

Fig. S1. FvStp1 domain and sequence alignment



Fig. S1. (A) Schematic depiction of *FvSTP1* locus with exons (gray box) and introns (line) that results in 2,118-bp transcript from 2,268 genomic DNA. (B) The 705-aa predicted protein harbors two putative functional domains (shown in light gray box): a N1221-like domain (pfam07923) and a conserved domain of unknown function (pfam 11882), in predicted protein. The N1221-like domain featured in this family are similar to a hypothetical protein product of ORF N1221 in the CPT1-SPC98 intergenic region of the yeast genome ([P53917](#)). This encodes an acidic polypeptide with several possible transmembrane regions. DFU3402 domain (pfam 11882) is functionally uncharacterized, but found in eukaryotes and is associated with [PF07923](#). This predicted domain is typically between 350 to 473 amino acids in length. (C) Amino acid alignment of four fungal *FvStp1* homologs by using CLUSTAL O (1.2.2) multiple sequence alignment. Sm (*S. macrospora*, accession no. AJ627567 [NCBI]), Nc (*N. crassa*, accession no. CAC28842 [NCBI]), Hs (*H. sapiens*, accession no. AAH19064 [NCBI]).