Supplementary Figures

Does Gut Microbiota Dysbiosis Impact the Metabolic Alterations of Hydrogen Sulfide and Lanthionine in Patients with Chronic Kidney Disease?

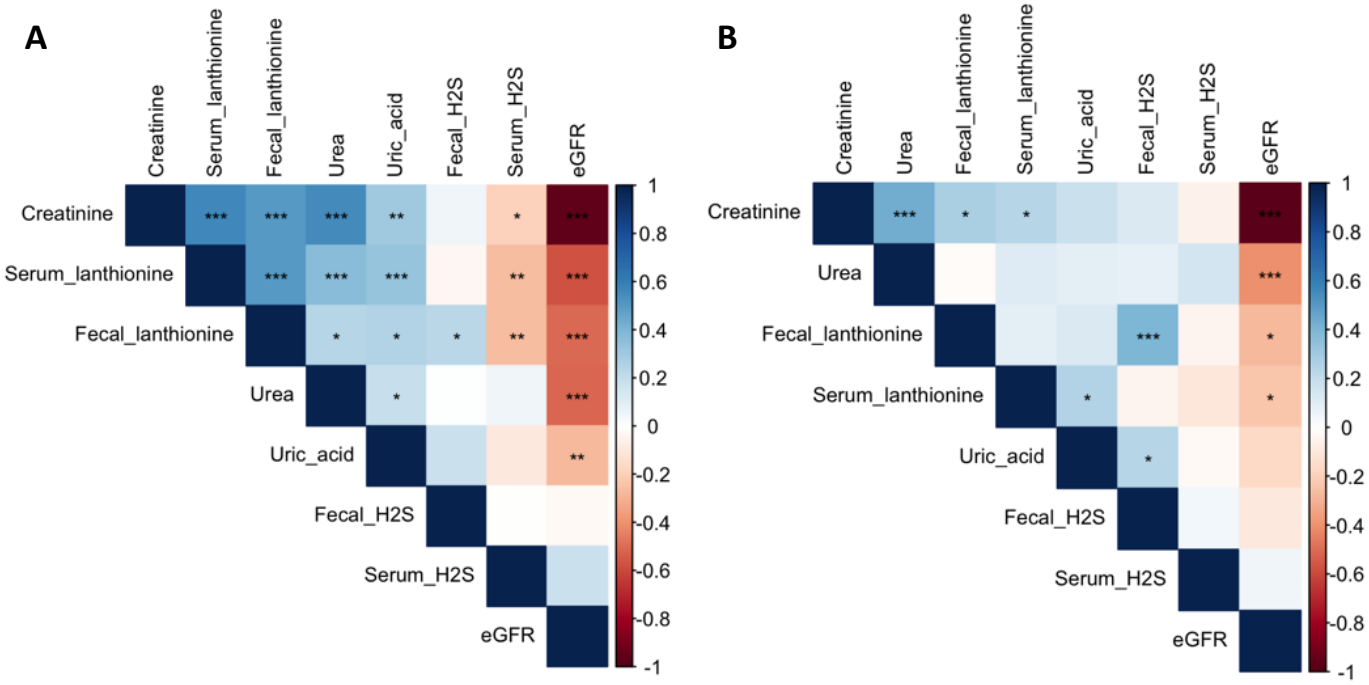

Figure S1: Correlogram shows positive (blue) or negative (red) Spearman's correlation between sulfur metabolites and markers of kidney function (***p ≤ 0.001, **p ≤ 0.01, *p ≤ 0.05). **A)** Correlations across the study cohort, including CKD patients and healthy controls. **B)** Correlations within the CKD population, encompassing non-dialysis, hemodialysis, and transplant patients. eGFR: estimated Glomerular Filtration Rate.

