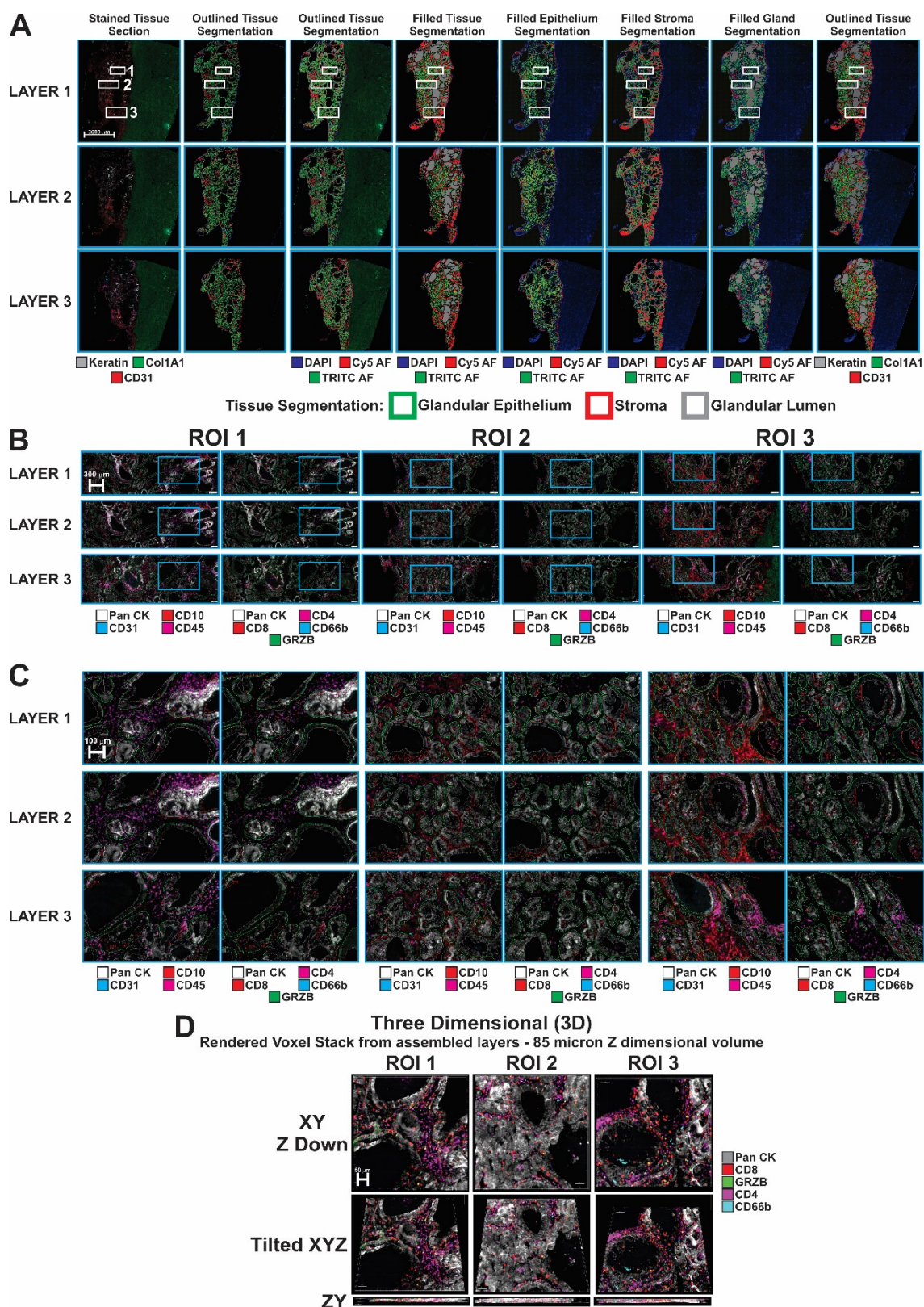
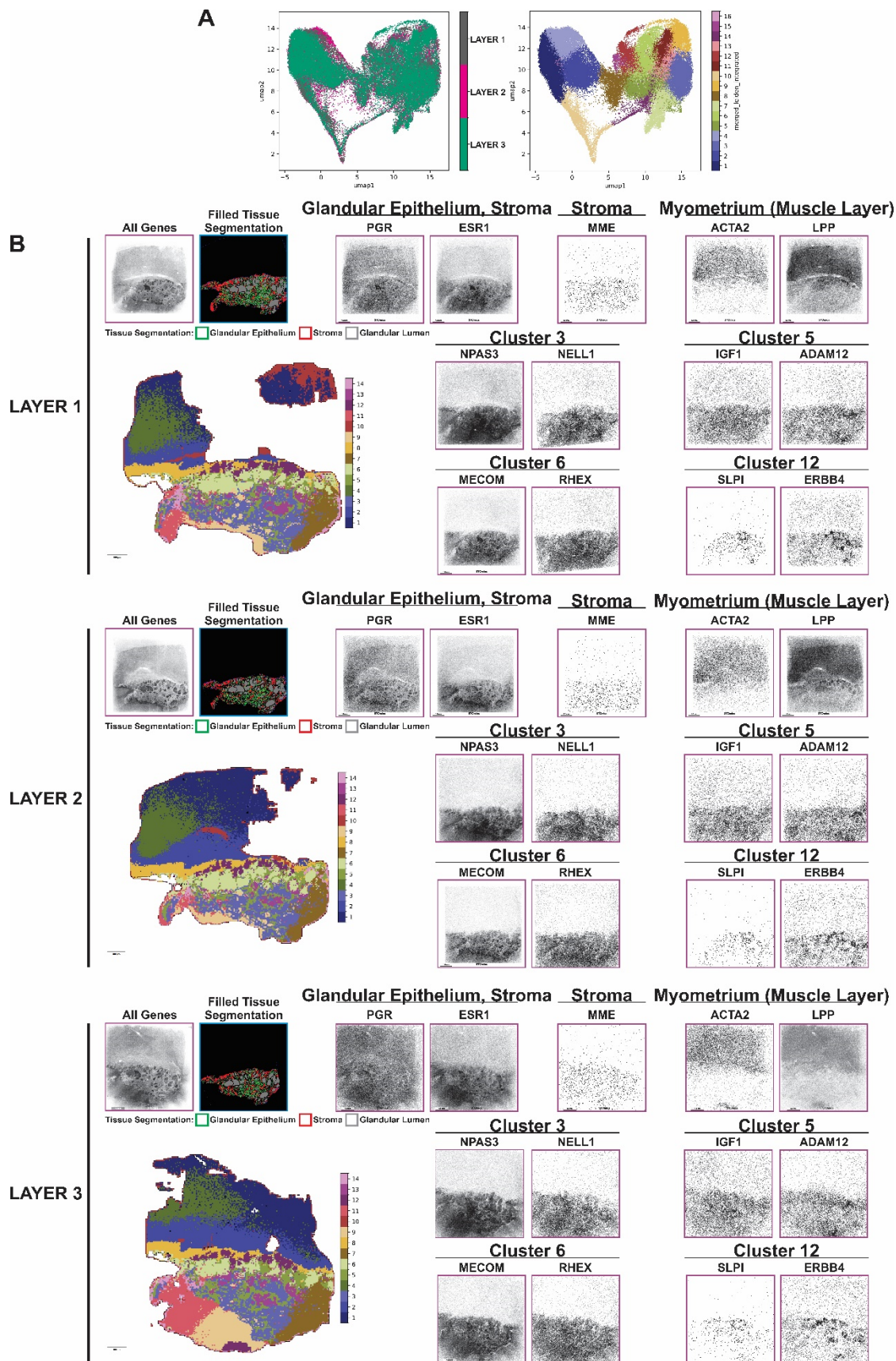


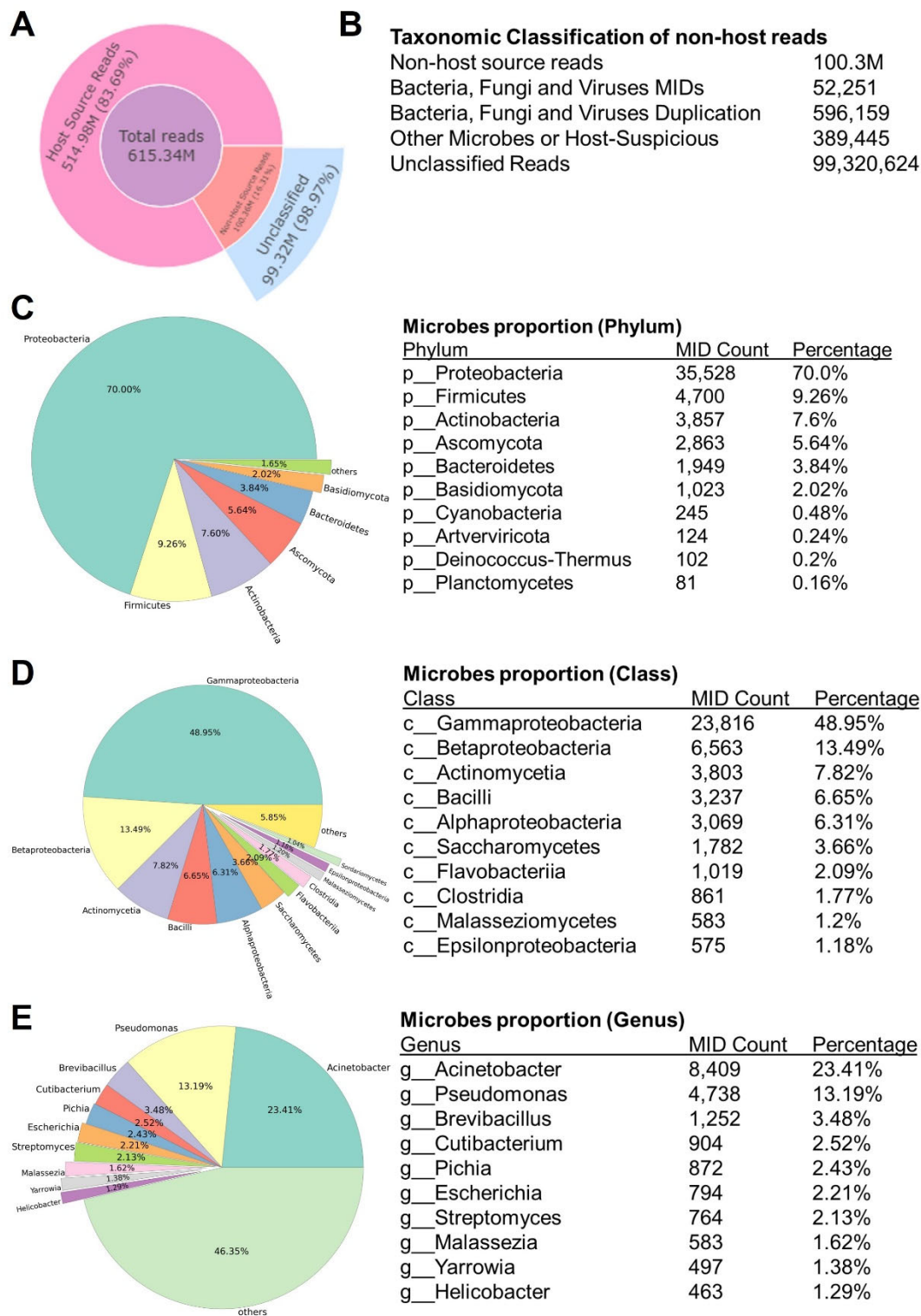
Supplementary figures



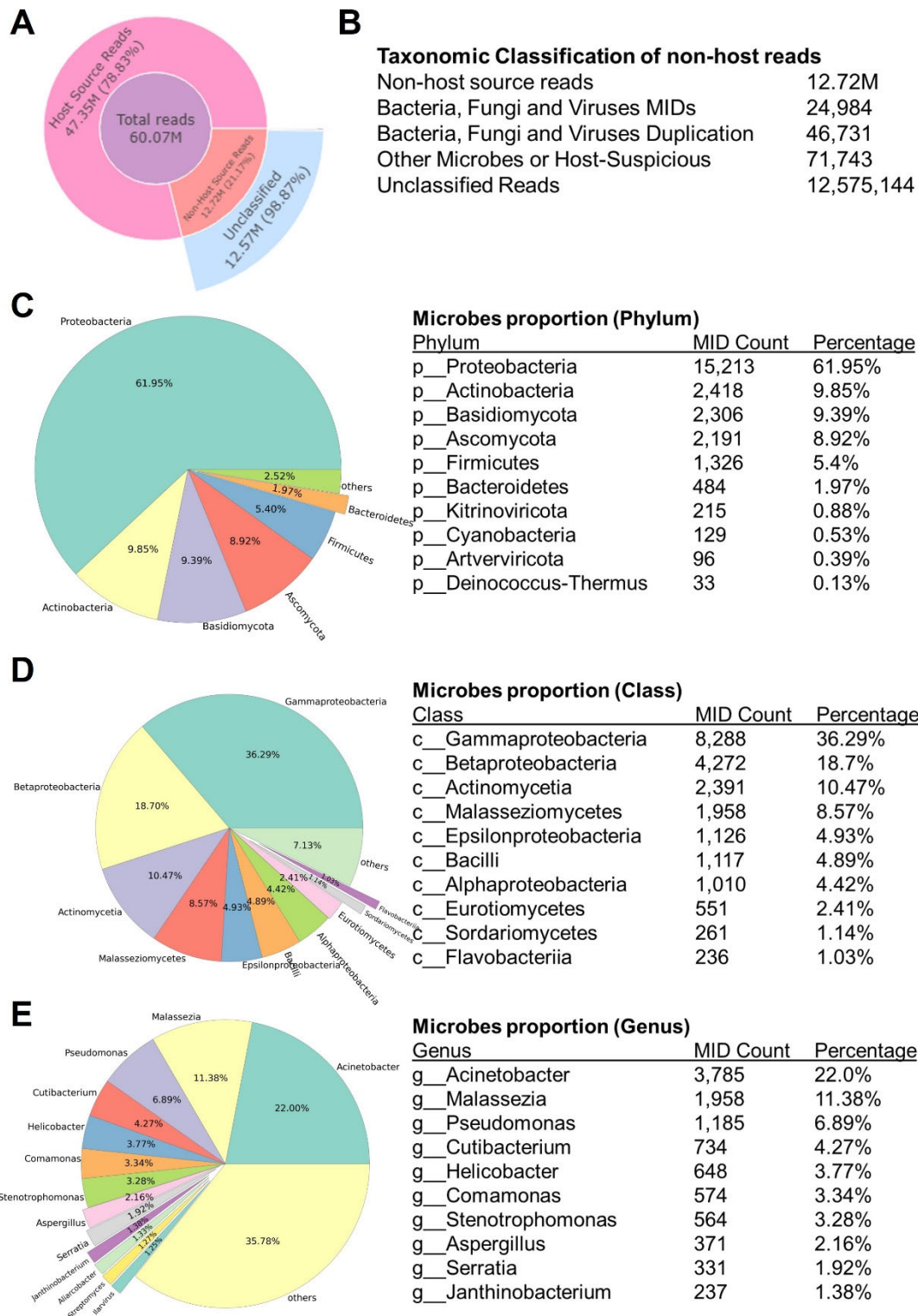
Supplementary Figure S1. Multiplex sequential immunofluorescence analysis on AEH sample. **A.** Whole tissue images overlaid with tissue segmentation mask were created based on Pan-Keratin, CD10 and α SMA markers in Visiopharm software for each layer. White boxes represent chosen ROIs shown in panel B. Scale bar is 3500 μ m. **B.** Chosen ROIs from panel A, highlighting corresponding marker expression in different tissue areas. Blue square represent chosen ROIs shown in panel C. Scale bar is 300 μ m. **C.** Chosen ROIs from panel B, showing differential expression of main immune markers. Scale bar is 100 μ m. **D.** 3D reconstruction through rendered voxel stack from assembled layers 1-3. Scale bar is 50 μ m.



