

Multi-platform metabolomics: enhancing the severity risk prognosis of SARS-CoV-2 infection

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1. Supporting Information

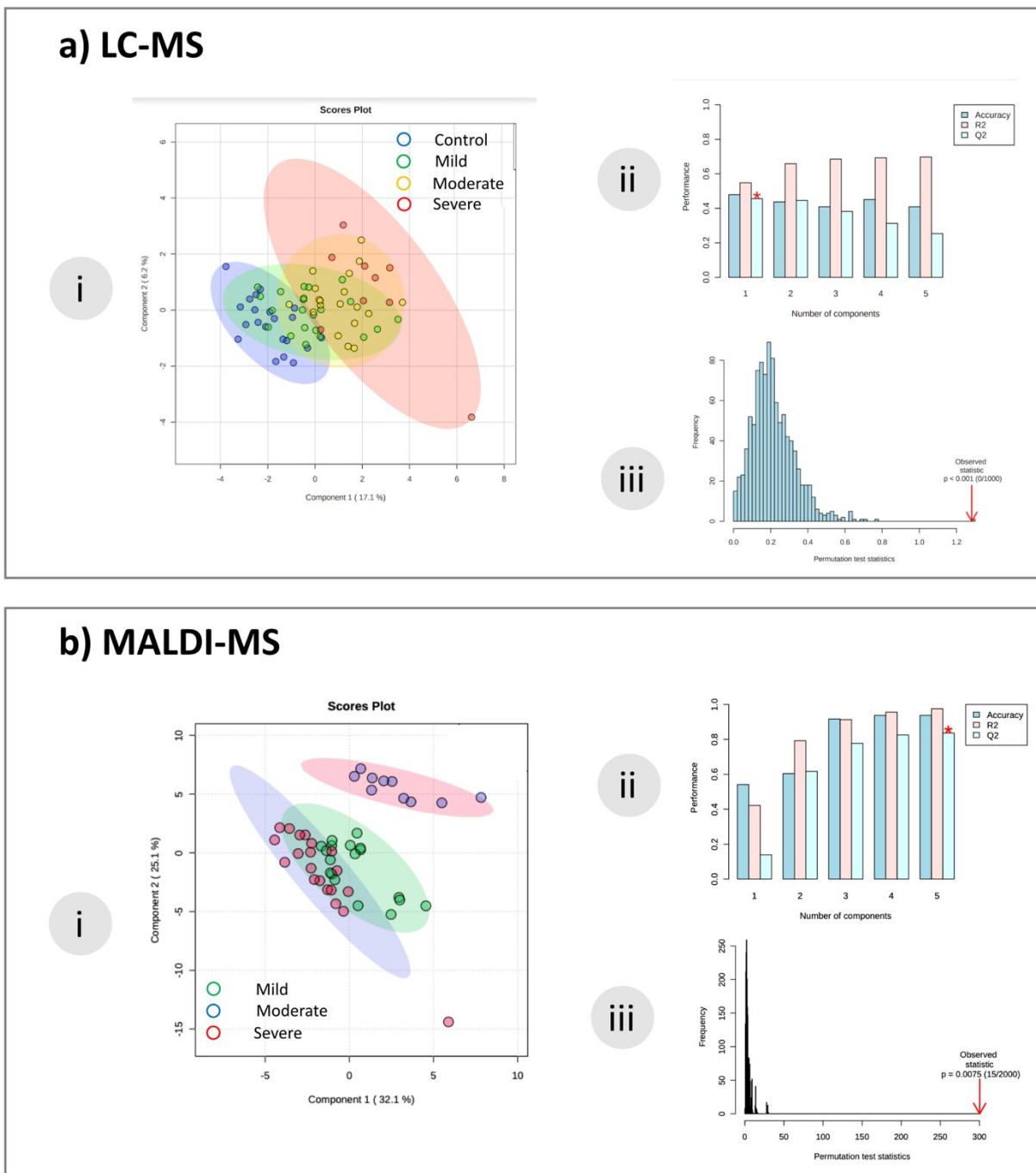


Figure S1. Statistical analysis for a) LC-MS and b) MALDI-MS datasets. The figure displays the plots of PLS-DA (i), cross-validation (ii), and permutation test (iii).

