Figure S1. Statistical testing of differences in community composition according to experimental variables with PERMANOVA (AB) and ANOSIM (C) based on Bray-Curtis dissimilarities (nperm = 999). Panel A shows the percent variability (R^2) explained by experimental variables in each soil layer, while panel B shows variability explained by variables in each ecozone with soil layers combined. In both panels, only statistically significant (p < 0.01) factors are plotted. Panel C summarizes the number (n) of statistically significant (p_{adj} < 0.05) pairwise ANOSIM contrasts and the average ANOSIM statistic (R) of the group. Comparisons were made separately for each ecozone and soil layer. Bacterial and fungal libraries were analyzed separately and both are included in the total number. A complete list of pairwise ANOSIM comparisons can be found in Table S7.
Figure S2. Rarefaction curves showing the number of OTUs as a function of sampling depth for each site. Ecozones are indicated by line colour. Inset: Shannon diversity estimates for fungal and bacterial communities among ecozones.
**Figure S3.** Differences in total carbon, total nitrogen, soil moisture and pH among treatments (left) and ecozones (right). Error bars correspond to one standard error of the mean.
Figure S4. All available long-term data on mean daily soil temperature data. Panel A contains the daily temperature data for the first 14 years following harvesting at JPOE at varying soil depth for OM2 and OM3 treatments. Consecutive 4 to 5-year periods were grouped and averaged (lines) and the transparent dots correspond to all daily measurements at a depth of 5 cm for OM2 (yellow) and OM3 (red). Panel B depicts soil temperatures in summer at PPCA averaged across the entire soil profile for REF, OM1 and OM3 plots five years after harvesting in PPCA (sourced from Paz, 2001 and reprinted with permission from Dr. Lucas Paz). Panel C illustrates the convergence of mean yearly soil temperatures at BSON over 14 years at the interface of organic and mineral layers (upper 5 cm) in OM2 and OM3 from 18 replicates per treatment.
**Figure S5.** Shannon diversity estimates of bacterial and fungal OTUs among OM treatments according to ecozone and soil layer. The estimation for a given sample was based on an average of 500 calculations on OTU tables rarefied to an equal sequencing depth. Tukey HSD supported, pairwise differences are grouped by lettering.
Figure S6. Relative abundances of *Basidiomycota* (top) to *Ascomycota* (bottom) according to ecozone and OM treatment. The log of the ratio of their abundances is denoted by a dot. Error bars correspond to one standard error of the mean. Significant (Tukey HSD; $p_{\text{adj}} < 0.05$) pairwise differences are grouped by lettering.
Figure S7. Abundance patterns of fungal and bacterial OTUs at-best classifiable to the taxonomic rank of Order. Error bars correspond to one standard error of the mean. Significant (Tukey HSD; \( p_{adj} < 0.05 \)) pairwise differences are grouped by lettering.
Figure S8. Co-association network of fungal OTUs with significant (p < 0.01) and relatively strong correlations (r > 0.3). Modules were calculated with Gephi using a ‘resolution’ of 0.5 and nodes with relative abundances greater than 15 reads per thousand were labeled. Bar plots showing the summed abundances of all OTUs in a given module are coloured and labeled accordingly. Modules which were part of the largest cluster of OTUs did not exhibit clear trends in abundance and, as a result, were not displayed.
Figure S9. Abundance patterns of pyrophilous fungal genera. Error bars correspond to one standard error of the mean.
**Figure S10.** Shannon diversity of ectomycorrhizal fungi by soil layer, ecozone and harvesting treatments based on OTU profiles within EM genera (A) or profiles of EM genera (B). Estimations were based on an average of 100 calculations on data rarefied to equal sequencing depth. Significant (Tukey HSD; \( p_{adj} < 0.05 \)) pairwise differences are grouped by lettering.
Figure S11. Evidence for declining populations of the methanotrophic bacterial genus, *Methylocapsa*, with increasing harvesting intensity. Abundances of *Methylocapsa* were estimated by (A) mapping shotgun metagenomic reads to *Methylocapsa acidophila*, (B) based on abundances in 16S pyrotag libraries and (C) based on enumeration of BLAST hits (E-value < 10^{-10}) to databases for *pmoA*, *mmoX* and *mcrA* genes derived from the ‘functional gene pipeline & repository’ (Fish et al., 2013). Error bars correspond to one standard error of the mean. Significant (Tukey HSD; p_{adj} < 0.05) pairwise differences are grouped by lettering.
Figure S12. Abundance profiles of taxa with increased abundance following intermediate intensities of OM removal (OM1 and OM2). Plots B and D each correspond to a single OTU, while plots A, C, E and F correspond to 20, 3, 17 and 4 aggregated OTUs (all showing similar abundance patterns), respectively. Error bars correspond to one standard error of the mean.

Average Counts per Thousand Reads

A  Thelephora sp. ECM1

B  Uncl. Dermateaceae spp.

C  Gymnopilus spp.

D  Uncl. Agaricomycotina sp.

E  Uncl. Agaricales spp.

F  Coniophora spp.

REF  OM1  OM3  OM2
Figure S13. Relative abundance of members of the actinobacterial family Geodermatophilaceae according to (A) the proportion of metagenomic reads mapped to three representative genomes (Sghai-er et al., 2016) and (B) the normalized read counts in pyrotag libraries. Significant (Tukey HSD; $p_{adj} < 0.05$) pairwise differences are grouped by lettering.
**Figure S14.** Abundance patterns for eight taxonomic groups exhibiting contrasting responses to harvesting (i.e. expansion or decline) between western and eastern sites. Error bars depict one standard error of the mean. The order AKIW781 is within the phylum *Chloroflexi*. 

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**WEST** | **EAST**
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![AKIW781 (Order)](image1) | ![Nostoc (Genus)](image2)
![Limnohabitans spp.](image3) | ![Aethiariales sp.](image4)
![Cupriavidus spp.](image5) | ![Kitasatospora spp.](image6)
![GAL15 (Phylum)](image7) | ![Rudaea spp.](image8)
Figure S15. Maximum-likelihood phylogenetic tree for predominant OTUs from the fungal genus, Rhizopogon, accompanied by abundance plots according to harvesting treatment. OTUs names are coloured according to whether they exhibited expanding (red) or declining (brown) relative abundances in harvested treatments. The barplot on the left shows the sum total of all reads classified as Rhizopogon, while barplots on the right correspond to the percent abundance of individual clades. On average, Rhizopogon spp. accounted for 0.7% of ITS reads per library. Aligned sequences were trimmed to 420 bp prior to tree building.
Figure S16. Differential responses to harvesting in two closely related ectomycorrhizal fungi from the family *Thelephoraceae: Tomentella* and *Pseudotomentella*. Error bars depict one standard error of the mean.