Supplementary Figure S2. Non-targeted spatially-resolved transcriptomics analysis. **A.** UMAPs generated after stereo-seq analysis for AEH sample. **B.** Quantitative Leiden cluster analysis and qualitative images for most differentiated genes exported from STereoMap software for each layer and overlaid to seqIF images through Visiopharm software (tissue segmentation overlay shown in the second panel). Scale bar is 1.5 mm.



Supplementary Figure S3. Stereo-seq non-host spatial transcriptomics results for HGSOC sample, section 9 (layer 2). **A.** Sunburst Chart of Mapping showing number of host (Number of reads that can be aligned to the host genome during denoising) and non-host (Number of reads that cannot be aligned to the host genome) reads. **B.** Taxonomic Classification of non-host reads: Bacteria, Fungi and Viruses MID (number of unique mRNA molecular assigned to bacteria, fungi or viruses); Bacteria, Fungi and Viruses Duplication (number of assigned reads that have been corrected due to duplicated MID); Other Microbes or Host-Suspicious (number of reads assigned to other microbes, exclude bacteria, fungi and viruses) or host; unclassified reads. **C.** The main proportion of microbes at the phylum level. **D.** The main proportion of microbes at the class level. **E.** The main proportion of microbes at the genus level.



Supplementary Figure S4. Stereo-seq non-host spatial transcriptomics results for AEH sample, section 9 (layer 2). **A.** Sunburst Chart of Mapping showing number of host (Number of reads that can be aligned to the host genome during denoising) and non-host (Number of reads that cannot be aligned to the host genome) reads. **B.** Taxonomic Classification of non-host reads: Bacteria, Fungi and Viruses MIDs (number of unique mRNA molecular assigned to bacteria, fungi or viruses); Bacteria, Fungi and Viruses Duplication (number of assigned reads that have been corrected due to duplicated MID); Other Microbes or Host-Suspicious (number of reads assigned to other microbes, exclude bacteria, fungi and viruses) or host; unclassified reads. **C.** The main proportion of microbes at the phylum level. **D.** The main proportion of microbes at the class level. **E.** The main proportion of microbes at the genus level