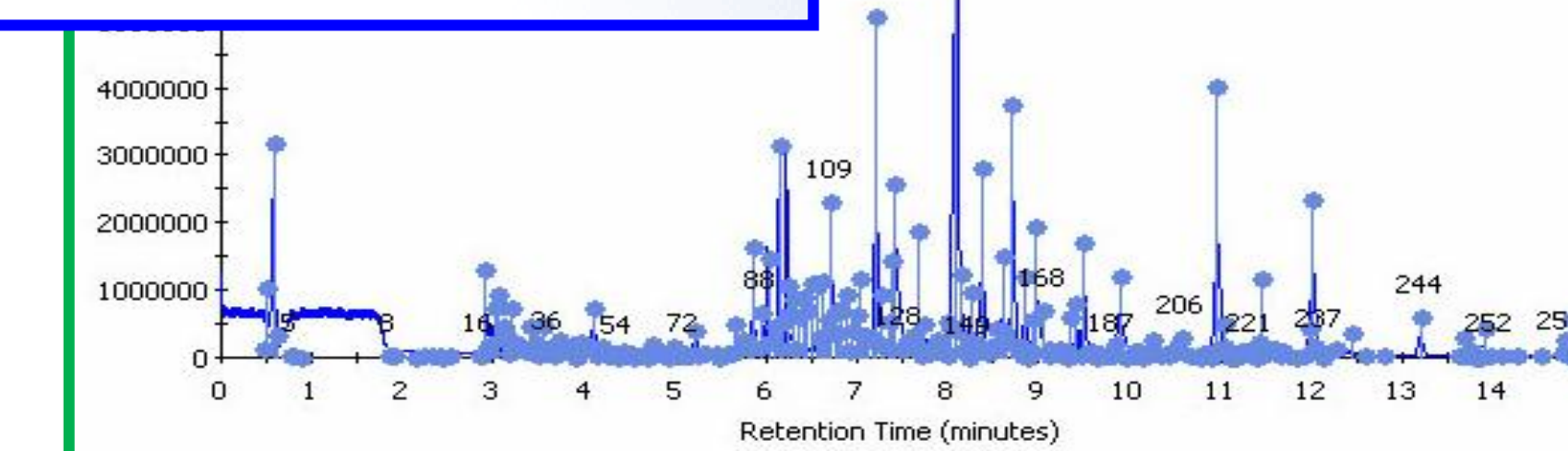
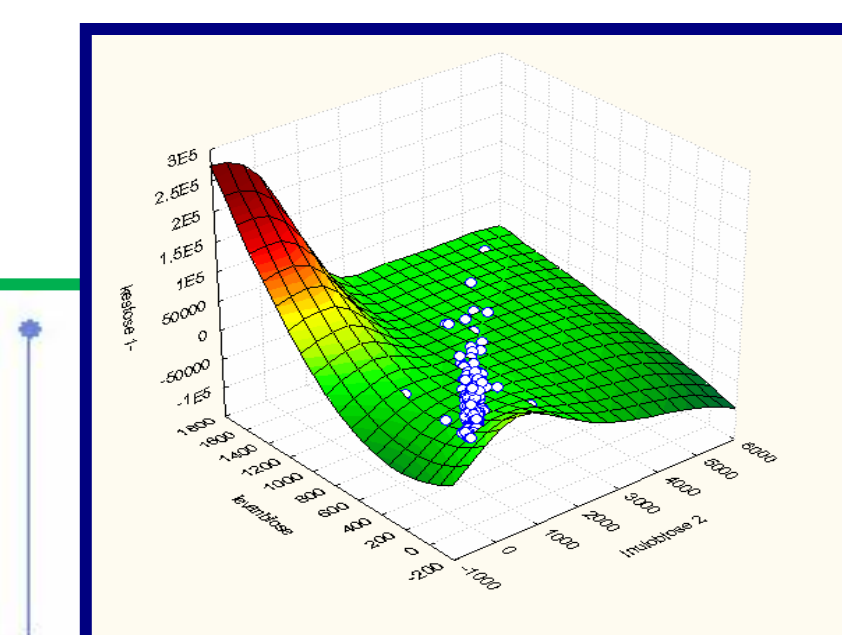


Biomarkers and Metabolomics: Practical Implication.

