

Guide:

This information matches the R scripts in the repository with the thesis chapter used in to produce the results. My thesis has three data chapters (Chapter 3 through 5).

Chapter 3: CORE AND DIFFERENTIALLY ABUNDANT BACTERIAL TAXA IN THE RHIZOSPHERE OF FIELD GROWN BRASSICA NAPUS GENOTYPES: IMPLICATIONS FOR CANOLA BREEDING

- Script file: **Summary_statistics_canola_sequence_data.R**

Taxonomic characterization (Appendices A – C).

- Script file: **core_genera.R**

B. napus rhizosphere core taxa (Tables 3.2 – 3.4 and Appendix D).

- Script files: **alpha_diversity_genetic_distance_heritability.R**

Genotype variation in alpha diversity measures (Figure 3.2).

Microbial patterns among B. napus genotypes.

Relationship between B. napus genotypes and rhizosphere microbial composition (Figure 3.3).

Heritability of microbial attributes (Tables 3.5 – 3.6).

- Script file: **differential_abundance.R**

Differentially abundant bacterial genera (Tables 3.7 and 3.8, Figure 3.4, Appendices E, F, G).

Chapter 4: ROOT GROWTH DYNAMICS, DOMINANT RHIZOSPHERE BACTERIA, AND CORRELATION BETWEEN DOMINANT BACTERIAL GENERA AND ROOT TRAITS THROUGH BRASSICA NAPUS DEVELOPMENT

- Script file: **root_growth_dynamics_dominat_taxa.R**

B. napus root growth dynamics across the growing season (Table 4.1, Figure 4.1 and Appendices H, I).

Dominant bacterial taxa based on frequency of occurrence (Table 4.2 and Appendices K, L, M, N).

Dominant bacterial taxa based on mean relative abundance (Figures 4. 2, 4.3, 4.4).

Proteobacteria to Acidobacteria ratios across growth stages.

Correlations between canola root traits and potentially growth promoting and dominant. genera under field conditions (Figures 4.5 and 4.6).

Correlation of rhizosphere bacteria with soil conditions and weather variables (Appendices P and Q).

Chapter 5: BRASSICA NAPUS RHIZOSPHERE BACTERIAL COMMUNITY ASSEMBLY: DRIVER AND CORE-HUB COMMUNITIES ACROSS GROWTH STAGES AND BETWEEN GENOTYPES.

- Script file: **Cooccurrence_network_analysis.R**

B. napus rhizosphere bacterial network complexity through plant development (Table 5.1, Appendix R).

Core-hub communities in *B. napus* rhizosphere microbial community and their conservation across growth stage (Figures 5.1, 5.2, 5.3).

Potential driver bacterial genera in *B. napus* rhizosphere at different growth stages (Tables 5.2, 5.3, 5.4, 5.5, Appendices S, T, U).

Dominant metabolic pathways and functional features of driver genera across *B. napus* growth stages (Tables 5.6 and 5.7, Appendices V, W, X, Y, Z, and AA).

Rhizosphere bacterial network complexity in genetically distinct *B. napus* genotypes (Table 5.8).

Core-hub communities in the rhizosphere of genetically distinct *B. napus* genotypes (Figure 5.4).

Potential driver genera resulting in microbial network variations between genetically distinct genotypes (Appendix AB).

Dominant metabolic pathways and functional features of driver genera in *B. napus* breeding lines (Tables 5.9 and 5.10, Appendices AC and AD).