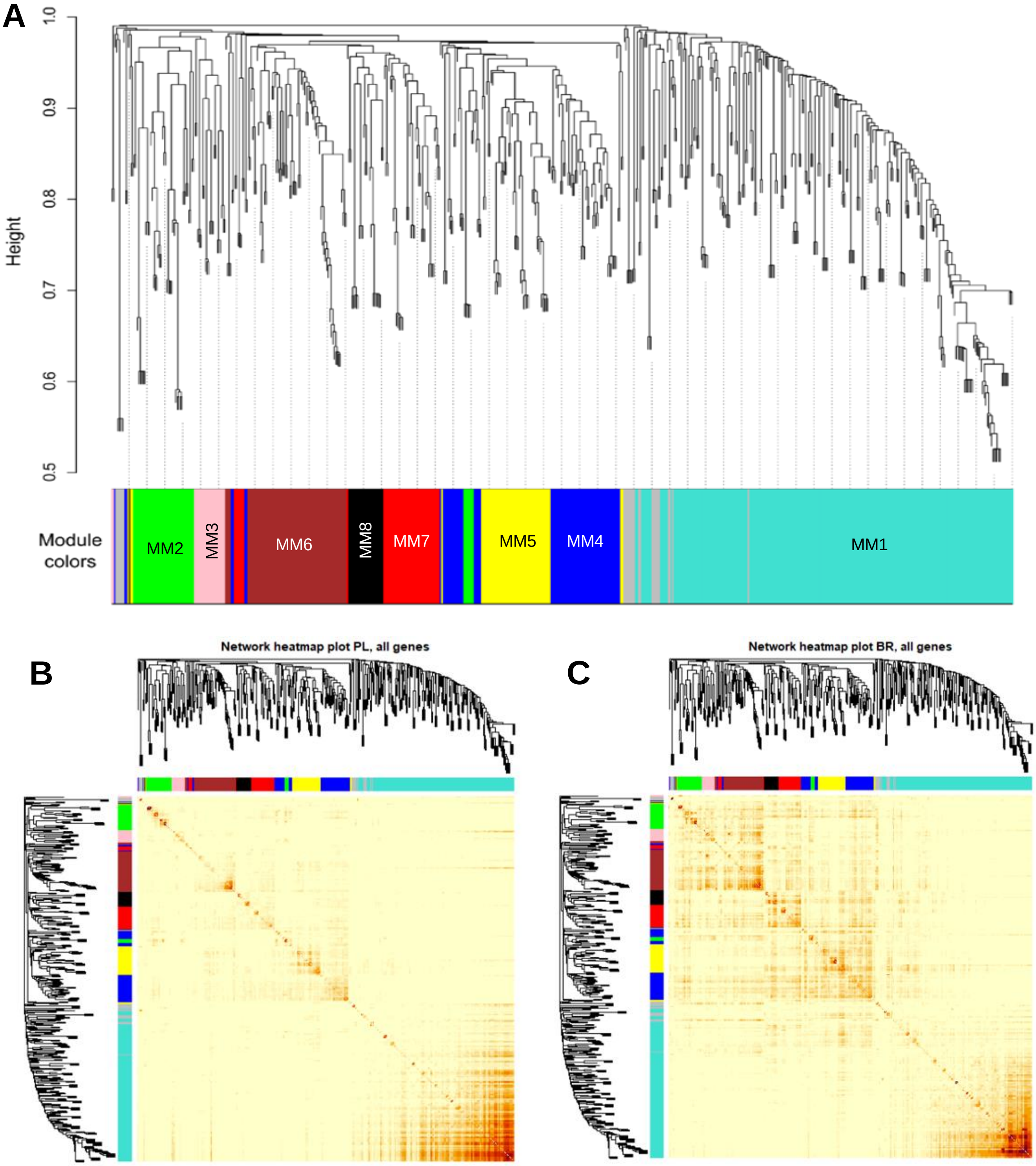

Fig. S1. A: Consensus gene dendrogram. Using a signed network where modules represent positively correlated taxonomic units (power >0.80), a total of eight distinct microbiome modules (MM1-MM8) were identified. **B, C**: Heatmaps illustrating the microbiome networks in placebo (PL) and nitrate conditions (BR). A darker colour indicates a high overlap between the taxonomic units. The horizontal and vertical colour blocks represent the modules MM1-MM8.