_01 0.825508 277 (-) NGAANNWTCK AGCCTCTTCT
M00255 V\$GC_01 0.792014 277 (-) NRGGGGCGGGGCK AGCCTCTTCTCCTT
M00127 V\$GATA1_03 0.820676 279 (-) RNSNNGATAANNNGN CCTCTTCTCCTTCC
M00084 V\$MZF1_02 0.820045 283 (-) KNNNKAGGGGNAA TTCTCCTTCTGA
M00025 V\$ELK1_02 0.863483 285 (-) NNNNCCGGAARYNN CTCCTTCTGATCG
M00074 V\$CETSIP54_02 0.835406 285 (-) NNAMMGGAWRWNN CTCCTTCTGATC
M00032 V\$CETSIP54_01 0.853341 286 (-) NCMGGAWGYN TCCTTCTGA
M00087 V\$IK2_01 0.865838 286 (-) NNNYGGGAWNNN TCCTTCTGATC
M00126 V\$GATA1_02 0.781563 289 (+) NNNNNGATANKGN TTCCTGATCGTGCC

M00075 V\$GATA1_01 0.928430 291 (+) SNNGATNNNN CCTGATCGTG
M00075 V\$GATA1_01 0.848963 291 (-) SNNGATNNNN CCTGATCGTG
M00076 V\$GATA2_01 0.885431 291 (+) NNGGATRNNN CCTGATCGTG
M00076 V\$GATA2_01 0.840325 291 (-) NNGGATRNNN CCTGATCGTG
M00180 V\$E2F_Q6 0.731721 291 (-) NNGCGCGAAANTK CCTGATCGTGGCA
M00278 V\$LMO2COM_02 0.799865 291 (-) NMGATANS GCTGATCGT
M00115 V\$TAXCREB_02 0.657965 297 (-) RTGACGCATAYCCCC CGTGGCAGGCGCCAC
M00196 V\$SP1_Q6 0.759074 297 (+) NGGGGGCGGGGYN CGTGGCAGGCGCC
M00222 V\$THIE47_01 0.792947 297 (-) NNNNGNRTCTGGMWTT CGTGGCAGGCGCCACC
M00236 V\$ARNT_01 0.766858 297 (-) NNNNNCACGTGNNNNN CGTGGCAGGCGCCACC
M00008 V\$SP1_01 0.784824 298 (+) GRGGCRGGGW GTGGCAGGCG
M00122 V\$USF_02 0.762585 298 (+) NNRNCACGTGNYNN GTGGCAGGCGCCAC
M00122 V\$USF_02 0.762585 298 (-) NNRNCACGTGNYNN GTGGCAGGCGCCAC
M00235 V\$AHRARNT_01 0.836710 299 (-) KNNKNNTYGCGTGCMS TGGCAGGCGCCACCAC
M00272 V\$P53_02 0.799238 299 (-) NGRCWTGYCY TGGCAGGCGC
M00017 V\$ATF_01 0.785733 300 (-) CNSTGACGTNNNYC GGCAGGCGCCACCA
M00184 V\$MYOD_Q6 0.830043 300 (-) NNCANCTGNY GGCAGGCGCC
M00177 V\$CREB_Q2 0.797052 301 (-) NSTGACGTAANN GCAGGCGCCACC
M00178 V\$CREB_Q4 0.790005 301 (-) NSTGACGTMANN GCAGGCGCCACC
M00179 V\$CREBP1_Q2 0.810303 301 (-) NSTGACGTMASN GCAGGCGCCACC
M00114 V\$TAXCREB_01 0.729293 302 (-) GGGGGTTGACGYANA CAGGCGCCACCACGC
M00085 V\$ZID_01 0.775931 303 (+) NGGCTCYATCAYC AGGCGCCACCACG
M00113 V\$CREB_02 0.827242 303 (-) NNGNTGACGYNN AGGCGCCACCAC
M00180 V\$E2F_Q6 0.754047 303 (+) NNGCGCGAAANTK AGGCGCCACCACG
M00196 V\$SP1_Q6 0.753288 304 (-) NGGGGGCGGGGYN GGCAGCCACCACGC
M00050 V\$E2F_02 0.743405 305 (-) TTTSGCGC GCGCCACC
M00237 V\$AHRARNT_02 0.718123 305 (-) GRGKATYGCGTGMSWNSCC GCGCCACCACGCTCTTCTG
M00189 V\$AP2_Q6 0.790901 306 (+) MKCCSCNNGGCG CGCCACCACGCT
M00211 V\$PADS_C 0.845010 307 (-) NGTGGTCTC GCCACCACG
M00236 V\$ARNT_01 0.840046 307 (-) NNNNNCACGTGNNNNN GCCACCACGCTCTTCT
M00273 V\$R_01 0.781276 307 (-) NNGKCCNCSNRNYGTGGTGYN GCCACCACGCTCTTCTGCCTG
M00255 V\$GC_01 0.795198 308 (-) NRGGGGCGGGGCKN CCACCACGCTCTTC
M00123 V\$MYCMAX_02 0.818492 309 (+) NANCACGTGNNW CACCACGCTCTT
M00235 V\$AHRARNT_01 0.783712 309 (-) KNNKNNTYGCGTGCMS CACCACGCTCTTCTGC
M00008 V\$SP1_01 0.815968 310 (-) GRGGCRGGGW ACCACGCTCT
M00271 V\$AML1_01 0.855588 310 (-) TGTGGT ACCACG
M00085 V\$ZID_01 0.762676 313 (+) NGGCTCYATCAYC ACGCTCTTCTGCC
M00108 V\$NRF2_01 0.812500 316 (-) ACCGGAAGNS CTCTTCTGCC
M00189 V\$AP2_Q6 0.802849 318 (+) MKCCSCNNGGCG CTTCTGCCTGCT
M00002 V\$E47_01 0.790880 320 (-) NSNGCAGGTGKNCNN TCTGCCTGCTGCACT
M00141 V\$LYF1_01 0.830820 320 (-) TTTGGGAGR TCTGCCTGC
M00277 V\$LMO2COM_01 0.792194 322 (+) SNNCAGGTGNNN TGCTGCTGCAC
M00143 V\$PAX5_01 0.778059 323 (+) NCNNNRNKCANNNGNWNKRGCSRSNNN
GCCTGCTGCACTTTGGAGTGATCGGCC
M00175 V\$AP4_Q5 0.814744 323 (-) NNCAGCTGNN GCCTGCTGCA
M00184 V\$MYOD_Q6 0.792721 323 (-) NNCANCTGNY GCCTGCTGCA
M00249 V\$CHOP_01 0.809385 323 (-) NNRTGCAATMCCC GCCTGCTGCACTT
M00134 V\$SHNF4_01 0.782214 326 (-) NNNRGGNCAAAGKTCANN TGCTGCACTTTGGAGTGAT
M00158 V\$COUP_01 0.842181 329 (+) TGAMCTTTGMMCYT TGCACCTTTGGAGTG
M00253 V\$CAP_01 0.893051 330 (+) NCANNNNN GCACTTTG
M00159 V\$CEBP_01 0.886224 332 (+) NNTKTGGWNANN ACTTTGGAGTGAT
M00033 V\$P300_01 0.802658 333 (+) NNNRGGAGTNNNNN CTTTGGAGTGATCG
M00124 V\$PBX1_02 0.752690 333 (-) NMATCAATCAANNW CTTTGGAGTGATCGG
M00050 V\$E2F_02 0.745904 334 (+) TTTSGCGC TTTGGAGT
M00221 V\$SREBP1_02 0.813935 335 (-) KATCACCCAC TTGGAGTGATC
M00115 V\$TAXCREB_02 0.611391 336 (-) RTGACGCATAYCCCC TGGAGTGATCGGCC
M00146 V\$HSF1_01 0.807404 337 (+) RGAANRTCN GGAGTGATCG
M00147 V\$HSF2_01 0.892052 337 (+) NGAANNWTCK GGAGTGATCG
M00147 V\$HSF2_01 0.800739 337 (-) NGAANNWTCK GGAGTGATCG
M00056 V\$MYOGNF1_01 0.767718 338 (-) CRSCTGTNNNNNTTTGGCACNSNGCCARNN
GAGTGATCGCCCCCAGAGGGAAGAGGTG

M00104 V\$CDPCR1_01 0.852165 338 (+) NATCGATCGS GAGTGATCGG
M00106 V\$CDPCR3HD_01 0.859285 338 (+) NATYGATSSS GAGTGATCGG
M00075 V\$GATA1_01 0.853406 339 (+) SNNGATNNNN AGTGATCGGC
M00075 V\$GATA1_01 0.841560 339 (-) SNNGATNNNN AGTGATCGGC
M00076 V\$GATA2_01 0.833559 339 (+) NNNGATRNNN AGTGATCGGC
M00076 V\$GATA2_01 0.853406 339 (-) NNNGATRNNN AGTGATCGGC
M00209 V\$NFY_C 0.770268 339 (+) NCTGATTGGYTASY AGTGATCGGCCCCC
M00185 V\$NFY_Q6 0.829651 340 (-) TRRCCAATSRN GTGATCGGCCC
M00255 V\$GC_01 0.803528 340 (-) NRGGGGCGGGGCNK GTGATCGGCCCCCA
M00196 V\$SP1_Q6 0.790637 341 (-) NGGGGGCGGGGYN TGATCGGCCCCCA
M00254 V\$CAAT_01 0.781700 341 (-) NNNRCCAATSA TGATCGGCCCCC
M00221 V\$SREBP1_02 0.720902 342 (+) KATCACCCAC GATCGGCCCCC
M00261 V\$OLF1_01 0.790264 344 (-) NNCNANTCCCYNGRGARNNKGN TCGGCCCCCAGAGGGAAGAGGT
M00189 V\$AP2_Q6 0.818704 345 (+) MKCCSCNNGGCG CGGCCCCCAGAG
M00189 V\$AP2_Q6 0.893842 346 (+) MKCCSCNNGGCG GGCCCCCAGAGG
M00141 V\$LYF1_01 0.835420 347 (-) TTTGGGAGR GCCCCAGA
M00025 V\$ELK1_02 0.804408 351 (+) NNNNCCGGAARYNN CCAGAGGGAAGAGG
M00086 V\$IK1_01 0.779380 352 (+) NNTTGGGAATRCC CAGAGGGAAGAGG
M00087 V\$IK2_01 0.858312 352 (+) NNNYGGGAWNNN CAGAGGGAAGAG
M00200 V\$CAAT_C 0.757857 352 (-) ACCAATCANCNNGCYYSNCNCWNNT CAGAGGGAAGAGGTGAGTGCCTGGC
M00058 V\$HEN1_02 0.720268 353 (+) NNGGGNCGCAGCTGCGNCCCN AGAGGGAAGAGGTGAGTGCCTG
M00058 V\$HEN1_02 0.718090 353 (-) NNGGGNCGCAGCTGCGNCCCN AGAGGGAAGAGGTGAGTGCCTG
M00068 V\$HEN1_01 0.747734 353 (+) NNNGGNCGCAGCTGCGNCCCN AGAGGGAAGAGGTGAGTGCCTG
M00196 V\$SP1_Q6 0.763546 353 (+) NGGGGGCGGGGYN AGAGGGAAGAGGT
M00255 V\$GC_01 0.873346 353 (+) NRGGGGCGGGGCNK AGAGGGAAGAGGTG
M00007 V\$ELK1_01 0.784903 354 (+) NNNACMGAAGTNCNN GAGGGAAGAGGTGAGT
M00108 V\$NRF2_01 0.816134 354 (+) ACCGGAAGNS GAGGGAAGAG
M00113 V\$CREB_02 0.770181 356 (+) NNGNTGACGYNN GGAAGAGGTGA
M00033 V\$P300_01 0.811861 357 (+) NNNRGGAGTNNNNS GGAAGAGGTGAGTG
M00115 V\$TAXCREB_02 0.653960 358 (-) RTGACGCATAYCCCC GAAGAGGTGAGTGCC
M00235 V\$AHRARNT_01 0.793534 358 (+) KNNKNNTYGCGTGCMS GAAGAGGTGAGTGCCT
M00073 V\$DELTAEF1_01 0.855426 359 (-) NNNCACCTNAN AAGAGGTGAGT
M00175 V\$AP4_Q5 0.838955 359 (-) NNCAGCTGNN AAGAGGTGAG
M00176 V\$AP4_Q6 0.823603 359 (-) CWCAGCTGGN AAGAGGTGAG
M00237 V\$AHRARNT_02 0.835744 359 (+) GRGKATYGCGTGMSWNSCC AAGAGGTGAGTGCCTGGCC
M00083 V\$MZF1_01 0.855686 360 (+) NGNGGGGA AGAGGTGA
M00155 V\$ARP1_01 0.764578 360 (-) TGARCCYTTGAMCCYW AGAGGTGAGTGCCTGG
M00194 V\$NFKB_Q6 0.783789 361 (-) NGGGGAMTTTCNN GAGGTGAGTGCCTG
M00051 V\$NFKAPPAB50_01 0.762772 363 (+) GGGGATYCCC GGTGAGTGCC
M00174 V\$AP1_Q6 0.796916 363 (+) NNTGACTCANN GGTGAGTGCCT
M00237 V\$AHRARNT_02 0.769923 363 (+) GRGKATYGCGTGMSWNSCC GGTGAGTGCCTGGCCAGCC
M00185 V\$NFY_Q6 0.784943 364 (-) TRRCCAATSRN GTGAGTGCCTG
M00244 V\$NGFIC_01 0.727130 364 (+) WTGCGTGGGYGG GTGAGTGCCTGG
M00035 V\$VMAF_01 0.781365 366 (-) NNTGCTGACTCAGCANN GAGTGCCTGGCCAGCCTTC
M00209 V\$NFY_C 0.767675 367 (+) NCTGATTGGYTASY AGTGCCTGGCCAGC
M00185 V\$NFY_Q6 0.786485 368 (-) TRRCCAATSRN GTGCCTGGCCA
M00254 V\$CAAT_01 0.835922 369 (-) NNNRCCAATSA TGCTGGCCAGC
M00193 V\$NF1_Q6 0.791858 370 (+) NNTTGGCNNNNNNCCNN GCCTGGCCAGCCTTCATC
M00255 V\$GC_01 0.792749 372 (-) NRGGGGCGGGGCNK CTGGCCAGCCTTCA
M00272 V\$P53_02 0.874560 373 (+) NGRCWTGYCY TGGCCAGCCT
M00272 V\$P53_02 0.847011 373 (-) NGRCWTGYCY TGGCCAGCCT
M00008 V\$SP1_01 0.856738 374 (-) GRGGCRGGGW GGCCAGCCTT
M00253 V\$CAP_01 0.920651 376 (+) NCANNNNN CCAGCCTT
M00114 V\$TAXCREB_01 0.722020 377 (-) GGGGGTTGACGYANA CAGCCTTCATCCACT
M00075 V\$GATA1_01 0.770484 378 (-) SNNGATNNNN AGCCTTCATC
M00074 V\$CETSIP54_02 0.835079 381 (-) NNAMMGGAWRWNN CTTTCATCCACTCT
M00075 V\$GATA1_01 0.788746 381 (-) SNNGATNNNN CTTTCATCCAC
M00253 V\$CAP_01 0.909808 383 (+) NCANNNNN TCATCCAC
M00033 V\$P300_01 0.853783 384 (-) NNNRGGAGTNNNNS CATCCACTCTCCCA
M00084 V\$MZF1_02 0.818795 384 (-) KNNNKAGGGGNAA CATCCACTCTCCC
M00185 V\$NFY_Q6 0.825540 384 (+) TRRCCAATSRN CATCCACTCTC

M00083 V\$MZF1_01 0.857575 386 (-) NGNGGGGA TCCACTCT
M00085 V\$ZID_01 0.783926 387 (+) NGGCTCYATCAYC CCACTCTCCCACC
M00253 V\$CAP_01 0.913751 387 (+) NCANNNNN CCACTCTC
M00008 V\$SP1_01 0.838335 389 (-) GRGGCRGGGW ACTCTCCCAC
M00255 V\$GC_01 0.801813 390 (-) NRGGGGCGGGGCNK CTCTCCCACCCAAG
M00141 V\$LYF1_01 0.855354 391 (-) TTTGGGAGR TCTCCCACC
M00196 V\$SP1_Q6 0.754603 391 (-) NGGGGGCGGGGYN TCTCCCACCCAAG
M00243 V\$EGR1_01 0.789516 391 (-) WTGCGTGGGCGK TCTCCCACCCA
M00244 V\$NGFIC_01 0.808227 391 (-) WTGCGTGGGYGG TCTCCCACCCA
M00245 V\$EGR3_01 0.771667 391 (-) NTGCGTGGGCGK TCTCCCACCCA
M00246 V\$EGR2_01 0.793938 391 (-) NTGCGTRGGCGK TCTCCCACCCA
M00261 V\$OLF1_01 0.780084 391 (-) NNCNANTCCCYNGRGARNNKGN TCTCCCACCCAAGGGGAAATGG
M00189 V\$AP2_Q6 0.857996 392 (+) MKCCCSCNNGCG CTCCCACCCAAG
M00261 V\$OLF1_01 0.787001 392 (-) NNCNANTCCCYNGRGARNNKGN CTCCCACCCAAGGGGAAATGGA
M00008 V\$SP1_01 0.834655 393 (-) GRGGCRGGGW TCCCACCCA
M00072 V\$CP2_01 0.856775 393 (+) GCNMNAMCMAG TCCCACCCAAG
M00254 V\$CAAT_01 0.814459 394 (+) NNNRRCCAATSA CCCACCCAAGGG
M00141 V\$LYF1_01 0.831587 395 (-) TTTGGGAGR CCACCCAAG
M00189 V\$AP2_Q6 0.824908 396 (+) MKCCCSCNNGCG CACCCAAGGGGA
M00025 V\$ELK1_02 0.828283 399 (+) NNNNCCGGAARYNN CCAAGGGGAAATGG
M00109 V\$CEBPB_01 0.817979 399 (+) RNRTKNNGMAAKNN CCAAGGGGAAATGG
M00143 V\$PAX5_01 0.782685 399 (+) NCNNNRNKCANNNGNWNRKRGRCSRSNN
CCAAGGGGAAATGGAGACGCAAGAGAGG
M00074 V\$CETSIP54_02 0.850785 400 (+) NNAMMGGAWRWNN CAAGGGGAAATGG
M00083 V\$MZF1_01 0.887798 400 (+) NGNGGGGA CAAGGGGA
M00059 V\$YY1_01 0.859109 401 (-) NNNNNCCATNTWNNNWN AAGGGGAAATGGAGACG
M00258 V\$ISRE_01 0.738038 404 (-) CAGTTTCWCTTTYCC GGGAAATGGAGACGC
M00085 V\$ZID_01 0.879024 405 (-) NGGCTCYATCAYC GGAAATGGAGACG
M00113 V\$CREB_02 0.818564 409 (+) NNGNTGACGYNN ATGGAGACGCAA
M00109 V\$CEBPB_01 0.815007 410 (+) RNRTKNNGMAAKNN TGGAGACGCAAGAG
M00072 V\$CP2_01 0.805317 411 (+) GCNMNAMCMAG GGAGACGCAAG
M00177 V\$CREB_Q2 0.841508 411 (+) NSTGACGTAANN GGAGACGCAAGA
M00178 V\$CREB_Q4 0.831398 411 (+) NSTGACGTMANNN GGAGACGCAAGA
M00179 V\$CREBP1_Q2 0.834424 411 (+) NSTGACGTMASN GGAGACGCAAGA
M00085 V\$ZID_01 0.803913 414 (-) NGGCTCYATCAYC GACGCAAGAGAGG
M00108 V\$NRF2_01 0.812500 414 (+) ACCGGAAGNS GACGCAAGAG
M00127 V\$GATA1_03 0.786624 416 (+) RNSNNGATAANNNGN CGCAAGAGAGGGAG
M00075 V\$GATA1_01 0.777887 418 (+) SNNGATNNNN CAAGAGAGGG
M00007 V\$ELK1_01 0.791583 419 (+) NNNACMGAAGTNCNN AAGAGAGGGAGAGAGA
M00077 V\$GATA3_01 0.858662 419 (+) NNGATARNG AAGAGAGGG
M00084 V\$MZF1_02 0.824044 419 (+) KNNNKAGGGGNAA AAGAGAGGGAGAG
M00244 V\$NGFIC_01 0.725563 419 (+) WTGCGTGGGYGG AAGAGAGGGAGA
M00278 V\$LMO2COM_02 0.810984 419 (+) NMGATANSG AAGAGAGGG
M00085 V\$ZID_01 0.767094 420 (-) NGGCTCYATCAYC AGAGAGGGAGAGA
M00200 V\$CAAT_C 0.763329 420 (-) ACCAATCANCNNGCYYSNCNCWNNT AGAGAGGGAGAGAGATGGGATGGGT
M00033 V\$P300_01 0.839127 422 (+) NNNRGGAGTNNNNS AGAGGGAGAGAGAT
M00108 V\$NRF2_01 0.808140 422 (+) ACCGGAAGNS AGAGGGAGAG
M00008 V\$SP1_01 0.848528 423 (+) GRGGCRGGGW GAGGGAGAGA
M00127 V\$GATA1_03 0.815287 424 (+) RNSNNGATAANNNGN AGGGAGAGAGATGG
M00066 V\$TAL1ALPHA47_01 0.760034 426 (+) NNNAACAGATGKTNNN GGAGAGAGATGGGATG
M00144 V\$PAX5_02 0.744475 426 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
GGAGAGAGATGGGATGGGTGAAAGATGT
M00084 V\$MZF1_02 0.828793 429 (+) KNNNKAGGGGNAA GAGAGATGGGATG
M00184 V\$MYOD_Q6 0.805059 429 (-) NNCANCTGNY GAGAGATGGG
M00075 V\$GATA1_01 0.863277 430 (+) SNNGATNNNN AGAGATGGGA
M00076 V\$GATA2_01 0.854759 430 (+) NNNGATRNNN AGAGATGGGA
M00077 V\$GATA3_01 0.911387 431 (+) NNGATARNG GAGATGGGA
M00097 V\$PAX6_01 0.751130 431 (-) NNNNTTACGCWTSANTKNNN GAGATGGGATGGGTGAAAGAT
M00115 V\$TAXCREB_02 0.693266 433 (-) RTGACGCATAYCCCC GATGGGATGGGTGAA
M00144 V\$PAX5_02 0.760356 433 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
GATGGGATGGGTGAAAGATGTGCGCTGA

M00196 V\$SP1_Q6 0.797212 433 (+) NGGGGGCGGGGYN GATGGGATGGGTG
M00235 V\$AHRARNT_01 0.813178 433 (+) KNNKNNTYGCCTGCMS GATGGGATGGGTGAAA
M00255 V\$GC_01 0.802303 433 (+) NRGGGGCGGGGCK GATGGGATGGGTGA
M00084 V\$MZF1_02 0.841540 434 (+) KNNNKAGGGGNAA ATGGGATGGGTGA
M00242 V\$PPARA_01 0.752275 434 (+) CWRRAWCTAGNCAAAGGTCA ATGGGATGGGTGAAAGATGT
M00008 V\$SP1_01 0.817950 435 (+) GRGGCRGGGW TGGGATGGGT
M00075 V\$GATA1_01 0.902764 435 (+) SNNGATNNNN TGGGATGGGT
M00076 V\$GATA2_01 0.931439 435 (+) NNNGATRNNN TGGGATGGGT
M00115 V\$TAXCREB_02 0.618807 435 (-) RTGACGCATAYCCCC TGGGATGGGTGAAAG
M00077 V\$GATA3_01 0.834293 436 (+) NNGATARNG GGGATGGGT
M00104 V\$CDPCR1_01 0.780528 436 (-) NATCGATCGS GGGATGGGTG
M00063 V\$IRF2_01 0.726112 438 (+) GAAAAGYGAAASY GATGGGTGAAAGA
M00221 V\$SREBP1_02 0.727547 438 (-) KATCACCCAC GATGGGTGAAA
M00050 V\$E2F_02 0.748403 441 (-) TTTSGCGC GGGTGAAG
M00200 V\$CAAT_C 0.786487 441 (-) ACCAATCANCNNGCYYSNCNCWNNT GGGTGAAAGATGTGCGCTGATAGGG
M00066 V\$TALIALPHAE47_01 0.777474 442 (+) NNNAACAGATGKTNNN GGTGAAAGATGTGCGC
M00001 V\$MYOD_01 0.813780 444 (-) SRACAGGTGKYG TGAAAGATGTGC
M00023 V\$HOX13_01 0.810856 445 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GAAAGATGTGCGCTGATAGGGAGGGATGGA
M00106 V\$CDPCR3HD_01 0.852653 445 (+) NATYGATSSS GAAAGATGTG
M00184 V\$MYOD_Q6 0.789944 445 (-) NNCANCTGNY GAAAGATGTG
M00075 V\$GATA1_01 0.808490 446 (+) SNNGATNNNN AAAGATGTGC
M00076 V\$GATA2_01 0.836265 446 (+) NNNGATRNNN AAAGATGTGC
M00152 V\$SRF_01 0.725283 452 (+) ATGCCCATATATGGWNNT GTGCGCTGATAGGGAGGG
M00175 V\$AP4_Q5 0.864527 452 (-) NNCAGCTGNN GTGCGCTGAT
M00176 V\$AP4_Q6 0.785517 452 (-) CWCAGCTGGN GTGCGCTGAT
M00215 V\$SRF_C 0.754919 452 (-) NCCWTATATGGNCWN GTGCGCTGATAGGGA
M00221 V\$SREBP1_02 0.813935 452 (-) KATCACCCAC GTGCGCTGATA
M00126 V\$GATA1_02 0.873438 454 (+) NNNNNGATANKGNN GCGCTGATAGGGAG
M00127 V\$GATA1_03 0.896864 454 (+) RNSNNGATAANNNGN GCGCTGATAGGGAG
M00128 V\$GATA1_04 0.893382 455 (+) NNCWGATARNNNN CGCTGATAGGGAG
M00075 V\$GATA1_01 0.987660 456 (+) SNNGATNNNN GCTGATAGGG
M00076 V\$GATA2_01 0.961660 456 (+) NNNGATRNNN GCTGATAGGG
M00173 V\$AP1_Q2 0.791801 456 (+) RSTGACTNMNW GCTGATAGGGA
M00077 V\$GATA3_01 0.953478 457 (+) NNGATARNG CTGATAGGG
M00143 V\$PAX5_01 0.780042 457 (+) NCNNNRNKCANNNGNWGNRKRGCSSNNN
CTGATAGGGAGGGATGGAGAGAAAAAAA
M00278 V\$LMO2COM_02 0.972372 457 (+) NMGATANSCTGATAGGG
M00203 V\$GATA_C 0.836906 458 (+) NGATAAGNMNN TGATAGGGAGG
M00141 V\$LYF1_01 0.831587 460 (+) TTTGGGAGR ATAGGGAGG
M00196 V\$SP1_Q6 0.815360 460 (+) NGGGGGCGGGGYN ATAGGGAGGGATG
M00255 V\$GC_01 0.856933 460 (+) NRGGGGCGGGGCK ATAGGGAGGGATGG
M00262 V\$STAF_01 0.750000 460 (-) NTTWCCCANMATGCAYYRCGN ATAGGGAGGGATGGAGAGAAAA
M00008 V\$SP1_01 0.874858 461 (+) GRGGCRGGGW TAGGGAGGGA
M00008 V\$SP1_01 0.795583 462 (+) GRGGCRGGGW AGGGAGGGAT
M00008 V\$SP1_01 0.881653 465 (+) GRGGCRGGGW GAGGGATGGA
M00084 V\$MZF1_02 0.836541 465 (+) KNNNKAGGGGNAA GAGGGATGGAGAG
M00075 V\$GATA1_01 0.853899 466 (+) SNNGATNNNN AGGGATGGAG
M00076 V\$GATA2_01 0.865584 466 (+) NNNGATRNNN AGGGATGGAG
M00085 V\$ZID_01 0.776562 466 (-) NGGCTCYATCAYC AGGGATGGAGAGA
M00077 V\$GATA3_01 0.860434 467 (+) NNGATARNG GGGATGGAG
M00024 V\$E2F_01 0.760394 470 (+) TWSGCGCGAAAAYKR ATGGAGAGAAAAAAA
M00127 V\$GATA1_03 0.801813 470 (+) RNSNNGATAANNNGN ATGGAGAGAAAAAAA
M00180 V\$E2F_Q6 0.776930 471 (+) NNGCGCGAAANTK TGGAGAGAAAAAAA
M00050 V\$E2F_02 0.748403 473 (-) TTTSGCGC GAGAGAAA
M00080 V\$EV11_03 0.716461 474 (+) AGATAAGATAA AGAGAAAAAAA
M00082 V\$EV11_05 0.789934 474 (+) AGATAAGATAN AGAGAAAAAAA
M00160 V\$SRY_02 0.761304 475 (+) NWWAACAANNWANN GAGAAAAAAACG
M00144 V\$PAX5_02 0.766096 476 (+) RRMSWGANWYCTNRAGCGKRACSRYSNM
AGAAAAAAACGTGGAGAAAGACGGGGAT
M00236 V\$ARNT_01 0.820483 478 (+) NNNNNCACGTGNNNNN AAAAAACGTGGAGAA

M00251 V\$XBP1_01 0.772863 478 (+) NNGNTGACGTGKNNNWT AAAAAACGTGGAGAAA
M00118 V\$MYCMAX_01 0.748890 479 (+) NNACCACGTGGTNN AAAAAACGTGGAGA
M00118 V\$MYCMAX_01 0.748890 479 (-) NNACCACGTGGTNN AAAAAACGTGGAGA
M00119 V\$MAX_01 0.769191 479 (+) NNANCACGTGNTNN AAAAAACGTGGAGA
M00119 V\$MAX_01 0.769191 479 (-) NNANCACGTGNTNN AAAAAACGTGGAGA
M00055 V\$NMYC_01 0.770377 480 (+) NNNCACGTGNNN AAAAAACGTGGAG
M00055 V\$NMYC_01 0.779574 480 (-) NNNCACGTGNNN AAAAAACGTGGAG
M00123 V\$MYCMAX_02 0.857631 480 (-) NANCACGTGNNW AAAAAACGTGGAG
M00187 V\$USF_Q6 0.838412 481 (-) GYCACGTGNC AAAACGTGGA
M00217 V\$USF_C 0.831936 482 (-) NCACGTGN AAACGTGG
M00262 V\$STAF_01 0.745809 483 (-) NTTWCCCANMATGCAYYRCGNY AACGTGGAGAAAGACGGGGATG
M00033 V\$P300_01 0.813906 484 (+) NNNRGGAGTNNNNS ACGTGGAGAAAGAC
M00109 V\$CEBPB_01 0.895988 484 (+) RNRTKNNGMAAKNN ACGTGGAGAAAGAC
M00127 V\$GATA1_03 0.804998 486 (+) RNSNNGATAANNNGN GTGGAGAAAGACGG
M00143 V\$PAX5_01 0.793259 489 (+) NCNNNRNKCANNNGNWGNRKRGCSSNNN
GAGAAAGACGGGGATGCAGAAAGAGATG
M00008 V\$SP1_01 0.801246 493 (+) GRGGCRGGGW AAGACGGGGA
M00162 V\$OCT1_06 0.821484 493 (+) CWNATWKWSATRYN AAGACGGGGATGCA
M00083 V\$MZF1_01 0.912731 495 (+) NGNGGGGA GACGGGGA
M00008 V\$SP1_01 0.818233 497 (+) GRGGCRGGGW CGGGGATGCA
M00051 V\$NFKAPPAB50_01 0.790315 498 (+) GGGGATYCCC GGGGATGCAG
M00075 V\$GATA1_01 0.892892 498 (+) SNNGATNNNN GGGGATGCAG
M00076 V\$GATA2_01 0.887235 498 (+) NNNGATRNNN GGGGATGCAG
M00201 V\$CEBP_C 0.824221 499 (+) NGWNTKNKGAAKNSAYA GGGATGCAGAAAGAGATG
M00109 V\$CEBPB_01 0.841506 500 (+) RNRTKNNGMAAKNN GGATGCAGAAAGAG
M00057 V\$COMP1_01 0.773772 501 (+) NNTNWKGATTGRCNRSRANMRRNN GATGCAGAAAGAGATGTGGCAAGA
M00108 V\$NRF2_01 0.808140 504 (+) ACCGGAAGNS GCAGAAAGAG
M00100 V\$CDXA_01 0.919568 505 (-) MTTTATR CAGAAAG
M00105 V\$CDPCR3_01 0.802872 505 (+) CACCRATANNTATNG CAGAAAGAGATGTGG
M00162 V\$OCT1_06 0.876172 505 (+) CWNATWKWSATRYN CAGAAAGAGATGTG
M00005 V\$AP4_01 0.828098 506 (+) WGARYCAGCTGYGGNCNK AGAAAGAGATGTGGCAAG
M00200 V\$CAAT_C 0.719303 507 (-) ACCAATCANCNNGCYYSNCNCWNNT GAAAGAGATGTGGCAAGAGATGGGG
M00001 V\$MYOD_01 0.821654 508 (-) SRACAGGTGKYG AAAGAGATGTGG
M00115 V\$TAXCREB_02 0.622071 508 (-) RTGACGCATAYCCCC AAAGAGATGTGGCAA
M00222 V\$TH1E47_01 0.822969 508 (+) NNNNGNRTCTGGMWTT AAAGAGATGTGGCAAG
M00122 V\$USF_02 0.802983 509 (+) NNRNCACGTGNYNN AAGAGATGTGGCAA
M00122 V\$USF_02 0.802983 509 (-) NNRNCACGTGNYNN AAGAGATGTGGCAA
M00175 V\$AP4_Q5 0.828074 509 (-) NNCAGCTGNN AAGAGATGTG
M00176 V\$AP4_Q6 0.823603 509 (-) CWCAGCTGGN AAGAGATGTG
M00184 V\$MYOD_Q6 0.772363 509 (-) NNCANCTGNY AAGAGATGTG
M00255 V\$GC_01 0.809897 509 (+) NRGGGGCGGGGNCNK AAGAGATGTGGCAA
M00001 V\$MYOD_01 0.840354 510 (+) SRACAGGTGKYG AGAGATGTGGCA
M00075 V\$GATA1_01 0.863277 510 (+) SNNGATNNNN AGAGATGTGG
M00076 V\$GATA2_01 0.861074 510 (+) NNNGATRNNN AGAGATGTGG
M00023 V\$HOX13_01 0.724414 511 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GAGATGTGGCAAGAGATGGGGAAGAGAGAG
M00077 V\$GATA3_01 0.886132 511 (+) NNGATARNG GAGATGTGG
M00187 V\$USF_Q6 0.875874 511 (-) GYCACGTGNC GAGATGTGGC
M00201 V\$CEBP_C 0.892693 511 (+) NGWNTKNKGAAKNSAYA GAGATGTGGCAAGAGATG
M00078 V\$EVII_01 0.727818 512 (+) WGAYAAGATAAGATAA AGATGTGGCAAGAGAT
M00109 V\$CEBPB_01 0.931402 512 (+) RNRTKNNGMAAKNN AGATGTGGCAAGAG
M00116 V\$CEBPA_01 0.863121 512 (-) NNATTRCNNAANN AGATGTGGCAAGAG
M00117 V\$CEBPB_02 0.853119 512 (-) NKNTTGCNYAAYNN AGATGTGGCAAGAG
M00271 V\$AML1_01 0.897865 515 (+) TGTGGT TGTGGC
M00066 V\$TAL1ALPHA47_01 0.800378 518 (+) NNNAACAGATGKTNNN GGCAAGAGATGGGGAA
M00070 V\$TAL1BETA1TF2_01 0.772358 518 (+) NNNAACAGATGKTNNN GGCAAGAGATGGGGAA
M00277 V\$LMO2COM_01 0.795155 520 (-) SNNCAGGTGNNN CAAGAGATGGGG
M00084 V\$MZF1_02 0.889528 521 (+) KNNNKAGGGGNAA AAGAGATGGGGAA
M00184 V\$MYOD_Q6 0.787477 521 (-) NNCANCTGNY AAGAGATGGG
M00075 V\$GATA1_01 0.910168 522 (+) SNNGATNNNN AGAGATGGGG
M00076 V\$GATA2_01 0.897609 522 (+) NNNGATRNNN AGAGATGGGG

M00077 V\$GATA3_01 0.946389 523 (+) NNGATARNG GAGATGGGG
M00278 V\$LMO2COM_02 0.816712 523 (+) NMGATANS GAGATGGGG
M00083 V\$MZF1_01 0.952399 525 (+) NGNGGGGA GATGGGGA
M00086 V\$IK1_01 0.783921 525 (+) NNNTGGGAATRCC GATGGGGAAGAGA
M00255 V\$GC_01 0.780500 526 (+) NRGGGGCGGGGCK ATGGGGAAGAGAGA
M00033 V\$P300_01 0.814928 527 (+) NNNRGGAGTNNNNS TGGGGAAGAGAGAG
M00008 V\$SP1_01 0.783692 528 (+) GRGGCRGGGW GGGGAAGAGA
M00057 V\$COMP1_01 0.789940 528 (+) NNTNWKGATTGRCNRSRANMRRNN GGGGAAGAGAGAGAGAGAGAAAGATG
M00127 V\$GATA1_03 0.787604 529 (+) RNSNNGATAANNNGN GGAAGAGAGAGAGAG
M00033 V\$P300_01 0.824131 531 (+) NNNRGGAGTNNNNS GAAGAGAGAGAGAGAG
M00063 V\$IRF2_01 0.700414 531 (+) GAAAAGYGAAASY GAAGAGAGAGAGAGA
M00085 V\$ZID_01 0.817799 531 (-) NGGCTCYATCAYC GAAGAGAGAGAGAGA
M00085 V\$ZID_01 0.768357 533 (-) NGGCTCYATCAYC AGAGAGAGAGAGAGA
M00077 V\$GATA3_01 0.835179 534 (+) NNGATARNG GAGAGAGAG
M00077 V\$GATA3_01 0.835179 536 (+) NNGATARNG GAGAGAGAG
M00127 V\$GATA1_03 0.782460 539 (+) RNSNNGATAANNNGN AGAGAGAAAGATGG
M00050 V\$E2F_02 0.748403 540 (-) TTTSGCGC GAGAGAAA
M00059 V\$YY1_01 0.849934 541 (-) NNNNNCCATNTWNNNWN AGAGAAAGATGGAGAGA
M00108 V\$NRF2_01 0.775678 541 (+) ACCGGAAGNS AGAGAAAGAT
M00238 V\$BARBIE_01 0.844124 541 (+) ATNNAAGCNGRNGG AGAGAAAGATGGAGA
M00184 V\$MYOD_Q6 0.825416 544 (-) NNCANCTGNY GAAAGATGGA
M00075 V\$GATA1_01 0.829714 545 (+) SNNGATNNNN AAAGATGGAG
M00076 V\$GATA2_01 0.843031 545 (+) NNNGATRNNN AAAGATGGAG
M00085 V\$ZID_01 0.839891 545 (-) NGGCTCYATCAYC AAAGATGGAGAGA
M00077 V\$GATA3_01 0.888347 546 (+) NNGATARNG AAGATGGAG
M00200 V\$CAAT_C 0.754040 546 (-) ACCAATCANCNNGCYYSNCNCWNNT AAGATGGAGAGACAGGATGTCTGGC
M00033 V\$P300_01 0.801977 547 (+) NNNRGGAGTNNNNS AGATGGAGAGACAG
M00007 V\$ELK1_01 0.832331 554 (+) NNNACMGAAGTNCNN GAGACAGGATGTCTGG
M00025 V\$ELK1_02 0.812978 554 (+) NNNNCCGGAARYNN GAGACAGGATGTCT
M00074 V\$CETSIP54_02 0.910995 555 (+) NNA MMGGAWRWNN AGACAGGATGTCT
M00080 V\$EV11_03 0.724691 555 (+) AGATAAGATAA AGACAGGATGT
M00082 V\$EV11_05 0.809128 555 (+) AGATAAGATAN AGACAGGATGT
M00032 V\$CETSIP54_01 0.966051 557 (+) NCMGGAWGYN ACAGGATGTC
M00108 V\$NRF2_01 0.819767 557 (+) ACCGGAAGNS ACAGGATGTC
M00075 V\$GATA1_01 0.875617 558 (+) SNNGATNNNN CAGGATGTCT
M00076 V\$GATA2_01 0.908435 558 (+) NNNGATRNNN CAGGATGTCT
M00115 V\$TAXCREB_02 0.677247 558 (-) RTGACGCATAYCCCC CAGGATGTCTGGCAC
M00222 V\$TH1E47_01 0.884441 558 (+) NNNNGNRTCTGGMWTT CAGGATGTCTGGCACA
M00264 V\$STAF_02 0.771290 561 (-) MNTTCCCAKMATKCMWNGCRN GATGTCTGGCACATGGAAGGT
M00050 V\$E2F_02 0.743405 565 (+) TTTSGCGC TCTGGCAC
M00118 V\$MYCMAX_01 0.750888 566 (+) NNACCACGTGGTNN CTGGCACATGGAAG
M00118 V\$MYCMAX_01 0.750888 566 (-) NNACCACGTGGTNN CTGGCACATGGAAG
M00121 V\$USF_01 0.773615 566 (+) NNRYCACGTGRYNN CTGGCACATGGAAG
M00121 V\$USF_01 0.773615 566 (-) NNRYCACGTGRYNN CTGGCACATGGAAG
M00122 V\$USF_02 0.791175 566 (+) NNRNCACGTGNYNN CTGGCACATGGAAG
M00122 V\$USF_02 0.791175 566 (-) NNRNCACGTGNYNN CTGGCACATGGAAG
M00199 V\$API_C 0.793878 566 (-) NTGASTCAG CTGGCACAT
M00055 V\$NMYC_01 0.823905 567 (+) NNNCACGTGNNN TGGCACATGGAA
M00055 V\$NMYC_01 0.874088 567 (-) NNNCACGTGNNN TGGCACATGGAA
M00123 V\$MYCMAX_02 0.853428 567 (+) NANCACGTGNNW TGGCACATGGAA
M00123 V\$MYCMAX_02 0.856055 567 (-) NANCACGTGNNW TGGCACATGGAA
M00277 V\$LMO2COM_01 0.843069 567 (-) SNNCAGGTGNNN TGGCACATGGAA
M00184 V\$MYOD_Q6 0.882480 568 (-) NNCANCTGNY GGCACATGGA
M00217 V\$USF_C 0.864475 569 (+) NCACGTGN GCACATGG
M00217 V\$USF_C 0.925193 569 (-) NCACGTGN GCACATGG
M00071 V\$E47_02 0.811725 572 (+) NNNMRCAGGTGTTMNN CATGGAAGGTGCTCAC
M00236 V\$ARNT_01 0.784120 572 (+) NNNNNCACGTGNNNNN CATGGAAGGTGCTCAC
M00255 V\$GC_01 0.800098 572 (+) NRGGGGCGGGGCK CATGGAAGGTGCTC
M00277 V\$LMO2COM_01 0.812921 574 (+) SNNCAGGTGNNN TGGAAGGTGCTC
M00023 V\$HOX13_01 0.770206 575 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GGAAGGTGCTCACTAAGTGTGTATGGAGTG

M00073 V\$DELTAEF1_01 0.845029 575 (-) NNNCACCTNAN GGAAGGTGCTC
M00146 V\$HSF1_01 0.860575 575 (+) RGAANRTTCN GGAAGGTGCT
M00147 V\$HSF2_01 0.891682 575 (+) NGAANNWTCK GGAAGGTGCT
M00147 V\$HSF2_01 0.829205 575 (-) NGAANNWTCK GGAAGGTGCT
M00184 V\$MYOD_Q6 0.845157 575 (-) NNCANCTGNY GGAAGGTGCT
M00279 V\$MIF1_01 0.778946 577 (+) NNGTTGCWWGGYACNGS AAGGTGCTCACTAAGTGT
M00035 V\$VMAF_01 0.791173 578 (+) NNNTGCTGACTCAGCANN AGGTGCTCACTAAGTGTGT
M00172 V\$APIFJ_Q2 0.818927 582 (+) RSTGACTNMNW GCTCACTAAGT
M00173 V\$API_Q2 0.847731 582 (+) RSTGACTNMNW GCTCACTAAGT
M00174 V\$API_Q6 0.793531 582 (+) NNTGACTCANN GCTCACTAAGT
M00188 V\$API_Q4 0.838365 582 (+) RSTGACTMANN GCTCACTAAGT
M00199 V\$API_C 0.787172 583 (+) NTGASTCAG CTCACTAAG
M00199 V\$API_C 0.807580 583 (-) NTGASTCAG CTCACTAAG
M00099 V\$S8_01 0.782301 584 (-) WNNANYYAATTANYNN TCACTAAGTGTGTATG
M00253 V\$CAP_01 0.875801 584 (+) NCANNNNN TCACTAAG
M00240 V\$NKX25_01 0.854040 587 (+) TYAAGTG CTAAGTG
M00059 V\$YY1_01 0.830275 589 (-) NNNNNCCATNTWNNNWN AAGTGTGTATGGAGTGA
M00222 V\$TH1E47_01 0.827496 589 (+) NNNNGNRTCTGGMWTT AAGTGTGTATGGAGTG
M00033 V\$P300_01 0.896728 595 (+) NNNRGGAGTNNNNS GTATGGAGTGAATG
M00023 V\$HOX13_01 0.742348 599 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GGAGTGAATGAATGAATGAATGAATGAACA
M00206 V\$HNF1_C 0.814442 599 (-) NGTTAATKAWTNACCAM GGAGTGAATGAATGAAT
M00173 V\$API_Q2 0.795900 601 (+) RSTGACTNMNW AGTGAATGAAT
M00174 V\$API_Q6 0.804814 601 (+) NNTGACTCANN AGTGAATGAAT
M00188 V\$API_Q4 0.794754 601 (+) RSTGACTMANN AGTGAATGAAT
M00206 V\$HNF1_C 0.829689 601 (+) NGTTAATKAWTNACCAM AGTGAATGAATGAATGA
M00097 V\$PAX6_01 0.769745 602 (-) NNNNTTCACGCWTSANTKNNN GTGAATGAATGAATGAATGAA
M00023 V\$HOX13_01 0.760282 603 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TGAATGAATGAATGAATGAATGAACAAGCA
M00106 V\$CDPCR3HD_01 0.822953 603 (-) NATYGATSSS TGAATGAATG
M00162 V\$OCT1_06 0.834375 603 (-) CWNATWKWSATRYN TGAATGAATGAATG
M00254 V\$CAAT_01 0.792714 603 (-) NNNRRCCAATSA TGAATGAATGAA
M00056 V\$MYOGNF1_01 0.742112 604 (-) CRSGTGTNNNNTTTGGCACNSNGCCARNN
GAATGAATGAATGAATGAATGAACAAGCA
M00174 V\$API_Q6 0.804814 605 (+) NNTGACTCANN AATGAATGAAT
M00096 V\$PBX1_01 0.892041 606 (-) ANCAATCAW ATGAATGAA
M00097 V\$PAX6_01 0.764685 606 (-) NNNNTTCACGCWTSANTKNNN ATGAATGAATGAATGAATGAA
M00199 V\$API_C 0.772886 606 (+) NTGASTCAG ATGAATGAA
M00106 V\$CDPCR3HD_01 0.822953 607 (-) NATYGATSSS TGAATGAATG
M00162 V\$OCT1_06 0.834375 607 (-) CWNATWKWSATRYN TGAATGAATGAATG
M00254 V\$CAAT_01 0.792714 607 (-) NNNRRCCAATSA TGAATGAATGAA
M00174 V\$API_Q6 0.804814 609 (+) NNTGACTCANN AATGAATGAAT
M00096 V\$PBX1_01 0.892041 610 (-) ANCAATCAW ATGAATGAA
M00097 V\$PAX6_01 0.772637 610 (-) NNNNTTCACGCWTSANTKNNN ATGAATGAATGAATGAACAAG
M00199 V\$API_C 0.772886 610 (+) NTGASTCAG ATGAATGAA
M00106 V\$CDPCR3HD_01 0.822953 611 (-) NATYGATSSS TGAATGAATG
M00162 V\$OCT1_06 0.834375 611 (-) CWNATWKWSATRYN TGAATGAATGAATG
M00254 V\$CAAT_01 0.792714 611 (-) NNNRRCCAATSA TGAATGAATGAA
M00098 V\$PAX2_01 0.769471 612 (-) NNNNGTCANGNRTKANNNN GAATGAATGAATGAACAAG
M00174 V\$API_Q6 0.804814 613 (+) NNTGACTCANN AATGAATGAAT
M00206 V\$HNF1_C 0.834436 613 (+) NGTTAATKAWTNACCAM AATGAATGAATGAACAA
M00096 V\$PBX1_01 0.892041 614 (-) ANCAATCAW ATGAATGAA
M00199 V\$API_C 0.772886 614 (+) NTGASTCAG ATGAATGAA
M00106 V\$CDPCR3HD_01 0.822953 615 (-) NATYGATSSS TGAATGAATG
M00254 V\$CAAT_01 0.792714 615 (-) NNNRRCCAATSA TGAATGAATGAA
M00174 V\$API_Q6 0.794284 617 (+) NNTGACTCANN AATGAATGAAC
M00096 V\$PBX1_01 0.892041 618 (-) ANCAATCAW ATGAATGAA
M00199 V\$API_C 0.772886 618 (+) NTGASTCAG ATGAATGAA
M00138 V\$OCT1_04 0.799456 619 (-) NNNNNNNWATGCAATNNNWNW TGAATGAACAAGCAGATATATAA
M00146 V\$HSF1_01 0.764868 619 (+) RGAANRTTCN TGAATGAACA
M00147 V\$HSF2_01 0.818484 619 (+) NGAANNWTCK TGAATGAACA

