

Additional file 1 — Table 1: Animal phenotypic traits and circulating fatty acids in the whole blood

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Phenotypic traits		
	Mean	Standard Deviation
age at slaughter	132.7	3.70
weight at slaughter	75.69	7.44
ADG	840.2	111.20
ADFI	2280	212.64
FCR	2.738	0.25
%backfat	7.093	1.56
%loin	28.26	1.05
Relative percentage of fatty acids		
	Mean	Standard Deviation
C14:0	0.36	0.16
C14:1	0.31	0.23
C15:0	0.17	0.05
C16:0	14.81	3.1
C16:1	1.03	0.3
C18:0	12.56	2.19
C18:1	27.12	2.14
n-6	33.41	4.93
n-3	5.93	1.95
C20:0	0.15	0.24
C20:1	0.34	0.33
C20:2	0.84	0.75
C22:0	1.37	0.94
C22:1	1.42	0.8

A total of 47 growing pigs were considered during a test period of 58 days.

Abbreviations used: ADG = average daily gain; ADFI: average daily feed intake ; FCR = food conversion ratio; %backfat = weight of dorsal subcutaneous fat tissue (relative to carcass weight); %loin = weight of dorsal subcutaneous fat tissue (relative to carcass weight).

Additional file 2 — Table 2: Number of probes significantly linked to the animal phenotypic traits of interest (linear models).

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Variable	<i>p.value</i> < 0.01	<i>p.value</i> < 0.05
line	1813	3726
age at slaughter	1174	4940
diet	50	335
%backfat	164	726
ADFI	213	1352
ADG	325	1756
FCR	425	1682
%loin	359	1918
weight at slaughter	90	596

Additional file 3 — Table 3: Adjacency matrix.

Weighted Gene Co-expression Network Analysis (WGCNA) were perform to build a network from the expression levels of 16,190 molecular probes expressed in the whole blood. The adjacency matrix was build using the signed hybrid method.

SP3 - adjacency_matrix_sh.csv <https://data-access.cesgo.org/index.php/s/YPz0J2ItxIEuN5M>

Additional file 4 — Table 4: Composition of the modules in probes with their annotation and GS.FCR and MM.

GS.FCR: Gene Significance for Feed Conversion Ratio (correlation between the FCR and each each probe), absGS: absolute value of the GS.FCR, MM: Module

SP4 - modules.csv

Additional file 5 — Figure 1: Correlation circle of the third and fourth dimensions of the principal component analysis summarizing the profiles of circulating metabolites in the blood.

