

SUPPLEMENTS

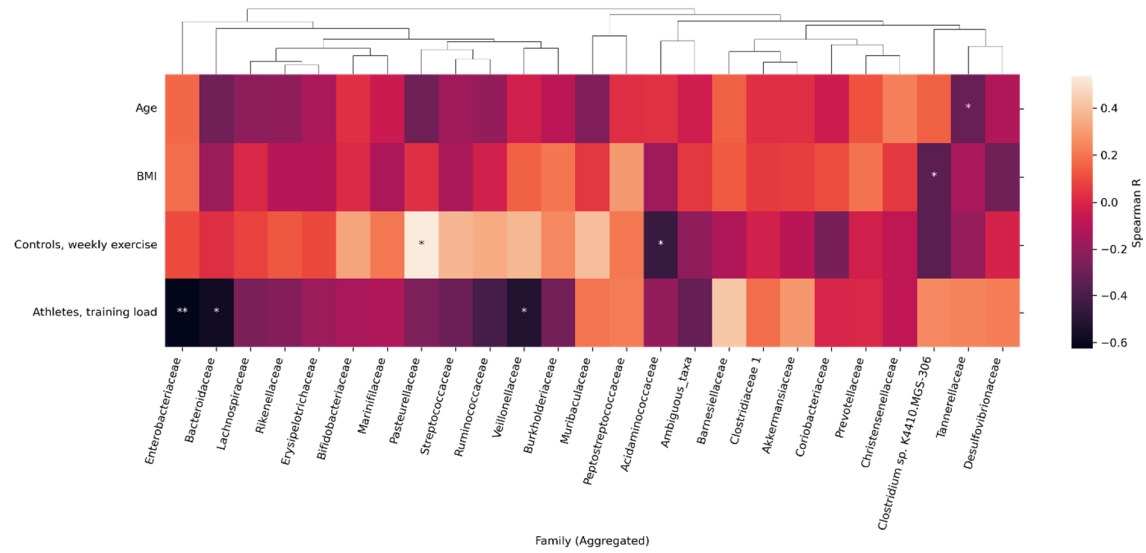


Figure S1. Clustered heatmap of Spearman correlation coefficients. between the bacterial families and background variables. Spearman p -value * < 0.05 ** < 0.01.

