

Supplementary Materials

Comprehensive Insight into Colorectal Cancer Metabolites and Lipids for Human Serum: A Proof-of-Concept Study

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Table S1. Metabolomics: A systematic feature reduction step

Omics Cascade

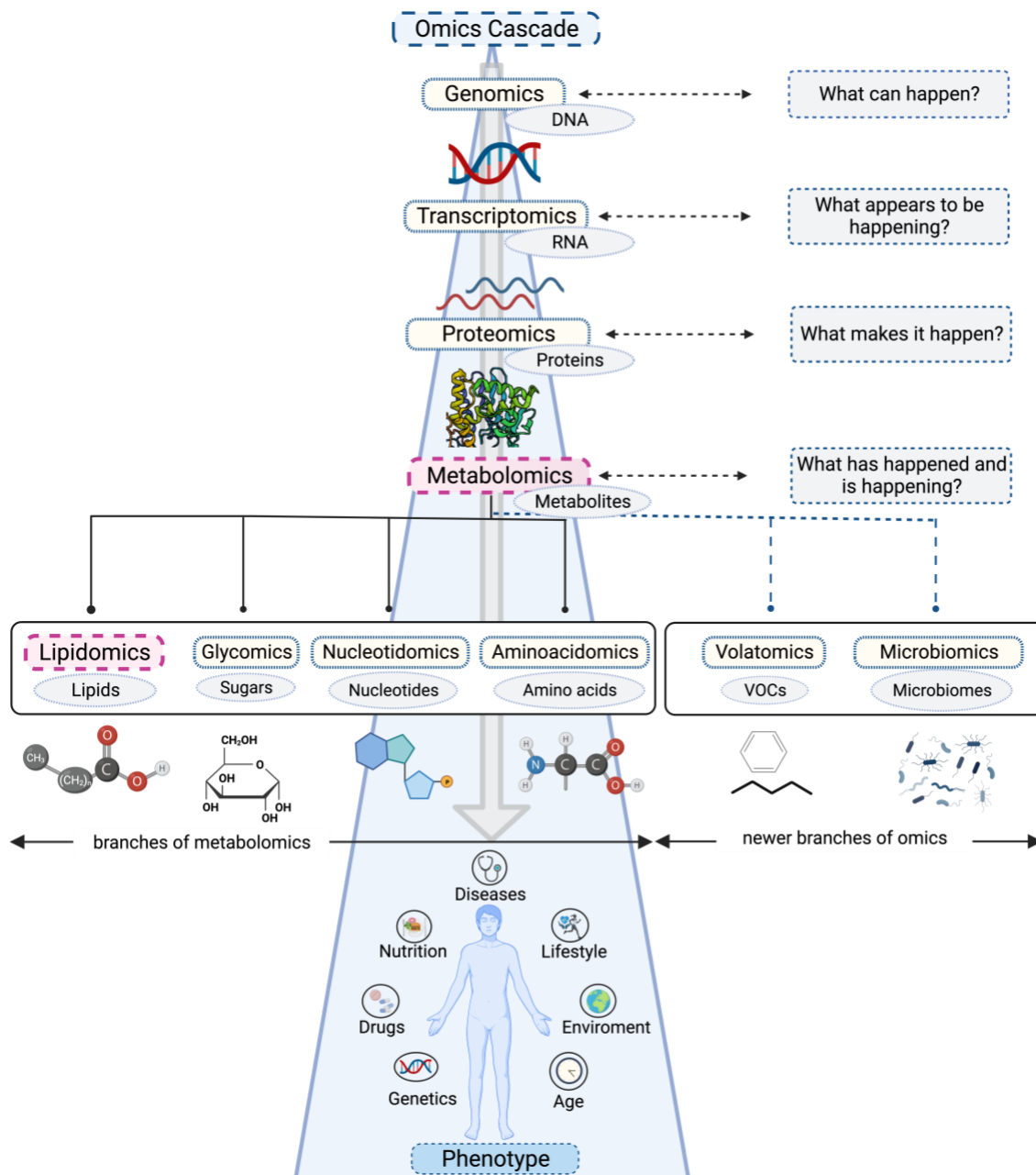


Figure S1: Overview of the omics cascade

Lipidomics: Unsupervised screening with all features

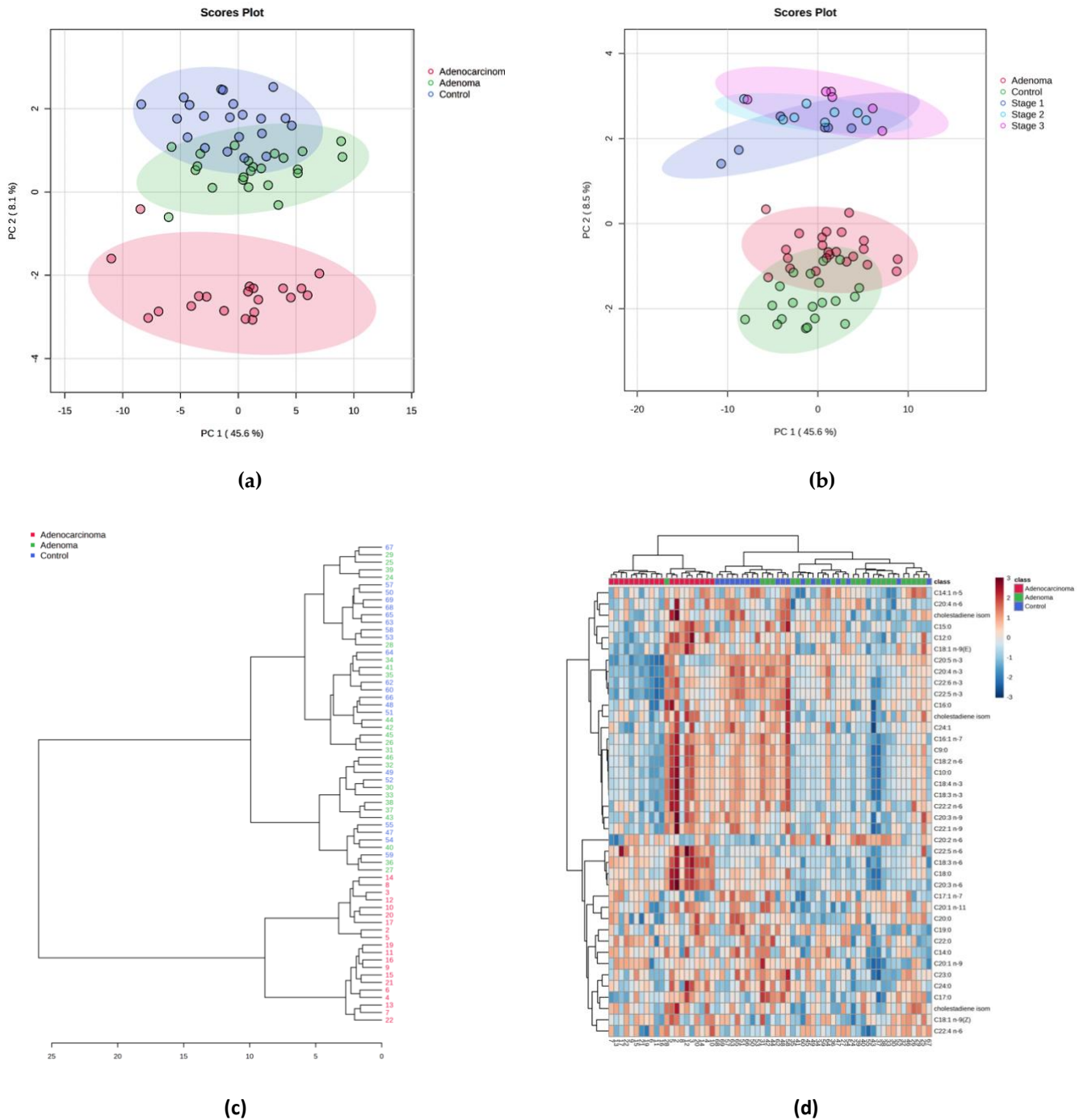
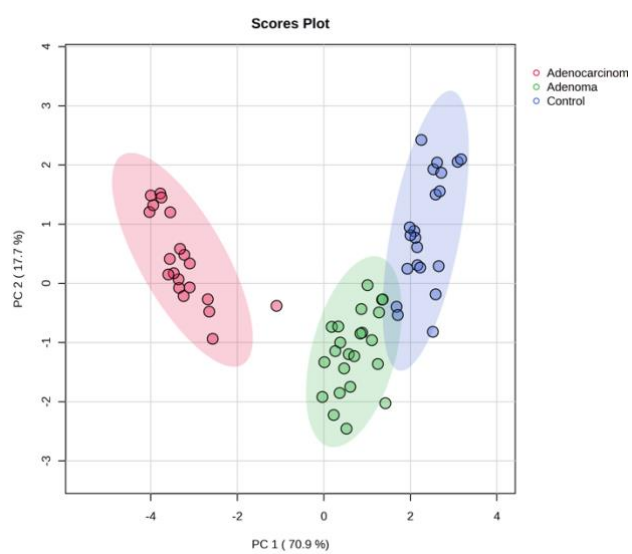