M00254 V\$CAAT_01 0.797232 619 (-) NNNRRCCAATSA TGAATGAACAAG
M00268 V\$XFD2_01 0.851600 619 (+) WNWATAAACAWNNR TGAATGAACAAGCA
M00072 V\$CP2_01 0.791166 620 (+) GCNMNAMCMAG GAATGAACAAG
M00129 V\$HFH1_01 0.807506 620 (-) NAWTGTTTATWT GAATGAACAAGC
M00138 V\$OCT1_04 0.798620 620 (+) NNNNNNNWATGCAAATNNNWNW GAATGAACAAGCAGATATATAAA
M00148 V\$SRV_01 0.907752 621 (+) AACWAM AATGAAC
M00174 V\$AP1_Q6 0.770967 621 (+) NNTGACTCANN AATGAACAAGC
M00160 V\$SRV_02 0.784498 622 (+) NWWAACA AWANN ATGAACAAGCAG
M00131 V\$HNF3B_01 0.874545 624 (-) NNNTRTTTRYTY GAACAAGCAGAT
M00235 V\$AHRARNT_01 0.768774 624 (-) KNNKNNTYGC GTG CMS GAACAAGCAGATATAT
M00272 V\$P53_02 0.837925 624 (-) NGRCWTGYCY GAACAAGCAG
M00222 V\$THIE47_01 0.806767 626 (-) NNNNGNRTCTGGMWTT ACAAGCAGATATATAA
M00127 V\$GATA1_03 0.786134 628 (+) RNSNNGATAANN GN AAGCAGATATATAA
M00131 V\$HNF3B_01 0.906576 628 (-) NNNTRTTTRYTY AAGCAGATATAT
M00138 V\$OCT1_04 0.801966 628 (+) NNNNNNNWATGCAAATNNNWNW AAGCAGATATATAAATAAGATAT
M00128 V\$GATA1_04 0.878983 629 (+) NNCWGATARNNNN AGCAGATATATAA
M00184 V\$MYOD_Q6 0.780382 629 (-) NNCANCTGNY AGCAGATATA
M00231 V\$MEF2_02 0.820629 629 (+) NNNNNNKCTAWAAATAGMNNNN AGCAGATATATAAATAAGATAT
M00232 V\$MEF2_03 0.791205 629 (+) NNNNNWKCTAWAAATAGMNNNN AGCAGATATATAAATAAGATAT
M00075 V\$GATA1_01 0.856861 630 (+) SNNGATNNNN GCAGATATAT
M00076 V\$GATA2_01 0.876861 630 (+) NNNGATRNNN GCAGATATAT
M00135 V\$OCT1_01 0.744563 630 (+) NNNNWTATGCAAATNTNNN GCAGATATATAAATAAGAT
M00138 V\$OCT1_04 0.784191 630 (+) NNNNNNNWATGCAAATNNNWNW GCAGATATATAAATAAGATATGG
M00133 V\$TST1_01 0.870616 631 (+) NNKGAWT WANANTNN CAGATATATAAATAA
M00045 V\$E4BP4_01 0.765591 632 (+) NRTTAYGTAAYN AGATATATAAAT
M00082 V\$EVII_05 0.792067 632 (+) AGATAAGATAN AGATATATAAA
M00195 V\$OCT1_Q6 0.881277 632 (+) NNNNATGCAAATNAN AGATATATAAATAAG
M00203 V\$GATA_C 0.871078 632 (+) NGATAAGNMNN AGATATATAAA
M00252 V\$TATA_01 0.804618 632 (+) STATAAAWRNNNNNNN AGATATATAAATAAG
M00026 V\$RSRFC4_01 0.830541 633 (-) RNKCTATTTWTAGMWN GATATATAAATAAGAT
M00162 V\$OCT1_06 0.886719 633 (-) CWNAWTKWSATRYN GATATATAAATAAG
M00216 V\$TATA_C 0.797465 633 (+) NCTATAAAAR GATATATAAA
M00210 V\$OCT_C 0.789176 634 (-) CTNATTTGCATAY ATATATAAATAAG
M00252 V\$TATA_01 0.863740 634 (+) STATAAAWRNNNNNNN ATATATAAATAAGAT
M00160 V\$SRV_02 0.767763 635 (+) NWWAACA AWANN TATATAAATAAG
M00216 V\$TATA_C 0.751782 635 (+) NCTATAAAAR TATATAAATA
M00267 V\$XFD1_01 0.950505 635 (+) YAWGTAAAYAWWRY TATATAAATAAGAT
M00268 V\$XFD2_01 0.905200 635 (+) WNWATAAACAWNNR TATATAAATAAGAT
M00269 V\$XFD3_01 0.789898 635 (+) WNWGTMAACAWWMW TATATAAATAAGAT
M00129 V\$HFH1_01 0.849462 636 (-) NAWTGTTTATWT ATATAAATAAGA
M00131 V\$HNF3B_01 0.903179 636 (-) NNNTRTTTRYTY ATATAAATAAGA
M00252 V\$TATA_01 0.862979 636 (+) STATAAAWRNNNNNNN ATATAAATAAGATAT
M00100 V\$CDXA_01 0.980873 637 (-) MTTTATR TATAAAT
M00101 V\$CDXA_02 1.000000 637 (-) WWTWMTR TATAAAT
M00162 V\$OCT1_06 0.860547 638 (+) CWNAWTKWSATRYN ATAAATAAGATATG
M00199 V\$AP1_C 0.771720 638 (+) NTGASTCAG ATAAATAAG
M00241 V\$NKX25_02 0.839809 639 (-) CWTAATTG TAAATAAG
M00079 V\$EVII_02 0.809473 640 (+) AGAYAAGATAA AAATAAGATAT
M00080 V\$EVII_03 0.868519 640 (+) AGATAAGATAA AAATAAGATAT
M00082 V\$EVII_05 0.930262 640 (+) AGATAAGATAN AAATAAGATAT
M00059 V\$YY1_01 0.880734 641 (-) NNNNNCCATNTWNNNWN AATAAGATATGGAGACA
M00126 V\$GATA1_02 0.795313 641 (+) NNNNNGATANKGN AATAAGATATGGAG
M00205 V\$GRE_C 0.773281 641 (-) GGTACAANN TGTYCTK AATAAGATATGGAGAC
M00011 V\$EVII_06 0.782419 642 (+) ACAAGATAA ATAAGATAT
M00128 V\$GATA1_04 0.918199 642 (+) NNCWGATARNNNN ATAAGATATGGAG
M00075 V\$GATA1_01 0.843040 643 (+) SNNGATNNNN TAAGATATGG
M00076 V\$GATA2_01 0.913848 643 (+) NNNGATRNNN TAAGATATGG
M00077 V\$GATA3_01 0.922463 644 (+) NNGATARNNG AAGATATGG
M00278 V\$LMO2COM_02 0.925202 644 (+) NMGATANS G AAGATATGG
M00085 V\$ZID_01 0.808963 645 (-) NGGCTCYATCAYC AGATATGGAGACA
M00203 V\$GATA_C 0.849953 645 (+) NGATAAGNMNN AGATATGGAGA

M00109 V\$CEBPB_01 0.871966 647 (+) RNRTKNNGMAAKNN ATATGGAGACAGAT
M00004 V\$CMYB_01 0.791892 648 (+) NCNRNNGRCNGTTGCKGG TATGGAGACAGATGTGGG
M00127 V\$GATA1_03 0.789319 649 (+) RNSNNGATAANNNGN ATGGAGACAGATGT
M00255 V\$GC_01 0.795688 650 (+) NRGGGCGGGGCK TGGAGACAGATGTG
M00002 V\$E47_01 0.815990 651 (-) NSNGCAGGTGKNCNN GGAGACAGATGTGGG
M00005 V\$AP4_01 0.781700 651 (+) WGARYCAGCTGYGGNCNK GGAGACAGATGTGGGGTG
M00065 V\$TALIBETA47_01 0.808752 651 (+) NNNAACAGATGKTNNN GGAGACAGATGTGGGG
M00066 V\$TALIALPHAE47_01 0.858794 651 (+) NNNAACAGATGKTNNN GGAGACAGATGTGGGG
M00070 V\$TALIBETA1TF2_01 0.815854 651 (+) NNNAACAGATGKTNNN GGAGACAGATGTGGGG
M00144 V\$PAX5_02 0.786473 651 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
GGAGACAGATGTGGGGTGTGAGAAGAGA
M00002 V\$E47_01 0.867015 652 (+) NSNGCAGGTGKNCNN GAGACAGATGTGGGG
M00122 V\$USF_02 0.774394 652 (+) NNRNCACGTGNYNN GAGACAGATGTGGG
M00122 V\$USF_02 0.774394 652 (-) NNRNCACGTGNYNN GAGACAGATGTGGG
M00001 V\$MYOD_01 0.819094 653 (+) SRACAGGTGKYG AGACAGATGTGG
M00001 V\$MYOD_01 0.904724 653 (-) SRACAGGTGKYG AGACAGATGTGG
M00277 V\$LMO2COM_01 0.843876 653 (+) SNNCAGGTGNNN AGACAGATGTGG
M00277 V\$LMO2COM_01 0.861642 653 (-) SNNCAGGTGNNN AGACAGATGTGG
M00139 V\$AHR_01 0.715281 654 (+) CYYCNRRSTNGCGTGASW GACAGATGTGGGGTGTGA
M00175 V\$AP4_Q5 0.830794 654 (+) NNCAGCTGNN GACAGATGTG
M00175 V\$AP4_Q5 0.823721 654 (-) NNCAGCTGNN GACAGATGTG
M00176 V\$AP4_Q6 0.813831 654 (+) CWCAGCTGGN GACAGATGTG
M00176 V\$AP4_Q6 0.840641 654 (-) CWCAGCTGGN GACAGATGTG
M00184 V\$MYOD_Q6 0.932449 654 (-) NNCANCTGNY GACAGATGTG
M00075 V\$GATA1_01 0.855380 655 (+) SNNGATNNNN ACAGATGTGG
M00076 V\$GATA2_01 0.861074 655 (+) NNNGATRNNN ACAGATGTGG
M00217 V\$USF_C 0.815498 655 (-) NCACGTGN ACAGATGT
M00253 V\$CAP_01 0.875308 655 (+) NCANNNNN ACAGATGT
M00077 V\$GATA3_01 0.863093 656 (+) NNGATARNG CAGATGTGG
M00187 V\$USF_Q6 0.818843 656 (-) GYCACGTGNC CAGATGTGGG
M00255 V\$GC_01 0.806467 656 (+) NRGGGCGGGGCK CAGATGTGGGGTGT
M00278 V\$LMO2COM_02 0.802898 656 (+) NMGATANSG CAGATGTGG
M00200 V\$CAAT_C 0.716376 657 (-) ACCAATCANCNNGCYYSNCNCWNNT AGATGTGGGGTGTGAGAAGAGAGAT
M00008 V\$SP1_01 0.793884 658 (+) GRGGCRGGGW GATGTGGGGT
M00023 V\$HOX13_01 0.736848 659 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
ATGTGGGGTGTGAGAAGAGAGATGGGGGAA
M00033 V\$P300_01 0.820041 659 (+) NNNRGGAGTNNNNS ATGTGGGGTGTGAG
M00235 V\$AHRARNT_01 0.788214 660 (+) KNNKNNTYGCGTGCMSTGTGGGGTGTGAGAAG
M00033 V\$P300_01 0.815269 661 (+) NNNRGGAGTNNNNS GTGGGGTGTGAGAA
M00221 V\$SREBP1_02 0.820580 661 (-) KATCACCCAC GTGGGGTGTGA
M00008 V\$SP1_01 0.844564 662 (+) GRGGCRGGGW TGGGGTGTGA
M00115 V\$TAXCREB_02 0.624740 662 (-) RTGACGCATAYCCCC TGGGGTGTGAGAAGA
M00271 V\$AML1_01 0.866053 662 (+) TGTGGT TGGGGT
M00221 V\$SREBP1_02 0.727547 663 (-) KATCACCCAC GGGGTGTGAGA
M00023 V\$HOX13_01 0.757652 665 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GGTGTGAGAAGAGAGATGGGGGAAGAAACA
M00115 V\$TAXCREB_02 0.611391 667 (-) RTGACGCATAYCCCC TGTGAGAAGAGAGAT
M00264 V\$STAF_02 0.759376 668 (-) MNTTCCCAKMATKCMWNGCRN GTGAGAAGAGAGATGGGGGAA
M00004 V\$CMYB_01 0.772166 669 (+) NCNRNNGRCNGTTGCKGG TGAGAAGAGAGATGGGGG
M00079 V\$EVII_02 0.775336 669 (+) AGAYAAGATAA TGAGAAGAGAG
M00080 V\$EVII_03 0.745885 669 (+) AGATAAGATAA TGAGAAGAGAG
M00082 V\$EVII_05 0.779697 669 (+) AGATAAGATAN TGAGAAGAGAG
M00139 V\$AHR_01 0.727245 669 (-) CYYCNRRSTNGCGTGASW TGAGAAGAGAGATGGGGG
M00144 V\$PAX5_02 0.740649 672 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
GAAGAGAGATGGGGGAAGAAACAAGTGA
M00126 V\$GATA1_02 0.789062 674 (+) NNNNNGATANKGNN AGAGAGATGGGGGA
M00127 V\$GATA1_03 0.807447 674 (+) RNSNNGATAANNNGN AGAGAGATGGGGGA
M00084 V\$MZF1_02 0.878530 675 (+) KNNNKAGGGGNAA GAGAGATGGGGGA
M00184 V\$MYOD_Q6 0.805059 675 (-) NNCANCTGNY GAGAGATGGG
M00075 V\$GATA1_01 0.910168 676 (+) SNNGATNNNN AGAGATGGGG
M00076 V\$GATA2_01 0.897609 676 (+) NNNGATRNNN AGAGATGGGG

M00077 V\$GATA3_01 0.946389 677 (+) NNGATARNG GAGATGGGG
M00084 V\$MZF1_02 0.846038 677 (+) KNNNKAGGGGNAA GAGATGGGGGAAG
M00278 V\$LMO2COM_02 0.816712 677 (+) NMGATANS GAGATGGGG
M00109 V\$CEBPB_01 0.828133 678 (+) RNRTKNNGMAAKNN AGATGGGGGAAGAA
M00281 V\$RFX1_02 0.752098 678 (+) NNGTNRNATRGYAACNNN AGATGGGGGAAGAAACAAG
M00083 V\$MZF1_01 0.849641 679 (+) NGNGGGGA GATGGGGG
M00083 V\$MZF1_01 0.931243 680 (+) NGNGGGGA ATGGGGGA
M00086 V\$IK1_01 0.792735 680 (+) NNNTGGAATRCC ATGGGGGAAGAAA
M00115 V\$TAXCREB_02 0.624740 681 (-) RTGACGCATAYCCCC TGGGGGAAGAAACAA
M00007 V\$SELK1_01 0.750835 682 (+) NNNACMGAAGTNCNN GGGGGAAGAAACAAGT
M00147 V\$HSF2_01 0.840296 685 (+) NGAANNWTCK GGAAGAAACA
M00072 V\$SCP2_01 0.791166 686 (+) GCNMNAMCMAG GAAGAAACAAG
M00098 V\$PAX2_01 0.766969 686 (-) NNNNGTCANGNRKANNNN GAAGAAACAAGTGATATGA
M00129 V\$HFH1_01 0.800759 686 (-) NAWTGTTTATWT GAAGAAACAAGT
M00131 V\$HNF3B_01 0.867751 686 (-) NNNTRTTTRYTY GAAGAAACAAGT
M00160 V\$SRYP_02 0.836171 688 (+) NWWAACA AWANN AGAAACAAGTGA
M00236 V\$ARNT_01 0.796087 688 (+) NNNNNCACGTGNNNNN AGAAACAAGTGATATG
M00236 V\$ARNT_01 0.792175 688 (-) NNNNNCACGTGNNNNN AGAAACAAGTGATATG
M00118 V\$MYCMAX_01 0.731350 689 (+) NNACCACGTGGTNN GAAACAAGTGATAT
M00118 V\$MYCMAX_01 0.731350 689 (-) NNACCACGTGGTNN GAAACAAGTGATAT
M00119 V\$MAX_01 0.837257 689 (+) NNANCACGTGNTNN GAAACAAGTGATAT
M00119 V\$MAX_01 0.837257 689 (-) NNANCACGTGNTNN GAAACAAGTGATAT
M00121 V\$USF_01 0.808443 689 (+) NNRYCACGTGRYNN GAAACAAGTGATAT
M00121 V\$USF_01 0.808443 689 (-) NNRYCACGTGRYNN GAAACAAGTGATAT
M00122 V\$USF_02 0.861094 689 (+) NNRNCACGTGNYNN GAAACAAGTGATAT
M00122 V\$USF_02 0.861094 689 (-) NNRNCACGTGNYNN GAAACAAGTGATAT
M00001 V\$MYOD_01 0.805906 690 (+) SRACAGGTGKYG AAACAAGTGATA
M00055 V\$NMYC_01 0.753041 690 (+) NNNCACGTGNNN AAACAAGTGATA
M00055 V\$NMYC_01 0.774939 690 (-) NNNCACGTGNNN AAACAAGTGATA
M00123 V\$MYCMAX_02 0.805621 690 (+) NANCACGTGNNW AAACAAGTGATA
M00123 V\$MYCMAX_02 0.846598 690 (-) NANCACGTGNNW AAACAAGTGATA
M00148 V\$SRYP_01 0.934109 690 (+) AAACWAM AAACAAG
M00162 V\$OCT1_06 0.821094 690 (+) CWNWTKWSATRYN AAACAAGTGATATG
M00220 V\$REBP1_01 0.784879 690 (+) NATCACGTGAY AAACAAGTGAT
M00272 V\$P53_02 0.860199 690 (-) NGRCWTGYCY AAACAAGTGA
M00003 V\$VMYB_01 0.776665 691 (+) AAYAACGGNN AACAAGTGAT
M00184 V\$MYOD_Q6 0.804750 691 (+) NNCANCTGNY AACAAGTGAT
M00184 V\$MYOD_Q6 0.862739 691 (-) NNCANCTGNY AACAAGTGAT
M00187 V\$USF_Q6 0.873637 691 (-) GYCACGTGNC AACAAGTGAT
M00220 V\$REBP1_01 0.816215 691 (-) NATCACGTGAY AACAAGTGATA
M00138 V\$OCT1_04 0.821832 692 (-) NNNNNNNWATGCAAATNNNWNW ACAAGTGATATGAATAAAGATGG
M00217 V\$USF_C 0.804764 692 (+) NCACGTGN ACAAGTGA
M00217 V\$USF_C 0.827239 692 (-) NCACGTGN ACAAGTGA
M00240 V\$NKX25_01 0.950176 692 (+) TYAAGTG ACAAGTG
M00023 V\$HOX13_01 0.751315 693 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
CAAGTGATATGAATAAAGATGGTGAGACAG
M00126 V\$GATA1_02 0.800312 693 (+) NNNNNGATANKGNN CAAGTGATATGAAT
M00138 V\$OCT1_04 0.791510 693 (+) NNNNNNNWATGCAAATNNNWNW CAAGTGATATGAATAAAGATGGT
M00128 V\$GATA1_04 0.875306 694 (+) NNCWGATARNNNN AGTGATATGAAT
M00075 V\$GATA1_01 0.837117 695 (+) SNNGATNNNN AGTGATATGA
M00076 V\$GATA2_01 0.835363 695 (+) NNNGATRNNN AGTGATATGA
M00077 V\$GATA3_01 0.881258 696 (+) NNGATARNG GTGATATGA
M00278 V\$LMO2COM_02 0.843666 696 (+) NMGATANS GTGATATGA
M00080 V\$EV11_03 0.712757 697 (+) AGATAAGATAA TGATATGAATA
M00082 V\$EV11_05 0.824270 697 (+) AGATAAGATAN TGATATGAATA
M00203 V\$GATA_C 0.881951 697 (+) NGATAAGNMNN TGATATGAATA
M00136 V\$OCT1_02 0.804277 698 (-) NNGAATATKCANNNN GATATGAATAAAGAT
M00160 V\$SRYP_02 0.780681 698 (+) NWWAACA AWANN GATATGAATAA
M00109 V\$CEBPB_01 0.823923 699 (+) RNRTKNNGMAAKNN ATATGAATAAAGAT
M00252 V\$TATA_01 0.817559 699 (+) STATAAAWRNNNNNN ATATGAATAAAGATG
M00133 V\$TST1_01 0.932190 700 (+) NNGAWT WANANTNN TATGAATAAAGATGG

M00174 V\$AP1_Q6 0.788642 700 (+) NNTGACTCANN TATGAATAAAG
M00069 V\$YY1_02 0.761335 701 (-) NNNCGGCCATCTTGNCTSNW ATGAATAAAGATGGTGAGAC
M00096 V\$PBX1_01 0.932272 701 (+) ANCAATCAW ATGAATAAA
M00152 V\$SRF_01 0.719847 701 (+) ATGCCCATATATGGWNNT ATGAATAAAGATGGTGAG
M00199 V\$AP1_C 0.847813 701 (+) NTGASTCAG ATGAATAAA
M00199 V\$AP1_C 0.779592 701 (-) NTGASTCAG ATGAATAAA
M00137 V\$OCT1_03 0.860529 702 (+) NNNRTAATNANNN TGAATAAAGATGG
M00216 V\$TATA_C 0.751518 702 (+) NCTATAAAAR TGAATAAAGA
M00267 V\$XFD1_01 0.850168 702 (+) YAWGTAAAYAWWRY TGAATAAAGATGGT
M00268 V\$XFD2_01 0.842000 702 (+) WNWATAAACAWNNR TGAATAAAGATGGT
M00059 V\$YY1_01 0.890891 703 (-) NNNNNCCATNTWNNNWN GAATAAAGATGGTGAGA
M00065 V\$TALIBETA47_01 0.782357 703 (+) NNNAACAGATGKTNNN GAATAAAGATGGTGAG
M00066 V\$TAL1ALPHA47_01 0.805631 703 (+) NNNAACAGATGKTNNN GAATAAAGATGGTGAG
M00070 V\$TALIBETA1TF2_01 0.808537 703 (+) NNNAACAGATGKTNNN GAATAAAGATGGTGAG
M00129 V\$SHFH1_01 0.793169 703 (-) NAWTGTTTATWT GAATAAAGATGG
M00131 V\$HNF3B_01 0.857316 703 (-) NNNTRTTTRYTY GAATAAAGATGG
M00238 V\$BARBIE_01 0.797703 703 (+) ATNNAAAGCNGRNGG GAATAAAGATGGTGA
M00241 V\$NKX25_02 0.839809 703 (-) CWTAATTG GAATAAAG
M00252 V\$TATA_01 0.812738 703 (+) STATAAAWRNNNNNNN GAATAAAGATGGTGA
M00127 V\$GATA1_03 0.786624 705 (+) RNSNNGATAANNNGN ATAAAGATGGTGAG
M00084 V\$MZF1_02 0.815046 706 (+) KNNNKAGGGGNAA TAAAGATGGTGAG
M00075 V\$GATA1_01 0.869200 707 (+) SNNGATNNNN AAAGATGGTG
M00076 V\$GATA2_01 0.883175 707 (+) NNNGATRNNN AAAGATGGTG
M00085 V\$ZID_01 0.771723 707 (-) NGGCTCYATCAYC AAAGATGGTGAGA
M00057 V\$COMP1_01 0.780838 708 (+) NNTNWKGATTGRCNRSRANMRRNN AAGATGGTGAGACAGAAAGAGCGG
M00077 V\$GATA3_01 0.908285 708 (+) NNGATARNG AAGATGGTG
M00083 V\$MZF1_01 0.847752 710 (+) NGNGGGGA GATGGTGA
M00144 V\$PAX5_02 0.745528 713 (+) RRMSWGANWYCTNRAGCGKRACSRYSNM
GGTGAGACAGAAAGAGCGGGAAATATGA
M00172 V\$APIFJ_Q2 0.817981 713 (+) RSTGACTNMNW GGTGAGACAGA
M00173 V\$AP1_Q2 0.824305 713 (+) RSTGACTNMNW GGTGAGACAGA
M00174 V\$AP1_Q6 0.817601 713 (+) NNTGACTCANN GGTGAGACAGA
M00037 V\$NFE2_01 0.799834 714 (-) TGCTGASTCAY GTGAGACAGAA
M00199 V\$AP1_C 0.852770 714 (+) NTGASTCAG GTGAGACAG
M00199 V\$AP1_C 0.856268 714 (-) NTGASTCAG GTGAGACAG
M00007 V\$ELK1_01 0.773213 716 (+) NNNACMGGAAAGTNCNN GAGACAGAAAGAGCGG
M00056 V\$MYOGNF1_01 0.751127 718 (-) CRSCTGTNNNNTTTGGCACNSNGCCARNN
GACAGAAAGAGCGGGAAATATGACAGCTA
M00005 V\$AP4_01 0.758357 719 (+) WGARYCAGCTGYGGNCNK ACAGAAAGAGCGGGAAAT
M00108 V\$NRF2_01 0.845930 719 (+) ACCGGAAGNS ACAGAAAGAG
M00100 V\$CDXA_01 0.919568 720 (-) MTTTATR CAGAAAG
M00146 V\$HSF1_01 0.842458 721 (+) RGAANRTTCN AGAAAGAGCG
M00147 V\$HSF2_01 0.864325 721 (+) NGAANNWTCK AGAAAGAGCG
M00084 V\$MZF1_02 0.822294 722 (+) KNNNKAGGGGNAA GAAAGAGCGGGAA
M00024 V\$E2F_01 0.738990 723 (+) TWSGCGCGAAAAYKR AAAGAGCGGGAAATA
M00242 V\$PPARA_01 0.760548 723 (+) CWRWCTAGGNCAAAGGTCA AAAGAGCGGGAAATATGACA
M00175 V\$AP4_Q5 0.781284 724 (+) NNCAGCTGNN AAGAGCGGGA
M00176 V\$AP4_Q6 0.806815 724 (+) CWCAGCTGGN AAGAGCGGGA
M00024 V\$E2F_01 0.809362 725 (+) TWSGCGCGAAAAYKR AGAGCGGGAAATATG
M00025 V\$ELK1_02 0.846954 725 (+) NNNNCCGGAARYNN AGAGCGGGAAATAT
M00074 V\$CETSIP54_02 0.845877 726 (+) NNAMMGGAWRWNN GAGCGGGAAATAT
M00086 V\$IK1_01 0.809028 726 (+) NNTGGGAATRCC GAGCGGGAAATAT
M00087 V\$IK2_01 0.896597 726 (+) NNNYGGGAWNNN GAGCGGGAAATA
M00180 V\$E2F_Q6 0.880930 726 (+) NNGCGCGAAANTK GAGCGGGAAATAT
M00032 V\$CETSIP54_01 0.841662 728 (+) NCMGGAWGYN GCGGGAAATA
M00050 V\$E2F_02 0.956679 728 (-) TTTSGCGC GCGGGAAA
M00059 V\$YY1_01 0.770642 729 (-) NNNNNCCATNTWNNNWN CGGGAAATATGACAGCT
M00023 V\$HOX13_01 0.762673 732 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GAAATATGACAGCTAAGGAGAGAGATGGGG
M00062 V\$IRF1_01 0.803160 732 (+) SAAAAGYGAAACC GAAATATGACAGC
M00063 V\$IRF2_01 0.760090 732 (+) GAAAAGYGAAASY GAAATATGACAGC

M00109 V\$CEBPB_01 0.825409 732 (+) RNRTKNNGMAAKNN GAAATATGACAGCT
M00057 V\$COMP1_01 0.790180 733 (+) NNTNWKGATTGRCNRSRANMRRNN AAATATGACAGCTAAGGAGAGAGA
M00076 V\$GATA2_01 0.783491 733 (-) NNGGATRNNN AAATATGACA
M00082 V\$EV11_05 0.807848 733 (+) AGATAAGATAN AAATATGACAG
M00177 V\$CREB_Q2 0.755496 733 (-) NSTGACGTAANN AAATATGACAGC
M00001 V\$MYOD_01 0.819291 738 (-) SRACAGGTGKYG TGACAGCTAAGG
M00128 V\$GATA1_04 0.835478 739 (+) NNCWGATARNNNN GACAGCTAAGGAG
M00175 V\$AP4_Q5 0.821817 739 (+) NNCAGCTGNN GACAGCTAAG
M00175 V\$AP4_Q5 0.834603 739 (-) NNCAGCTGNN GACAGCTAAG
M00176 V\$AP4_Q6 0.840641 739 (-) CWCAGCTGGN GACAGCTAAG
M00278 V\$LMO2COM_02 0.841307 741 (+) NMGATANS GAGCTAAGG
M00073 V\$DELTAEF1_01 0.878493 744 (-) NNCACCTNAN CTAAGGAGAGA
M00141 V\$LYF1_01 0.858165 744 (+) TTTGGGAGR CTAAGGAGA
M00004 V\$CMYB_01 0.761327 745 (+) NCNRNNGRCNGTTGKKGG TAAGGAGAGAGATGGGGG
M00127 V\$GATA1_03 0.789319 746 (+) RNSNNGATAANNNGN AAGGAGAGAGATGG
M00126 V\$GATA1_02 0.789062 750 (+) NNNNNGATANKGNN AGAGAGATGGGGGA
M00127 V\$GATA1_03 0.807447 750 (+) RNSNNGATAANNNGN AGAGAGATGGGGGA
M00084 V\$MZF1_02 0.878530 751 (+) KNNNKAGGGGNAA GAGAGATGGGGGA
M00184 V\$MYOD_Q6 0.805059 751 (-) NNCANCTGNY GAGAGATGGG
M00075 V\$GATA1_01 0.910168 752 (+) SNGGATNNNN AGAGATGGGG
M00076 V\$GATA2_01 0.897609 752 (+) NNGGATRNNN AGAGATGGGG
M00077 V\$GATA3_01 0.946389 753 (+) NNGATARNNG GAGATGGGG
M00084 V\$MZF1_02 0.843789 753 (+) KNNNKAGGGGNAA GAGATGGGGGAGA
M00278 V\$LMO2COM_02 0.816712 753 (+) NMGATANS GAGATGGGG
M00083 V\$MZF1_01 0.849641 755 (+) NGNGGGGA GATGGGGG
M00085 V\$ZID_01 0.788555 755 (-) NGGCTCYATCAYC GATGGGGGAGATA
M00008 V\$SP1_01 0.808324 756 (+) GRGGCRGGGW ATGGGGGAGA
M00083 V\$MZF1_01 0.931243 756 (+) NGNGGGGA ATGGGGGA
M00023 V\$HOX13_01 0.727284 757 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TGGGGGAGATAAGGAGAGAAGAAGATAGGG
M00221 V\$SREBP1_02 0.720902 757 (-) KATCACCCAC TGGGGGAGATA
M00008 V\$SP1_01 0.815119 758 (+) GRGGCRGGGW GGGGAGATA
M00126 V\$GATA1_02 0.865312 759 (+) NNNNNGATANKGNN GGGGAGATAAGGAG
M00127 V\$GATA1_03 0.956149 759 (+) RNSNNGATAANNNGN GGGGAGATAAGGAG
M00128 V\$GATA1_04 0.951900 760 (+) NNCWGATARNNNN GGGAGATAAGGAG
M00075 V\$GATA1_01 0.909674 761 (+) SNGGATNNNN GGAGATAAGG
M00076 V\$GATA2_01 0.921516 761 (+) NNGGATRNNN GGAGATAAGG
M00252 V\$TATA_01 0.770870 761 (+) STATAAAWRNNNNNN GGAGATAAGGAGAGA
M00077 V\$GATA3_01 0.971644 762 (+) NNGATARNNG GAGATAAGG
M00278 V\$LMO2COM_02 0.969340 762 (+) NMGATANS GAGATAAGG
M00080 V\$EV11_03 0.715638 763 (+) AGATAAGATAA AGATAAGGAGA
M00203 V\$GATA_C 0.922336 763 (+) NGATAAGNMNN AGATAAGGAGA
M00073 V\$DELTAEF1_01 0.853476 765 (-) NNCACCTNAN ATAAGGAGAGA
M00024 V\$E2F_01 0.746535 767 (+) TWSGCGCGAAAAYKR AAGGAGAGAAGAAGA
M00127 V\$GATA1_03 0.833660 767 (+) RNSNNGATAANNNGN AAGGAGAGAAGAAG
M00200 V\$CAAT_C 0.719812 770 (-) ACCAATCANCNNGCYYSNCNCWNNT GAGAGAAGAAGATAGGGTGTCTGGC
M00080 V\$EV11_03 0.717284 771 (+) AGATAAGATAA AGAGAAGAAGA
M00108 V\$NRF2_01 0.775678 773 (+) ACCGGAAGNS AGAAGAAGAT
M00082 V\$EV11_05 0.792067 774 (+) AGATAAGATAN GAAGAAGATAG
M00126 V\$GATA1_02 0.899375 775 (+) NNNNNGATANKGNN AAGAAGATAGGGTG
M00127 V\$GATA1_03 0.898334 775 (+) RNSNNGATAANNNGN AAGAAGATAGGGTG
M00205 V\$GRE_C 0.799368 775 (-) GGTACAANNTGTCTK AAGAAGATAGGGTGTCTGTC
M00011 V\$EV11_06 0.855027 776 (+) ACAAGATAA AGAAGATAG
M00128 V\$GATA1_04 0.913297 776 (+) NNCWGATARNNNN AGAAGATAGGGTG
M00255 V\$GC_01 0.793484 776 (+) NRGGGGCGGGGCK AGAAGATAGGGTGT
M00075 V\$GATA1_01 0.946199 777 (+) SNGGATNNNN GAAGATAGGG
M00076 V\$GATA2_01 0.964817 777 (+) NNGGATRNNN GAAGATAGGG
M00237 V\$AHRARNT_02 0.751476 777 (+) GRGKATYCGGTGMSWNSCC GAAGATAGGGTGTCTGGCA
M00056 V\$MYOGNF1_01 0.740194 778 (+) CRSCTGTNNNNTTTGGCACNSNGCCARNN
AAGATAGGGTGTCTGGCACACAGAAGACA
M00077 V\$GATA3_01 0.982720 778 (+) NNGATARNNG AAGATAGGG

M00278 V\$LMO2COM_02 0.966644 778 (+) NMGATANS G AAGATAGGG
M00203 V\$GATA_C 0.846847 779 (+) NGATAAGNMNN AGATAGGGTGT
M00008 V\$SP1_01 0.810306 782 (+) GRGGCRGGGW TAGGGTGTCT
M00115 V\$TAXCREB_02 0.728419 782 (-) RTGACGCATAYCCCC TAGGGTGTCTGGCAC
M00222 V\$TH1E47_01 0.924708 782 (+) NNNNGNRTCTGGMWTT TAGGGTGTCTGGCACA
M00115 V\$TAXCREB_02 0.654702 784 (-) RTGACGCATAYCCCC GGGTGTCTGGCACAC
M00278 V\$LMO2COM_02 0.791105 784 (-) NMGATANS G GGTGTCTG
M00050 V\$E2F_02 0.743405 789 (+) TTTSGCGC TCTGGCAC
M00192 V\$GR_Q6 0.827567 790 (-) NNNNNNCNNTNTGTNCTNN CTGGCACACAGAAGACACT
M00199 V\$AP1_C 0.781341 790 (-) NTGASTCAG CTGGCACAC
M00235 V\$AHRARNT_01 0.818703 791 (-) KNNKNNTYGCGTGCMS TGGCACACAGAAGACA
M00189 V\$AP2_Q6 0.790901 792 (+) MKCCSCNNGGCG GGCACACAGAAG
M00072 V\$CP2_01 0.844340 793 (+) GCNMNAMCMAG GCACACAGAAG
M00108 V\$NRF2_01 0.796027 796 (+) ACCGGAAGNS CACAGAAGAC
M00179 V\$CREBP1_Q2 0.751431 797 (-) NSTGACGTMASN ACAGAAGACACT
M00146 V\$HSF1_01 0.794013 799 (+) RGAANRTTCN AGAAGACACT
M00147 V\$HSF2_01 0.848799 799 (+) NGAANNWTCK AGAAGACACT
M00185 V\$NFY_Q6 0.771840 801 (+) TRRCCAATSRN AAGACACTCAG
M00086 V\$IK1_01 0.780182 807 (+) NNNTGGAATRCC CTCAGGGAAAGAG
M00087 V\$IK2_01 0.888089 807 (+) NNNYGGGAWNNN CTCAGGGAAAGA
M00200 V\$CAAT_C 0.715231 807 (-) ACCAATCANCNNGCYYSNCNCWNNT CTCAGGGAAAGAGCTGTTGAATGCC
M00141 V\$LYF1_01 0.900843 808 (+) TTTGGGAGR TCAGGGAAA
M00050 V\$E2F_02 0.764788 809 (-) TTTSGCGC CAGGGAAA
M00255 V\$GC_01 0.833170 809 (+) NRGGGGCGGGGCGNK CAGGGAAAGAGCTG
M00005 V\$AP4_01 0.783285 810 (-) WGARYCAGCTGYGGNCNK AGGGAAAGAGCTGTTGAA
M00004 V\$CMYB_01 0.772816 812 (+) NCNRNNGRCNGTTGKGKGG GGAAAGAGCTGTTGAATG
M00005 V\$AP4_01 0.810231 812 (+) WGARYCAGCTGYGGNCNK GGAAAGAGCTGTTGAATG
M00066 V\$TAL1ALPHA47_01 0.783568 812 (+) NNNAACAGATGKTNNN GGAAAGAGCTGTTGAA
M00066 V\$TAL1ALPHA47_01 0.798697 812 (-) NNNAACAGATGKTNNN GGAAAGAGCTGTTGAA
M00070 V\$TAL1BETA1F2_01 0.772764 812 (+) NNNAACAGATGKTNNN GGAAAGAGCTGTTGAA
M00070 V\$TAL1BETA1F2_01 0.764634 812 (-) NNNAACAGATGKTNNN GGAAAGAGCTGTTGAA
M00071 V\$E47_02 0.767756 812 (+) NNNMRCAGGTGTTMNN GGAAAGAGCTGTTGAA
M00071 V\$E47_02 0.784442 812 (-) NNNMRCAGGTGTTMNN GGAAAGAGCTGTTGAA
M00146 V\$HSF1_01 0.791256 812 (+) RGAANRTTCN GGAAAGAGCT
M00147 V\$HSF2_01 0.849538 812 (+) NGAANNWTCK GGAAAGAGCT
M00001 V\$MYOD_01 0.869291 814 (+) SRACAGGTGKYG AAAGAGCTGTTG
M00001 V\$MYOD_01 0.861417 814 (-) SRACAGGTGKYG AAAGAGCTGTTG
M00175 V\$AP4_Q5 0.841676 815 (+) NNCAGCTGNN AAGAGCTGTT
M00175 V\$AP4_Q5 0.942873 815 (-) NNCAGCTGNN AAGAGCTGTT
M00176 V\$AP4_Q6 0.830619 815 (+) CWCAGCTGGN AAGAGCTGTT
M00176 V\$AP4_Q6 0.912553 815 (-) CWCAGCTGGN AAGAGCTGTT
M00184 V\$MYOD_Q6 0.799506 815 (+) NNCANCTGNY AAGAGCTGTT
M00184 V\$MYOD_Q6 0.799506 815 (-) NNCANCTGNY AAGAGCTGTT
M00262 V\$STAF_01 0.755058 817 (-) NTTWCCCANMATGCAYYRCGNY GAGCTGTTGAATGCCTGGAAGG
M00183 V\$MYB_Q6 0.824481 818 (-) NNNAACKGNC AGCTGTTGAA
M00249 V\$CHOP_01 0.801118 818 (-) NNRTGCAATMCCC AGCTGTTGAATGC
M00057 V\$COMP1_01 0.771737 819 (+) NNTNWKGATTGRCNRSRANMRRNN GCTGTTGAATGCCTGGAAGGTGAA
M00227 V\$VMBYB_02 0.818592 819 (-) NSYAACGGN GCTGTTGAA
M00209 V\$NFY_C 0.766811 822 (+) NCTGATTGGYTASY GTTGAATGCCTGGA
M00224 V\$STAT1_01 0.722707 822 (+) NNN SANTCCGGGAANTGNSN GTTGAATGCCTGGAAGGTGAA
M00008 V\$SP1_01 0.799264 824 (-) GRGGCRGGGW TGAATGCCTG
M00155 V\$ARP1_01 0.769231 824 (+) TGARCCYTTGAMCCYW TGAATGCCTGGAAGGT
M00162 V\$OCT1_Q6 0.813672 824 (-) CWNATWKWSATRYN TGAATGCCTGGAAG
M00254 V\$CAAT_01 0.832533 824 (-) NNNRRCCAATSA TGAATGCCTGGA
M00243 V\$EGR1_01 0.773850 827 (+) WTGCGTGGGCGK ATGCCTGGAAGG
M00244 V\$NGFIC_01 0.785504 827 (+) WTGCGTGGGYGG ATGCCTGGAAGG
M00245 V\$EGR3_01 0.740625 827 (+) NTGCGTGGGCGK ATGCCTGGAAGG
M00246 V\$EGR2_01 0.746580 827 (+) NTGCGTRGGCGK ATGCCTGGAAGG
M00223 V\$STAT_01 0.856819 828 (+) TTCCRKAA TGCCTGGAA
M00223 V\$STAT_01 0.832871 828 (-) TTCCRKAA TGCCTGGAA
M00108 V\$NRF2_01 0.795785 830 (+) ACCGGAAGNS CCTGGAAGGT

M00239 V\$T3R_01 0.758092 831 (+) SNNTRAGGTCACGSNN CTGGAAGGTGAATACA
M00073 V\$DELTAEF1_01 0.922027 833 (-) NNNCACCTNAN GGAAGGTGAAT
M00184 V\$MYOD_Q6 0.791795 833 (-) NNCANCTGNY GGAAGGTGAA
M00133 V\$TST1_01 0.888932 834 (-) NNKGAWTWANANTNN GAAGGTGAATACACA
M00136 V\$OCT1_02 0.805631 835 (-) NNGAATATKCANNNN AAGGTGAATACACAG
M00133 V\$TST1_01 0.887763 837 (+) NNKGAWTWANANTNN GGTGAATACACAGAT
M00174 V\$AP1_Q6 0.796916 837 (+) NNTGACTCANN GGTGAATACAC
M00023 V\$HOX13_01 0.723219 839 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TGAATACACAGATGAATGGAGAGAGAGAAAAC
M00097 V\$PAX6_01 0.754744 839 (+) NNNNTTCACGCWTSANTKNNN TGAATACACAGATGAATGGAG
M00268 V\$XFD2_01 0.830400 839 (+) WNWATAAACAWNNR TGAATACACAGATG
M00105 V\$CDPCR3_01 0.751772 843 (+) CACCRATANNTATNG TACACAGATGAATGG
M00122 V\$USF_02 0.761964 843 (+) NNRNCACGTGNYNN TACACAGATGAATG
M00122 V\$USF_02 0.761964 843 (-) NNRNCACGTGNYNN TACACAGATGAATG
M00127 V\$GATA1_03 0.780010 844 (+) RNSNNGATAANNNGN ACACAGATGAATGG
M00262 V\$STAF_01 0.721532 844 (-) NTTWCCCANMATGCAYYRCGNY ACACAGATGAATGGAGAGAGAA
M00277 V\$LMO2COM_01 0.782234 844 (-) SNNCAGGTGNNN ACACAGATGAAT
M00175 V\$AP4_Q5 0.805767 845 (+) NNCAGCTGNN CACAGATGAA
M00176 V\$AP4_Q6 0.764219 845 (+) CWCAGCTGGN CACAGATGAA
M00184 V\$MYOD_Q6 0.792412 845 (-) NNCANCTGNY CACAGATGAA
M00057 V\$COMP1_01 0.834611 846 (+) NNTNWKGATTGRCNRSRANMRRNN ACAGATGAATGGAGAGAGAAAACC
M00059 V\$YY1_01 0.804391 846 (-) NNNNNCCATNTWNNNWN ACAGATGAATGGAGAGA
M00075 V\$GATA1_01 0.773939 846 (+) SNNGATNNNN ACAGATGAAT
M00076 V\$GATA2_01 0.786649 846 (+) NNNGATRNNN ACAGATGAAT
M00217 V\$USF_C 0.829587 846 (-) NCACGTGN ACAGATGA
M00104 V\$CDPCR1_01 0.774015 847 (-) NATCGATCGS CAGATGAATG
M00106 V\$CDPCR3HD_01 0.904268 847 (-) NATYGATSSS CAGATGAATG
M00252 V\$TATA_01 0.770109 848 (+) STATAAAWRNNNNNNN AGATGAATGGAGAGA
M00104 V\$CDPCR1_01 0.782807 849 (+) NATCGATCGS GATGAATGGA
M00185 V\$NFY_Q6 0.778777 850 (-) TRRCCAATSRN ATGAATGGAGA
M00057 V\$COMP1_01 0.787784 851 (+) NNTNWKGATTGRCNRSRANMRRNN TGAATGGAGAGAGAAAACCAGACA
M00254 V\$CAAT_01 0.824061 851 (-) NNNRRCCAATSA TGAATGGAGAGA
M00063 V\$IRF2_01 0.702656 856 (+) GAAAAGYGAAASY GGAGAGAGAGAAAAC
M00007 V\$ELK1_01 0.768871 857 (+) NNNACMGGAAGTNCNN GAGAGAGAGAAAACCAGA
M00127 V\$GATA1_03 0.833660 858 (+) RNSNNGATAANNNGN AGAGAGAGAAAACCAG
M00050 V\$E2F_02 0.748403 859 (-) TTTSGCGC GAGAGAAA
M00078 V\$EV11_01 0.767857 860 (+) WGAYAAGATAAGATAA AGAGAGAAAACCAGACAC
M00072 V\$CP2_01 0.805746 861 (+) GCNMNAMCMAG GAGAGAAAACCAG
M00160 V\$SRY_02 0.760129 863 (+) NWWAACAANWANN GAGAGAAAACCAGACA
M00254 V\$CAAT_01 0.786501 863 (+) NNNRRCCAATSA GAGAGAAAACCAGACA
M00222 V\$TH1E47_01 0.923040 864 (-) NNNNGNRTCTGGMWTT AAAACCAGACACCTCA
M00185 V\$NFY_Q6 0.771069 865 (+) TRRCCAATSRN AAACCAGACAC
M00144 V\$PAX5_02 0.817373 866 (+) RRMSWGANWYCTNRAGCGKRACSRYSNM
AACCAGACACCTCAGGGCTAAGAGCGCA
M00214 V\$SEF1_C 0.767568 866 (-) AACACGGATATCTGTGGTY AACCAGACACCTCAGGGCT
M00239 V\$T3R_01 0.745788 867 (-) SNNTRAGGTCACGSNN ACCAGACACCTCAGGG
M00271 V\$AML1_01 0.873587 867 (-) TGTGGT ACCAGA
M00002 V\$E47_01 0.770189 868 (-) NSNGCAGGTGKNCNN CCAGACACCTCAGGG
M00076 V\$GATA2_01 0.782138 868 (+) NNNGATRNNN CCAGACACCT
M00261 V\$OLF1_01 0.798356 868 (-) NNCNANTCCCYNGRGARNNKGN CCAGACACCTCAGGGCTAAGAG
M00017 V\$ATF_01 0.803304 869 (-) CNSTGACGTNNNYC CAGACACCTCAGGG
M00001 V\$MYOD_01 0.845866 870 (-) SRACAGGTGKYG AGACACCTCAGG
M00073 V\$DELTAEF1_01 0.840156 870 (+) NNNCACCTNAN AGACACCTCAG
M00179 V\$CREBP1_Q2 0.768397 870 (-) NSTGACGTMASN AGACACCTCAGG
M00272 V\$P53_02 0.797773 870 (-) NGRCWTGYCY AGACACCTCA
M00277 V\$LMO2COM_01 0.786272 870 (-) SNNCAGGTGNNN AGACACCTCAGG
M00175 V\$AP4_Q5 0.788357 871 (+) NNCAGCTGNN GACACCTCAG
M00211 V\$PADS_C 0.852823 871 (-) NGTGGTCTC GACACCTCA
M00189 V\$AP2_Q6 0.838695 873 (+) MKCCSCSNGGCG CACCTCAGGGCT
M00271 V\$AML1_01 0.910841 874 (-) TGTGGT ACCTCA
M00134 V\$HNF4_01 0.760436 876 (+) NNNRGGNCAAAGKTCANNN CTCAGGGCTAAGAGCGCAG

