	spruce	beech
Total no. of 18S rRNA sequences	73	85
Putative chimeric sequences	4	23
"good quality" 18S rRNA sequences	60	42
No. of MOTUs (97 % nt identity threshold)	49	30

Table S1 Characteristics of the PCR-amplified 18S rRNA sequence datasets.

Putative chimeric sequences were identified using the CHECK_CHIMERA program