

## New Phytologist Supporting Information

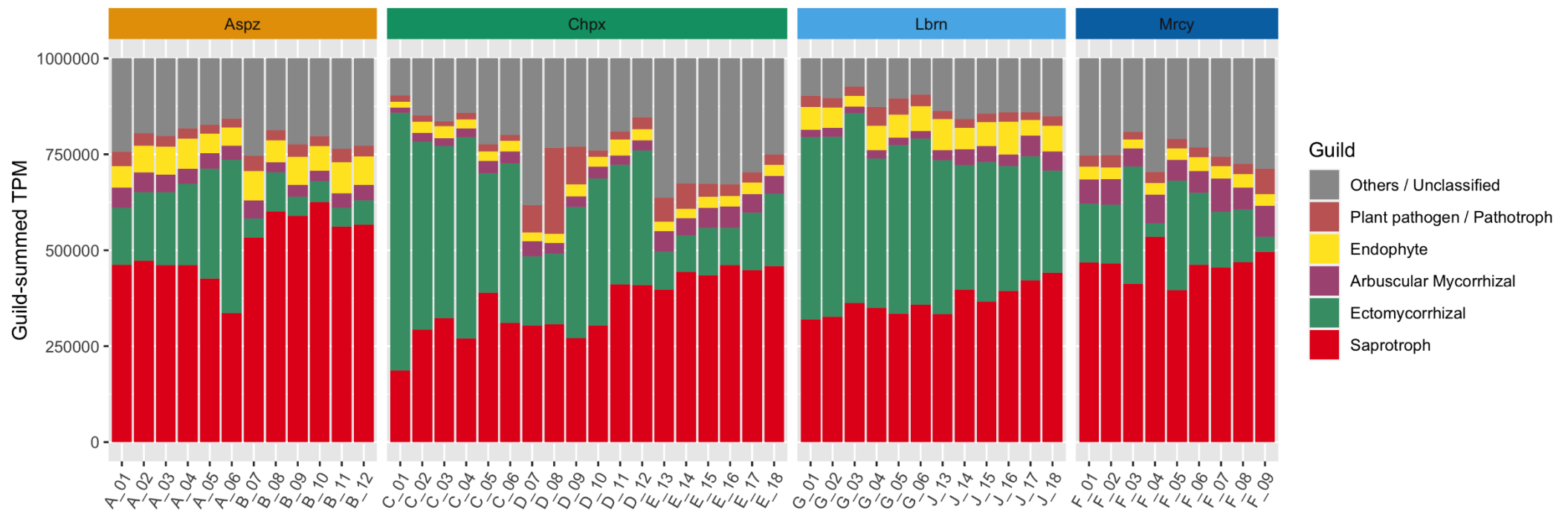
Article title: **Metatranscriptomics sheds light on the links between the functional traits of fungal guilds and ecological processes in forest soil ecosystems.**

