

Sympatric *Lepus* spp. in the central Italian Alps host significantly different gut microbiotas

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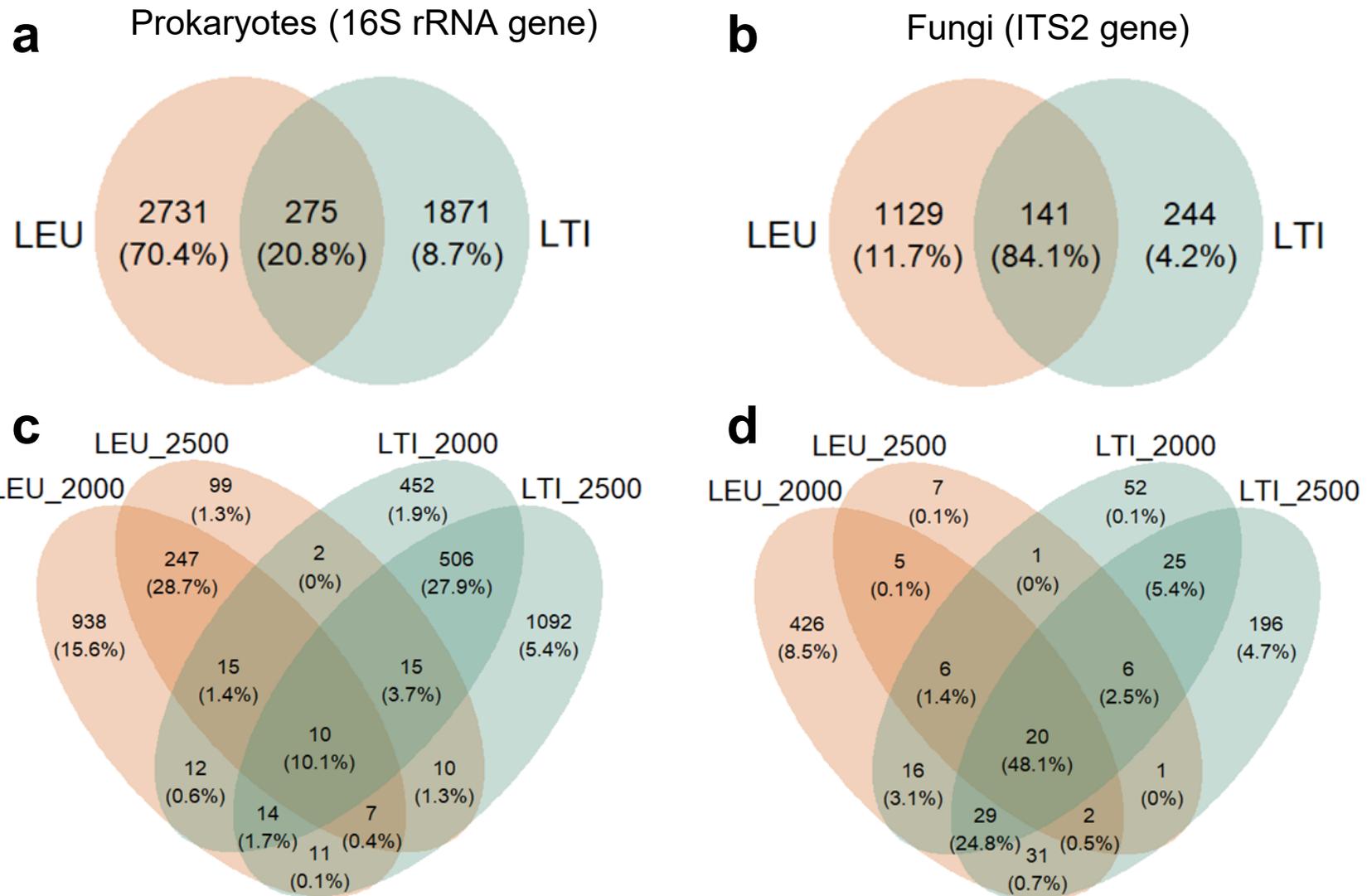


Figure S1. Venn diagrams illustrating shared and unique bacterial (a,c) and fungal (b,d) ASVs between the two hare species and across elevational levels (2000 and 2500 m a.s.l.). ASVs are represented by integers, with the relative abundance of sequences per group shown as percentages. Diagrams were generated using the microeco R package. LEU = *Lepus europaeus*, LTI = *Lepus timidus*.

