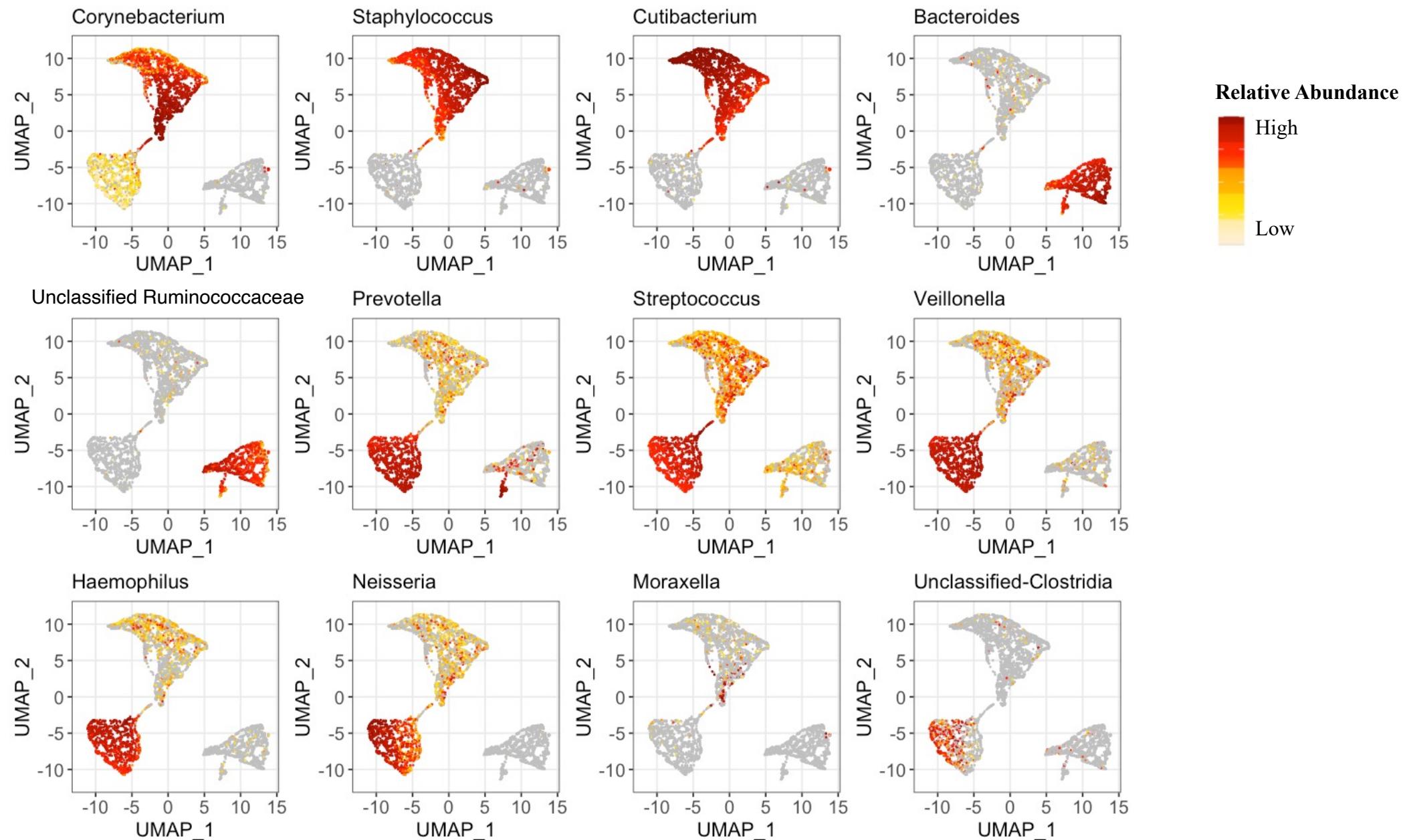
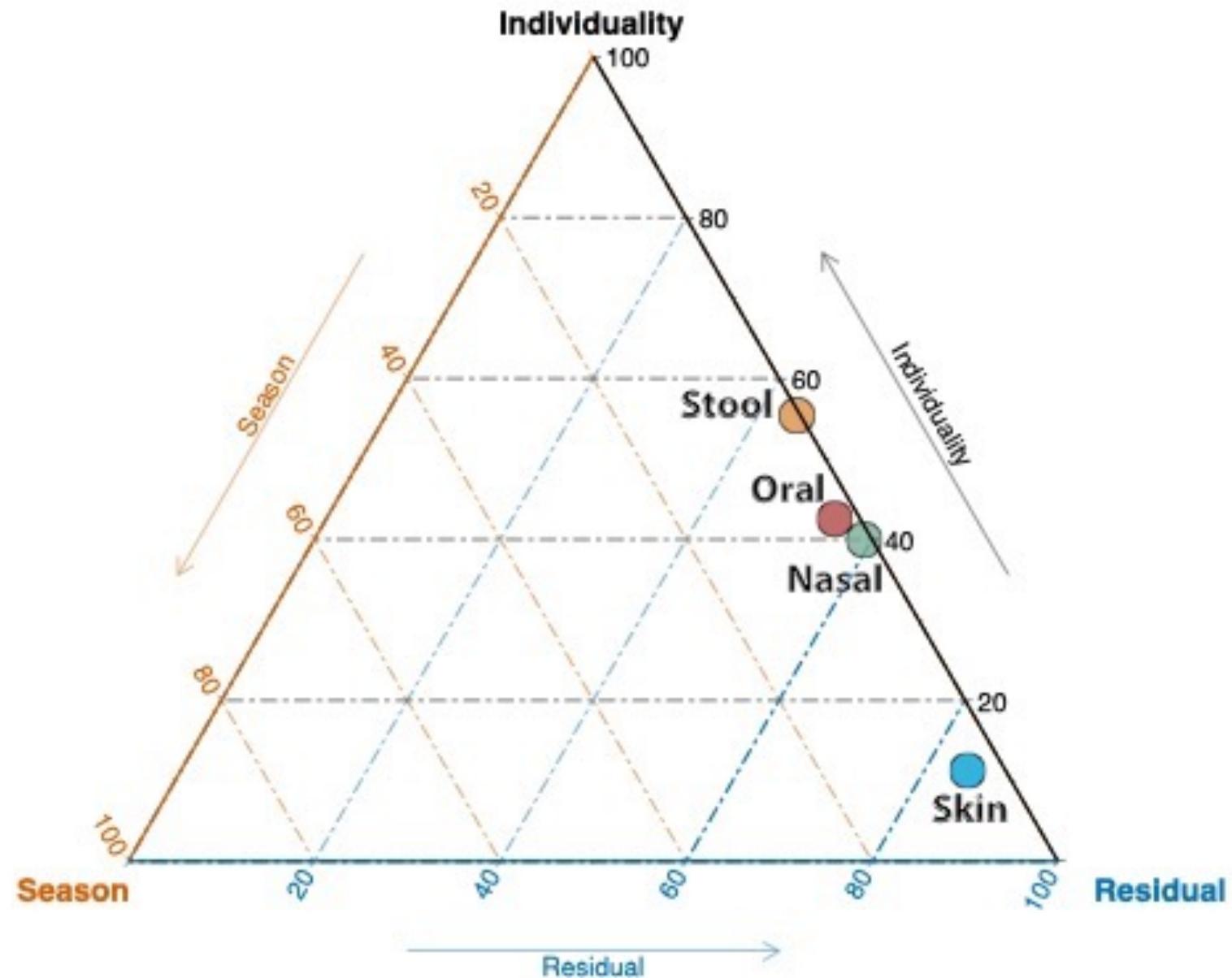


Extended Data Fig. 1: Relative abundance of representative genera on UMAP

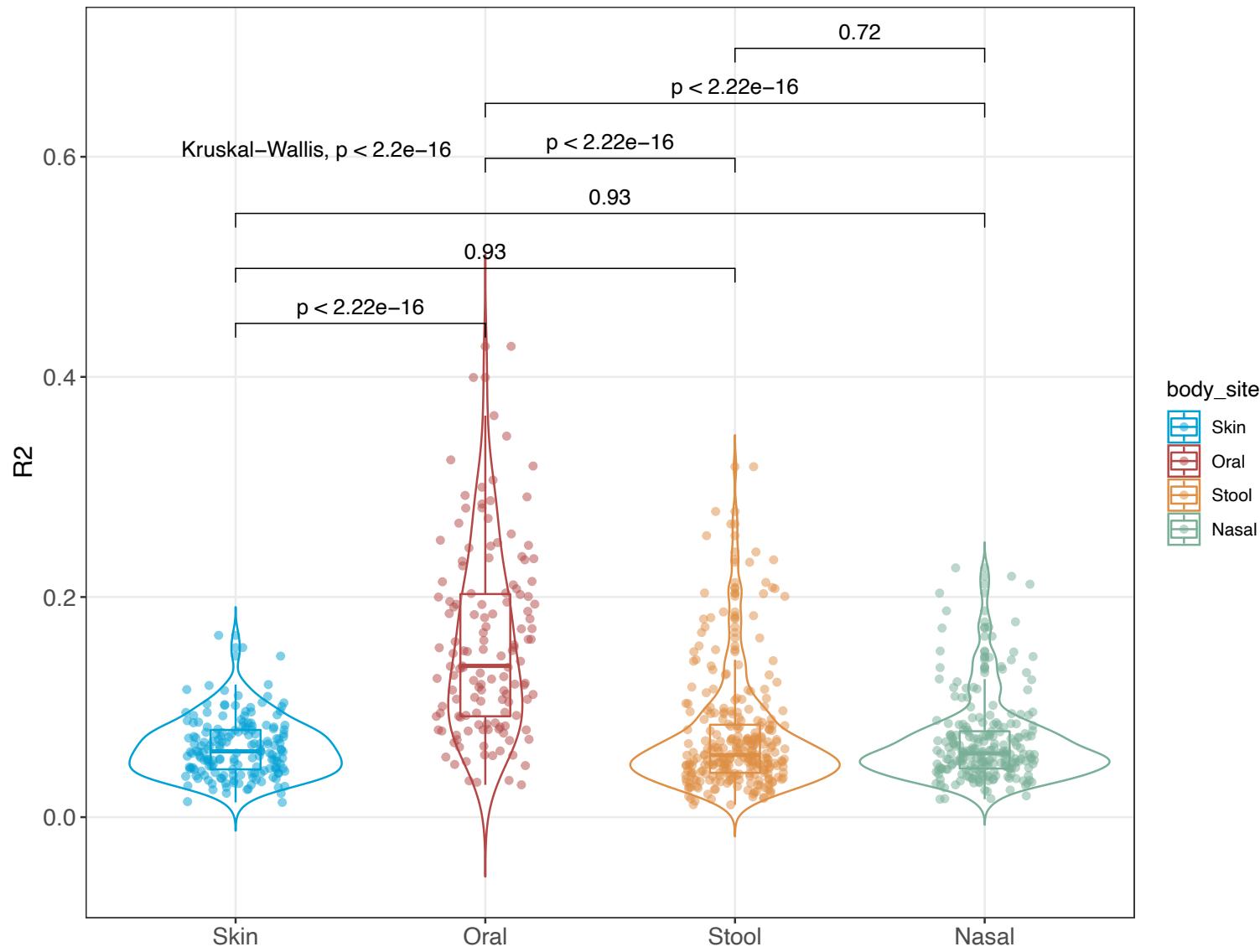


Extended Data Fig. 2: Microbiome variance explained by the individuality, season, and residuals



