Figure S3  A comparison of the conserved transcription regulator targets of the Mit1 regulon in *S. cerevisiae* and the Wor1 regulon in *C. albicans*. Each node represents one orthologous pair of factors, where at least one member of the pair is bound by either Wor1 or Mit1. Orthologous pairs bound in both species are indicated in blue, those bound only in *S. cerevisiae* are in pink, and those bound only in *C. albicans* are in green. For example: ScSOK2 and ScPHD1 participate in a 2:2 relationship with CaEFG1 and CaEFH1. Therefore there are 4 possible pairs of interactions — ScSOK2:CaEFG1, ScSOK2:CaEFH1, ScPHD1:CaEFG1, and ScPHD1:CaEFH1. Two of these pairs are represented as blue nodes bound by both Mit1 and Wor1, because SOK2 and PHD1 are bound by Mit1, and EFG1 is bound by Wor1. Two of these pairs are represented as pink nodes bound only by Mit1, because EFH1 is not a Wor1 target.