

Supplementary Figures

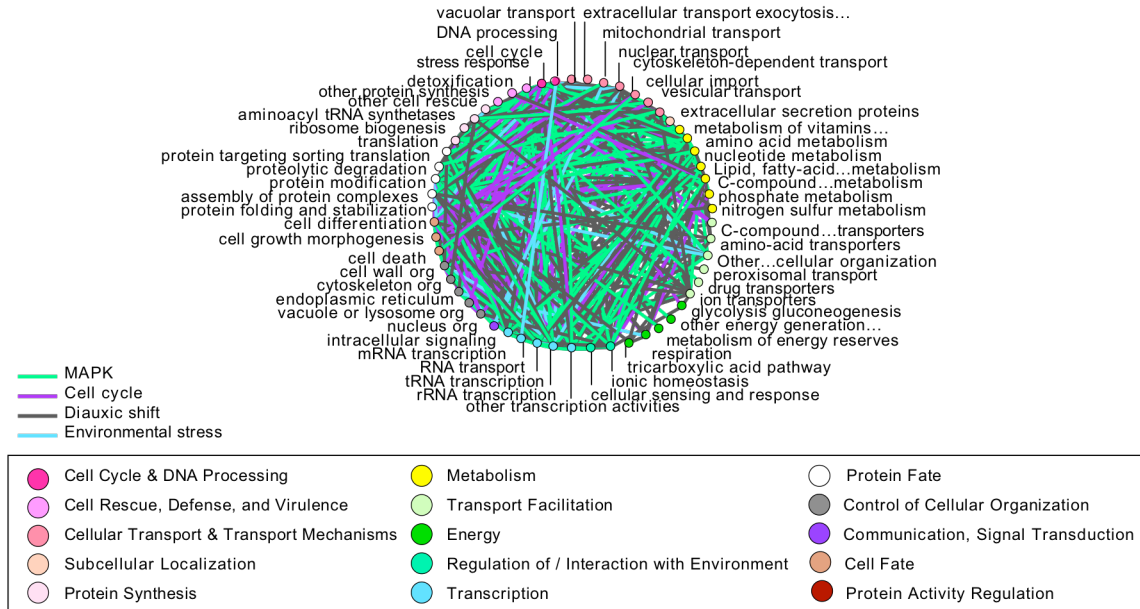


Figure S4. Summary of results obtained using the MSA TFBS data set.

Each node represents a module. Node color represents the corresponding top-level MIPS category (see legend). Edge color represents the expression data set in which the interaction was identified: purple = cell cycle, gray = diauxic shift, turquoise = environmental stress, green = MAPK.