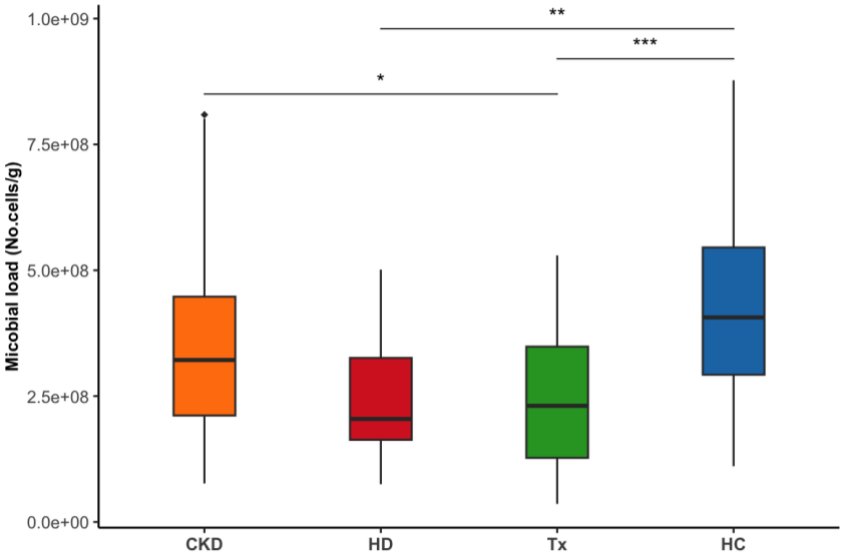

Figure S2: Microbial load distribution across the study cohort (***p ≤ 0.001, **p ≤ 0.01, *p ≤ 0.05). CKD: non-dialysis Chronic Kidney Disease (orange), HD: Hemodialysis (red), Tx: Kidney transplant (green), HC: Healthy Controls (blue).