M00176 V\$AP4_Q6 0.772989 876 (+) CWCAGCTGGN CTCAGGGCTA
M00155 V\$ARP1_01 0.793515 878 (-) TGARCCYTTGAMCCYW CAGGGCTAAGAGCGCA
M00143 V\$PAX5_01 0.813085 884 (+) NCNNNRNKCANNNGNWNRKRKGCSRSNNN
TAAGAGCGCAGGCCAGACAGGCAGCCAG
M00007 V\$ELK1_01 0.773547 885 (+) NNNACMGGAAGTNCNN AAGAGCGCAGGCCAGA
M00072 V\$CP2_01 0.806175 889 (+) GCMNAMCMAG GCGCAGGCCAG
M00162 V\$OCT1_06 0.808594 890 (-) CWNATKWSATRYN CGCAGGCCAGACAG
M00059 V\$YY1_01 0.792595 891 (+) NNNNNCCATNTWNNNWN GCAGGCCAGACAGGCAG
M00254 V\$CAAT_01 0.806269 891 (+) NNNRCCAATSA GCAGGCCAGACA
M00215 V\$SRF_C 0.750527 892 (-) NCCWTATATGGNCWN CAGGCCAGACAGGCA
M00222 V\$TH1E47_01 0.798904 892 (-) NNNNGNRTCTGGMWTT CAGGCCAGACAGGCAG
M00127 V\$GATA1_03 0.809652 894 (+) RNSNNGATAANNNGN GGCCAGACAGGCAG
M00237 V\$AHRARNT_02 0.781877 894 (-) GRGKATYGCGTGMSWNSCC GGCCAGACAGGCAGGCCAGC
M00075 V\$GATA1_01 0.772458 896 (+) SNNGATNNNN CCAGACAGGC
M00076 V\$GATA2_01 0.791159 896 (+) NNNGATRNNN CCAGACAGGC
M00193 V\$NF1_Q6 0.802877 896 (-) NNTTGGCNNNNNNCCNNN CCAGACAGGCAGGCCAGCT
M00007 V\$ELK1_01 0.864061 897 (+) NNNACMGGAAGTNCNN CAGACAGGCAGGCCAGC
M00278 V\$LMO2COM_02 0.815701 897 (+) NMGATANS GAGACAGGC
M00272 V\$P53_02 0.834115 898 (-) NGRCWTGYCY AGACAGGCAG
M00032 V\$CETS1P54_01 0.845464 900 (+) NCMGGAAGYN ACAGGCAGGCC
M00108 V\$NRF2_01 0.803779 900 (+) ACCGGAAGNS ACAGGCAGGCC
M00058 V\$HEN1_02 0.781072 901 (+) NNGGGNCGCAGCTGCGNCCCN CAGGCAGCCAGCTGTTCTCCT
M00058 V\$HEN1_02 0.768174 901 (-) NNGGGNCGCAGCTGCGNCCCN CAGGCAGCCAGCTGTTCTCCT
M00068 V\$HEN1_01 0.743629 901 (+) NNGGGNCNCAGCTGCGNCCCN CAGGCAGCCAGCTGTTCTCCT
M00068 V\$HEN1_01 0.779203 901 (-) NNGGGNCNCAGCTGCGNCCCN CAGGCAGCCAGCTGTTCTCCT
M00005 V\$AP4_01 0.814265 902 (-) WGARYCAGCTGYGGNCNK AGGCAGCCAGCTGTTCTCCT
M00188 V\$AP1_Q4 0.809088 902 (-) RSTGACTMANN AGGCAGCCAGC
M00192 V\$GR_Q6 0.791295 902 (+) NNNNNNCNNTNTGTNCTNN AGGCAGCCAGCTGTTCTCCT
M00002 V\$E47_01 0.895942 904 (-) NSNGCAGGTGKNCNN GCAGCCAGCTGTTCC
M00065 V\$TAL1BETAE47_01 0.799259 904 (+) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00065 V\$TAL1BETAE47_01 0.839546 904 (-) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00066 V\$TAL1ALPHAE47_01 0.851439 904 (+) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00066 V\$TAL1ALPHAE47_01 0.850809 904 (-) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00070 V\$TAL1BETAIF2_01 0.821748 904 (+) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00070 V\$TAL1BETAIF2_01 0.854268 904 (-) NNNAACAGATGKTNNN GCAGCCAGCTGTTCTCCT
M00071 V\$E47_02 0.829989 904 (+) NNNMRCAGGTGTTMNN GCAGCCAGCTGTTCTCCT
M00071 V\$E47_02 0.801353 904 (-) NNNMRCAGGTGTTMNN GCAGCCAGCTGTTCTCCT
M00002 V\$E47_01 0.855163 905 (+) NSNGCAGGTGKNCNN CAGCCAGCTGTTCTCCT
M00122 V\$USF_02 0.836234 905 (+) NNRNCACGTGNYNN CAGCCAGCTGTTCC
M00122 V\$USF_02 0.836234 905 (-) NNRNCACGTGNYNN CAGCCAGCTGTTCC
M00001 V\$MYOD_01 0.798031 906 (+) SRACAGGTGKYG AGCCAGCTGTTC
M00001 V\$MYOD_01 0.944488 906 (-) SRACAGGTGKYG AGCCAGCTGTTC
M00277 V\$LMO2COM_01 0.904980 906 (+) SNNCAGGTGNNN AGCCAGCTGTTC
M00277 V\$LMO2COM_01 0.857873 906 (-) SNNCAGGTGNNN AGCCAGCTGTTC
M00175 V\$AP4_Q5 0.875136 907 (+) NNCAGCTGNN GCCAGCTGTT
M00175 V\$AP4_Q5 0.949402 907 (-) NNCAGCTGNN GCCAGCTGTT
M00176 V\$AP4_Q6 0.853170 907 (+) CWCAGCTGGN GCCAGCTGTT
M00176 V\$AP4_Q6 0.956402 907 (-) CWCAGCTGGN GCCAGCTGTT
M00184 V\$MYOD_Q6 0.942011 907 (+) NNCANCTGNY GCCAGCTGTT
M00184 V\$MYOD_Q6 0.926897 907 (-) NNCANCTGNY GCCAGCTGTT
M00253 V\$CAP_01 0.884179 908 (+) NCANNNNN CCAGCTGT
M00255 V\$GC_01 0.846644 909 (-) NRGGGGCGGGGCNK CAGCTGTTCTCCTCCT
M00108 V\$NRF2_01 0.770349 912 (-) ACCGGAAGNS CTGTTCTCCTCCT
M00255 V\$GC_01 0.870897 912 (-) NRGGGGCGGGGCNK CTGTTCTCCTCCTTTA
M00073 V\$DELTAEF1_01 0.818389 915 (+) NNNCACCTNAN TTCCTCCTTTA
M00083 V\$MZF1_01 0.838685 916 (-) NGNGGGGA TCCTCCTT
M00215 V\$SRF_C 0.758609 916 (-) NCCWTATATGGNCWN TCCTCCTTTAAGGGT
M00107 V\$E2_01 0.743072 917 (-) NNACCRNNANCGGTRN CCTCCTTTAAGGGTGA
M00181 V\$E2_Q6 0.763032 917 (+) NNACCRNNANCGGTRN CCTCCTTTAAGGGTGA
M00098 V\$PAX2_01 0.829528 918 (+) NNNNGTCANGNRTKANNNN CTCCTTTAAGGGTGACTCC
M00215 V\$SRF_C 0.786367 919 (+) NCCWTATATGGNCWN TCCTTTAAGGGTGAC

M00227 V\$VMBYB_02 0.803550 919 (-) NSYAACGGN TCCTTTAAG
M00100 V\$CDXA_01 0.937224 921 (+) MTTTATR CTTTAAG
M00156 V\$RORA1_01 0.761559 921 (+) NWAOWNAGGTGAN CTTTAAGGGTGAC
M00227 V\$VMBYB_02 0.812876 922 (+) NSYAACGGN TTTAAGGGT
M00008 V\$SP1_01 0.792186 925 (+) GRGGCRGGGW AAGGGTGACT
M00083 V\$MZF1_01 0.836796 925 (+) NGNGGGGA AAGGGTGA
M00239 V\$T3R_01 0.740299 925 (-) SNNTAGGTACAGSNN AAGGGTGACTCCCTCG
M00113 V\$CREB_02 0.891664 926 (+) NNGNTGACGYNN AAGGGTGACTCCC
M00194 V\$NFKB_Q6 0.819030 926 (-) NGGGGAMTTTCCNN AAGGGTGACTCCCTC
M00033 V\$P300_01 0.826858 927 (-) NNNRGGAGTNNNNS GGGTGACTCCCTCG
M00194 V\$NFKB_Q6 0.803068 927 (+) NGGGGAMTTTCCNN GGGTGACTCCCTCG
M00208 V\$NFKB_C 0.773640 927 (-) NGGGACTTTCCA GGGTGACTCCCT
M00051 V\$NFKAPPAB50_01 0.798756 928 (+) GGGGATYCCC GGTGACTCCC
M00054 V\$NFKAPPAB_01 0.789763 928 (+) GGGAMTTYCC GGTGACTCCC
M00054 V\$NFKAPPAB_01 0.811486 928 (-) GGGAMTTYCC GGTGACTCCC
M00172 V\$AP1FJ_Q2 0.961830 928 (+) RSTGACTNMNW GGTGACTCCCT
M00173 V\$AP1_Q2 0.944656 928 (+) RSTGACTNMNW GGTGACTCCCT
M00174 V\$AP1_Q6 0.939075 928 (+) NNTGACTCANN GGTGACTCCCT
M00177 V\$CREB_Q2 0.778449 928 (+) NSTGACGTAANN GGTGACTCCCTC
M00178 V\$CREB_Q4 0.791267 928 (+) NSTGACGTMANN GGTGACTCCCTC
M00188 V\$AP1_Q4 0.950290 928 (+) RSTGACTMANN GGTGACTCCCT
M00051 V\$NFKAPPAB50_01 0.760107 929 (-) GGGGATYCCC GTGACTCCCT
M00199 V\$AP1_C 0.801166 929 (+) NTGASTCAG GTGACTCCC
M00199 V\$AP1_C 0.808746 929 (-) NTGASTCAG GTGACTCCC
M00008 V\$SP1_01 0.832390 930 (-) GRGGCRGGGW TGACTCCCTC
M00057 V\$COMP1_01 0.796527 932 (-) NNTNWKGATTGRCNRSRANMRRNN ACTCCCTCGATGTAAACCATTCTC
M00059 V\$YY1_01 0.773263 933 (-) NNNNNCCATNTWNNNWN CTCCCTCGATGTAAACC
M00104 V\$CDPCR1_01 0.797134 934 (-) NATCGATCGS TCCCTCGATG
M00023 V\$HOX13_01 0.755022 937 (+) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
CTCGATGTAAACCATTCTCCTTCTCCCCAA
M00075 V\$GATA1_01 0.823297 937 (+) SNNGATNNNN CTGATGTAA
M00098 V\$PAX2_01 0.757585 939 (+) NNNNGTCANGNRTKANNNN CGATGTAAACCATTCTCCT
M00134 V\$HNF4_01 0.781987 942 (-) NNNRGGNCAAAGKTCANNN TGTTAACCATTCTCCTTCT
M00206 V\$HNF1_C 0.816312 942 (+) NGTTAATKAWTNACCAM TGTTAACCATTCTCCTT
M00059 V\$YY1_01 0.776868 943 (+) NNNNNCCATNTWNNNWN GTTAACCATTCTCCTTC
M00160 V\$SRY_02 0.784204 943 (+) NWWAACAANWANN GTTAACCATTCT
M00209 V\$NFY_C 0.777528 943 (-) NCTGATTGGYTASY GTTAACCATTCTCC
M00254 V\$CAAT_01 0.802881 943 (+) NNNRCCAATSA GTTAACCATTCT
M00262 V\$STAF_01 0.721821 943 (+) NTTWCCCANMATGCAYYRCGY GTTAACCATTCTCCTTCTCCCC
M00042 V\$SOX5_01 0.822409 944 (+) NNAACAATNN TTAACCATTC
M00185 V\$NFY_Q6 0.853289 945 (+) TRRCCAATSRN TAACCATTCCTC
M00255 V\$GC_01 0.799608 945 (-) NRGGGGCGGGGCNK TAACCATTCCTT
M00127 V\$GATA1_03 0.814307 947 (-) RNSNNGATAANNGN ACCATTCTCCTTCT
M00200 V\$CAAT_C 0.714976 947 (+) ACCAATCANCNNGCYYSNCNCWNNT ACCATTCTCCTTCTCCCCAACAGTT
M00253 V\$CAP_01 0.919665 948 (+) NCANNNNN CCATTCTC
M00115 V\$TAXCREB_02 0.631415 950 (+) RTGACGCATAYCCCC ATTCTCCTTCTCCCC
M00084 V\$MZF1_02 0.854536 951 (-) KNNNKAGGGGNAA TTCTCCTTCTCCC
M00114 V\$TAXCREB_01 0.731313 952 (-) GGGGGTTGACGYANA TCTCCTTCTCCCCAA
M00143 V\$PAX5_01 0.828285 952 (-) NCNNNRNKCANNNGWGNRKRKGRCSRSNNN
TCTCCTTCTCCCCAACAGTTCCCCAGGG
M00033 V\$P300_01 0.818678 953 (-) NNNRGGAGTNNNNS CTCCTTCTCCCCAA
M00084 V\$MZF1_02 0.815296 956 (-) KNNNKAGGGGNAA CTTCTCCCCAACAA
M00084 V\$MZF1_02 0.832292 957 (-) KNNNKAGGGGNAA TTCTCCCCAACAG
M00141 V\$LYF1_01 0.887043 958 (-) TTTGGGAGR TCTCCCCAA
M00141 V\$LYF1_01 0.902632 959 (-) TTTGGGAGR CTCCCCAAC
M00004 V\$CMYB_01 0.795144 960 (-) NCNRNNGRCNGTTGGKGG TCCCCAACAGTTCCCCAG
M00083 V\$MZF1_01 0.942199 960 (-) NGNGGGGA TCCCCAAC
M00075 V\$GATA1_01 0.775420 961 (-) SNNGATNNNN CCCCCAACAGT
M00183 V\$MYB_Q6 0.826556 962 (+) NNNAACKGNC CCCCCAACAGTT
M00227 V\$VMBYB_02 0.845367 962 (+) NSYAACGGN CCCCCAACAGT
M00261 V\$OLF1_01 0.788958 964 (+) NNCNANTCCCYNGRGARNNKGN CAACAGTTCCCCAGGGACCTCT

M00176 V\$AP4_Q6 0.780005 965 (+) CWCAGCTGGN AACAGTTCCC
M00183 V\$MYB_Q6 0.862241 965 (-) NNNAACKGNC AACAGTTCCC
M00261 V\$OLF1_01 0.872749 965 (+) NNCNANTCCCYNGRGARNKGN AACAGTTCCCCAGGGACCTCTC
M00261 V\$OLF1_01 0.867398 965 (-) NNCNANTCCCYNGRGARNKGN AACAGTTCCCCAGGGACCTCTC
M00086 V\$IK1_01 0.777244 966 (-) NNNTGGGAATRCC ACAGTTCCCCAGG
M00227 V\$VMYB_02 0.792419 966 (-) NSYAACGN ACAGTTCCC
M00253 V\$CAP_01 0.902908 966 (+) NCANNNNN ACAGTTCC
M00279 V\$MIF1_01 0.759698 966 (-) NNGTTGCWWGGYACNGS ACAGTTCCCCAGGGACCT
M00280 V\$RFX1_01 0.782638 967 (+) NNGTNRCNWRGYAACNN CAGTTCCCCAGGGACCT
M00189 V\$AP2_Q6 0.835018 969 (+) MKCCSCNNGGCG GTTCCCCAGGGA
M00141 V\$LYF1_01 0.866343 970 (-) TTTGGGAGR TTCCCCAGG
M00189 V\$AP2_Q6 0.809513 970 (+) MKCCSCNNGGCG TTCCCCAGGGAC
M00189 V\$AP2_Q6 0.783778 970 (-) MKCCSCNNGGCG TTCCCCAGGGAC
M00083 V\$MZF1_01 0.902909 971 (-) NGNGGGGA TCCCCAGG
M00239 V\$T3R_01 0.769071 973 (-) SNNTRAGGTCACGSNN CCCAGGGACCTCTCTC
M00194 V\$NFKB_Q6 0.785862 975 (+) NGGGGAMTTTCNN CAGGGACCTCTCTC
M00179 V\$CREBP1_Q2 0.765331 976 (+) NSTGACGTMASN AGGGACCTCTCT
M00054 V\$NFKAPPAB_01 0.829213 977 (+) GGGAMTTYCC GGGACCTCTC
M00023 V\$HOX13_01 0.758847 978 (+) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GGACCTCTCTCTAATCAGCCCTCTGGCCCA
M00146 V\$HSF1_01 0.763293 978 (-) RGAANRTTCN GGACCTCTCT
M00272 V\$P53_02 0.796307 978 (+) NGRCWTGYCY GGACCTCTCT
M00063 V\$IRF2_01 0.703174 981 (-) GAAAAGYGAAASY CCTCTCTCTAATC
M00085 V\$ZID_01 0.790659 981 (+) NGGCTCYATCAYC CCTCTCTCTAATC
M00099 V\$S8_01 0.773957 983 (+) WNNANYYAATTANYNN TCTCTCTAATCAGCCC
M00141 V\$LYF1_01 0.889854 983 (-) TTTGGGAGR TCTCTCTAA
M00080 V\$EV11_03 0.776955 984 (-) AGATAAGATAA CTCTCTAATCA
M00082 V\$EV11_05 0.815099 984 (-) AGATAAGATAN CTCTCTAATCA
M00072 V\$CP2_01 0.797170 985 (+) GCNMNAMCMAG TCTCTAATCAG
M00099 V\$S8_01 0.784576 985 (-) WNNANYYAATTANYNN TCTCTAATCAGCCCTC
M00127 V\$GATA1_03 0.837335 985 (-) RNSNNGATAANNGN TCTCTAATCAGCCC
M00143 V\$PAX5_01 0.770239 985 (+) NCNNNRNKCANNNGNWGNRKRGCSSRSNN
TCTCTAATCAGCCCTCTGGCCAGGCAG
M00185 V\$NFY_Q6 0.788541 985 (+) TRRCCAATSRN TCTCTAATCAG
M00174 V\$AP1_Q6 0.765325 986 (-) NNTGACTCANN CTCTAATCAGC
M00075 V\$GATA1_01 0.851925 987 (-) SNNGATNNNN TCTAATCAGC
M00076 V\$GATA2_01 0.802887 987 (-) NNGATRNNN TCTAATCAGC
M00077 V\$GATA3_01 0.856447 987 (-) NNGATARNG TCTAATCAG
M00200 V\$CAAT_C 0.713450 987 (+) ACCAATCANCNNGCYYSNCNCWNNT TCTAATCAGCCCTCTGGCCAGGCA
M00255 V\$GC_01 0.816512 988 (-) NRGGGGCGGGGCKN CTAATCAGCCCTCT
M00008 V\$SP1_01 0.831257 990 (-) GRGGCRGGGW AATCAGCCCT
M00221 V\$SREBP1_02 0.737616 990 (+) KATCACCCAC AATCAGCCCTC
M00134 V\$HNF4_01 0.807623 991 (-) NNNRGGNCAAAGKTCANN ATCAGCCCTCTGGCCAGG
M00175 V\$AP4_Q5 0.808215 991 (+) NNCAGCTGNN ATCAGCCCTC
M00176 V\$AP4_Q6 0.785517 991 (+) CWCAGCTGGN ATCAGCCCTC
M00066 V\$TAL1ALPHA47_01 0.769910 992 (-) NNNAACAGATGKTNNN TCAGCCCTCTGGCCCA
M00070 V\$TAL1BETA1F2_01 0.766260 992 (-) NNNAACAGATGKTNNN TCAGCCCTCTGGCCCA
M00155 V\$ARP1_01 0.801221 992 (+) TGARCCYTTGAMCCYW TCAGCCCTCTGGCCCA
M00253 V\$CAP_01 0.963529 992 (+) NCANNNNN TCAGCCCT
M00075 V\$GATA1_01 0.774926 994 (-) SNNGATNNNN AGCCCTCTGG
M00189 V\$AP2_Q6 0.845588 994 (+) MKCCSCNNGGCG AGCCCTCTGGCC
M00189 V\$AP2_Q6 0.792969 994 (-) MKCCSCNNGGCG AGCCCTCTGGCC
M00184 V\$MYOD_Q6 0.784392 995 (+) NNCANCTGNY GCCCTCTGGC
M00187 V\$USF_Q6 0.798994 995 (-) GYCACGTGNC GCCCTCTGGC
M00254 V\$CAAT_01 0.808811 997 (-) NNNRRCCAATSA CCTCTGGCCAG
M00050 V\$E2F_02 0.743405 999 (+) TTTSGCGC TCTGGCCC
M00072 V\$CP2_01 0.791595 1000 (-) GCNMNAMCMAG CTGGCCAGGC
M00245 V\$EGR3_01 0.741250 1001 (-) NTGCGTGGGCGK TGGCCAGGCAG
M00007 V\$ELK1_01 0.809619 1002 (+) NNNACMGGAAGTNCNN GGCCAGGCAGTCAGT
M00254 V\$CAAT_01 0.822084 1004 (+) NNNRRCCAATSA CCCAGGCAGTCA
M00032 V\$CETSIP54_01 0.820478 1005 (+) NCMGGAWGYN CCAGGCAGTC

M00108 V\$NRF2_01 0.781977 1005 (+) ACCGGAAGNS CCAGGCAGTC
M00007 V\$ELK1_01 0.798263 1006 (+) NNNACMGGAAGTNCNN CAGGCAGTCAGTAAGT
M00008 V\$SP1_01 0.822480 1006 (+) GRGGCRGGGW CAGGCAGTCA
M00172 V\$AP1FJ_Q2 0.897161 1007 (-) RSTGACTNMNW AGGCAGTCAGT
M00173 V\$AP1_Q2 0.903953 1007 (-) RSTGACTNMNW AGGCAGTCAGT
M00174 V\$AP1_Q6 0.854833 1007 (-) NNTGACTCANN AGGCAGTCAGT
M00188 V\$AP1_Q4 0.897530 1007 (-) RSTGACTMANN AGGCAGTCAGT
M00037 V\$NFE2_01 0.826123 1008 (-) TGCTGASTCAY GGCAGTCAGTA
M00253 V\$CAP_01 0.886151 1009 (+) NCANNNNN GCAGTCAG
M00007 V\$ELK1_01 0.755177 1010 (+) NNNACMGGAAGTNCNN CAGTCAGTAAGTGTCT
M00188 V\$AP1_Q4 0.791095 1011 (-) RSTGACTMANN AGTCAGTAAGT
M00199 V\$AP1_C 0.802915 1012 (+) NTGASTCAG GTCAGTAAG
M00032 V\$CETS1P54_01 0.830798 1013 (+) NCMGGAWGYN TCAGTAAGTG
M00253 V\$CAP_01 0.896008 1013 (+) NCANNNNN TCAGTAAG
M00240 V\$NKX25_01 0.941233 1016 (+) TYAAGTG GTAAGTG
M00172 V\$AP1FJ_Q2 0.811041 1019 (+) RSTGACTNMNW AGTGTCTCCAA
M00173 V\$AP1_Q2 0.804978 1019 (+) RSTGACTNMNW AGTGTCTCCAA
M00115 V\$TAXCREB_02 0.642094 1020 (+) RTGACGCATAYCCCC GTGTCTCCAAACCTC
M00159 V\$CEBP_01 0.904700 1020 (-) NNTKTGGWNANNN GTGTCTCCAAACC
M00057 V\$COMP1_01 0.824192 1021 (-) NNTNWKGATTGRCNRSRANMRRNN TGTCTCCAAACCTCTTTCCTAATT
M00050 V\$E2F_02 0.745904 1023 (-) TTTSGCGC TCTCCAAA
M00141 V\$LYF1_01 0.852543 1023 (-) TTTGGGAGR TCTCCAAAC
M00004 V\$CMYB_01 0.762627 1024 (-) NCNRNNGRCNGTTGGKGG CTCCAAACCTCTTTCCTA
M00008 V\$SP1_01 0.852492 1025 (-) GRGGCRGGGW TCCAAACCTC
M00200 V\$CAAT_C 0.721084 1025 (+) ACCAATCANCNNGCYYSNCNCWNNT TCCAAACCTCTTTCCTAATTCTGGG
M00242 V\$PPARA_01 0.788796 1028 (-) CWRWCTAGGNCAAAGGTCA AAACCTCTTTCCTAATTCTG
M00201 V\$CEBP_C 0.886902 1029 (-) NGWNTKNKGAAKNSAYA AACCTCTTTCCTAATTCT
M00086 V\$IK1_01 0.801282 1032 (-) NNNTGGGAATRCC CTCTTTCCTAATT
M00109 V\$CEBPB_01 0.936355 1032 (-) RNRTKNNGMAAKNN CTCTTTCCTAATTC
M00116 V\$CEBPA_01 0.804067 1032 (-) NNATTRCNNAANN CTCTTTCCTAATTC
M00117 V\$CEBPB_02 0.854435 1032 (+) NKNTTGCNYAAYNN CTCTTTCCTAATTC
M00045 V\$E4BP4_01 0.770824 1033 (-) NRTTAYGTAAYN TCTTTCCTAATT
M00087 V\$IK2_01 0.894634 1033 (-) NNNYGGGAWNNN TCTTTCCTAATT
M00248 V\$OCT1_07 0.805173 1033 (+) TNTATGNTAATT TCTTTCCTAATT
M00157 V\$RORA2_01 0.771145 1034 (-) NWAWNTAGGTCAN CTTTCCTAATTCT
M00040 V\$CREBP1_01 0.749109 1035 (+) TTACGTAA TTTCTTAA
M00040 V\$CREBP1_01 0.746641 1035 (-) TTACGTAA TTTCTTAA
M00141 V\$LYF1_01 0.831587 1035 (-) TTTGGGAGR TTTCTTAA
M00098 V\$PAX2_01 0.753832 1038 (+) NNNNGTCANGNRTKANNNN CCTAATTCTGGGTTTGGGT
M00241 V\$NKX25_02 0.853885 1038 (+) CWTAATTG CCTAATTC
M00257 V\$RREB1_01 0.846532 1043 (-) CCCCACACMMCCCC TTCTGGGTTTGGGT
M00255 V\$GC_01 0.798873 1044 (+) NRGGGGCGGGGCGNK TCTGGGTTTGGGT
M00072 V\$CP2_01 0.951973 1045 (-) GCNMNAMCMAG CTGGGTTTGGG
M00189 V\$AP2_Q6 0.786075 1046 (-) MKCCCSCNGGCG TGGGTTTGGGT
M00008 V\$SP1_01 0.782843 1047 (+) GRGGCRGGGW GGGTTTGGGT
M00062 V\$IRF1_01 0.747770 1047 (-) SAAAAGYGAAACC GGGTTTGGGTTTG
M00257 V\$RREB1_01 0.817704 1047 (-) CCCCACACMMCCCC GGGTTTGGGTTTGG
M00062 V\$IRF1_01 0.800186 1048 (-) SAAAAGYGAAACC GGTTTGGGTTTGG
M00063 V\$IRF2_01 0.754226 1048 (-) GAAAAGYGAAASY GGTTTGGGTTTGG
M00257 V\$RREB1_01 0.864338 1048 (-) CCCCACACMMCCCC GGTTTGGGTTTGGG
M00257 V\$RREB1_01 0.933526 1049 (-) CCCCACACMMCCCC GTTTGGGTTTGGGG
M00072 V\$CP2_01 0.804889 1050 (-) GCNMNAMCMAG TTTGGGTTTGG
M00257 V\$RREB1_01 0.828048 1050 (-) CCCCACACMMCCCC TTTGGGTTTGGGGG
M00072 V\$CP2_01 0.852916 1051 (-) GCNMNAMCMAG TTGGGTTTGGG
M00235 V\$AHRARNT_01 0.771639 1051 (+) KNNKNNTYGCGTGCMs TTGGGTTTGGGGGTAG
M00257 V\$RREB1_01 0.802611 1051 (-) CCCCACACMMCCCC TTGGGTTTGGGGGT
M00084 V\$MZF1_02 0.845789 1053 (+) KNNNKAGGGGNAA GGGTTTGGGGGTA
M00084 V\$MZF1_02 0.859535 1054 (+) KNNNKAGGGGNAA GGTTTGGGGGTAG
M00189 V\$AP2_Q6 0.781020 1054 (-) MKCCCSCNGGCG GGTTTGGGGGTA
M00257 V\$RREB1_01 0.814143 1055 (-) CCCCACACMMCCCC GTTTGGGGGTAGGG
M00050 V\$E2F_02 0.808109 1056 (+) TTTSGCGC TTTGGGGG

M00139 V\$AHR_01 0.784038 1056 (+) CYYCNRSTNGCGTGASW TTTGGGGGTAGGGTTAGT
M00141 V\$LYF1_01 0.859954 1056 (+) TTTGGGAGR TTTGGGGGT
M00257 V\$RREB1_01 0.818382 1056 (-) CCCCCAACMMCCCC TTTGGGGGTAGGGT
M00115 V\$TAXCREB_02 0.628004 1058 (-) RTGACGCATAYCCCC TGGGGGTAGGGTTAG
M00196 V\$SP1_Q6 0.813519 1058 (+) NGGGGGCGGGGYN TGGGGGTAGGGTT
M00255 V\$GC_01 0.906173 1058 (+) NRGGGGCGGGGCK TGGGGGTAGGGTTA
M00115 V\$TAXCREB_02 0.657372 1059 (-) RTGACGCATAYCCCC GGGGGTAGGGTTAGT
M00008 V\$SP1_01 0.924689 1060 (+) GRGGCRGGGW GGGGTAGGGT
M00084 V\$MZF1_02 0.863784 1060 (+) KNNNKAGGGGNAA GGGGTAGGGTTAG
M00008 V\$SP1_01 0.803228 1064 (+) GRGGCRGGGW TAGGGTTAGT
M00023 V\$HOX13_01 0.747011 1066 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
GGGTAGTACCGGTATGGAAGCAGTGGGGG
M00032 V\$CETS1P54_01 0.815318 1070 (-) NCMGGAWGYN TAGTACCGGT
M00003 V\$VMYB_01 0.786361 1071 (+) AAYAACGGNN AGTACCGGTA
M00227 V\$VMYB_02 0.807160 1071 (+) NSYAACGGN AGTACCGGT
M00059 V\$YY1_01 0.778178 1072 (-) NNNNNCCATNTWNNNNWN GTACCGGTATGGAAGCA
M00107 V\$E2_01 0.769896 1072 (-) NNACCRNNANCGGTRN GTACCGGTATGGAAGC
M00181 V\$E2_Q6 0.793080 1072 (-) NNACCRNNANCGGTRN GTACCGGTATGGAAGC
M00227 V\$VMYB_02 0.811673 1074 (-) NSYAACGGN ACCGGTATG
M00008 V\$SP1_01 0.786240 1075 (+) GRGGCRGGGW CCGGTATGGA
M00278 V\$LMO2COM_02 0.794811 1075 (+) NMGATANS GCGGTATGG
M00025 V\$ELK1_02 0.780533 1076 (+) NNNNCCGGAARYNN CCGGTATGGAAGCAG
M00045 V\$E4BP4_01 0.763846 1076 (+) NRTTAYGTAAYN CCGGTATGGAAGC
M00004 V\$CMYB_01 0.746586 1079 (+) NCNRNNGRCNGTTGGKGG TATGGAAGCAGTGGGGGA
M00032 V\$CETS1P54_01 0.845464 1079 (+) NCMGGAWGYN TATGGAAGCA
M00264 V\$STAF_02 0.783350 1079 (-) MNTTCCCAKMATKCMWNGCRN TATGGAAGCAGTGGGGGAAAT
M00005 V\$AP4_01 0.756484 1082 (+) WGARYCAGCTGYGGNCKN GGAAGCAGTGGGGGAAAT
M00033 V\$P300_01 0.826858 1082 (+) NNNRGGAGTNNNS GGAAGCAGTGGGGG
M00175 V\$AP4_Q5 0.788357 1082 (+) NNCAGCTGNN GGAAGCAGTG
M00187 V\$USF_Q6 0.806262 1084 (-) GYCACGTGNC AAGCAGTGGG
M00242 V\$PPARA_01 0.737383 1084 (+) CWRWCTAGGNCAAAGGTCA AAGCAGTGGGGGAAATTTAA
M00175 V\$AP4_Q5 0.799238 1085 (+) NNCAGCTGNN AGCAGTGGGG
M00176 V\$AP4_Q6 0.790028 1085 (+) CWCAGCTGGN AGCAGTGGGG
M00183 V\$MYB_Q6 0.832365 1085 (-) NNNAAACKGNC AGCAGTGGGG
M00084 V\$MZF1_02 0.874531 1086 (+) KNNNKAGGGGNAA GCAGTGGGGGAAA
M00227 V\$VMYB_02 0.793622 1086 (-) NSYAACGGN GCAGTGGGG
M00083 V\$MZF1_01 0.897242 1088 (+) NGNGGGGA AGTGGGGG
M00200 V\$CAAT_C 0.775671 1088 (-) ACCAATCANCNNGCYYSNCNCWNNT AGTGGGGGAAATTTAAAGTTTTGGT
M00008 V\$SP1_01 0.785957 1089 (+) GRGGCRGGGW GTGGGGGAAA
M00083 V\$MZF1_01 0.920665 1089 (+) NGNGGGGA GTGGGGGA
M00086 V\$IK1_01 0.794071 1089 (+) NNNTGGGAATRCC GTGGGGGAAATTT
M00180 V\$E2F_Q6 0.763163 1089 (+) NNGCGCGAAANTK GTGGGGGAAATTT
M00050 V\$E2F_02 0.828381 1091 (-) TTTSGCGC GGGGGAAA
M00232 V\$MEF2_03 0.781135 1091 (-) NNNNNWKCTAWAAATAGMNNNN GGGGGAAATTTAAAGTTTTGGT
M00194 V\$NFKB_Q6 0.788350 1092 (+) NGGGGAMTTTCCNN GGGGAAATTTAAAG
M00208 V\$NFKB_C 0.763180 1092 (+) NGGGACTTTCCA GGGGAAATTTAA
M00053 V\$CREL_01 0.837875 1093 (+) SGRNWTTCC GGGAATTTAA
M00133 V\$TST1_01 0.908807 1093 (+) NNKGAWTWANANTNN GGGAATTTAAAGTT
M00208 V\$NFKB_C 0.759623 1093 (+) NGGGACTTTCCA GGGAATTTAAAGTT
M00258 V\$ISRE_01 0.758914 1093 (-) CAGTTTCWCTTTYCC GGGAATTTAAAGTT
M00053 V\$CREL_01 0.820634 1094 (-) SGRNWTTCC GGGAATTTAA
M00062 V\$IRF1_01 0.756320 1094 (+) SAAAAGYGAAACC GGGAATTTAAAGT
M00063 V\$IRF2_01 0.752156 1094 (+) GAAAAGYGAAASY GGGAATTTAAAGT
M00133 V\$TST1_01 0.871005 1094 (+) NNKGAWTWANANTNN GGGAATTTAAAGTTT
M00134 V\$HNF4_01 0.773820 1094 (+) NNNRGGNCAAAGKTCANN GGGAATTTAAAGTTTTGGT
M00158 V\$COUP_01 0.808170 1094 (+) TGAMCTTTGMMCYT GGGAATTTAAAGTT
M00162 V\$OCT1_06 0.834375 1094 (+) CWNWTKWSATRYN GGGAATTTAAAGTT
M00162 V\$OCT1_06 0.834375 1095 (+) CWNWTKWSATRYN GAAATTTAAAGTTT
M00162 V\$OCT1_06 0.885547 1095 (-) CWNWTKWSATRYN GAAATTTAAAGTTT
M00162 V\$OCT1_06 0.813672 1096 (-) CWNWTKWSATRYN AAATTTAAAGTTTT
M00062 V\$IRF1_01 0.742007 1098 (-) SAAAAGYGAAACC ATTTAAAGTTTTG

M00100 V\$CDXA_01 0.937224 1098 (+) MTTTATR ATTAAAG
M00212 V\$POLY_C 0.767810 1098 (+) CAATAAAACCCYYYKCTN ATTAAAGTTTGGTCTT
M00238 V\$BARBIE_01 0.803078 1098 (+) ATNNAAAGCNGRNGG ATTAAAGTTTGGT
M00023 V\$SHOX13_01 0.723816 1099 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TTTAAAGTTTGGTCTTGGGGGAGGATGGA
M00100 V\$CDXA_01 0.918097 1099 (-) MTTTATR TTAAAG
M00160 V\$SRX_02 0.799178 1099 (-) NWWAACAANWANN TTAAAGTTTGG
M00129 V\$HFH1_01 0.802867 1101 (+) NAWTGTTTATWT TAAAGTTTGGT
M00062 V\$IRF1_01 0.820446 1104 (-) SAAAAGYGAAACC AGTTTGGTCTTG
M00063 V\$IRF2_01 0.746292 1104 (-) GAAAAGYGAAASY AGTTTGGTCTTG
M00257 V\$RREB1_01 0.789384 1105 (-) CCCCACMMCCCC GTTTGGTCTTGGG
M00257 V\$RREB1_01 0.817026 1106 (-) CCCCACMMCCCC TTTTGGTCTTGGG
M00261 V\$OLF1_01 0.775255 1106 (-) NNCNANTCCYNGRGARNKGN TTTGGTCTTGGGGGAGGATGG
M00072 V\$CP2_01 0.838336 1107 (-) GCNMNAMCMAG TTTGGTCTTGG
M00098 V\$PAX2_01 0.789803 1107 (+) NNNNGTCANGNRTKANNNN TTTGGTCTTGGGGGAGGAT
M00211 V\$PADS_C 0.856603 1107 (+) NGTGGTCTC TTTGGTCTT
M00271 V\$AMLI_01 0.853077 1107 (+) TGTGGT TTTGGT
M00189 V\$AP2_Q6 0.884881 1111 (-) MKCCCSCNGGCG GTCTTGGGGGAG
M00262 V\$STAF_01 0.759393 1111 (-) NTTWCCCANMATGCAYYRCGY GTCTTGGGGGAGGATGGATGGA
M00141 V\$LYF1_01 0.820598 1112 (+) TTTGGGAGR TCTTGGGGG
M00264 V\$STAF_02 0.796294 1112 (-) MNTTCCCAKMATKCMWNGCRN TCTTGGGGGAGGATGGATGGA
M00072 V\$CP2_01 0.842624 1113 (-) GCNMNAMCMAG CTTGGGGGAGG
M00141 V\$LYF1_01 0.911832 1113 (+) TTTGGGAGR CTTGGGGGA
M00083 V\$MZF1_01 0.895731 1114 (+) NGNGGGGA TTGGGGGA
M00141 V\$LYF1_01 0.824176 1114 (+) TTTGGGAGR TTGGGGGAG
M00008 V\$SP1_01 0.794734 1115 (+) GRGGCRGGGW TGGGGGGAGGA
M00115 V\$TAXCREB_02 0.617324 1115 (-) RTGACGCATAYCCCC TGGGGGAGGATGGAT
M00196 V\$SP1_Q6 0.834561 1115 (+) NGGGGGCGGGGYN TGGGGGGAGGATGG
M00255 V\$GC_01 0.852278 1115 (+) NRGGGGCGGGGCKN TGGGGGGAGGATGGA
M00008 V\$SP1_01 0.890430 1116 (+) GRGGCRGGGW GGGGGAGGAT
M00084 V\$MZF1_02 0.841540 1116 (+) KNNNKAGGGGNAA GGGGGAGGATGGA
M00114 V\$TAXCREB_01 0.723838 1116 (+) GGGGGTTGACGYANA GGGGGAGGATGGATG
M00083 V\$MZF1_01 0.865130 1117 (+) NGNGGGGA GGGGAGGA
M00124 V\$PBX1_02 0.740874 1118 (-) NNMATCAATCAANNW GGGAGGATGGATGGA
M00127 V\$GATA1_03 0.788829 1118 (+) RNSNNGATAANNNGN GGGAGGATGGATGG
M00196 V\$SP1_Q6 0.770910 1118 (+) NGGGGGCGGGGYN GGGAGGATGGATG
M00262 V\$STAF_01 0.735694 1118 (-) NTTWCCCANMATGCAYYRCGY GGGAGGATGGATGGAGGTGAAA
M00059 V\$YY1_01 0.822412 1120 (-) NNNNNCCATNTWNNNNWN GAGGATGGATGGAGGTG
M00075 V\$GATA1_01 0.878578 1120 (+) SNNGATNNNN GAGGATGGAT
M00076 V\$GATA2_01 0.891295 1120 (+) NNNGATRNNN GAGGATGGAT
M00104 V\$CDPCR1_01 0.795506 1121 (-) NATCGATCGS AGGATGGATG
M00106 V\$CDPCR3HD_01 0.880911 1121 (-) NATYGATSSS AGGATGGATG
M00124 V\$PBX1_02 0.780333 1122 (-) NNMATCAATCAANNW GGATGGATGGAGGTG
M00104 V\$CDPCR1_01 0.841420 1123 (+) NATCGATCGS GATGGATGGA
M00106 V\$CDPCR3HD_01 0.868512 1123 (+) NATYGATSSS GATGGATGGA
M00255 V\$GC_01 0.807937 1123 (+) NRGGGGCGGGGCKN GATGGATGGAGGTG
M00075 V\$GATA1_01 0.789240 1124 (+) SNNGATNNNN ATGGATGGAG
M00189 V\$AP2_Q6 0.791820 1125 (-) MKCCCSCNGGCG TGATGGAGGTG
M00084 V\$MZF1_02 0.843789 1126 (+) KNNNKAGGGGNAA GGATGGAGGTGAA
M00156 V\$RORA1_01 0.799322 1126 (+) NWAANNAGGTCAN GGATGGAGGTGAA
M00084 V\$MZF1_02 0.813047 1127 (+) KNNNKAGGGGNAA GATGGAGGTGAAA
M00239 V\$T3R_01 0.794814 1127 (+) SNNTRAGGTCACGSNN GATGGAGGTGAAAGTA
M00073 V\$DELTAEF1_01 0.887589 1129 (-) NNNCACCTNAN TGGAGGTGAAA
M00109 V\$CEBPB_01 0.822189 1129 (+) RNRTKNNGMAAKNN TGGAGGTGAAAGTA
M00004 V\$CMYB_01 0.775851 1130 (+) NCNRNNGRCNGTTGGKGG GGAGGTGAAAGTAGGGGG
M00083 V\$MZF1_01 0.845108 1130 (+) NGNGGGGA GGAGGTGA
M00127 V\$GATA1_03 0.797158 1131 (+) RNSNNGATAANNNGN GAGGTGAAAGTAGG
M00238 V\$BARBIE_01 0.805766 1133 (+) ATNNAAAGCNGRNGG GGTGAAAGTAGGGGG
M00084 V\$MZF1_02 0.814796 1137 (+) KNNNKAGGGGNAA AAAGTAGGGGGGT
M00212 V\$POLY_C 0.791557 1138 (-) CAATAAAACCCYYYKCTN AAGTAGGGGGGTATTTTC
M00008 V\$SP1_01 0.782843 1140 (+) GRGGCRGGGW GTAGGGGGGT

M00141 V\$LYF1_01 0.869921 1140 (+) TTTGGGAGR GTAGGGGGG
M00221 V\$SREBP1_02 0.720902 1140 (-) KATCACCCAC GTAGGGGGGTA
M00008 V\$SP1_01 0.841450 1141 (+) GRGGCRGGGW TAGGGGGGTA
M00255 V\$GC_01 0.833660 1141 (+) NRGGGGCGGGGCKN TAGGGGGGTATTTT
M00008 V\$SP1_01 0.841166 1142 (+) GRGGCRGGGW AGGGGGGTAT
M00008 V\$SP1_01 0.829841 1143 (+) GRGGCRGGGW GGGGGGTATT
M00255 V\$GC_01 0.822391 1143 (+) NRGGGGCGGGGCKN GGGGGGTATTTTCT
M00194 V\$NFKB_Q6 0.804519 1144 (+) NGGGGAMTTTCCNN GGGGGTATTTTCTA
M00008 V\$SP1_01 0.810872 1145 (+) GRGGCRGGGW GGGGTATTTT
M00194 V\$NFKB_Q6 0.802446 1145 (+) NGGGGAMTTTCCNN GGGGTATTTTCTAG
M00051 V\$NFKAPPAB50_01 0.752999 1146 (+) GGGGATYCCC GGGTATTTTC
M00052 V\$NFKAPPAB65_01 0.790419 1146 (+) GGGRATTTCC GGGTATTTTC
M00053 V\$CREL_01 0.905729 1146 (+) SGRNWTTC GGGTATTTTC
M00054 V\$NFKAPPAB_01 0.812984 1146 (+) GGGAMTTYCC GGGTATTTTC
M00208 V\$NFKB_C 0.789749 1146 (+) NGGGACTTTCCA GGGTATTTTCTA
M00261 V\$OLF1_01 0.786870 1146 (-) NNCNANTCCYNGRGARNKGN GGGTATTTTCTAGGAAGTTAA
M00054 V\$NFKAPPAB_01 0.782022 1147 (+) GGGAMTTYCC GGTATTTTCT
M00146 V\$HSF1_01 0.827491 1147 (+) RGAANRTTCN GGTATTTTCT
M00146 V\$HSF1_01 0.842064 1147 (-) RGAANRTTCN GGTATTTTCT
M00147 V\$HSF2_01 0.794455 1147 (+) NGAANNWTCK GGTATTTTCT
M00147 V\$HSF2_01 0.871349 1147 (-) NGAANNWTCK GGTATTTTCT
M00088 V\$IK3_01 0.817871 1153 (+) TNYTGGAATACC TTCTAGGAAGTTT
M00223 V\$STAT_01 0.850769 1153 (+) TTCCCRKAA TTCTAGGAA
M00223 V\$STAT_01 0.956138 1153 (-) TTCCCRKAA TTCTAGGAA
M00141 V\$LYF1_01 0.912599 1154 (+) TTTGGGAGR TCTAGGAAG
M00255 V\$GC_01 0.786624 1154 (+) NRGGGGCGGGGCKN TCTAGGAAGTTAA
M00033 V\$P300_01 0.815951 1155 (+) NNNRGGAGTNNNS CTAGGAAGTTAAG
M00108 V\$NRF2_01 0.773983 1155 (+) ACCGGAAGNS CTAGGAAGTT
M00134 V\$HNF4_01 0.820780 1158 (+) NNNRGGNCAAAGKTCANN GGAAGTTTAAGGGTCTCAG
M00183 V\$MYB_Q6 0.880083 1158 (-) NNNAACKGNC GGAAGTTAA
M00148 V\$SRY_01 0.908527 1159 (-) AAACWAM GAAGTTT
M00155 V\$ARP1_01 0.818962 1160 (-) TGARCCYTTGAMCCYW AAGTTTAAGGGTCTCA
M00158 V\$COUP_01 0.861976 1160 (-) TGAMCTTTGMMCYT AAGTTTAAGGGTCT
M00156 V\$RORA1_01 0.789881 1162 (+) NWAANNAGGTCAN GTTTAAGGGTCTC
M00227 V\$VMYB_02 0.812876 1163 (+) NSYAACGGN TTTAAGGGT
M00058 V\$HEN1_02 0.798492 1166 (+) NNGGGNCGCAGCTGCGNCCCNN AAGGGTCTCAGCTTTTTCTTTT
M00058 V\$HEN1_02 0.736851 1166 (-) NNGGGNCGCAGCTGCGNCCCNN AAGGGTCTCAGCTTTTTCTTTT
M00068 V\$HEN1_01 0.804686 1166 (+) NNNGGNCNCAGCTGCGNCCCNN AAGGGTCTCAGCTTTTTCTTTT
M00068 V\$HEN1_01 0.770994 1166 (-) NNNGGNCNCAGCTGCGNCCCNN AAGGGTCTCAGCTTTTTCTTTT
M00005 V\$AP4_01 0.778530 1167 (-) WGARYCAGCTGYGGNCKN AGGGTCTCAGCTTTTTCT
M00174 V\$AP1_Q6 0.776232 1167 (-) NNTGACTCANN AGGGTCTCAGC
M00037 V\$NFE2_01 0.847030 1168 (-) TGCTGASTCAY GGGTCTCAGCT
M00199 V\$AP1_C 0.773761 1168 (+) NTGASTCAG GGGTCTCAG
M00063 V\$IRF2_01 0.721283 1169 (-) GAAAAGYGAAASY GGTCTCAGCTTTT
M00238 V\$BARBIE_01 0.848278 1170 (-) ATNNAAAGCNGRNGG GTCTCAGCTTTTTCT
M00175 V\$AP4_Q5 0.872416 1172 (+) NNCAGCTGNN CTCAGCTTTT
M00175 V\$AP4_Q5 0.812840 1172 (-) NNCAGCTGNN CTCAGCTTTT
M00176 V\$AP4_Q6 0.862942 1172 (+) CWCAGCTGGN CTCAGCTTTT
M00242 V\$PPARA_01 0.734310 1173 (-) CWRAWCTAGGNCAAAGGTCA TCAGCTTTTTCTTTTCTCTC
M00253 V\$CAP_01 0.960079 1173 (+) NCANNNNN TCAGCTTT
M00146 V\$HSF1_01 0.799134 1175 (-) RGAANRTTCN AGCTTTTTCT
M00147 V\$HSF2_01 0.798891 1175 (+) NGAANNWTCK AGCTTTTTCT
M00147 V\$HSF2_01 0.853974 1175 (-) NGAANNWTCK AGCTTTTTCT
M00062 V\$IRF1_01 0.859108 1176 (-) SAAAAGYGAAACC GCTTTTTCTTTTC
M00063 V\$IRF2_01 0.849086 1176 (-) GAAAAGYGAAASY GCTTTTTCTTTTC
M00160 V\$SRY_02 0.821491 1177 (-) NWWAACA AWANN CTTTTCTTTTC
M00258 V\$ISRE_01 0.738962 1177 (+) CAGTTTCWCTTTYCC CTTTTCTTTTCTCT
M00269 V\$XFD3_01 0.829183 1178 (-) WNWGTMAACAWWMW TTTTCTTTTCTCT
M00011 V\$EV11_06 0.775619 1179 (-) ACAAGATAA TTTTCTTTT
M00079 V\$EV11_02 0.822488 1179 (-) AGAYAAGATAA TTTTCTTTTCT
M00080 V\$EV11_03 0.811523 1179 (-) AGATAAGATAA TTTTCTTTTCT