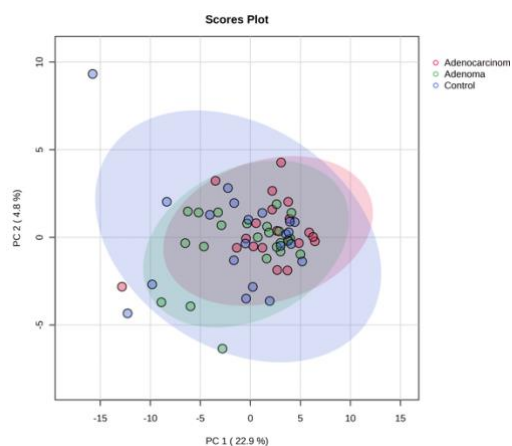
Figure S2. Lipidomics: Unsupervised screening with all features (a) PCA score plot for three different groups: control, adenoma, adenocarcinoma. (b) PCA score plot: Here, adenocarcinoma is divided in three stages based on pTNM staging: Stage 1, Stage 2, and stage 3 (c) Hierarchical Clustering Dendrogram (d) Heat map



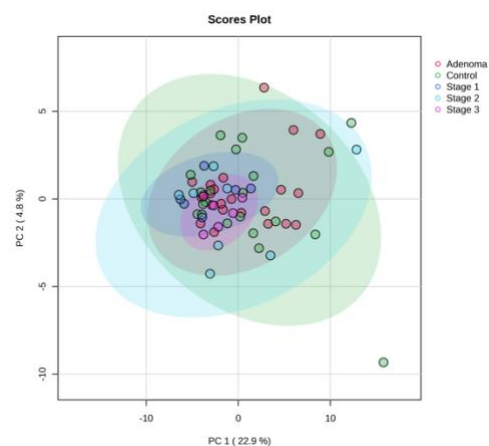
(a)

Figure S3. Lipidomics: PCA score plot using significant features (adenocarcinoma, adenoma, and control).

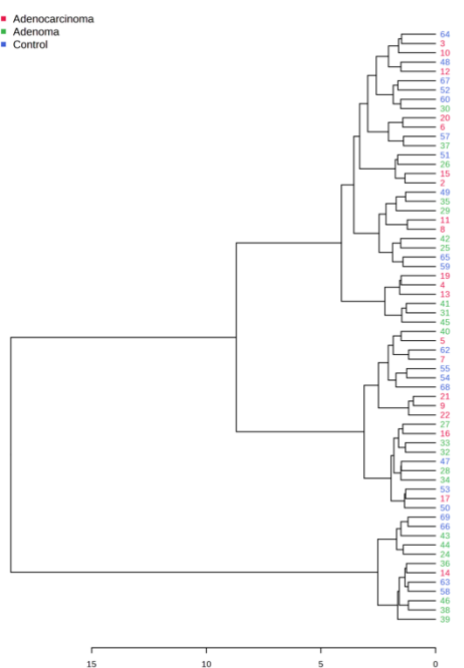
Metabolomics Approach: Unsupervised screening with all features