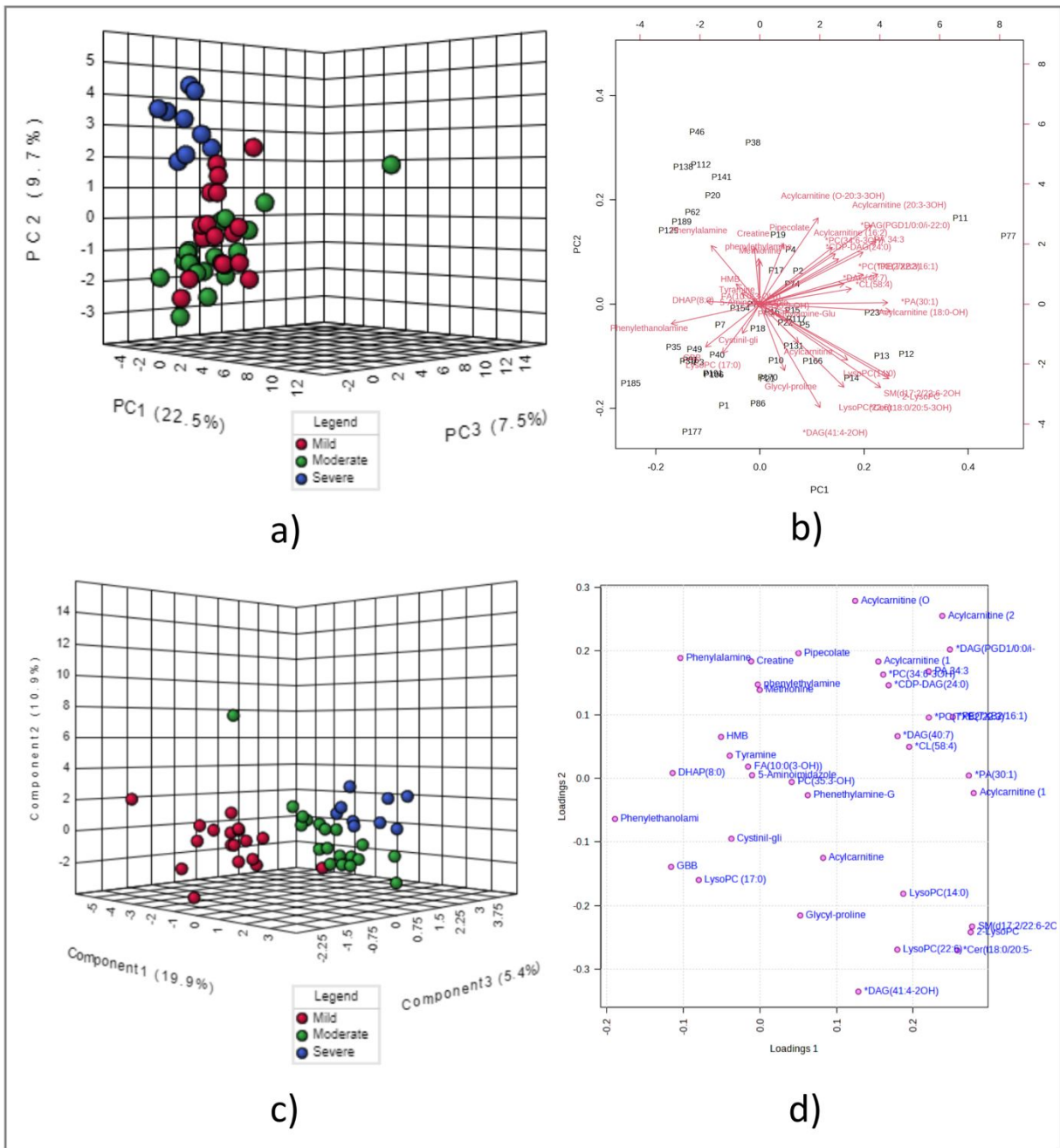


Figure S2. Multi-platform statistical analysis: 3D PCA (a) and biplot (b); 3D PLS-DA (c) and loadings plot (d).

