Supplementary Figure 1.
Phylogenetic relationships among environmental nucleic acid sequences of cbhl 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.molecularevolution.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.