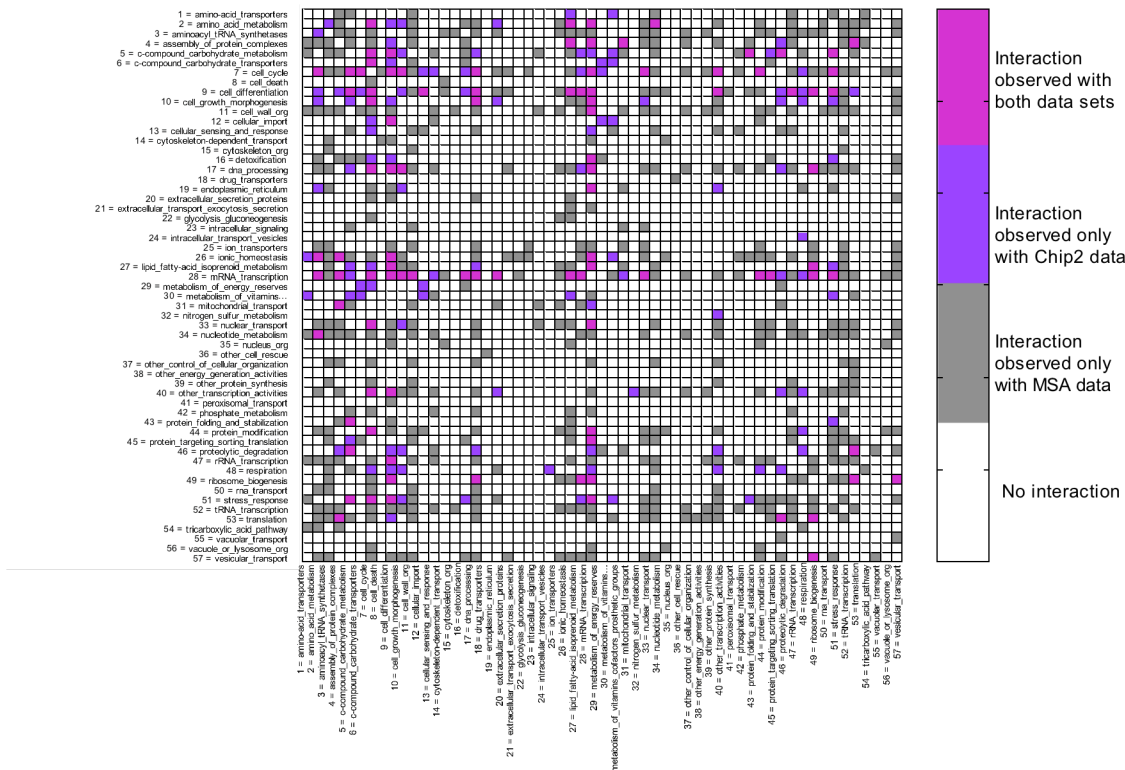


Figure S5. Comparison of MSA and Chip2 Results

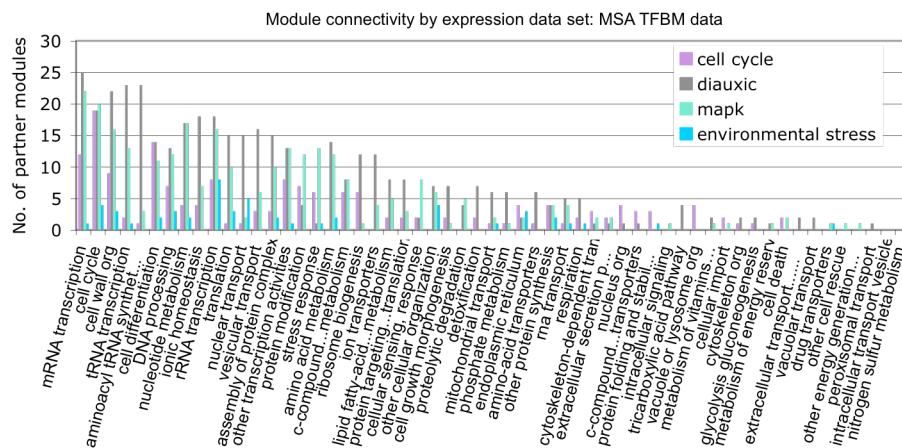


Figure S6-A. Distribution of Module Connectivity (MSA) by Expression Data Set

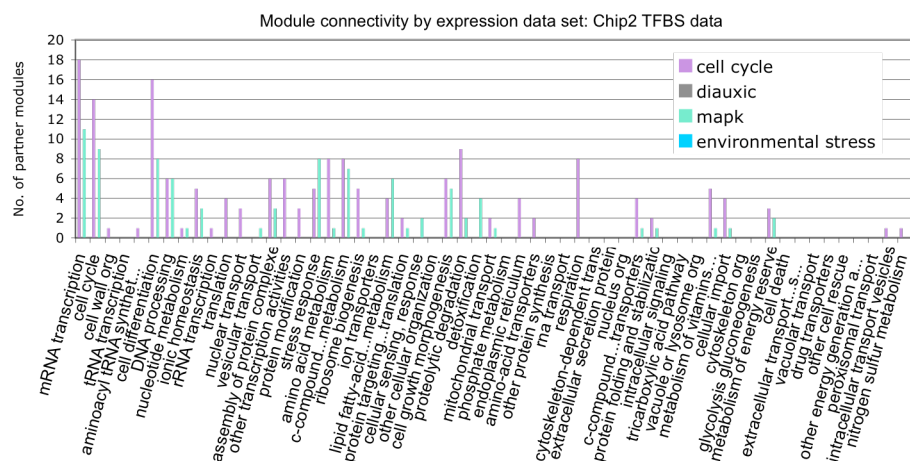


