

### Supplement S3 – Schematic overview of the microbiome composition

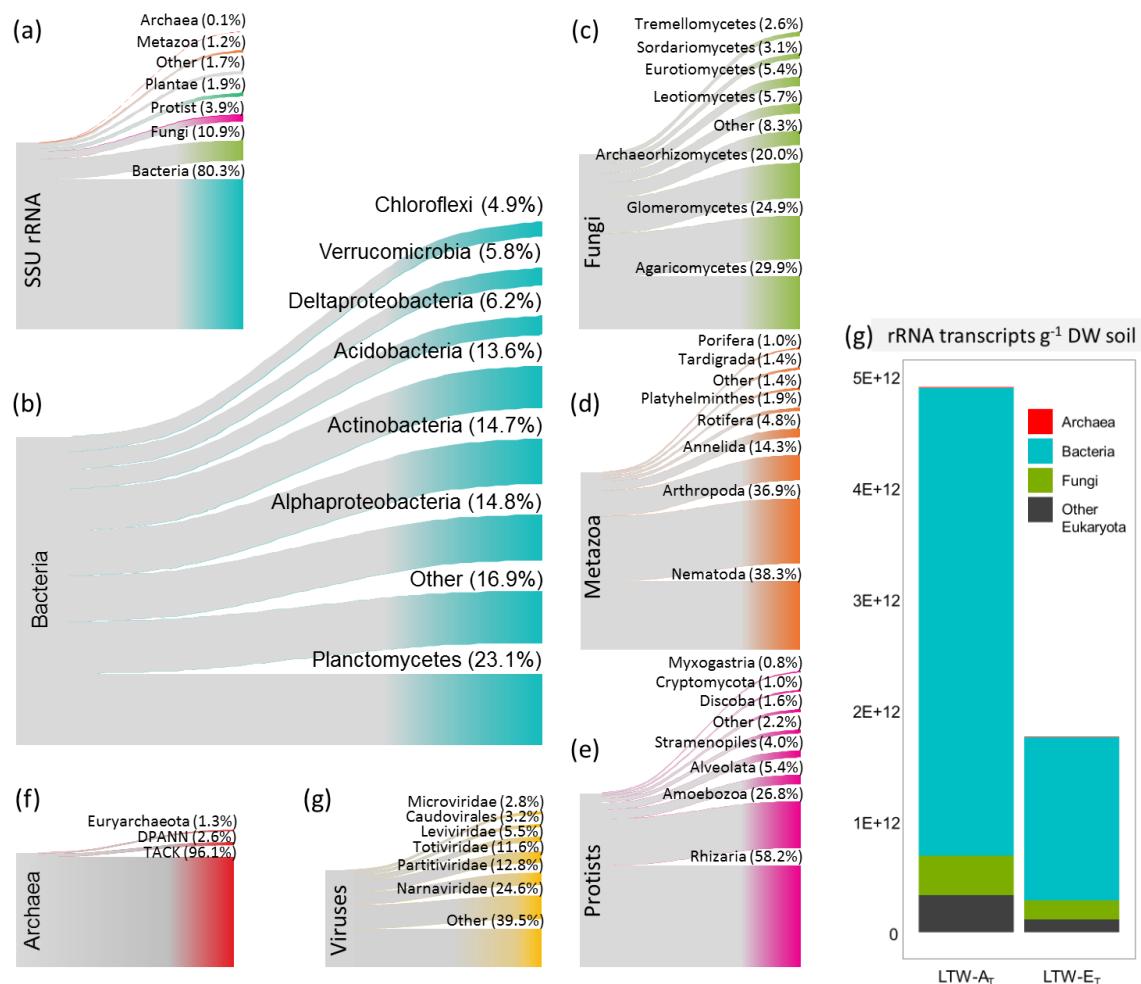


Figure S3 Holistic community profile. Sankey diagrams of the census (mean of all samples) relative abundances of SSU rRNA sequences for major soil (micro-)biota groups. Bars reflect the proportions of reads for all SSU rRNA data (a), Bacteria (phyla-level; b), Fungi (class-level; c), Metazoa (phyla-level; d), ‘Protists’ (major lineages; e), Archaea (major lineages; f) and viruses (major groups; e) normalized to mRNA library sizes. SSU rRNA transcripts g<sup>-1</sup> DW soil identified to main domains at LTW-A<sub>T</sub> and LTW-E<sub>T</sub> (g).