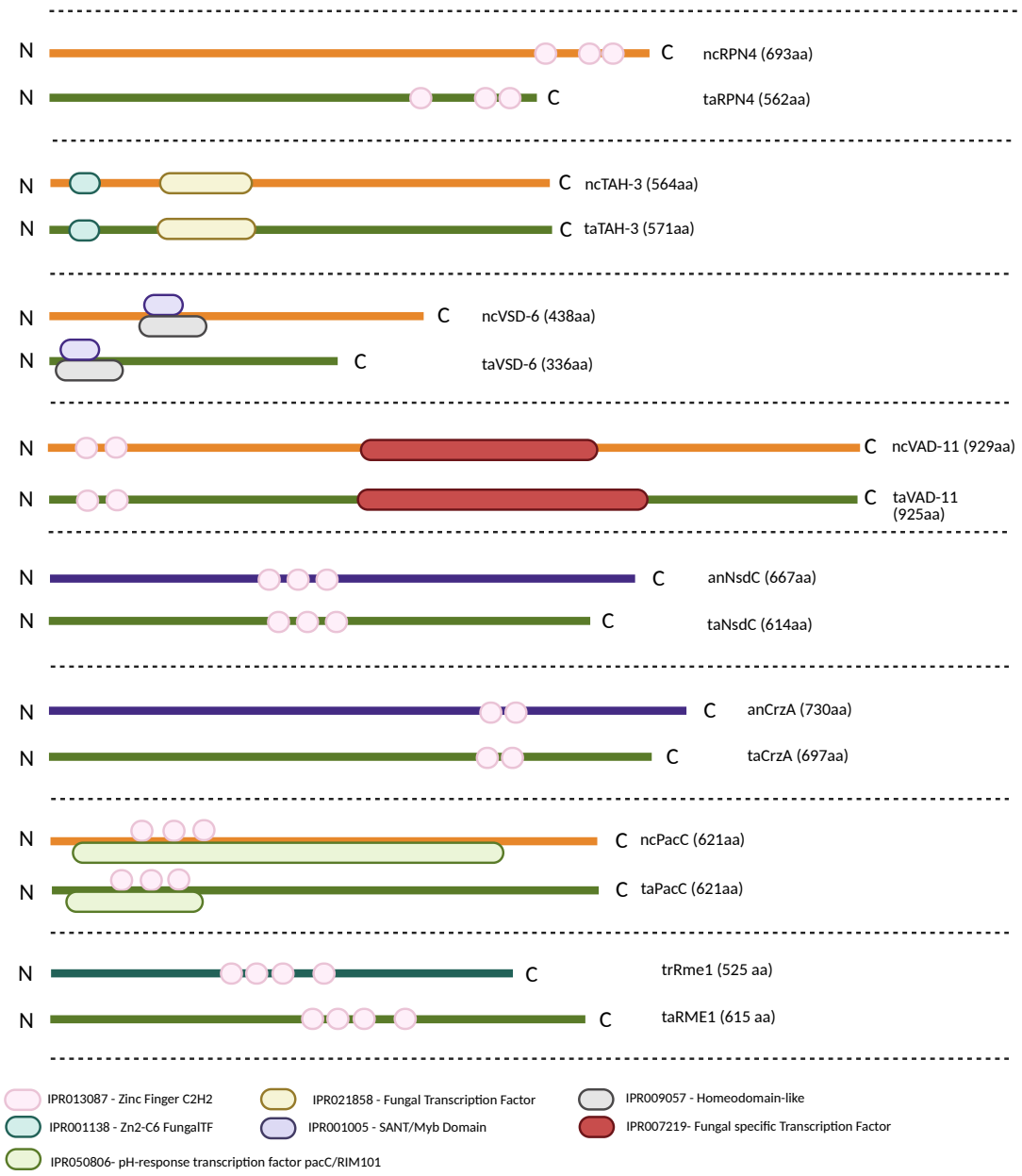


Figure S6. Conserved domain architecture of *T. atroviride* transcription factors. Domain organization of *T. atroviride* TFs RPN4, TAH3, VSD-6, NsdC, VAD11, CrzA, PacC, RME1 compared with their homologs in representative fungi. Protein sequences of the *T. atroviride* TFs were analyzed with blastp. A protein was considered homolog when the results showed a conserved sequence (between 100-300 aa) with an identity > 70%, or more than one conserved sequence with identities of 50-90%. Domains of the *T. atroviride* TF and its determined homolog

were identified using InterProScan. Conservation of domain composition and arrangement supports functional relatedness across species. As illustrated in the figure above, a conserved domain architecture was observed across all homologs, with each transcription factor exhibiting the same number of domains, which were furthermore positioned at comparably similar distances from one another.