Figure S6-B. Distribution of Module Connectivity (Chip2) by Expression Data Set

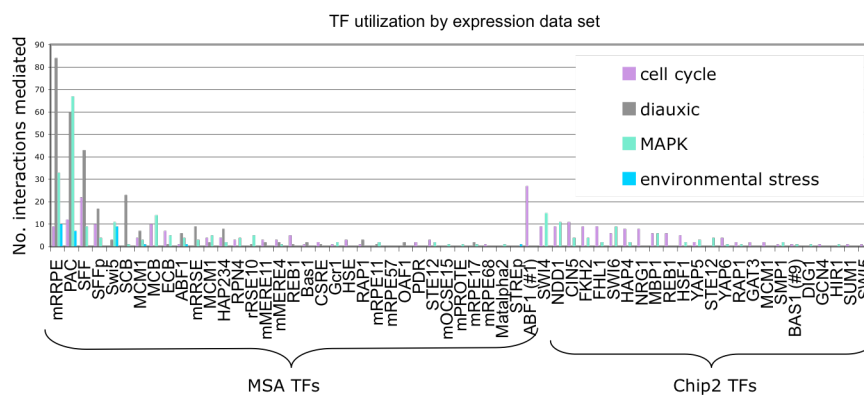


Figure S6-C. TF utilization by expression data set

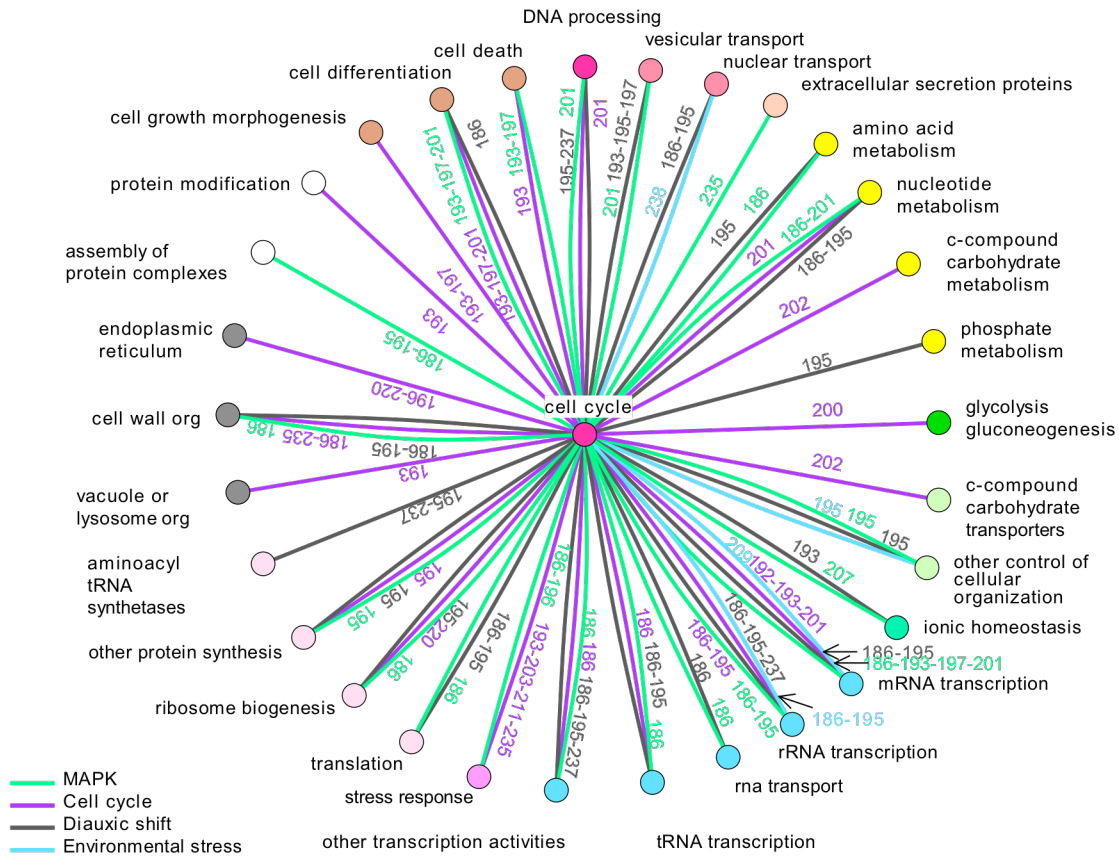


Figure S7. Subset of modules in S4 that are coordinated with the *Cell cycle* module (all TFs from MSA data set)