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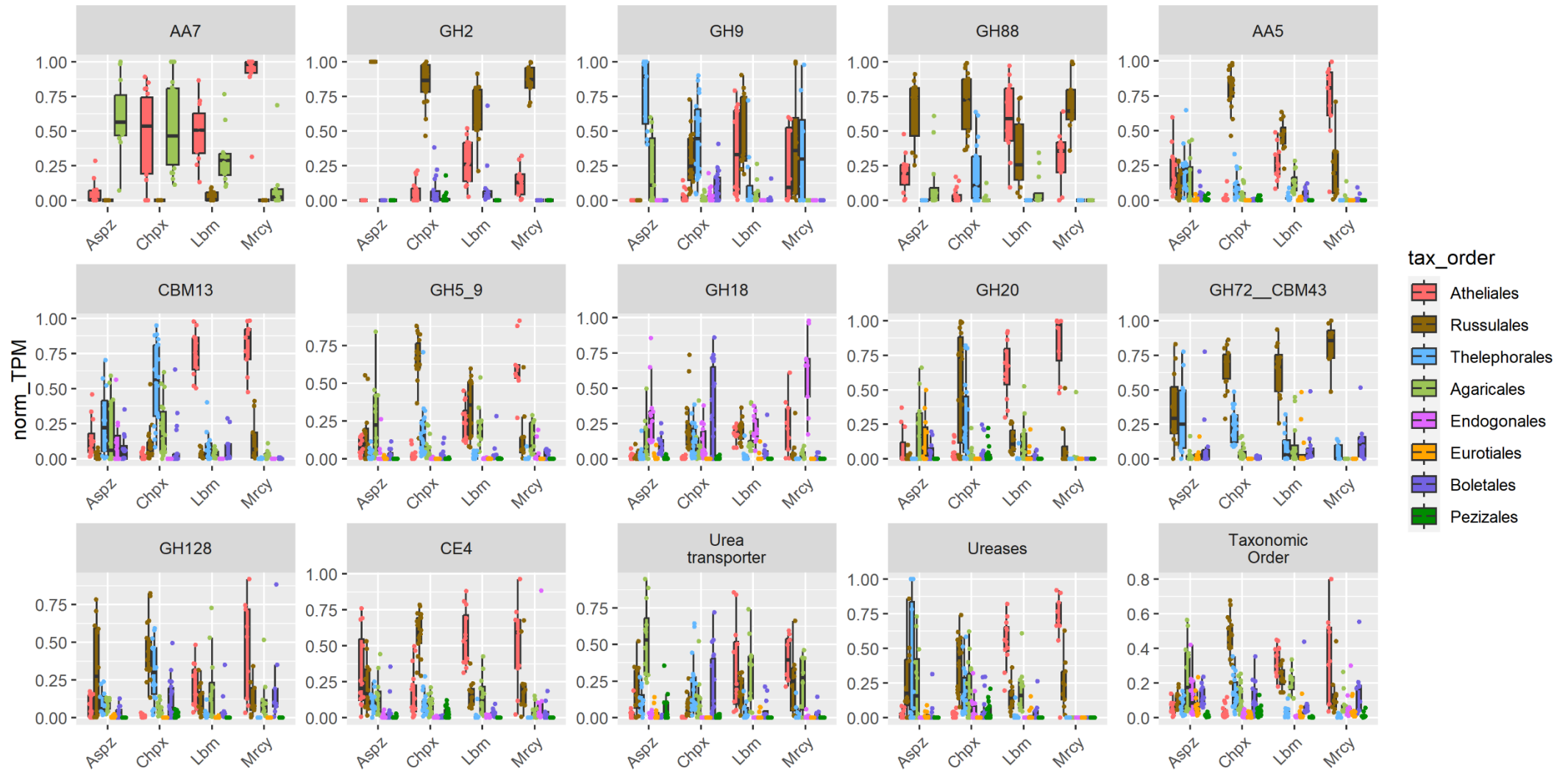
**Figure S1:** Fungal trophic guilds transcript TPM abundances across sites, according to FungalTraits database and genus annotation based on Mycocosm.

Guilds were constructed based on FungalTraits LifeStyle annotations, merging the different types of saprotrophs, endophytes and plant pathogen in one guild each. Genus with no or other LifeStyle annotation were placed in the Others / Unclassified group. Samples were ordered according their site, with Aspz (Aspurz, submediterranean forest) in orange, Chpx (Champenoux, temperate forest) in green and Lbrn and Mrcy (Lamborn and Montmorency, boreal forests) in blue.



**Figure S2:** Boxplots of the overexpressed functions according to ECM fungal order in each site.

Only ECM transcripts were considered and total expression was normalised to 1 for each family/function, so the proportion of the expression due to each of the 8 main orders can be visualised for each of the sites. Boxplots and dots (corresponding to individual samples) are coloured according to taxonomic orders using the Figure 1 colour code.



**Methods S1** To ensure the reliability of fungal guild annotations based on the taxonomy of the best hits in Mycocosm, coding sequences from 20 unpublished genomes (here designated by their taxonomic family level) were annotated following the same process as metatranscriptomic transcripts. For 10 (respectively, 6 and 4) of these genomes, a genome of the same genus (respectively, family and order-or-higher) is available in Mycocosm. Genomes were chosen to best encompass fungi diversity. (A) Proportion of correctly annotated genes at different taxonomic ranks and within the trophic guild (as defined in the metatranscriptomics analysis), represented for each of the genomes. Genomes annotated with a star are the 3 ectomycorrhizal genomes among the 20 genomes. (B) Distribution of correctly annotated genes for the 3 categories of genomes (with the closest reference at the genus, family, or order level). Genes with no hits in Mycocosm were excluded from the error calculation, as they would have been in the metatranscriptomic analysis where NoHits are discarded. As expected, the proportion of NoHits increases with the distance to the nearest reference genome, while the quality of taxonomic annotation decreases. Apart from a few outliers, the trophic guild annotation (ectomycorrhizal or saprotrophic) is accurate for over 90% of annotated genes, and even for over 95% of genes when reference genomes from the same genus or family are available.

