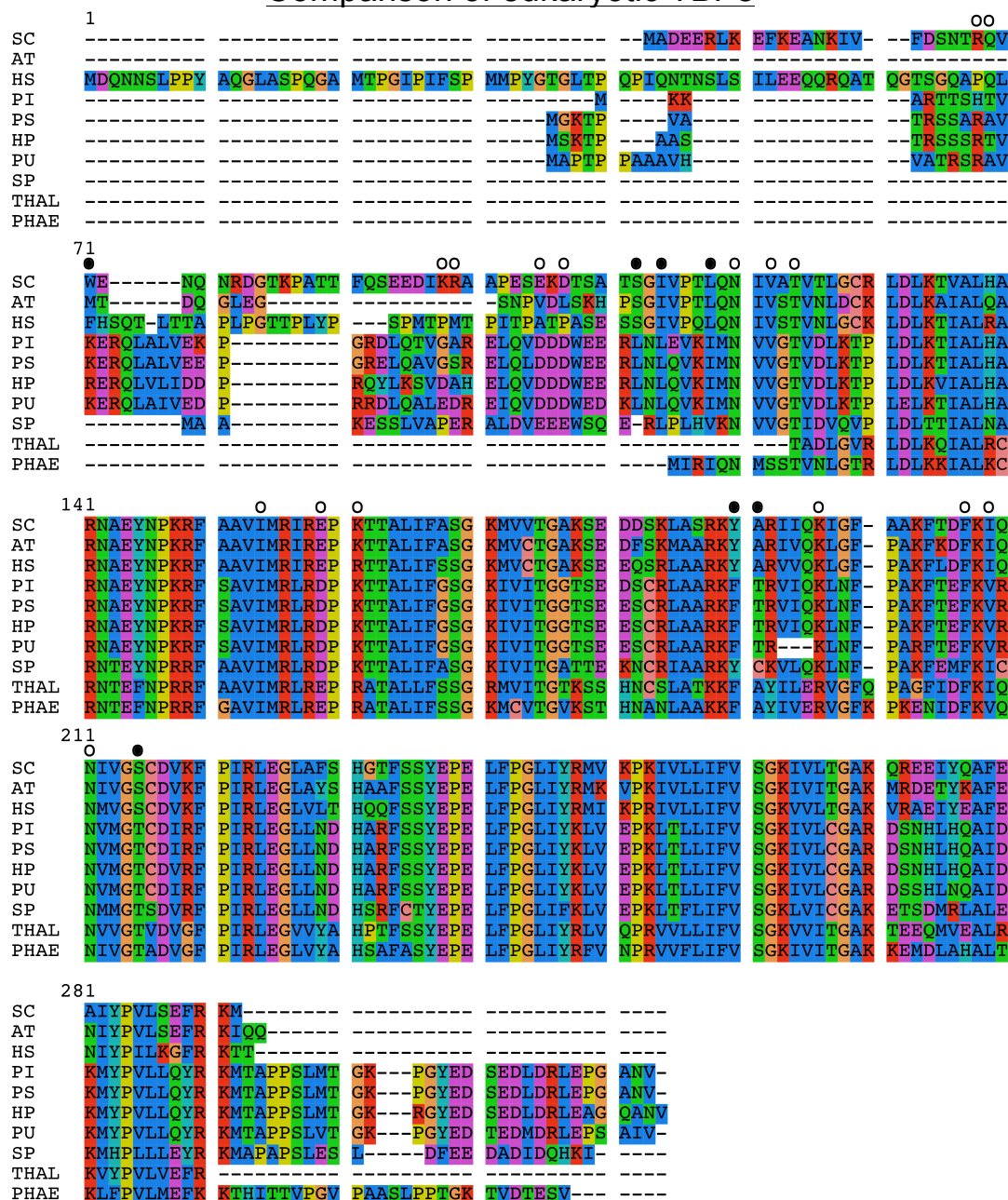