Extended Data Fig. 3: Microbiome variance explained by diet and exposome

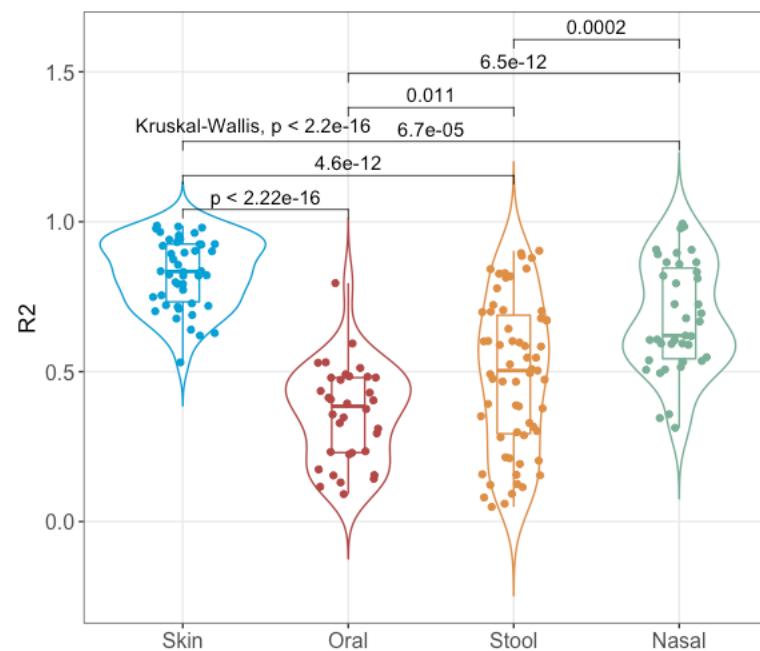
a)



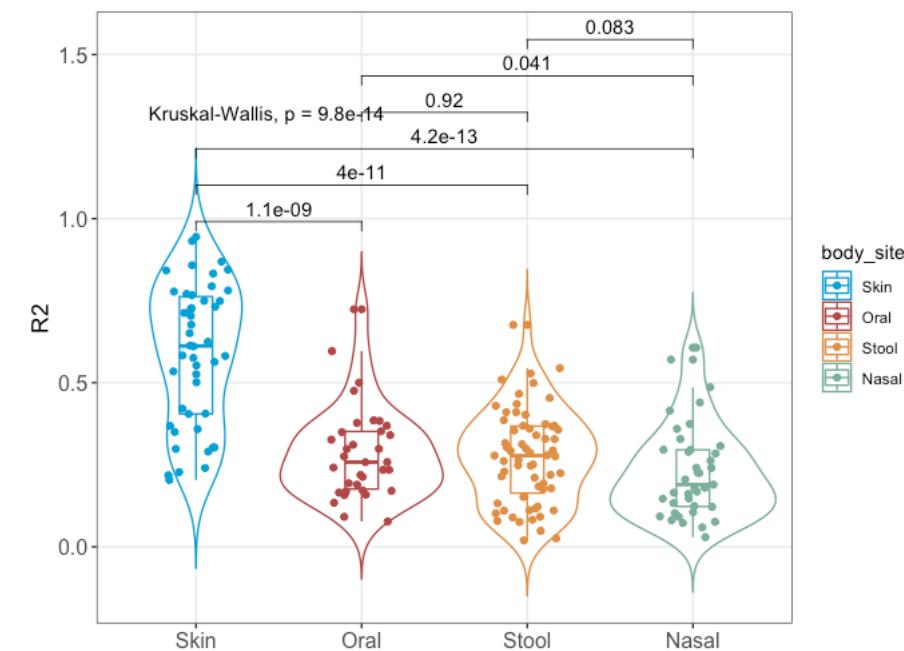
Extended Data Fig. 3: Microbiome variance explained by diet and exposome

b)

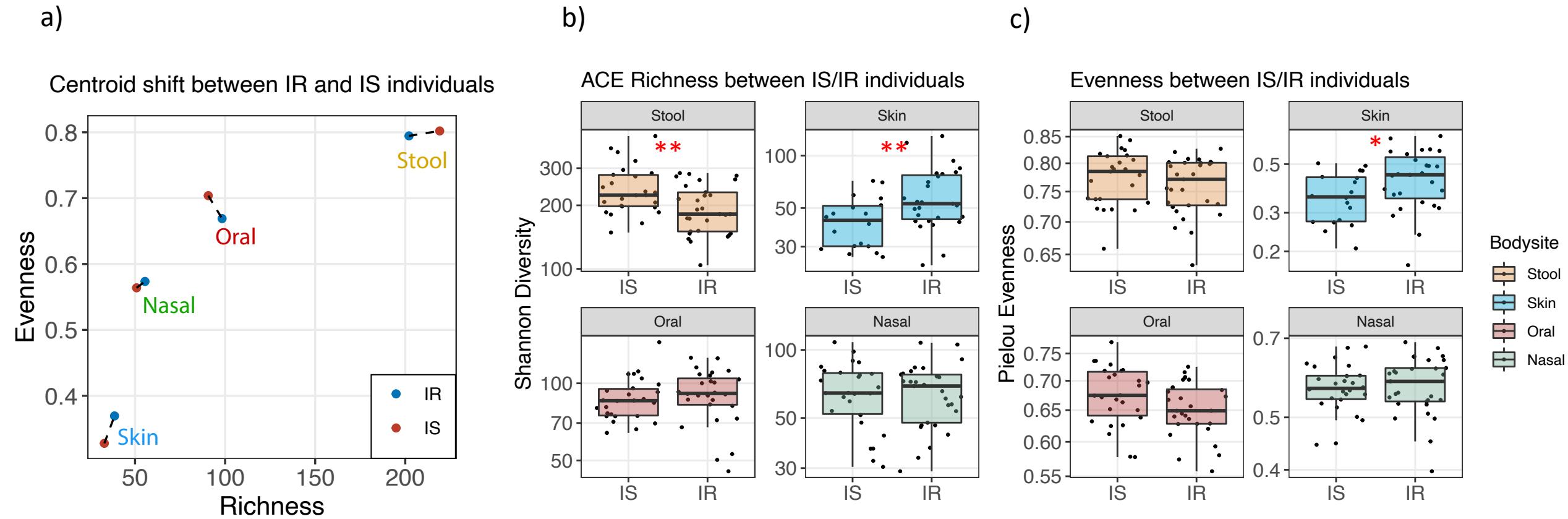
Participant 1



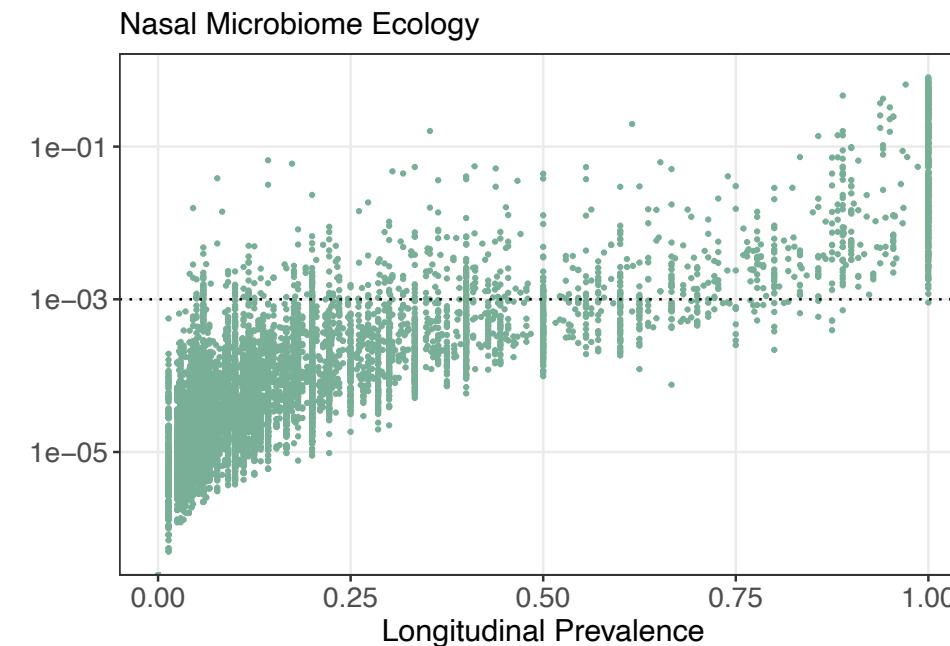
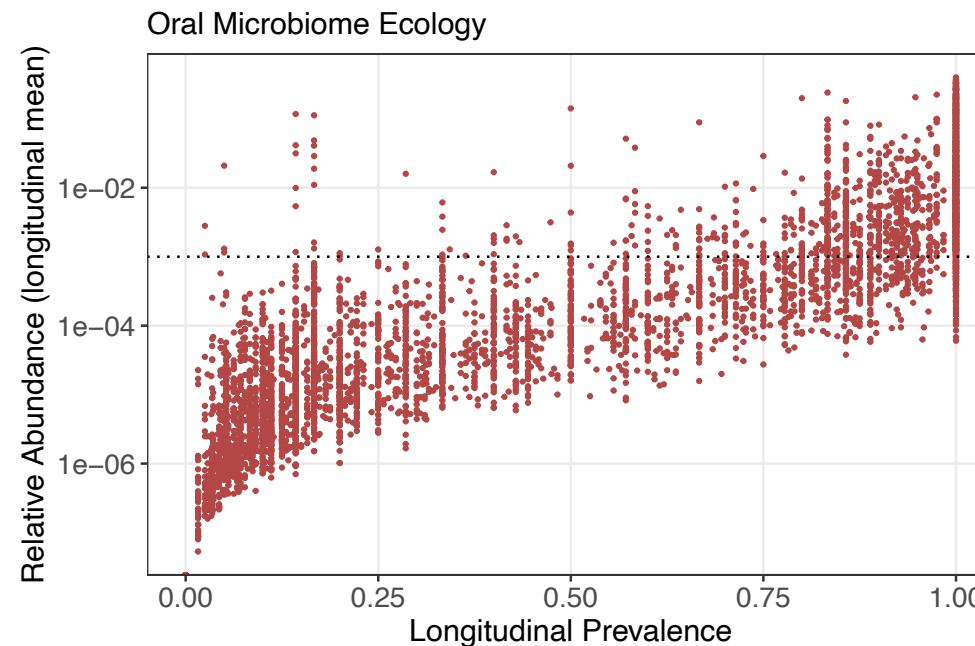
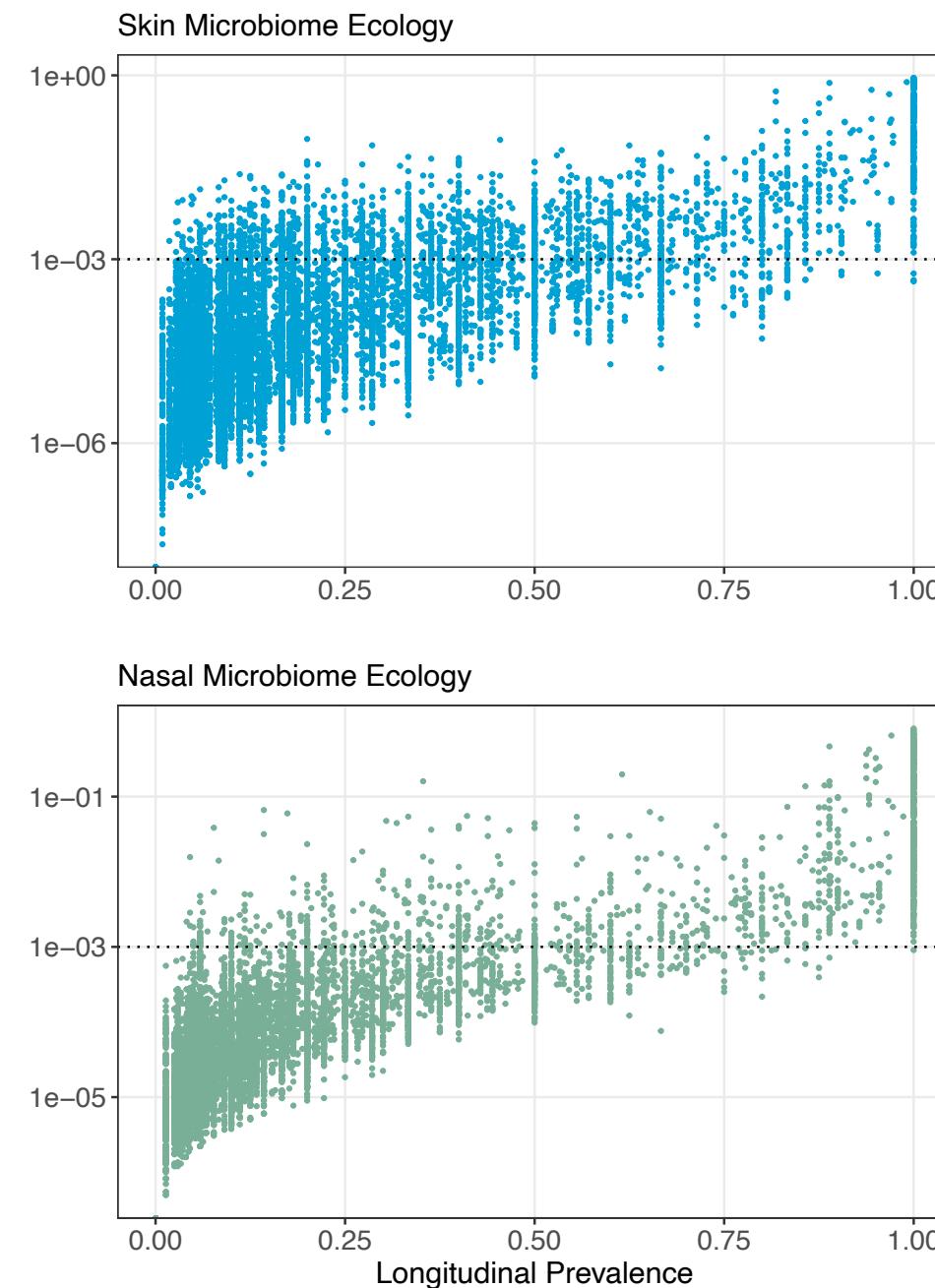
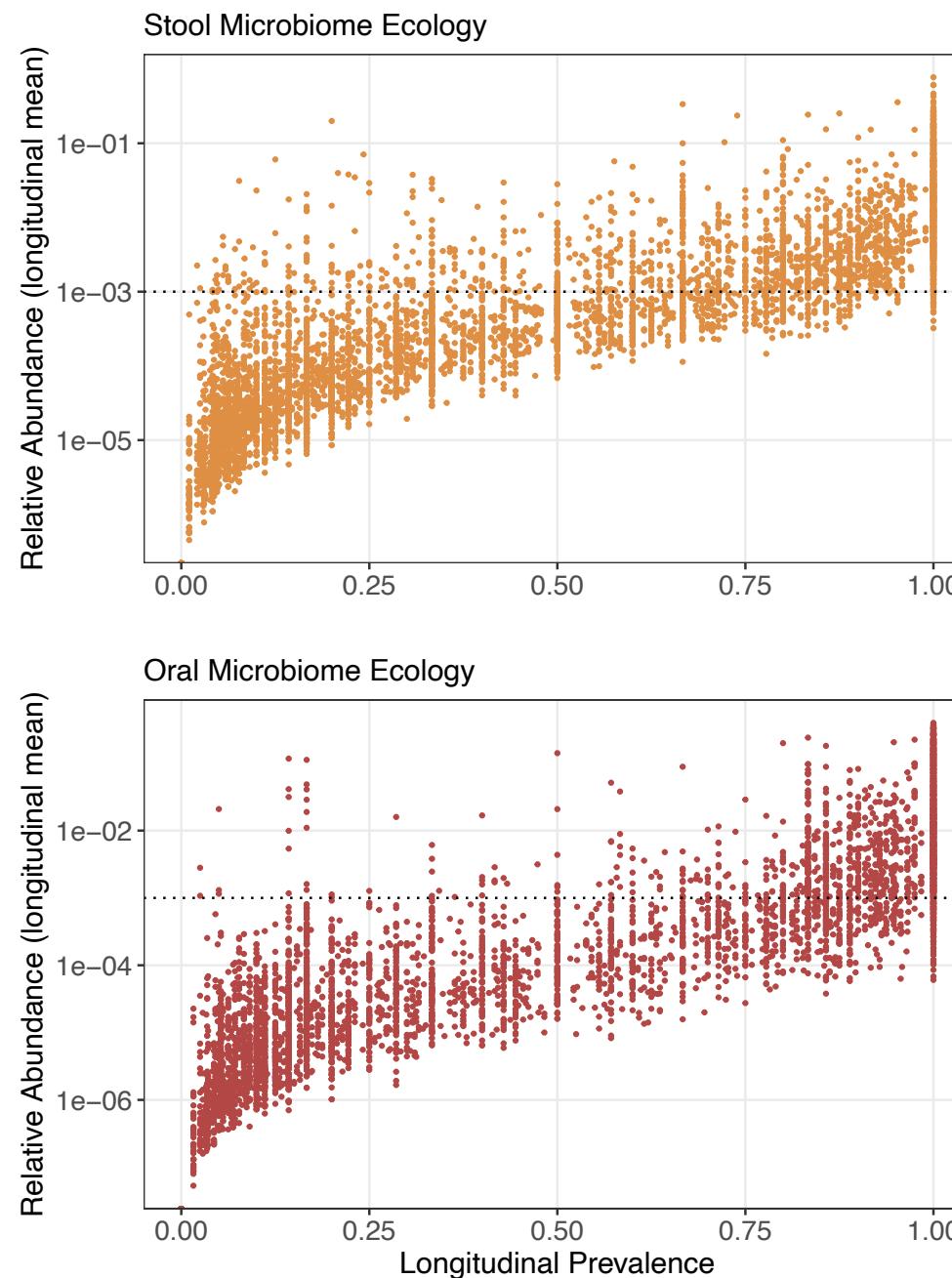
Participant 2



