

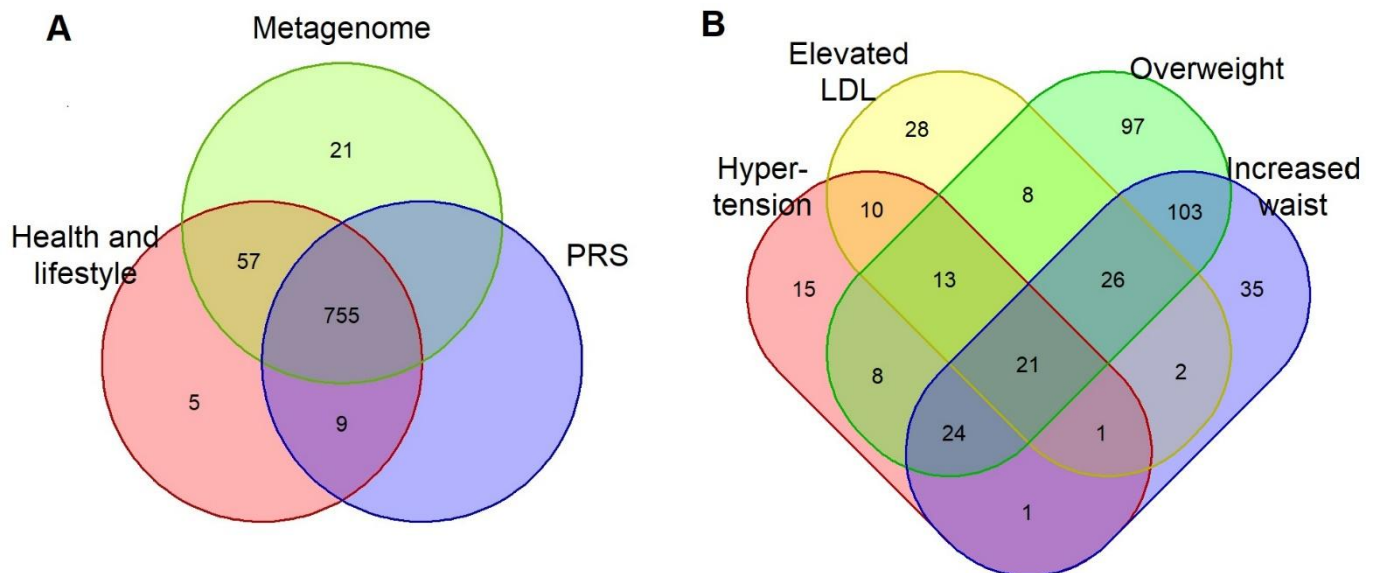
Polygenic risk for type 2 diabetes modulates gut microbiome associations across metabolic health traits

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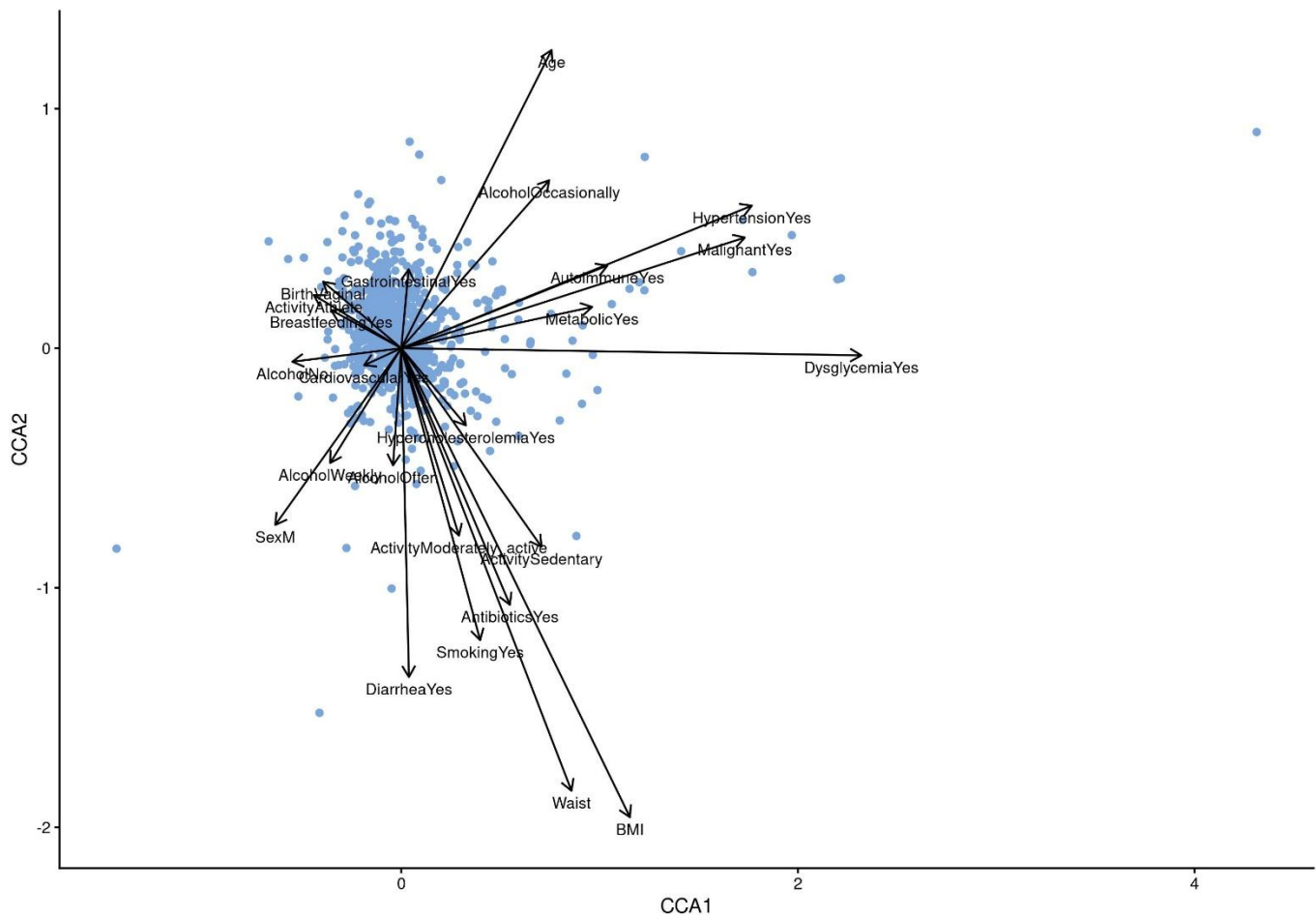
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Supplementary material