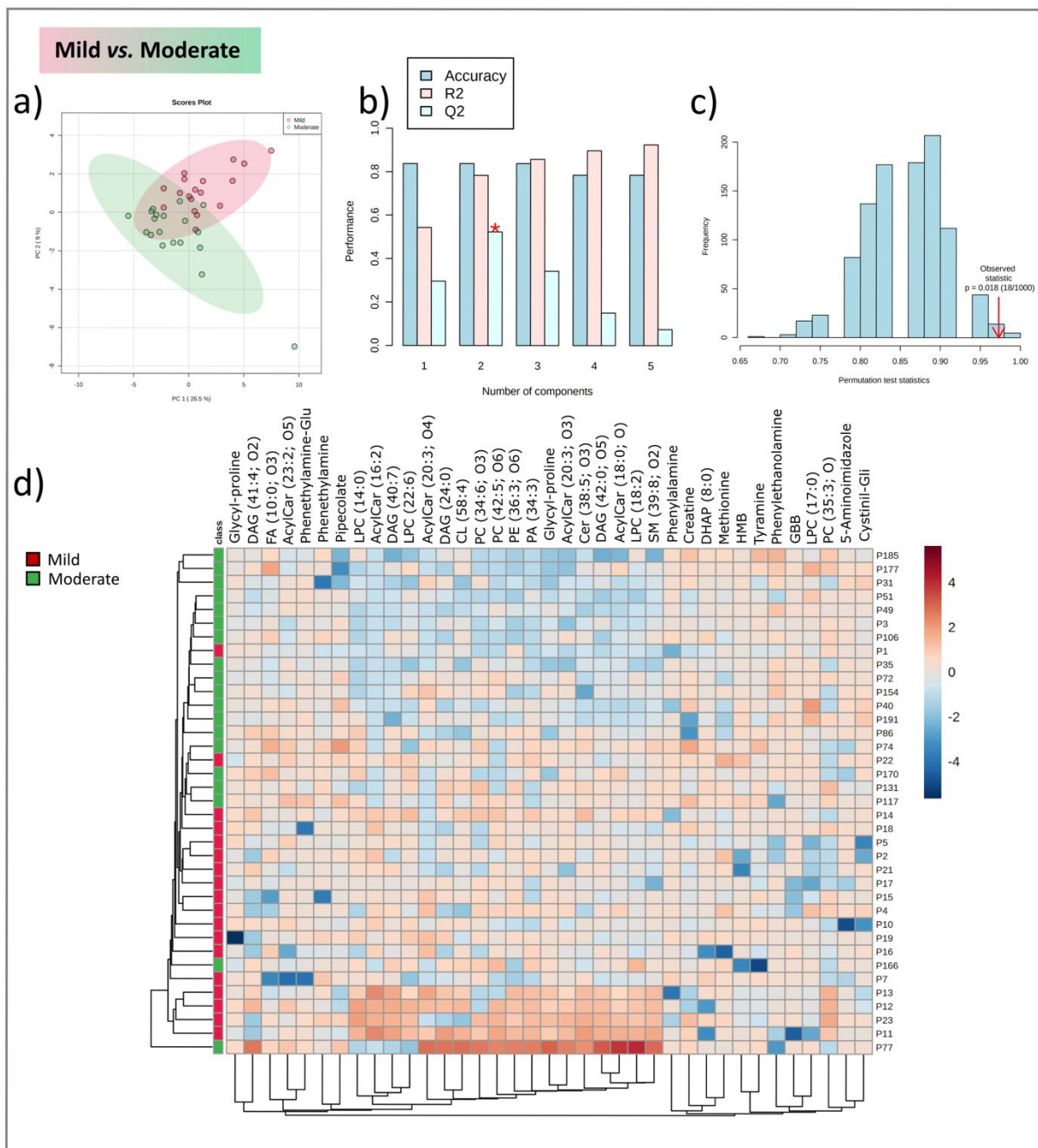


Figure S3. Mild vs. Moderate PCA and PLS-DA validation metrics: a) PCA, b) cross-validation, c) permutation test, and d) heatmap.