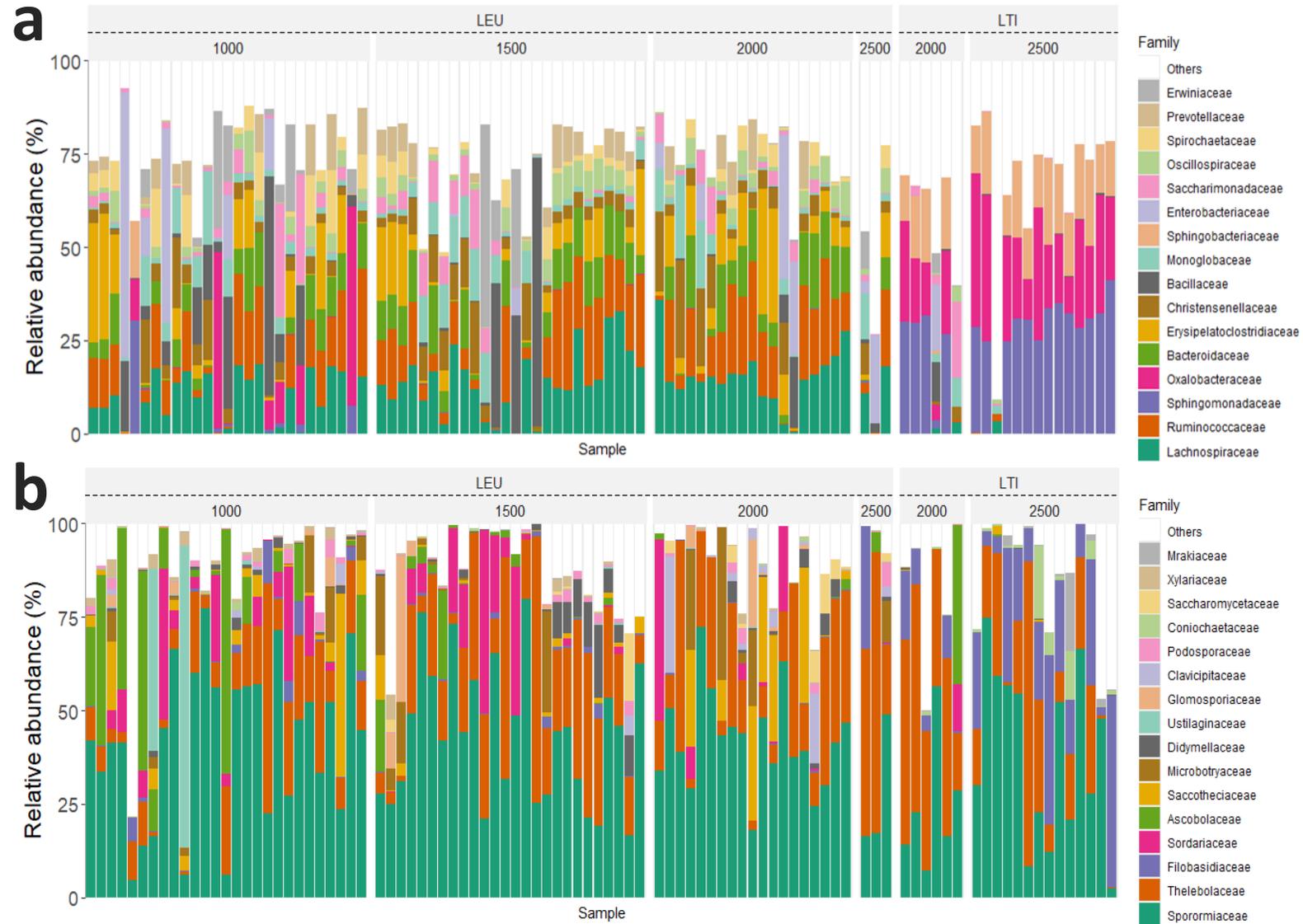
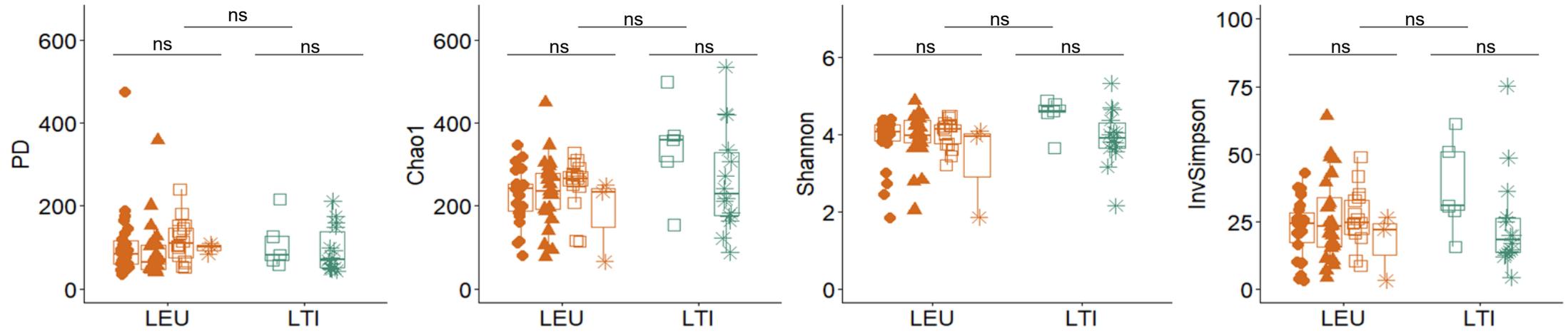


