

SUPPLEMENTARY INFORMATION

SI-A and SI-B

for

Fungal and beetle diversity in deciduous fine woody debris in spruce-dominated forests in relation to substrate quantity and quality

Biodiversity and Conservation

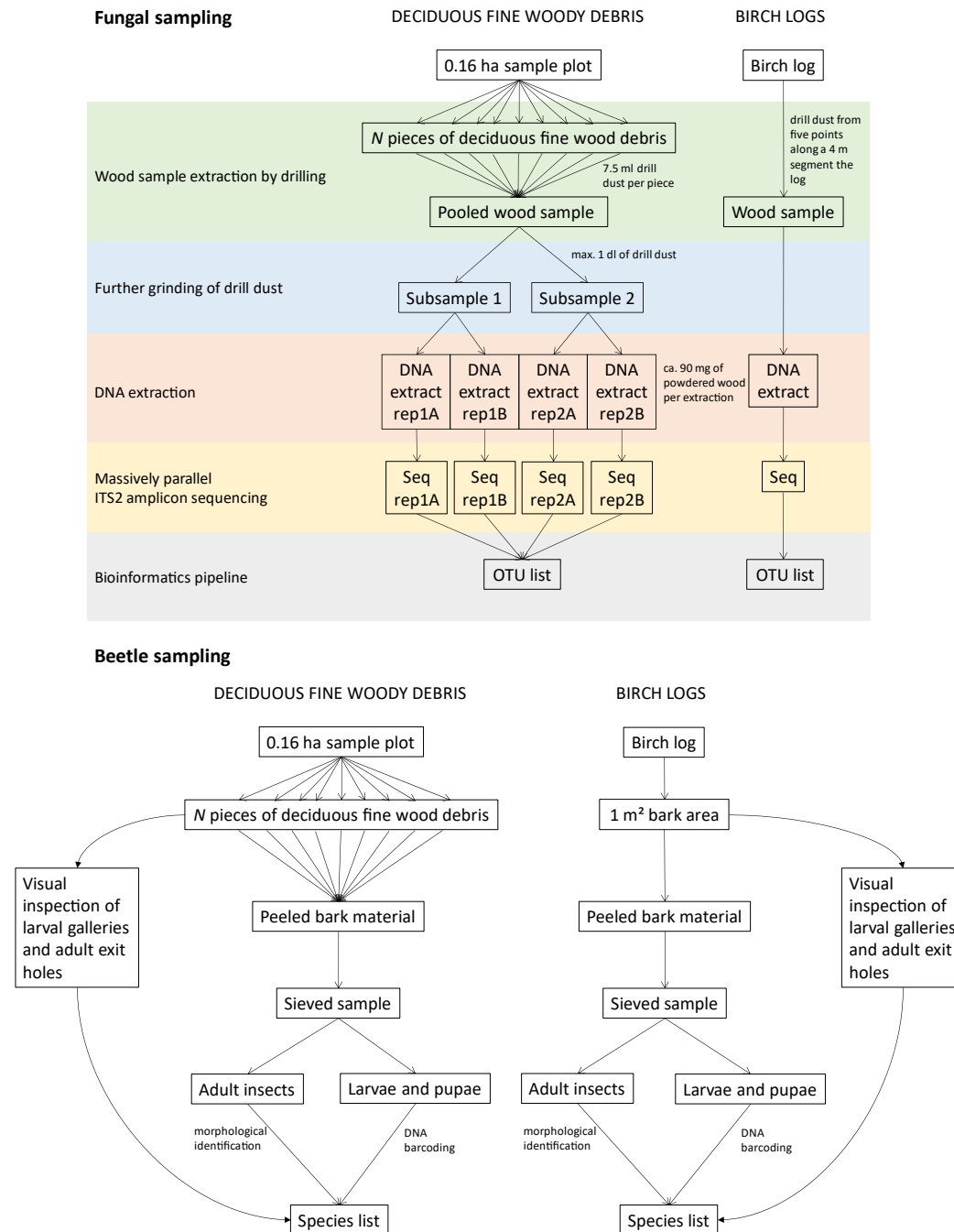
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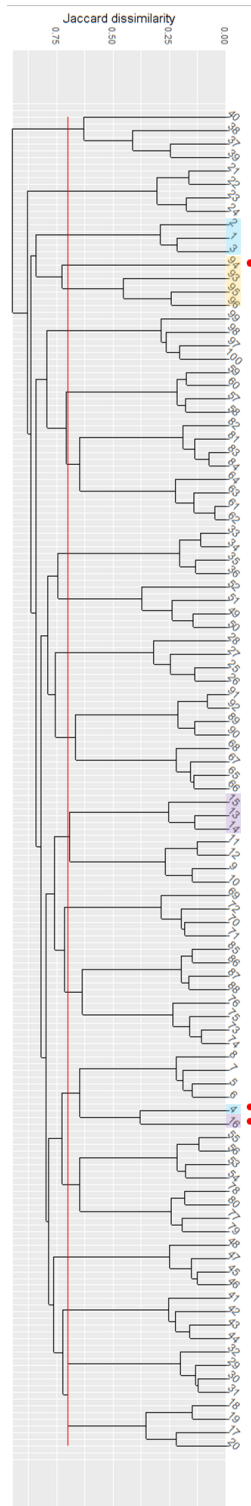
SI-A: Sampling and sample processing design