Extended Data Fig. 4: Diversity and evenness shift between IS and IR individuals

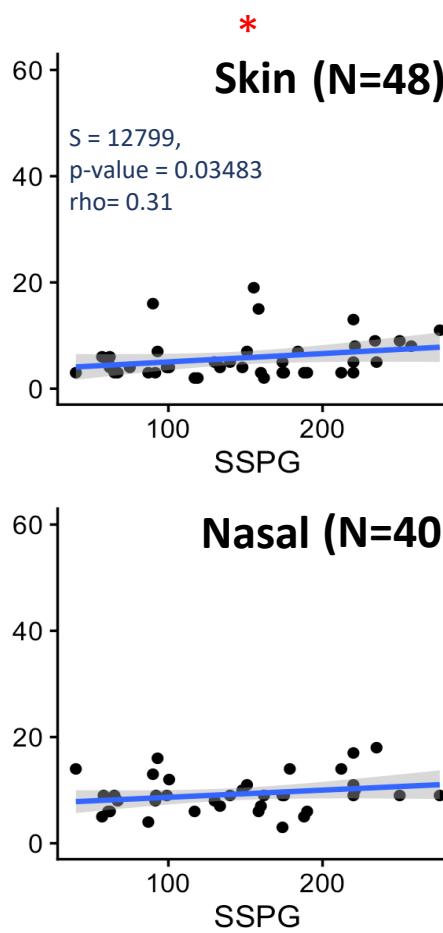
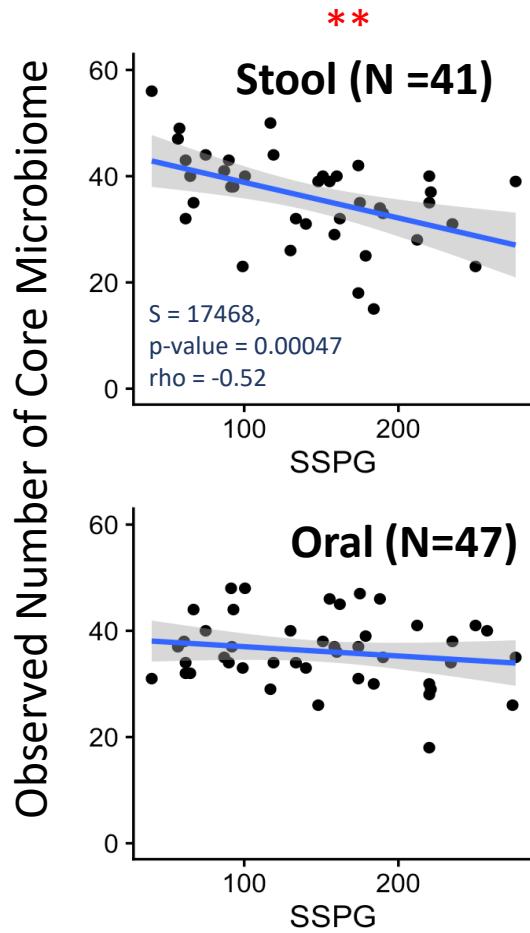


Extended Data Fig. 5: Prevalence by relative abundance plot

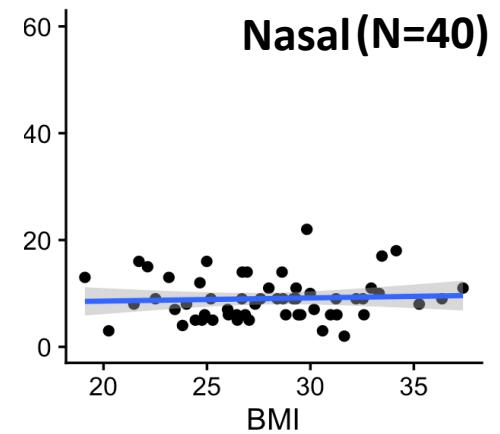
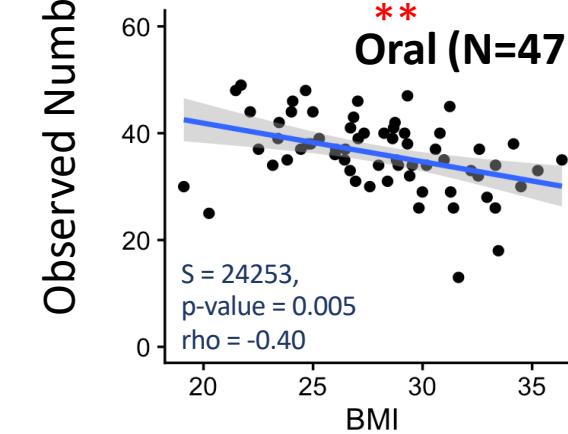
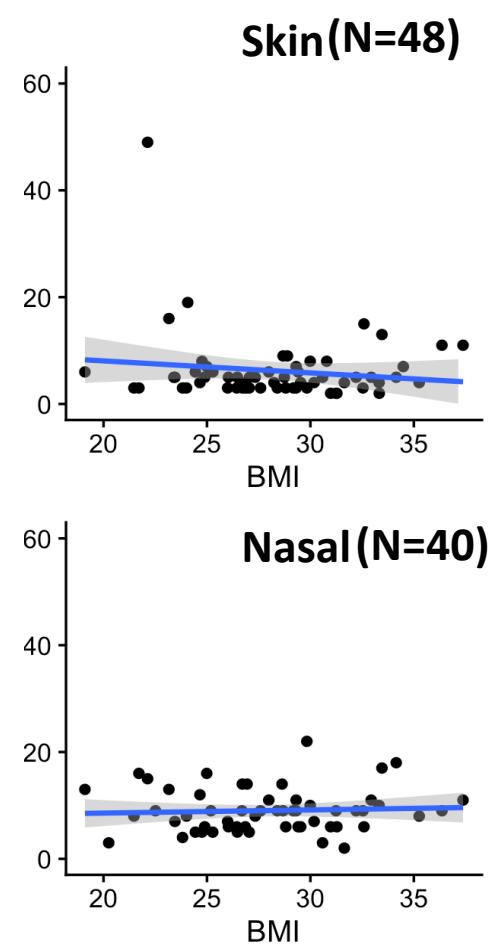
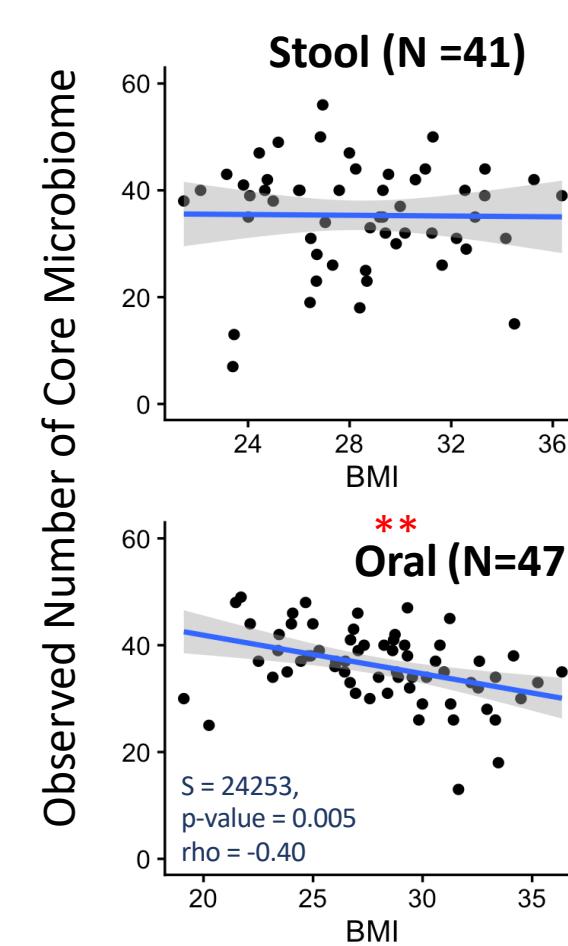