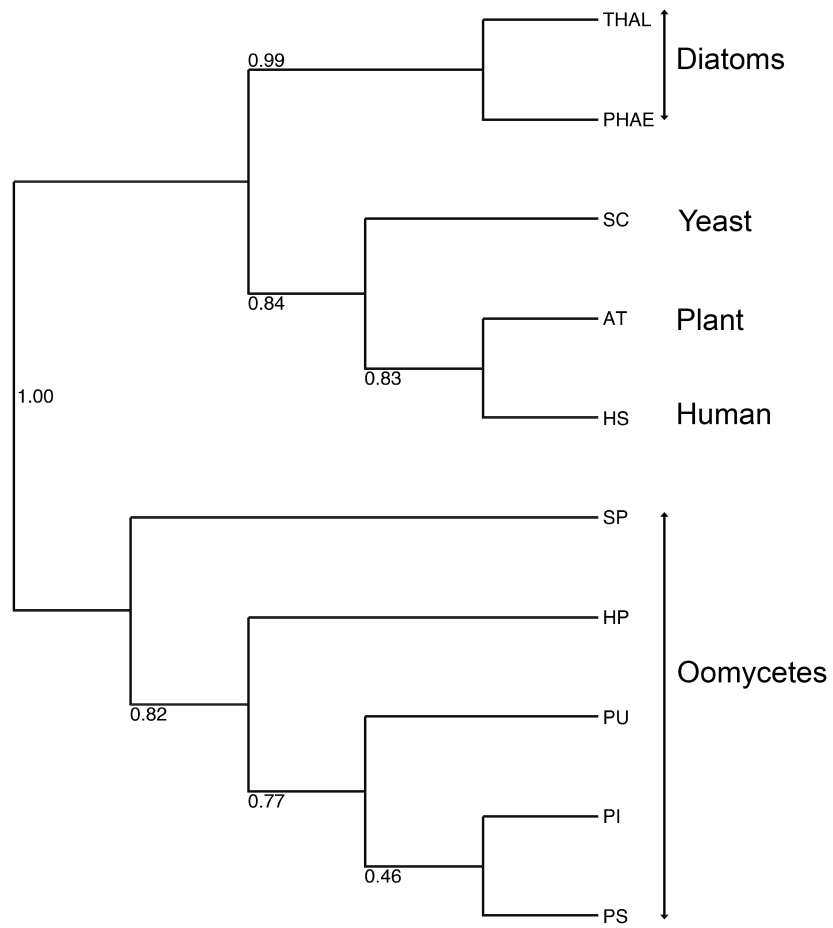


