

Supplementary Material

Transcriptional Regulation in the G1-S Cell Cycle Stage in Fungi: Insights through Computational Analysis

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SUPPLEMENTARY MATERIAL

Table S1 – List of fungal species used in the study.

File format – XLS.

Description of data – Left column lists fungal species sorted in alphabetical order. Right column lists genome version as implemented in SCOPE.

Table S2. MBF STAMP analyses.

File format – XLS.

Description of data - Motifs are the highest-scoring motifs identified by SCOPE in each run. Number of instances is the motif count in the upstream sequences of the genes from each SCOPE run. Sig value is the measure of motif statistical significance; Sig value of 10 is roughly equivalent to the p-value of 10^{-3} . Coverage is the fraction of upstream sequences in the input gene set that have at least one instance of the highest-scoring motif. STAMP p-value is the measure of similarity between motif identified by SCOPE and the reference motif as calculated by STAMP. Reference motif is the one to which all motifs from all SCOPE runs were compared.

Table S3. SBF STAMP analyses.

File format – XLS.

Description of data - Motifs are the highest-scoring motifs identified by SCOPE in each run. Number of instances is the motif count in the upstream sequences of the genes from each SCOPE run. Sig value is the measure of motif statistical significance; Sig value of 10 is roughly equivalent to the p-value of 10^{-3} . Coverage is the fraction of upstream sequences in the input gene set that have at least one instance of the highest-scoring motif. STAMP p-value is the measure of similarity between motif identified by SCOPE and the reference motif as calculated by STAMP. Reference motif is the one to which all motifs from all SCOPE runs were compared.

Table S4. MBF motif pair analyses.

File format – XLS.

Description of data – Modules are combinations of SCOPE motifs that are the best matches to MBF recognition site as identified by STAMP. Modular score shows the overall quality of a module (see Motif pattern analysis section in the Methods).

Table S5. SBF motif pair analyses.

File format - XLS.

Description of data – Modules are combinations of SCOPE motifs that are the best matches to SBF recognition site as identified by STAMP. Modular score shows the overall quality of a module (see Motif pattern analysis section in the Methods).

Table S6. Functional analysis of MBF targets.

File format – XLS.

Description of data – The primary functional enrichment tool used in the analysis is DAVID. When a different tool is used, it is indicated in the Notes column.

Table S7. Functional analysis of SBF targets.

File format – XLS.

Description of data – The primary functional enrichment tool used in the analysis is DAVID. When a different tool is used, it is indicated in the Notes column.

Table S8. Relationship between MBF module and gene function in fungi.

File format – XLS.

Description of data – Comparison of unique and enriched functional categories in gene subsets with and without modules in *N. crassa*, *U. maydis* and *F. graminearum*.

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Table S9. Relationship between SBF module and gene function in fungi.

File format – XLS.

Description of data – Comparison of unique and enriched functional categories in gene subsets with and without modules in *S. cerevisiae* and *U. maydis*.

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