Extended Data Fig.6 Relationship between number of core microbiome, steady-state plasma glucose and body mass index

a)

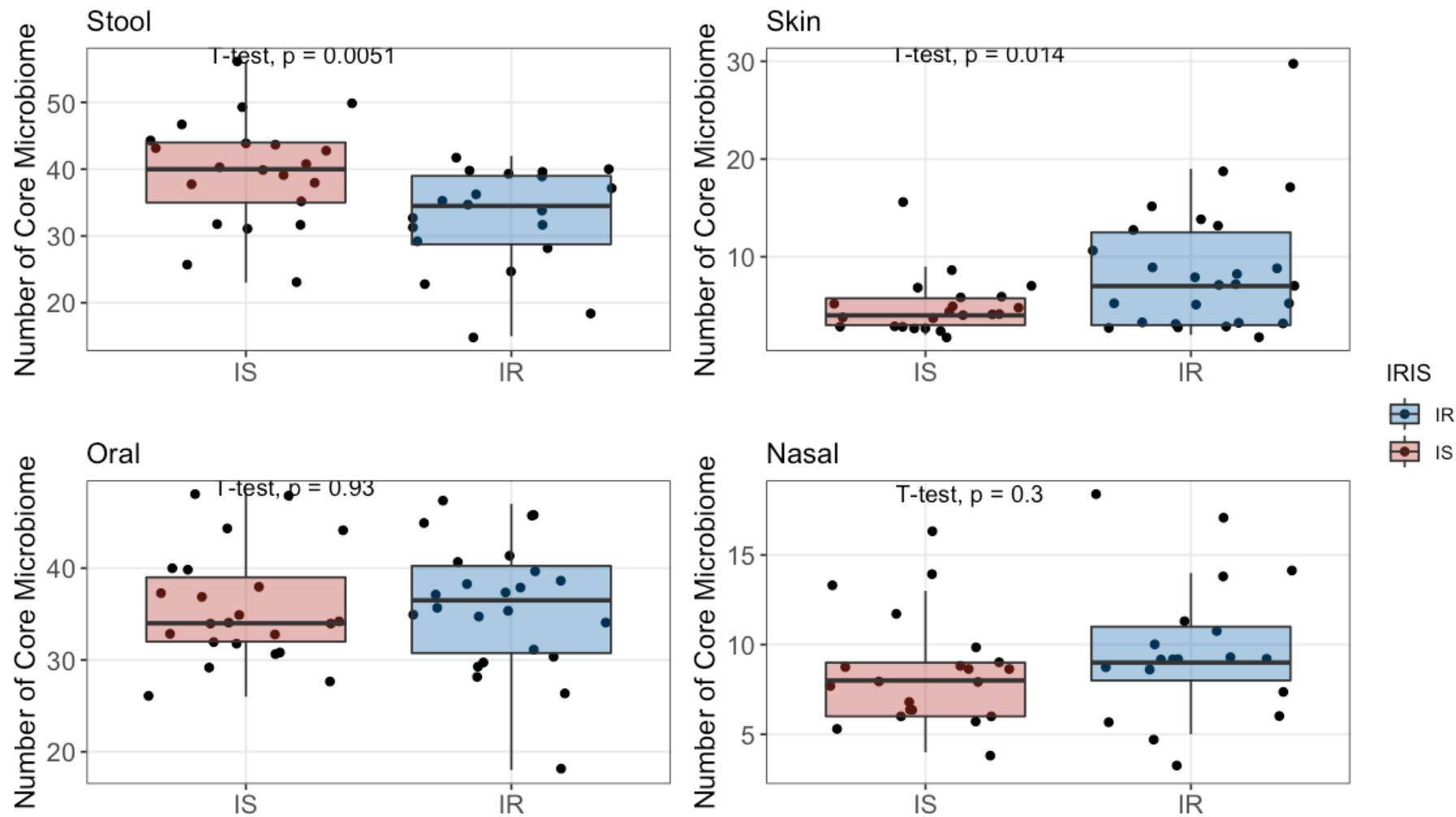


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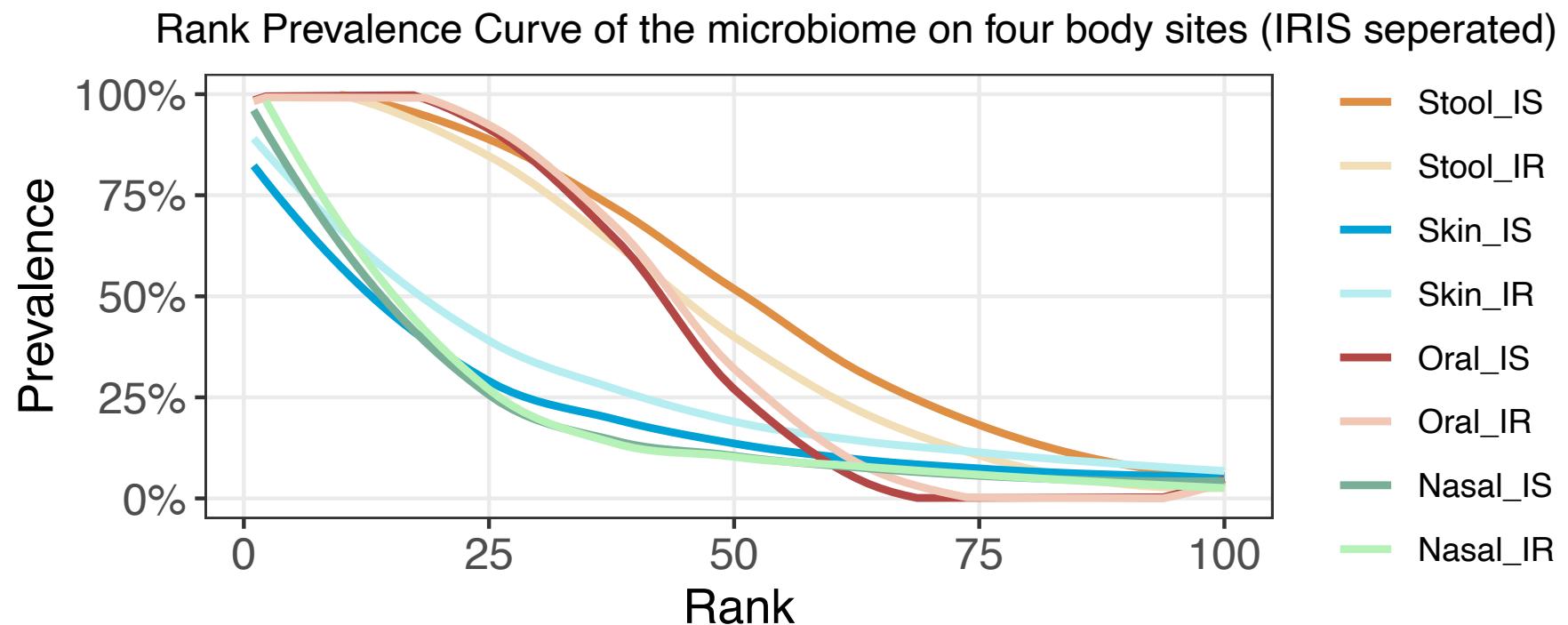


