

A spatial microbiome technological approach to analyze the host-microbiome interaction in Parkinson disease

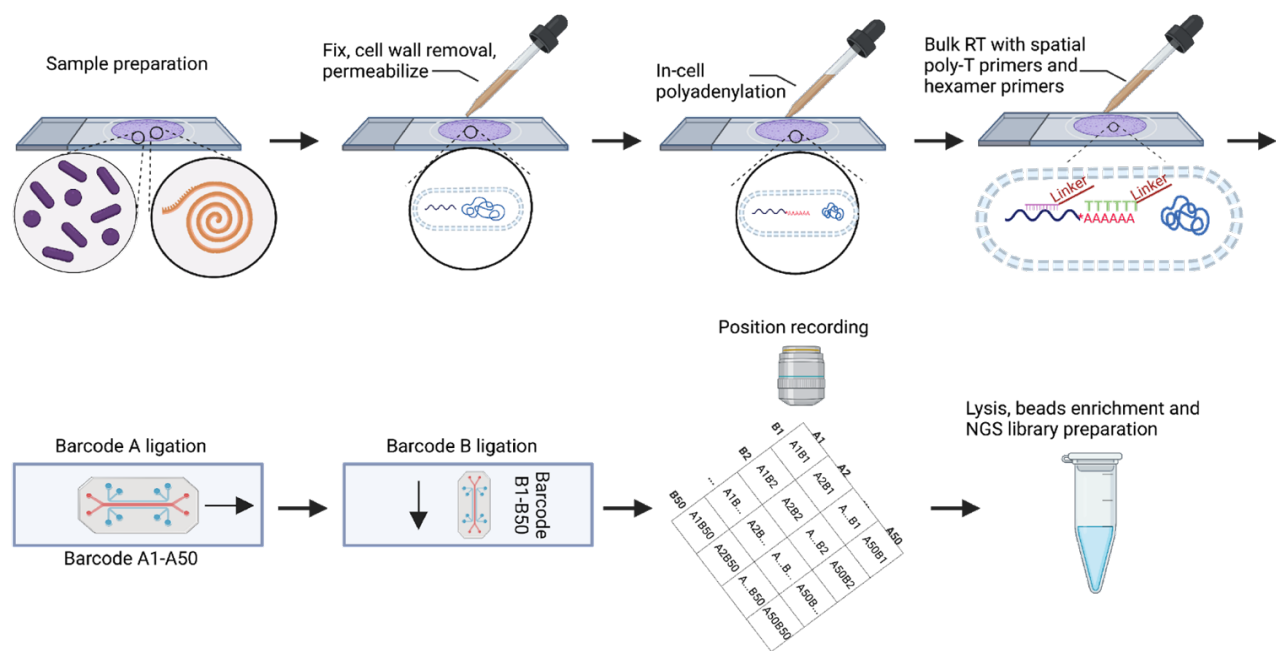


Figure 1. Spatial host-microbiome transcriptome sequencing technology (microDBiT) with mouse models.