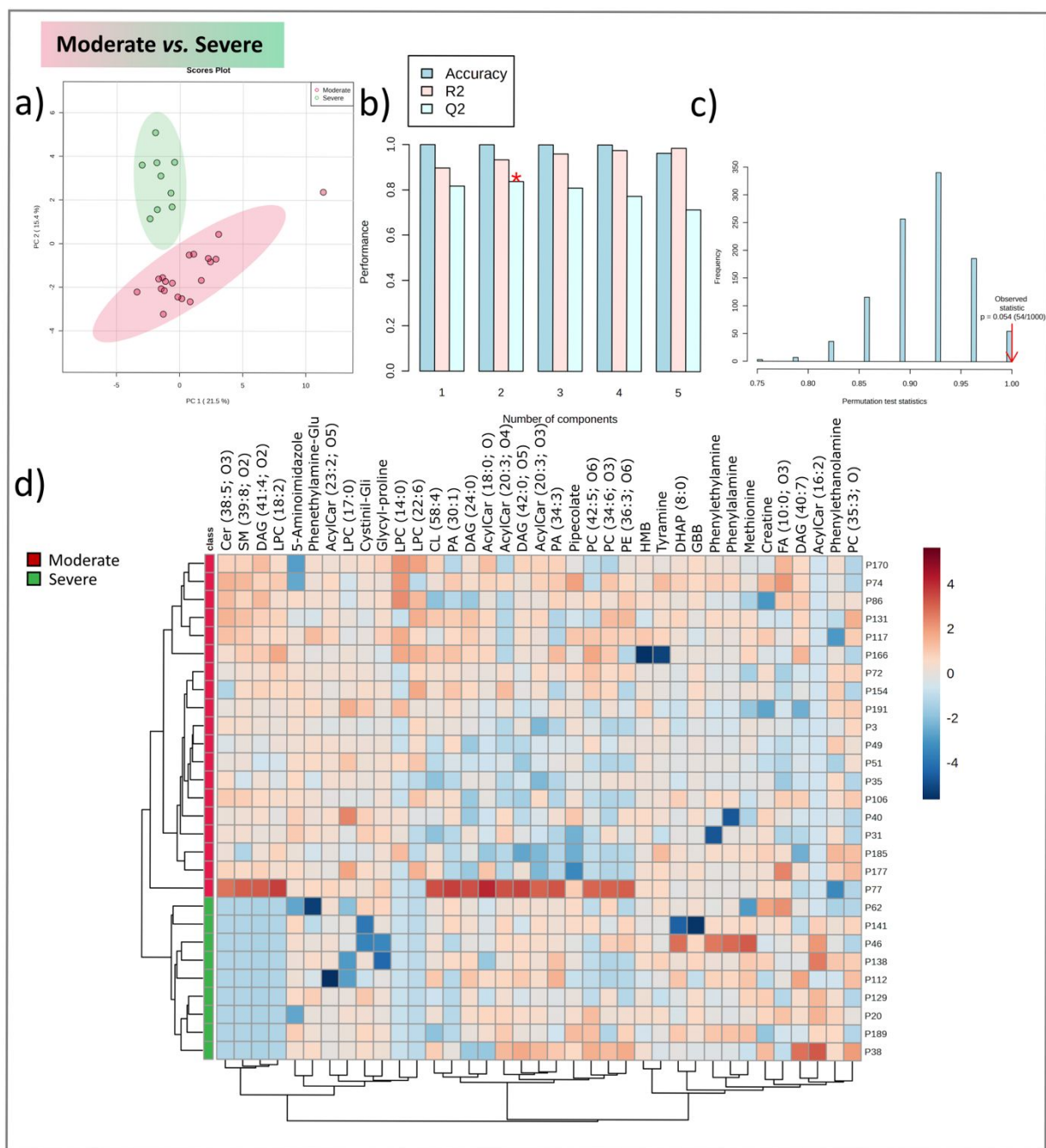


Figure S4. Moderate vs. Severe PCA and PLS-DA validation metrics: a) PCA, b) cross-validation, c) permutation test, and d) heatmap.