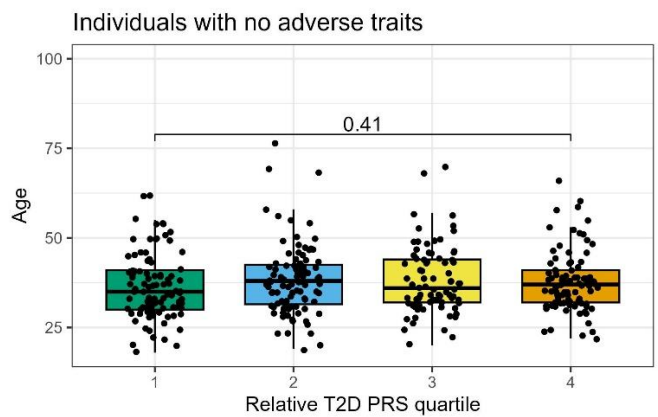
Supplementary Figure S1. A: overlap of available data in the analysed cohort. **B:** overlap of analysed traits in the study cohort



Supplementary figure S2. CCA visualisation of microbiome taxonomic diversity and phenotype data in study cohort



Supplementary figure S3. Age differences between T2D PRS quartiles for individuals with no adverse traits of metabolic health



Supplementary table S1. Beta diversity dissimilarities of microbiome composition for different phenotypes (PERMANOVA test)

	R2	p
Sex	0.004263	1.00E-04
Age	0.003128	1.00E-04
Smoking	0.001532	0.1269
Frequency of alcohol use	0.005915	0.0515
Physical activity	0.004915	0.019
History of malignant diseases	0.001572	0.1426
History of cardiovascular diseases	0.001532	0.1945
History of metabolic or endocrine diseases	0.001646	0.2188
History of autoimmune diseases	0.001686	0.2365
History of gastrointestinal diseases	0.001345	0.6782
Hypertension	0.002096	0.055
Hypercholesterolemia	0.001451	0.526
Dysglycemia	0.002749	0.0053
Waist circumference	0.004589	1.00E-04
BMI	0.004464	1.00E-04
Use of antibiotics in the past 2 months	0.003507	8.00E-04
Diarrhea in the past week	0.002726	0.0115
Type of birth	0.0018	0.3321
Breastfeeding	0.001863	0.4488

Supplementary table S2. Linear dependencies between different phenotypes

	VIF
SexM	1.459082
Age	1.486213
SmokingYes	1.072766
AlcoholNo	12.16894
AlcoholOccasionally	23.72877
AlcoholOften	7.655555
AlcoholWeekly	20.04681
ActivityAthlete	1.067932
ActivityModerately_active	1.629058
ActivitySedentary	1.683706
MalignantYes	1.061095
CardiovascularYes	2.553581
MetabolicYes	1.565009
AutoimmuneYes	1.259709
GastrointestinalYes	1.092286
HypertensionYes	1.801717
HypercholesterolemiaYes	2.009822
DysglycemiaYes	1.193982
Waist	4.167207
BMI	3.506977
AntibioticsYes	1.103749
DiarrheaYes	1.088037
BirthVaginal	1.099821
BreastfeedingYes	1.044605

Supplementary data 1. Gut microbiome associations with traits of metabolic health, MaAsLin2 coefficient (Log_2FC)
Provided in a separate file.

Supplementary data 2. Microbiome associations with phenotype in high and low PRS groups, and with PRS in healthy and adverse phenotype groups, MaAsLin2 coefficient (Log_2FC)
Provided in a separate file.