M00082 V\$EV11_05 0.848155 1179 (-) AGATAAGATAN TTTCTTTTCT
M00127 V\$GATA1_03 0.810632 1180 (-) RNSNNGATAANNNGN TTTCTTTTCTCTCT
M00148 V\$SR1_01 0.960465 1180 (-) AAACWAM TTTCTTT
M00080 V\$EV11_03 0.716461 1181 (-) AGATAAGATAA TTCTTTTCTCT
M00127 V\$GATA1_03 0.782460 1182 (-) RNSNNGATAANNNGN TCTTTTCTCTCTCC
M00050 V\$E2F_02 0.748403 1185 (+) TTSGCGC TTTCTCTC
M00144 V\$PAX5_02 0.757295 1185 (-) RRMSWGAWYCTNRAGCGKRACSRYSNM
TTTCTCTCTCCTCTTCAGGATCATCTTC
M00033 V\$P300_01 0.800273 1186 (-) NNNRGGAGTNNNS TTCTCTCTCCTCTT
M00084 V\$MZF1_02 0.829043 1189 (-) KNNNKAGGGGNA TCTCTCCTCTTCA
M00261 V\$OLF1_01 0.767163 1190 (-) NNCNANTCCCYNGRGARNNKGN CTCTCCTCTTCAGGATCATCTT
M00085 V\$ZID_01 0.772354 1194 (+) NGGCTCYATCAYC CCTCTTCAGGATC
M00189 V\$AP2_Q6 0.809743 1194 (-) MKCCCSCNGGCG CCTCTTCAGGAT
M00035 V\$VMAF_01 0.780548 1195 (-) NNNTGCTGACTCAGCANN CTCTTCAGGATCATCTTCT
M00108 V\$NRF2_01 0.784157 1195 (-) ACCGGAAGNS CTCTTCAGGA
M00156 V\$RORA1_01 0.791092 1196 (+) NWAOWNAGGTCAN TCTTCAGGATCAT
M00074 V\$CETS1P54_02 0.887762 1197 (+) NNAMMGAWRWNN CTTCAGGATCATC
M00086 V\$IK1_01 0.790598 1197 (+) NNNTGGGAATRCC CTTCAGGATCATC
M00032 V\$CETS1P54_01 0.813417 1199 (+) NCMGGAWGYN TCAGGATCAT
M00173 V\$AP1_Q2 0.790044 1199 (-) RSTGACTNMNW TCAGGATCATC
M00059 V\$YY1_01 0.774574 1200 (+) NNNNNCCATNTWNNNWN CAGGATCATCTTCTCGA
M00075 V\$GATA1_01 0.791214 1200 (+) SNNGATNNNN CAGGATCATC
M00075 V\$GATA1_01 0.877591 1200 (-) SNNGATNNNN CAGGATCATC
M00076 V\$GATA2_01 0.834912 1200 (+) NNNGATRNNN CAGGATCATC
M00076 V\$GATA2_01 0.857465 1200 (-) NNNGATRNNN CAGGATCATC
M00066 V\$TAL1ALPHA47_01 0.764656 1201 (-) NNNAACAGATGKTNNN AGGATCATCTTCTCGA
M00146 V\$HSF1_01 0.792438 1201 (-) RGAANRTTCN AGGATCATCT
M00147 V\$HSF2_01 0.874677 1201 (+) NGAANNWTCK AGGATCATCT
M00075 V\$GATA1_01 0.842547 1203 (-) SNNGATNNNN GATCATCTTC
M00076 V\$GATA2_01 0.861976 1203 (-) NNNGATRNNN GATCATCTTC
M00011 V\$EV11_06 0.777076 1205 (-) ACAAGATAA TCATCTTCT
M00079 V\$EV11_02 0.776830 1205 (-) AGAYAAGATAA TCATCTTCTCG
M00080 V\$EV11_03 0.720576 1205 (-) AGATAAGATAA TCATCTTCTCG
M00253 V\$CAP_01 0.936915 1205 (+) NCANNNNN TCATCTTC
M00141 V\$LYF1_01 0.864298 1209 (-) TTTGGGAGR CTCTCGAA
M00139 V\$AHR_01 0.788581 1212 (+) CYYCNRRSTNGCGTGASW CTCGAACCCCGAGTGACA
M00261 V\$OLF1_01 0.782955 1212 (-) NNCNANTCCCYNGRGARNNKGN CTCGAACCCCGAGTGACAAGCC
M00098 V\$PAX2_01 0.770723 1214 (-) NNNNGTCANGNRTKANNNN CGAACCCCGAGTGACAAGC
M00237 V\$AHRARNT_02 0.751181 1215 (+) GRGKATYGCGTGMSWNSCC GAACCCCGAGTGACAAGCC
M00123 V\$MYCMAX_02 0.795114 1216 (+) NANCACGTGNNW AACCCCGAGTGA
M00055 V\$NMYC_01 0.761557 1218 (+) NNNCACGTGNNN CCCCAGGTGACA
M00187 V\$USF_Q6 0.876992 1219 (-) GYCACGTGNC CCCGAGTGAC
M00172 V\$AP1FJ_Q2 0.823659 1223 (+) RSTGACTNMNW AGTGACAAGCC
M00173 V\$AP1_Q2 0.798829 1223 (+) RSTGACTNMNW AGTGACAAGCC
M00174 V\$AP1_Q6 0.773599 1223 (+) NNTGACTCANN AGTGACAAGCC
M00188 V\$AP1_Q4 0.817017 1223 (+) RSTGACTMANN AGTGACAAGCC
M00203 V\$GATA_C 0.832246 1225 (+) NGATAAGNMNN TGACAAGCCTG
M00272 V\$P53_02 0.936108 1225 (+) NGRCWTGYCY TGACAAGCCT
M00272 V\$P53_02 0.935815 1225 (-) NGRCWTGYCY TGACAAGCCT
M00008 V\$SP1_01 0.797282 1226 (-) GRGGCRGGGW GACAAGCCTG
M00007 V\$ELK1_01 0.798263 1228 (+) NNNACMGGAAGTNCNN CAAGCCTGTAGCCCAT
M00189 V\$AP2_Q6 0.780790 1230 (+) MKCCCSCNGGCG AGCCTGTAGCCC
M00192 V\$GR_Q6 0.770647 1232 (+) NNNNNNCNNTNTGTNCTNN CCTGTAGCCCATGTTGTAG
M00069 V\$YY1_02 0.763120 1234 (+) NNNCGGCCATCTTGNCTSNW TGTAGCCCATGTTGTAGGTA
M00162 V\$OCT1_06 0.847266 1234 (-) CWNATKWSATRYN TGTAGCCCATGTTG
M00059 V\$YY1_01 0.797837 1235 (+) NNNNNCCATNTWNNNWN GTAGCCCATGTTGTAGG
M00122 V\$USF_02 0.776569 1235 (+) NNRNCACGTGNYNN GTAGCCCATGTTGT
M00122 V\$USF_02 0.776569 1235 (-) NNRNCACGTGNYNN GTAGCCCATGTTGT
M00001 V\$MYOD_01 0.848228 1236 (-) SRACAGGTGKYG TAGCCCATGTTG
M00185 V\$NFY_Q6 0.807811 1236 (+) TRRCCAATSRN TAGCCCATGTT
M00076 V\$GATA2_01 0.790708 1238 (+) NNNGATRNNN GCCCATGTTG

M00076 V\$GATA2_01 0.806495 1238 (-) NNNGATRNNN GCCCATGTTG
M00123 V\$MYCMAX_02 0.793013 1238 (-) NANCACGTGNNW GCCCATGTTGTA
M00217 V\$USF_C 0.839651 1238 (+) NCACGTGN GCCCATGT
M00242 V\$PPARA_01 0.750502 1242 (+) CWRWCTAGGNCAAAGGTCA ATGTTGTAGGTAAGAGCTCT
M00126 V\$GATA1_02 0.775000 1245 (+) NNNNGATANKGNN TTGTAGGTAAGAGC
M00073 V\$DELTAEF1_01 0.881741 1246 (-) NNNCACCTNAN TGTAAGGTAAGA
M00040 V\$CREBP1_01 0.746641 1247 (+) TTACGTAA GTAGGTAA
M00040 V\$CREBP1_01 0.795723 1247 (-) TTACGTAA GTAGGTAA
M00175 V\$AP4_Q5 0.806311 1253 (+) NNCAGCTGNN AAGAGCTCTG
M00175 V\$AP4_Q5 0.828074 1253 (-) NNCAGCTGNN AAGAGCTCTG
M00176 V\$AP4_Q6 0.780005 1253 (+) CWCAGCTGGN AAGAGCTCTG
M00176 V\$AP4_Q6 0.823603 1253 (-) CWCAGCTGGN AAGAGCTCTG
M00176 V\$AP4_Q6 0.772989 1255 (-) CWCAGCTGGN GAGCTCTGAG
M00189 V\$AP2_Q6 0.785386 1256 (-) MKCCCSCNGGCG AGCTCTGAGGAT
M00007 V\$ELK1_01 0.784903 1258 (+) NNNACMGGAAGTNCNN CTCTGAGGATGTGTCT
M00017 V\$ATF_01 0.750328 1258 (+) CNSTGACGTNNNYC CTCTGAGGATGTGT
M00074 V\$CETS1P54_02 0.853076 1259 (+) NNAMMGAWRWNN TCTGAGGATGTGT
M00115 V\$TAXCREB_02 0.643874 1260 (-) RTGACGCATAYCCCC CTGAGGATGTGTCTT
M00255 V\$GC_01 0.783195 1260 (+) NRGGGGCGGGGCGNK CTGAGGATGTGTCT
M00032 V\$CETS1P54_01 0.820206 1261 (+) NCMGGAWGYN TGAGGATGTG
M00122 V\$USF_02 0.791175 1261 (+) NNRNCACGTGNYNN TGAGGATGTGTCTT
M00122 V\$USF_02 0.791175 1261 (-) NNRNCACGTGNYNN TGAGGATGTGTCTT
M00255 V\$GC_01 0.830475 1261 (+) NRGGGGCGGGGCGNK TGAGGATGTGTCTT
M00001 V\$MYOD_01 0.832480 1262 (+) SRACAGGTGKYG GAGGATGTGTCT
M00008 V\$SP1_01 0.790770 1262 (+) GRGGCRGGGW GAGGATGTGT
M00075 V\$GATA1_01 0.883514 1262 (+) SNNGATNNNN GAGGATGTGT
M00076 V\$GATA2_01 0.901218 1262 (+) NNNGATRNNN GAGGATGTGT
M00115 V\$TAXCREB_02 0.618807 1262 (-) RTGACGCATAYCCCC GAGGATGTGTCTTGG
M00123 V\$MYCMAX_02 0.782243 1262 (+) NANCACGTGNNW GAGGATGTGTCT
M00187 V\$USF_Q6 0.805703 1263 (-) GYCACGTGNC AGGATGTGTC
M00146 V\$HSF1_01 0.764868 1264 (+) RGAANRTTCN GGATGTGTCT
M00147 V\$HSF2_01 0.820333 1264 (+) NGAANNWTCK GGATGTGTCT
M00147 V\$HSF2_01 0.799261 1264 (-) NGAANNWTCK GGATGTGTCT
M00272 V\$P53_02 0.850821 1264 (+) NGRCWTGYCY GGATGTGTCT
M00155 V\$ARP1_01 0.753090 1267 (+) TGARCCYTTGAMCCYW TGTGTCTTGGAACCTG
M00201 V\$CEBP_C 0.800204 1267 (-) NGWNTKNKGAAKNSAYA TGTGTCTTGGAACCTGGA
M00264 V\$STAF_02 0.751581 1268 (-) MNTTCCCAKMATKCMWNGCRN GTGTCTTGGAACCTGGAGGGC
M00139 V\$AHR_01 0.764047 1269 (-) CYYCNRRSTNGCGTGASW TGTCTTGGAACCTGGAGG
M00223 V\$STAT_01 0.812957 1270 (+) TTCCCRKAA GTCTTGGA
M00236 V\$ARNT_01 0.770311 1272 (+) NNNNNCACGTGNNNNN CTTGGAACCTGGAGGG
M00200 V\$CAAT_C 0.722484 1276 (-) ACCAATCANCNNGCYYSNCNCWNT GAACTTGAGGGGCTAGGATTTGGGG
M00250 V\$GF1_01 0.804997 1280 (-) NNNNNNNAAATCASWGYNNNNNN TTGGAGGGCTAGGATTTGGGGATT
M00008 V\$SP1_01 0.802945 1284 (+) GRGGCRGGGW AGGGCTAGGA
M00257 V\$RREB1_01 0.786162 1287 (-) CCCCACMMCCCC GCTAGGATTTGGGG
M00075 V\$GATA1_01 0.814906 1289 (+) SNNGATNNNN TAGGATTTGG
M00076 V\$GATA2_01 0.863780 1289 (+) NNNGATRNNN TAGGATTTGG
M00115 V\$TAXCREB_02 0.614654 1289 (-) RTGACGCATAYCCCC TAGGATTTGGGGATT
M00077 V\$GATA3_01 0.843598 1290 (+) NNGATARNG AGGATTTGG
M00050 V\$E2F_02 0.745904 1294 (+) TTTSGCGC TTTGGGGA
M00083 V\$MZF1_01 0.917265 1294 (+) NGNGGGGA TTTGGGGA
M00086 V\$IK1_01 0.777778 1294 (+) NNNTGGGAATRCC TTTGGGGATTGAA
M00141 V\$LYF1_01 0.838998 1294 (+) TTTGGGAGR TTTGGGGAT
M00033 V\$P300_01 0.813565 1295 (+) NNNRGGAGTNNNS TTGGGGATTGAAGC
M00008 V\$SP1_01 0.832390 1296 (+) GRGGCRGGGW TGGGGATTGA
M00075 V\$GATA1_01 0.847976 1297 (+) SNNGATNNNN GGGGATTGAA
M00076 V\$GATA2_01 0.833559 1297 (+) NNNGATRNNN GGGGATTGAA
M00114 V\$TAXCREB_01 0.806667 1297 (+) GGGGGTTGACGYANA GGGGATTGAAGCCCC
M00249 V\$CHOP_01 0.874787 1297 (-) NNRTGCAATMCCC GGGGATTGAAGCC
M00077 V\$GATA3_01 0.845370 1298 (+) NNGATARNG GGGATTGAA
M00113 V\$CREB_02 0.789377 1299 (+) NNGNTGACGYNN GGATTGAAGCCC
M00106 V\$CDPCR3HD_01 0.844291 1300 (+) NATYGATSSS GATTGAAGCC

M00005 V\$AP4_01 0.750865 1305 (+) WGARYCAGCTGYGGN CNK AAGCCCGGCTGATGGTAG
M00069 V\$YY1_02 0.772760 1306 (-) NNNCGGCCATCTTG NCTSNW AGCCCGGCTGATGGTAGGCA
M00189 V\$AP2_Q6 0.848805 1306 (+) MKCCCSCNGGCG AGCCCGGCTGAT
M00262 V\$STAF_01 0.744653 1306 (-) NTTWCCCANMATGCAYYRCGNY AGCCCGGCTGATGGTAGGCAGA
M00066 V\$TAL1ALPHA E47_01 0.782727 1308 (+) NNNAACAGATGKTNNN CCCGGCTGATGGTAGG
M00070 V\$TAL1BETA IFT2_01 0.760366 1308 (+) NNNAACAGATGKTNNN CCCGGCTGATGGTAGG
M00175 V\$AP4_Q5 0.861534 1308 (-) NNCAGCTGNN CCCGGCTGAT
M00176 V\$AP4_Q6 0.846154 1308 (-) CWCAGCTGGN CCCGGCTGAT
M00002 V\$E47_01 0.803134 1309 (+) NSNGCAGGTGKNCNN CCGGCTGATGGTAGG
M00004 V\$CMYB_01 0.781921 1309 (+) NCNRNNGRCNGTTG KGG CCGGCTGATGGTAGGCAG
M00127 V\$GATA1_03 0.806957 1310 (+) RNSNNGATAANN GN CGGCTGATGGTAGG
M00184 V\$MYOD_Q6 0.819864 1311 (-) NNCANCTGNY GGCTGATGGT
M00075 V\$GATA1_01 0.928430 1312 (+) SNNGATNNNN GCTGATGGTA
M00076 V\$GATA2_01 0.884078 1312 (+) NNNGATRNNN GCTGATGGTA
M00077 V\$GATA3_01 0.844041 1313 (+) NNGATARNG CTGATGGTA
M00127 V\$GATA1_03 0.790544 1313 (+) RNSNNGATAANN GN CTGATGGTAGGCAG
M00115 V\$TAXCREB_02 0.631415 1315 (-) RTGACGCATAYCCCC GATGGTAGGCAGAAC
M00008 V\$SP1_01 0.793318 1316 (+) GRGGCRGGGW ATGGTAGGCA
M00084 V\$MZF1_02 0.810797 1316 (+) KNNNKAGGGGNAA ATGGTAGGCAGAA
M00196 V\$SP1_Q6 0.755129 1318 (+) NGGGGGCGGGGYN GGTAGGCAGAACT
M00255 V\$GC_01 0.888535 1318 (+) NRGGGGCGGGG CNK GGTAGGCAGAACTT
M00141 V\$LYF1_01 0.855354 1319 (+) TTTGGGAGR GTAGGCAGA
M00008 V\$SP1_01 0.793318 1320 (+) GRGGCRGGGW TAGGCAGAAC
M00253 V\$CAP_01 0.889601 1323 (+) NCANNNNN GCAGAACT
M00280 V\$RFX1_01 0.796028 1323 (+) NNGTNR CNWRGYAACNN GCAGAACTTG GAGACAA
M00183 V\$MYB_Q6 0.847718 1324 (+) NNNAACKGNC CAGAACTTG
M00205 V\$GRE_C 0.776126 1324 (-) GGTACAANNTGT YCTK CAGAACTTG GAGACAA
M00277 V\$LMO2COM_01 0.796501 1324 (-) SNNCAGGTGNNN CAGAACTTG GAG
M00162 V\$OCT1_06 0.805859 1325 (+) CWN AWT KWSATRYN AGAACTTG GAGACA
M00085 V\$ZID_01 0.804755 1326 (-) NGGCTCYATCAYC GAACTTG GAGACA
M00007 V\$ELK1_01 0.757515 1331 (+) NNNACM GGAAGTNCNN TGGAGACAATGTGAGA
M00160 V\$SR Y_02 0.802114 1332 (+) NWWAACA AWANN GGAGACAATGTG
M00042 V\$SOX5_01 0.843397 1333 (+) NNAACAATNN GAGACAATGT
M00185 V\$NFY_Q6 0.796506 1333 (+) TRRCCAATSRN GAGACAATGTG
M00122 V\$USF_02 0.761964 1334 (+) NNRNCACGTGNYNN AGACAATGTGAGAA
M00122 V\$USF_02 0.761964 1334 (-) NNRNCACGTGNYNN AGACAATGTGAGAA
M00123 V\$MYC MAX_02 0.780667 1335 (-) NANCACGTGNNW GACAATGTGAGA
M00187 V\$USF_Q6 0.854627 1336 (-) GYCACGTGNC ACAATGTGAG
M00128 V\$GATA1_04 0.815870 1339 (+) NNCWGATARNNNN ATGTGAGAAGGAC
M00077 V\$GATA3_01 0.824103 1341 (+) NNGATARNG GTGAGAAGG
M00203 V\$GATA_C 0.841876 1342 (+) NGATAAGNMNN TGAGAAGGACT
M00191 V\$ER_Q6 0.771625 1345 (+) NNARGNNANNTG ACCYNN GAAGGACTCGCTGAGCTCA
M00205 V\$GRE_C 0.812964 1346 (-) GGTACAANNTGT YCTK AAGGACTCGCTGAGCT
M00235 V\$AHRARNT_01 0.772662 1348 (-) KNNKNNTY GCGTGCMS GGACTCGCTGAGCTCA
M00272 V\$P53_02 0.813892 1348 (-) NGRCWTGYCY GGACTCGCTG
M00056 V\$MYOGNF1_01 0.744797 1349 (-) CRSCTGTNNNTTTGGCACNSNGCCARNN
GACTCGCTGAGCTCAAGGGAAGGGTGGAG
M00175 V\$AP4_Q5 0.840860 1350 (-) NNCAGCTGNN ACTCGCTGAG
M00176 V\$AP4_Q6 0.855926 1350 (-) CWCAGCTGGN ACTCGCTGAG
M00239 V\$T3R_01 0.763581 1351 (-) SNNTRAGGTCACGSNN CTCGCTGAGCTCAAGG
M00239 V\$T3R_01 0.835321 1353 (+) SNNTRAGGTCACGSNN CGCTGAGCTCAAGGGA
M00175 V\$AP4_Q5 0.792165 1355 (+) NNCAGCTGNN CTGAGCTCAA
M00039 V\$CREB_01 0.774627 1356 (+) TGACGTMA TGAGCTCA
M00039 V\$CREB_01 0.774627 1356 (-) TGACGTMA TGAGCTCA
M00155 V\$ARP1_01 0.794532 1356 (-) TGARCCYTTGAMCCYW TGAGCTCAAGGGAAGG
M00143 V\$PAX5_01 0.809891 1359 (+) NCNNNRNKCANNGNWGNRKRGC SRNN
GCTCAAGGGAAGGGTGGAGGAACAGCAC
M00025 V\$ELK1_02 0.797980 1360 (+) NNNNCCGGAARYNN CTCAAGGGAAGGGT
M00143 V\$PAX5_01 0.803833 1360 (+) NCNNNRNKCANNGNWGNRKRGC SRNN
CTCAAGGGAAGGGTGGAGGAACAGCACA
M00227 V\$V MYB_02 0.797533 1360 (+) NSYAACGN CTCAAGGGA

M00004 V\$CMYB_01 0.742900 1361 (+) NCNRNNGRCNGTTGKGKG TCAAGGGAAGGGTGGAGG
M00141 V\$LYF1_01 0.826220 1361 (+) TTTGGGAGR TCAAGGGA
M00240 V\$NKX25_01 0.852443 1361 (+) TYAAGTG TCAAGG
M00196 V\$SP1_Q6 0.776696 1362 (+) NGGGGGCGGGGYN CAAGGGAAGGGTG
M00255 V\$GC_01 0.864527 1362 (+) NRGGGGCGGGGCKN CAAGGGAAGGGTGG
M00108 V\$NRF2_01 0.828246 1363 (+) ACCGGAAGNS AAGGGAAGGG
M00255 V\$GC_01 0.780990 1363 (+) NRGGGGCGGGGCKN AAGGGAAGGGTGA
M00008 V\$SP1_01 0.828992 1364 (+) GRGGCRGGGW AGGGAAGGGT
M00196 V\$SP1_Q6 0.790637 1367 (+) NGGGGGCGGGGYN GAAGGGTGGAGGA
M00255 V\$GC_01 0.833415 1367 (+) NRGGGGCGGGGCKN GAAGGGTGGAGGAA
M00083 V\$MZF1_01 0.875708 1369 (+) NGNGGGGA AGGGTGA
M00196 V\$SP1_Q6 0.757759 1370 (+) NGGGGGCGGGGYN GGGTGGAGGAACA
M00086 V\$IK1_01 0.778312 1372 (+) NNNTGGGAATRCC GTGGAGGAACAGC
M00058 V\$HEN1_02 0.723786 1373 (-) NNGGGNCGCAGCTGCGNCCCN TGGAGGAACAGCACAGGCCTTA
M00108 V\$NRF2_01 0.770349 1374 (+) ACCGGAAGNS GGAGGAACAG
M00003 V\$VMYB_01 0.778604 1376 (+) AAYAACGGNN AGGAACAGCA
M00005 V\$AP4_01 0.813401 1376 (+) WGARYCAGCTGYGGNCKN AGGAACAGCACAGGCCTT
M00175 V\$AP4_Q5 0.871600 1379 (+) NNCAGCTGNN AACAGCACAG
M00211 V\$PADS_C 0.832157 1379 (-) NGTGGTCTC AACAGCAC
M00122 V\$USF_02 0.777191 1380 (+) NNRNCACGTGNYNN ACAGCACAGGCCTT
M00122 V\$USF_02 0.777191 1380 (-) NNRNCACGTGNYNN ACAGCACAGGCCTT
M00001 V\$MYOD_01 0.835039 1381 (-) SRACAGGTGKYG CAGCACAGGCCT
M00123 V\$MYCMAX_02 0.804571 1381 (+) NANCACGTGNNW CAGCACAGGCCT
M00277 V\$LMO2COM_01 0.786810 1381 (-) SNNCAGGTGNNN CAGCACAGGCCT
M00262 V\$STAF_01 0.737572 1382 (-) NTTWCCCANMATGCAYYRCGNY AGCACAGGCCTTAGTGGGATAC
M00217 V\$USF_C 0.824556 1383 (-) NCACGTGN GCACAGGC
M00272 V\$P53_02 0.810961 1383 (+) NGRCWTGYCY GCACAGGCCT
M00272 V\$P53_02 0.804513 1383 (-) NGRCWTGYCY GCACAGGCCT
M00215 V\$SRF_C 0.833099 1386 (-) NCCWTATATGGNCWN CAGGCCTTAGTGGGA
M00186 V\$SRF_Q6 0.808115 1388 (+) GNCCAWATAWGGMN GGCCTTAGTGGGAT
M00186 V\$SRF_Q6 0.765427 1388 (-) GNCCAWATAWGGMN GGCCTTAGTGGGAT
M00215 V\$SRF_C 0.751405 1389 (+) NCCWTATATGGNCWN GCCTTAGTGGGATAC
M00189 V\$AP2_Q6 0.790671 1390 (-) MKCCCSCNGGCG CCTTAGTGGGAT
M00162 V\$OCT1_06 0.878906 1391 (+) CWNATKWSATRYN CTTAGTGGGATACT
M00086 V\$IK1_01 0.803152 1393 (+) NNNTGGGAATRCC TAGTGGGATACTC
M00087 V\$IK2_01 0.857984 1393 (+) NNNYGGGAWNNN TAGTGGGATACT
M00180 V\$E2F_Q6 0.745488 1393 (+) NNGCGCGAAANTK TAGTGGGATACTC
M00127 V\$GATA1_03 0.814797 1394 (+) RNSNNGATAANNNGN AGTGGGATACTCAG
M00144 V\$PAX5_02 0.766096 1394 (+) RRMSWGANWYCTNRAGCGKRACSRYSM
AGTGGGATACTCAGAACGTCATGGCCAG
M00008 V\$SP1_01 0.780861 1395 (+) GRGGCRGGGW GTGGGATACT
M00221 V\$SREBP1_02 0.720902 1395 (-) KATCACCCAC GTGGGATACTC
M00075 V\$GATA1_01 0.849951 1396 (+) SNNGATNNNN TGGGATACTC
M00076 V\$GATA2_01 0.924673 1396 (+) NNGGATRNNN TGGGATACTC
M00115 V\$TAXCREB_02 0.625482 1396 (-) RTGACGCATAYCCCC TGGGATACTCAGAAC
M00208 V\$NFKB_C 0.788703 1396 (+) NGGGACTTTCCA TGGGATACTCAG
M00199 V\$AP1_C 0.804373 1399 (+) NTGASTCAG GATACTCAG
M00223 V\$STAT_01 0.822536 1401 (+) TTCCCRKAA TACTCAGAA
M00036 V\$VJUN_01 0.732309 1403 (+) NYGATGACGTCATNCY CTCAGAACGTCATGGC
M00175 V\$AP4_Q5 0.807399 1403 (+) NNCAGCTGNN CTCAGAACGT
M00017 V\$ATF_01 0.800682 1404 (-) CNSTGACGTNNNYC TCAGAACGTCATGG
M00253 V\$CAP_01 0.894529 1404 (+) NCANNNNN TCAGAACG
M00177 V\$CREB_Q2 0.829427 1405 (-) NSTGACGTAANN CAGAACGTCATG
M00178 V\$CREB_Q4 0.828874 1405 (-) NSTGACGTMANN CAGAACGTCATG
M00205 V\$GRE_C 0.778972 1405 (-) GGTACAANNTGTCTK CAGAACGTCATGGCCA
M00162 V\$OCT1_06 0.803125 1406 (-) CWNATKWSATRYN AGAACGTCATGGCC
M00174 V\$AP1_Q6 0.763821 1406 (-) NNTGACTCANN AGAACGTCATG
M00039 V\$CREB_01 0.806489 1407 (-) TGACGTMA GAACGTCA
M00040 V\$SREBP1_01 0.787497 1407 (-) TTACGTAA GAACGTCA
M00041 V\$SREBP1CJUN_01 0.793611 1407 (+) TGACGTYA GAACGTCA
M00041 V\$SREBP1CJUN_01 0.907222 1407 (-) TGACGTYA GAACGTCA

M00113 V\$CREB_02 0.890876 1407 (-) NNGNTGACGYNN GAACGTCATGGC
M00150 V\$BRACH_01 0.725237 1408 (+) MKNNTSACACCTAGGTGTGAAATT AACGTCATGGCCAGGTGGGATGTG
M00076 V\$GATA2_01 0.815968 1410 (+) NNNGATRNNN CGTCATGGCC
M00076 V\$GATA2_01 0.794768 1410 (-) NNNGATRNNN CGTCATGGCC
M00264 V\$STAF_02 0.818503 1410 (-) MNTTCCCAKMATKCMWNGCRN CGTCATGGCCAGGTGGGATGT
M00059 V\$YY1_01 0.773591 1413 (+) NNNNNCCATNTWNNNWN CATGGCCAGGTGGGATG
M00065 V\$TALIBETAE47_01 0.778421 1414 (+) NNNAACAGATGKTNNN ATGGCCAGGTGGGATG
M00066 V\$TALIALPHAE47_01 0.812566 1414 (+) NNNAACAGATGKTNNN ATGGCCAGGTGGGATG
M00071 V\$E47_02 0.810372 1414 (+) NNNMRCAGGTGTTMNN ATGGCCAGGTGGGATG
M00236 V\$ARNT_01 0.780898 1414 (+) NNNNNCACGTGNNNNN ATGGCCAGGTGGGATG
M00236 V\$ARNT_01 0.752819 1414 (-) NNNNNCACGTGNNNNN ATGGCCAGGTGGGATG
M00118 V\$MYCMAX_01 0.782194 1415 (+) NNACCACGTGGTNN TGGCCAGGTGGGAT
M00118 V\$MYCMAX_01 0.782194 1415 (-) NNACCACGTGGTNN TGGCCAGGTGGGAT
M00119 V\$MAX_01 0.745650 1415 (+) NNANCACGTGNTNN TGGCCAGGTGGGAT
M00119 V\$MAX_01 0.745650 1415 (-) NNANCACGTGNTNN TGGCCAGGTGGGAT
M00121 V\$USF_01 0.781266 1415 (+) NNRYCACGTGRYNN TGGCCAGGTGGGAT
M00121 V\$USF_01 0.781266 1415 (-) NNRYCACGTGRYNN TGGCCAGGTGGGAT
M00122 V\$USF_02 0.883157 1415 (+) NNRNCACGTGNYNN TGGCCAGGTGGGAT
M00122 V\$USF_02 0.883157 1415 (-) NNRNCACGTGNYNN TGGCCAGGTGGGAT
M00001 V\$MYOD_01 0.816732 1416 (+) SRACAGGTGKYG GGCCAGGTGGGA
M00055 V\$NMYC_01 0.752737 1416 (+) NNNCACGTGNNN GGCCAGGTGGGA
M00055 V\$NMYC_01 0.842457 1416 (-) NNNCACGTGNNN GGCCAGGTGGGA
M00123 V\$MYCMAX_02 0.787759 1416 (-) NANCACGTGNNW GGCCAGGTGGGA
M00262 V\$STAF_01 0.742052 1416 (-) NTTWCCCANMATGCAYYRCGY GGCCAGGTGGGATGTGGGATGA
M00277 V\$LMO2COM_01 0.904172 1416 (+) SNNCAGGTGNNN GGCCAGGTGGGA
M00073 V\$DELTAEF1_01 0.930474 1417 (-) NNNCACCTNAN GCCAGGTGGGA
M00143 V\$PAX5_01 0.776627 1417 (+) NCNNNRNKCANNNGNWNRKRGRCSRSNN
GCCAGGTGGGATGTGGGATGACAGACAG
M00176 V\$AP4_Q6 0.774242 1417 (-) CWCAGCTGGN GCCAGGTGGG
M00184 V\$MYOD_Q6 0.940160 1417 (-) NNCANCTGNY GCCAGGTGGG
M00187 V\$USF_Q6 0.825832 1417 (+) GYCACGTGNC GCCAGGTGGG
M00187 V\$USF_Q6 0.847638 1417 (-) GYCACGTGNC GCCAGGTGGG
M00189 V\$AP2_Q6 0.837086 1417 (-) MKCCCSCNGGCG GCCAGGTGGGAT
M00196 V\$SP1_Q6 0.771173 1417 (+) NGGGGGCGGGGYN GCCAGGTGGGATG
M00255 V\$GC_01 0.781725 1417 (+) NRGGGGCGGGGNC GCCAGGTGGGATGT
M00217 V\$USF_C 0.805434 1418 (+) NCACGTGN CCAGGTGG
M00217 V\$USF_C 0.889634 1418 (-) NCACGTGN CCAGGTGG
M00008 V\$SP1_01 0.824179 1419 (+) GRGGCRGGGW CAGGTGGGAT
M00115 V\$TAXCREB_02 0.705874 1421 (-) RTGACGCATAYCCCC GGTGGGATGTGGGAT
M00257 V\$RREB1_01 0.834492 1421 (-) CCCCAAACMMCCCC GGTGGGATGTGGGA
M00139 V\$AHR_01 0.741784 1422 (+) CYYCNRRSTNGCGTGASW GTGGGATGTGGGATGACA
M00055 V\$NMYC_01 0.765815 1423 (-) NNNCACGTGNNN TGGGATGTGGGA
M00075 V\$GATA1_01 0.867226 1423 (+) SNNGATNNNN TGGGATGTGG
M00076 V\$GATA2_01 0.907984 1423 (+) NNNGATRNNN TGGGATGTGG
M00115 V\$TAXCREB_02 0.618807 1423 (-) RTGACGCATAYCCCC TGGGATGTGGGATGA
M00077 V\$GATA3_01 0.840939 1424 (+) NNGATARNG GGGATGTGG
M00187 V\$USF_Q6 0.824154 1424 (-) GYCACGTGNC GGGATGTGGG
M00189 V\$AP2_Q6 0.846507 1424 (-) MKCCCSCNGGCG GGGATGTGGGAT
M00057 V\$COMP1_01 0.792695 1426 (+) NNTNWKGATTGRCNRSRANMRRNN GATGTGGGATGACAGACAGAGAGG
M00086 V\$IK1_01 0.836271 1427 (+) NNNTGGGAATRCC ATGTGGGATGACA
M00087 V\$IK2_01 0.925393 1427 (+) NNNYGGGAWNNN ATGTGGGATGAC
M00056 V\$MYOGNF1_01 0.756593 1428 (-) CRSCTGTNNNTTTGGCACNSNGCCARNN
TGTGGGATGACAGACAGAGAGGACAGGAA
M00115 V\$TAXCREB_02 0.611391 1428 (-) RTGACGCATAYCCCC TGTGGGATGACAGAC
M00141 V\$LYF1_01 0.837976 1428 (+) TTTGGGAGR TGTGGGATG
M00008 V\$SP1_01 0.789071 1429 (+) GRGGCRGGGW GTGGGATGAC
M00114 V\$TAXCREB_01 0.805051 1429 (+) GGGGGTTGACGYANA GTGGGATGACAGACA
M00221 V\$SREBP1_02 0.888844 1429 (-) KATCACCCAC GTGGGATGACA
M00075 V\$GATA1_01 0.789733 1430 (+) SNNGATNNNN TGGGATGACA
M00076 V\$GATA2_01 0.862878 1430 (+) NNNGATRNNN TGGGATGACA
M00115 V\$TAXCREB_02 0.618807 1430 (-) RTGACGCATAYCCCC TGGGATGACAGACAG

M00127 V\$GATA1_03 0.784664 1431 (+) RNSNNGATAANNNGN GGGATGACAGACAG
M00162 V\$OCT1_06 0.834766 1431 (-) CWNATKWSATRYN GGGATGACAGACAG
M00172 V\$APIFJ_Q2 0.864669 1433 (+) RSTGACTNMNW GATGACAGACA
M00173 V\$API_Q2 0.871449 1433 (+) RSTGACTNMNW GATGACAGACA
M00174 V\$API_Q6 0.819857 1433 (+) NNTGACTCANN GATGACAGACA
M00188 V\$API_Q4 0.849344 1433 (+) RSTGACTMANN GATGACAGACA
M00083 V\$MZF1_01 0.857575 1443 (+) NGNGGGGA AGAGAGGA
M00179 V\$CREBP1_Q2 0.751431 1443 (-) NSTGACGTMASN AGAGAGGACAGG
M00280 V\$RFX1_01 0.750948 1443 (+) NNGTNRNWRGYAACNN AGAGAGGACAGGAACCG
M00127 V\$GATA1_03 0.783684 1444 (+) RNSNNGATAANNNGN GAGAGGACAGGAAC
M00007 V\$ELK1_01 0.798263 1447 (+) NNNACMGGAAGTNCNN AGGACAGGAACCGGAT
M00025 V\$ELK1_02 0.809305 1447 (+) NNNNCCGGAARYNN AGGACAGGAACCGG
M00001 V\$MYOD_01 0.797047 1448 (+) SRACAGGTGKYG GGACAGGAACCG
M00074 V\$CETSIP54_02 0.862893 1448 (+) NNAMMGAWRWNN GGACAGGAACCGG
M00181 V\$E2_Q6 0.740269 1448 (+) NNACCRNNANCGGTRN GGACAGGAACCGGATG
M00181 V\$E2_Q6 0.750967 1448 (-) NNACCRNNANCGGTRN GGACAGGAACCGGATG
M00203 V\$GATA_C 0.834731 1448 (+) NGATAAGNMNN GGACAGGAACC
M00032 V\$CETSIP54_01 0.911733 1450 (+) NCMGGAWGYN ACAGGAACCG
M00108 V\$NRF2_01 0.820252 1450 (+) ACCGGAAGNS ACAGGAACCG
M00007 V\$ELK1_01 0.832331 1453 (+) NNNACMGGAAGTNCNN GGAACCGGATGTGGGG
M00025 V\$ELK1_02 0.887052 1453 (+) NNNNCCGGAARYNN GGAACCGGATGTGG
M00074 V\$CETSIP54_02 0.939791 1454 (+) NNAMMGAWRWNN GAACCGGATGTGG
M00107 V\$E2_01 0.747949 1454 (+) NNACCRNNANCGGTRN GAACCGGATGTGGGGT
M00107 V\$E2_01 0.794724 1454 (-) NNACCRNNANCGGTRN GAACCGGATGTGGGGT
M00181 V\$E2_Q6 0.772593 1454 (-) NNACCRNNANCGGTRN GAACCGGATGTGGGGT
M00001 V\$MYOD_01 0.821654 1455 (-) SRACAGGTGKYG AACCGGATGTGG
M00032 V\$CETSIP54_01 0.981803 1456 (+) NCMGGAWGYN ACCGGATGTG
M00108 V\$NRF2_01 0.878391 1456 (+) ACCGGAAGNS ACCGGATGTG
M00139 V\$AHR_01 0.715281 1456 (+) CYYCNRRSTNGCGTGASW ACCGGATGTGGGGTGGGC
M00176 V\$AP4_Q6 0.773991 1456 (-) CWCAGCTGGN ACCGGATGTG
M00271 V\$AML1_01 0.832985 1456 (-) TGTGGT ACCGGA
M00075 V\$GATA1_01 0.920039 1457 (+) SNNGATNNNN CCGGATGTGG
M00076 V\$GATA2_01 0.917005 1457 (+) NNNGATRNNN CCGGATGTGG
M00277 V\$LMO2COM_01 0.789233 1457 (+) SNNCAGGTGNNN CCGGATGTGGGG
M00187 V\$USF_Q6 0.790327 1458 (-) GYCACGTGNC CGGATGTGGG
M00189 V\$AP2_Q6 0.788833 1458 (-) MKCCCSCNGGCG CGGATGTGGGGT
M00255 V\$GC_01 0.790544 1458 (+) NRGGGGCGGGGCK CGGATGTGGGGTGG
M00008 V\$SP1_01 0.793884 1460 (+) GRGGCRGGGW GATGTGGGGT
M00257 V\$RREB1_01 0.788028 1460 (-) CCCCACMMCCCC GATGTGGGGTGGGC
M00072 V\$CP2_01 0.867496 1463 (-) GCNMNAMCMAG GTGGGGTGGGC
M00084 V\$MZF1_02 0.854536 1463 (+) KNNNKAGGGGNAA GTGGGGTGGGCAG
M00196 V\$SP1_Q6 0.772751 1463 (+) NGGGGGCGGGGYN GTGGGGTGGGCAG
M00221 V\$SREBP1_02 0.820580 1463 (-) KATCACCCAC GTGGGGTGGGC
M00008 V\$SP1_01 0.871744 1464 (+) GRGGCRGGGW TGGGGTGGGC
M00115 V\$TAXCREB_02 0.611391 1464 (-) RTGACGCATAYCCCC TGGGGTGGGCAGAGC
M00243 V\$EGR1_01 0.753565 1464 (+) WTGCGTGGGCGK TGGGGTGGGCAG
M00244 V\$NGFIC_01 0.769833 1464 (+) WTGCGTGGGYGG TGGGGTGGGCAG
M00245 V\$EGR3_01 0.742500 1464 (+) NTGCGTGGGCGK TGGGGTGGGCAG
M00246 V\$EGR2_01 0.780046 1464 (+) NTGCGTRGGCGK TGGGGTGGGCAG
M00271 V\$AML1_01 0.866053 1464 (+) TGTGGT TGGGGT
M00008 V\$SP1_01 0.890430 1465 (+) GRGGCRGGGW GGGGTGGGCA
M00134 V\$HNF4_01 0.777223 1466 (+) NNNRGGNCAAAGKTCANN GGGTGGGCAGAGCTCGAGG
M00056 V\$MYOGNF1_01 0.761197 1467 (-) CRSCTGTNNNTTTGGCACNSNGCCARN
GGTGGGCAGAGCTCGAGGGCCAGGATGTG
M00196 V\$SP1_Q6 0.834298 1467 (+) NGGGGGCGGGGYN GGTGGGCAGAGCT
M00255 V\$GC_01 0.895639 1467 (+) NRGGGGCGGGGCK GGTGGGCAGAGCTC
M00072 V\$CP2_01 0.805746 1468 (-) GCNMNAMCMAG GTGGGCAGAGC
M00221 V\$SREBP1_02 0.727547 1468 (-) KATCACCCAC GTGGGCAGAGC
M00008 V\$SP1_01 0.864666 1469 (+) GRGGCRGGGW TGGGCAGAGC
M00253 V\$CAP_01 0.874322 1472 (+) NCANNNN GCAGAGCT
M00134 V\$HNF4_01 0.793557 1473 (+) NNNRGGNCAAAGKTCANN CAGAGCTCGAGGGCCAGGA

M00175 V\$AP4_Q5 0.810120 1473 (+) NNCAGCTGNN CAGAGCTCGA
M00176 V\$AP4_Q6 0.833626 1473 (+) CWCAGCTGNN CAGAGCTCGA
M00055 V\$NMYC_01 0.742701 1475 (-) NNNCACGTGNNN GAGCTCGAGGGC
M00085 V\$ZID_01 0.811908 1475 (+) NGGCTCYATCAYC GAGCTCGAGGGCC
M00158 V\$COUP_01 0.802231 1475 (-) TGAMCTTTGMMCYT GAGCTCGAGGGCCA
M00189 V\$AP2_Q6 0.820772 1476 (+) MKCCCSCNGGCG AGCTCGAGGGCC
M00189 V\$AP2_Q6 0.789062 1476 (-) MKCCCSCNGGCG AGCTCGAGGGCC
M00143 V\$PAX5_01 0.830818 1478 (+) NCNNNRNKCANNNGNWGNRKRGC SRNN
CTCGAGGGGCCAGGATGTGGAGAGTGAAC
M00008 V\$SP1_01 0.797848 1483 (+) GRGGCRGGGW GGGCCAGGAT
M00025 V\$ELK1_02 0.782369 1483 (+) NNNNCCGGAARYNN GGGCCAGGATGTGG
M00074 V\$CETS1P54_02 0.868128 1484 (+) NNAMMGAWRWNN GGCCAGGATGTGG
M00032 V\$CETS1P54_01 0.933460 1486 (+) NCMGGAWGYN CCAGGATGTG
M00108 V\$NRF2_01 0.798450 1486 (+) ACCGGAAGNS CCAGGATGTG
M00139 V\$AHR_01 0.711949 1486 (+) CYYCNRRSTNGCGTASW CCAGGATGTGGAGAGTGA
M00075 V\$GATA1_01 0.899309 1487 (+) SNNGATNNNN CAGGATGTGG
M00076 V\$GATA2_01 0.908886 1487 (+) NNNGATRNNN CAGGATGTGG
M00277 V\$LMO2COM_01 0.789233 1487 (+) SNNCAGGTGNNN CAGGATGTGGAG
M00077 V\$GATA3_01 0.823660 1488 (+) NNGATARNG AGGATGTGG
M00097 V\$PAX6_01 0.781312 1488 (-) NNNNTTCACGCWTSANTKNNN AGGATGTGGAGAGTGAACCGA
M00083 V\$MZF1_01 0.849641 1490 (+) NGNGGGGA GATGTGGA
M00159 V\$CEBP_01 0.905348 1490 (+) NNTKTGGWNANNN GATGTGGAGAGTG
M00235 V\$AHRARNT_01 0.796399 1490 (+) KNNKNNTYGCGTGCMS GATGTGGAGAGTGAAC
M00271 V\$AML1_01 0.853077 1492 (+) TGTGGT TGTGGA
M00033 V\$P300_01 0.857192 1493 (+) NNNRGGAGTNNNS GTGGAGAGTGAACC
M00063 V\$IRF2_01 0.738013 1495 (+) GAAAAGYGAAASY GGAGAGTGAACCG
M00085 V\$ZID_01 0.765411 1495 (-) NGGCTCYATCAYC GGAGAGTGAACCG
M00249 V\$CHOP_01 0.786044 1495 (-) NNRTGCAATMCCC GGAGAGTGAACCG
M00239 V\$T3R_01 0.759228 1496 (-) SNNTRAGGTCACGSNN GAGAGTGAACCGACAT
M00147 V\$HSF2_01 0.800000 1497 (+) NGAANNWTCK AGAGTGAACC
M00183 V\$MYB_Q6 0.853112 1500 (+) NNNAACKGNC GTGAACCGAC
M00144 V\$PAX5_02 0.786090 1501 (-) RRMSWGANWYCTNRAGCGKRACSRYSM
TGAACCGACATGGCCACACTGACTCTCC
M00059 V\$YY1_01 0.826999 1502 (-) NNNNNCCATNTWNNNWN GAACCGACATGGCCACA
M00131 V\$HNF3B_01 0.867508 1502 (-) NNNTTRTTTRYTY GAACCGACATGG
M00122 V\$USF_02 0.770665 1503 (+) NNRNCACGTGNYNN AACCGACATGGCCA
M00122 V\$USF_02 0.770665 1503 (-) NNRNCACGTGNYNN AACCGACATGGCCA
M00215 V\$SRF_C 0.754392 1503 (+) NCCWTATATGGNCWN AACCGACATGGCCAC
M00055 V\$NMYC_01 0.771594 1504 (+) NNNCACGTGNNN AACCGACATGGCC
M00187 V\$USF_Q6 0.798994 1505 (+) GYCACGTGNC CCGACATGGC
M00255 V\$GC_01 0.783684 1505 (-) NRGGGGCGGGGCKN CCGACATGGCCACA
M00278 V\$LMO2COM_02 0.794811 1505 (+) NMGATANS GCGACATGG
M00076 V\$GATA2_01 0.827244 1506 (+) NNNGATRNNN CGACATGGCC
M00076 V\$GATA2_01 0.809653 1506 (-) NNNGATRNNN CGACATGGCC
M00272 V\$P53_02 0.843787 1506 (+) NGRCW TG YCY CGACATGGCC
M00272 V\$P53_02 0.833236 1506 (-) NGRCW TG YCY CGACATGGCC
M00109 V\$CEBPB_01 0.833086 1508 (-) RNRTKNNGMAAKNN ACATGGCCACACTG
M00271 V\$AML1_01 0.897865 1513 (-) TGTGGT GCCACA
M00008 V\$SP1_01 0.793035 1516 (-) GRGGCRGGGW AACTGACTC
M00033 V\$P300_01 0.844922 1517 (-) NNNRGGAGTNNNS CACTGACTCTCCTC
M00037 V\$NFE2_01 0.849100 1517 (+) TGCTGASTCAY CACTGACTCTC
M00172 V\$AP1FJ_Q2 0.856467 1518 (+) RSTGACTNMNW ACTGACTCTCC
M00173 V\$AP1_Q2 0.847731 1518 (+) RSTGACTNMNW ACTGACTCTCC
M00174 V\$AP1_Q6 0.867243 1518 (+) NNTGACTCANN ACTGACTCTCC
M00188 V\$AP1_Q4 0.858493 1518 (+) RSTGACTMANN ACTGACTCTCC
M00033 V\$P300_01 0.822427 1519 (-) NNNRGGAGTNNNS CTGACTCTCCTCTC
M00115 V\$TAXCREB_02 0.687333 1519 (+) RTGACGCATAYCCCC CTGACTCTCCTCTC
M00127 V\$GATA1_03 0.783684 1519 (-) RNSNNGATAANNGN CTGACTCTCCTCTC
M00199 V\$AP1_C 0.793003 1519 (+) NTGASTCAG CTGACTCTC
M00199 V\$AP1_C 0.852770 1519 (-) NTGASTCAG CTGACTCTC
M00255 V\$GC_01 0.783684 1519 (-) NRGGGGCGGGGCKN CTGACTCTCCTCTC