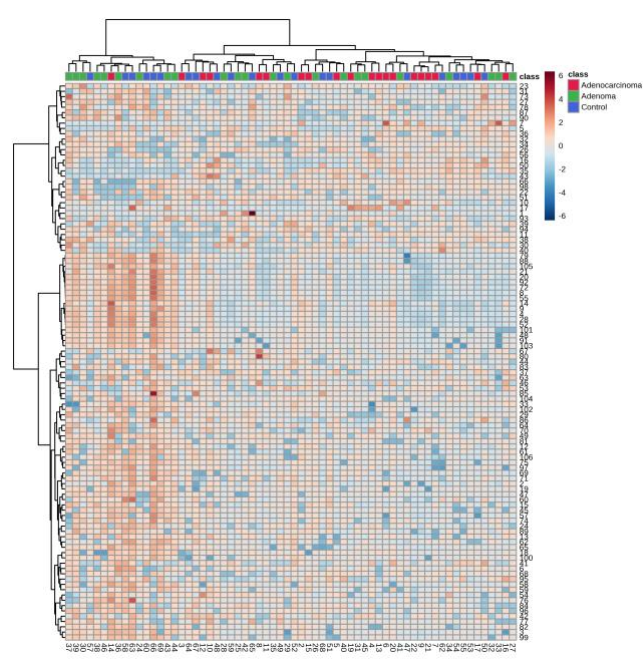
(a)



(b)



(c)



(d)

Figure S4. Metabolomics: Unsupervised screening with all features (a) PCA score plot for three different groups: control, adenoma, adenocarcinoma. (b) PCA score plot: Here, adenocarcinoma is divided in three stages based on pTNM staging: Stage 1, Stage 2, and stage 3 (c) Hierarchical Clustering Dendrogram (d) Heat map

Metabolomics Approach: significant features

Top feature	PLS-DA (Validation)			RF (1000 trees)	RF Confusion matrix (Class error)		
	Accuracy	R ²	Q ²	OOB error	Adenocarcinoma	Adenoma	Control
11	0.65	0.74	0.62	0.2500	0.250	0.261	0.238
10	0.76	0.78	0.73	0.1880	0.150	0.217	0.190
9	0.73	0.76	0.70	0.0938	0.000	0.130	0.143
8	0.79	0.81	0.75	0.0476	0.000	0.087	0.050
7	0.80	0.81	0.78	0.0476	0.000	0.087	0.050

Table S1. Metabolomics: A systematic feature reduction step [Top 11 features (feature number: 20,60,92,72,14,88,8,71,70,55,30)]

The chemometric tools were used in conjunction to identify and select a subset of features that achieves high classification accuracy in distinguishing adenocarcinoma, adenoma, and control group with fewer variables, a systematic feature reduction step was conducted. As per one way ANOVA, and VIP score top 11 metabolites (feature number (from 1 to 11): 20,60,92,72,14,88,8,71,70,55,30) were same. While according to MCA score from RF out of 11 there were 8 metabolites common with the above list. The top 11 metabolites which were common in ANOVA and VIP were again projected turn by turn by reducing one feature which was a least significant in time of p-value and VIP score at a time (as shown in Table S1).