Extended Data Fig. 7: Core Microbiome in IS and IR individuals

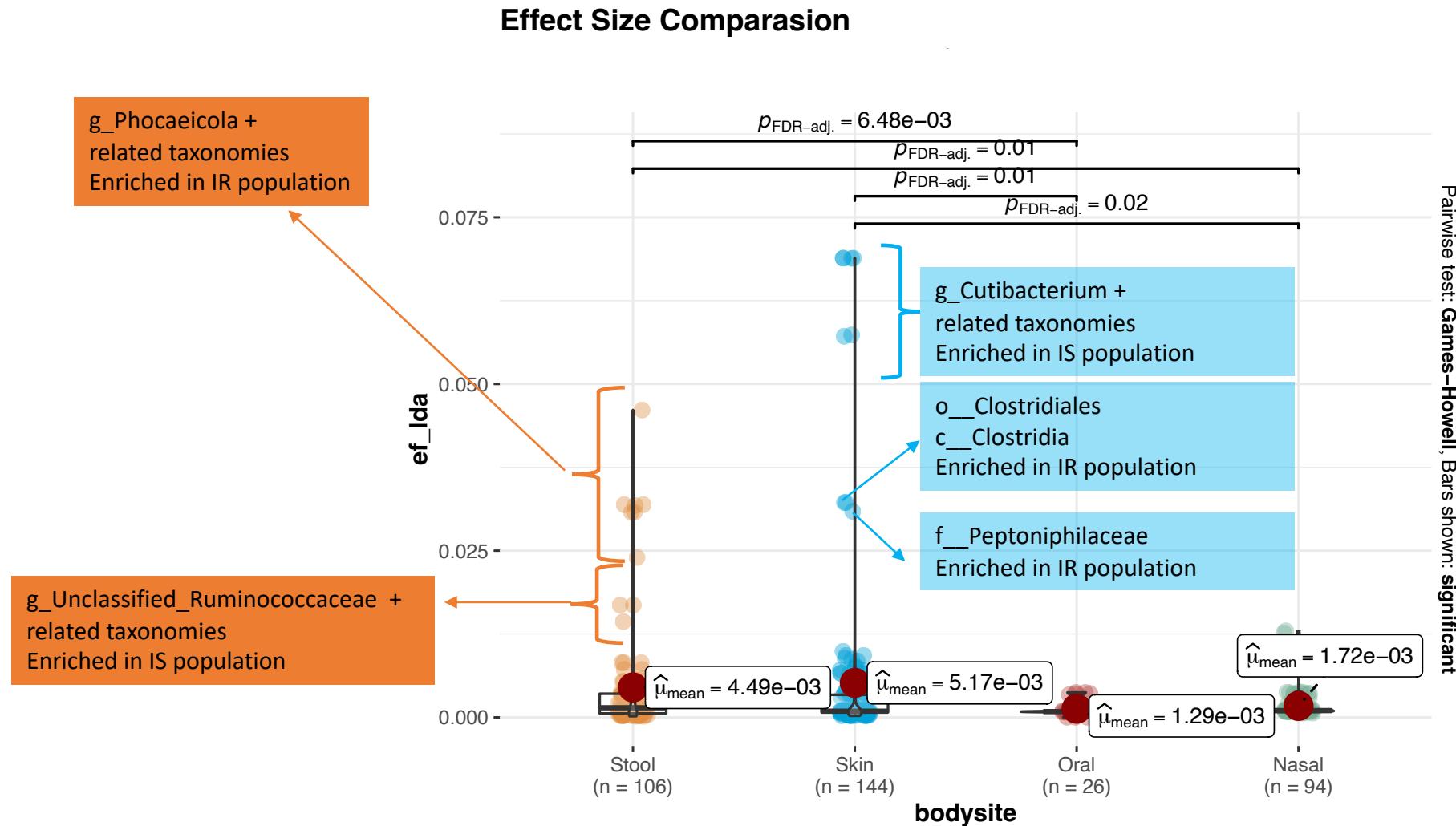
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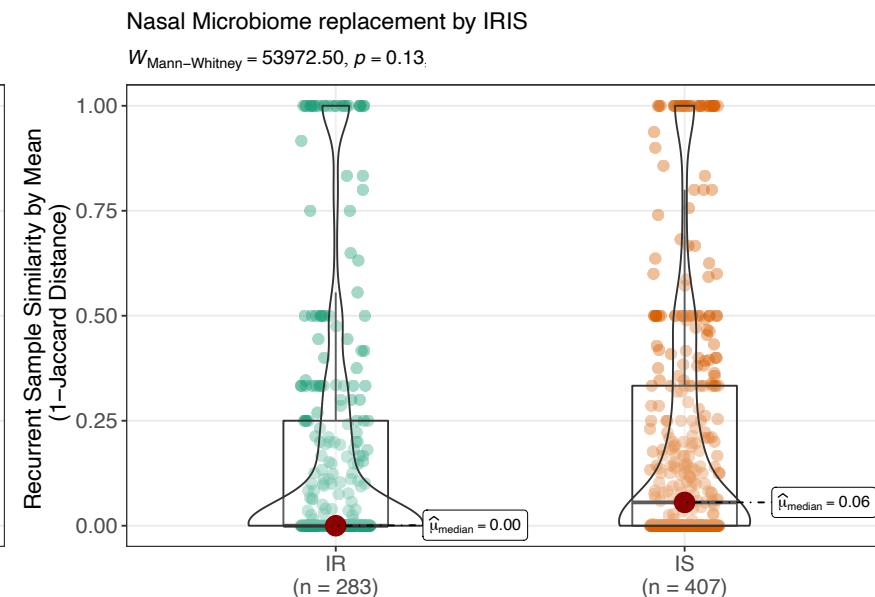
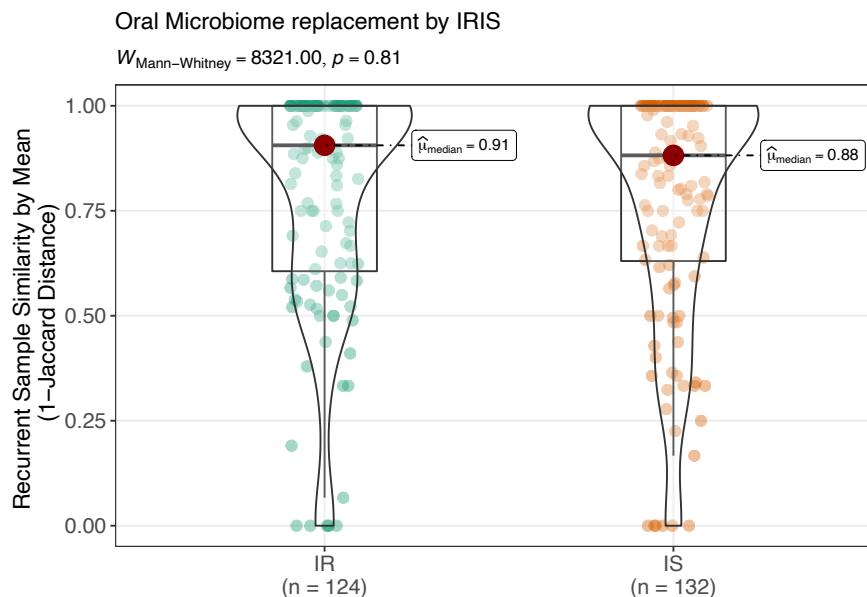
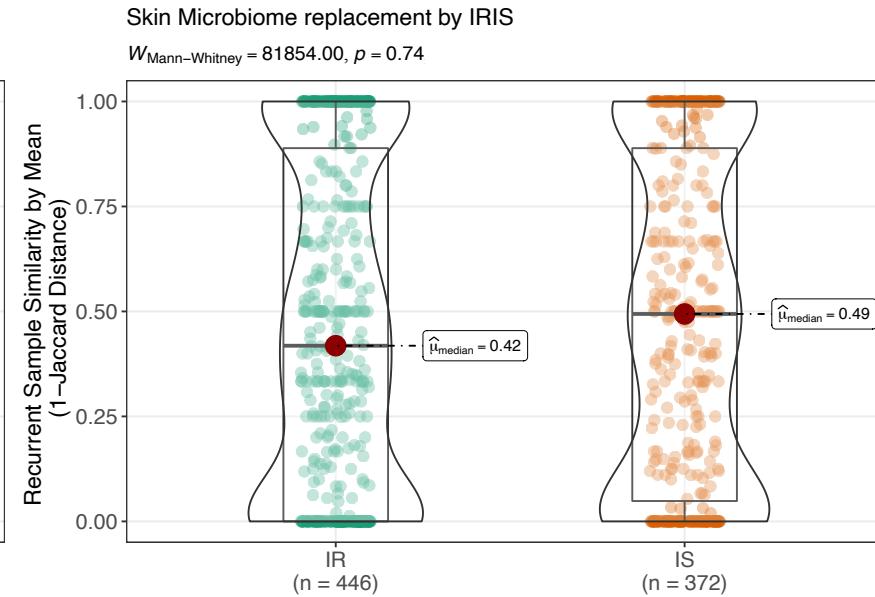
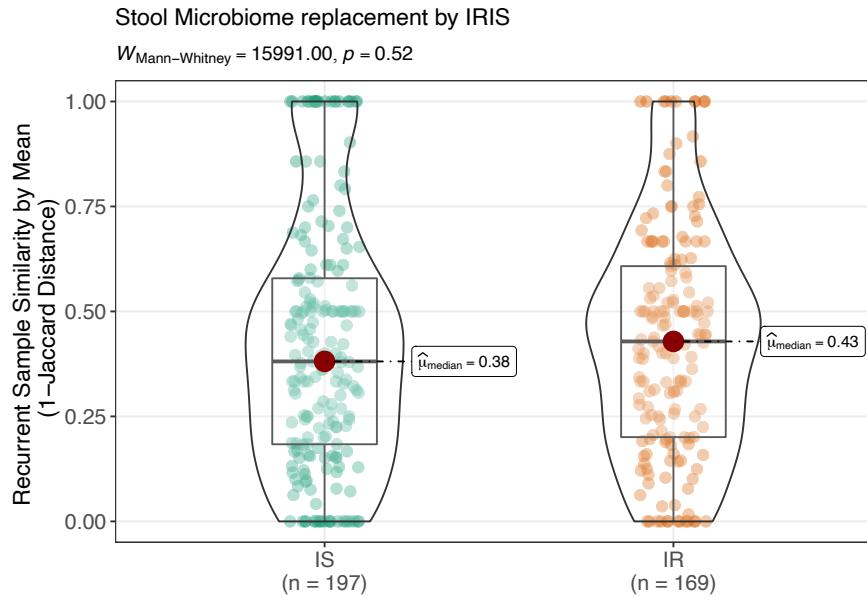
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Extended Data Fig. 8: Effect size of taxa that are significantly differ in relative abundance between IR and IS individuals

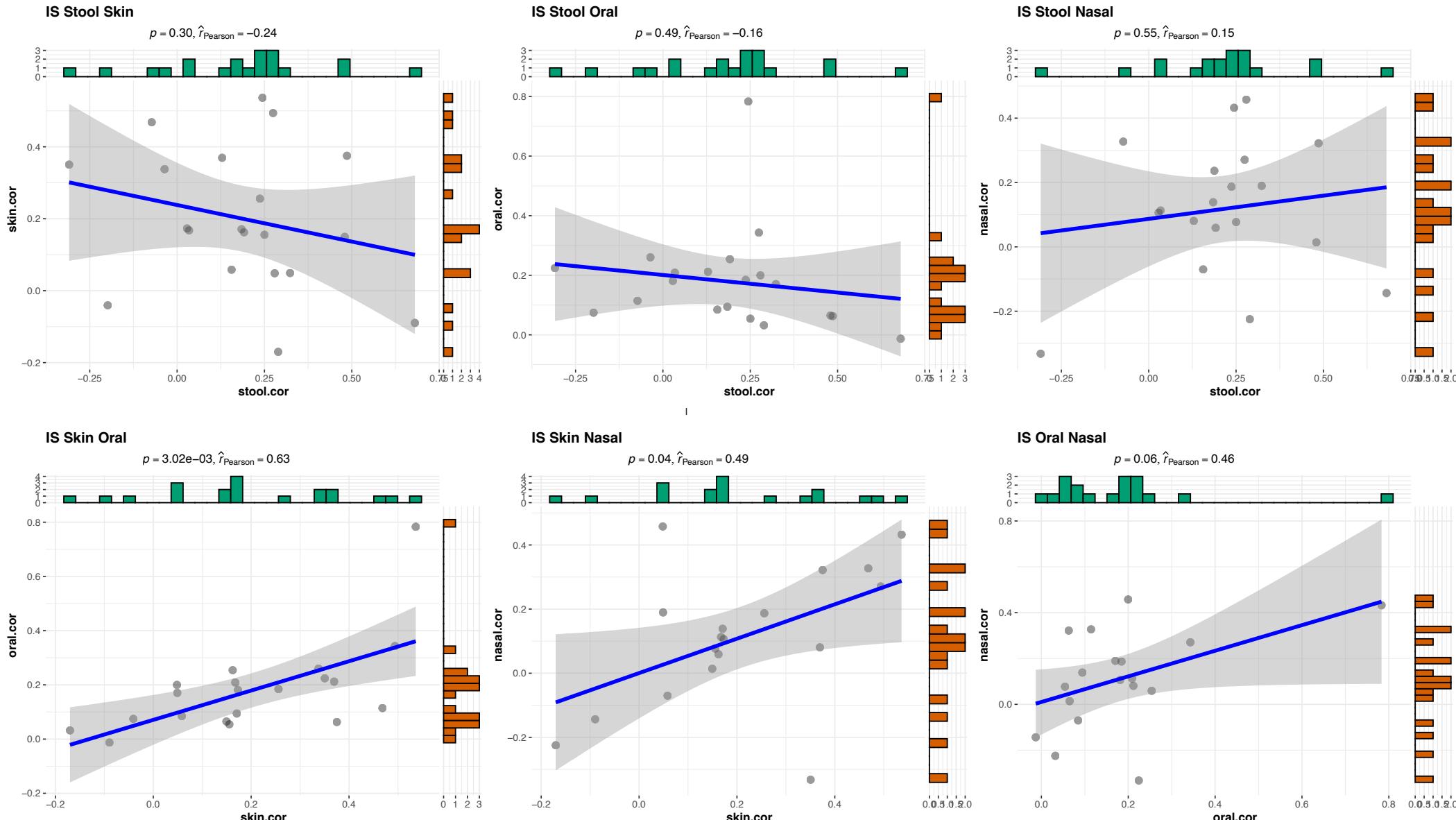


Extended Data Fig. 9: Strain replacement rate by body site in IS and IR individuals