Figure S2. Relative abundances of faecal prokaryote (16S) and fungal (ITS2) families: (a) 16S rRNA gene and (b) ITS2 family composition. Each bar represents a different sample, with colors indicating the most abundant taxa as shown in the legend. Samples are grouped by species (LEU = *L. europaeus*, LTI = *L. timidus*) and ordered by elevation.

Prokaryotes



Fungi

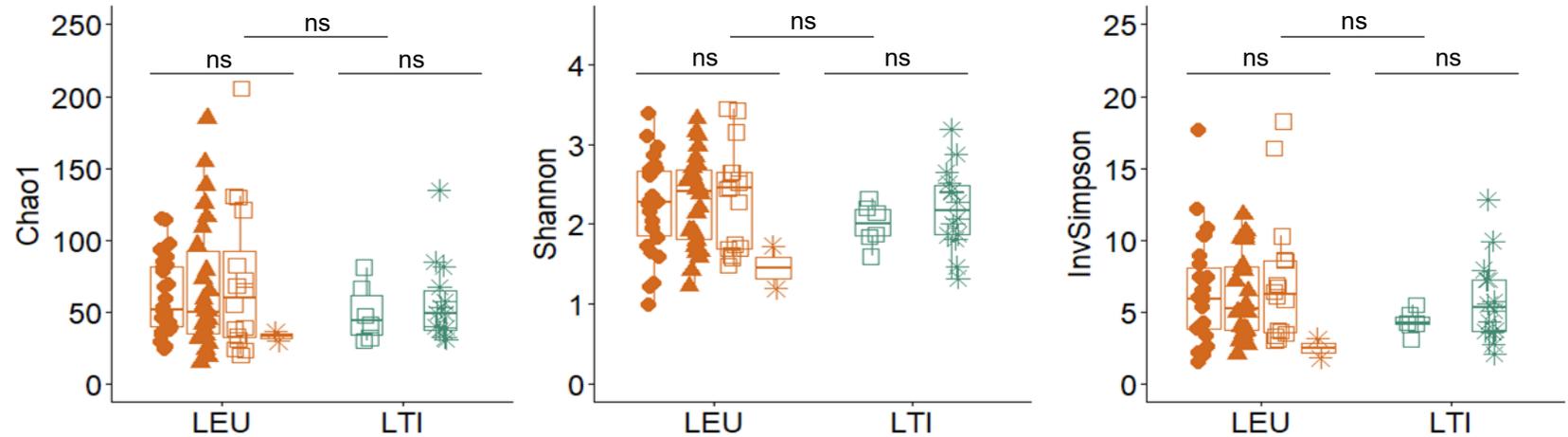
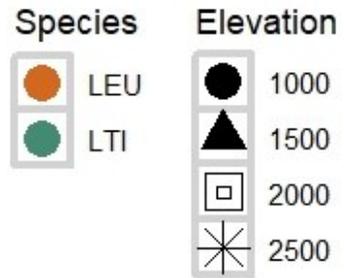


Figure S3. 16S rRNA gene and ITS2 richness based on alpha-diversity. Chao1, Shannon and InvSimpson were calculated for both 16S rRNA gene and ITS2 data, while phylogenetic diversity (PD) was computed for 16S rRNA gene data only. Group difference were assessed using the Wilcoxon rank-sum test. (LEU = *L. europaeus*; LTI = *Lepus timidus*)