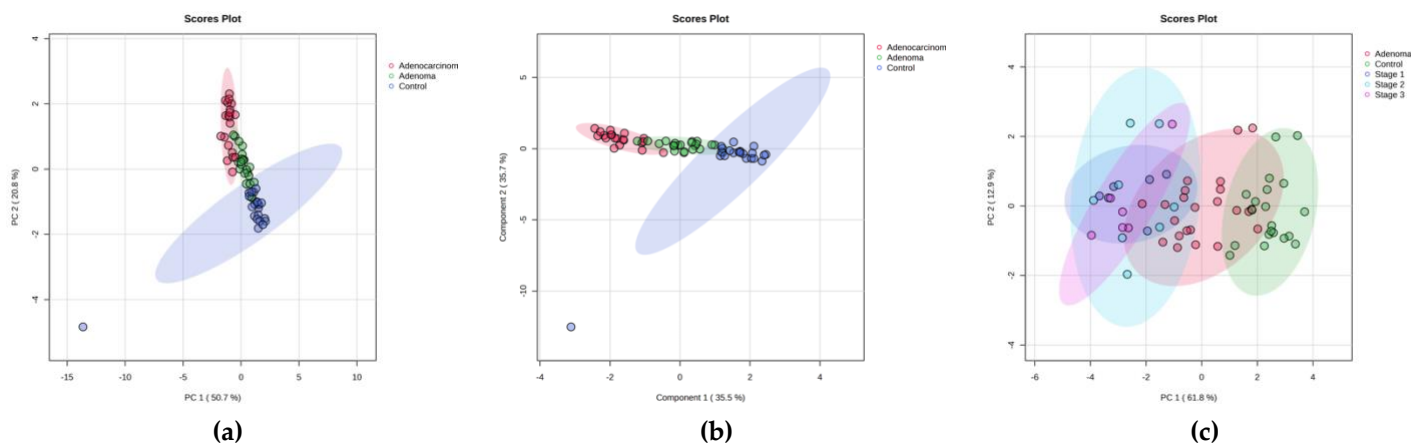


Figure S5. Metabolomics: Unsupervised screening with selected features (a) PCA score plot for three different groups: control, adenoma, adenocarcinoma. (control sample no 47 at bottom left corner) **(b)** PLS-DA score plot for three different groups: control, adenoma, adenocarcinoma. (control sample no 47 at bottom left corner) **(c)** PCA score plot: Here, adenocarcinoma is divided in three stages based on pTNM staging: Stage 1, Stage 2, and stage 3 (without sample no 47)

Lipidomics: QC Chart (Pooled human plasma)

