Table S1. Conda environments used by 16S-Pipeline

Environment	**Components**
microbiome_16S	Python 3.11, FastAPI, Dash, FastQC, Cutadapt, MAFFT, FastTree, vsearch, sra-tools
dada2_16S	R 4.3, DADA2 for denoising and taxonomy assignment
analysis_16S	R 4.4, ALDEx2, DESeq2, ANCOM-BC2
maaslin2_16S	R 4.3, MaAsLin2, LinDA, vegan
picrust2_16S	PICRUSt2 for functional prediction