Supplementary Fig. A1. Fungal and beetle sampling and sample processing design for deciduous fine woody debris and birch logs.

SI-B: Consistency of sequencing replicates from deciduous fine woody debris

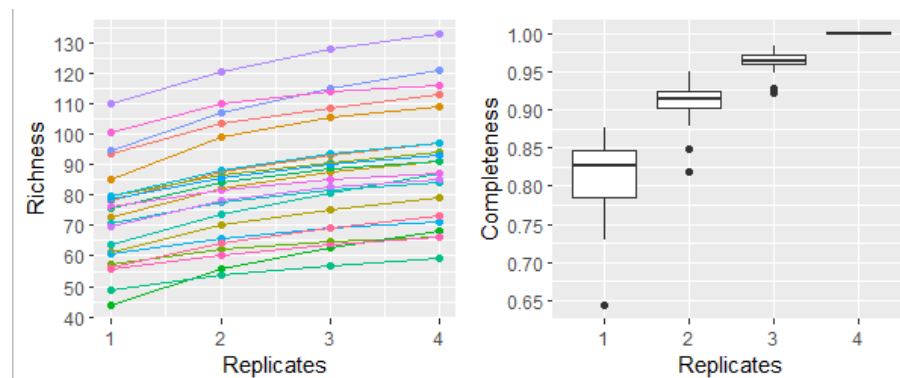
Based on the analysis of pairwise dissimilarities of fungal OTU composition between replicates across all deciduous fine woody debris (DFWD) samples, we identified three spurious, potentially contaminated, sample replicates that were removed from further analyses (Supplementary Fig. B1).



Single replicates of DFWD samples (one out of four) captured, on average, 81% of fungal OTUs recovered by the full set of four replicates. Coverage increased to 91% with two replicates and to 96% with three replicates (Supplementary Fig. B2).

The number of deadwood pieces pooled into a DFWD sample had no significant effect on how dissimilar the fungal OTU composition was between individual replicates. Correlation between average Jaccard dissimilarity between replicates and the number of pooled deadwood pieces was -0.29 ($t = -1.434$, $df = 23$, $p = 0.165$).

Supplementary Fig. B1. (left) Hierarchical clustering of DFWD samples based on Jaccard dissimilarities calculated from fungal OTU presence-absence data. Tree graph shows individual replicates and their relative distances in terms of fungal community composition. Replicates originating from the same sample generally group together in groups of four. Three deviant replicates, that differed strongly (> 0.7 , indicated by the vertical red line) from their sister replicates (shaded with same color), are denoted with red dots.



Supplementary Fig. B2. (above) Number (richness) and proportion (completeness) of fungal OTUs captured in one, two and three sample replicates compared to the full set of four replicates.