M00127 V\$GATA1_03 0.797648 1524 (-) RNSNNGATAANNNGN TCTCCTCTCCCTCT
M00083 V\$MZF1_01 0.846997 1526 (-) NGNGGGGA TCCTCTCC
M00085 V\$ZID_01 0.768988 1527 (+) NGGCTCYATCAYC CCTCTCCCTCTCT
M00084 V\$MZF1_02 0.854036 1528 (-) KNNNKAGGGGNAA CTCTCCCTCTCTC
M00108 V\$NRF2_01 0.808140 1528 (-) ACCGGAAGNS CTCTCCCTCT
M00084 V\$MZF1_02 0.821045 1530 (-) KNNNKAGGGGNAA CTCCCTCTCTCCC
M00127 V\$GATA1_03 0.836110 1530 (-) RNSNNGATAANNNGN CTCCCTCTCTCCCT
M00033 V\$P300_01 0.852761 1532 (-) NNNRGGAGTNNNS CCCTCTCTCCCTCC
M00075 V\$GATA1_01 0.802073 1532 (-) SNNGATNNNN CCCTCTCTCC
M00077 V\$GATA3_01 0.875942 1532 (-) NNGATARNG CCCTCTCTC
M00278 V\$LMO2COM_02 0.816712 1532 (-) NMGATANS G CCTCTCTC
M00085 V\$ZID_01 0.771934 1533 (+) NGGCTCYATCAYC CCTCTCTCCCTCC
M00008 V\$SP1_01 0.848528 1535 (-) GRGGCRGGGW TCTCTCCCTC
M00139 V\$AHR_01 0.741178 1535 (-) CYYCNRRSTNGCGTGASW TCTCTCCCTCCCTCCAGC
M00033 V\$P300_01 0.807430 1536 (-) NNNRGGAGTNNNS CTCTCCCTCCCTCC
M00084 V\$MZF1_02 0.870282 1536 (-) KNNNKAGGGGNAA CTCTCCCTCCCTC
M00108 V\$NRF2_01 0.770349 1536 (-) ACCGGAAGNS CTCTCCCTCC
M00255 V\$GC_01 0.801078 1536 (-) NRGGGGCGGGGCKN CTCTCCCTCCCTCC
M00264 V\$STAF_02 0.756582 1536 (+) MNTTCCCAKMATKCMWNGCRN CTCTCCCTCCCTCCAGCAAAC
M00084 V\$MZF1_02 0.817296 1537 (-) KNNNKAGGGGNAA TCTCCCTCCCTCC
M00196 V\$SP1_Q6 0.826407 1537 (-) NGGGGGCGGGGYN TCTCCCTCCCTCC
M00008 V\$SP1_01 0.904870 1539 (-) GRGGCRGGGW TCCCTCCCTC
M00005 V\$AP4_01 0.753314 1542 (-) WGARYCAGCTGYGGNCKN CTCCCTCCAGCAAACCTT
M00189 V\$AP2_Q6 0.806526 1542 (+) MKCCCSCNNGGCG CTCCCTCCAGCA
M00115 V\$TAXCREB_02 0.648027 1546 (+) RTGACGCATAYCCCC CTCCAGCAAACCTC
M00050 V\$E2F_02 0.764788 1548 (-) TTTSGCGC CCAGCAAA
M00212 V\$POLY_C 0.802732 1549 (+) CAATAAAACCCYYYKCTN CAGCAAACCCTCAAGCTG
M00008 V\$SP1_01 0.826161 1550 (-) GRGGCRGGGW AGCAAACCTT
M00008 V\$SP1_01 0.821348 1551 (-) GRGGCRGGGW GCAAACCTC
M00189 V\$AP2_Q6 0.786075 1554 (+) MKCCCSCNNGGCG AACCTCAAGCT
M00277 V\$LMO2COM_01 0.797308 1558 (-) SNNCAGGTGNNN CTCAAGCTGAGG
M00175 V\$AP4_Q5 0.854461 1559 (-) NNCAGCTGNN TCAAGCTGAG
M00176 V\$AP4_Q6 0.872964 1559 (-) CWCAGCTGGN TCAAGCTGAG
M00084 V\$MZF1_02 0.868783 1562 (+) KNNNKAGGGGNAA AGCTGAGGGGCGAG
M00075 V\$GATA1_01 0.788746 1563 (+) SNNGATNNNN GCTGAGGGGC
M00141 V\$LYF1_01 0.842576 1563 (+) TTTGGGAGR GCTGAGGGG
M00143 V\$PAX5_01 0.771340 1563 (-) NCNNNRNKCANNNGNWNKRGCSRSNNN
GCTGAGGGGCGAGCTCCAGTGGCTGAACC
M00209 V\$NFY_C 0.764391 1563 (+) NCTGATTGGYTASY GCTGAGGGGCGAGCT
M00007 V\$ELK1_01 0.775551 1564 (+) NNNACMGGAAGTNCNN CTGAGGGGCGAGTCCA
M00008 V\$SP1_01 0.804077 1566 (+) GRGGCRGGGW GAGGGGCGAGC
M00115 V\$TAXCREB_02 0.628004 1566 (-) RTGACGCATAYCCCC GAGGGGCGAGCTCCAG
M00196 V\$SP1_Q6 0.768017 1566 (+) NGGGGGCGGGGYN GAGGGGCGAGCTCC
M00255 V\$GC_01 0.810387 1566 (+) NRGGGGCGGGGCKN GAGGGGCGAGTCCA
M00002 V\$E47_01 0.777220 1567 (-) NSNGCAGGTGKNCNN AGGGGCGAGTCCAGT
M00005 V\$AP4_01 0.763689 1567 (+) WGARYCAGCTGYGGNCKN AGGGGCGAGTCCAGTGGC
M00194 V\$NFKB_Q6 0.830431 1567 (+) NGGGGAMTTTCCNN AGGGGCGAGTCCAG
M00054 V\$NFKAPPAB_01 0.789014 1568 (+) GGGAMTTYCC GGGGCGAGCTC
M00208 V\$NFKB_C 0.764017 1568 (+) NGGGACTTTCCA GGGGCGAGTCCA
M00051 V\$NFKAPPAB50_01 0.813194 1569 (+) GGGGATYCCC GGGCAGCTCC
M00051 V\$NFKAPPAB50_01 0.791648 1569 (-) GGGGATYCCC GGGCAGCTCC
M00054 V\$NFKAPPAB_01 0.817728 1569 (-) GGGAMTTYCC GGGCAGCTCC
M00277 V\$LMO2COM_01 0.827187 1569 (+) SNNCAGGTGNNN GGGCAGTCCAG
M00277 V\$LMO2COM_01 0.797039 1569 (-) SNNCAGGTGNNN GGGCAGTCCAG
M00072 V\$CP2_01 0.834048 1570 (+) GCNMNAMCMAG GGCAGTCCAG
M00175 V\$AP4_Q5 0.896083 1570 (+) NNCAGCTGNN GGCAGTCCA
M00176 V\$AP4_Q6 0.878978 1570 (+) CWCAGCTGGN GGCAGTCCA
M00184 V\$MYOD_Q6 0.813078 1570 (-) NNCANCTGNY GGCAGTCCA
M00253 V\$CAP_01 0.899951 1571 (+) NCANNNNN GCAGTCC
M00001 V\$MYOD_01 0.791732 1572 (-) SRACAGGTGKYG CAGTCCAGTGG
M00085 V\$ZID_01 0.778245 1572 (+) NGGCTCYATCAYC CAGTCCAGTGGC

M00185 V\$NFY_Q6 0.789054 1574 (+) TRRCCAATSRN GCTCCAGTGGC
M00187 V\$USF_Q6 0.880347 1575 (-) GYCACGTGNC CTCCAGTGGC
M00189 V\$AP2_Q6 0.798713 1575 (-) MKCCCSCNGGCG CTCCAGTGGCTG
M00185 V\$NFY_Q6 0.826310 1576 (-) TRRCCAATSRN TCCAGTGGCTG
M00240 V\$NKX25_01 0.852443 1576 (+) TYAAGTG TCCAGTG
M00253 V\$CAP_01 0.872844 1577 (+) NCANNNNN CCAGTGGC
M00254 V\$CAAT_01 0.878283 1577 (-) NNNRRCCAATSA CCAGTGGCTGAA
M00188 V\$AP1_Q4 0.817627 1579 (+) RSTGACTMANN AGTGGCTGAAC
M00008 V\$SP1_01 0.783126 1580 (+) GRGGCRGGGW GTGGCTGAAC
M00144 V\$PAX5_02 0.744571 1580 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
GTGGCTGAACCGCCGGGCCAATGCCCTC
M00085 V\$ZID_01 0.795287 1581 (+) NGGCTCYATCAYC TGGCTGAACCGCC
M00183 V\$MYB_Q6 0.896266 1584 (+) NNNAACKGNC CTGAACCGCC
M00155 V\$ARP1_01 0.752654 1585 (+) TGARCCYTTGAMCCYW TGAACCGCCGGGCCAA
M00008 V\$SP1_01 0.783126 1586 (-) GRGGCRGGGW GAACCGCCGG
M00189 V\$AP2_Q6 0.797105 1586 (+) MKCCCSCNGGCG GAACCGCCGGGC
M00189 V\$AP2_Q6 0.833869 1587 (+) MKCCCSCNGGCG AACCGCCGGGCC
M00189 V\$AP2_Q6 0.819623 1587 (-) MKCCCSCNGGCG AACCGCCGGGCC
M00271 V\$AML1_01 0.835496 1588 (-) TGTGGT ACCGCC
M00180 V\$E2F_Q6 0.747907 1590 (+) NNGCGCGAAANTK CGCCGGGCCAATG
M00254 V\$CAAT_01 0.865010 1592 (+) NNNRRCCAATSA CCGGGCCAATGC
M00050 V\$E2F_02 0.743405 1594 (-) TTTSGCGC GGGCCAAT
M00185 V\$NFY_Q6 0.831963 1594 (+) TRRCCAATSRN GGGCCAATGCC
M00255 V\$GC_01 0.787359 1595 (-) NRGGGGCGGGGCGNK GGCCAATGCCCTCC
M00076 V\$GATA2_01 0.798376 1596 (-) NNNGATRNNN GCCAATGCC
M00239 V\$T3R_01 0.762067 1596 (-) SNNTRAGGTCACGSNN GCCAATGCCCTCCTGG
M00193 V\$NF1_Q6 0.851240 1600 (-) NNTTGGCNNNNNNCCNNN ATGCCCTCCTGGCCAATG
M00122 V\$USF_02 0.793971 1601 (+) NNRNCACGTGNYNN TGCCCTCCTGGCCA
M00122 V\$USF_02 0.793971 1601 (-) NNRNCACGTGNYNN TGCCCTCCTGGCCA
M00055 V\$NMYC_01 0.753041 1602 (+) NNNCACGTGNNN GCCCTCCTGGCC
M00189 V\$AP2_Q6 0.780790 1602 (+) MKCCCSCNGGCG GCCCTCCTGGCC
M00189 V\$AP2_Q6 0.783548 1602 (-) MKCCCSCNGGCG GCCCTCCTGGCC
M00277 V\$LMO2COM_01 0.804576 1602 (-) SNNCAGGTGNNN GCCCTCCTGGCC
M00056 V\$MYOGNF1_01 0.743359 1603 (+) CRSCTGTNNNNTTTGGCACNSNGCCARN
CCCTCCTGGCCAATGGCGTGGAGCTGAGA
M00184 V\$MYOD_Q6 0.797656 1603 (+) NNCANCTGNY CCCTCCTGGC
M00141 V\$LYF1_01 0.845387 1604 (-) TTTGGGAGR CCTCCTGGC
M00254 V\$CAAT_01 0.816154 1605 (-) NNNRRCCAATSA CTCCTGGCCAAT
M00193 V\$NF1_Q6 0.823691 1606 (+) NNTTGGCNNNNNNCCNNN TCCTGGCCAATGGCGTGG
M00254 V\$CAAT_01 0.952273 1607 (+) NNNRRCCAATSA CCTGGCCAATGG
M00185 V\$NFY_Q6 0.945529 1609 (+) TRRCCAATSRN TGGCCAATGGC
M00242 V\$PPARA_01 0.780404 1609 (-) CWRAWCTAGGNCAAAGGTCA TGGCCAATGGCGTGGAGCTG
M00144 V\$PAX5_02 0.801588 1610 (+) RRMSWGANWYCTNRAGCGKRACSRYSNM
GGCCAATGGCGTGGAGCTGAGAGATAAC
M00235 V\$AHRARNT_01 0.800082 1610 (+) KNNKNNTYGCGTGCMS GGCCAATGGCGTGGAG
M00185 V\$NFY_Q6 0.772097 1611 (-) TRRCCAATSRN GCCAATGGCGT
M00227 V\$VMBYB_02 0.837545 1611 (+) NSYAACGGN GCCAATGGC
M00254 V\$CAAT_01 0.794691 1612 (-) NNNRRCCAATSA CCAATGGCGTGG
M00017 V\$ATF_01 0.742985 1613 (+) CNSTGACGTNNNYC CAATGGCGTGGAGC
M00008 V\$SP1_01 0.879672 1615 (+) GRGGCRGGGW ATGGCGTGGGA
M00255 V\$GC_01 0.851053 1615 (+) NRGGGGCGGGGCGNK ATGGCGTGGAGCTG
M00180 V\$E2F_Q6 0.734326 1616 (+) NNGCGCGAAANTK TGGCGTGGAGCTG
M00083 V\$MZF1_01 0.846997 1617 (+) NGNGGGGA GCGTGGGA
M00115 V\$TAXCREB_02 0.637941 1620 (-) RTGACGCATAYCCCC GTGGAGCTGAGAGAT
M00175 V\$AP4_Q5 0.917845 1621 (-) NNCAGCTGNN TGGAGCTGAG
M00176 V\$AP4_Q6 0.922576 1621 (-) CWCAGCTGGN TGGAGCTGAG
M00280 V\$RFX1_01 0.753850 1623 (+) NNGTNRNCRNWRGYAACNN GAGCTGAGAGATAACCA
M00037 V\$NFE2_01 0.795280 1624 (+) TGCTGASTCAY AGCTGAGAGAT
M00056 V\$MYOGNF1_01 0.776638 1624 (-) CRSCTGTNNNNTTTGGCACNSNGCCARN
AGCTGAGAGATAACCAGCTGGTGGTGCCA
M00141 V\$LYF1_01 0.884488 1625 (+) TTTGGGAGR GCTGAGAGA

M00199 V\$AP1_C 0.792420 1626 (-) NTGASTCAG CTGAGAGAT
M00126 V\$GATA1_02 0.772812 1627 (+) NNNNGATANKGN TGAGAGATAACCAG
M00127 V\$GATA1_03 0.847134 1627 (+) RNSNNGATAANN GN TGAGAGATAACCAG
M00128 V\$GATA1_04 0.890319 1628 (+) NNCWGATARNNNN GAGAGATAACCAG
M00075 V\$GATA1_01 0.806515 1629 (+) SNNGATNNNN AGAGATAACC
M00076 V\$GATA2_01 0.870546 1629 (+) NNNGATRNNN AGAGATAACC
M00072 V\$CP2_01 0.805746 1630 (+) GCNMNAMCMAG GAGATAACCAG
M00077 V\$GATA3_01 0.867966 1630 (+) NNGATARNG GAGATAACC
M00278 V\$LMO2COM_02 0.930593 1630 (+) NMGATANS GAGATAACC
M00005 V\$AP4_01 0.789049 1631 (-) WGARYCAGCTGYGGNCNK AGATAACCAGCTGGTGGT
M00183 V\$MYB_Q6 0.840664 1632 (+) NNNAACKGNC GATAACCAGC
M00002 V\$E47_01 0.808759 1633 (-) NSNGCAGGTGKNCNN ATAACCAGCTGGTGG
M00005 V\$AP4_01 0.773487 1633 (+) WGARYCAGCTGYGGNCNK ATAACCAGCTGGTGGTGC
M00065 V\$TAL1BETAE47_01 0.829590 1633 (+) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00065 V\$TAL1BETAE47_01 0.839546 1633 (-) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00066 V\$TAL1ALPHAE47_01 0.850389 1633 (+) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00066 V\$TAL1ALPHAE47_01 0.862576 1633 (-) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00070 V\$TAL1BETAITF2_01 0.815244 1633 (+) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00070 V\$TAL1BETAITF2_01 0.835772 1633 (-) NNNAACAGATGKTNNN ATAACCAGCTGGTGGT
M00071 V\$E47_02 0.829087 1633 (+) NNNMRCAGGTGTTMNN ATAACCAGCTGGTGGT
M00071 V\$E47_02 0.827057 1633 (-) NNNMRCAGGTGTTMNN ATAACCAGCTGGTGGT
M00118 V\$MYCMAX_01 0.743561 1634 (+) NNACCACGTGGTNN TAACCAGCTGGTGG
M00118 V\$MYCMAX_01 0.743561 1634 (-) NNACCACGTGGTNN TAACCAGCTGGTGG
M00122 V\$USF_02 0.839030 1634 (+) NNRNCACGTGNYNN TAACCAGCTGGTGG
M00122 V\$USF_02 0.839030 1634 (-) NNRNCACGTGNYNN TAACCAGCTGGTGG
M00001 V\$MYOD_01 0.879134 1635 (+) SRACAGGTGKYG AACCAGCTGGTG
M00001 V\$MYOD_01 0.871260 1635 (-) SRACAGGTGKYG AACCAGCTGGTG
M00075 V\$GATA1_01 0.774926 1635 (-) SNNGATNNNN AACCAGCTGG
M00277 V\$LMO2COM_01 0.890713 1635 (+) SNNCAGGTGNNN AACCAGCTGGTG
M00277 V\$LMO2COM_01 0.911709 1635 (-) SNNCAGGTGNNN AACCAGCTGGTG
M00066 V\$TAL1ALPHAE47_01 0.784829 1636 (+) NNNAACAGATGKTNNN ACCAGCTGGTGGTGCC
M00071 V\$E47_02 0.794814 1636 (+) NNNMRCAGGTGTTMNN ACCAGCTGGTGGTGCC
M00175 V\$AP4_Q5 0.886017 1636 (+) NNCAGCTGNN ACCAGCTGGT
M00175 V\$AP4_Q5 0.886017 1636 (-) NNCAGCTGNN ACCAGCTGGT
M00176 V\$AP4_Q6 0.879980 1636 (+) CWCAGCTGGN ACCAGCTGGT
M00176 V\$AP4_Q6 0.879980 1636 (-) CWCAGCTGGN ACCAGCTGGT
M00184 V\$MYOD_Q6 0.924429 1636 (+) NNCANCTGNY ACCAGCTGGT
M00184 V\$MYOD_Q6 0.924429 1636 (-) NNCANCTGNY ACCAGCTGGT
M00002 V\$E47_01 0.863801 1637 (+) NSNGCAGGTGKNCNN CCAGCTGGTGGTGCC
M00075 V\$GATA1_01 0.786278 1637 (+) SNNGATNNNN CCAGCTGGTG
M00001 V\$MYOD_01 0.887992 1638 (+) SRACAGGTGKYG CAGCTGGTGGTG
M00277 V\$LMO2COM_01 0.830148 1638 (+) SNNCAGGTGNNN CAGCTGGTGGTG
M00184 V\$MYOD_Q6 0.827576 1639 (-) NNCANCTGNY AGCTGGTGGT
M00085 V\$ZID_01 0.801178 1640 (-) NGGCTCYATCAYC GCTGGTGGTGCCA
M00072 V\$CP2_01 0.834048 1641 (-) GCNMNAMCMAG CTGGTGGTGCC
M00109 V\$CEBPB_01 0.856117 1642 (+) RNRTKNGMAAKNN TGGTGGTGCCATCA
M00211 V\$PADS_C 0.821069 1643 (+) NGTGGTCTC GGTGGTGCC
M00239 V\$T3R_01 0.757335 1643 (-) SNNTRAGGTCACGSNN GGTGGTGCCATCAGAG
M00271 V\$AML1_01 0.876099 1643 (+) TGTGGT GGTGGT
M00221 V\$SREBP1_02 0.720902 1644 (-) KATCACCCAC GTGGTGCCATC
M00017 V\$ATF_01 0.761605 1645 (-) CNSTGACGTNNNYC TGGTGCCATCAGAG
M00177 V\$CREB_Q2 0.771926 1646 (+) NSTGACGTAANN GGTGCCATCAGA
M00178 V\$CREB_Q4 0.781424 1646 (+) NSTGACGTMANN GGTGCCATCAGA
M00178 V\$CREB_Q4 0.750631 1646 (-) NSTGACGTMANN GGTGCCATCAGA
M00179 V\$CREBP1_Q2 0.769828 1646 (+) NSTGACGTMASN GGTGCCATCAGA
M00039 V\$CREB_01 0.775797 1648 (-) TGACGTMA TGCCATCA
M00041 V\$CREBP1CJUN_01 0.793611 1648 (+) TGACGTYA TGCCATCA
M00075 V\$GATA1_01 0.872162 1648 (-) SNNGATNNNN TGCCATCAGA
M00076 V\$GATA2_01 0.888588 1648 (-) NNNGATRNNN TGCCATCAGA
M00077 V\$GATA3_01 0.828090 1648 (-) NNGATARNG TGCCATCAG
M00065 V\$TAL1BETAE47_01 0.776106 1649 (+) NNNAACAGATGKTNNN GCCATCAGAGGGCCTG

M00070 V\$TALIBETAITF2_01 0.804472 1649 (+) NNNAACAGATGKTNNN GCCATCAGAGGGCCTG
M00215 V\$SRF_C 0.752284 1649 (+) NCCWTATATGGNCWN GCCATCAGAGGGCCT
M00122 V\$USF_02 0.750155 1650 (+) NNRNCACGTGNYNN CCATCAGAGGGCCT
M00122 V\$USF_02 0.750155 1650 (-) NNRNCACGTGNYNN CCATCAGAGGGCCT
M00175 V\$AP4_Q5 0.792165 1652 (+) NNCAGCTGNN ATCAGAGGGC
M00176 V\$AP4_Q6 0.806815 1652 (+) CWCAGCTGGN ATCAGAGGGC
M00253 V\$CAP_01 0.8174815 1653 (+) NCANNNNN TCAGAGGG
M00057 V\$COMP1_01 0.790060 1656 (-) NNTNWKGATTGRCNRSRANMRRNN GAGGGCCTGTACCTCATCTACTCC
M00115 V\$TAXCREB_02 0.713290 1658 (-) RTGACGCATAYCCCC GGGCCTGTACCTCAT
M00272 V\$P53_02 0.813599 1658 (-) NGRCWTGYCY GGGCCTGTAC
M00239 V\$T3R_01 0.736513 1659 (-) SNNTRAGGTCACGSNN GGCCTGTACCTCATCT
M00068 V\$HEN1_01 0.739011 1662 (+) NNNGGNCNCAGCTGCGNCCCNN CTGTACCTCATCTACTCCCAGG
M00068 V\$HEN1_01 0.732683 1662 (-) NNNGGNCNCAGCTGCGNCCCNN CTGTACCTCATCTACTCCCAGG
M00177 V\$CREB_Q2 0.769751 1662 (-) NSTGACGTAANN CTGTACCTCATC
M00174 V\$AP1_Q6 0.776984 1663 (-) NNTGACTCANN TGTACCTCATC
M00205 V\$GRE_C 0.772016 1663 (+) GGTACAANNTGTYCTK TGTACCTCATCTACTC
M00037 V\$NFE2_01 0.857379 1664 (-) TGCTGASTCAY GTACCTCATCT
M00039 V\$CREB_01 0.781058 1664 (-) TGACGTMA GTACCTCA
M00040 V\$CREBP1_01 0.751028 1664 (-) TTACGTAA GTACCTCA
M00078 V\$EVII_01 0.757254 1664 (-) WGAYAAGATAAGATAA GTACCTCATCTACTCC
M00080 V\$EVII_03 0.754733 1664 (-) AGATAAGATAA GTACCTCATCT
M00113 V\$CREB_02 0.865369 1664 (-) NNGNTGACGYNN GTACCTCATCTA
M00115 V\$TAXCREB_02 0.673984 1664 (+) RTGACGCATAYCCCC GTACCTCATCTACTC
M00126 V\$GATA1_02 0.780312 1665 (-) NNNNNGATANKGNN TACCTCATCTACTC
M00271 V\$AML1_01 0.910841 1666 (-) TGTGGT ACCTCA
M00075 V\$GATA1_01 0.845015 1667 (-) SNNGATNNNN CCTCATCTAC
M00076 V\$GATA2_01 0.803338 1667 (-) NNNGATRNNN CCTCATCTAC
M00077 V\$GATA3_01 0.876385 1667 (-) NNGATARNG CCTCATCTA
M00278 V\$LMO2COM_02 0.807951 1667 (-) NMGATANS GCTCATCTA
M00253 V\$CAP_01 0.892065 1669 (+) NCANNNNN TCATCTAC
M00033 V\$P300_01 0.836060 1670 (-) NNNRGGAGTNNNS CATCTACTCCCAGG
M00255 V\$GC_01 0.798138 1670 (-) NRGGGGCGGGGCKN CATCTACTCCCAGG
M00071 V\$E47_02 0.791206 1675 (+) NNNMRCAGGTGTTMNN ACTCCCAGGTCCTCTT
M00141 V\$LYF1_01 0.821876 1675 (-) TTTGGGAGR ACTCCCAGG
M00222 V\$TH1E47_01 0.800334 1675 (-) NNNNGNRTCTGGMWTT ACTCCCAGGTCCTCTT
M00189 V\$AP2_Q6 0.804228 1676 (+) MKCCCSCNGGCG CTCCCAGGTCCT
M00277 V\$LMO2COM_01 0.815343 1677 (+) SNNCAGGTGNNN TCCCAGGTCCTC
M00255 V\$GC_01 0.784174 1680 (-) NRGGGGCGGGGCKN CAGGTCCTCTTCAA
M00017 V\$ATF_01 0.747181 1682 (-) CNSTGACGTNNNYC GGTCTCTTCAAGG
M00098 V\$PAX2_01 0.786049 1685 (+) NNNNGTCANGNRTKANNNN CCTCTTCAAGGGCCAAGGC
M00193 V\$NF1_Q6 0.792164 1685 (-) NNTTGGCNNNNNNCCNNN CCTCTTCAAGGGCCAAGG
M00158 V\$COUP_01 0.870074 1686 (-) TGAMCTTTGMMCYT CTCTTCAAGGGCCA
M00227 V\$VMYB_02 0.812876 1689 (+) NSYAACGGN TTCAAGGGC
M00134 V\$HNF4_01 0.783802 1690 (+) NNNRGGNCAAAGKTCANN TCAAGGGCCAAGGCTGCCC
M00240 V\$NKX25_01 0.852443 1690 (+) TYAAGTG TCAAGGG
M00254 V\$CAAT_01 0.813894 1690 (-) NNNRRCCAATSA TCAAGGGCCAAG
M00058 V\$HEN1_02 0.720938 1692 (+) NNGGGNCGCAGCTGCGNCCCNN AAGGGCCAAGGCTGCCCCCTCCA
M00058 V\$HEN1_02 0.711893 1692 (-) NNGGGNCGCAGCTGCGNCCCNN AAGGGCCAAGGCTGCCCCCTCCA
M00155 V\$ARP1_01 0.857496 1692 (-) TGARCCYTTGAMCCYW AAGGGCCAAGGCTGCC
M00254 V\$CAAT_01 0.787066 1692 (+) NNNRRCCAATSA AAGGGCCAAGGC
M00005 V\$AP4_01 0.779107 1693 (-) WGARYCAGCTGYGGNCKN AGGGCCAAGGCTGCCCCCT
M00050 V\$E2F_02 0.743405 1694 (-) TTTSGCGC GGGCCAAG
M00255 V\$GC_01 0.791769 1698 (-) NRGGGGCGGGGCKN CAAGGCTGCCCCCTC
M00008 V\$SP1_01 0.824745 1700 (-) GRGGCRGGGW AGGCTGCCCC
M00054 V\$NFKAPPAB_01 0.801248 1700 (-) GGGAMTTYCC AGGCTGCCCC
M00115 V\$TAXCREB_02 0.614654 1700 (+) RTGACGCATAYCCCC AGGCTGCCCCCTCCAC
M00143 V\$PAX5_01 0.797775 1700 (-) NCNNNRNKCANNNGNWNKRKRGRCSRSNN
AGGCTGCCCCCTCCACCATGTGCTCCTC
M00255 V\$GC_01 0.780745 1700 (-) NRGGGGCGGGGCKN AGGCTGCCCCCTCCA
M00008 V\$SP1_01 0.804077 1702 (-) GRGGCRGGGW GCTGCCCCCTC
M00143 V\$PAX5_01 0.774094 1702 (-) NCNNNRNKCANNNGNWNKRKRGRCSRSNN

GCTGCCCTCCACCATGTGCTCCTCAC
M00084 V\$MZF1_02 0.913772 1703 (-) KNNKAGGGGNA CTGCCCCCTCCACC
M00115 V\$TAXCREB_02 0.612133 1703 (+) RTGACGCATAYCCCC CTGCCCCCTCCACCCA
M00255 V\$GC_01 0.799853 1703 (-) NRGGGGCGGGGCKN CTGCCCCCTCCACCC
M00273 V\$R_01 0.766783 1703 (+) NNGKCCNCSNRNYGTGGTGYN CTGCCCCCTCCACCATGTGCT
M00196 V\$SP1_Q6 0.827459 1704 (-) NGGGGGCGGGGYN TGCCCCCTCCACCC
M00008 V\$SP1_01 0.799830 1705 (-) GRGGCRGGGW GCCCTCCAC
M00083 V\$MZF1_01 0.846997 1705 (-) NGNGGGGA GCCCTCC
M00255 V\$GC_01 0.870162 1706 (-) NRGGGGCGGGGCKN CCCCTCCACCCATG
M00196 V\$SP1_Q6 0.816675 1707 (-) NGGGGGCGGGGYN CCCTCCACCCATG
M00244 V\$NGFIC_01 0.740646 1707 (-) WTGCGTGGGYGG CCCTCCACCCAT
M00072 V\$CP2_01 0.791595 1708 (+) GCMNAMCMAG CCTCCACCCAT
M00083 V\$MZF1_01 0.840196 1710 (-) NGNGGGGA TCCACCCA
M00155 V\$ARP1_01 0.775047 1710 (+) TGARCCYTTGAMCCYW TCCACCCATGTGCTCC
M00002 V\$E47_01 0.800522 1711 (-) NSNGCAGGTGKNCNN CCACCCATGTGCTCC
M00071 V\$E47_02 0.809019 1711 (+) NNNMRCAGGTGTTMNN CCACCCATGTGCTCCT
M00236 V\$ARNT_01 0.783659 1711 (-) NNNNNCACGTGNNNNN CCACCCATGTGCTCCT
M00244 V\$NGFIC_01 0.761998 1711 (-) WTGCGTGGGYGG CCACCCATGTGC
M00118 V\$MYCMAX_01 0.775977 1712 (+) NNACCACGTGGTNN CACCCATGTGCTCC
M00118 V\$MYCMAX_01 0.775977 1712 (-) NNACCACGTGGTNN CACCCATGTGCTCC
M00119 V\$MAX_01 0.755885 1712 (+) NNANCACGTGNTNN CACCCATGTGCTCC
M00119 V\$MAX_01 0.755885 1712 (-) NNANCACGTGNTNN CACCCATGTGCTCC
M00121 V\$USF_01 0.792876 1712 (+) NNRYCACGTGRYNN CACCCATGTGCTCC
M00121 V\$USF_01 0.792876 1712 (-) NNRYCACGTGRYNN CACCCATGTGCTCC
M00122 V\$USF_02 0.836234 1712 (+) NNRNCACGTGNYNN CACCCATGTGCTCC
M00122 V\$USF_02 0.836234 1712 (-) NNRNCACGTGNYNN CACCCATGTGCTCC
M00055 V\$NMYC_01 0.844586 1713 (+) NNNCACGTGNNN ACCCATGTGCTC
M00055 V\$NMYC_01 0.774331 1713 (-) NNNCACGTGNNN ACCCATGTGCTC
M00076 V\$GATA2_01 0.823636 1713 (-) NNNGATRNNN ACCCATGTGC
M00123 V\$MYCMAX_02 0.790649 1713 (+) NANCACGTGNNW ACCCATGTGCTC
M00123 V\$MYCMAX_02 0.914894 1713 (-) NANCACGTGNNW ACCCATGTGCTC
M00217 V\$USF_C 0.857095 1713 (+) NCACGTGN ACCCATGT
M00277 V\$LMO2COM_01 0.898789 1713 (+) SNNCAGGTGNNN ACCCATGTGCTC
M00184 V\$MYOD_Q6 0.844540 1714 (+) NNCANCTGNY CCCATGTGCT
M00217 V\$USF_C 0.925193 1715 (+) NCACGTGN CCATGTGC
M00217 V\$USF_C 0.864475 1715 (-) NCACGTGN CCATGTGC
M00056 V\$MYOGNF1_01 0.759087 1716 (-) CRSCTGTNNNNNTTGGCACNSNGCCARNN
CATGTGCTCCTCACCCACACCATCAGCCG
M00084 V\$MZF1_02 0.894526 1719 (-) KNNKAGGGGNA GTGCTCCTCACCC
M00115 V\$TAXCREB_02 0.634678 1719 (+) RTGACGCATAYCCCC GTGCTCCTCACCCAC
M00255 V\$GC_01 0.791769 1719 (-) NRGGGGCGGGGCKN GTGCTCCTCACCCA
M00114 V\$TAXCREB_01 0.729697 1720 (-) GGGGGTTGACGYANA TGCTCCTCACCCACA
M00196 V\$SP1_Q6 0.758285 1720 (-) NGGGGGCGGGGYN TGCTCCTCACCCA
M00237 V\$AHRARNT_02 0.721960 1720 (-) GRGKATYGCGTGMSWNSCC TGCTCCTCACCCACACCAT
M00113 V\$CREB_02 0.853800 1721 (-) NNGNTGACGYNN GCTCCTCACCCA
M00083 V\$MZF1_01 0.886664 1723 (-) NGNGGGGA TCCTCACC
M00235 V\$AHRARNT_01 0.770002 1724 (-) KNNKNNTYGCGTGCMS CCTCACCCACACCATC
M00257 V\$RREB1_01 0.827031 1724 (+) CCCCCAACMMCCCC CCTCACCCACACCA
M00115 V\$TAXCREB_02 0.693266 1725 (+) RTGACGCATAYCCCC CTCACCCACACCATC
M00243 V\$EGR1_01 0.753766 1726 (-) WTGCGTGGGCGK TCACCCACACCA
M00244 V\$NGFIC_01 0.788443 1726 (-) WTGCGTGGGYGG TCACCCACACCA
M00246 V\$EGR2_01 0.800253 1726 (-) NTGCGTRGGCGK TCACCCACACCA
M00253 V\$CAP_01 0.903894 1726 (+) NCANNNNN TCACCCAC
M00033 V\$P300_01 0.825494 1727 (-) NNNRGGAGTNNNS CACCCACACCATCA
M00189 V\$AP2_Q6 0.801471 1727 (+) MKCCCSCNGGCG CACCCACACCAT
M00255 V\$GC_01 0.791279 1727 (-) NRGGGGCGGGGCKN CACCCACACCATCA
M00257 V\$RREB1_01 0.838223 1728 (+) CCCCCAACMMCCCC ACCCACACCATCAG
M00002 V\$E47_01 0.796906 1731 (-) NSNGCAGGTGKNCNN CACACCATCAGCCGC
M00066 V\$TAL1ALPHA E47_01 0.807733 1731 (-) NNNAACAGATGKTNNN CACACCATCAGCCGCA
M00070 V\$TAL1BETA ITF2_01 0.773780 1731 (-) NNNAACAGATGKTNNN CACACCATCAGCCGCA
M00173 V\$AP1_Q2 0.791801 1732 (-) RSTGACTNMNW ACACCATCAGC

M00001 V\$MYOD_01 0.801378 1733 (-) SRACAGGTGKYG CACCATCAGCCG
M00075 V\$GATA1_01 0.975321 1733 (-) SNNGATNNNN CACCATCAGC
M00076 V\$GATA2_01 0.926928 1733 (-) NNNGATRNNN CACCATCAGC
M00077 V\$GATA3_01 0.879043 1733 (-) NNGATARNG CACCATCAG
M00277 V\$LMO2COM_01 0.795962 1733 (-) SNNCAGGTGNNN CACCATCAGCCG
M00184 V\$MYOD_Q6 0.819864 1734 (+) NNCANCTGNY ACCATCAGCC
M00004 V\$CMYB_01 0.751788 1735 (-) NCNRNNGRCNGTTGGKGG CCATCAGCCGCATCGCCG
M00115 V\$TAXCREB_02 0.631415 1737 (+) RTGACGCATAYCCCC ATCAGCCGCATCGCC
M00175 V\$AP4_Q5 0.814744 1737 (+) NNCAGCTGNN ATCAGCCGCA
M00176 V\$AP4_Q6 0.819344 1737 (+) CWCAGCTGGN ATCAGCCGCA
M00184 V\$MYOD_Q6 0.775139 1737 (-) NNCANCTGNY ATCAGCCGCA
M00253 V\$CAP_01 0.950222 1738 (+) NCANNNNN TCAGCCGC
M00271 V\$AML1_01 0.857262 1741 (-) TGTGGT GCCGCA
M00075 V\$GATA1_01 0.963968 1742 (-) SNNGATNNNN CCGCATCGCC
M00076 V\$GATA2_01 0.805593 1742 (+) NNNGATRNNN CCGCATCGCC
M00076 V\$GATA2_01 0.916103 1742 (-) NNNGATRNNN CCGCATCGCC
M00077 V\$GATA3_01 0.837395 1742 (-) NNGATARNG CCGCATCGC
M00278 V\$LMO2COM_02 0.794137 1742 (-) NMGATANS CCGCATCGC
M00057 V\$COMP1_01 0.779162 1748 (-) NNTNWKGATTGRCNRSRANMRRN CGCCGTCTCTACCAGACCAAGGT
M00075 V\$GATA1_01 0.789733 1748 (-) SNNGATNNNN CGCCGTCTCC
M00076 V\$GATA2_01 0.797474 1748 (-) NNNGATRNNN CGCCGTCTCC
M00189 V\$AP2_Q6 0.815257 1754 (+) MKCCCSCNGGCG CTCCTACCAGAC
M00141 V\$LYF1_01 0.855098 1756 (-) TTTGGGAGR CCTACCAGA
M00222 V\$TH1E47_01 0.806528 1756 (-) NNNNGNRTCTGGMWTT CCTACCAGACCAAGGT
M00072 V\$CP2_01 0.875643 1759 (+) GCNMNAMCMAG ACCAGACCAAG
M00271 V\$AML1_01 0.873587 1759 (-) TGTGGT ACCAGA
M00211 V\$PADS_C 0.827117 1761 (-) NGTGGTCTC CAGACCAAG
M00156 V\$RORA1_01 0.902929 1762 (+) NWAOWNAGGTCAN AGACCAAGGTCAA
M00157 V\$RORA2_01 0.793403 1762 (+) NWAOWNAGGTCAN AGACCAAGGTCAA
M00185 V\$NFY_Q6 0.779291 1762 (+) TRRCCAATSRN AGACCAAGGTC
M00017 V\$ATF_01 0.750328 1763 (-) CNSTGACGTNNNYC GACCAAGGTCAACC
M00239 V\$T3R_01 0.843271 1763 (+) SNNTRAGGTCACGSNN GACCAAGGTCAACCTC
M00073 V\$DELTAEF1_01 0.825211 1765 (-) NNNCACCTNAN CCAAGGTCAAC
M00114 V\$TAXCREB_01 0.711111 1765 (-) GGGGGTTGACGYANA CCAAGGTCAACCTCC
M00113 V\$CREB_02 0.786484 1766 (-) NNGNTGACGYNN CAAGGTCAACCT
M00191 V\$ER_Q6 0.801806 1766 (-) NNARGNANNTGACCYNN CAAGGTCAACCTCCTCTCT
M00255 V\$GC_01 0.828025 1767 (-) NRGGGGCGGGGCKN AAGGTCAACCTCCT
M00269 V\$XFD3_01 0.813399 1767 (+) WNWGTMAACAWWMW AAGGTCAACCTCCT
M00004 V\$CMYB_01 0.771949 1768 (-) NCNRNNGRCNGTTGGKGG AGGTCAACCTCCTCTCTG
M00212 V\$POLY_C 0.775105 1768 (+) CAATAAAACCYYYKCTN AGGTCAACCTCCTCTCTG
M00007 V\$ELK1_01 0.802939 1770 (-) NNNACMGGAAGTNCNN GTCAACCTCCTCTCTG
M00183 V\$MYB_Q6 0.892946 1770 (+) NNNAACKGNC GTCAACCTCC
M00253 V\$CAP_01 0.894529 1771 (+) NCANNNNN TCAACCTC
M00057 V\$COMP1_01 0.815090 1773 (-) NNTNWKGATTGRCNRSRANMRRN AACCTCCTCTCTGCCATCAAGAGC
M00057 V\$COMP1_01 0.791138 1775 (+) NNTNWKGATTGRCNRSRANMRRN CCTCCTCTCTGCCATCAAGAGCCC
M00128 V\$GATA1_04 0.814645 1775 (-) NNCWGATARNNN CCTCCTCTCTGCC
M00083 V\$MZF1_01 0.857575 1777 (-) NGNGGGGA TCCTCTCT
M00085 V\$ZID_01 0.808963 1778 (+) NGGCTCYATCAYC CCTCTCTGCCATC
M00141 V\$LYF1_01 0.826220 1778 (-) TTTGGGAGR CCTCTCTGC
M00008 V\$SP1_01 0.827576 1780 (-) GRGGCRGGGW TCTCTGCCAT
M00069 V\$YY1_02 0.763834 1780 (+) NNNCGGCCATCTTGNCTSNW TCTCTGCCATCAAGAGCCCC
M00178 V\$CREB_Q4 0.752398 1782 (+) NSTGACGTMANN TCTGCCATCAAG
M00039 V\$CREB_01 0.775797 1784 (-) TGACGTMA TGCCATCA
M00041 V\$CREBP1CJUN_01 0.793611 1784 (+) TGACGYA TGCCATCA
M00075 V\$GATA1_01 0.876111 1784 (-) SNNGATNNNN TGCCATCAAG
M00076 V\$GATA2_01 0.807848 1784 (-) NNNGATRNNN TGCCATCAAG
M00104 V\$CDPCR1_01 0.816346 1785 (-) NATCGATCGS GCCATCAAGA
M00004 V\$CMYB_01 0.768480 1786 (-) NCNRNNGRCNGTTGGKGG CCATCAAGAGCCCCTGCC
M00056 V\$MYOGNF1_01 0.760909 1789 (-) CRSCTGTNNNTTTGGCACNSNGCCARNN
TCAAGAGCCCCTGCCAGAGGGAGACCCCA
M00143 V\$PAX5_01 0.760656 1789 (+) NCNNNRNKCANNGNWGNRKRGCSSNNN

TCAAGAGCCCCTGCCAGAGGGAGACCCC
M00240 V\$NKX25_01 0.852443 1789 (+) TYAAGTG TCAAGAG
M00193 V\$NF1_Q6 0.831038 1790 (-) NNTTGGCNNNNNNCCNN CAAGAGCCCCTGCCAGAG
M00071 V\$E47_02 0.763021 1791 (-) NNNMRCAGGTGTTMNN AAGAGCCCCTGCCAGA
M00122 V\$USF_02 0.768800 1792 (+) NNRNCACGTGNYNN AGAGCCCCTGCCAG
M00122 V\$USF_02 0.768800 1792 (-) NNRNCACGTGNYNN AGAGCCCCTGCCAG
M00255 V\$GC_01 0.801568 1793 (-) NRGGGGCGGGGCKN GAGCCCCTGCCAGA
M00277 V\$LMO2COM_01 0.812921 1793 (-) SNNCAGGTGNNN GAGCCCCTGCCA
M00175 V\$AP4_Q5 0.781284 1794 (-) NNCAGCTGNN AGCCCCTGCC
M00176 V\$AP4_Q6 0.780005 1794 (-) CWCAGCTGGN AGCCCCTGCC
M00184 V\$MYOD_Q6 0.845157 1794 (+) NNCANCTGNY AGCCCCTGCC
M00196 V\$SP1_Q6 0.788795 1794 (-) NGGGGGCGGGGYN AGCCCCTGCCAGA
M00072 V\$CP2_01 0.806175 1795 (+) GCNMNAMCMAG GCCCCTGCCAG
M00139 V\$AHR_01 0.712706 1795 (+) CYYCNRRSTNGCGTGASW GCCCCTGCCAGAGGGAGA
M00217 V\$USF_C 0.831600 1795 (+) NCACGTGN GCCCCTGC
M00261 V\$OLF1_01 0.791830 1795 (-) NNCNANTCCCYNGRGARNNKGN GCCCCTGCCAGAGGGAGACCCC
M00189 V\$AP2_Q6 0.781939 1796 (+) MKCCCSCNGGCG CCCCTGCCAGAG
M00141 V\$LYF1_01 0.914388 1798 (-) TTTGGGAGR CCTGCCAGA
M00189 V\$AP2_Q6 0.822151 1800 (-) MKCCCSCNGGCG TGCCAGAGGGAG
M00184 V\$MYOD_Q6 0.792721 1801 (-) NNCANCTGNY GCCAGAGGGA
M00115 V\$TAXCREB_02 0.648027 1803 (+) RTGACGCATAYCCCC CAGAGGGAGACCCCA
M00108 V\$NRF2_01 0.791667 1804 (+) ACCGGAAGNS AGAGGGAGAC
M00194 V\$NFKB_Q6 0.803068 1804 (-) NGGGGAMTTTCCNN AGAGGGAGACCCCA
M00008 V\$SP1_01 0.803228 1805 (+) GRGGCRGGGW GAGGGAGACC
M00194 V\$NFKB_Q6 0.783167 1805 (+) NGGGGAMTTTCCNN GAGGGAGACCCCAG
M00239 V\$T3R_01 0.816771 1805 (-) SNNTRAGGTCACGSNN GAGGGAGACCCCAGAG
M00051 V\$NFKAPPAB50_01 0.772990 1806 (+) GGGGATYCCC AGGGAGACCC
M00208 V\$NFKB_C 0.812762 1806 (+) NGGGACTTTCCA AGGGAGACCCCA
M00261 V\$OLF1_01 0.798225 1806 (+) NNCNANTCCCYNGRGARNNKGN AGGGAGACCCCAGAGGGGGGCTG
M00017 V\$ATF_01 0.754524 1807 (-) CNSTGACGTNNNYC GGGAGACCCCAGAG
M00051 V\$NFKAPPAB50_01 0.843403 1807 (-) GGGGATYCCC GGGAGACCCC
M00052 V\$NFKAPPAB65_01 0.776287 1807 (+) GGGRATTTCC GGGAGACCCC
M00052 V\$NFKAPPAB65_01 0.807425 1807 (-) GGGRATTTCC GGGAGACCCC
M00054 V\$NFKAPPAB_01 0.831710 1807 (+) GGGAMTTYCC GGGAGACCCC
M00054 V\$NFKAPPAB_01 0.870162 1807 (-) GGGAMTTYCC GGGAGACCCC
M00052 V\$NFKAPPAB65_01 0.829701 1808 (-) GGGRATTTCC GGAGACCCCA
M00053 V\$CREL_01 0.835651 1808 (-) SGRNWTTC GGAGACCCCA
M00068 V\$HEN1_01 0.736446 1808 (-) NNNGGNCNCAGCTGCGNCCCN GGAGACCCCAGAGGGGGGCTGAG
M00072 V\$CP2_01 0.842624 1808 (+) GCNMNAMCMAG GGAGACCCCAG
M00261 V\$OLF1_01 0.764683 1808 (+) NNCNANTCCCYNGRGARNNKGN GGAGACCCCAGAGGGGGGCTGAG
M00261 V\$OLF1_01 0.783346 1808 (-) NNCNANTCCCYNGRGARNNKGN GGAGACCCCAGAGGGGGGCTGAG
M00005 V\$AP4_01 0.763112 1809 (-) WGARYCAGCTGYGGNCNK GAGACCCCAGAGGGGGGCT
M00211 V\$PADS_C 0.883569 1809 (-) NGTGGTCTC GAGACCCCA
M00189 V\$AP2_Q6 0.797794 1810 (+) MKCCCSCNGGCG AGACCCCAGAGG
M00189 V\$AP2_Q6 0.824678 1811 (+) MKCCCSCNGGCG GACCCCAGAGGG
M00189 V\$AP2_Q6 0.802849 1812 (+) MKCCCSCNGGCG ACCCCAGAGGGG
M00271 V\$AML1_01 0.866053 1812 (-) TGTGGT ACCCA
M00075 V\$GATA1_01 0.798618 1815 (+) SNNGATNNNN CCAGAGGGGG
M00083 V\$MZF1_01 0.857575 1817 (+) NGNGGGGA AGAGGGGG
M00134 V\$HNF4_01 0.794011 1818 (+) NNNRGGNCAAAGKTCANNN GAGGGGGGCTGAGGCCAAGC
M00008 V\$SP1_01 0.822197 1819 (+) GRGGCRGGGW AGGGGGGCTGA
M00193 V\$NF1_Q6 0.842975 1819 (-) NNTTGGCNNNNNNCCNNN AGGGGGGCTGAGGCCAAGC
M00196 V\$SP1_Q6 0.849027 1819 (+) NGGGGGCGGGGYN AGGGGGGCTGAGGC
M00255 V\$GC_01 0.817491 1819 (+) NRGGGGCGGGGCKN AGGGGGGCTGAGGCC
M00114 V\$TAXCREB_01 0.855354 1820 (+) GGGGGTTGACGYANA GGGGGGCTGAGGCCAA
M00158 V\$COUP_01 0.859816 1820 (-) TGAMCTTTGMMCYT GGGGGGCTGAGGCCA
M00175 V\$AP4_Q5 0.801143 1820 (-) NNCAGCTGNN GGGGGGCTGAG
M00176 V\$AP4_Q6 0.812328 1820 (-) CWCAGCTGGN GGGGGGCTGAG
M00008 V\$SP1_01 0.799830 1821 (+) GRGGCRGGGW GGGGGGCTGAGG
M00113 V\$CREB_02 0.856166 1822 (+) NNGNTGACGYNN GGGGCTGAGGCCA
M00017 V\$ATF_01 0.742722 1823 (+) CNSTGACGTNNNYC GGCTGAGGCCAAGC