Each node represents a module; see color key in Fig. S4. Edge color represents the expression data set in which the interaction was identified, as in Fig. S4. Each edge is labeled with the TF that mediates the interaction (TF color corresponds to the expression data set with which the interaction was identified), as follows: 186 = PAC; 192 = MCM1; 193 = SFF; 195 = mRRPE3; 196 = RPN4; 197 = SFFp; 200 = GCR1; 201 = MCB; 202 = mMERE11; 207 = MATA1PHA2; 209 = STREp; 211 = CSRE; 220 = REB1; 235 = ECB; 237 = SCB; 238 = SWI5.

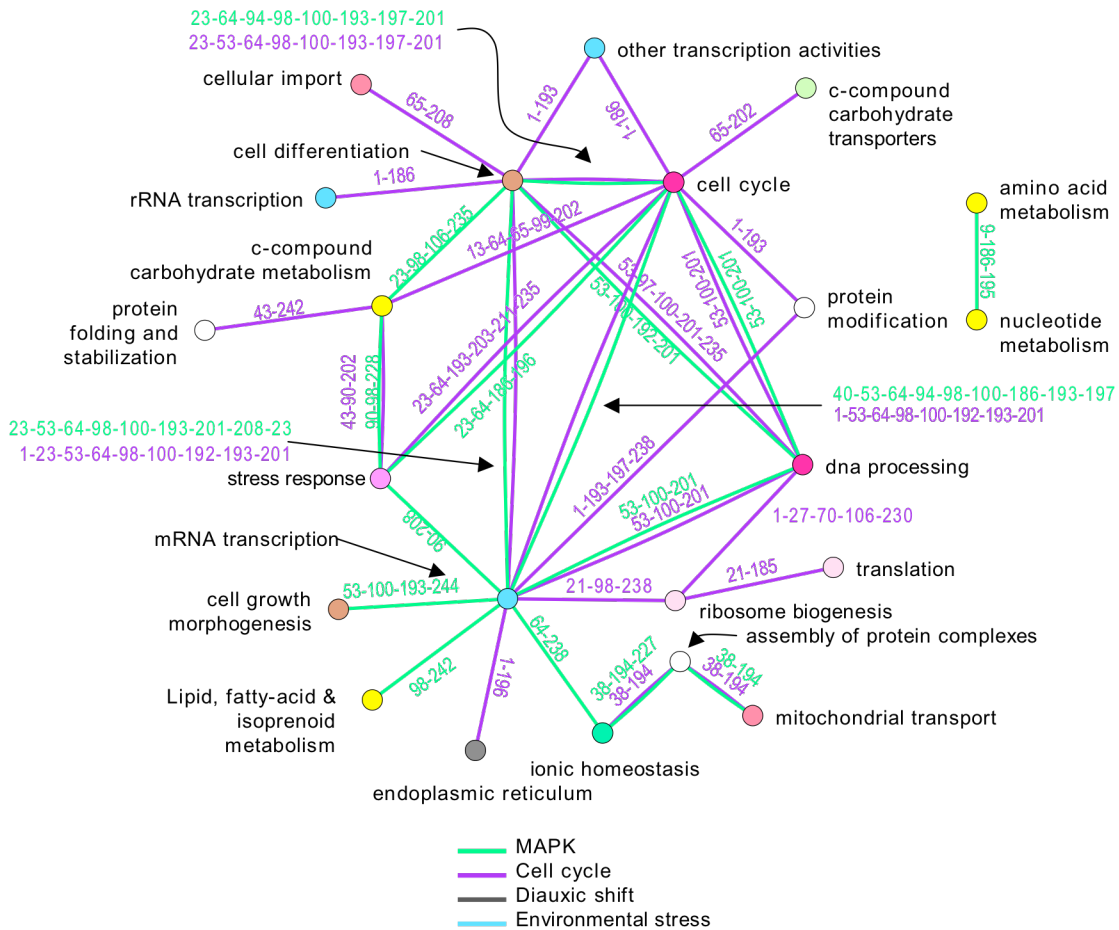


Figure S8. Module pairs found to be coordinated using both the MSA and Chip2 TFBS data sets.