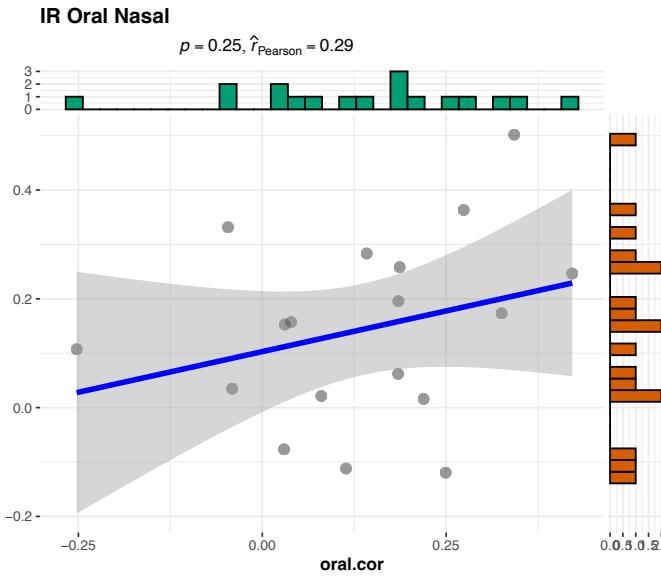
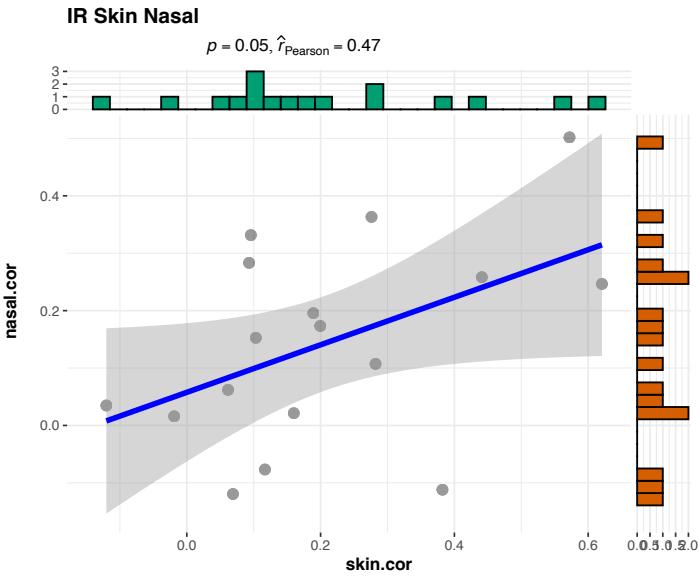
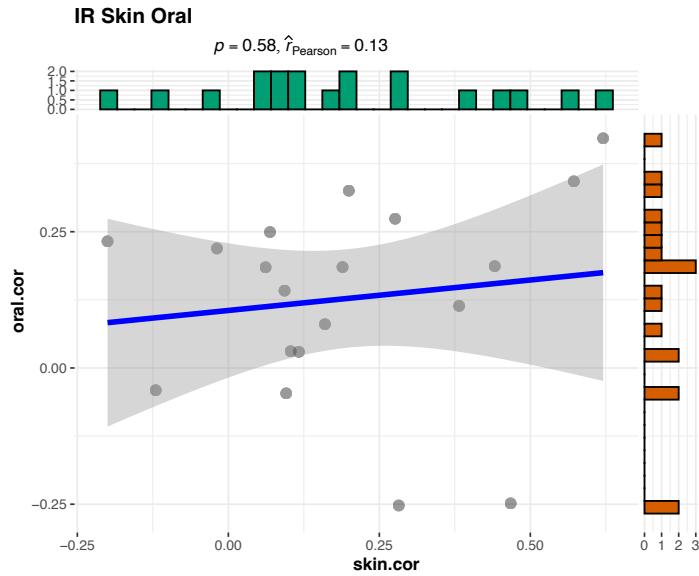
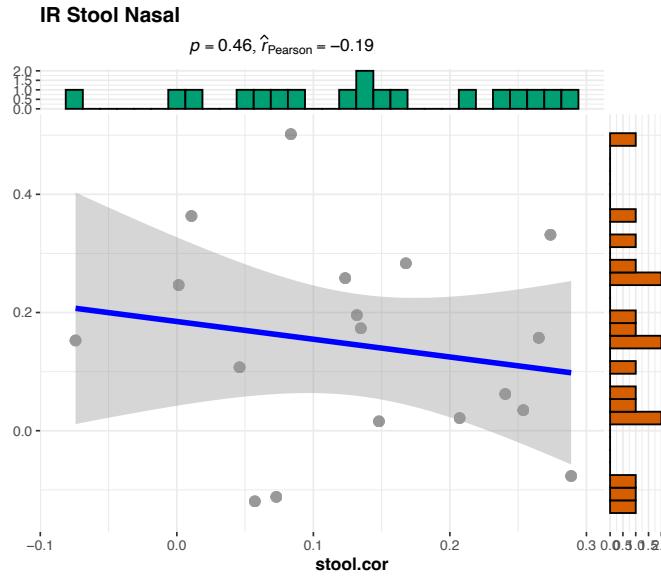
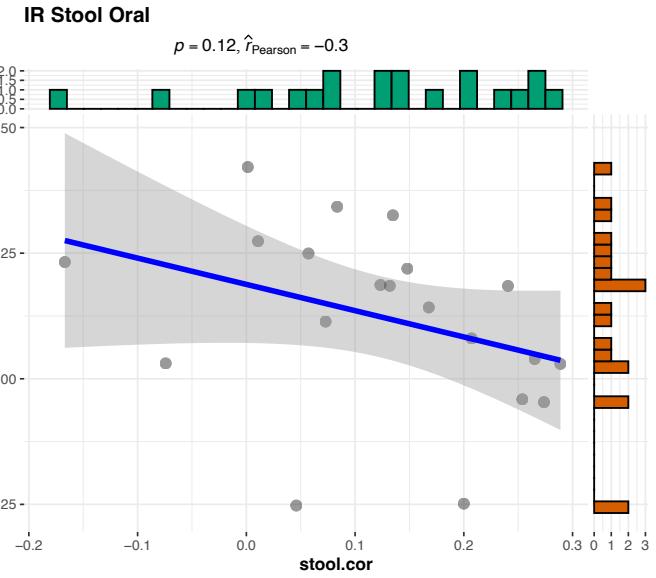
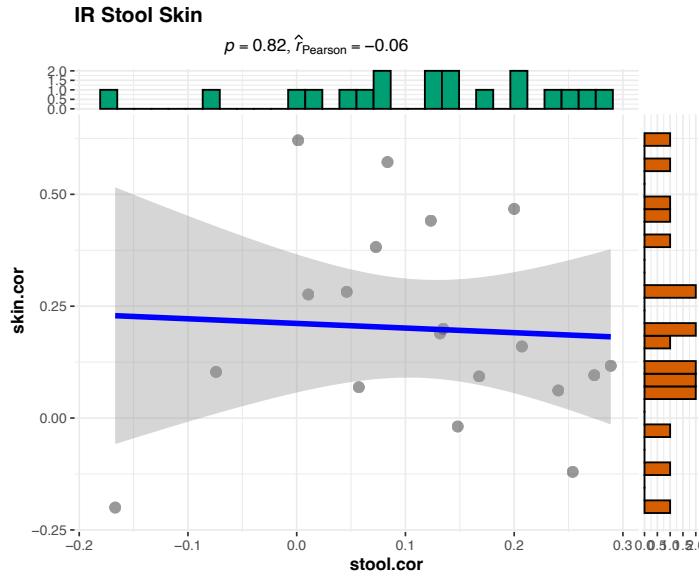


Extended Data Fig. 10: Time-related microbiome stability correlation between body sites among IR and IS individuals