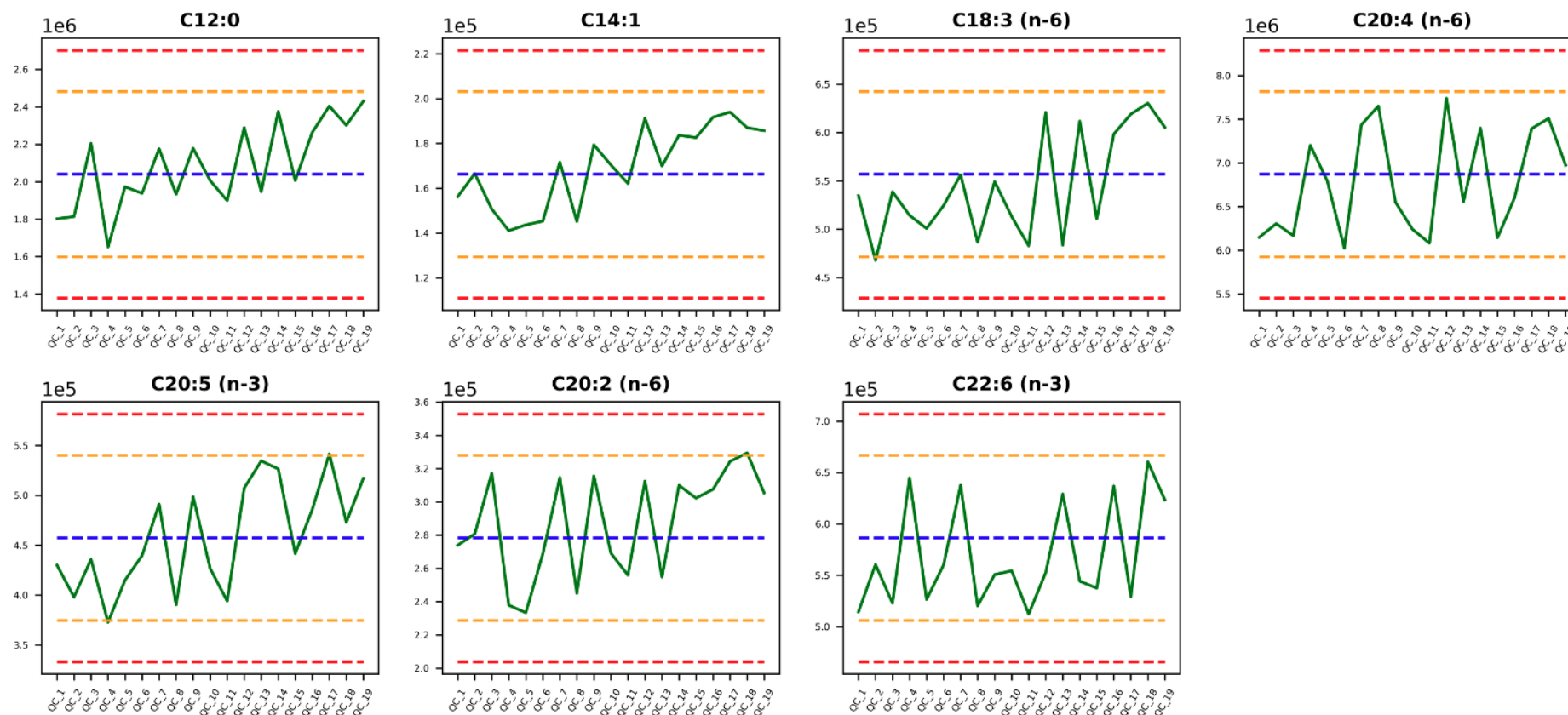


Figure S6: Lipidomics: QC Chart

Metabolomics: QC Chart (Pooled human plasma)

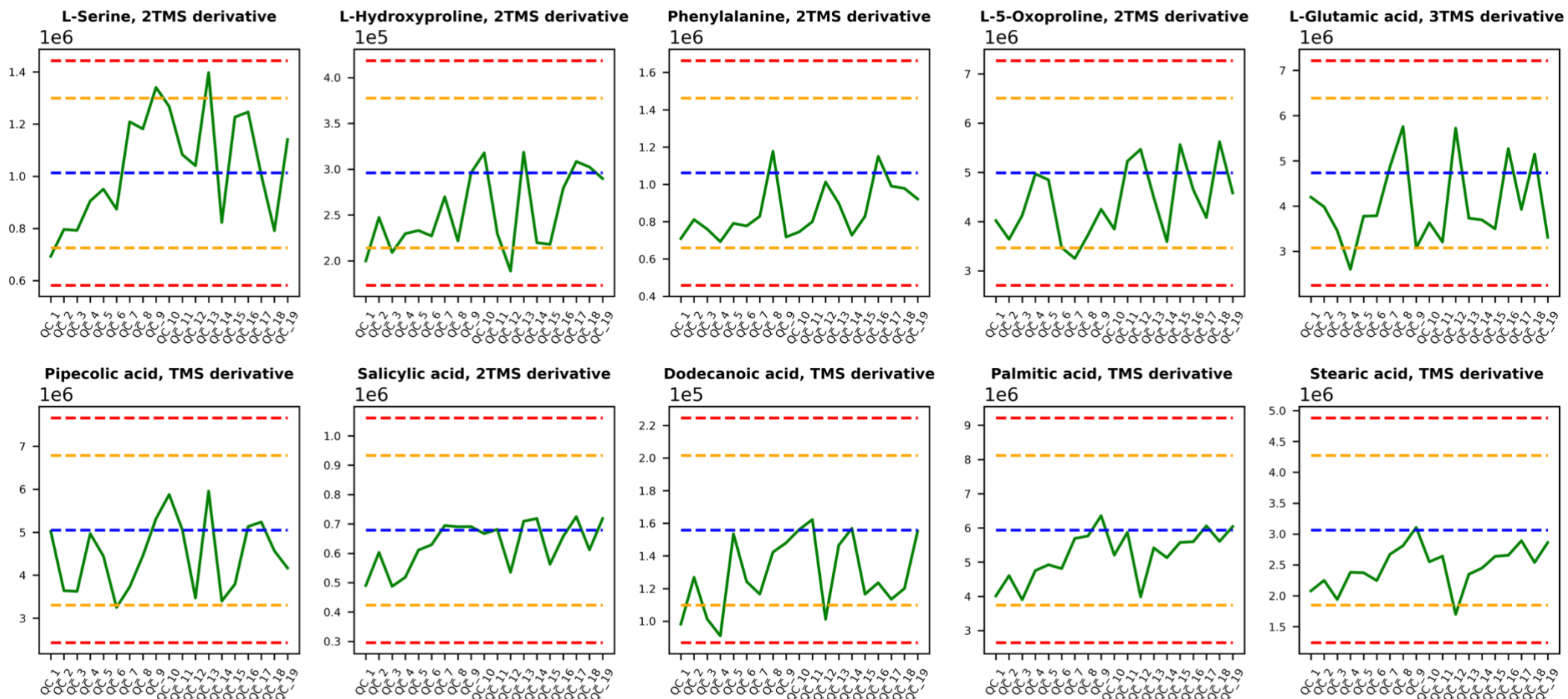


Figure S7: Metabolomics: QC Chart