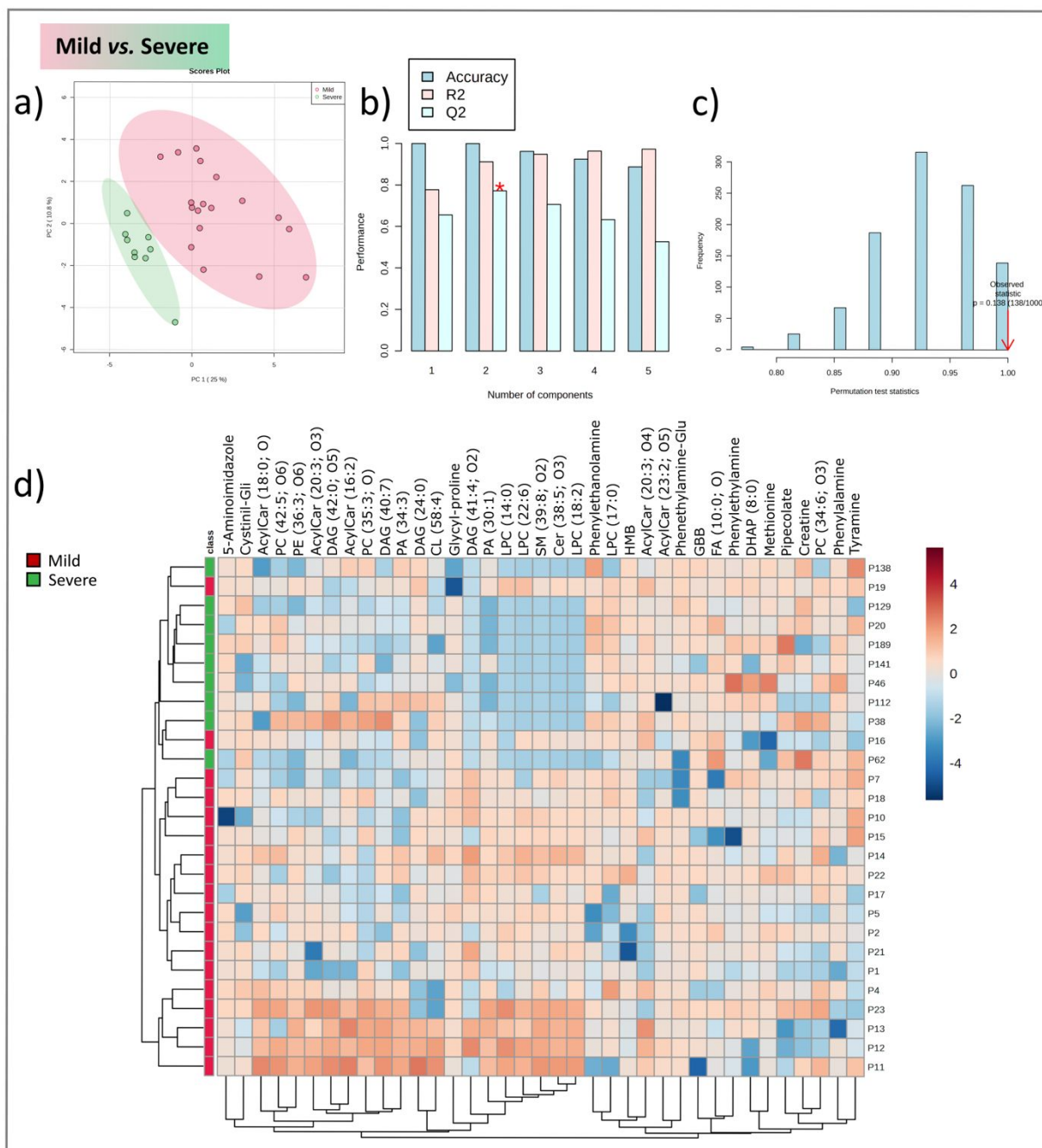
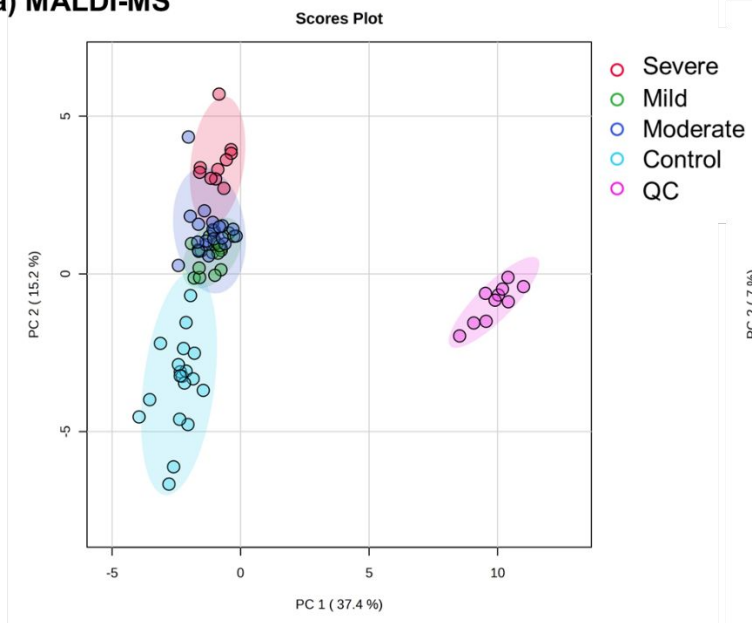