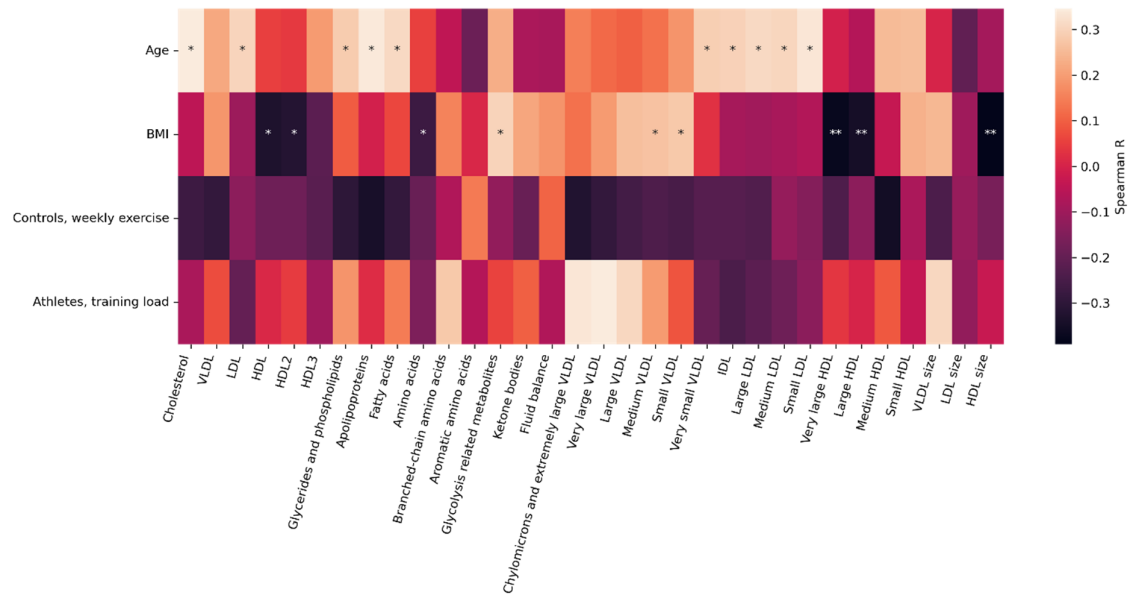
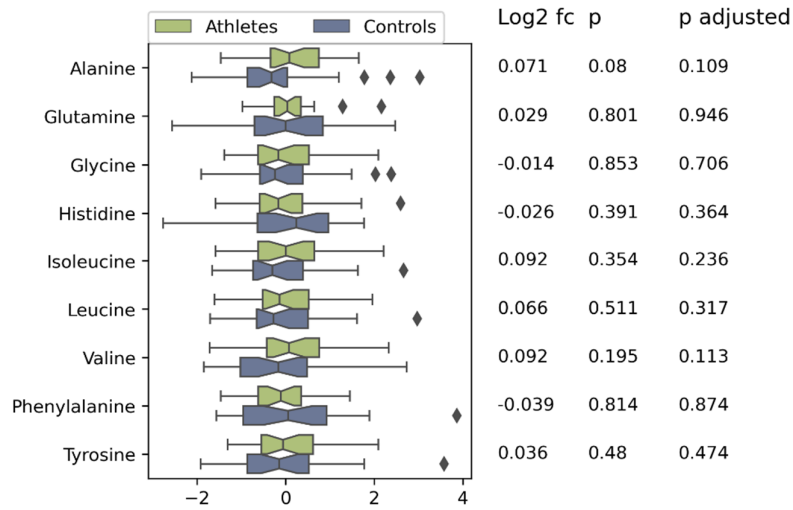
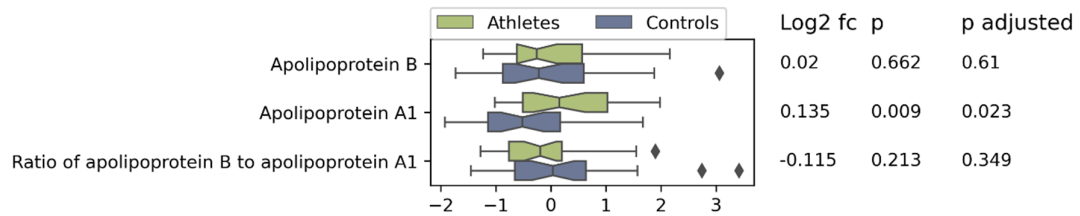


Figure S2. Heatmap of Spearman correlation coefficients between the metabolite groups and back-ground variables. Spearman p -value * < 0.05 ** < 0.01.