Each node represents a module; see color key in Fig. S4. Edge color represents the expression data set in which the interaction was identified, as in Fig. S4. Each edge is labeled with the TF that mediates the interaction (TF color corresponds to the expression data set with which the interaction was identified), as follows (where a superscripts “1” and “2” signify the Chip2 and MSA data sets, respectively): 1 = ABF1¹; 9 = BAS1¹; 13 = CIN5¹; 21 = FHL1¹; 23 = FKH2¹; 27 = GAT3¹; 38 = HAP4¹; 43 = HSF1¹; 53 = MBP1¹; 64 = NDD1¹; 65 = NRG1¹; 70 = RAP1¹; 90 = SMP1¹; 94 = STE12¹; 97 = SUM1¹; 98 = SWI4¹; 99 = SWI5¹; 100 = SWI6¹; 106 = YAP5¹; 185 = RAP1²; 186 = PAC²; 192 = MCM1²; 193 = SFF²; 194 = HAP2/3/4²; 195 = mRRPE3²; 196 = RPN4²; 197 = SFFp²; 201 = MCB²; 202 = mMERE11²; 203 = HSE²; 208 = MCM1-short²; 211 = CSRE²; 227 = ABF1²; 228 = rRSE10²; 230 = mRPE68²; 235 = ECB²; 238 = SWI5²; 242 = mMERE4²; 244 = STE12².