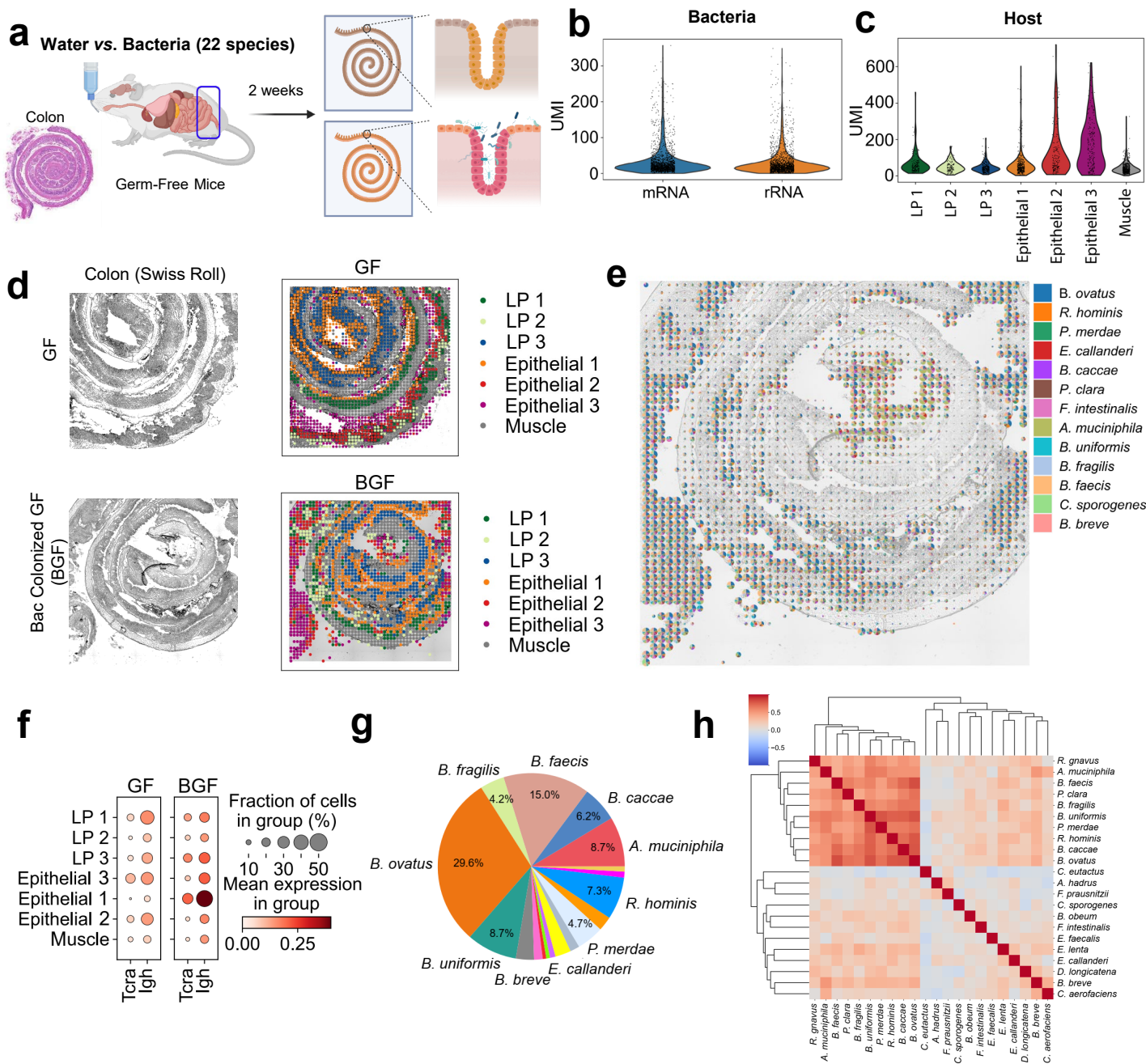


Figure 2. microDBiT working with mouse models. (a) Germ free mice (GF) and Bacteria loaded germ (BGF) free mice. (b) Bacteria UMI for each spatial pixel. (c) Host UMI counts for each spatial pixel. (d) Colon “Swiss roll” of GF and BGF and the host cell distribution based on gene expression. (e) Spatial piechart of bacteria species based on gene expression. (f) Host responses with Bacteria. (g) Bacteria piechart. (h) Colocalization heatmap of different bacteria species.

