Bench sheet · EnGeL-BIOINF-COMMUNITY

From OTU table to community data: identified OTUs, incidence and shared OTUs between groups (R) · version 1.0.1 (2026-11-17). Full protocol: EnGeL-BIOINF-COMMUNITY. Tick each step when done; write deviations in Notes.

Date	
Operator	
Plate ID / samples	
R and package versions	
Input files (names and dates)	

1. Set up

☐	No.	Step
☐	1	Open the project's R project (paths below are relative to the project folder; do not use `setwd()` with personal paths).
☐	2	Load the packages:

2. Read and join the tables

☐	No.	Step
☐	3	Read the identification table and the curated OTU table, and check the dimensions (OTUs × samples) against the EnGeL-BIOINF-OBITOOLS4 report:
☐	4	Give both tables the same OTU column name and keep only OTUs that have an identification:
☐	5	Keep only the sample columns, with OTU names as row names:
!		**CRITICAL** Every sample column of the OTU table must appear in the sample-group table, spelled the same way. Check that `length(samples)` equals the number of samples you expect.

3. Incidence (presence/absence)

☐	No.	Step
☐	6	Convert read counts to presence/absence (1/0) and save the incidence table:

4. OTUs shared between groups

☐	No.	Step
☐	7	List, for each group, the OTUs present in at least one of its samples. Negative controls are never counted in a sample group:
☐	8	Draw and save the Venn diagram (8 × 6 inches, 300 dpi):

Notes / deviations