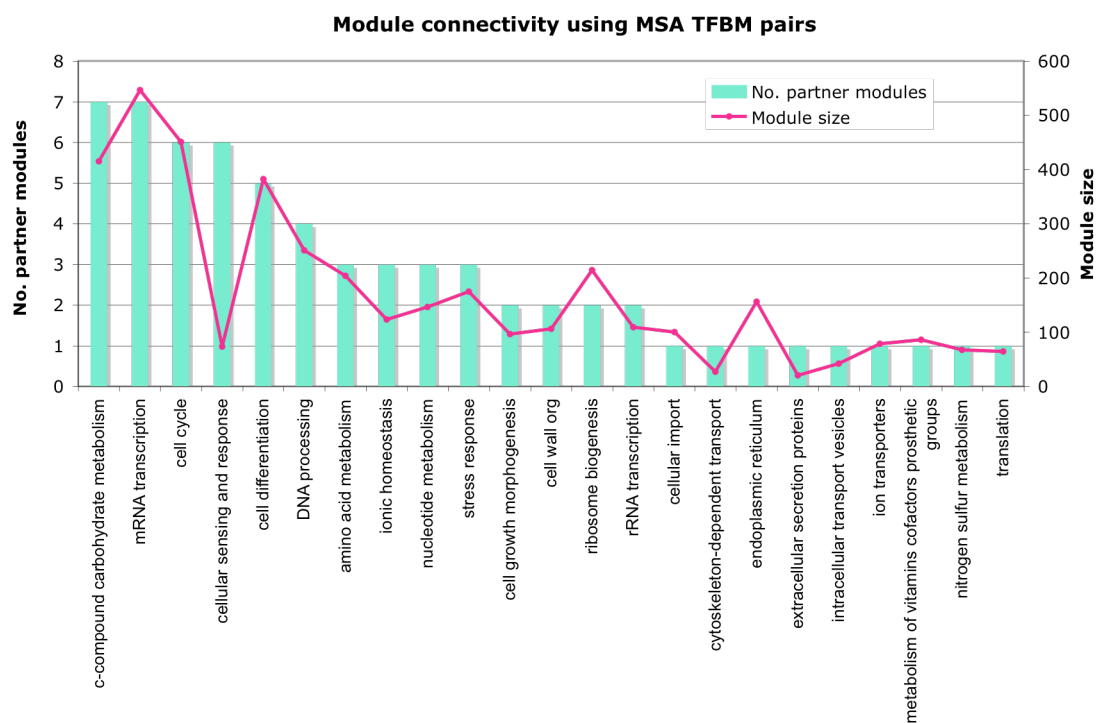


Figure S11. Module Connectivity using MSA TFBM pairs

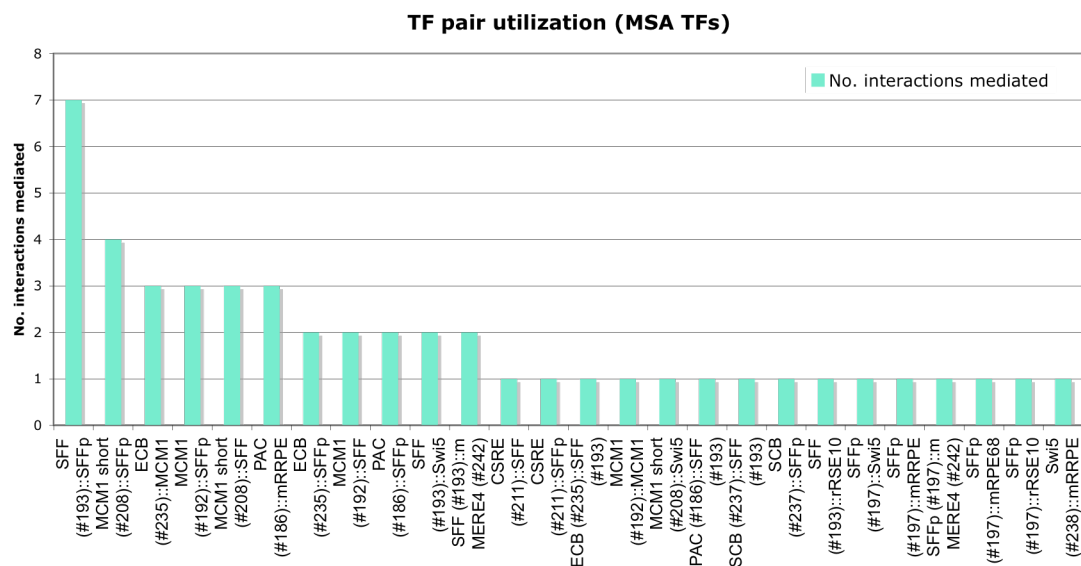


Figure S12. Utilization of TF pairs

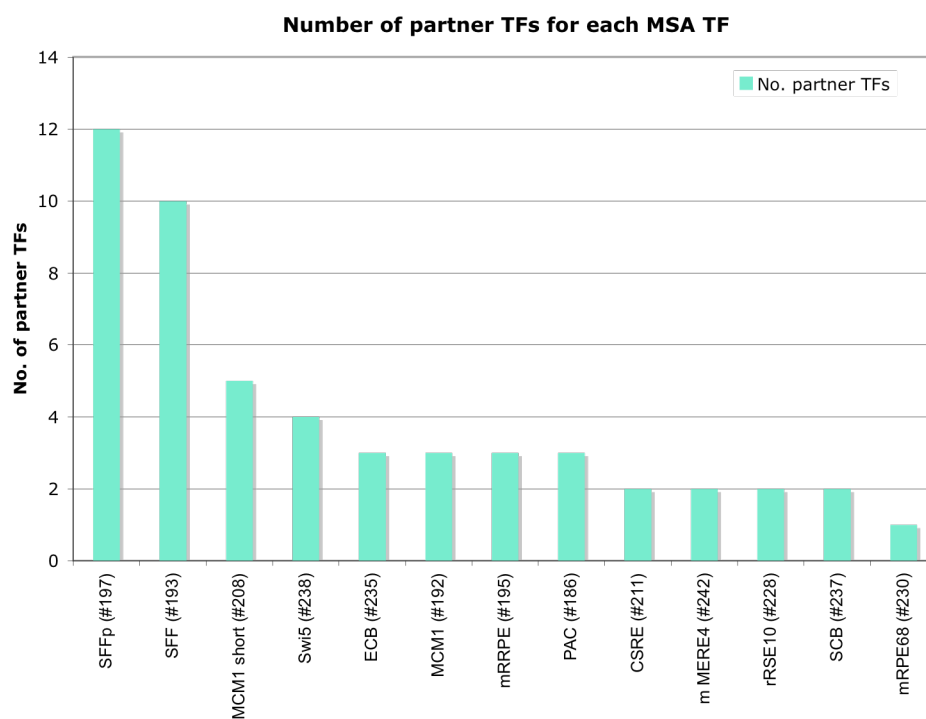


Figure S13. Number of Partner TFs for each MSA TF

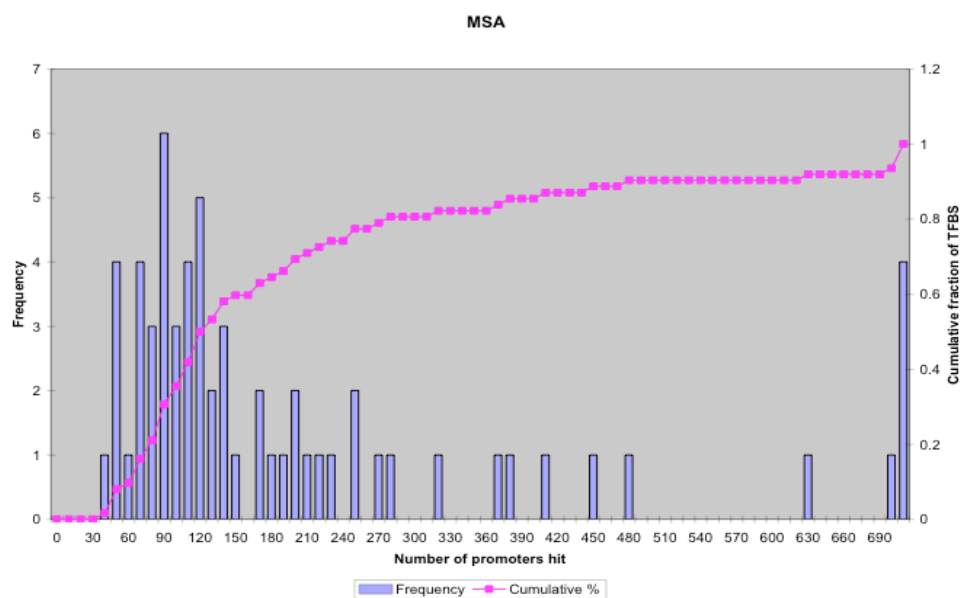


Figure S15. Number of Promoter Targets for Each MSA TF