M00037 V\$NFE2_01 0.806251 1823 (+) TGCTGASTCAY GGCTGAGGCCA
M00109 V\$CEBPB_01 0.811540 1823 (+) RNRTKNNGMAAKNN GGCTGAGGCCAAGC
M00239 V\$T3R_01 0.847057 1823 (+) SNNTRAGGTCACGSNN GGCTGAGGCCAAGCCC
M00174 V\$AP1_Q6 0.767582 1824 (+) NNTGACTCANN GCTGAGGCCAA
M00177 V\$CREB_Q2 0.808649 1824 (+) NSTGACGTAANN GCTGAGGCCAAG
M00178 V\$CREB_Q4 0.805149 1824 (+) NSTGACGTMANN GCTGAGGCCAAG
M00179 V\$CREBP1_Q2 0.801308 1824 (+) NSTGACGTMASN GCTGAGGCCAAG
M00115 V\$TAXCREB_02 0.610205 1825 (+) RTGACGCATAYCCCC CTGAGGCCAAGCCCT
M00039 V\$CREB_01 0.775797 1826 (+) TGACGTMA TGAGGCCA
M00039 V\$CREB_01 0.774627 1826 (-) TGACGTMA TGAGGCCA
M00155 V\$ARP1_01 0.824924 1826 (-) TGARCCYTTGAMCCYW TGAGGCCAAGCCCTGG
M00254 V\$CAAT_01 0.809941 1826 (+) NNNRRCOAATSA TGAGGCCAAGCC
M00005 V\$AP4_01 0.796398 1828 (+) WGARYCAGCTGYGGNCK AGGCCAAGCCCTGGTATG
M00255 V\$GC_01 0.827536 1828 (-) NRGGGGCGGGGCK AGGCCAAGCCCTGG
M00196 V\$SP1_Q6 0.767491 1829 (-) NGGGGGCGGGGYN GGCCAAGCCCTGG
M00272 V\$P53_02 0.849648 1829 (+) NGRCWTGYCY GGCCAAGCCC
M00272 V\$P53_02 0.834408 1829 (-) NGRCWTGYCY GGCCAAGCCC
M00008 V\$SP1_01 0.886750 1830 (-) GRGGCRGGGW GCCAAGCCCT
M00072 V\$CP2_01 0.791166 1830 (+) GCNMNAMCMAG GCCAAGCCCTG
M00155 V\$ARP1_01 0.777374 1831 (+) TGARCCYTTGAMCCYW CCAAGCCCTGGTATGA
M00127 V\$GATA1_03 0.804998 1837 (-) RNSNNGATAANNGN CCTGGTATGAGCCC
M00072 V\$CP2_01 0.896226 1838 (-) GCNMNAMCMAG CTGGTATGAGC
M00076 V\$GATA2_01 0.798376 1839 (-) NNNGATRNNN TGGTATGAGC
M00239 V\$T3R_01 0.757903 1839 (-) SNNTRAGGTCACGSNN TGGTATGAGCCCATCT
M00201 V\$CEBP_C 0.818259 1840 (+) NGWNTKNKGAAKNSAYA GGTATGAGCCCATCTATC
M00221 V\$SREBP1_02 0.720902 1842 (+) KATCACCCAC TATGAGCCCAT
M00059 V\$YY1_01 0.798820 1844 (+) NNNNNCCATNTWNNNNWN TGAGCCCATCTATCTGG
M00002 V\$E47_01 0.790277 1845 (-) NSNGCAGGTGKNCNN GAGCCCATCTATCTG
M00066 V\$TAL1ALPHA47_01 0.769279 1845 (-) NNNAACAGATGKTNNN GAGCCCATCTATCTGG
M00070 V\$TAL1BETA1F2_01 0.763211 1845 (-) NNNAACAGATGKTNNN GAGCCCATCTATCTGG
M00084 V\$MZF1_02 0.821295 1845 (-) KNNNKAGGGGNA GAGCCCATCTATC
M00075 V\$GATA1_01 0.819348 1847 (-) SNNGATNNNN GCCCATCTAT
M00076 V\$GATA2_01 0.791159 1847 (-) NNNGATRNNN GCCCATCTAT
M00077 V\$GATA3_01 0.837838 1847 (-) NNGATARNNG GCCCATCTA
M00104 V\$CDPCR1_01 0.807555 1848 (-) NATCGATCGS CCCATCTATC
M00106 V\$CDPCR3HD_01 0.935698 1848 (-) NATYGATSSS CCCATCTATC
M00184 V\$MYOD_Q6 0.805059 1848 (+) NNCANCTGNY CCCATCTATC
M00105 V\$CDPCR3_01 0.757180 1849 (-) CACCRATANNTATNG CCATCTATCTGGGAG
M00126 V\$GATA1_02 0.839375 1849 (-) NNNNNGATANKGNN CCATCTATCTGGGA
M00127 V\$GATA1_03 0.786134 1849 (-) RNSNNGATAANNGN CCATCTATCTGGGA
M00128 V\$GATA1_04 0.860294 1849 (-) NNCWGATARNNNN CCATCTATCTGGG
M00104 V\$CDPCR1_01 0.810485 1850 (+) NATCGATCGS CATCTATCTG
M00106 V\$CDPCR3HD_01 0.843426 1850 (+) NATYGATSSS CATCTATCTG
M00075 V\$GATA1_01 0.908193 1851 (-) SNNGATNNNN ATCTATCTGG
M00076 V\$GATA2_01 0.907984 1851 (-) NNNGATRNNN ATCTATCTGG
M00077 V\$GATA3_01 0.869296 1851 (-) NNGATARNNG ATCTATCTG
M00278 V\$LMO2COM_02 0.826819 1851 (-) NMGATANSNG ATCTATCTG
M00115 V\$TAXCREB_02 0.620587 1856 (-) RTGACGCATAYCCCC TCTGGGAGGGGTCTT
M00141 V\$LYF1_01 0.970866 1856 (+) TTTGGGAGR TCTGGGAGG
M00196 V\$SP1_Q6 0.875855 1856 (+) NGGGGGCGGGGYN TCTGGGAGGGGTCT
M00255 V\$GC_01 0.916707 1856 (+) NRGGGGCGGGGCK TCTGGGAGGGGTCT
M00008 V\$SP1_01 0.847961 1858 (+) GRGGCRGGGW TGGGAGGGGT
M00146 V\$HSF1_01 0.763293 1860 (+) RGAANRTTCN GGAGGGGTCT
M00147 V\$HSF2_01 0.821072 1860 (+) NGAANNWTCK GGAGGGGTCT
M00221 V\$SREBP1_02 0.720902 1861 (-) KATCACCCAC GAGGGGTCTTC
M00194 V\$NFKB_Q6 0.782338 1862 (+) NGGGGAMTTTCCNN AGGGGTCTTCCAGC
M00208 V\$NFKB_C 0.779707 1862 (+) NGGGACTTTCCA AGGGGTCTTCCA
M00211 V\$PADS_C 0.843498 1862 (+) NGTGGTCTC AGGGGTCTT
M00007 V\$ELK1_01 0.755177 1863 (-) NNNACMGGAAGTNCNN GGGGTCTTCCAGCTGG
M00051 V\$NFKAPPAB50_01 0.798978 1863 (+) GGGGATYCCC GGGGTCTTCC
M00052 V\$NFKAPPAB65_01 0.844790 1863 (+) GGGRATTTC GGGGTCTTCC

M00053 V\$CREL_01 0.921023 1863 (+) SGGRNWTTCC GGGGTCTTCC
M00054 V\$NFKAPPAB_01 0.872909 1863 (+) GGGAMTTYCC GGGGTCTTCC
M00144 V\$PAX5_02 0.753564 1863 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
GGGGTCTTCCAGCTGGAGAAGGGTGACC
M00208 V\$NFKB_C 0.789540 1863 (+) NGGGACTTTCCA GGGGTCTTCCAG
M00025 V\$ELK1_02 0.847873 1865 (-) NNNNCCGGAARYNN GGTCTTCCAGCTGG
M00074 V\$CETSIP54_02 0.842605 1865 (-) NNAMMGGAWRWNN GGTCTTCCAGCTG
M00086 V\$IK1_01 0.772703 1865 (-) NNNTGGGAATRCC GGTCTTCCAGCTG
M00032 V\$CETSIP54_01 0.862303 1866 (-) NCMGGAWGYN GTCTTCCAGC
M00108 V\$NRF2_01 0.837452 1866 (-) ACCGGAAGNS GTCTTCCAGC
M00005 V\$AP4_01 0.802017 1867 (+) WGARYCAGCTGYGGNCKN TCTTCCAGCTGGAGAAGG
M00066 V\$TALIALPHA47_01 0.760874 1867 (+) NNNAACAGATGKTNNN TCTTCCAGCTGGAGAA
M00071 V\$E47_02 0.787148 1867 (+) NNNMRCAGGTGTTMNN TCTTCCAGCTGGAGAA
M00071 V\$E47_02 0.793010 1867 (-) NNNMRCAGGTGTTMNN TCTTCCAGCTGGAGAA
M00141 V\$LYF1_01 0.825198 1867 (-) TTTGGGAGR TCTTCCAGC
M00189 V\$AP2_Q6 0.781939 1869 (-) MKCCCSCNGGCG TTCCAGCTGGAG
M00277 V\$LMO2COM_01 0.900942 1869 (+) SNNCAGGTGNNN TTCCAGCTGGAG
M00277 V\$LMO2COM_01 0.904441 1869 (-) SNNCAGGTGNNN TTCCAGCTGGAG
M00176 V\$AP4_Q6 0.786770 1870 (+) CWCAGCTGGN TCCAGCTGGA
M00176 V\$AP4_Q6 0.786770 1870 (-) CWCAGCTGGN TCCAGCTGGA
M00184 V\$MYOD_Q6 0.806292 1870 (+) NNCANCTGNY TCCAGCTGGA
M00184 V\$MYOD_Q6 0.806292 1870 (-) NNCANCTGNY TCCAGCTGGA
M00109 V\$CEBPB_01 0.812531 1873 (+) RNRTKNNGMAAKNN AGCTGGAGAAGGGT
M00127 V\$GATA1_03 0.821166 1873 (+) RNSNNGATAANNNGN AGCTGGAGAAGGGT
M00098 V\$PAX2_01 0.788239 1874 (+) NNNNGTCANGNRTKANNNN GCTGGAGAAGGGTGACCGA
M00115 V\$TAXCREB_02 0.632008 1875 (-) RTGACGCATAYCCCC CTGGAGAAGGGTGAC
M00191 V\$ER_Q6 0.766635 1875 (+) NNARGNNANNNTGACCYN CTGGAGAAGGGTGACCGAC
M00084 V\$MZF1_02 0.840290 1876 (+) KNNNKAGGGGNAA TGGAGAAGGGTGA
M00075 V\$GATA1_01 0.790721 1877 (+) SNNGATNNNN GGAGAAGGGT
M00239 V\$T3R_01 0.731213 1878 (+) SNNTRAGGTCACGSNN GAGAAGGGTGACCGAC
M00114 V\$TAXCREB_01 0.712121 1880 (+) GGGGGTTGACGYANA GAAGGGTGACCGACT
M00221 V\$SREBP1_02 0.795812 1880 (-) KATCACCCAC GAAGGGTGACC
M00083 V\$MZF1_01 0.836796 1881 (+) NGNGGGGA AAGGGTGA
M00115 V\$TAXCREB_02 0.614654 1881 (-) RTGACGCATAYCCCC AAGGGTGACCGACTC
M00155 V\$ARP1_01 0.778683 1881 (-) TGARCCYTTGAMCCYW AAGGGTGACCGACTCA
M00172 V\$APIFJ_Q2 0.890852 1884 (+) RSTGACTNMNW GGTGACCGACT
M00173 V\$AP1_Q2 0.872621 1884 (+) RSTGACTNMNW GGTGACCGACT
M00174 V\$AP1_Q6 0.849191 1884 (+) NNTGACTCANN GGTGACCGACT
M00188 V\$AP1_Q4 0.890515 1884 (+) RSTGACTMANN GGTGACCGACT
M00072 V\$CP2_01 0.805746 1887 (+) GCNMNAMCMAG GACCGACTCAG
M00143 V\$PAX5_01 0.772001 1887 (+) NCNNNRNKCANNNGNWGNRKRGCSSNNN
GACCGACTCAGCGCTGAGATCAATCGGC
M00173 V\$AP1_Q2 0.805564 1888 (+) RSTGACTNMNW ACCGACTCAGC
M00173 V\$AP1_Q2 0.803807 1888 (-) RSTGACTNMNW ACCGACTCAGC
M00174 V\$AP1_Q6 0.795412 1888 (+) NNTGACTCANN ACCGACTCAGC
M00174 V\$AP1_Q6 0.846559 1888 (-) NNTGACTCANN ACCGACTCAGC
M00188 V\$AP1_Q4 0.811528 1888 (+) RSTGACTMANN ACCGACTCAGC
M00037 V\$NFE2_01 0.809356 1889 (-) TGCTGASTCAY CCGACTCAGCG
M00199 V\$AP1_C 0.837026 1889 (+) NTGASTCAG CCGACTCAG
M00199 V\$AP1_C 0.844606 1889 (-) NTGASTCAG CCGACTCAG
M00175 V\$AP4_Q5 0.911317 1893 (+) NNCAGCTGNN CTCAGCGCTG
M00176 V\$AP4_Q6 0.888750 1893 (+) CWCAGCTGGN CTCAGCGCTG
M00253 V\$CAP_01 0.921143 1894 (+) NCANNNNN TCAGCGCT
M00175 V\$AP4_Q5 0.911317 1895 (-) NNCAGCTGNN CAGCGCTGAG
M00176 V\$AP4_Q6 0.888750 1895 (-) CWCAGCTGGN CAGCGCTGAG
M00017 V\$ATF_01 0.745607 1898 (+) CNSTGACGTNNNYC CGCTGAGATCAATC
M00239 V\$T3R_01 0.795760 1898 (+) SNNTRAGGTCACGSNN CGCTGAGATCAATCGG
M00179 V\$CREBP1_Q2 0.764105 1899 (+) NSTGACGTMASN GCTGAGATCAAT
M00039 V\$CREB_01 0.774627 1901 (-) TGACGTMA TGAGATCA
M00041 V\$CREBP1CJUN_01 0.793611 1901 (+) TGACGTYA TGAGATCA
M00076 V\$GATA2_01 0.783040 1901 (+) NNNGATRNNN TGAGATCAAT

M00254 V\$CAAT_01 0.795538 1901 (+) NNNRRCCAATSA TGAGATCAATCG
M00104 V\$CDPCR1_01 0.885705 1902 (-) NATCGATCGS GAGATCAATC
M00106 V\$CDPCR3HD_01 0.972607 1902 (-) NATYGATSSS GAGATCAATC
M00160 V\$SR_02 0.837052 1902 (+) NWWAACA AWANN GAGATCAATCGG
M00211 V\$PADS_C 0.839718 1902 (-) NGTGGTCTC GAGATCAAT
M00146 V\$HSF1_01 0.850729 1903 (+) RGAANRTTCN AGATCAATCG
M00146 V\$HSF1_01 0.780228 1903 (-) RGAANRTTCN AGATCAATCG
M00147 V\$HSF2_01 0.902033 1903 (+) NGAANNWTCK AGATCAATCG
M00147 V\$HSF2_01 0.895379 1903 (-) NGAANNWTCK AGATCAATCG
M00185 V\$NFY_Q6 0.805755 1903 (+) TRRCCAATSRN AGATCAATCGG
M00104 V\$CDPCR1_01 0.927385 1904 (+) NATCGATCGS GATCAATCGG
M00106 V\$CDPCR3HD_01 0.865340 1904 (+) NATYGATSSS GATCAATCGG
M00075 V\$GATA1_01 0.894867 1905 (-) SNNGATNNNN ATCAATCGGC
M00076 V\$GATA2_01 0.845737 1905 (-) NNNGATRNNN ATCAATCGGC
M00200 V\$CAAT_C 0.712941 1905 (+) ACCAATCANCNNGCYYSNCNCWNNT ATCAATCGGCCCGACTATCTCGACT
M00253 V\$CAP_01 0.874815 1906 (+) NCANNNNN TCAATCGG
M00085 V\$ZID_01 0.773406 1911 (+) NGGCTCYATCAYC CGGCCCGACTATC
M00126 V\$GATA1_02 0.915937 1915 (-) NNNNNGATANKGN CCGACTATCTCGAC
M00127 V\$GATA1_03 0.926507 1915 (-) RNSNNGATAANNNGN CCGACTATCTCGAC
M00128 V\$GATA1_04 0.863051 1915 (-) NNCWGATARNNNN CCGACTATCTCGA
M00075 V\$GATA1_01 0.940770 1917 (-) SNNGATNNNN GACTATCTCG
M00076 V\$GATA2_01 0.944520 1917 (-) NNNGATRNNN GACTATCTCG
M00077 V\$GATA3_01 0.912273 1917 (-) NNGATARNNG GACTATCTC
M00278 V\$LMO2COM_02 0.901280 1917 (-) NMGATANSNG GACTATCTC
M00079 V\$EV11_02 0.775976 1919 (-) AGAYAAGATAA CTATCTCGACT
M00080 V\$EV11_03 0.730247 1919 (-) AGATAAGATAA CTATCTCGACT
M00082 V\$EV11_05 0.774366 1919 (-) AGATAAGATAN CTATCTCGACT
M00261 V\$OLF1_01 0.771600 1921 (-) NNCNANTCCCYNGRGARNNKGN ATCTCGACTTTGCCGAGTCTGG
M00086 V\$IK1_01 0.782585 1926 (-) NNNTGGGAATRCC GACTTTGCCGAGT
M00050 V\$E2F_02 0.830880 1929 (+) TTTSGCGC TTTGCCGA
M00186 V\$SRF_Q6 0.771344 1931 (-) GNCCAWATAWGGMN TGCCGAGTCTGGGC
M00272 V\$P53_02 0.806272 1931 (+) NGRCWTGYCY TGCCGAGTCT
M00215 V\$SRF_C 0.771082 1932 (+) NCCWTATATGGNCWN GCCGAGTCTGGGCAG
M00008 V\$SP1_01 0.790204 1935 (+) GRGGCRGGGW GAGTCTGGGC
M00141 V\$LYF1_01 0.836954 1938 (+) TTTGGGAGR TCTGGGCAG
M00196 V\$SP1_Q6 0.775118 1938 (+) NGGGGGCGGGGYN TCTGGGCAGGTCT
M00255 V\$GC_01 0.901764 1938 (+) NRGGGGGCGGGGCK TCTGGGCAGGTCTA
M00071 V\$E47_02 0.766178 1939 (+) NNNMRCAGGTGTTMNN CTGGGCAGGTCTACTT
M00072 V\$CP2_01 0.809605 1939 (-) GCNMNAMCMAG CTGGGCAGGTCT
M00002 V\$E47_01 0.784652 1940 (+) NSNGCAGGTGKNCNN TGGGCAGGTCTACTT
M00008 V\$SP1_01 0.868630 1940 (+) GRGGCRGGGW TGGGCAGGTCT
M00272 V\$P53_02 0.886284 1941 (+) NGRCWTGYCY GGGCAGGTCT
M00272 V\$P53_02 0.938453 1941 (-) NGRCWTGYCY GGGCAGGTCT
M00277 V\$LMO2COM_01 0.826380 1941 (+) SNNCAGGTGNNN GGGCAGGTCTAC
M00175 V\$AP4_Q5 0.788357 1942 (+) NNCAGCTGNN GGCAGGTCTA
M00176 V\$AP4_Q6 0.763217 1942 (+) CWCAGCTGNN GGCAGGTCTA
M00184 V\$MYOD_Q6 0.823257 1942 (-) NNCANCTGNY GGCAGGTCTA
M00186 V\$SRF_Q6 0.770499 1946 (-) GNCCAWATAWGGMN GGTCTACTTTGGGA
M00189 V\$AP2_Q6 0.798943 1949 (-) MKCCCSNNGGCG CTACTTTGGGAT
M00086 V\$IK1_01 0.843483 1952 (+) NNNTGGGAATRCC CTTTGGGATCATT
M00087 V\$IK2_01 0.914267 1952 (+) NNNYGGGAWNNN CTTTGGGATCAT
M00239 V\$T3R_01 0.789135 1952 (+) SNNTRAGGTCACGSNN CTTTGGGATCATTGCC
M00141 V\$LYF1_01 0.849987 1953 (+) TTTGGGAGR TTTGGGATC
M00134 V\$HNF4_01 0.795599 1954 (-) NNNRGGNCAAAGKTCANN TTGGGATCATTGCCCTGTG
M00057 V\$COMP1_01 0.822036 1955 (+) NNTNWKGATTGRCNRSRANMRRNN TGGGATCATTGCCCTGTGAGGAGG
M00075 V\$GATA1_01 0.773939 1955 (+) SNNGATNNNN TGGGATCATT
M00076 V\$GATA2_01 0.837618 1955 (+) NNNGATRNNN TGGGATCATT
M00076 V\$GATA2_01 0.786649 1955 (-) NNNGATRNNN TGGGATCATT
M00104 V\$CDPCR1_01 0.830023 1956 (-) NATCGATCGS GGGATCATTG
M00106 V\$CDPCR3HD_01 0.927624 1956 (-) NATYGATSSS GGGATCATTG
M00264 V\$STAF_02 0.775261 1958 (-) MNTTCCCAKMATKCMWNGCRN GATCATTGCCCTGTGAGGAGG

M00185 V\$NFY_Q6 0.782888 1959 (-) TRRCCAATSRN ATCATTGCCCT
M00143 V\$PAX5_01 0.780262 1960 (+) NCNNNRNKCANNNGNWGNRKRGC SRSNNN
TCATTGCCCTGTGAGGAGGACGAACATC
M00253 V\$CAP_01 0.920158 1960 (+) NCANNNNN TCATTGCC
M00254 V\$CAAT_01 0.827450 1960 (-) NNNRRCCAATSA TCATTGCCCTGT
M00215 V\$SRF_C 0.764582 1962 (-) NCCWTATATGGNCWN ATTGCCCTGTGAGGA
M00122 V\$USF_02 0.772840 1963 (+) NNRNCACGTGNYNN TTGCCCTGTGAGGA
M00122 V\$USF_02 0.772840 1963 (-) NNRNCACGTGNYNN TTGCCCTGTGAGGA
M00186 V\$SRF_Q6 0.789096 1964 (-) GNCCA WATAWGGMN TGCCCTGTGAGGAG
M00187 V\$USF_Q6 0.916131 1965 (-) GYCACGTGNC GCCCTGTGAG
M00189 V\$AP2_Q6 0.803079 1966 (-) MKCCCSCNGGCG CCCTGTGAGGAG
M00217 V\$USF_C 0.856424 1966 (+) NCACGTGN CCCTGTGA
M00017 V\$ATF_01 0.773145 1968 (+) CNSTGACGTNNNYC CTGTGAGGAGGACG
M00084 V\$MZF1_02 0.849038 1968 (+) KNNNKAGGGGNAA CTGTGAGGAGGAC
M00083 V\$MZF1_01 0.861730 1969 (+) NGNGGGGA TGTGAGGA
M00244 V\$NGFIC_01 0.729285 1970 (+) WTGCGTGGGYGG GTGAGGAGGACG
M00007 V\$ELK1_01 0.796259 1971 (+) NNNACMGGAAGTNCNN TGAGGAGGACGAACAT
M00114 V\$TAXCREB_01 0.710707 1971 (+) GGGGGTTGACGYANA TGAGGAGGACGAACA
M00113 V\$CREB_02 0.775440 1973 (+) NNGNTGACGYNN AGGAGGACGAAC
M00255 V\$GC_01 0.793484 1973 (+) NRGGGGCGGGGCGNK AGGAGGACGAACAT
M00235 V\$AHRARNT_01 0.788623 1975 (-) KNNKNNTYGC GTGMS GAGGACGAACATCCAA
M00115 V\$TAXCREB_02 0.751706 1976 (+) RTGACGCATAYCCCC AGGACGAACATCCAA
M00194 V\$NFKB_Q6 0.786692 1978 (-) NGGGGAMTTTCCNN GACGAACATCCAAAC
M00200 V\$CAAT_C 0.721084 1978 (+) ACCAATCANCNNGCYYSNCNCWNNT GACGAACATCCAAACCTTCCCAAACG
M00007 V\$ELK1_01 0.814295 1979 (-) NNNACMGGAAGTNCNN ACGAACATCCAAACCTT
M00136 V\$OCT1_02 0.784515 1979 (+) NNGAATATKCANNNN ACGAACATCCAAACCT
M00146 V\$HSF1_01 0.787712 1980 (+) RGAANRTTCN CGAACATCCA
M00146 V\$HSF1_01 0.832611 1980 (-) RGAANRTTCN CGAACATCCA
M00147 V\$HSF2_01 0.873567 1980 (-) NGAANNWTCK CGAACATCCA
M00076 V\$GATA2_01 0.795219 1981 (-) NNGGATRNNN GAACATCCAA
M00221 V\$SREBP1_02 0.720902 1981 (+) KATCACCCAC GAACATCCAAAC
M00264 V\$STAF_02 0.766877 1982 (+) MNTTCCCAKMATKCMWNGCRN AACATCCAAACCTTCCCAAACG
M00008 V\$SP1_01 0.812288 1985 (-) GRGGCRGGGW ATCCAAACCTT
M00200 V\$CAAT_C 0.722484 1986 (+) ACCAATCANCNNGCYYSNCNCWNNT TCCAAACCTTCCCAAACGCCTCCCCT
M00146 V\$HSF1_01 0.772351 1987 (-) RGAANRTTCN CCAACCTTCC
M00147 V\$HSF2_01 0.812200 1987 (-) NGAANNWTCK CCAACCTTCC
M00255 V\$GC_01 0.849584 1987 (-) NRGGGGCGGGGCGNK CCAACCTTCCCAAAC
M00086 V\$IK1_01 0.887821 1989 (-) NNNTGGGAATRCC AACCTTCCCAAAC
M00088 V\$IK3_01 0.826409 1989 (-) TNYTGGGAATACC AACCTTCCCAAAC
M00087 V\$IK2_01 0.919503 1990 (-) NNNYGGGAWNNN ACCTTCCCAAAC
M00109 V\$CEBPB_01 0.844477 1990 (-) RNRTKNGMAAKNN ACCTTCCCAAACGC
M00159 V\$CEBP_01 0.910211 1990 (-) NNTKTGGWNANN ACCTTCCCAAACG
M00280 V\$RFX1_01 0.757420 1990 (-) NNGTNRCNWRGYAACNN ACCTTCCCAAACGCCTC
M00264 V\$STAF_02 0.784968 1991 (+) MNTTCCCAKMATKCMWNGCRN CCTTCCCAAACGCCTCCCCTG
M00141 V\$LYF1_01 0.974444 1992 (-) TTTGGGAGR CTCCCAAAC
M00200 V\$CAAT_C 0.736608 1994 (+) ACCAATCANCNNGCYYSNCNCWNNT TCCCAAACGCCTCCCCTGCCCAAT
M00075 V\$GATA1_01 0.818361 1995 (-) SNNGATNNNN CCCAAACGCC
M00200 V\$CAAT_C 0.804046 1995 (+) ACCAATCANCNNGCYYSNCNCWNNT CCCAAACGCCTCCCCTGCCCAATC
M00255 V\$GC_01 0.809407 1995 (-) NRGGGGCGGGGCGNK CCCAAACGCCTCCC
M00115 V\$TAXCREB_02 0.628004 1997 (+) RTGACGCATAYCCCC CAAACGCCTCCCCTG
M00255 V\$GC_01 0.851053 1998 (-) NRGGGGCGGGGCGNK AAACGCCTCCCCTG
M00196 V\$SP1_Q6 0.835876 1999 (-) NGGGGGCGGGGYN AACGCCTCCCCTG
M00115 V\$TAXCREB_02 0.611391 2000 (+) RTGACGCATAYCCCC ACGCCTCCCCTGCCC
M00243 V\$EGR1_01 0.766620 2000 (-) WTGCGTGGGCGK ACGCCTCCCCTG
M00245 V\$EGR3_01 0.762708 2000 (-) NTGCGTGGGCGK ACGCCTCCCCTG
M00002 V\$E47_01 0.773202 2001 (-) NSNGCAGGTGKNCNN CGCCTCCCCTGCCCC
M00072 V\$CP2_01 0.800600 2001 (+) GCNMNAMCMAG CGCCTCCCCTG
M00243 V\$EGR1_01 0.762000 2003 (-) WTGCGTGGGCGK CCTCCCCTGCCC
M00244 V\$NGFIC_01 0.759647 2003 (-) WTGCGTGGGYGG CCTCCCCTGCCC
M00141 V\$LYF1_01 0.824431 2004 (-) TTTGGGAGR CTCCCCTGC
M00184 V\$MYOD_Q6 0.771437 2004 (+) NNCANCTGNY CTCCCCTGCC

M00196 V\$SP1_Q6 0.781694 2004 (-) NGGGGGCGGGGYN CTCCCCTGCCCCA
M00255 V\$GC_01 0.856688 2004 (-) NRGGGGCGGGGCKN CTCCCCTGCCCCA
M00083 V\$MZF1_01 0.888175 2005 (-) NGNGGGGA TCCCCTGC
M00196 V\$SP1_Q6 0.784850 2005 (-) NGGGGGCGGGGYN TCCCCTGCCCCA
M00217 V\$USF_C 0.863133 2005 (+) NCACGTGN TCCCCTGC
M00008 V\$SP1_01 0.867214 2006 (-) GRGGCRGGGW CCCCTGCCCC
M00201 V\$CEBP_C 0.800545 2006 (+) NGWNTKNKGAAKNSAYA CCCCTGCCCCAATCCCTT
M00250 V\$GFI1_01 0.752598 2008 (+) NNNNNNNAAATCASWGYNNNNNNN CCTGCCCCAATCCCTTTATTACCC
M00033 V\$P300_01 0.845262 2011 (-) NNNRRGAGTNNNS GCCCAATCCCTTT
M00050 V\$E2F_02 0.743405 2011 (-) TTTSGCGC GCCCAAT
M00083 V\$MZF1_01 0.850019 2011 (-) NGNGGGGA GCCCAAT
M00127 V\$GATA1_03 0.787849 2011 (-) RNSNNGATAANNNGN GCCCAATCCCTTT
M00185 V\$NFY_Q6 0.781860 2011 (+) TRRCCAATSRN GCCCAATCCC
M00023 V\$HOX13_01 0.766858 2012 (+) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
CCCCAATCCCTTTATTACCCCTCCTTCAG
M00075 V\$GATA1_01 0.882034 2013 (-) SNNGATNNNN CCCAATCCCT
M00076 V\$GATA2_01 0.875959 2013 (-) NNNGATRNNN CCCAATCCCT
M00077 V\$GATA3_01 0.921134 2013 (-) NNGATARNG CCCAATCCC
M00200 V\$CAAT_C 0.775417 2013 (+) ACCAATCANCNNGCYYSNCNCWNNT CCCAATCCCTTTATTACCCCTCCT
M00059 V\$YY1_01 0.789318 2014 (+) NNNNNCCATNTWNNNNWN CCAATCCCTTTATTACC
M00104 V\$CDPCR1_01 0.795832 2014 (-) NATCGATCGS CCAATCCCTT
M00137 V\$OCT1_03 0.847886 2017 (-) NNNRTAATNANNN ATCCCTTTATTAC
M00003 V\$VMYB_01 0.807692 2018 (-) AAYAACGGNN TCCCTTTATT
M00127 V\$GATA1_03 0.821656 2019 (-) RNSNNGATAANNNGN CCCTTTATTACCCC
M00160 V\$SRY_02 0.763946 2019 (-) NWWAACAANWANN CCCTTTATTACC
M00137 V\$OCT1_03 0.890557 2020 (-) NNNRTAATNANNN CCTTTATTACCCC
M00216 V\$TATA_C 0.749670 2020 (+) NCTATAAAAR CCTTTATTAC
M00241 V\$NKX25_02 0.839809 2021 (+) CWTAATTG CTTTATTA
M00127 V\$GATA1_03 0.784174 2022 (-) RNSNNGATAANNNGN TTTATTACCCCTC
M00116 V\$CEBPA_01 0.816973 2023 (+) NNATTRCNNAANNN TTATTACCCCTCCTC
M00212 V\$POLY_C 0.749030 2024 (+) CAATAAAACCYYYKCTN TATTACCCCTCCTTCAG
M00221 V\$SREBP1_02 0.720902 2024 (+) KATCACCCAC TATTACCCCT
M00008 V\$SP1_01 0.799830 2025 (-) GRGGCRGGGW ATTACCCCT
M00115 V\$TAXCREB_02 0.620587 2025 (+) RTGACGCATAYCCCC ATTACCCCTCCTTC
M00008 V\$SP1_01 0.833239 2026 (-) GRGGCRGGGW TTACCCCTC
M00084 V\$MZF1_02 0.921020 2027 (-) KNNNKAGGGGNA TACCCCTCCTTC
M00255 V\$GC_01 0.877756 2027 (-) NRGGGGCGGGGCKN TACCCCTCCTTCA
M00008 V\$SP1_01 0.800963 2028 (-) GRGGCRGGGW ACCCCCTCCT
M00196 V\$SP1_Q6 0.833772 2028 (-) NGGGGGCGGGGYN ACCCCCTCCTTCA
M00083 V\$MZF1_01 0.846997 2029 (-) NGNGGGGA CCCCCTCC
M00238 V\$BARBIE_01 0.791840 2029 (-) ATNNAAAGCNRRNG CCCCCTCCTTCAGAC
M00073 V\$DELTAEF1_01 0.810916 2030 (+) NNNCACCTNAN CCCCTCCTTCA
M00235 V\$AHRARNT_01 0.767137 2036 (-) KNNKNNTYGC GTGMS CTTAGACACCCTCAA
M00098 V\$PAX2_01 0.750704 2038 (-) NNNNGTCANGNRTKANNNN TCAGACACCCTCAACCTCT
M00253 V\$CAP_01 0.914243 2038 (+) NCANNNNN TCAGACAC
M00278 V\$LMO2COM_02 0.791105 2039 (+) NMGATANS GAGACACCC
M00008 V\$SP1_01 0.840317 2040 (-) GRGGCRGGGW AGACACCCTC
M00084 V\$MZF1_02 0.870532 2041 (-) KNNNKAGGGGNA GACACCCTCAACC
M00115 V\$TAXCREB_02 0.618807 2041 (+) RTGACGCATAYCCCC GACACCCTCAACCTC
M00253 V\$CAP_01 0.892558 2042 (+) NCANNNNN ACACCCTC
M00255 V\$GC_01 0.812347 2044 (-) NRGGGGCGGGGCKN ACCCTCAACCTCTT
M00004 V\$CMYB_01 0.851073 2045 (-) NCNRNNGRCNGTTGGKGG CCCTCAACCTCTTCTGGC
M00183 V\$MYB_Q6 0.856017 2047 (+) NNNAACKGNC CTCAACCTCT
M00253 V\$CAP_01 0.894529 2048 (+) NCANNNNN TCAACCTC
M00107 V\$E2_01 0.768122 2049 (-) NNACCRNNANCGGTRN CAACCTCTTCTGGCTC
M00057 V\$COMP1_01 0.799042 2050 (-) NNTNWKGATTGRCNRSRANMRRNN AACCTCTTCTGGCTCAAAAAGAGA
M00222 V\$THIE47_01 0.802240 2050 (+) NNNNGNRTCTGGMWTT AACCTCTTCTGGCTCA
M00001 V\$MYOD_01 0.792717 2052 (+) SRACAGGTGKYG CCTCTTCTGGCT
M00108 V\$NRF2_01 0.850291 2053 (-) ACCGGAAGNS CTCTTCTGGC
M00156 V\$RORA1_01 0.771968 2054 (+) NWAANNAGGTCAN TCTTCTGGCTCAA
M00254 V\$CAAT_01 0.796385 2055 (-) NNNRRCCAATSA CTTCTGGCTCAA

M00193 V\$NF1_Q6 0.793695 2056 (+) NNTTGGCNNNNNNCCNNN TTCTGGCTCAAAAAGAGA
M00050 V\$E2F_02 0.743405 2057 (+) TTTSGCGC TCTGGCTC
M00199 V\$AP1_C 0.786589 2058 (+) NTGASTCAG CTGGCTCAA
M00199 V\$AP1_C 0.829155 2058 (-) NTGASTCAG CTGGCTCAA
M00023 V\$HOX13_01 0.733620 2059 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TGGCTCAAAAAGAGAATTGGGGGCTTAGGG
M00216 V\$TATA_C 0.767098 2060 (+) NCTATAAAAR GGCTCAAAAA
M00050 V\$E2F_02 0.762288 2061 (-) TTTSGCGC GCTCAAAA
M00216 V\$TATA_C 0.752311 2061 (+) NCTATAAAAR GCTCAAAAAG
M00004 V\$CMYB_01 0.787123 2064 (+) NCNRNNGRCNGTTGGKGG CAAAAAGAGAATTGGGGG
M00127 V\$GATA1_03 0.804998 2065 (+) RNSNNGATAANNNGN AAAAAGAGAATTGG
M00011 V\$EVII_06 0.775619 2066 (+) ACAAGATAA AAAAGAGAA
M00237 V\$AHRARNT_02 0.715762 2070 (+) GRGKATYGCGTGMSWNSCC GAGAATTGGGGGCTTAGGG
M00084 V\$MZF1_02 0.815046 2072 (+) KNNNKAGGGGNAA GAATTGGGGGCTT
M00083 V\$MZF1_01 0.850019 2074 (+) NGNGGGGA ATTGGGGG
M00050 V\$E2F_02 0.743405 2075 (+) TTTSGCGC TTGGGGGC
M00257 V\$RREB1_01 0.802611 2075 (-) CCCCCAACMMCCCC TTGGGGGCTTAGGG
M00134 V\$SHNF4_01 0.773593 2076 (+) NNNRGGNCAAAGKTCANNN TGGGGGCTTAGGGTCGGAA
M00155 V\$ARP1_01 0.755417 2076 (-) TGARCCYTTGAMCCYW TGGGGGCTTAGGGTCG
M00196 V\$SP1_Q6 0.768543 2076 (+) NGGGGGCGGGGYN TGGGGGCTTAGGG
M00255 V\$GC_01 0.817246 2076 (+) NRGGGGCGGGGCKN TGGGGGCTTAGGGT
M00257 V\$RREB1_01 0.802611 2076 (-) CCCCCAACMMCCCC TGGGGGCTTAGGGT
M00189 V\$AP2_Q6 0.789292 2079 (-) MKCCCSCNGGCG GGGCTTAGGGTC
M00008 V\$SP1_01 0.811438 2084 (+) GRGGCRGGGW TAGGGTCGGA
M00196 V\$SP1_Q6 0.773803 2084 (+) NGGGGGCGGGGYN TAGGGTCGGAACC
M00255 V\$GC_01 0.819451 2084 (+) NRGGGGCGGGGCKN TAGGGTCGGAACCC
M00025 V\$ELK1_02 0.801959 2085 (+) NNNNCCGGAARYNN AGGGTCGGAACCCA
M00072 V\$CP2_01 0.794597 2090 (+) GCNMNAMCMAG CGGAACCCAAG
M00097 V\$PAX6_01 0.782035 2090 (-) NNNNTTCACGCWTSANTKNNN CGGAACCCAAGCTTAGAACTT
M00155 V\$ARP1_01 0.826669 2096 (+) TGARCCYTTGAMCCYW CCAAGCTTAGAACTTT
M00216 V\$TATA_C 0.747293 2099 (+) NCTATAAAAR AGCTTAGAAC
M00134 V\$SHNF4_01 0.785163 2101 (-) NNNRGGNCAAAGKTCANNN CTTAGAACTTTAAGCAACA
M00281 V\$RFX1_02 0.787175 2103 (+) NNGTNRCNATRGYACNNN TAGAACTTTAAGCAACAAG
M00280 V\$RFX1_01 0.777505 2104 (+) NNGTNRCNWRGYACNN AGAACTTTAAGCAACAA
M00109 V\$CEBPB_01 0.823180 2107 (+) RNRTKNNGMAAKNN ACTTTAAGCAACAA
M00116 V\$CEBPA_01 0.802894 2107 (+) NNATTRCNNAANNN ACTTTAAGCAACAA
M00116 V\$CEBPA_01 0.882675 2107 (-) NNATTRCNNAANNN ACTTTAAGCAACAA
M00117 V\$CEBPB_02 0.881285 2107 (-) NKNTTGCNYAAYNN ACTTTAAGCAACAA
M00190 V\$CEBP_Q2 0.898049 2107 (-) NNNTTGCNNAANNN ACTTTAAGCAACAA
M00269 V\$XFD3_01 0.781831 2107 (+) WNWGTMAACAWWMW ACTTTAAGCAACAA
M00100 V\$CDXA_01 0.937224 2108 (+) MTTTATR CTTTAAG
M00260 V\$HLF_01 0.822791 2109 (-) RTTACRYAAT TTTAAGCAAC
M00040 V\$CREBP1_01 0.746641 2110 (+) TTACGTAA TTAAGCAA
M00040 V\$CREBP1_01 0.749109 2110 (-) TTACGTAA TTAAGCAA
M00042 V\$SOX5_01 0.795286 2114 (+) NNAACAATNN GCAACAAGAC
M00079 V\$EVII_02 0.781737 2115 (+) AGAYAAGATAA CAACAAGACCA
M00011 V\$EVII_06 0.777076 2117 (+) ACAAGATAA ACAAGACCA
M00255 V\$GC_01 0.789319 2118 (-) NRGGGGCGGGGCKN CAAGACCACCACTT
M00211 V\$PADS_C 0.876512 2119 (-) NGTGGTCTC AAGACCACC
M00008 V\$SP1_01 0.823046 2120 (-) GRGGCRGGGW AGACCACCAC
M00271 V\$AML1_01 0.876099 2122 (-) TGTGGT ACCACC
M00280 V\$RFX1_01 0.791341 2123 (+) NNGTNRCNWRGYACNN CCACCACTTCGAAACCT
M00271 V\$AML1_01 0.908330 2125 (-) TGTGGT ACCACT
M00109 V\$CEBPB_01 0.827390 2126 (-) RNRTKNNGMAAKNN CCACTTCGAAACCT
M00180 V\$E2F_Q6 0.733209 2127 (+) NNGCGCGAAANTK CACTTCGAAACCT
M00059 V\$YY1_01 0.812910 2130 (-) NNNNNCCATNTWNNNNWN TTCGAAACCTGGGATTC
M00277 V\$LMO2COM_01 0.800808 2132 (-) SNNCAGGTGNNN CGAAACCTGGGA
M00162 V\$OCT1_06 0.877734 2134 (+) CWNWTKWSATRYN AAACCTGGGATTCA
M00086 V\$IK1_01 0.785524 2136 (+) NNNTGGGAATRCC ACCTGGGATTCA
M00087 V\$IK2_01 0.884817 2136 (+) NNNYGGGAWNNN ACCTGGGATTCA
M00143 V\$PAX5_01 0.837757 2138 (+) NCNNNRNKCANNNGWGNRKRGC SRSNNN

CTGGGATTCAGGAATGTGTGGCCTGCAC
M00224 V\$STAT1_01 0.729129 2138 (+) NNNSANTCCGGAANTGNSN CTGGGATTCAGGAATGTGTGG
M00075 V\$GATA1_01 0.812932 2139 (+) SNNGATNNNN TGGGATTCAG
M00076 V\$GATA2_01 0.836716 2139 (+) NNNGATRNNN TGGGATTCAG
M00174 V\$AP1_Q6 0.796540 2139 (-) NNTGACTCANN TGGGATTCAGG
M00086 V\$IK1_01 0.846688 2143 (+) NNNTGGGAATRCC ATTCAGGAATGTG
M00087 V\$IK2_01 0.861257 2143 (+) NNNYGGGAWNNN ATTCAGGAATGT
M00191 V\$ER_Q6 0.769487 2145 (+) NNARGNNANNNTGACCYN TCAGGAATGTGTGGCCTGC
M00235 V\$AHRARNT_01 0.775118 2145 (+) KNNKNNTYGCGTGCMS TCAGGAATGTGTGGCC
M00115 V\$TAXCREB_02 0.634678 2147 (-) RTGACGCATAYCCCC AGGAATGTGTGGCCT
M00187 V\$USF_Q6 0.805703 2148 (-) GYCACGTGNC GGAATGTGTG
M00255 V\$GC_01 0.792504 2148 (+) NRGGGGCGGGGCK GGAATGTGTGGCCT
M00056 V\$MYOGNF1_01 0.745948 2149 (-) CRSCTGTNNNNTTTGGCACNSNGCCARNN
GAATGTGTGGCCTGCACAGTGAAGTGCTG
M00235 V\$AHRARNT_01 0.823409 2150 (+) KNNKNNTYGCGTGCMS AATGTGTGGCCTGCAC
M00244 V\$NGFIC_01 0.729677 2151 (+) WTGCGTGGGYGG ATGTGTGGCCTG
M00246 V\$EGR2_01 0.758367 2151 (+) NTGCGTRGGCGK ATGTGTGGCCTG
M00254 V\$CAAT_01 0.784807 2152 (-) NNNRRCCAATSA TGTGTGGCCTGC
M00211 V\$PADS_C 0.837702 2154 (+) NGTGGTCTC TGTGGCCTG
M00271 V\$AML1_01 0.897865 2154 (+) TGTGGT TGTGGC
M00273 V\$R_01 0.746627 2156 (+) NNGKCCNCNSRNYGTGGTGYN TGGCCTGCACAGTGAAGTGCT
M00262 V\$STAF_01 0.738728 2161 (-) NTTWCCCANMATGCAYYRCGNY TGCACAGTGAAGTGCTGGCAAC
M00273 V\$R_01 0.731801 2161 (-) NNGKCCNCNSRNYGTGGTGYN TGCACAGTGAAGTGCTGGCAA
M00187 V\$USF_Q6 0.826111 2162 (-) GYCACGTGNC GCACAGTGAA
M00113 V\$CREB_02 0.772548 2164 (+) NNGNTGACGYNN ACAGTGAAGTGC
M00281 V\$RFX1_02 0.858834 2167 (+) NNGTNRCNATRGYACNN GTGAAGTGCTGGCAACCAC
M00240 V\$NKX25_01 0.870010 2168 (+) TYAAGTG TGAAGTG
M00280 V\$RFX1_01 0.763222 2168 (+) NNGTNRCNWRGYACNN TGAAGTGCTGGCAACCA
M00175 V\$AP4_Q5 0.808215 2170 (-) NNCAGCTGNN AAGTGCTGGC
M00235 V\$AHRARNT_01 0.788418 2172 (-) KNNKNNTYGCGTGCMS GTGCTGGCAACCACTA
M00193 V\$NF1_Q6 0.823691 2173 (+) NNTTGGCNNNNNNCCNN TGCTGGCAACCACTAAGA
M00223 V\$STAT_01 0.808419 2173 (-) TTCCCRKAA TGCTGGCAA
M00209 V\$NFY_C 0.801037 2177 (-) NCTGATTGGYTASY GGCAACCACTAAGA
M00254 V\$CAAT_01 0.812200 2177 (+) NNNRRCCAATSA GGCAACCACTAA
M00211 V\$PADS_C 0.827873 2178 (-) NGTGGTCTC GCAACCACT
M00185 V\$NFY_Q6 0.881809 2179 (+) TRRCCAATSRN CAACCACTAAG
M00271 V\$AML1_01 0.908330 2181 (-) TGTGGT ACCACT
M00042 V\$SOX5_01 0.811108 2185 (+) NNAACAATNN CTAAGAATTC
M00258 V\$ISRE_01 0.791798 2186 (-) CAGTTTCWCTTTYCC TAAGAATTCAAACCTG
M00160 V\$SRY_02 0.793893 2189 (+) NWWAACA AWANN GAATTCAAACCTG
M00059 V\$YY1_01 0.795872 2190 (-) NNNNNCCATNTWNNNWN AATTCAAACCTGGGGCCT
M00183 V\$MYB_Q6 0.861411 2193 (+) NNNAACKGNC TCAAACCTGGG
M00083 V\$MZF1_01 0.835663 2197 (+) NGNGGGGA ACTGGGGC
M00072 V\$CP2_01 0.842624 2198 (-) GCNMNAMCMAG CTGGGGGCCTCC
M00085 V\$ZID_01 0.766042 2202 (+) NGGCTCYATCAYC GGCCTCCAGAACT
M00189 V\$AP2_Q6 0.840993 2202 (+) MKCCCSCNGGCG GGCCTCCAGAAC
M00189 V\$AP2_Q6 0.834329 2202 (-) MKCCCSCNGGCG GGCCTCCAGAAC
M00262 V\$STAF_01 0.726590 2202 (+) NTTWCCCANMATGCAYYRCGNY GGCCTCCAGAACTCACTGGGGC
M00222 V\$TH1E47_01 0.801763 2203 (-) NNNNGNRTCTGGMWTT GCCTCCAGAACTCACT
M00141 V\$LYF1_01 0.828776 2204 (-) TTTGGGAGR CCTCCAGAA
M00174 V\$AP1_Q6 0.772471 2208 (-) NNTGACTCANN CAGAACTCACT
M00205 V\$GRE_C 0.802846 2208 (-) GGTACAANNTGTCTK CAGAACTCACTGGGGC
M00261 V\$OLF1_01 0.795745 2208 (+) NNCNANTCCCYNGRGARNNKGN CAGAACTCACTGGGGCCTACAG
M00261 V\$OLF1_01 0.777865 2208 (-) NNCNANTCCCYNGRGARNNKGN CAGAACTCACTGGGGCCTACAG
M00113 V\$CREB_02 0.774126 2209 (-) NNGNTGACGYNN AGAACTCACTGG
M00146 V\$HSF1_01 0.792438 2209 (+) RGAANRTTCN AGAACTCACT
M00147 V\$HSF2_01 0.818854 2209 (+) NGAANNWTCK AGAACTCACT
M00185 V\$NFY_Q6 0.800874 2213 (-) TRRCCAATSRN CTCCTGGGGC
M00187 V\$USF_Q6 0.882304 2213 (+) GYCACGTGNC CTCCTGGGGC
M00189 V\$AP2_Q6 0.863511 2213 (-) MKCCCSCNGGCG CTCCTGGGGC
M00253 V\$CAP_01 0.886644 2214 (+) NCANNNNN TCACTGGG

