



Supplementary Fig. S1. *In silico* analysis of the *tvcp2* gene and zymogen and identification of TvCP2 peptides by MS/MS. (A) Genomic organization of the *tvcp2* gene (TVAG_057000; contig DS113412) and putative transcription start site (+1 arrow) predicted from the *T. vaginalis* genomic sequence (Carlton et al., 2007; www.trichdb.org). Arrows indicated the position of primers used for cloning, RT-PCR and qRT-PCR assays). The bar represents 100 bp. (B) Schematic representation of the zymogen TvCP2 protein sequence. The predicted protein sequence is 315-aa. The catalytic triad is indicated in light gray boxes. A prepro-peptide of 72-aa (light gray boxes; 8-kDa molecular weight) and a mature proteinase sequence (dark gray box; 27-kDa molecular weight) are shown. (C) Amino acid sequence of the complete TvCP2 zymogen. Peptides identified by MS/MS from *in vitro* secretion assays (Black rectangle) and from patient vaginal secretions (bold letters).