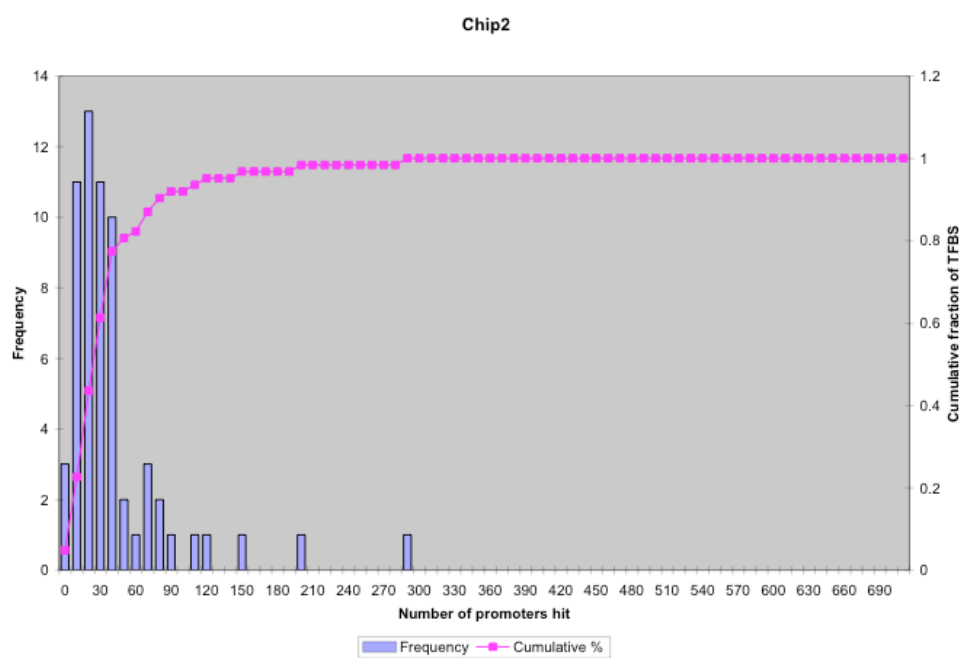


Figure S17. Number of Promoter Targets for each Chip2 TF

Convergence Score (C)

C compares the inter-module coherence of target genes to that of non-target genes. If the TF coordinates a module pair, it may “draw together” its target genes in both modules, as shown to the right and in the alternative representation below.