M00083 V\$MZF1_01 0.835663 2216 (+) NGNGGGGA ACTGGGGC
M00072 V\$SCP2_01 0.780875 2217 (-) GCNMNAMCMAG CTGGGGCCTAC
M00059 V\$YY1_01 0.777523 2221 (+) NNNNNCCATNTWNNNWN GGCCTACAGCTTTGATC
M00071 V\$E47_02 0.760541 2222 (-) NNNMRCAGGTGTTMNN GCCTACAGCTTTGATC
M00002 V\$E47_01 0.784050 2223 (+) NSNGCAGGTGKNCNN CCTACAGCTTTGATC
M00238 V\$BARBIE_01 0.833130 2223 (-) ATNNAAGCNGRNGG CCTACAGCTTTGATC
M00155 V\$ARP1_01 0.825651 2225 (+) TGARCCYTTGAMCCYW TACAGCTTTGATCCCT
M00175 V\$AP4_Q5 0.823721 2225 (-) NNCAGCTGNN TACAGCTTTG
M00176 V\$AP4_Q6 0.840641 2225 (-) CWCAGCTGGN TACAGCTTTG
M00253 V\$CAP_01 0.903894 2226 (+) NCANNNNN ACAGCTTT
M00160 V\$SR_Y_02 0.764240 2228 (-) NWWAACA AWANN AGCTTTGATCCC
M00098 V\$PAX2_01 0.751329 2229 (-) NNNNGTCANGNRTKANNNN GCTTTGATCCCTGACATCT
M00106 V\$CDPCR3HD_01 0.903114 2230 (+) NATYGATSSS CTTTGATCCC
M00075 V\$GATA1_01 0.773939 2231 (+) SNGGATNNNN TTTGATCCCT
M00087 V\$IK2_01 0.878927 2232 (-) NNNYGGGAWNNN TTGATCCCTGAC
M00155 V\$ARP1_01 0.798459 2232 (+) TGARCCYTTGAMCCYW TTGATCCCTGACATCT
M00280 V\$RFX1_01 0.751841 2232 (-) NNGTNRCNWRGYAACNN TTGATCCCTGACATCTG
M00158 V\$COUP_01 0.812489 2233 (+) TGAMCTTTGMMCYT TGATCCCTGACATC
M00162 V\$OCT1_06 0.816406 2235 (+) CWNWTKWSATRYN ATCCCTGACATCTG
M00069 V\$YY1_02 0.797751 2236 (+) NNNCGGCCATCTTGNCTSNW TCCCTGACATCTGGAATCTG
M00017 V\$ATF_01 0.793076 2237 (+) CNSTGACGTNNNYC CCCTGACATCTGGA
M00065 V\$TALIBETA47_01 0.839546 2238 (-) NNNAACAGATGKTNNN CCTGACATCTGGAATC
M00066 V\$TALIALPHA47_01 0.832738 2238 (-) NNNAACAGATGKTNNN CCTGACATCTGGAATC
M00070 V\$TALIBETAITF2_01 0.836789 2238 (-) NNNAACAGATGKTNNN CCTGACATCTGGAATC
M00174 V\$AP1_Q6 0.760812 2238 (+) NNTGACTCANN CCTGACATCTG
M00177 V\$CREB_Q2 0.854071 2238 (+) NSTGACGTAANN CCTGACATCTGG
M00178 V\$CREB_Q4 0.837456 2238 (+) NSTGACGTMANNN CCTGACATCTGG
M00179 V\$CREBP1_Q2 0.810303 2238 (+) NSTGACGTMASN CCTGACATCTGG
M00222 V\$TH1E47_01 0.892304 2238 (+) NNNNGNRTCTGGMWTT CCTGACATCTGGAATC
M00122 V\$USF_02 0.788067 2239 (+) NNRNCACGTGNYNN CTGACATCTGGAAT
M00122 V\$USF_02 0.788067 2239 (-) NNRNCACGTGNYNN CTGACATCTGGAAT
M00039 V\$CREB_01 0.840690 2240 (+) TGACGTMA TGACATCT
M00041 V\$CREBP1CJUN_01 0.843889 2240 (+) TGACGTYA TGACATCT
M00055 V\$NMYC_01 0.760949 2240 (-) NNNCACGTGNNN TGACATCTGGAA
M00075 V\$GATA1_01 0.865252 2240 (-) SNGGATNNNN TGACATCTGG
M00076 V\$GATA2_01 0.872350 2240 (-) NNNGATRNNN TGACATCTGG
M00123 V\$MYCMAX_02 0.817967 2240 (-) NANCACGTGNNW TGACATCTGGAA
M00158 V\$COUP_01 0.813748 2240 (+) TGAMCTTTGMMCYT TGACATCTGGAATC
M00277 V\$LMO2COM_01 0.818035 2240 (+) SNNCAGGTGNNN TGACATCTGGAA
M00277 V\$LMO2COM_01 0.812382 2240 (-) SNNCAGGTGNNN TGACATCTGGAA
M00032 V\$CETSIP54_01 0.834058 2241 (-) NCMGGAWGYN GACATCTGGA
M00056 V\$MYOGNF1_01 0.773856 2241 (+) CRSCTGTNNNNTTTGGCACNSNGCCARN
GACATCTGGAATCTGGAGACCAGGGAGCC
M00175 V\$AP4_Q5 0.823721 2241 (+) NNCAGCTGNN GACATCTGGA
M00176 V\$AP4_Q6 0.840641 2241 (+) CWCAGCTGGN GACATCTGGA
M00184 V\$MYOD_Q6 0.782850 2241 (+) NNCANCTGNY GACATCTGGA
M00184 V\$MYOD_Q6 0.830043 2241 (-) NNCANCTGNY GACATCTGGA
M00057 V\$COMP1_01 0.778204 2243 (+) NNTNWKGATTGRCNRSRANMRRNN CATCTGGAATCTGGAGACCAGGGA
M00074 V\$CETSIP54_02 0.845877 2243 (+) NNAMMGGAWRWNN CATCTGGAATCTG
M00261 V\$OLF1_01 0.767946 2244 (-) NNCNANTCCCYNGRGARNNKGN ATCTGGAATCTGGAGACCAGGG
M00059 V\$YY1_01 0.818480 2245 (-) NNNNNCCATNTWNNNWN TCTGGAATCTGGAGACC
M00222 V\$TH1E47_01 0.853943 2245 (+) NNNNGNRTCTGGMWTT TCTGGAATCTGGAGAC
M00280 V\$RFX1_01 0.794466 2246 (+) NNGTNRCNWRGYAACNN CTGGAATCTGGAGACCA
M00075 V\$GATA1_01 0.862784 2247 (-) SNGGATNNNN TGGAATCTGG
M00076 V\$GATA2_01 0.847542 2247 (-) NNNGATRNNN TGGAATCTGG
M00085 V\$ZID_01 0.831896 2249 (-) NGGCTCYATCAYC GAATCTGGAGACC
M00122 V\$USF_02 0.760721 2249 (+) NNRNCACGTGNYNN GAATCTGGAGACCA
M00122 V\$USF_02 0.760721 2249 (-) NNRNCACGTGNYNN GAATCTGGAGACCA
M00189 V\$AP2_Q6 0.800781 2250 (+) MKCCCSCNGGCG AATCTGGAGACC
M00261 V\$OLF1_01 0.764683 2251 (-) NNCNANTCCCYNGRGARNNKGN ATCTGGAGACCAGGGAGCCTTT
M00280 V\$RFX1_01 0.758982 2254 (+) NNGTNRCNWRGYAACNN TGGAGACCAGGGAGCCT

M00211 V\$PADS_C 0.872984 2256 (-) NGTGGTCTC GAGACCAGG
M00085 V\$ZID_01 0.855460 2258 (-) NGGCTCYATCAYC GACCAGGGAGCCT
M00214 V\$SEF1_C 0.705327 2258 (+) AACACGGATATCTGTGGTY GACCAGGGAGCCTTTGGTT
M00032 V\$CETS1P54_01 0.812873 2260 (+) NCMGGAWGYN CCAGGGAGCC
M00134 V\$HNF4_01 0.776316 2262 (-) NNNRGGNCAAAGKTCANNN AGGGAGCCTTTGGTTCTGG
M00158 V\$COUP_01 0.803131 2265 (+) TGAMCTTTGMMCYT GAGCCTTTGGTTCT
M00185 V\$NFY_Q6 0.828109 2267 (-) TRRCCAATSRN GCCTTTGGTTC
M00227 V\$VMYB_02 0.817990 2267 (-) NSYAACGGN GCCTTTGGT
M00160 V\$SRY_02 0.769818 2268 (-) NWWAACA AWANN CCTTTGGTTCTG
M00254 V\$CAAT_01 0.837052 2268 (-) NNNRCCAATSA CCTTTGGTTCTG
M00193 V\$NF1_Q6 0.866238 2269 (-) NNTTGGC NNNNNNCCNNN CTTTGGTTCTGGCCAGAA
M00222 V\$TH1E47_01 0.815344 2269 (+) NNNNGNRTCTGGMWTT CTTTGGTTCTGGCCAG
M00050 V\$E2F_02 0.743405 2270 (+) TTTSGCGC TTTGGTTC
M00271 V\$AML1_01 0.853077 2270 (+) TGTGGT TTTGGT
M00072 V\$CP2_01 0.877787 2271 (-) GCNMNAMCMAG TTGGTTCTGGC
M00256 V\$NRSF_01 0.746875 2273 (-) TTCAGCACCACGGACAGMGSC GGTTCCTGGCCAGAATGCTGCA
M00072 V\$CP2_01 0.786878 2274 (+) GCNMNAMCMAG GTTCTGGCCAG
M00193 V\$NF1_Q6 0.832262 2275 (+) NNTTGGC NNNNNNCCNNN TTCTGGCCAGAATGCTGC
M00262 V\$STAF_01 0.762861 2276 (+) NTTWCCCANMATGCAYYRCGNY TCTGGCCAGAATGCTGCAGGAC
M00098 V\$PAX2_01 0.756647 2283 (-) NNNNGTCANGNRTKANNNN AGAATGCTGCAGGACTTGA
M00189 V\$AP2_Q6 0.812500 2286 (-) MKCCCSCNGGCG ATGCTGCAGGAC
M00205 V\$GRE_C 0.822134 2292 (-) GGTACAANNTGTCTK CAGGACTTGAGAAGAC
M00240 V\$NKX25_01 0.857234 2295 (-) TYAAGTG GACTTGA
M00086 V\$IK1_01 0.825321 2296 (+) NNNTGGGAATRCC ACTTGAGAAGACC
M00088 V\$IK3_01 0.794536 2296 (+) TNYTGGGAATACC ACTTGAGAAGACC
M00141 V\$LYF1_01 0.867110 2297 (+) TTTGGGAGR CTTGAGAAG
M00203 V\$GATA_C 0.840012 2299 (+) NGATAAGNMNN TGAGAAGACCT
M00239 V\$T3R_01 0.750710 2299 (-) SNNTRAGGTCACGSNN TGAGAAGACCTCACCT
M00036 V\$VJUN_01 0.734898 2300 (+) NYGATGACGTCATNCY GAGAAGACCTCACCTA
M00036 V\$VJUN_01 0.758371 2300 (-) NYGATGACGTCATNCY GAGAAGACCTCACCTA
M00017 V\$ATF_01 0.813533 2301 (-) CNSTGACGTNNNYC AGAAGACCTCACCT
M00177 V\$CREB_Q2 0.813482 2302 (-) NSTGACGTAANN GAAGACCTCACC
M00178 V\$CREB_Q4 0.815497 2302 (-) NSTGACGTMANN GAAGACCTCACC
M00179 V\$CREBP1_Q2 0.776574 2302 (-) NSTGACGTMASN GAAGACCTCACC
M00221 V\$SREBP1_02 0.720902 2302 (+) KATCACCCAC GAAGACCTCAC
M00211 V\$PADS_C 0.856603 2303 (-) NGTGGTCTC AAGACCTCA
M00039 V\$CREB_01 0.774627 2304 (+) TGACGTMA AGACCTCA
M00039 V\$CREB_01 0.839813 2304 (-) TGACGTMA AGACCTCA
M00041 V\$CREBP1CJUN_01 0.793611 2304 (-) TGACGTYA AGACCTCA
M00113 V\$CREB_02 0.860899 2304 (-) NNGNTGACGYNN AGACCTCACCTA
M00255 V\$GC_01 0.821411 2304 (-) NRGGGGCGGGGCKN AGACCTCACCTAGA
M00271 V\$AML1_01 0.910841 2306 (-) TGTGGT ACCTCA
M00073 V\$DELTAEF1_01 0.944769 2307 (+) NNNCACCTNAN CCTCACCTAGA
M00156 V\$RORA1_01 0.822561 2308 (-) NWA WNNAGGTCAN CTCACCTAGAAAT
M00157 V\$RORA2_01 0.795832 2308 (-) NWA WNTAGGTCAN CTCACCTAGAAAT
M00024 V\$E2F_01 0.736218 2309 (+) TWSGCGCGAAAAYKR TCACCTAGAAATTGA
M00141 V\$LYF1_01 0.825198 2309 (-) TTTGGGAGR TCACCTAGA
M00180 V\$E2F_Q6 0.757581 2310 (+) NNGCGCGAAANTK CACCTAGAAATTG
M00252 V\$TATA_01 0.793200 2313 (+) STATAA W RNNNNNN CTAGAAATTGACACA
M00100 V\$CDXA_01 0.919568 2314 (-) MTTTATR TAGAAAT
M00101 V\$CDXA_02 0.981893 2314 (-) WWTWMTR TAGAAAT
M00269 V\$XFD3_01 0.823571 2314 (-) WNWGTMAACAWWMW TAGAAATTGACACA
M00116 V\$CEBPA_01 0.814627 2317 (+) NNATTRCNNAANN AAATTGACACAAGT
M00174 V\$AP1_Q6 0.793907 2319 (+) NNTGACTCANN ATTGACACAAG
M00177 V\$CREB_Q2 0.751631 2319 (+) NSTGACGTAANN ATTGACACAAGT
M00178 V\$CREB_Q4 0.782181 2319 (+) NSTGACGTMANN ATTGACACAAGT
M00179 V\$CREBP1_Q2 0.820523 2319 (+) NSTGACGTMASN ATTGACACAAGT
M00122 V\$USF_02 0.770665 2320 (+) NNRNCACGTGNYNN TTGACACAAGTGGA
M00122 V\$USF_02 0.770665 2320 (-) NNRNCACGTGNYNN TTGACACAAGTGGA
M00199 V\$AP1_C 0.839942 2320 (-) NTGASTCAG TTGACACAA
M00228 V\$VBP_01 0.814485 2320 (-) GTTACRTMAK TTGACACAAG

M00001 V\$MYOD_01 0.840354 2321 (-) SRACAGGTGKYG TGACACAAGTGG
M00040 V\$CREBP1_01 0.768851 2321 (+) TTACGTAA TGACACAA
M00055 V\$NMYC_01 0.802920 2321 (-) NNNCACGTGNNN TGACACAAGTGG
M00160 V\$SR_02 0.772167 2321 (+) NWWAACA AWANN TGACACAAGTGG
M00002 V\$E47_01 0.798313 2322 (+) NSNGCAGGTGKNCNN GACACAAGTGGACCT
M00187 V\$USF_Q6 0.833380 2322 (+) GYCACGTGNC GACACAAGTG
M00055 V\$NMYC_01 0.782543 2323 (+) NNNCACGTGNNN ACACAAGTGGAC
M00055 V\$NMYC_01 0.770377 2323 (-) NNNCACGTGNNN ACACAAGTGGAC
M00123 V\$MYCMAX_02 0.806672 2323 (-) NANCACGTGNNW ACACAAGTGGAC
M00277 V\$LMO2COM_01 0.843338 2323 (+) SNNCAGGTGNNN ACACAAGTGGAC
M00063 V\$IRF2_01 0.710935 2324 (+) GAAAAGYGAAASY CACAAGTGGACCT
M00184 V\$MYOD_Q6 0.791178 2324 (-) NNCANCTGNY CACAAGTGGA
M00187 V\$USF_Q6 0.851831 2324 (-) GYCACGTGNC CACAAGTGGA
M00217 V\$USF_C 0.841999 2325 (-) NCACGTGN ACAAGTGG
M00240 V\$NKX25_01 0.950176 2325 (+) TYAAGTG ACAAGTG
M00239 V\$T3R_01 0.741435 2326 (-) SNNTRAGGTCACGSNN CAAGTGGACCTTAGGC
M00134 V\$HNF4_01 0.801951 2327 (-) NNNRGGNCAAAGKTCANNN AAGTGGACCTTAGGCCTTC
M00134 V\$HNF4_01 0.834392 2328 (-) NNNRGGNCAAAGKTCANNN AGTGGACCTTAGGCCTTC
M00073 V\$DELTAEF1_01 0.818713 2329 (+) NNNCACCTNAN GTGGACCTTAG
M00155 V\$ARP1_01 0.761960 2330 (+) TGARCCYTTGAMCCYW TGGACCTTAGGCCTTC
M00158 V\$COUP_01 0.861436 2330 (+) TGAMCTTTGMMCYT TGGACCTTAGGCCTTC
M00158 V\$COUP_01 0.905165 2331 (+) TGAMCTTTGMMCYT GGACCTTAGGCCTTC
M00242 V\$PPARA_01 0.781113 2331 (-) CWRWCTAGGNCAAAGGTCA GGACCTTAGGCCTTCCTCTC
M00069 V\$YY1_02 0.801142 2335 (+) NNNCGGCCATCTTGNCTSNW CTTAGGCCTTCCTCTCTCCA
M00007 V\$ELK1_01 0.820975 2337 (-) NNNACMGGAAGTNCNN TAGGCCTTCCTCTCTC
M00255 V\$GC_01 0.845419 2337 (-) NRGGGGCGGGGCK TAGGCCTTCCTCTC
M00272 V\$P53_02 0.803048 2338 (+) NGRCWTGYCY AGGCCTTCCTTC
M00025 V\$ELK1_02 0.797062 2339 (-) NNNNCCGGAARYNN GGCCTTCCTCTCTC
M00108 V\$NRF2_01 0.877907 2340 (-) ACCGGAAGNS GCCTTCCTCTC
M00127 V\$GATA1_03 0.793484 2342 (-) RNSNNGATAANNGN CTTCTCTCTCCAG
M00077 V\$GATA3_01 0.840939 2344 (-) NNGATARNG TCCTCTCTC
M00083 V\$MZF1_01 0.857575 2344 (-) NGNGGGGA TCCTCTCTC
M00072 V\$CP2_01 0.848628 2345 (+) GCNMNAMCMAG CCTCTCTCCAG
M00005 V\$AP4_01 0.766282 2346 (-) WGARYCAGCTGYGGNCK CTCTCTCCAGATGTTTCC
M00065 V\$TALIBETA47_01 0.888632 2348 (+) NNNAACAGATGKTNNN CTCTCCAGATGTTTCC
M00066 V\$TALIALPHA47_01 0.858794 2348 (+) NNNAACAGATGKTNNN CTCTCCAGATGTTTCC
M00070 V\$TALIBETA1F2_01 0.883740 2348 (+) NNNAACAGATGKTNNN CTCTCCAGATGTTTCC
M00071 V\$E47_02 0.780834 2348 (+) NNNMRCAGGTGTTMNN CTCTCCAGATGTTTCC
M00122 V\$USF_02 0.773462 2349 (+) NNRNCACGTGNYNN TCTCCAGATGTTTC
M00122 V\$USF_02 0.773462 2349 (-) NNRNCACGTGNYNN TCTCCAGATGTTTC
M00001 V\$MYOD_01 0.852559 2350 (-) SRACAGGTGKYG CTCCAGATGTTT
M00123 V\$MYCMAX_02 0.782769 2350 (+) NANCACGTGNNW CTCCAGATGTTT
M00277 V\$LMO2COM_01 0.890713 2350 (+) SNNCAGGTGNNN CTCCAGATGTTT
M00277 V\$LMO2COM_01 0.831763 2350 (-) SNNCAGGTGNNN CTCCAGATGTTT
M00032 V\$CETSIP54_01 0.816133 2351 (+) NCMGGAWGYN TCCAGATGTT
M00175 V\$AP4_Q5 0.823721 2351 (-) NNCAGCTGNN TCCAGATGTT
M00176 V\$AP4_Q6 0.840641 2351 (-) CWCAGCTGGN TCCAGATGTT
M00184 V\$MYOD_Q6 0.812461 2351 (+) NNCANCTGNY TCCAGATGTT
M00184 V\$MYOD_Q6 0.797964 2351 (-) NNCANCTGNY TCCAGATGTT
M00075 V\$GATA1_01 0.900790 2352 (+) SNNGATNNNN CCAGATGTTT
M00076 V\$GATA2_01 0.883175 2352 (+) NNNGATRNNN CCAGATGTTT
M00253 V\$CAP_01 0.874322 2352 (+) NCANNNNN CCAGATGT
M00269 V\$XFD3_01 0.825675 2353 (-) WNWGTMAACAWWMW CAGATGTTTCCAGA
M00146 V\$HSF1_01 0.834187 2354 (+) RGAANRTTCN AGATGTTTCC
M00146 V\$HSF1_01 0.774714 2354 (-) RGAANRTTCN AGATGTTTCC
M00147 V\$HSF2_01 0.866913 2354 (+) NGAANNWTCK AGATGTTTCC
M00147 V\$HSF2_01 0.925693 2354 (-) NGAANNWTCK AGATGTTTCC
M00086 V\$IK1_01 0.788996 2355 (-) NNNTGGGAATRCC GATGTTTCCAGAC
M00088 V\$IK3_01 0.847467 2355 (-) TNYTGGGAATACC GATGTTTCCAGAC
M00143 V\$PAX5_01 0.817821 2355 (-) NCNNNRNKCANNNGNWGNRKRGRSNNN
GATGTTTCCAGACTTCCTTGAGACACGG

M00148 V\$SRV_01 0.929845 2355 (-) AAACWAM GATGTTT
M00281 V\$RFX1_02 0.824618 2355 (-) NNGTNRCNATRGYAAACNNN GATGTTTCCAGACTTCCTT
M00074 V\$CETSIP54_02 0.855694 2356 (-) NNAMMGGAWRWNN ATGTTTCCAGACT
M00280 V\$RFX1_01 0.860969 2356 (-) NNGTNRCNWRGYAACNN ATGTTTCCAGACTTCCTT
M00032 V\$CETSIP54_01 0.889462 2357 (-) NCMGGAWGYN TGTTCAGAG
M00262 V\$STAF_01 0.763150 2357 (+) NTTWCCCANMATGCAYYRCGY TGTTCAGACTTCCTTGAGAC
M00264 V\$STAF_02 0.868951 2357 (+) MNTTCCCAKMATKCMWNGCRN TGTTCAGACTTCCTTGAGA
M00205 V\$GRE_C 0.774229 2358 (+) GGTACAANNTGTCTK GTTTCAGACTTCCTT
M00222 V\$THIE47_01 0.889683 2358 (-) NNNNGNRTCTGGMWTT GTTTCAGACTTCCTT
M00139 V\$AHR_01 0.813570 2360 (+) CYYCNRRSTNGCGTGASW TTCCAGACTTCCTTGAGA
M00191 V\$SER_Q6 0.731939 2362 (+) NNARGNNANNNTGACCYN CCAGACTTCCTTGAGACAC
M00253 V\$CAP_01 0.910793 2362 (+) NCANNNNN CCAGACTT
M00261 V\$OLF1_01 0.785304 2362 (+) NNCNANTCCCYNGRGARNNKGN CCAGACTTCCTTGAGACACGGA
M00261 V\$OLF1_01 0.782694 2362 (-) NNCNANTCCCYNGRGARNNKGN CCAGACTTCCTTGAGACACGGA
M00025 V\$ELK1_02 0.836547 2364 (-) NNNNCCGGAARYNN AGACTTCCTTGAGA
M00074 V\$CETSIP54_02 0.868455 2364 (-) NNAMMGGAWRWNN AGACTTCCTTGAG
M00272 V\$P53_02 0.825029 2364 (+) NGRCWTGYCY AGACTTCCTT
M00032 V\$CETSIP54_01 0.877784 2365 (-) NCMGGAWGYN GACTTCCTTG
M00108 V\$NRF2_01 0.856105 2365 (-) ACCGGAAGNS GACTTCCTTG
M00141 V\$LYF1_01 0.858932 2367 (-) TTTGGGAGR CTTCCTTG
M00174 V\$AP1_Q6 0.760436 2371 (-) NNTGACTCANN CTGAGACACG
M00199 V\$AP1_C 0.785131 2372 (+) NTGASTCAG TTGAGACAC
M00199 V\$AP1_C 0.855977 2372 (-) NTGASTCAG TTGAGACAC
M00155 V\$ARP1_01 0.769085 2373 (+) TGARCCYTTGAMCCYW TGAGACACGGAGCCCA
M00115 V\$TAXCREB_02 0.642094 2374 (+) RTGACGCATAYCCCC GAGACACGGAGCCCA
M00278 V\$LMO2COM_02 0.802224 2374 (+) NMGATANS GAGACACGG
M00085 V\$ZID_01 0.820955 2375 (-) NGGCTCYATCAYC AGACACGGAGCCC
M00143 V\$PAX5_01 0.762969 2375 (-) NCNNNRNKCANNNGNWNKRGCSRSNN
AGACACGGAGCCCAGCCCTCCCCATGGA
M00187 V\$USF_Q6 0.823036 2376 (+) GYCACGTGNC GACACGGAGC
M00189 V\$AP2_Q6 0.780790 2376 (+) MKCCCSCNGGCG GACACGGAGCCC
M00196 V\$SP1_Q6 0.764335 2382 (-) NGGGGGCGGGGYN GAGCCCAGCCCTC
M00255 V\$GC_01 0.832190 2382 (-) NRGGGGCGGGGCKN GAGCCCAGCCCTCC
M00196 V\$SP1_Q6 0.859548 2383 (-) NGGGGGCGGGGYN AGCCCAGCCCTCC
M00272 V\$P53_02 0.813013 2383 (+) NGRCWTGYCY AGCCCAGCCC
M00008 V\$SP1_01 0.909966 2384 (-) GRGGCRGGGW GCCCAGCCCT
M00253 V\$CAP_01 0.906358 2386 (+) NCANNNNN CCAGCCCT
M00255 V\$GC_01 0.856198 2386 (-) NRGGGGCGGGGCKN CCAGCCCTCCCCAT
M00196 V\$SP1_Q6 0.841399 2387 (-) NGGGGGCGGGGYN CAGCCCTCCCCAT
M00255 V\$GC_01 0.827536 2387 (-) NRGGGGCGGGGCKN CAGCCCTCCCCATG
M00008 V\$SP1_01 0.843715 2388 (-) GRGGCRGGGW AGCCCTCCCC
M00075 V\$GATA1_01 0.773939 2388 (-) SNNGATNNNN AGCCCTCCCC
M00261 V\$OLF1_01 0.761942 2388 (-) NNCNANTCCCYNGRGARNNKGN AGCCCTCCCCATGGAGCCAGCT
M00008 V\$SP1_01 0.882786 2389 (-) GRGGCRGGGW GCCCTCCCCA
M00072 V\$CP2_01 0.867496 2389 (+) GCNMNAMCMAG GCCCTCCCCAT
M00059 V\$YY1_01 0.806356 2391 (+) NNNNNCCATNTWNNNWN CCTCCCCATGGAGCCAG
M00189 V\$AP2_Q6 0.896599 2392 (+) MKCCCSCNGGCG CTCCCCATGGAG
M00277 V\$LMO2COM_01 0.804307 2392 (-) SNNCAGGTGNNN CTCCCCATGGAG
M00083 V\$MZF1_01 0.927465 2393 (-) NGNGGGGA TCCCCATG
M00076 V\$GATA2_01 0.781687 2394 (+) NNNGATRNNN CCCCATGGAG
M00085 V\$ZID_01 0.811487 2394 (-) NGGCTCYATCAYC CCCCATGGAGCCA
M00217 V\$USF_C 0.856424 2394 (+) NCACGTGN CCCCATGG
M00109 V\$CEBPB_01 0.812531 2396 (+) RNRTKNNGMAAKNN CCATGGAGCCAGCT
M00058 V\$HEN1_02 0.712730 2397 (+) NNGGGNCGCAGCTGCGNCCCN CATGGAGCCAGCTCCCTCTATT
M00173 V\$AP1_Q2 0.804100 2398 (-) RSTGACTNMNW ATGGAGCCAGC
M00188 V\$AP1_Q4 0.821287 2398 (-) RSTGACTMANN ATGGAGCCAGC
M00037 V\$NFE2_01 0.803146 2399 (-) TGCTGASTCAY TGGAGCCAGCT
M00002 V\$E47_01 0.824628 2400 (-) NSNGCAGGTGKNCNN GGAGCCAGCTCCCTC
M00272 V\$P53_02 0.806272 2401 (+) NGRCWTGYCY GAGCCAGCTC
M00272 V\$P53_02 0.801876 2401 (-) NGRCWTGYCY GAGCCAGCTC
M00001 V\$MYOD_01 0.819291 2402 (-) SRACAGGTGKYG AGCCAGCTCCCT

M00008 V\$SP1_01 0.804926 2402 (-) GRGGCRGGGW AGCCAGCTCC
M00075 V\$GATA1_01 0.778381 2402 (-) SNNGATNNNN AGCCAGCTCC
M00255 V\$GC_01 0.794463 2402 (-) NRGGGGCGGGGCK AGCCAGCTCCCTCT
M00175 V\$AP4_Q5 0.803863 2403 (+) NNCAGCTGNN GCCAGCTCCC
M00175 V\$AP4_Q5 0.823721 2403 (-) NNCAGCTGNN GCCAGCTCCC
M00176 V\$AP4_Q6 0.802556 2403 (+) CWCAGCTGGN GCCAGCTCCC
M00176 V\$AP4_Q6 0.823854 2403 (-) CWCAGCTGGN GCCAGCTCCC
M00184 V\$MYOD_Q6 0.804750 2403 (+) NNCANCTGNY GCCAGCTCCC
M00184 V\$MYOD_Q6 0.784392 2403 (-) NNCANCTGNY GCCAGCTCCC
M00253 V\$CAP_01 0.879744 2404 (+) NCANNNNN CCAGCTCC
M00059 V\$Y1_01 0.778834 2405 (+) NNNNNCCATNTWNNNWN CAGCTCCCTCTATTAT
M00255 V\$GC_01 0.783439 2405 (-) NRGGGGCGGGGCK CAGCTCCCTCTATT
M00147 V\$HSF2_01 0.792606 2406 (-) NGAANNWTCK AGCTCCCTCT
M00143 V\$PAX5_01 0.812424 2407 (-) NCNNNRNKCANNNGNWNKRKGRCSRSNN
GCTCCCTCTATTATGTTTGCACCTGTG
M00267 V\$XFD1_01 0.861953 2411 (-) YAWGTAAAYAWWRY CCTCTATTTATGTT
M00268 V\$XFD2_01 0.855200 2411 (-) WNWATAAACAWNNR CCTCTATTTATGTT
M00129 V\$HFH1_01 0.788530 2412 (+) NAWTGTTTATWT CTCTATTTATGT
M00131 V\$HNF3B_01 0.879884 2412 (+) NNNTRTTTRYTY CTCTATTTATGT
M00252 V\$TATA_01 0.794976 2414 (+) STATAAAWRNNNNNN CTATTTATGTTTGCA
M00100 V\$CDXA_01 1.000000 2416 (+) MTTTATR ATTTATG
M00101 V\$CDXA_02 0.997531 2416 (+) WWTWMTR ATTTATG
M00160 V\$SR_Y_02 0.844392 2416 (-) NWWAACAAWANN ATTTATGTTTGC
M00144 V\$PAX5_02 0.771071 2417 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
TTTATGTTTGCACCTGTGATTATTTATT
M00268 V\$XFD2_01 0.850000 2417 (-) WNWATAAACAWNNR TTTATGTTTGCACCT
M00269 V\$XFD3_01 0.888109 2417 (-) WNWGTMAACAWWMW TTTATGTTTGCACCT
M00129 V\$HFH1_01 0.799916 2418 (+) NAWTGTTTATWT TTATGTTTGCAC
M00131 V\$HNF3B_01 0.903664 2418 (+) NNNTRTTTRYTY TTATGTTTGCAC
M00148 V\$SR_Y_01 0.945349 2419 (-) AAACWAM TATGTTT
M00180 V\$E2F_Q6 0.730977 2419 (-) NNGCGCGAAANTK TATGTTTGCACCT
M00062 V\$IRF1_01 0.775093 2422 (-) SAAAAGYGAAACC GTTTGCACCTGTG
M00063 V\$IRF2_01 0.729562 2422 (-) GAAAAGYGAAASY GTTTGCACCTGTG
M00071 V\$E47_02 0.828410 2422 (-) NNNMRCAGGTGTTMNN GTTTGCACCTGTGATT
M00236 V\$ARNT_01 0.790334 2422 (+) NNNNNCACGTGNNNN GTTTGCACCTGTGATT
M00055 V\$NMYC_01 0.776764 2424 (+) NNNCACGTGNNN TTGCACCTGTGA
M00055 V\$NMYC_01 0.815998 2424 (-) NNNCACGTGNNN TTGCACCTGTGA
M00123 V\$MYCMAX_02 0.827423 2424 (+) NANCACGTGNNW TTGCACCTGTGA
M00277 V\$LMO2COM_01 0.833378 2424 (-) SNNCAGGTGNNN TTGCACCTGTGA
M00122 V\$USF_02 0.814481 2425 (+) NNRNCACGTGNYNN TGCACCTGTGATTA
M00122 V\$USF_02 0.814481 2425 (-) NNRNCACGTGNYNN TGCACCTGTGATTA
M00184 V\$MYOD_Q6 0.791178 2425 (+) NNCANCTGNY TGCACCTGTG
M00123 V\$MYCMAX_02 0.848700 2426 (-) NANCACGTGNNW GCACCTGTGATT
M00217 V\$USF_C 0.819188 2426 (-) NCACGTGN GCACCTGT
M00253 V\$CAP_01 0.906358 2426 (+) NCANNNNN GCACCTGT
M00187 V\$USF_Q6 0.811294 2427 (-) GYCACGTGNC CACTTGTGAT
M00240 V\$NKX25_01 0.950176 2427 (-) TYAAGTG CACTTGT
M00098 V\$PAX2_01 0.750704 2428 (+) NNNNGTCANGNRTKANNNN ACTTGTGATTATTTATTAT
M00160 V\$SR_Y_02 0.765708 2428 (-) NWWAACAAWANN ACTTGTGATTAT
M00136 V\$OCT1_02 0.777477 2429 (-) NNGAATATKANNNN CTTGTGATTATTTAT
M00137 V\$OCT1_03 0.897274 2430 (-) NNNRTAATNANNN TTGTGATTATTTA
M00075 V\$GATA1_01 0.826752 2431 (+) SNNGATNNNN TGTGATTATT
M00076 V\$GATA2_01 0.811908 2431 (+) NNNGATRNNN TGTGATTATT
M00098 V\$PAX2_01 0.791680 2431 (+) NNNNGTCANGNRTKANNNN TGTGATTATTTATTATTTA
M00148 V\$SR_Y_01 0.926744 2431 (-) AAACWAM TGTGATT
M00271 V\$AML1_01 0.850984 2431 (+) TGTGGT TGTGAT
M00077 V\$GATA3_01 0.826761 2432 (+) NNGATARNG GTGATTATT
M00136 V\$OCT1_02 0.819166 2432 (+) NNGAATATKANNNN GTGATTATTTATTAT
M00023 V\$HOX13_01 0.721664 2433 (+) TGCNNNNWYCCYCACTAKTNNNNNMNNYCN
TGATTATTTATTTATTTATTTATTTATT
M00042 V\$SOX5_01 0.854698 2433 (-) NNAACAATNN TGATTATTTA

M00099 V\$S8_01 0.791909 2433 (-) WNNANYYAATTANYNN TGATTATTTATTATT
M00268 V\$XFD2_01 0.947200 2433 (-) WNWATAAACAWNNR TGATTATTTATTAT
M00269 V\$XFD3_01 0.847071 2433 (-) WNWGTMAACAWWMW TGATTATTTATTAT
M00045 V\$E4BP4_01 0.762756 2434 (+) NRTTAYGTAAYN GATTATTTATTA
M00099 V\$S8_01 0.768900 2434 (+) WNNANYYAATTANYNN GATTATTTATTATTA
M00129 V\$HFH1_01 0.840396 2434 (+) NAWTGTTTATWT GATTATTTATTA
M00130 V\$HFH2_01 0.917874 2434 (+) NAWTGTTTTRTTT GATTATTTATTA
M00131 V\$HNF3B_01 0.857074 2434 (+) NNNTRTTTRYTY GATTATTTATTA
M00162 V\$OCT1_06 0.821094 2434 (+) CWNATKWSATRYN GATTATTTATTAT
M00095 V\$CDP_01 0.758760 2435 (-) CCAATAATCGAT ATTATTTATTAT
M00096 V\$PBX1_01 0.899855 2435 (-) ANCAATCAW ATTATTTAT
M00102 V\$CDP_02 0.847598 2435 (+) NWNATCGATTANYNN ATTATTTATTATTTA
M00103 V\$CLOX_01 0.851669 2435 (+) NNTATCGATTANYNW ATTATTTATTATTTA
M00160 V\$SR_02 0.763065 2435 (-) NWWAACAANWANN ATTATTTATTAT
M00099 V\$S8_01 0.793679 2436 (-) WNNANYYAATTANYNN TTATTTATTATTTATT
M00138 V\$OCT1_04 0.795901 2436 (-) NNNNNNNWATGCAAATNNNNWNNW TTATTTATTATTTATTATTTATT
M00160 V\$SR_02 0.768350 2436 (-) NWWAACAANWANN TTATTTATTATT
M00206 V\$HNF1_C 0.819620 2436 (-) NGTTAATKAWTNACCAM TTATTTATTATTTATTT
M00129 V\$HFH1_01 0.805187 2437 (+) NAWTGTTTATWT TATTTATTATTT
M00137 V\$OCT1_03 0.860529 2437 (-) NNNRTAATNANNN TATTTATTATTTA
M00082 V\$EV11_05 0.774579 2438 (-) AGATAAGATAN ATTTATTTATTT
M00095 V\$CDP_01 0.759723 2438 (-) CCAATAATCGAT ATTTATTTATTTA
M00099 V\$S8_01 0.798736 2438 (+) WNNANYYAATTANYNN ATTTATTTATTTATTTA
M00145 V\$BRN2_01 0.865303 2438 (-) NNCATNSRWAATNMRN ATTTATTTATTTATTTA
M00096 V\$PBX1_01 0.923589 2439 (-) ANCAATCAW TTTATTATT
M00136 V\$OCT1_02 0.775041 2439 (+) NNGAATATKCANNNN TTTATTTATTTATTTA
M00160 V\$SR_02 0.832355 2439 (-) NWWAACAANWANN TTTATTTATTAT
M00023 V\$HOX13_01 0.765901 2440 (+) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TTATTTATTTATTTATTTATTTATTTATTTAC
M00042 V\$SOX5_01 0.891831 2440 (-) NNAACAATNN TTATTTATTTA
M00099 V\$S8_01 0.793679 2440 (-) WNNANYYAATTANYNN TTATTTATTTATTTATT
M00138 V\$OCT1_04 0.796529 2440 (-) NNNNNNNWATGCAAATNNNNWNNW TTATTTATTTATTTATTTATTTATT
M00267 V\$XFD1_01 0.902020 2440 (-) YAWGTAAAYAWWRY TTATTTATTTATTTA
M00268 V\$XFD2_01 0.926000 2440 (-) WNWATAAACAWNNR TTATTTATTTATTTA
M00269 V\$XFD3_01 0.866012 2440 (-) WNWGTMAACAWWMW TTATTTATTTATTTA
M00045 V\$E4BP4_01 0.761666 2441 (+) NRTTAYGTAAYN TATTATTTATTT
M00101 V\$CDXA_02 0.995062 2441 (-) WWTWMTR TATTATT
M00129 V\$HFH1_01 0.902593 2441 (+) NAWTGTTTATWT TATTATTTATTT
M00130 V\$HFH2_01 0.960913 2441 (+) NAWTGTTTTRTTT TATTATTTATTT
M00131 V\$HNF3B_01 0.955593 2441 (+) NNNTRTTTRYTY TATTATTTATTT
M00096 V\$PBX1_01 0.899855 2442 (-) ANCAATCAW ATTATTTAT
M00097 V\$PAX6_01 0.750768 2442 (+) NNNNTTCACGCWTSANTKNNN ATTATTTATTTATTTATTTATT
M00098 V\$PAX2_01 0.791992 2442 (+) NNNNGTCANGNRTKANNNN ATTATTTATTTATTTATTTA
M00099 V\$S8_01 0.809102 2442 (+) WNNANYYAATTANYNN ATTATTTATTTATTAT
M00103 V\$CLOX_01 0.779521 2442 (+) NNTATCGATTANYNW ATTATTTATTTATTA
M00160 V\$SR_02 0.762184 2442 (-) NWWAACAANWANN ATTATTTATTTA
M00124 V\$PBX1_02 0.741296 2443 (-) NNMATCAATCAANNW TTATTTATTTATTAT
M00138 V\$OCT1_04 0.799875 2443 (-) NNNNNNNWATGCAAATNNNNWNNW TTATTTATTTATTTATTTATTTATT
M00160 V\$SR_02 0.782443 2443 (-) NWWAACAANWANN TTATTTATTTAT
M00206 V\$HNF1_C 0.794448 2443 (-) NGTTAATKAWTNACCAM TTATTTATTTATTTATTT
M00026 V\$RSRFC4_01 0.791099 2444 (+) RNKCTATTTWTAGMWN TATTTATTTATTTATTT
M00267 V\$XFD1_01 0.850505 2444 (-) YAWGTAAAYAWWRY TATTTATTTATTAT
M00268 V\$XFD2_01 0.934000 2444 (-) WNWATAAACAWNNR TATTTATTTATTAT
M00269 V\$XFD3_01 0.842511 2444 (-) WNWGTMAACAWWMW TATTTATTTATTAT
M00099 V\$S8_01 0.801011 2445 (+) WNNANYYAATTANYNN ATTTATTTATTTATTTA
M00129 V\$HFH1_01 0.786000 2445 (+) NAWTGTTTATWT ATTTATTTATTA
M00130 V\$HFH2_01 0.890426 2445 (+) NAWTGTTTTRTTT ATTTATTTATTA
M00131 V\$HNF3B_01 0.856103 2445 (+) NNNTRTTTRYTY ATTTATTTATTA
M00145 V\$BRN2_01 0.850411 2445 (-) NNCATNSRWAATNMRN ATTTATTTATTTATTTA
M00162 V\$OCT1_06 0.813281 2445 (+) CWNATKWSATRYN ATTTATTTATTATT
M00096 V\$PBX1_01 0.914327 2446 (-) ANCAATCAW TTTATTTAT

M00102 V\$CDP_02 0.852838 2446 (+) NWNATCGATTANYNN TTTATTTATTTATTTA
M00103 V\$CLOX_01 0.860632 2446 (+) NNTATCGATTANYNW TTTATTTATTTATTTA
M00160 V\$SR_02 0.780388 2446 (-) NWWAACAAWANN TTTATTTATTTAT
M00099 V\$S8_01 0.793679 2447 (-) WNNANYYAATTANYNN TTTATTTATTTATTTAT
M00138 V\$OCT1_04 0.813258 2447 (-) NNNNNNNWATGCAAATNNNWNW TTTATTTATTTATTTATTTAC
M00160 V\$SR_02 0.768350 2447 (-) NWWAACAAWANN TTTATTTATTTAT
M00206 V\$HNF1_C 0.819620 2447 (-) NGTTAATKAWTNACCAM TTTATTTATTTATTTATTT
M00129 V\$HFI1_01 0.805187 2448 (+) NAWTGTTTATWT TTTATTTATTTATTT
M00137 V\$OCT1_03 0.860529 2448 (-) NNNRTAATNANNN TTTATTTATTTATTTA
M00082 V\$EV1_05 0.774579 2449 (-) AGATAAGATAN ATTTATTTATTT
M00095 V\$CDP_01 0.759723 2449 (-) CCAATAATCGAT ATTTATTTATTTA
M00099 V\$S8_01 0.798736 2449 (+) WNNANYYAATTANYNN ATTTATTTATTTATTTA
M00145 V\$BRN2_01 0.865303 2449 (-) NNCATNSRWAATNMRN ATTTATTTATTTATTTA
M00096 V\$PBX1_01 0.923589 2450 (-) ANCAATCAW TTTATTTATTT
M00136 V\$OCT1_02 0.775041 2450 (+) NNGAATATKCANNNN TTTATTTATTTATTTA
M00160 V\$SR_02 0.832355 2450 (-) NWWAACAAWANN TTTATTTATTTAT
M00042 V\$SOX5_01 0.891831 2451 (-) NNAACAATNN TTTATTTATTTA
M00099 V\$S8_01 0.793679 2451 (-) WNNANYYAATTANYNN TTTATTTATTTATTTATTT
M00267 V\$XFD1_01 0.902020 2451 (-) YAWGTAAAYAWWRY TTTATTTATTTATTTA
M00268 V\$XFD2_01 0.926000 2451 (-) WNWATAAACAWNNR TTTATTTATTTATTTA
M00269 V\$XFD3_01 0.866012 2451 (-) WNWGTMAACAWWMW TTTATTTATTTATTTA
M00045 V\$E4BP4_01 0.761666 2452 (+) NRTTAYGTAAYN TTTATTTATTTATTT
M00101 V\$CDXA_02 0.995062 2452 (-) WWTWMTR TTTATTTATTT
M00129 V\$HFI1_01 0.902593 2452 (+) NAWTGTTTATWT TTTATTTATTTATTT
M00130 V\$HFI2_01 0.960913 2452 (+) NAWTGTTTTRTTT TTTATTTATTTATTT
M00131 V\$HNF3B_01 0.955593 2452 (+) NNNTRTTTRYTY TTTATTTATTTATTT
M00206 V\$HNF1_C 0.807106 2452 (+) NGTTAATKAWTNACCAM TTTATTTATTTATTTATTTA
M00096 V\$PBX1_01 0.899855 2453 (-) ANCAATCAW ATTTATTTATTT
M00099 V\$S8_01 0.813148 2453 (+) WNNANYYAATTANYNN ATTTATTTATTTATTTA
M00103 V\$CLOX_01 0.781761 2453 (+) NNTATCGATTANYNW ATTTATTTATTTATTT
M00160 V\$SR_02 0.762184 2453 (-) NWWAACAAWANN ATTTATTTATTTA
M00160 V\$SR_02 0.782443 2454 (-) NWWAACAAWANN TTTATTTATTTAT
M00206 V\$HNF1_C 0.854430 2454 (-) NGTTAATKAWTNACCAM TTTATTTATTTATTTATTTA
M00267 V\$XFD1_01 0.884175 2455 (-) YAWGTAAAYAWWRY TTTATTTATTTATTTA
M00268 V\$XFD2_01 0.926000 2455 (-) WNWATAAACAWNNR TTTATTTATTTATTTA
M00269 V\$XFD3_01 0.854437 2455 (-) WNWGTMAACAWWMW TTTATTTATTTATTTA
M00129 V\$HFI1_01 0.834071 2456 (+) NAWTGTTTATWT ATTTATTTATTTATTT
M00130 V\$HFI2_01 0.951471 2456 (+) NAWTGTTTTRTTT ATTTATTTATTTATTT
M00131 V\$HNF3B_01 0.954623 2456 (+) NNNTRTTTRYTY ATTTATTTATTTATTT
M00206 V\$HNF1_C 0.809839 2456 (+) NGTTAATKAWTNACCAM ATTTATTTATTTATTTACAGA
M00096 V\$PBX1_01 0.914327 2457 (-) ANCAATCAW TTTATTTATTT
M00099 V\$S8_01 0.763843 2457 (+) WNNANYYAATTANYNN TTTATTTATTTATTTACAGA
M00138 V\$OCT1_04 0.859055 2457 (-) NNNNNNNWATGCAAATNNNWNW TTTATTTATTTATTTACAGATGAATGT
M00160 V\$SR_02 0.779507 2457 (-) NWWAACAAWANN TTTATTTATTTATTTA
M00231 V\$MEF2_02 0.786888 2457 (-) NNNNNNKCTAWAAATAGMNNN TTTATTTATTTATTTACAGATGAATG
M00232 V\$MEF2_03 0.811850 2457 (-) NNNNNWKCTAWAAATAGMNNN TTTATTTATTTATTTACAGATGAATG
M00160 V\$SR_02 0.796829 2458 (-) NWWAACAAWANN TTTATTTATTTATTTAC
M00252 V\$TATA_01 0.784572 2458 (+) STATAAAWRNNNNNNN TTTATTTATTTATTTACAGA
M00026 V\$RSRFC4_01 0.824956 2459 (+) RNKCTATTTWTAGMWN TTTATTTATTTATTTACAGATG
M00135 V\$OCT1_01 0.750668 2459 (-) NNNNWTATGCAAATNTNNN TTTATTTATTTATTTACAGATGAAT
M00268 V\$XFD2_01 0.895200 2459 (-) WNWATAAACAWNNR TTTATTTATTTATTTACAGA
M00269 V\$XFD3_01 0.928446 2459 (-) WNWGTMAACAWWMW TTTATTTATTTATTTACAGA
M00131 V\$HNF3B_01 0.860713 2460 (+) NNNTRTTTRYTY ATTTATTTATTTATTTACAG
M00252 V\$TATA_01 0.772139 2460 (+) STATAAAWRNNNNNNN ATTTATTTATTTATTTACAGATG
M00097 V\$PAX6_01 0.829749 2461 (+) NNNNTTCACGCWTSANTKNNN TTTATTTATTTATTTACAGATGAATGTAT
M00098 V\$PAX2_01 0.774163 2461 (+) NNNNGTCANGNRTKANNNN TTTATTTATTTATTTACAGATGAATGT
M00145 V\$BRN2_01 0.855301 2461 (-) NNCATNSRWAATNMRN TTTATTTATTTATTTACAGATGAA
M00210 V\$OCT_C 0.768780 2461 (+) CTNATTTGCATAY TTTATTTATTTATTTACAGAT
M00138 V\$OCT1_04 0.788791 2463 (-) NNNNNNNWATGCAAATNNNWNW TTTATTTATTTATTTACAGATGAATGTATTTAT
M00059 V\$YY1_01 0.780144 2464 (-) NNNNNCCATNTWNNNNWN ATTTATTTATTTATTTACAGATGAATGTA
M00100 V\$CDXA_01 0.923982 2464 (+) MTTTATR ATTTATTTATTTATTTACAGAT