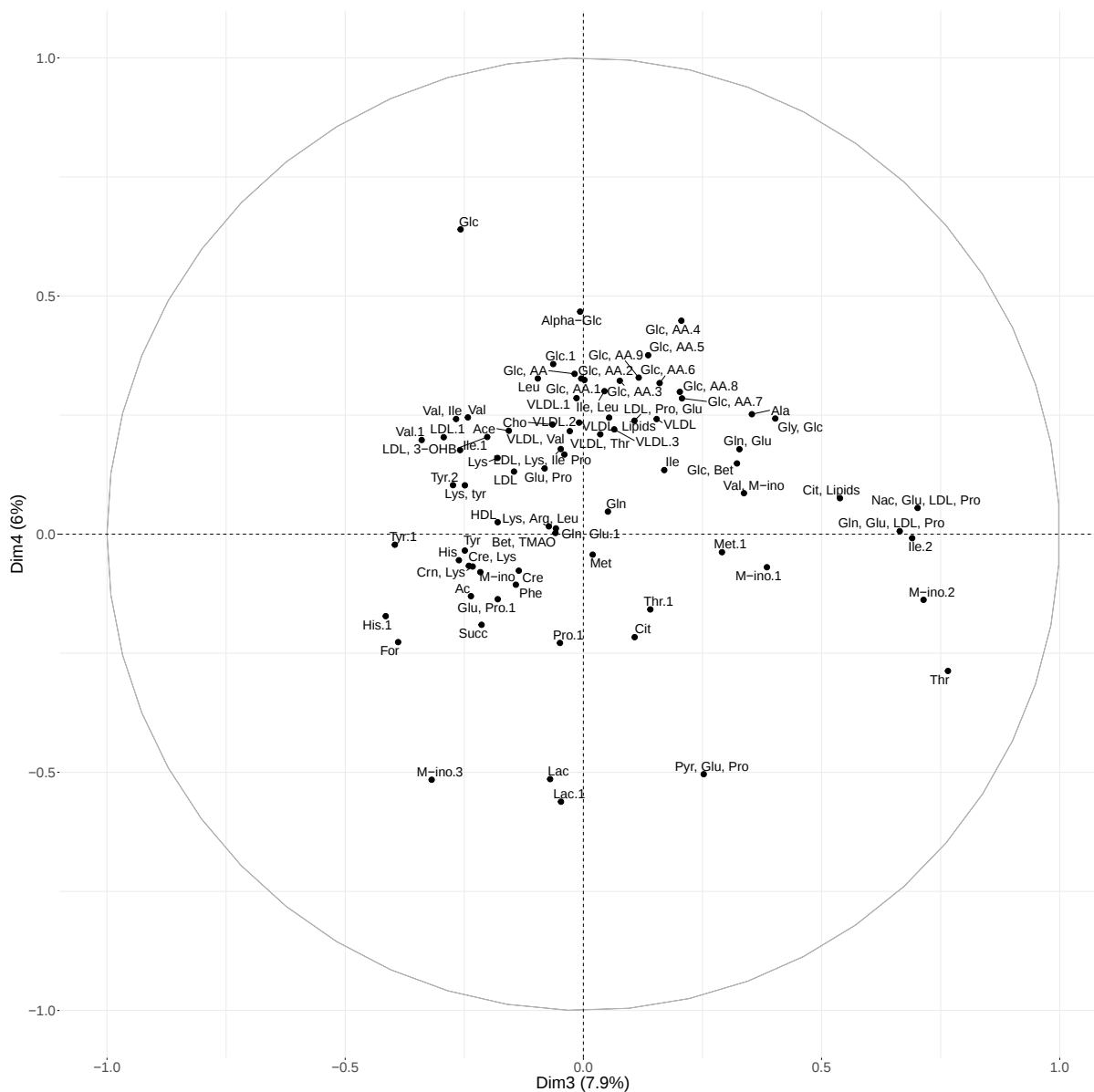


Figure 1: Correlation circle of the third and fourth dimensions of the principal component analysis summarizing the profiles of circulating metabolites in the blood.

¹H-NMR spectra were obtained in the plasma prepared from the whole blood of 47 growing pigs. The matrix of correlations was calculated from 94 individual variables corresponding to the different annotated spectra.

Additional file 6 — Figure 2: Correlation circle of the third and fifth dimensions of the principal component analysis summarizing the profiles of circulating metabolites in the blood.