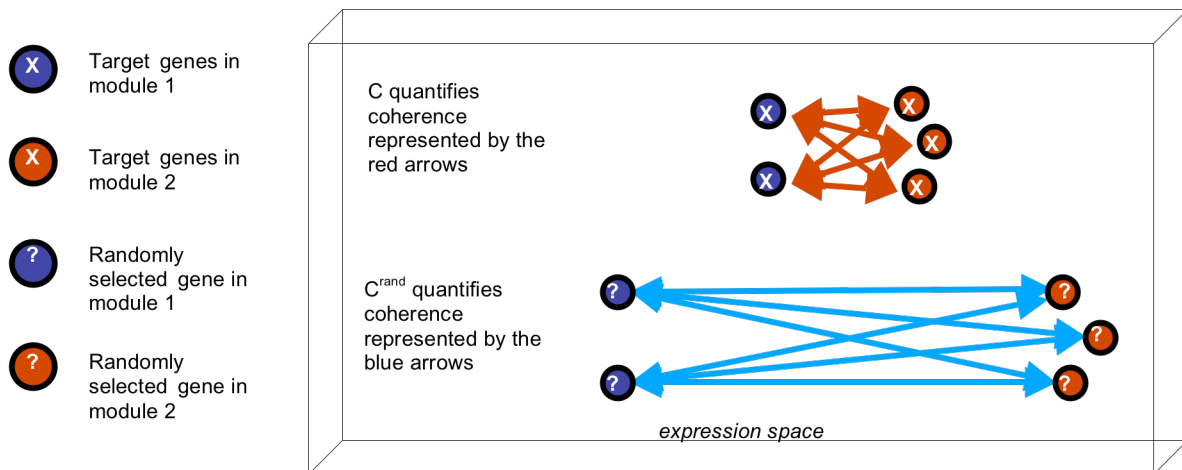
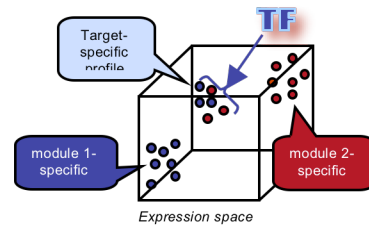
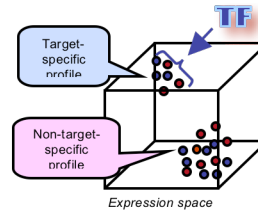


Figure S18. Convergence Score Diagram

Distinctness Score (D)

D quantifies the difference in expression profiles between the target genes and the non-target genes, shown to the right.



D is computed by comparing the coherence, within the aggregate target genes (numerator) to that between the aggregate target genes and the aggregate non-target genes (denominator)

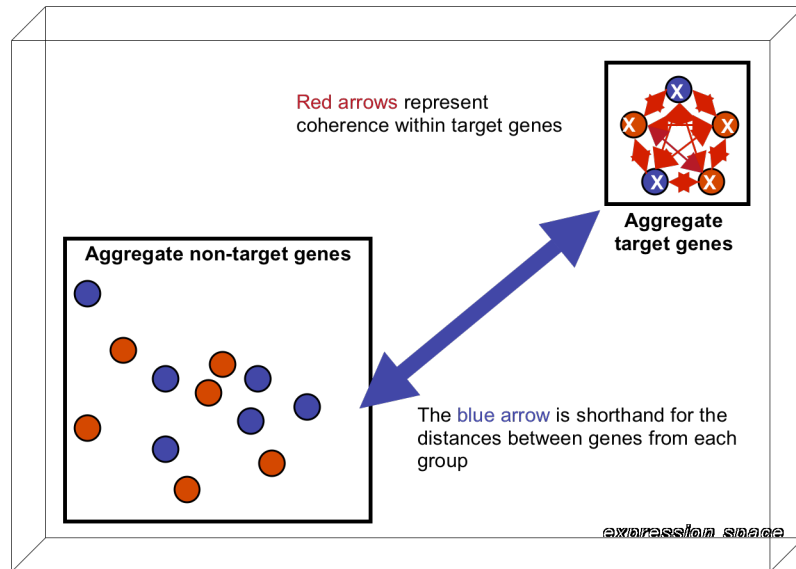


Figure S19. Distinctness Score Diagram