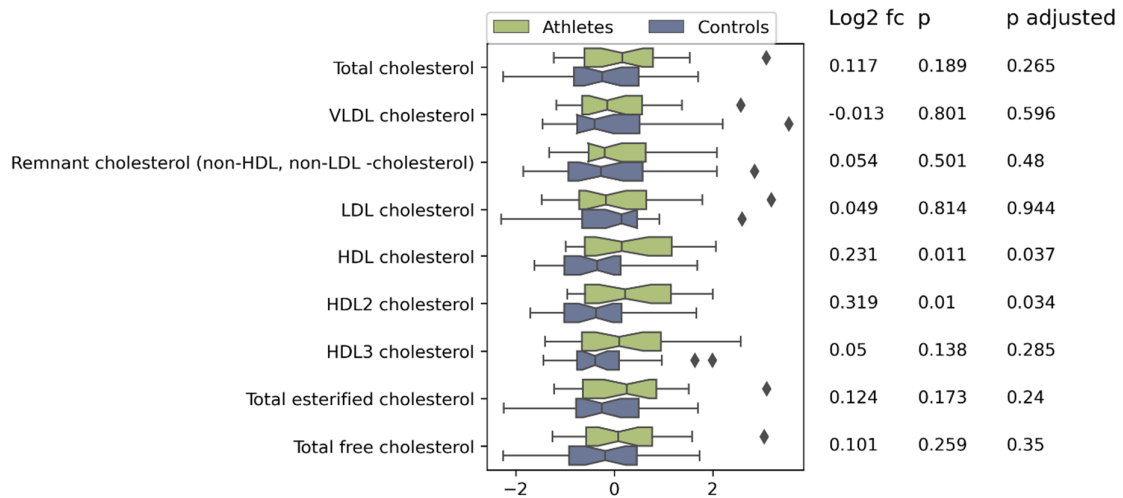
Amino acids



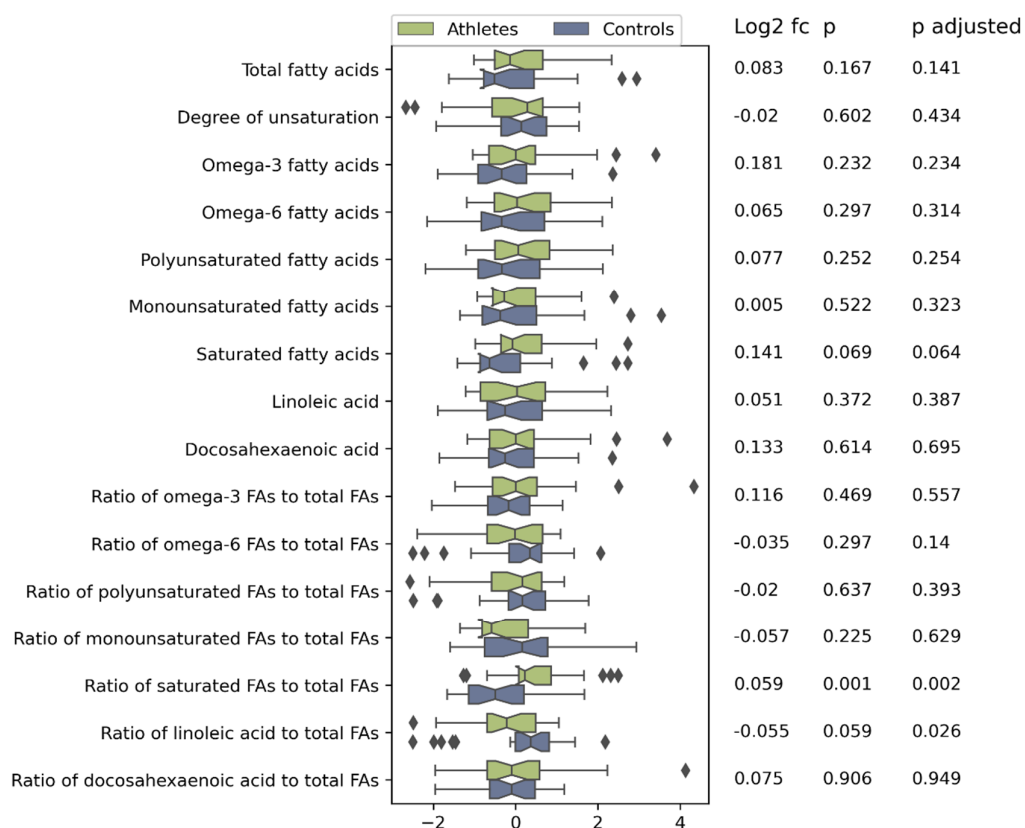
Apolipoproteins



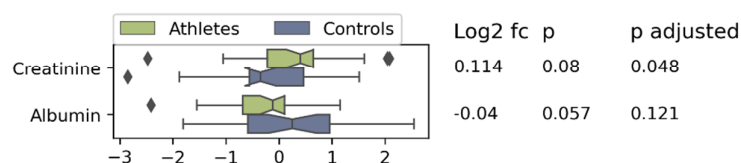
Cholesterol



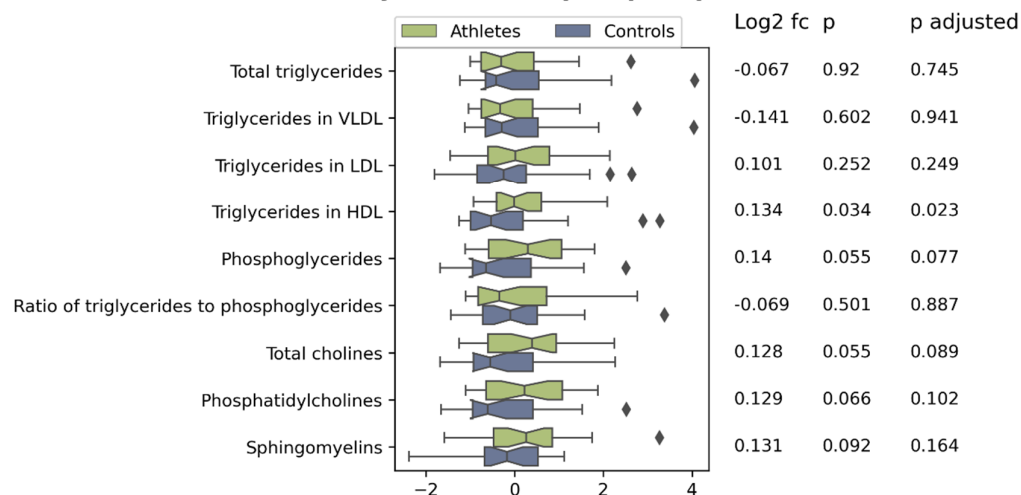
Fatty acids



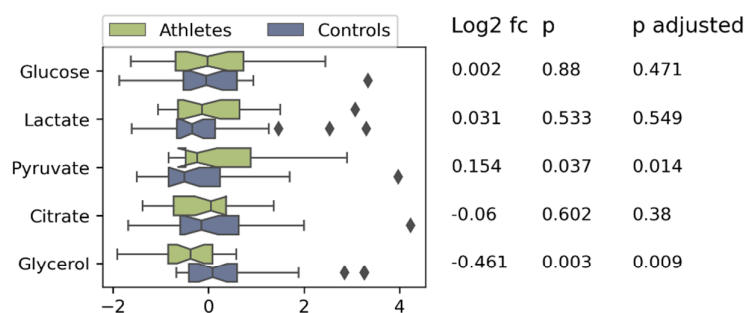
Fluid balance



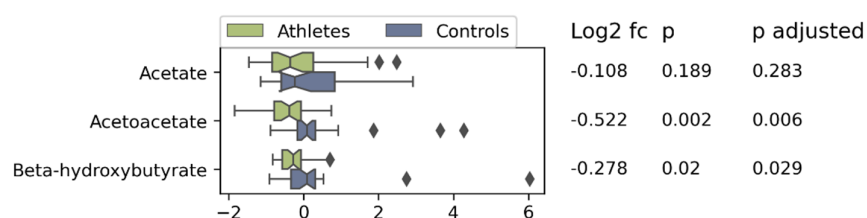
Glycerides and phospholipids



Glycolysis related metabolites



Ketone bodies



Lipoprotein particle sizes

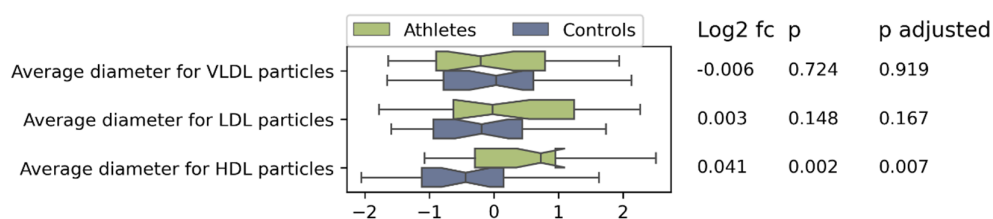


Figure S3. The metabolites and derived parameters. For boxplots, all values were mean centered. Whiskers indicate 1.5 times the interquartile range. Fold change between skiers and controls log2-transformed. *p*-values derived from Kruskal Wallis test. Adjusted *p*-values derived from Quade's ANCOVA adjusted for BMI and age.

Table S1. Results summary for linear regression model using *Butyricicoccus* and *Ruminococcus torques* group as dependent variables and associated metabolites as regressors.

Dep. Variable:	Butyricicoccus			
F-statistic:	82.88	R-squared (uncentered):	0.864	
Prob (F-statistic):	5.68E-17	Adj. R-squared (uncentered):	0.854	
	Coefficient	Std error	t	P> t
HDL2 cholesterol	0.767	0.509	1.507	0.14
HDL size	0.2151	0.066	3.26	0.002
Acetoacetate	-18.6707	7.912	-2.36	0.023
Dep. Variable:	[Ruminococcus] torques group			
F-statistic:	103.7	R-squared (uncentered):	0.838	
Prob (F-statistic):	1.49E-16	Adj. R-squared (uncentered):	0.83	
	Coefficient	Std error	t	P> t
Acetate	-13.756	11.906	-1.155	0.255
Total cholesterol	0.7533	0.116	6.499	0

Method: Ordinary least squares. R² is computed without centering (uncentered) since the model does not contain a constant. Standard Errors assume that the covariance matrix of the errors is correctly specified.