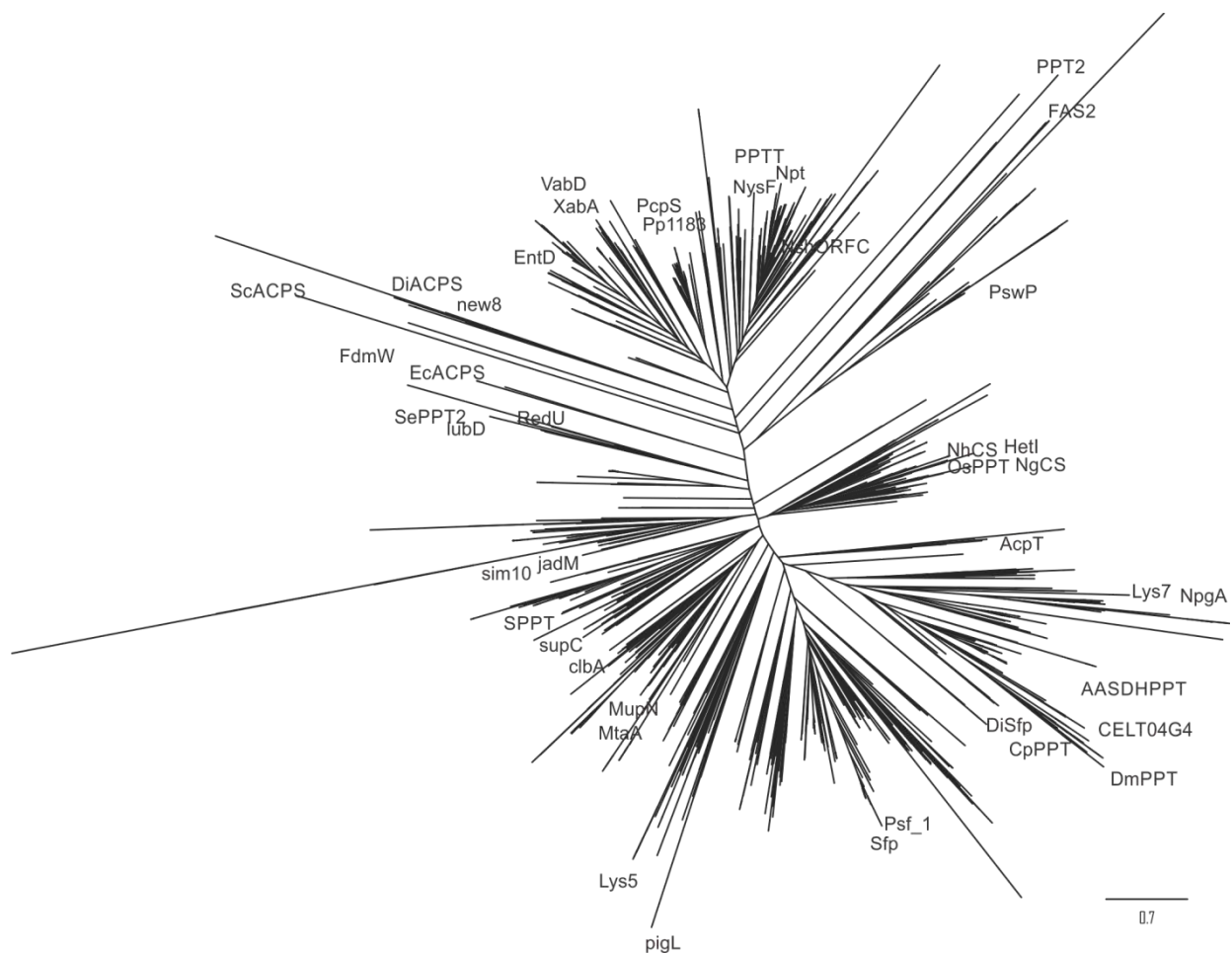## Supporting Information

Fig. S1 - Unbiased phylogenetic tree constructed from ~1700 unique PPTase sequences using Fasttree. The ~60 annotated PPTases are shown. Unrooted phylogenetic tree was constructed in the following way: several PPTases, including Sfp, AASDHPPT and PptTwere separately blasted against the UniProt database and top 500 hits combined, until >3000 sequences were collected. Duplicates were removed, leading to 1700 unique sequences. Taxon names were condensed using Mesquite and protein sequences aligned using Muscle. Fasttree was used to create a phylogenetic tree and Dendroscope and Figtree used to visualize the tree.