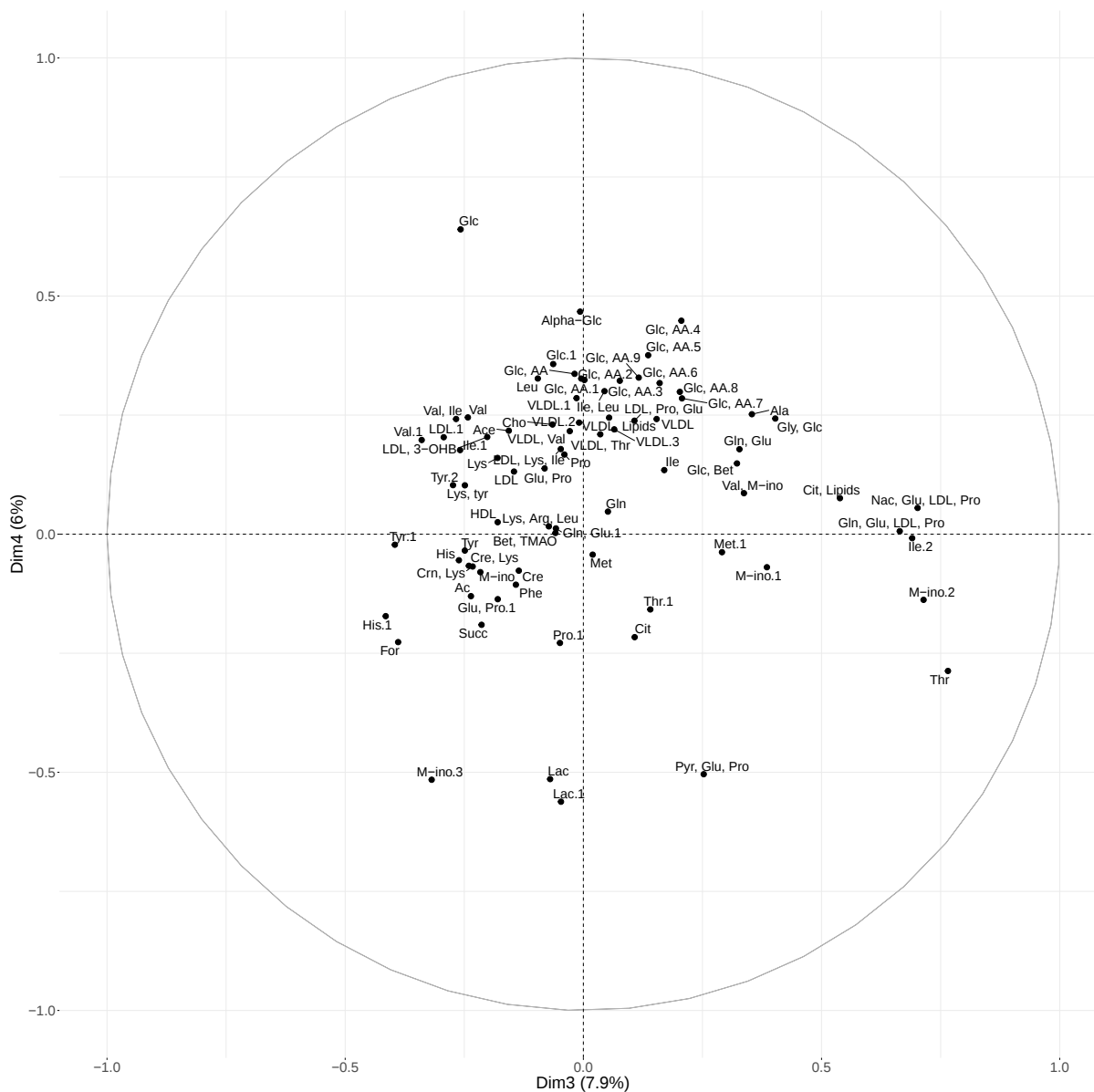


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Additional file 7 — Figure 3: Correlation circle of the third and fourth dimensions of the principal component analysis summarizing fatty acid composition in blood.

