



**Figure S3.** Contribution of phenotypic factors to faecal microbiome changes. Shown are the correlations between different phenotypic factors at SHIP-2 and global changes in the faecal microbiome from SHIP-2 to SHIP-3 using **a)** Jaccard distance or **b)** Euclidean distance as measurement of beta diversity. Large positive associations indicate greater variation or instability in the faecal microbiome if the respective factor is distinctly elevated (continuous variables) or positive (binary variables). On the other hand, large negative associations suggest stability of the faecal microbiome. \* indicates significant associations ( $q < 0.05$ ). BMI: Body mass index; eGFR, estimated glomerular filtration rate, HbA1c: Glycated hemoglobin, HDL: High-density lipoprotein; LDL: Low-density lipoprotein. NT-proBNP: N-terminal brain natriuretic peptide. TSH: Thyroid-stimulating hormone.