M00222 V\$TH1E47_01 0.822016 2464 (-) NNNNGNRTCTGGMWTT ATTTACAGATGAATGT
M00277 V\$LMO2COM_01 0.788156 2466 (-) SNNCAGGTGNNN TTACAGATGAAT
M00184 V\$MYOD_Q6 0.792412 2467 (-) NNCANCTGNY TACAGATGAA
M00075 V\$GATA1_01 0.773939 2468 (+) SNNGATNNNN ACAGATGAAT
M00076 V\$GATA2_01 0.786649 2468 (+) NNNGATRNNN ACAGATGAAT
M00217 V\$USF_C 0.829587 2468 (-) NCACGTGN ACAGATGA
M00104 V\$CDPCR1_01 0.774015 2469 (-) NATCGATCGS CAGATGAATG
M00106 V\$CDPCR3HD_01 0.904268 2469 (-) NATYGATSSS CAGATGAATG
M00160 V\$SR_Y_02 0.784792 2472 (-) NWWAACA AWANN ATGAATGTATTT
M00162 V\$OCT1_06 0.862891 2473 (-) CWNATWKWSATRYN TGAATGTATTTATT
M00267 V\$XFD1_01 0.932660 2475 (-) YAWGTAAAYAWWRY AATGTATTTATTG
M00131 V\$HNF3B_01 0.920165 2476 (+) NNNTRTTTRYTY ATGTATTTATTT
M00137 V\$OCT1_03 0.841169 2476 (-) NNNRTAATNANNN ATGTATTTATTTG
M00160 V\$SR_Y_02 0.770699 2477 (-) NWWAACA AWANN TGTATTTATTTG
M00186 V\$SRF_Q6 0.806847 2478 (-) GNCCAWATAWGGMN GTATTTATTTGGGA
M00252 V\$TATA_01 0.824664 2478 (+) STATAA AWRNNNNNN GTATTTATTTGGGAG
M00087 V\$IK2_01 0.884162 2484 (+) NNNYGGGAWNNN ATTTGGGAGACC
M00072 V\$CP2_01 0.819468 2485 (-) GCNMNAMCMAG TTTGGGAGACC
M00141 V\$LYF1_01 1.000000 2485 (+) TTTGGGAGR TTTGGGAGA
M00262 V\$STAF_01 0.769220 2491 (-) NTTWCCCANMATGCAYYRCGY AGACCGGGGTATCCTGGGGGAC
M00143 V\$PAX5_01 0.785219 2492 (+) NCNNNRNKCANNNGWGNRKRGRSNN
GACCGGGGTATCCTGGGGGACCCAATGT
M00052 V\$NFKAPPAB65_01 0.829701 2495 (+) GGGRATTTCC CGGGGTATCC
M00053 V\$CREL_01 0.895439 2495 (+) SGRNWTTC CGGGGTATCC
M00127 V\$GATA1_03 0.820921 2495 (-) RNSNNGATAANNNGN CGGGGTATCCTGGG
M00054 V\$NFKAPPAB_01 0.845693 2496 (+) GGGAMTTYCC GGGGTATCCT
M00281 V\$RF1_02 0.756832 2496 (-) NNGTNRCNATRGYACNNN GGGGTATCCTGGGGGACCC
M00025 V\$ELK1_02 0.807775 2497 (-) NNNNCCGGAARYNN GGGTATCCTGGGGG
M00074 V\$CETSIP54_02 0.861911 2497 (-) NNAMMGAWRWNN GGGTATCCTGGGG
M00075 V\$GATA1_01 0.882034 2497 (-) SNNGATNNNN GGGTATCCTG
M00076 V\$GATA2_01 0.944520 2497 (-) NNNGATRNNN GGGTATCCTG
M00032 V\$CETSIP54_01 0.901684 2498 (-) NCMGGAWGYN GGTATCCTGG
M00189 V\$AP2_Q6 0.847656 2501 (+) MKCCCSCNNGGCG ATCCTGGGGGAC
M00189 V\$AP2_Q6 0.896369 2501 (-) MKCCCSCNNGGCG ATCCTGGGGGAC
M00189 V\$AP2_Q6 0.798943 2502 (-) MKCCCSCNNGGCG TCCTGGGGGACC
M00141 V\$LYF1_01 0.887299 2503 (+) TTTGGGAGR CCTGGGGGA
M00083 V\$MZF1_01 0.895731 2504 (+) NGNGGGGA CTGGGGGA
M00177 V\$CREB_Q2 0.751872 2507 (+) NSTGACGTAANN GGGGACCCAATG
M00185 V\$NFY_Q6 0.823227 2510 (+) TRRCCAATSRN GACCCAATGTA
M00186 V\$SRF_Q6 0.788462 2511 (+) GNCCAWATAWGGMN ACCCAATGTAGGAG
M00255 V\$GC_01 0.836355 2517 (+) NRGGGGCGGGGCGNK TG TAGGAGCTGCCT
M00001 V\$MYOD_01 0.813976 2519 (-) SRACAGGTGKYG TAGGAGCTGCCT
M00175 V\$AP4_Q5 0.794886 2520 (+) NNCAGCTGNN AGGAGCTGCC
M00175 V\$AP4_Q5 0.924918 2520 (-) NNCAGCTGNN AGGAGCTGCC
M00176 V\$AP4_Q6 0.797043 2520 (+) CWCAGCTGGN AGGAGCTGCC
M00176 V\$AP4_Q6 0.895765 2520 (-) CWCAGCTGGN AGGAGCTGCC
M00184 V\$MYOD_Q6 0.819864 2520 (+) NNCANCTGNY AGGAGCTGCC
M00184 V\$MYOD_Q6 0.787168 2520 (-) NNCANCTGNY AGGAGCTGCC
M00255 V\$GC_01 0.783439 2520 (-) NRGGGGCGGGGCGNK AGGAGCTGCCTTG
M00144 V\$PAX5_02 0.741797 2521 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
GGAGCTGCCTTGGCTCAGACATGTTTTTC
M00272 V\$P53_02 0.797773 2521 (+) NGRCWTGYCY GGAGCTGCCT
M00201 V\$CEBP_C 0.846023 2524 (-) NGWNTKNKGAAKNSAYA GCTGCCTTGGCTCAGACA
M00254 V\$CAAT_01 0.812200 2527 (-) NNNRRCCAATSA GCCTTGGCTCAG
M00193 V\$NF1_Q6 0.799816 2528 (+) NNTTGGCNNNNNNCCNNN CCTTGGCTCAGACATGTT
M00050 V\$E2F_02 0.743405 2529 (+) TTTSGCGC CTTGGCTC
M00191 V\$ER_Q6 0.734553 2530 (-) NNARGNNANNNTGACCYN TTGGCTCAGACATGTTTTTC
M00199 V\$AP1_C 0.823615 2530 (+) NTGASTCAG TTGGCTCAG
M00199 V\$AP1_C 0.792128 2530 (-) NTGASTCAG TTGGCTCAG
M00162 V\$OCT1_06 0.803125 2532 (+) CWNATWKWSATRYN GGCTCAGACATGTT
M00072 V\$CP2_01 0.782590 2533 (+) GCNMNAMCMAG GCTCAGACATG

M00144 V\$PAX5_02 0.744571 2533 (+) RRMSWGANWYCTNRAGCGKRACSRYSNM
GCTCAGACATGTTTTCCGTGAAAACGGA
M00098 V\$PAX2_01 0.758836 2534 (+) NNNNGTCANGNRTKANNNN CTCAGACATGTTTTCCGTG
M00199 V\$AP1_C 0.790087 2534 (-) NTGASTCAG CTCAGACAT
M00055 V\$NMYC_01 0.757299 2535 (+) NNNCACGTGNNN TCAGACATGTTT
M00253 V\$CAP_01 0.923115 2535 (+) NCANNNNN TCAGACAT
M00057 V\$COMP1_01 0.815210 2537 (+) NNTNWKGATTGRCNRSRANMRRNN AGACATGTTTTCCGTGAAAACGGA
M00082 V\$EV11_05 0.811260 2537 (+) AGATAAGATAN AGACATGTTTT
M00123 V\$MYCMAX_02 0.799580 2537 (-) NANCACGTGNNW AGACATGTTTTT
M00160 V\$SR1_02 0.771873 2537 (-) NWWAACA AWANN AGACATGTTTTT
M00272 V\$P53_02 0.976553 2537 (+) NGRCWTGYCY AGACATGTTT
M00272 V\$P53_02 0.964244 2537 (-) NGRCWTGYCY AGACATGTTT
M00024 V\$E2F_01 0.758854 2540 (-) TWSGCGCGAAAAYKR CATGTTTTCCGTGAA
M00224 V\$STAT1_01 0.815742 2540 (+) NNNSANTTCCGGGAANTGNSN CATGTTTTCCGTGAAAACGGA
M00224 V\$STAT1_01 0.742137 2540 (-) NNNSANTTCCGGGAANTGNSN CATGTTTTCCGTGAAAACGGA
M00225 V\$STAT3_01 0.727009 2540 (+) NGNNATTTCCSGGAARTGNNN CATGTTTTCCGTGAAAACGGA
M00225 V\$STAT3_01 0.754960 2540 (-) NGNNATTTCCSGGAARTGNNN CATGTTTTCCGTGAAAACGGA
M00235 V\$AHRARNT_01 0.760999 2540 (+) KNNKNNTYGCGTGCMS CATGTTTTCCGTGAAA
M00180 V\$E2F_Q6 0.736186 2541 (-) NNGCGCGAAANTK ATGTTTTCCGTGA
M00237 V\$AHRARNT_02 0.727420 2541 (+) GRGKATYGCGTGMSWNSCC ATGTTTTCCGTGAAAACGG
M00025 V\$ELK1_02 0.786654 2542 (-) NNNNCCGGGAARYNN TGTTTTCCGTGAAA
M00074 V\$CETS1P54_02 0.835079 2542 (-) NNAMMGGAWRWNN TGTTTTCCGTGAA
M00032 V\$CETS1P54_01 0.816133 2543 (-) NCMGGAWGYN GTTTTCCGTG
M00108 V\$NRF2_01 0.796027 2543 (-) ACCGGAAGNS GTTTTCCGTG
M00024 V\$E2F_01 0.848014 2545 (+) TWSGCGCGAAAAYKR TTTCCGTGAAAACGG
M00040 V\$CREBP1_01 0.751577 2546 (+) TTACGTAA TTCCGTGA
M00040 V\$CREBP1_01 0.751577 2546 (-) TTACGTAA TTCCGTGA
M00180 V\$E2F_Q6 0.791442 2546 (+) NNGCGCGAAANTK TTCCGTGAAAACG
M00223 V\$STAT_01 0.860852 2546 (+) TTCCCRKAA TTCCGTGAA
M00223 V\$STAT_01 0.887320 2546 (-) TTCCCRKAA TTCCGTGAA
M00227 V\$VMYB_02 0.812876 2547 (-) NSYAACGGN TCCGTGAAA
M00050 V\$E2F_02 0.813107 2548 (-) TTTSGCGC CCGTGAAA
M00258 V\$ISRE_01 0.757805 2550 (-) CAGTTTCWCTTTYCC GTGAAAACGGAGCTG
M00003 V\$VMYB_01 0.849063 2552 (+) AAYAACGGNN GAAAACGGAG
M00085 V\$ZID_01 0.812750 2552 (-) NGGCTCYATCAYC GAAAACGGAGCTG
M00227 V\$VMYB_02 0.821300 2552 (+) NSYAACGGN GAAAACGGA
M00175 V\$AP4_Q5 0.805767 2557 (+) NNCAGCTGNN CGGAGCTGAA
M00175 V\$AP4_Q5 0.832699 2557 (-) NNCAGCTGNN CGGAGCTGAA
M00176 V\$AP4_Q6 0.819344 2557 (-) CWCAGCTGGN CGGAGCTGAA
M00129 V\$HFH1_01 0.794856 2560 (-) NAWTGTTTATWT AGCTGAACAATA
M00174 V\$AP1_Q6 0.766077 2561 (+) NNTGACTCANN GCTGAACAATA
M00200 V\$CAAT_C 0.732154 2561 (+) ACCAATCANCNNGCYYSNCNCWNNT GCTGAACAATAGGCTGTTCCCATGT
M00160 V\$SR1_02 0.926894 2562 (+) NWWAACA AWANN CTGAACAATAGG
M00042 V\$SOX5_01 0.964805 2563 (+) NNAACAATNN TGAACAATAG
M00185 V\$NFY_Q6 0.817831 2563 (+) TRRCCAATSRN TGAACAATAGG
M00104 V\$CDPCR1_01 0.781179 2564 (+) NATCGATCGS GAACAATAGG
M00005 V\$AP4_01 0.754035 2566 (+) WGARYCAGCTGYGGNCKN ACAATAGGCTGTTCCCAT
M00255 V\$GC_01 0.810877 2568 (+) NRGGGGCGGGGCKN AATAGGCTGTTCCC
M00008 V\$SP1_01 0.800396 2570 (+) GRGGCRGGGW TAGGCTGTTC
M00144 V\$PAX5_02 0.768775 2570 (-) RRMSWGANWYCTNRAGCGKRACSRYSNM
TAGGCTGTTCCCATGTAGCCCCCTGGCC
M00146 V\$HSF1_01 0.790863 2571 (-) RGAANRTTCN AGGCTGTTCC
M00255 V\$GC_01 0.834885 2571 (-) NRGGGGCGGGGCKN AGGCTGTTCCCATG
M00183 V\$MYB_Q6 0.837344 2572 (-) NNNAACKGNC GGCTGTTCCC
M00086 V\$IK1_01 0.885150 2573 (-) NNNTGGGAATRCC GCTGTTCCCATGT
M00088 V\$IK3_01 0.795864 2573 (-) TNYTGGGAATACC GCTGTTCCCATGT
M00279 V\$MIF1_01 0.763696 2573 (-) NNGTTGCWWGGYACNGS GCTGTTCCCATGTAGCCC
M00281 V\$RFX1_02 0.814934 2573 (-) NNGTNRCNATRGYACNNN GCTGTTCCCATGTAGCCCC
M00087 V\$IK2_01 0.862893 2574 (-) NNNYGGGAWNNN CTGTTCCCATGT
M00279 V\$MIF1_01 0.740154 2574 (+) NNGTTGCWWGGYACNGS CTGTTCCCATGTAGCCCC
M00280 V\$RFX1_01 0.850703 2574 (-) NNGTNRCNWRGYACNN CTGTTCCCATGTAGCCC

M00059 V\$YY1_01 0.804391 2575 (+) NNNNNCCATNTWNNNWN TGTTCCCATGTAGCCCC
M00217 V\$USF_C 0.871184 2578 (+) NCACGTGN TCCCATGT
M00200 V\$CAAT_C 0.714086 2579 (+) ACCAATCANCNNGCYYSNCNCWNNT CCCATGTAGCCCCCTGGCCTCTGTG
M00105 V\$CDPCR3_01 0.761283 2580 (-) CACCRATANNTATNG CCATGTAGCCCCCTG
M00127 V\$GATA1_03 0.780500 2580 (-) RNSNNGATAANNNGN CCATGTAGCCCCCT
M00249 V\$CHOP_01 0.784585 2580 (+) NNRTGCAATMCCC CCATGTAGCCCCC
M00134 V\$HNF4_01 0.767241 2583 (-) NNNRGGNCAAGKTCANNN TGTAGCCCCCTGGCCTCTG
M00118 V\$MYCMAX_01 0.726909 2585 (+) NNACCACGTGGTNN TAGCCCCCTGGCCT
M00118 V\$MYCMAX_01 0.726909 2585 (-) NNACCACGTGGTNN TAGCCCCCTGGCCT
M00122 V\$USF_02 0.816967 2585 (+) NNRNCACGTGNYNN TAGCCCCCTGGCCT
M00122 V\$USF_02 0.816967 2585 (-) NNRNCACGTGNYNN TAGCCCCCTGGCCT
M00155 V\$ARP1_01 0.757307 2585 (+) TGARCCYTTGAMCCYW TAGCCCCCTGGCCTCT
M00001 V\$MYOD_01 0.799016 2586 (-) SRACAGGTGKYG AGCCCCCTGGCC
M00189 V\$AP2_Q6 0.930147 2586 (+) MKCCCSCNGGCG AGCCCCCTGGCC
M00189 V\$AP2_Q6 0.801930 2586 (-) MKCCCSCNGGCG AGCCCCCTGGCC
M00277 V\$LMO2COM_01 0.802961 2586 (-) SNNCAGGTGNNN AGCCCCCTGGCC
M00184 V\$MYOD_Q6 0.809685 2587 (+) NNCANCTGNY GCCCCTGGC
M00187 V\$USF_Q6 0.836455 2587 (-) GYCACGTGNC GCCCCTGGC
M00217 V\$USF_C 0.835290 2588 (+) NCACGTGN CCCCCTGG
M00139 V\$AHR_01 0.730426 2589 (+) CYYCNRRSTNGCGTGASW CCCCTGGCCTCTGTGCCT
M00254 V\$CAAT_01 0.800056 2589 (-) NNNRRCCAATSA CCCCTGGCCTCT
M00134 V\$HNF4_01 0.808984 2590 (-) NNNRGGNCAAGKTCANNN CCCTGGCCTCTGTGCCTTC
M00158 V\$COUP_01 0.827785 2593 (+) TGAMCTTTGMMCYT TGGCCTCTGTGCCT
M00176 V\$AP4_Q6 0.806815 2594 (-) CWCAGCTGGN GGCCTCTGTG
M00189 V\$AP2_Q6 0.805377 2594 (-) MKCCCSCNGGCG GGCCTCTGTGCC
M00008 V\$SP1_01 0.804360 2598 (-) GRGGCRGGGW TCTGTGCCTT
M00146 V\$HSF1_01 0.790075 2600 (-) RGAANRTTCN TGTGCCTTCT
M00147 V\$HSF2_01 0.796673 2600 (-) NGAANNWTCK TGTGCCTTCT
M00238 V\$BARBIE_01 0.823846 2601 (-) ATNNAAGCNGRNGG GTGCCTTCTTTTGAT
M00250 V\$GFI1_01 0.753924 2601 (-) NNNNNNNAAATCASWGYNNNNNNN GTGCCTTCTTTTGATTATGTTTT
M00186 V\$SRF_Q6 0.786137 2602 (-) GNCCAWATAWGGMN TGCCTTCTTTTGAT
M00162 V\$OCT1_06 0.844922 2605 (+) CWNATWKWSATRYN CTTCTTTTGATTAT
M00099 V\$S8_01 0.819975 2606 (+) WNNANYAATTANYNN TTCTTTTGATTATGTT
M00062 V\$IRF1_01 0.750372 2607 (-) SAAAAGYGAAACC TCTTTTGATTATG
M00103 V\$CLOX_01 0.806632 2607 (+) NNTATCGATTANYNW TCTTTTGATTATGTT
M00160 V\$SRY_02 0.916618 2607 (-) NWWAACAANWANN TCTTTTGATTAT
M00129 V\$SHF1_01 0.830909 2609 (+) NAWTGTTTATWT TTTTGATTATGT
M00137 V\$OCT1_03 0.899644 2609 (-) NNNRTAATNANNN TTTTGATTATGTT
M00138 V\$OCT1_04 0.802593 2609 (+) NNNNNNNWATGCAAATNNNWNW TTTTGATTATGTTTTTAAATA
M00075 V\$GATA1_01 0.773445 2610 (+) SNNGATNNNN TTTGATTATG
M00148 V\$SRY_01 0.962791 2610 (-) AAACWAM TTTGATT
M00077 V\$GATA3_01 0.852016 2611 (+) NNGATARNG TTGATTATG
M00127 V\$GATA1_03 0.784664 2611 (-) RNSNNGATAANNNGN TTGATTATGTTTTT
M00241 V\$NKX25_02 0.834741 2612 (-) CWTAATTG TGATTATG
M00160 V\$SRY_02 0.802408 2613 (-) NWWAACAANWANN GATTATGTTTTT
M00268 V\$XFD2_01 0.851600 2614 (-) WNWATAAACAWNNR ATTATGTTTTTTAA
M00269 V\$XFD3_01 0.800421 2614 (-) WNWGTMAACAWWMW ATTATGTTTTTTAA
M00011 V\$EV11_06 0.775619 2615 (-) ACAAGATAA TTATGTTTTT
M00080 V\$EV11_03 0.716461 2615 (-) AGATAAGATAA TTATGTTTTTTT
M00129 V\$SHF1_01 0.795488 2615 (+) NAWTGTTTATWT TTATGTTTTTTT
M00138 V\$OCT1_04 0.810749 2616 (-) NNNNNNNWATGCAAATNNNWNW TATGTTTTTTAAATATTTATCT
M00148 V\$SRY_01 0.945349 2616 (-) AAACWAM TATGTTT
M00231 V\$MEF2_02 0.774825 2616 (+) NNNNNNKCTAWAAATAGMNNNN TATGTTTTTTAAATATTTATC
M00232 V\$MEF2_03 0.812017 2616 (+) NNNNNWKTAWAAATAGMNNNN TATGTTTTTTAAATATTTATC
M00233 V\$MEF2_04 0.743165 2616 (+) NNTGTACTAAAAATAGAAMNN TATGTTTTTTAAATATTTATC
M00109 V\$CEBPB_01 0.813522 2617 (+) RNRTKNNGMAAKNN ATGTTTTTTAAAT
M00116 V\$CEBPA_01 0.825968 2617 (-) NNATRCNNAANNN ATGTTTTTTAAAT
M00160 V\$SRY_02 0.765708 2618 (-) NWWAACAANWANN TGTTTTTTAAAA
M00109 V\$CEBPB_01 0.810797 2619 (+) RNRTKNNGMAAKNN GTTTTTTTAAATAT
M00216 V\$TATA_C 0.768154 2620 (+) NCTATAAAAR TTTTTTAAAA
M00216 V\$TATA_C 0.872722 2621 (+) NCTATAAAAR TTTTTTAAAT

M00136 V\$OCT1_02 0.776394 2622 (-) NNGAATATKCANNNN TTTTAAATATTTAT
M00138 V\$OCT1_04 0.790673 2622 (-) NNNNNNNWATGCAAATNNNWNW TTTTAAATATTTATCTGATTAA
M00206 V\$HNF1_C 0.845081 2622 (-) NGTTAATKAWTNACCAM TTTTAAATATTTATCT
M00099 V\$S8_01 0.790645 2624 (+) WNNANYYAATTANYNN TTAATAATTTATCTG
M00138 V\$OCT1_04 0.791719 2624 (-) NNNNNNNWATGCAAATNNNWNW TTAATAATTTATCTGATTAAAGT
M00136 V\$OCT1_02 0.772334 2625 (+) NNGAATATKCANNNN TAAATATTTATCTG
M00099 V\$S8_01 0.777244 2626 (-) WNNANYYAATTANYNN AAAATATTTATCTGAT
M00267 V\$XFD1_01 0.890909 2626 (-) YAWGTAAAYAWWRY AAAATATTTATCTG
M00129 V\$HFH1_01 0.782838 2627 (+) NAWTGTTTATWT AAATATTTATCT
M00130 V\$HFH2_01 0.915459 2627 (+) NAWTGTTTTRTTT AAATATTTATCT
M00131 V\$HNF3B_01 0.921864 2627 (+) NNNTRTTRYTY AAATATTTATCT
M00137 V\$OCT1_03 0.849467 2627 (-) NNNRTAATNANNN AAATATTTATCTG
M00203 V\$GATA_C 0.946567 2628 (-) NGATAAGNMNN AATATTTATCT
M00127 V\$GATA1_03 0.789809 2629 (-) RNSNNGATAANNGN ATATTTATCTGATT
M00128 V\$GATA1_04 0.952819 2629 (-) NNCWGATARNNNN ATATTTATCTGAT
M00104 V\$CDPCR1_01 0.778248 2630 (+) NATCGATCGS TATTTATCTG
M00075 V\$GATA1_01 0.782330 2631 (-) SNNGATNNNN ATTTATCTGA
M00076 V\$GATA2_01 0.847542 2631 (-) NNNGATRNNN ATTTATCTGA
M00077 V\$GATA3_01 0.840939 2631 (-) NNGATARNG ATTTATCTG
M00100 V\$CDXA_01 0.948504 2631 (+) MTTTATR ATTTATC
M00131 V\$HNF3B_01 0.853191 2631 (+) NNNTRTTRYTY ATTTATCTGATT
M00278 V\$LMO2COM_02 0.823787 2631 (-) NMGATANSNG ATTTATCTG
M00099 V\$S8_01 0.875853 2632 (+) WNNANYYAATTANYNN TTTATCTGATTAAAGTT
M00162 V\$OCT1_06 0.822656 2632 (-) CWNATKWSATRYN TTTATCTGATTAAAG
M00011 V\$EVII_06 0.777076 2633 (-) ACAAGATAA TTATCTGAT
M00079 V\$EVII_02 0.784084 2633 (-) AGAYAAGATAA TTATCTGATTA
M00080 V\$EVII_03 0.775926 2633 (-) AGATAAGATAA TTATCTGATTA
M00082 V\$EVII_05 0.818298 2633 (-) AGATAAGATAN TTATCTGATTA
M00099 V\$S8_01 0.772946 2634 (-) WNNANYYAATTANYNN TATCTGATTAAAGTTGT
M00124 V\$PBX1_02 0.741929 2634 (-) NNMATCAATCAANNW TATCTGATTAAAGTTG
M00137 V\$OCT1_03 0.879494 2635 (-) NNNRTAATNANNN ATCTGATTAAAGTT
M00075 V\$GATA1_01 0.790721 2636 (+) SNNGATNNNN TCTGATTAAAG
M00076 V\$GATA2_01 0.784844 2636 (+) NNNGATRNNN TCTGATTAAAG
M00172 V\$APIFJ_Q2 0.820189 2636 (+) RSTGACTNMNW TCTGATTAAAGT
M00173 V\$API_Q2 0.795900 2636 (+) RSTGACTNMNW TCTGATTAAAGT
M00174 V\$API_Q6 0.839037 2636 (+) NNTGACTCANN TCTGATTAAAGT
M00188 V\$API_Q4 0.845990 2636 (+) RSTGACTMANN TCTGATTAAAGT
M00077 V\$GATA3_01 0.850687 2637 (+) NNGATARNG CTGATTAAAG
M00199 V\$API_C 0.808163 2637 (+) NTGASTCAG CTGATTAAAG
M00199 V\$API_C 0.894752 2637 (-) NTGASTCAG CTGATTAAAG
M00241 V\$NKX25_02 0.846002 2638 (-) CWTAATTG TGATTAAAG
M00269 V\$XFD3_01 0.788495 2640 (-) WNWGTMAACAWWMW ATTAAGTTGTCTAA
M00003 V\$VMYB_01 0.812864 2641 (-) AAYAACGGNN TTAAGTTGTC
M00011 V\$EVII_06 0.775619 2641 (-) ACAAGATAA TTAAGTTGT
M00078 V\$EVII_01 0.752651 2641 (-) WGAYAAGATAAGATAA TTAAGTTGTCTAAACA
M00079 V\$EVII_02 0.802859 2641 (-) AGAYAAGATAA TTAAGTTGTCT
M00080 V\$EVII_03 0.760288 2641 (-) AGATAAGATAA TTAAGTTGTCT
M00082 V\$EVII_05 0.816805 2641 (-) AGATAAGATAN TTAAGTTGTCT
M00023 V\$HOX13_01 0.725012 2642 (-) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
TAAGTTGTCTAAACAATGCTGATTGGTGA
M00272 V\$P53_02 0.798359 2642 (+) NGRCWTGYCY TAAGTTGTCT
M00116 V\$CEBPA_01 0.848260 2643 (+) NNATTRCNNAANNN AAGTTGTCTAAACA
M00116 V\$CEBPA_01 0.817364 2643 (-) NNATTRCNNAANNN AAGTTGTCTAAACA
M00117 V\$CEBPB_02 0.863912 2643 (-) NKNTTGCNYAAYNN AAGTTGTCTAAACA
M00143 V\$PAX5_01 0.772882 2643 (-) NCNNNRNKCANNNGNWGNRKRGRCSRSNN
AAGTTGTCTAAACAATGCTGATTGGTG
M00269 V\$XFD3_01 0.786741 2643 (-) WNWGTMAACAWWMW AAGTTGTCTAAACA
M00109 V\$CEBPB_01 0.838782 2644 (-) RNRTKNGMAAKNN AGTTGTCTAAACAA
M00200 V\$CAAT_C 0.733299 2644 (-) ACCAATCANCNNGCYYSNCNCWNNT AGTTGTCTAAACAATGCTGATTGG
M00080 V\$EVII_03 0.712757 2646 (-) AGATAAGATAA TTGTCTAAACA
M00199 V\$API_C 0.776385 2646 (+) NTGASTCAG TTGTCTAAA

M00267 V\$XFD1_01 0.888215 2647 (+) YAWGTAAAYAWWRY TGTCTAAACAATGC
M00129 V\$HFH1_01 0.919460 2648 (-) NAWTGTATTATWT GTCTAAACAATG
M00138 V\$OCT1_04 0.806985 2649 (+) NNNNNNNWATGCAAATNNWNW TCTAAACAATGCTGATTGGTGA
M00160 V\$SR5_02 0.913388 2650 (+) NWWAACA AWANN TAAACAATGCT
M00042 V\$SOX5_01 0.979658 2651 (+) NNAACAATNN TAAACAATGC
M00135 V\$OCT1_01 0.738649 2651 (+) NNNNWTATGCAAATNTNNN TAAACAATGCTGATTGGT
M00148 V\$SR5_01 0.910853 2652 (+) AACWAM AACAAAT
M00076 V\$GATA2_01 0.782138 2653 (-) NNNGATRNNN AACAAATGCTG
M00248 V\$OCT1_07 0.828705 2654 (+) TNTATGNTAATT ACAATGCTGATT
M00035 V\$VMAF_01 0.768492 2655 (+) NNNTGCTGACTCAGCANNN CAATGCTGATTGGTGACC
M00105 V\$CDPCR3_01 0.784595 2655 (-) CACCRATANNTATNG CAATGCTGATTGGT
M00131 V\$HNF3B_01 0.864111 2655 (+) NNNTRTTTRYTY CAATGCTGATT
M00175 V\$AP4_Q5 0.808215 2655 (-) NNCAGCTGNN CAATGCTGAT
M00281 V\$RFX1_02 0.757908 2656 (-) NNGTNRCNATRGYACNNN AATGCTGATTGGTGACCA
M00281 V\$RFX1_02 0.757908 2657 (+) NNGTNRCNATRGYACNNN ATGCTGATTGGTGACCAA
M00191 V\$ER_Q6 0.743584 2658 (+) NNARGNNANNNTGACCYNNTGCTGATTGGTGACCAAC
M00235 V\$AHRARNT_01 0.789441 2658 (+) KNNKNNTYGCGTGCMS TGCTGATTGGTGACC
M00280 V\$RFX1_01 0.771926 2658 (+) NNGTNRCNWRGYACNN TGCTGATTGGTGACCA
M00075 V\$GATA1_01 0.917078 2659 (+) SNNGATNNNN GCTGATTGG
M00076 V\$GATA2_01 0.860622 2659 (+) NNNGATRNNN GCTGATTGG
M00172 V\$APIFJ_Q2 0.816719 2659 (+) RSTGACTNMNW GCTGATTGGT
M00173 V\$API_Q2 0.834261 2659 (+) RSTGACTNMNW GCTGATTGGT
M00174 V\$API_Q6 0.791275 2659 (+) NNTGACTCANN GCTGATTGGT
M00209 V\$NFY_C 0.788245 2659 (+) NCTGATTGGYTASY GCTGATTGGTGAC
M00077 V\$GATA3_01 0.859548 2660 (+) NNGATARNNG CTGATTGG
M00185 V\$NFY_Q6 0.788541 2660 (-) TRRCCAATSRN CTGATTGGTG
M00159 V\$CEBP_01 0.897245 2662 (+) NNTKTGGWNANNN GATTGGTGACCA
M00269 V\$XFD3_01 0.782182 2662 (-) WNWGTMAACAWWMW GATTGGTGACCAA
M00050 V\$E2F_02 0.745904 2664 (+) TTTSGCGC TTTGGTGA
M00271 V\$AML1_01 0.853077 2664 (+) TGTGGT TTTGGT
M00068 V\$HEN1_01 0.759535 2665 (+) NNNGGNCNCAGCTGCGNCCCNN TTGGTGACCAACTGTCACTCAT
M00113 V\$CREB_02 0.808572 2665 (+) NNGNTGACGYNN TTGGTGACCAAC
M00057 V\$COMP1_01 0.774731 2667 (-) NNTNWKGATTGRCNRSRANMRRNN GGTGACCAACTGTCACTCATTGCT
M00172 V\$APIFJ_Q2 0.911356 2667 (+) RSTGACTNMNW GGTGACCAACT
M00173 V\$API_Q2 0.891947 2667 (+) RSTGACTNMNW GGTGACCAACT
M00174 V\$API_Q6 0.882663 2667 (+) NNTGACTCANN GGTGACCAACT
M00177 V\$CREB_Q2 0.782073 2667 (+) NSTGACGTAANN GGTGACCAACTG
M00178 V\$CREB_Q4 0.750126 2667 (+) NSTGACGTMANN GGTGACCAACTG
M00188 V\$API_Q4 0.922537 2667 (+) RSTGACTMANN GGTGACCAACT
M00065 V\$TALIBETA47_01 0.850660 2668 (-) NNNAACAGATGKTNNN GTGACCAACTGTCACT
M00066 V\$TALIALPHA47_01 0.844295 2668 (-) NNNAACAGATGKTNNN GTGACCAACTGTCACT
M00070 V\$TALIBETAITF2_01 0.825813 2668 (-) NNNAACAGATGKTNNN GTGACCAACTGTCACT
M00071 V\$E47_02 0.806313 2668 (-) NNNMRCAGGTGTTMNN GTGACCAACTGTCACT
M00157 V\$RORA2_01 0.784703 2668 (-) NWA WNTAGGTCAN GTGACCAACTGTC
M00205 V\$GRE_C 0.781502 2668 (+) GGTACAANNTGTYCTK GTGACCAACTGTCACT
M00004 V\$CMYB_01 0.779970 2669 (-) NCNRRNNGRCNGTTGGKGG TGACCAACTGTCACTCAT
M00122 V\$USF_02 0.795836 2669 (+) NNRNCACGTGNYNN TGACCAACTGTCACT
M00122 V\$USF_02 0.795836 2669 (-) NNRNCACGTGNYNN TGACCAACTGTCACT
M00185 V\$NFY_Q6 0.778777 2669 (+) TRRCCAATSRN TGACCAACTGT
M00277 V\$LMO2COM_01 0.798116 2670 (+) SNNCAGGTGNNN GACCAACTGTCA
M00277 V\$LMO2COM_01 0.795155 2670 (-) SNNCAGGTGNNN GACCAACTGTCA
M00003 V\$VMBYB_01 0.840659 2671 (+) AAYAACGGNN ACCAACTGTC
M00175 V\$AP4_Q5 0.852557 2671 (-) NNCAGCTGNN ACCAACTGTC
M00176 V\$AP4_Q6 0.857429 2671 (-) CWCAGCTGGN ACCAACTGTC
M00183 V\$MYB_Q6 0.936515 2671 (+) NNNAACKGNC ACCAACTGTC
M00184 V\$MYOD_Q6 0.943245 2671 (+) NNCANCTGNY ACCAACTGTC
M00184 V\$MYOD_Q6 0.821098 2671 (-) NNCANCTGNY ACCAACTGTC
M00227 V\$VMBYB_02 0.898917 2671 (+) NSYAACGGN ACCAACTGT
M00023 V\$HOX13_01 0.748804 2672 (+) TGCNNNNWYCCYCATTAKTNNNNNMNNYCN
CCAACCTGTCACTCATTGCTGAGCCTCTGCT
M00143 V\$PAX5_01 0.818482 2672 (-) NCNNNRNKCANNNGNWGNRKRGRCSRSNNN

CCAACTGTCACCTATTGCTGAGCCTCTG
M00173 V\$AP1_Q2 0.790922 2673 (-) RSTGACTNMNW CAACTGTCACCT
M00097 V\$PAX6_01 0.791072 2674 (+) NNNNTTCACGCWTSANTKNNN AACTGTCACCTATTGCTGAGC
M00098 V\$PAX2_01 0.815765 2674 (+) NNNNGTCANGNRTKANNNN AACTGTCACCTATTGCTGA
M00063 V\$IRF2_01 0.708693 2675 (-) GAAAGYGAASY ACTGTCACCTATT
M00143 V\$PAX5_01 0.775416 2676 (+) NCNNNRNKCANNNGNWGNRKRGCSSNNN
CTGTCACCTATTGCTGAGCCTCTGCTCC
M00139 V\$AHR_01 0.741633 2677 (-) CYYCNRRSTNGCGTGASW TGTCACCTATTGCTGAGC
M00174 V\$AP1_Q6 0.774351 2677 (+) NNTGACTCANN TGTCACCTATT
M00174 V\$AP1_Q6 0.805942 2677 (-) NNTGACTCANN TGTCACCTATT
M00235 V\$AHRARNT_01 0.772048 2677 (-) KNNKNNTYGCGTGCMS TGTCACCTATTGCTGA
M00037 V\$NFE2_01 0.821776 2678 (-) TGCTGASTCAY GTCACCTATTG
M00199 V\$AP1_C 0.823032 2678 (+) NTGASTCAG GTCACCTCAT
M00199 V\$AP1_C 0.825073 2678 (-) NTGASTCAG GTCACCTCAT
M00253 V\$CAP_01 0.934943 2679 (+) NCANNNNN TCACCTCAT
M00185 V\$NFY_Q6 0.832991 2682 (-) TRRCCAATSRN CTCATTGCTGA
M00042 V\$SOX5_01 0.858250 2683 (-) NNAACAATNN TCATTGCTGA
M00116 V\$CEBPA_01 0.811889 2683 (+) NNATTRCNNAANN TCATTGCTGAGCCT
M00159 V\$CEBP_01 0.889141 2683 (+) NNTKTGGWNANN TCATTGCTGAGCC
M00253 V\$CAP_01 0.929029 2683 (+) NCANNNNN TCATTGCT
M00279 V\$MIF1_01 0.755848 2683 (+) NNGTTGCWWGGYACNGS TCATTGCTGAGCCTCTGC
M00280 V\$RFX1_01 0.752957 2683 (-) NNGTNRCNWRGYAACNN TCATTGCTGAGCCTCTG
M00175 V\$AP4_Q5 0.819097 2684 (-) NNCAGCTGNN CATTGCTGAG
M00058 V\$HEN1_02 0.717923 2686 (-) NNGGGNCGCAGCTGCGNCCCN TTGCTGAGCCTCTGCTCCCCAG
M00037 V\$NFE2_01 0.813703 2687 (+) TGCTGASTCAY TGCTGAGCCTC
M00008 V\$SP1_01 0.812288 2688 (-) GRGGCRGGGW GCTGAGCCTC
M00134 V\$HNF4_01 0.783348 2688 (-) NNNRGGNCAAAGKTCANN GCTGAGCCTCTGCTCCCCA
M00066 V\$TAL1ALPHA47_01 0.783358 2689 (-) NNNAACAGATGKTNN CTGAGCCTCTGCTCCC
M00070 V\$TAL1BETA1F2_01 0.783740 2689 (-) NNNAACAGATGKTNN CTGAGCCTCTGCTCCC
M00155 V\$ARP1_01 0.792788 2690 (+) TGARCCYTTGAMCCYW TGAGCCTCTGCTCCCC
M00115 V\$TAXCREB_02 0.628745 2691 (+) RTGACGCATAYCCCC GAGCCTCTGCTCCCC
M00158 V\$COUP_01 0.802951 2691 (+) TGAMCTTTGMMCYT GAGCCTCTGCTCCCC
M00175 V\$AP4_Q5 0.781284 2692 (-) NNCAGCTGNN AGCCTCTGCT
M00176 V\$AP4_Q6 0.780005 2692 (-) CWCAGCTGGN AGCCTCTGCT
M00184 V\$MYOD_Q6 0.802283 2692 (+) NNCANCTGNY AGCCTCTGCT
M00255 V\$GC_01 0.780010 2692 (-) NRGGGGCGGGGCKN AGCCTCTGCTCCCC
M00175 V\$AP4_Q5 0.792165 2695 (+) NNCAGCTGNN CTCTGCTCCC
M00176 V\$AP4_Q6 0.806815 2695 (+) CWCAGCTGGN CTCTGCTCCC
M00261 V\$OLF1_01 0.956800 2695 (+) NNCNANTCCCYNGRGARNNKGN CTCTGCTCCCCAGGGGAGTTGT
M00261 V\$OLF1_01 0.808797 2695 (-) NNCNANTCCCYNGRGARNNKGN CTCTGCTCCCCAGGGGAGTTGT
M00261 V\$OLF1_01 0.888410 2696 (-) NNCNANTCCCYNGRGARNNKGN TCTGCTCCCCAGGGGAGTTGTG
M00273 V\$R_01 0.723138 2697 (+) NNGKCCNCSNRNYGTGGTGYN CTGCTCCCCAGGGGAGTTGTG
M00189 V\$AP2_Q6 0.800781 2699 (+) MKCCCSCNNGGCG GCTCCCCAGGGG
M00141 V\$LYF1_01 0.861743 2700 (-) TTTGGGAGR CTCCCCAGG
M00189 V\$AP2_Q6 0.851333 2700 (+) MKCCCSCNNGGCG CTCCCCAGGGGA
M00083 V\$MZF1_01 0.902909 2701 (-) NGNGGGGA TCCCCAGG
M00189 V\$AP2_Q6 0.786994 2701 (-) MKCCCSCNNGGCG TCCCCAGGGGAG
M00004 V\$CMYB_01 0.746152 2702 (+) NCNRNNGRCNGTTGGKGG CCCCAGGGGAGTTGTGTC
M00073 V\$DELTAEF1_01 0.811241 2703 (-) NNNCACCTNAN CCCAGGGGAGT
M00083 V\$MZF1_01 0.863241 2704 (+) NGNGGGGA CCAGGGGA
M00217 V\$USF_C 0.820530 2704 (-) NCACGTGN CCAGGGGA
M00033 V\$P300_01 0.806408 2705 (+) NNNRGGAGTNNNS CAGGGGAGTTGTGT
M00139 V\$AHR_01 0.710435 2705 (+) CYYCNRRSTNGCGTGASW CAGGGGAGTTGTGTCTGT
M00196 V\$SP1_Q6 0.781431 2705 (+) NGGGGGCGGGGYN CAGGGGAGTTGTG
M00255 V\$GC_01 0.865752 2705 (+) NRGGGGCGGGGCKN CAGGGGAGTTGTGT
M00257 V\$RREB1_01 0.782601 2705 (-) CCCCACMMCCCC CAGGGGAGTTGTGT
M00002 V\$E47_01 0.783849 2706 (+) NSNGCAGGTGKNCNN AGGGGAGTTGTGTCT
M00008 V\$SP1_01 0.816535 2707 (+) GRGGCRGGGW GGGGAGTTGT
M00115 V\$TAXCREB_02 0.710620 2707 (-) RTGACGCATAYCCCC GGGGAGTTGTGTCTG
M00175 V\$AP4_Q5 0.781284 2708 (-) NNCAGCTGNN GGGAGTTGTG
M00176 V\$AP4_Q6 0.806815 2708 (-) CWCAGCTGGN GGGAGTTGTG

M00183 V\$MYB_Q6 0.870954 2708 (-) NNNAACKGNC GGGAGTTGTG
M00237 V\$AHRARNT_02 0.720779 2708 (+) GRGKATYGCGTGMSWNSCC GGGAGTTGTGTCTGTAATC
M00255 V\$GC_01 0.786379 2708 (+) NRGGGGCGGGGCK GGGAGTTGTGTCTG
M00187 V\$USF_Q6 0.805703 2710 (-) GYCACGTGNC GAGTTGTGTC
M00237 V\$AHRARNT_02 0.716647 2710 (+) GRGKATYGCGTGMSWNSCC GAGTTGTGTCTGTAATCGC
M00179 V\$CREBP1_Q2 0.753475 2711 (-) NSTGACGTMASN AGTTGTGTCTGT
M00211 V\$PADS_C 0.839718 2711 (+) NGTGGTCTC AGTTGTGTC
M00222 V\$TH1E47_01 0.857756 2711 (+) NNNNGNRTCTGGMWTT AGTTGTGTCTGTAATC
M00228 V\$VBP_01 0.825921 2712 (+) GTTACRTMAK GTTGTGTCTG
M00116 V\$CEBPA_01 0.817755 2714 (-) NNATTRCNNAANN TGTGTCTGTAATCG
M00133 V\$TST1_01 0.874513 2715 (-) NNKGAWTANANTNN GTGTCTGTAATCGCC
M00057 V\$COMP1_01 0.802275 2716 (-) NNTNWKGATTGRCNRSRANMRRNN TGTCTGTAATCGCCCTACTATTCA
M00114 V\$TAXCREB_01 0.758990 2716 (-) GGGGGTTGACGYANA TGTCTGTAATCGCCC
M00249 V\$CHOP_01 0.853149 2717 (+) NNRTGCAATMCCC GTCTGTAATCGCC
M00075 V\$GATA1_01 0.841560 2720 (-) SNNGATNNNN TGTAATCGCC
M00076 V\$GATA2_01 0.823636 2720 (-) NNNGATRNNN TGTAATCGCC
M00077 V\$GATA3_01 0.836509 2720 (-) NNGATARNNG TGTAATCGC
M00180 V\$E2F_Q6 0.741395 2720 (-) NNGCGCGAAANTK TGTAATCGCCCTA
M00221 V\$SREBP1_02 0.737616 2723 (+) KATCACCCAC AATCGCCCTAC
M00136 V\$OCT1_02 0.772875 2729 (+) NNGAATATKCANNNN CCTACTATTTCAGTGG
M00095 V\$CDP_01 0.779938 2730 (+) CCAATAATCGAT CTACTATTTCAGT
M00057 V\$COMP1_01 0.781916 2732 (+) NNTNWKGATTGRCNRSRANMRRNN ACTATTTCAGTGGCGAGAAATAAAG
M00241 V\$NKX25_02 0.831926 2733 (-) CWTAAATTG CTATTTCAG
M00235 V\$AHRARNT_01 0.764886 2735 (+) KNNKNNTYGCGTGCMs ATTCAGTGGCGAGAAA
M00185 V\$NFY_Q6 0.841470 2736 (-) TRRCCAATSRN TTCAGTGGCGA
M00098 V\$PAX2_01 0.754770 2737 (-) NNNNGTCANGNRTKANNNN TCAGTGGCGAGAAATAAAG
M00253 V\$CAP_01 0.930015 2737 (+) NCANNNNN TCAGTGGC
M00254 V\$CAAT_01 0.819825 2737 (-) NNNRRCCAATSA TCAGTGGCGAGA
M00221 V\$SREBP1_02 0.727547 2740 (-) KATCACCCAC GTGGCGAGAAA
M00180 V\$E2F_Q6 0.850233 2741 (+) NNGCGCGAAANTK TGGCGAGAAATAA
M00223 V\$STAT_01 0.791782 2741 (-) TTCCCRKAA TGGCGAGAA
M00050 V\$E2F_02 0.876701 2743 (-) TTTSGCGC GCGAGAAA
M00133 V\$TST1_01 0.865549 2745 (+) NNKGAWTANANTNN GAGAAATAAAGTTTG
M00212 V\$POLY_C 0.747167 2745 (-) CAATAAAACCYYYKCTN GAGAAATAAAGTTTGCTT
M00162 V\$OCT1_06 0.839844 2746 (-) CWNWTKWSATRYN AGAAATAAAGTTTG
M00129 V\$SHFH1_01 0.837445 2748 (-) NAWTGTTTATWT AAATAAAGTTTG
M00057 V\$COMP1_01 0.784072 2749 (+) NNTNWKGATTGRCNRSRANMRRNN AATAAAGTTTGCTTAGAAAAGAAA
M00269 V\$XFD3_01 0.793406 2750 (-) WNWGTMAACAWWMW ATAAAGTTTGCTTA
M00129 V\$SHFH1_01 0.851149 2751 (+) NAWTGTTTATWT TAAAGTTTGCTT
M00131 V\$HNF3B_01 0.863625 2751 (+) NNNTRTTTRYTY TAAAGTTTGCTT
M00272 V\$P53_02 0.834701 2753 (+) NGRCWYGYCY AAGTTTGCTT
M00116 V\$CEBPA_01 0.846304 2754 (+) NNATTRCNNAANN AGTTTGCTTAGAAA
M00159 V\$CEBP_01 0.899838 2754 (+) NNTKTGGWNANN AGTTTGCTTAGAA
M00190 V\$CEBP_Q2 0.866765 2754 (+) NNNTTGCNNAANN AGTTTGCTTAGAAA
M00269 V\$XFD3_01 0.798316 2754 (-) WNWGTMAACAWWMW AGTTTGCTTAGAAA
M00080 V\$EVII_03 0.712757 2758 (+) AGATAAGATAA TGCTTAGAAAA
M00081 V\$EVII_04 0.908601 2758 (+) NGATANGANWAGATA TGCTTAGAAAAGAAA
M00082 V\$EVII_05 0.799318 2758 (+) AGATAAGATAN TGCTTAGAAAA
M00116 V\$CEBPA_01 0.817755 2758 (+) NNATTRCNNAANN TGCTTAGAAAAGAA
M00216 V\$TATA_C 0.780829 2758 (+) NCTATAAAAR TGCTTAGAAA
M00223 V\$STAT_01 0.795815 2758 (+) TTCCCRKAA TGCTTAGAA
M00160 V\$SRV_02 0.766882 2759 (+) NWWAACAANN GCTTAGAAAAGA
M00199 V\$AP1_C 0.788047 2760 (-) NTGASTCAG CTTAGAAAA
M00216 V\$TATA_C 0.804595 2760 (+) NCTATAAAAR CTTAGAAAAG
M00148 V\$SRV_01 0.960465 2766 (+) AAACWAM AAAGAAA