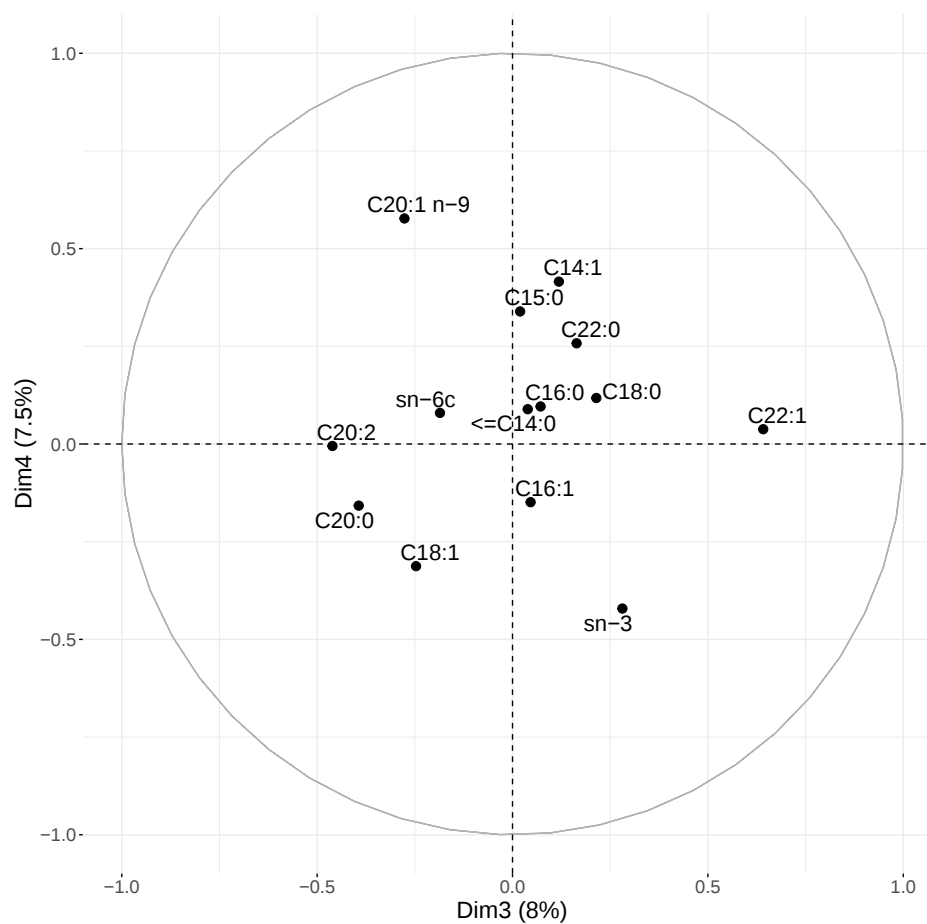


Figure 3: Correlation circle of the third and fourth dimensions of the principal component analysis summarizing fatty acid composition in blood.

The fatty acid composition (in percentage) was obtained in the plasma prepared from the whole blood of 47 growing pigs by using gas chromatography. Some of the individual FA were grouped in biologically relevant families (saturated FA with 14 carbons or less, omega-6 sum of $n - 6$ and omega-3 sum of $n - 3$), whereas the other fatty acids were kept as these.

Additional file 8 — Figure 4: Correlation circle of the third and fifth dimensions of the principal component analysis summarizing fatty acid composition in blood.

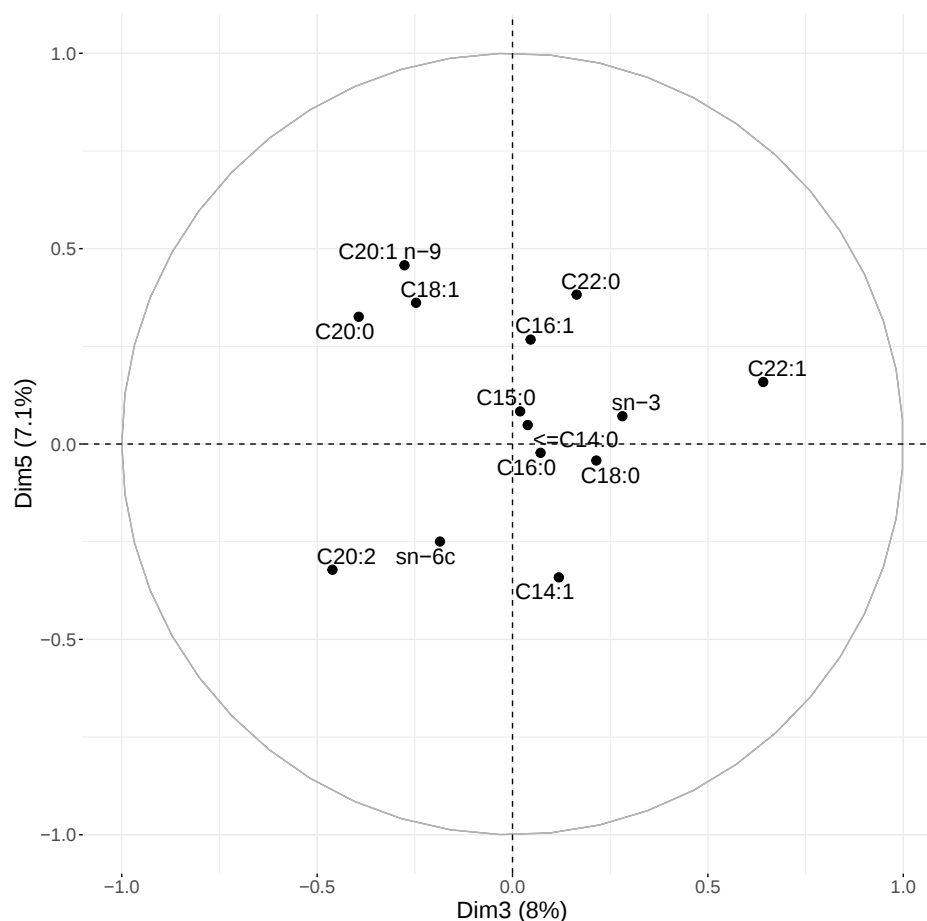


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Additional file 9 — Figure 5: Heatmap of correlations between module eigengenes of molecular modules of co-expressed genes in the whole blood and the first dimensions of principal component analyses summarizing the metabolites obtained by 1H-NMR high throughput method in plasma.