Figure S5. Mild vs. Severe PCA and PLS-DA validation metrics: a) PCA, b) cross-validation, c) permutation test, and d) heatmap.

a) MALDI-MS



a) LC-MS

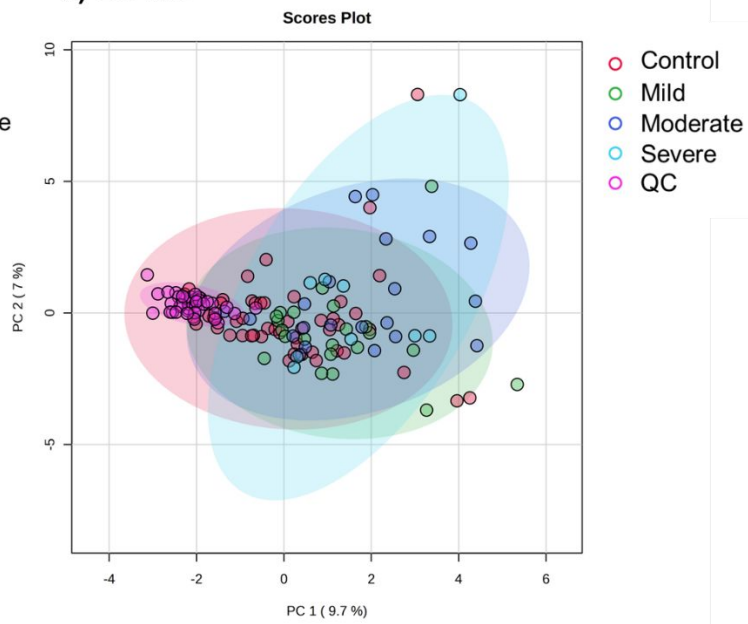


Figure S6. PCA Scores Plot analysis of LC-MS and MALDI-TOF data separately.