2nd Microorganisms Identification and filtering 1st Filter by Quality by Alignment (SURPI): (Trimmomatic) Sequenced Microbiota, genomic edit distances (ED) and reference genome options **Identification of sequenced Microbiota** (Taxonomic clasification) Alignment to **FastQC** Raw files Mycobacterium reads Complete genome Aligment to human GRCh38 Non-Mycobacterium reads **Bacterial reference** database Not assigned reads **Trimmomatic** Virus reference database Adjustment parameters for alignment with Mycobacterium for reads **FastQC** elimination **Clean files** Genomic edit Reference genome distance (ED) options options Complete ED = 3 H37Rv genome (NC_000962.3)

