



Supplementary Figure 1.  
 Phylogenetic relationships among environmental nucleic acid sequences of *cbhI* genes (50 most abundant OUs) and the sequences of identified fungal taxa obtained from GeneBank. Introns were removed and DNA dataset was aligned using software SeaView version 4 (<http://pbil.univ-lyon1.fr/software/seaview.html>) with external program Muscle (<http://www.drive5.com/muscle/>). Maximum likelihood phylogenetic tree computed with GTR substitutions model was obtained using GARLI Web Service ([http://www.molcularevolution.org/software/phylogenetics/garli/garli\\_create\\_job](http://www.molcularevolution.org/software/phylogenetics/garli/garli_create_job)). Bootstrapping was performed with 1000 replications. Bootstrap frequencies above 60% are shown at supported branches. Scale bar indicate number of nucleotide substitutions per site.