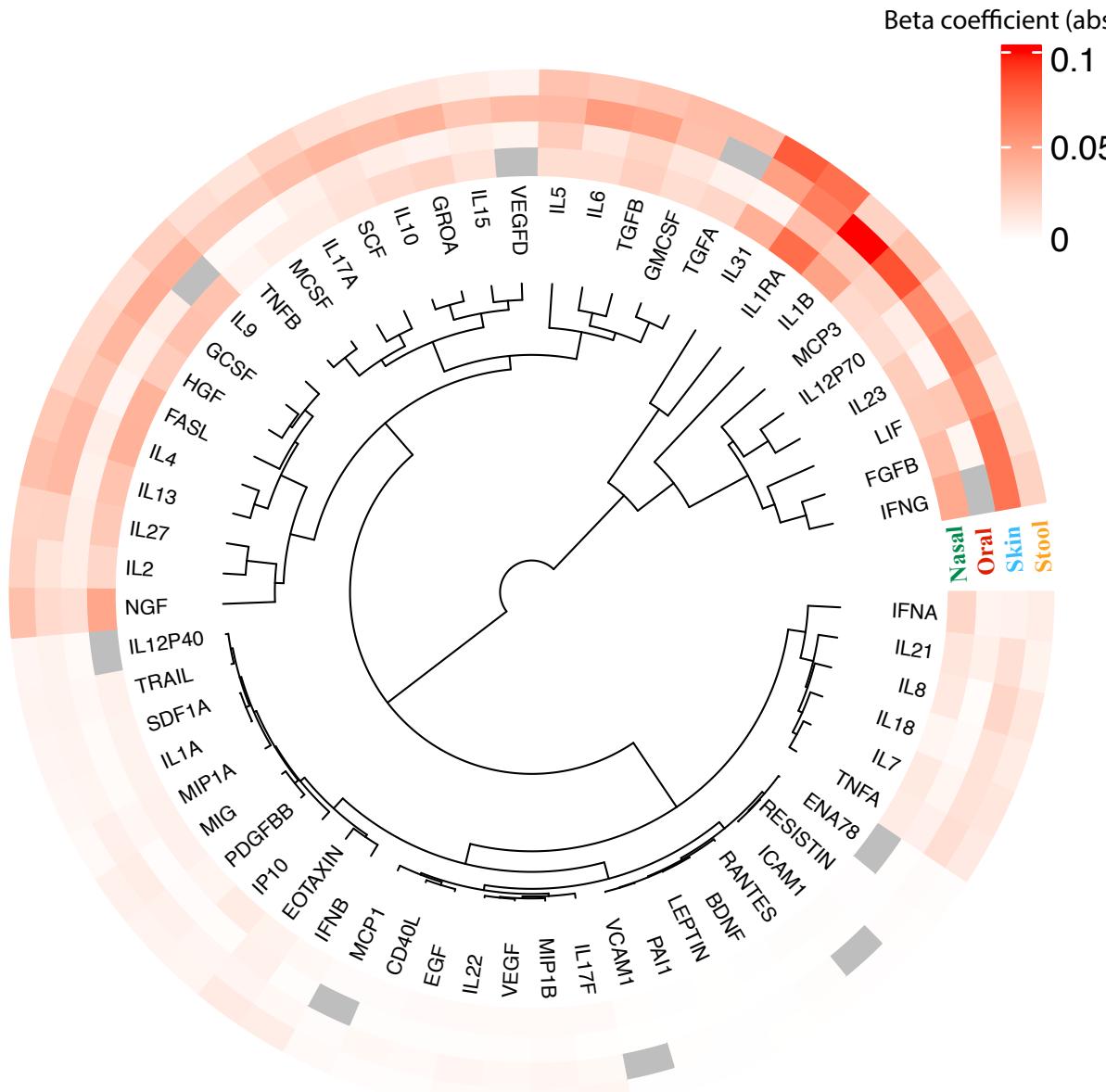
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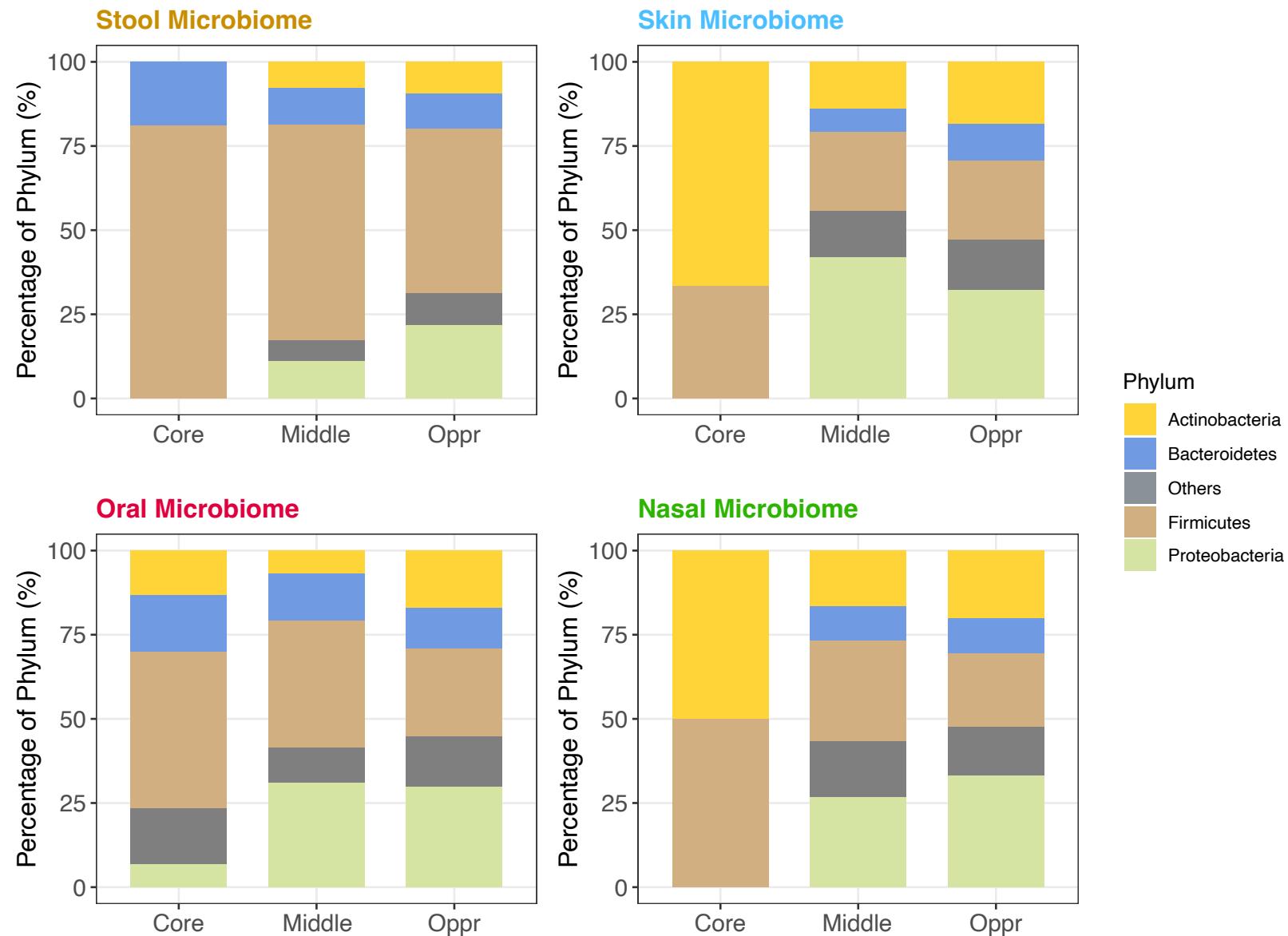
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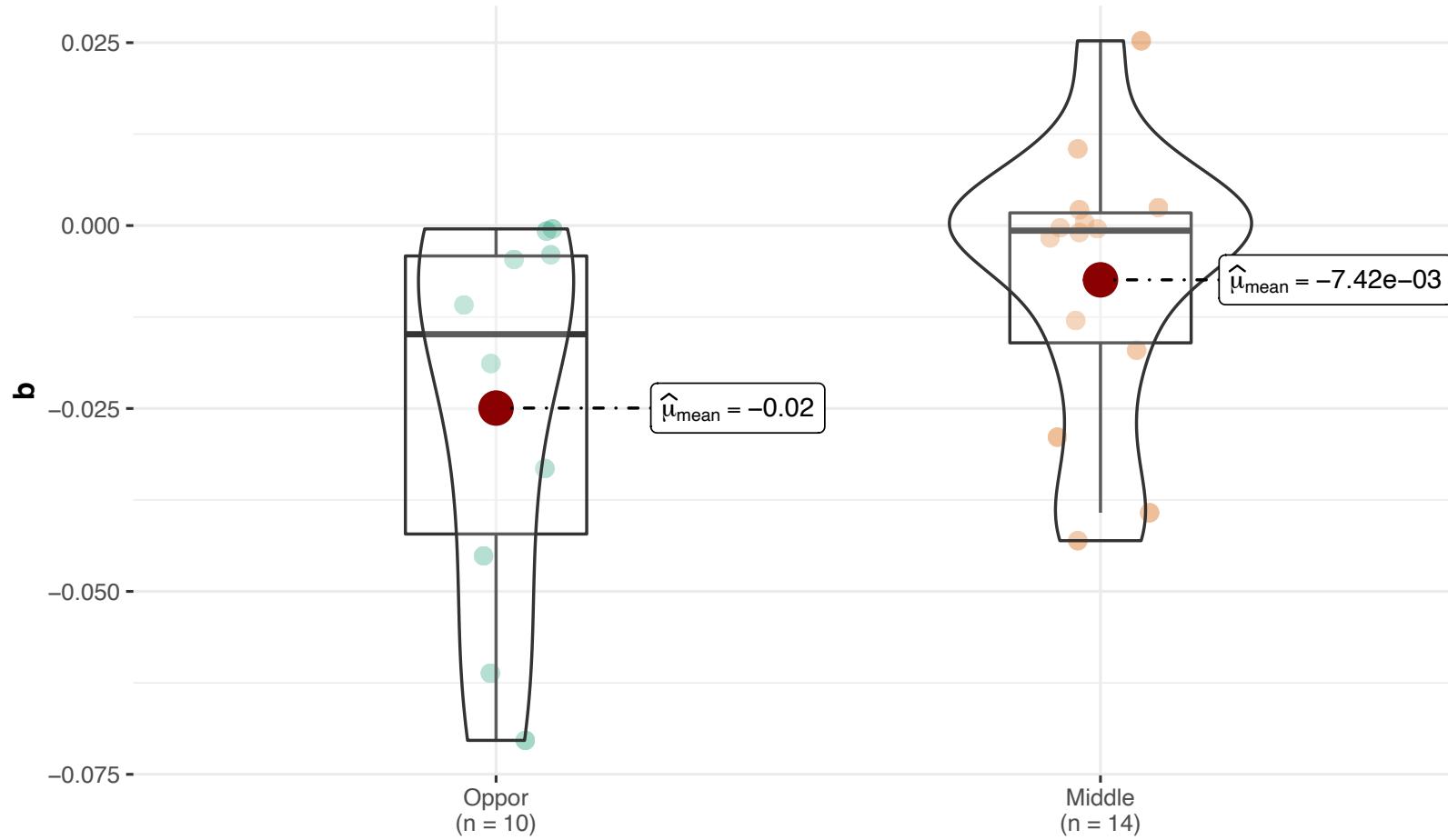
Extended Data Fig. 11: Beta coefficient comparison between cytokines and genera from different body sites



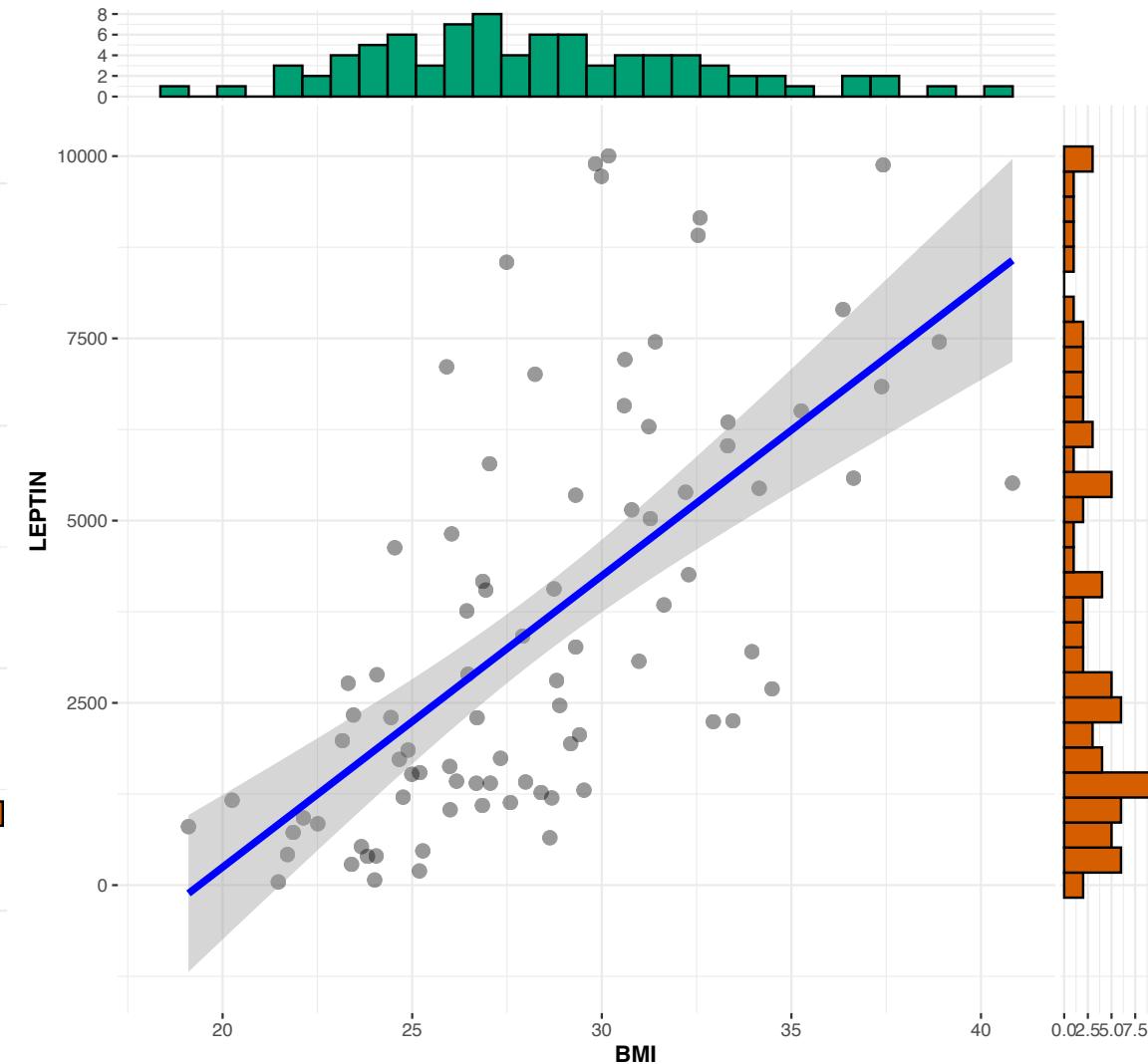
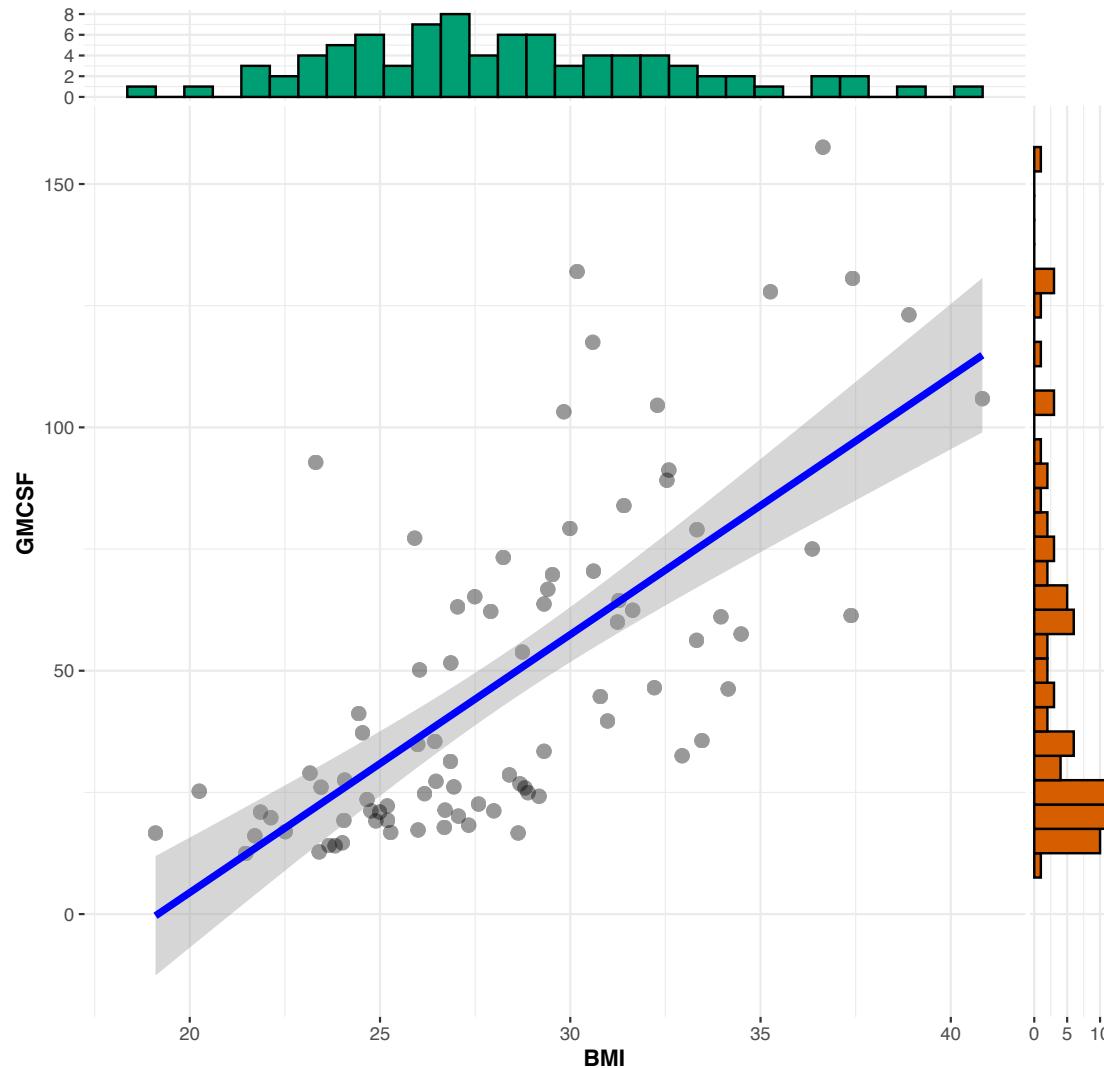
Extended Data Fig. 12: Phyla composition of core, middle and opportunistic genera of microbiome