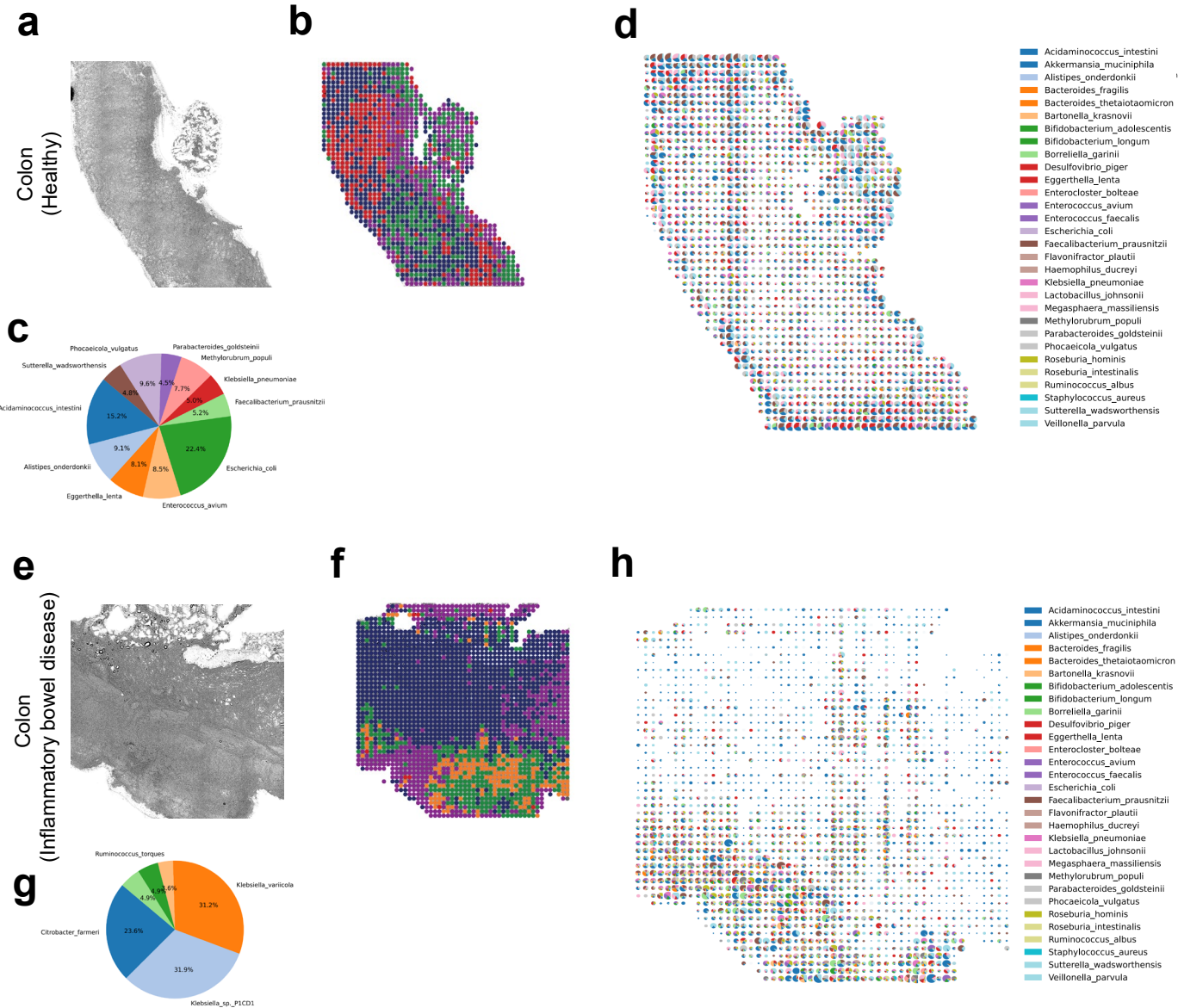


Figure 3. microDBiT working with human colon tissue from healthy and Inflammatory bowel disease. (a-d) Healthy donor tissue. (a) Microscope image of colon section. (b) Host cell distribution (c) Host UMI counts. (d) Spatial piechart of bacteria species based on gene expression. (e-h) IBD tissue. (e) Microscope image of colon section. (f) Host cell distribution (g) Host UMI counts. (h) Spatial piechart of bacteria species based on gene expression.

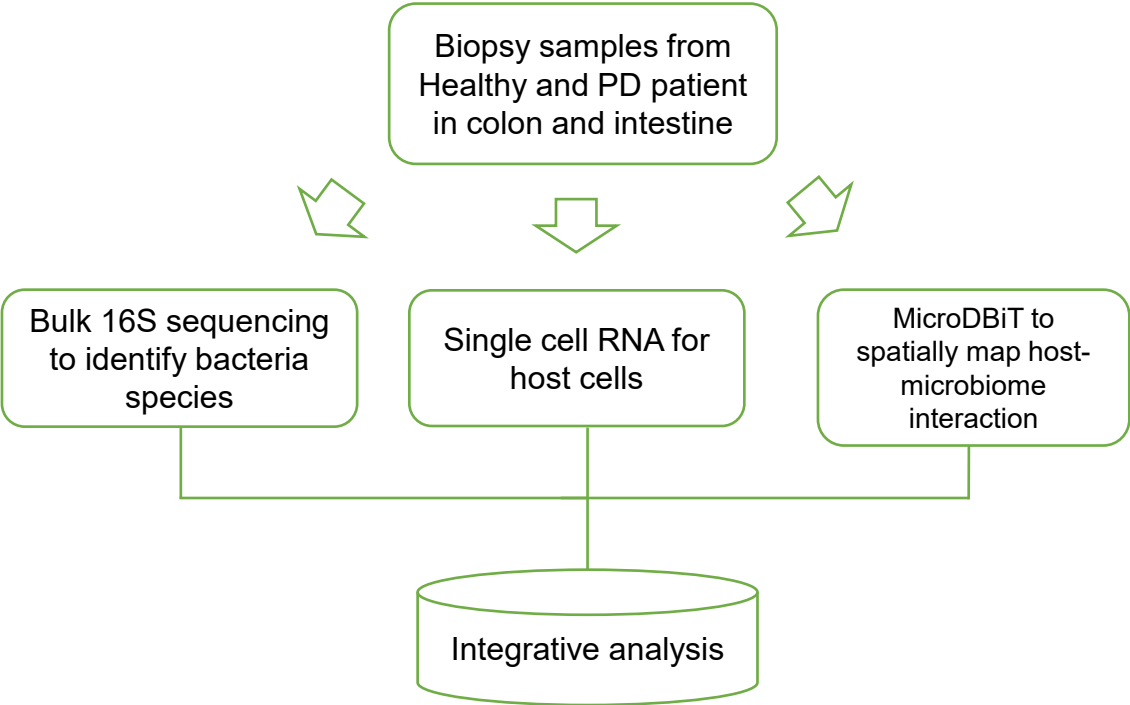


Figure 4. Standard workflow for the integrated analysis of spatial microbiome data.