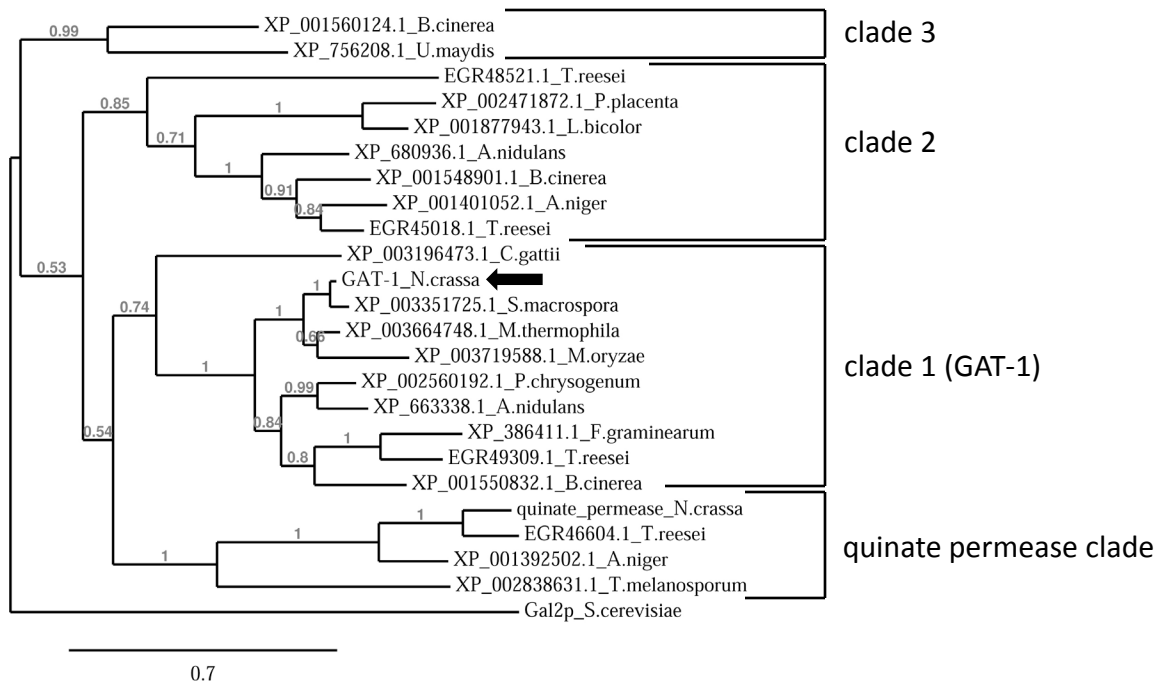




**Figure S2 Maximum likelihood phylogenetic analysis of the GAT-1 transporter.** The tree was generated with the help of the phylogeny.fr software workflow [60]: In this case, the alignment was performed by MUSCLE, the phylogeny calculated by PhyML, and the tree rendered by TreeDyn (see Materials & Methods). The *S. cerevisiae* galactose transporter Gal2p was used as outgroup. From the Ascomycota: *A.nidulans* (*Aspergillus nidulans*, Eurotiomycetes); *A.niger* (*Aspergillus niger*, Eurotiomycetes); *B.cinerea* (*Botrytis cinerea*, Leotiomycetes); *F.graminearum* (*Fusarium graminearum*, Sordariomycetes); *M.thermophila* (*Myceliophthora thermophila*, Sordariomycetes); *M.oryzae* (*Magnapotha oryzae*, Sordariomycetes); *N.crassa* (*Neurospora crassa*, Sordariomycetes); *P.chrysogenum* (*Penicillium chrysogenum*, Eurotiomycetes); *S.cerevisiae* (*Saccharomyces cerevisiae*, Saccharomycotina); *S.macrospora* (*Sordaria macrospora*, Sordariomycetes); *T.melanosporum* (*Tuber melanosporum*, Pezizomycetes); *T.reesei* (*Trichoderma reesei*, Sordariomycetes). From the Basidiomycota: *C.gattii* (*Cryptococcus gattii*, Tremellomycetes); *L.bicolor* (*Laccaria bicolor*, Agaricomycetes); *P.placenta* (*Postia placenta*, Agaricomycetes); *U.maydis* (*Ustilago maydis*, Ustilaginomycotina); the arrow indicates the position of GAT-1 in the tree; GAT-1: XP\_963898.1; quinate permease: XP\_959616.1.