Comparison of eukaryotic TBPs

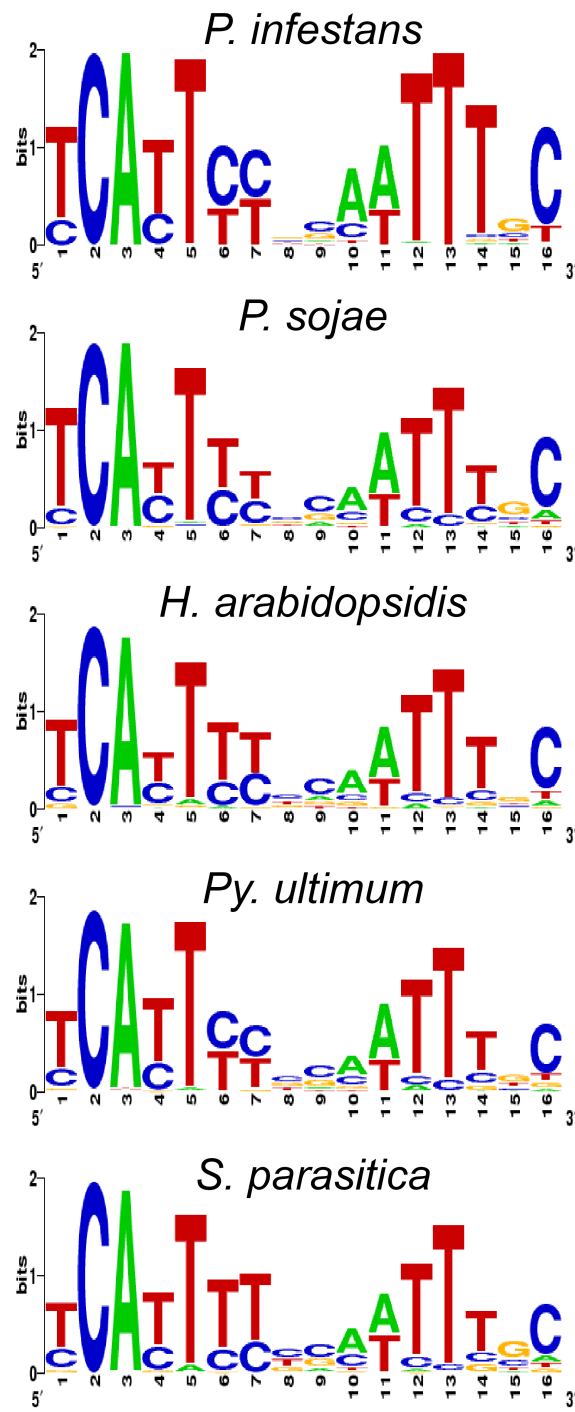


Alignments of TATA binding protein (TBP) orthologs, created using MUSCLE. Symbols above alignment denote DNA-interacting residues; filled circles are cases where the sequence is well conserved in humans, *Saccharomyces cerevisiae*, and *Arabidopsis thaliana*, but different in all oomycetes. Sequences are from *S. cerevisiae* (SC; GenBank AEP68421.1), *A. thaliana* (AT; NP_187953.1), human (HS; AAI09055.1), *Phytophthora infestans* (PI; EEE53626.1 [PITG_07312]), *Phytophthora sojae* (PS; EGZ26194.1), *Hyaloperonospora arabidopsidis* (HP; correction of gene model 813721), *Pythium ultimum* (PU; correction of model PYU1_G013989), *Saprolegnia parasitica* (SP; Broad Institute SPRG_03180.2), and the diatoms *Thalassiosira pseudonana* (THAE; XP_002293666.1 [lacks N-terminus]), and *Phaeodactylum tricornutum* (PHAE; XP_002186321.1). Numbers indicate location within the *S. cerevisiae* protein.

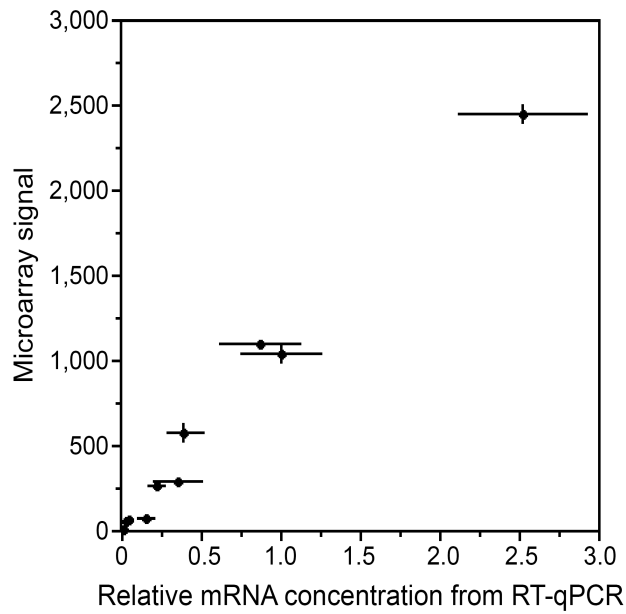


Cladogram showing relationships between TATA-binding proteins shown on the preceding page, made using the PhyML program. Branch support is indicated by aLRT values.

Sequence logos of INR+FPR supramotif from different oomycetes



Correlation analysis of microarray and qRT-PCR data



Expression values from Affymetrix arrays compared relative values determined by reverse transcription qPCR. Error bars reflect variation in array data (from duplicates) and qRT-PCR (from triplicates). Genes tested were PITG_00527, PITG_00805, PITG_00988, PITG_03546, PITG_03864, PITG_11913, PITG_15771, PITG_15786, and PITG_16528.