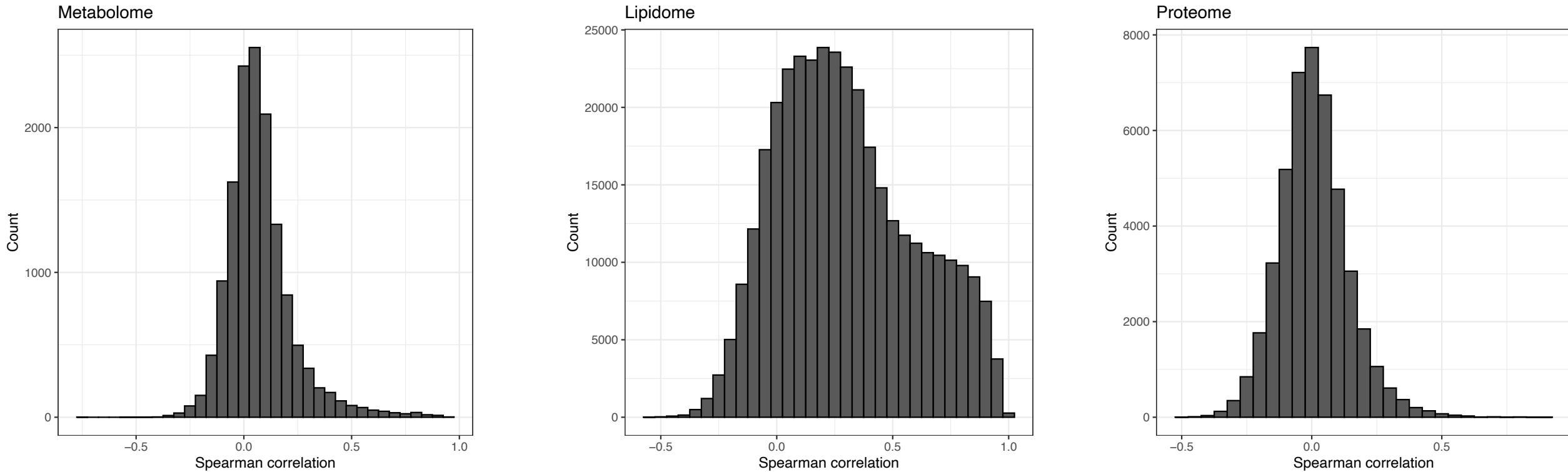
Extended Data Fig. 13: Correlation between genera of stool Proteobacteria and plasma cytokines grouped by prevalence



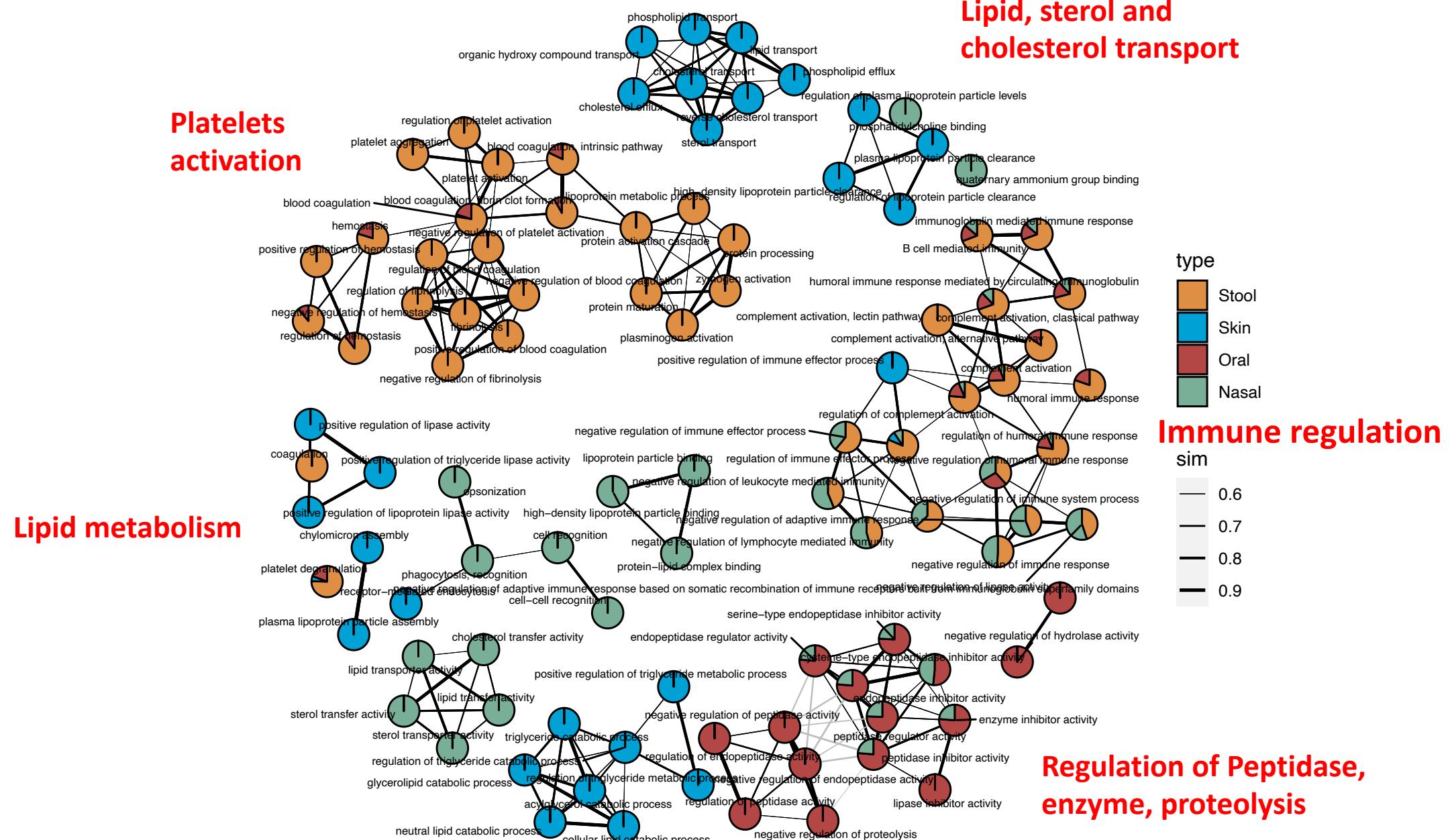
Extended Data Fig. 14: The correlation between body mass index and plasma leptin and granulocyte-macrophage colony-stimulating factor



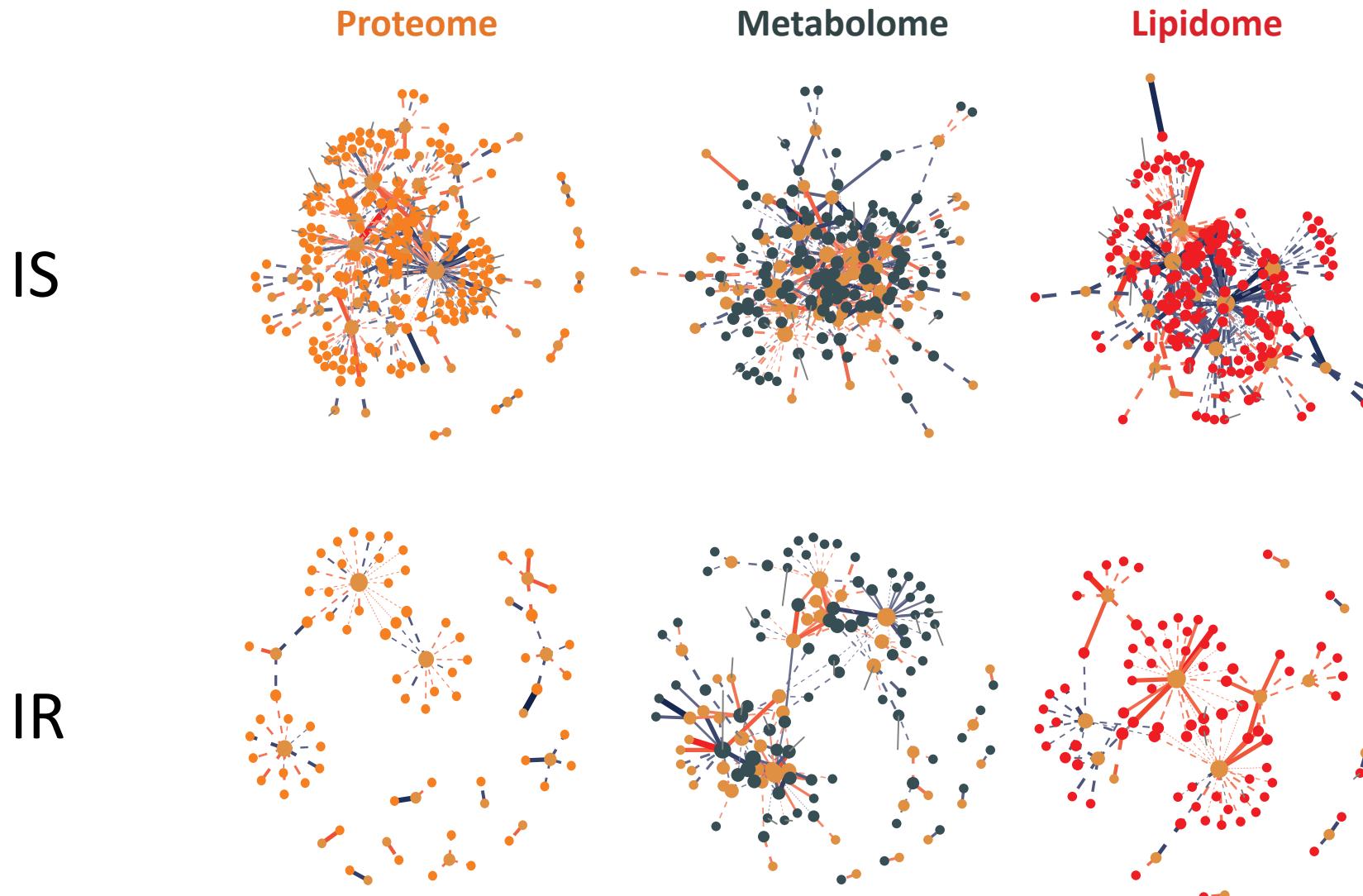
Extended Data Fig. 15: High collinearity of omics is specific to the lipidome data



Extended Data Fig. 16: Pathway enrichment analysis of proteomics and microbiome interactions



Extended Data Fig. 17: Different interactome of the stool microbiome and internal plasma analytes



Extended Data Fig. 18: Correlation network of microbiome richness and multiple internal analytes on four body sites

