Fig. S1. FvStp1 domain and sequence alignment

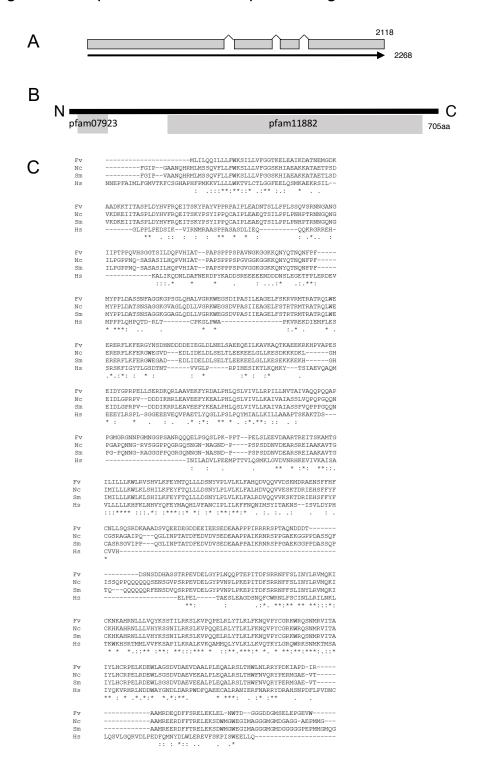


Fig. S1. (A) Schematic depiction of *FvSTP1* locus with exons (gray box) and introns (line) that results in 2,118-bp transcript from 2,268 genomic DNA. (B) The 705-aa predicted protein harbors two putative functional domains (shown in light gray box): a N1221-like domain (pfam07923) and a conserved domain 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. (B) 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]).