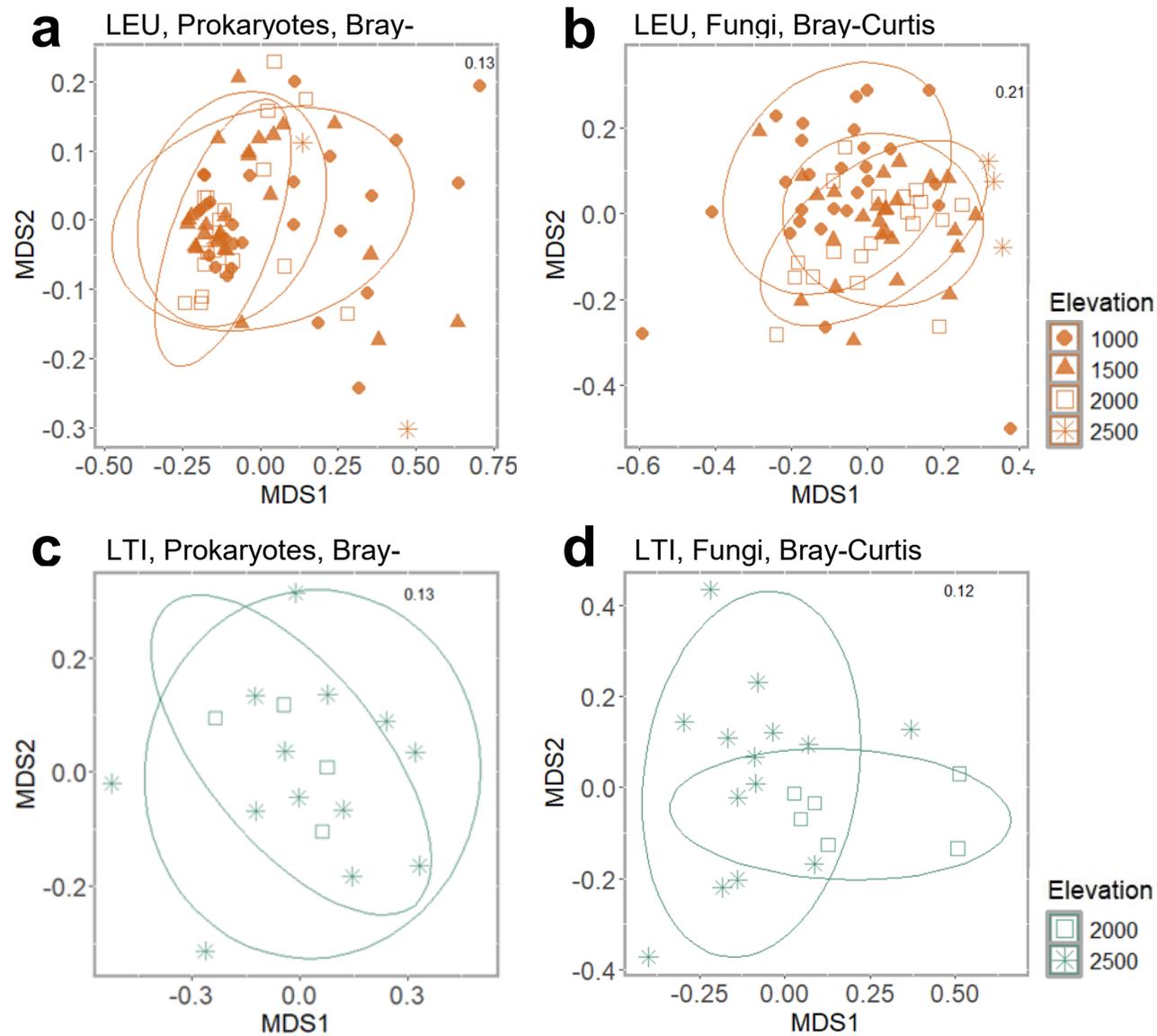


Figure S4. Microbial community structure of *Lepus* spp. Panels (a) and (b) showing microbial community composition of *L. europaeus* (LEU) samples, while panels (c) and (d) represent that of *L. timidus* (LTI) samples. Community composition was analyzed using Bray-Curtis-based PcoA of faecal bacterial and fungal sequences. Each dot represent a single faecal pellet sample. Sample elevations are indicated with different shapes, as detailed in the legend. NMDS shown in panel (c) (LTI, Prokaryotes, Bray-Curtis) was performed after the removal of outlier samples, LTI_72, LTI_106, LTI_679, to avoid convergence failure.