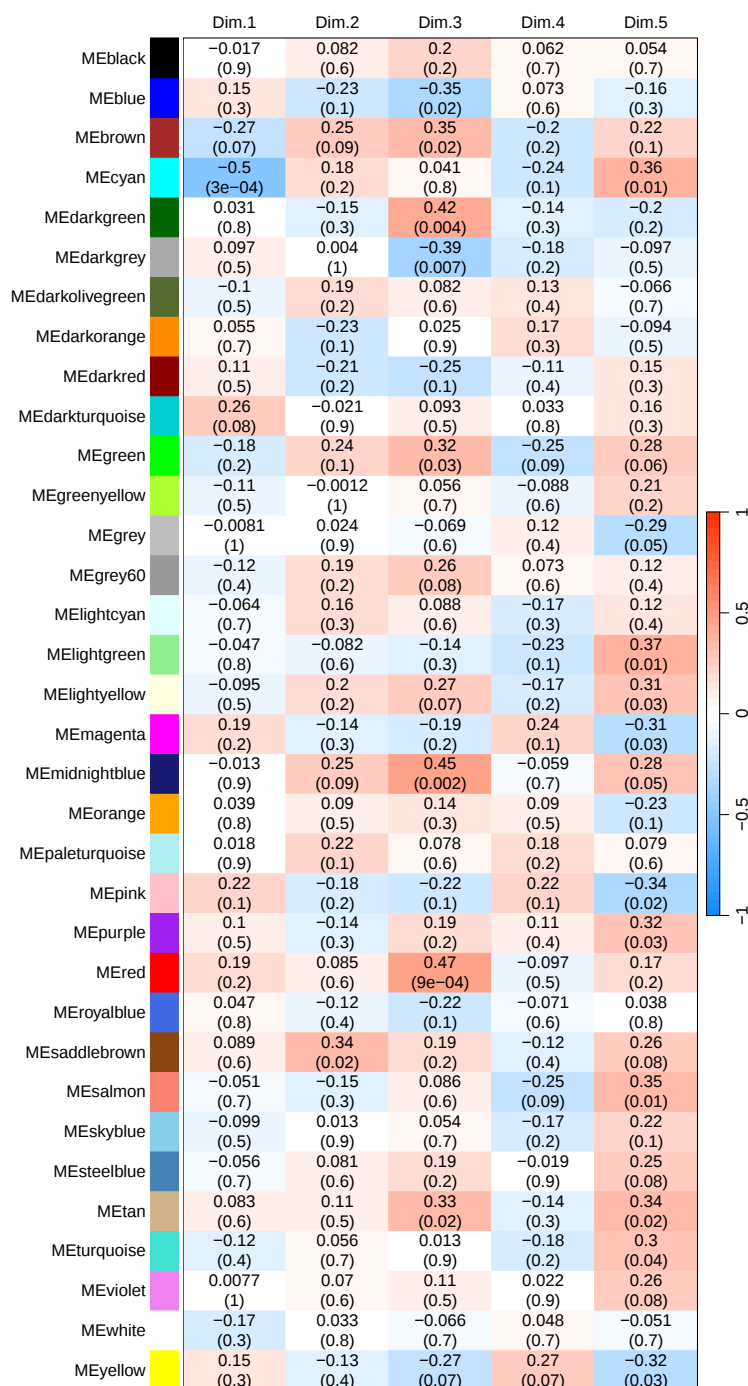


Figure 5: Heatmap of correlations between module eigengenes of molecular modules of co-expressed genes in the whole blood and the first dimensions of principal component analyses summarizing the metabolites obtained by 1H-NMR high throughput method in plasma.

Modules of co-expressed probes were obtained from a weighted gene correlation network analysis (WGCNA) from microarray data in the whole blood of 47 growing pigs. The eigengene of each module (ME) was considered as a mathematical representative of the expression levels of the molecular probes within the module. Circulating biochemical molecules were analyzed and the data were summarized by weighted linear correlation using principal component analysis (PCA). The i th dimensions of the PCA were called dim_i met.