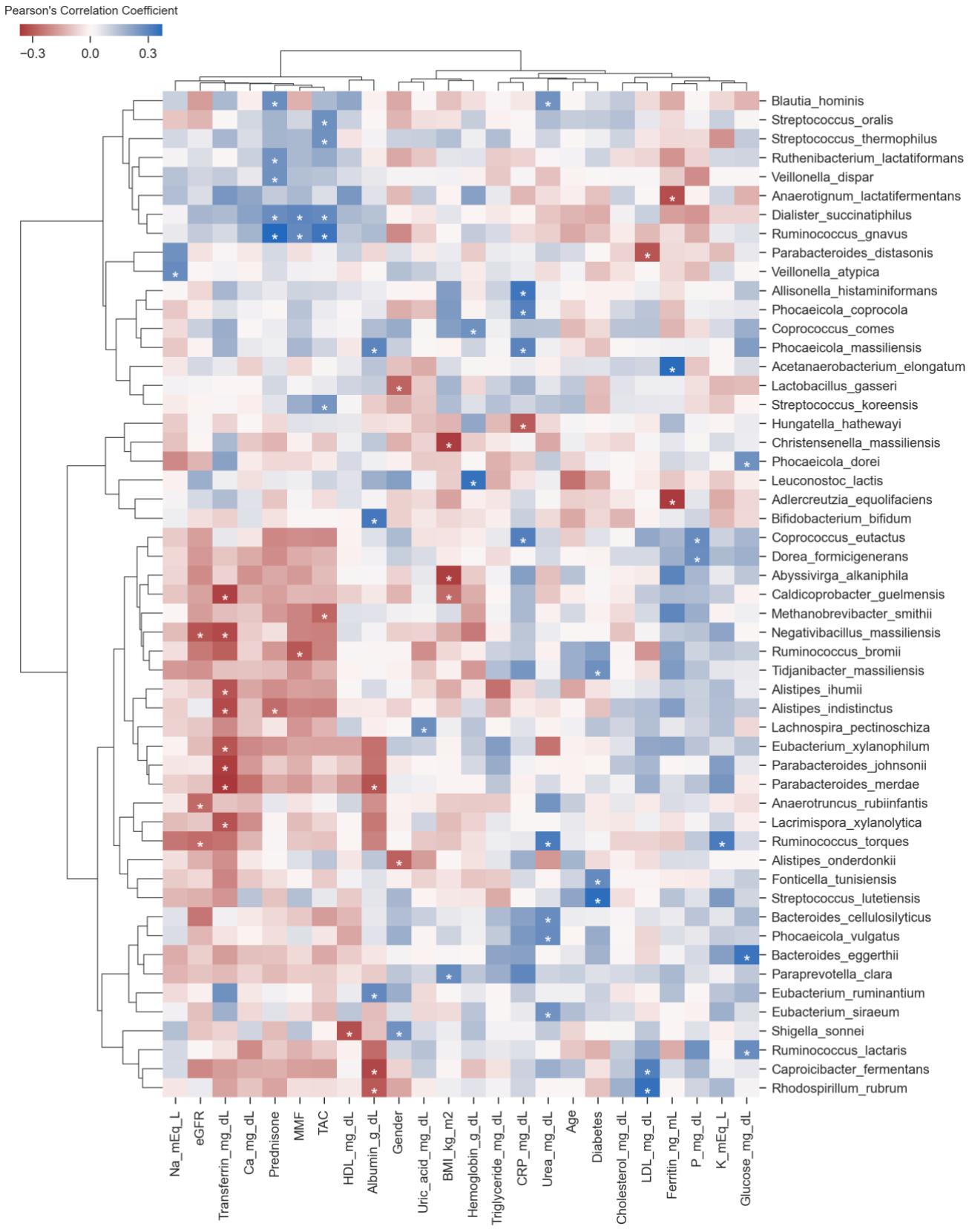

Figure S3: Correlogram of bacterial species and metadata variables shows positive (blue) or negative (red) Pearson's correlation on normalized and standardized abundances and metadata parameters. Only species having at least one significant correlation after 10% two-stage Benjamini–Hochberg FDR were reported. eGFR: estimated glomerular filtration rate, MMF: Mycophenolate mofetil, TAC: Tacrolimus, HDL: High-density lipoprotein, BMI: Body Mass Index, CRP: C-Reactive protein, LDL: Low-density lipoprotein.

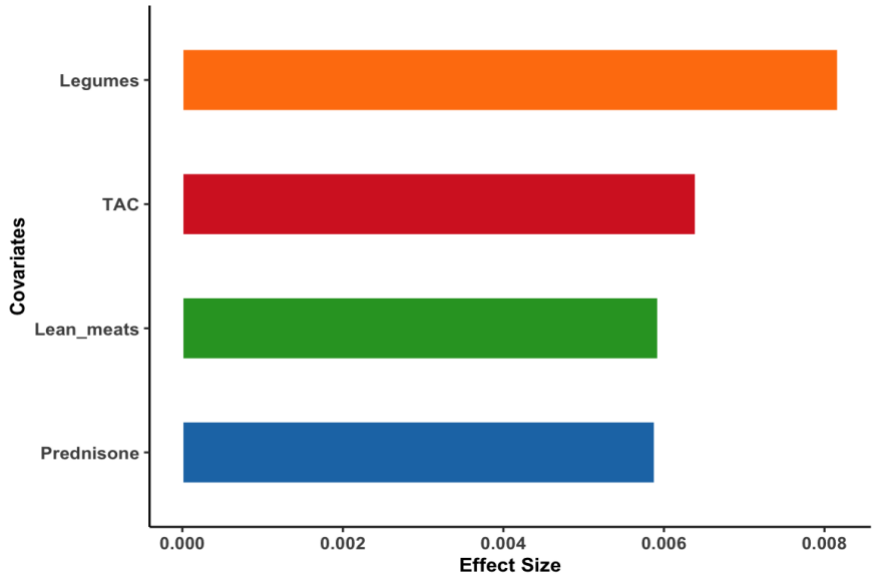

Figure S4: Covariates accounting for about 3% of the inter-individual microbiota community variation observed as determined by single distance-based redundancy analysis (db-RDA) on species-level Bray–Curtis dissimilarity (FDR ≤ 0.05).