



**S1 Figure. Phylogenetic analysis of all identified *T. atroviride* chitin synthases and chitin deacetylases.**

Extended evolutionary tree representing the analysis on which the compressed tree shown in Figure 1A is based. The tree was generated by use of the whole sequence of the indicated enzymes with the phylogenetic analysis software MEGA7, 1,000 bootstraps and the neighbor-joining-method. Numbers next to nodes indicate the bootstrap value. The bar marker indicates the genetic distance, which is proportional to the number of amino acid substitutions. Fungal chitin synthase classes are indicated in roman numbers (I-VII and CV). The following complete or relevant enzyme sets were mined from respective databases for CHS and also for CDA analysis: Ar, *Amylomyces rouxii*; Af, *A. fumigatus*; An, *Aspergillus nidulans*; Cl, *Colletotrichum lindemuthianum*; Cn, *Cryptococcus neoformans*; Fusgr, *Fusarium graminearum*; Fox, *F. oxysporum*; Fv, *Flammulina velutipes*; Gb, *Gongronella butleri*; Mgg, *Magnaporthe oryzae*; Nc, *Neurospora crassa*; Pd, *Penicillium digitatum*, PENCH, *P. chrysogenum*; Pa, *Podospira anserina*; Pb, *Phycomyces blakesleeanus*; Pc, *Pochonia chlamydosporia*; Pes, *Pestalotiopsis* sp.; Pgt, *Puccinia graminis*; Rs, *Rhizopus stolonifer* (*nigricans*); Sc, *Saccharomyces cerevisiae*; Sch, *Schizophyllum commune*; Ta, *T. atroviride*; Tr, *T. reesei*; Tv, *T. virens*.