Additional file 10 — Figure 6: Heatmap of correlations between module eigengenes of molecular modules of co-expressed genes in the whole blood and the five first dimensions of principal component analyses summarizing the fatty acids analyzed by target gas chromatography.

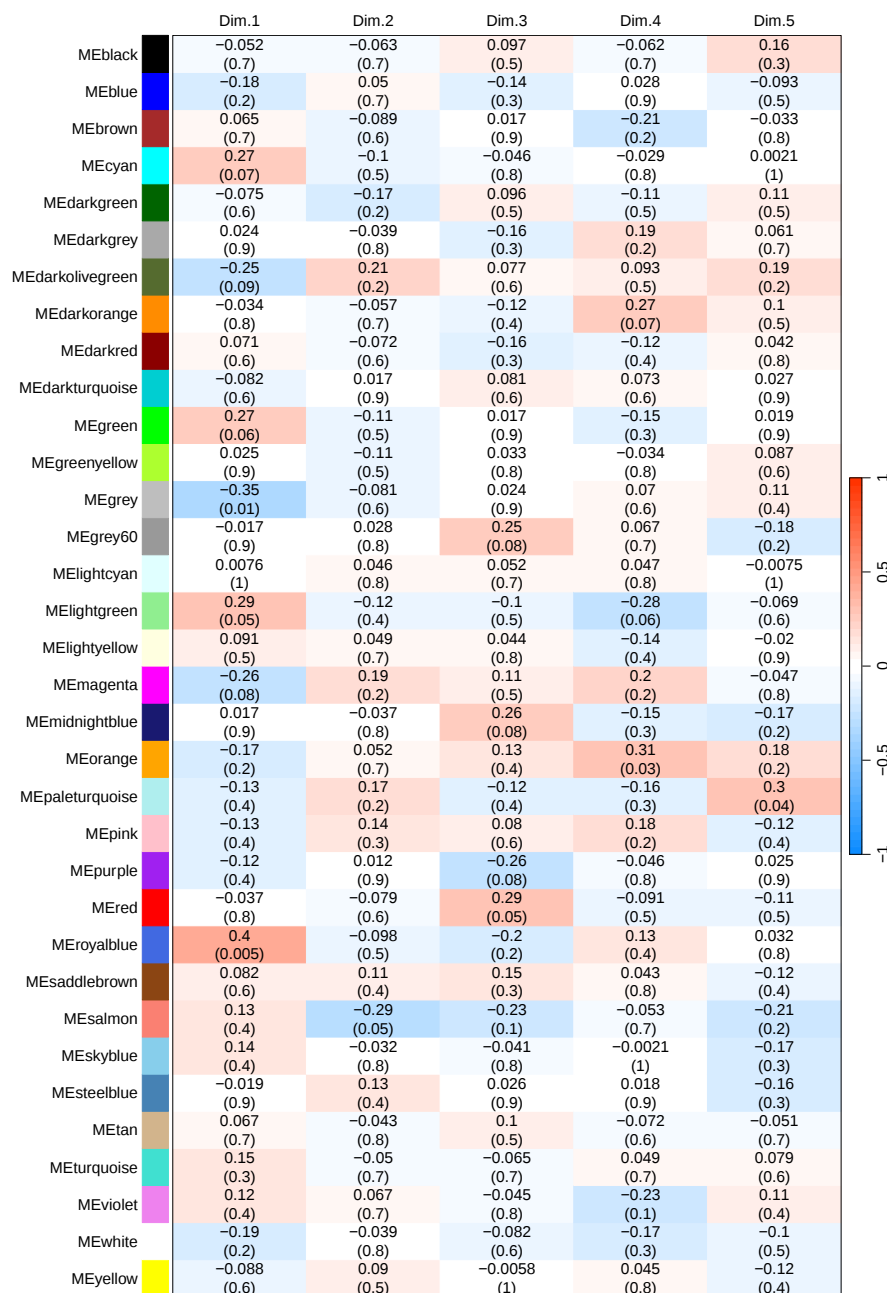


Figure 6: **Heatmap of correlations between module eigengenes of molecular modules of co-expressed genes in the whole blood and the five first dimensions of principal component analyses summarizing the fatty acids analyzed by target gas chromatography.**

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