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Phase I. **Aim:** Find potential small molecule biomarkers for metastatic kidney cancer (RCC). Metabolomics pilot study. Proof of the concept. Phase 1 is completed.

Phase II. **Aim:** Use Phase I proof of concept methodology to carry out next set of studies:

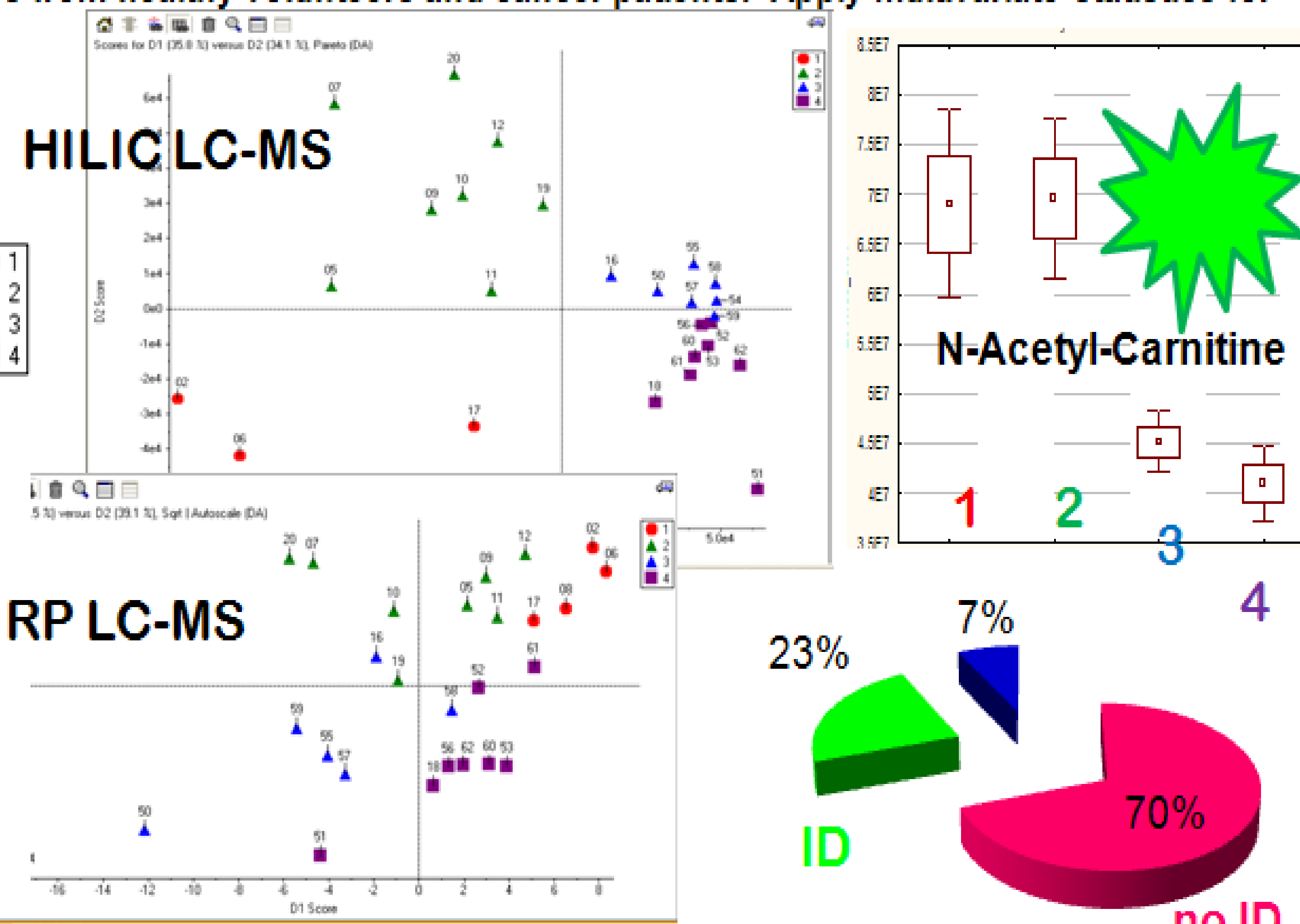
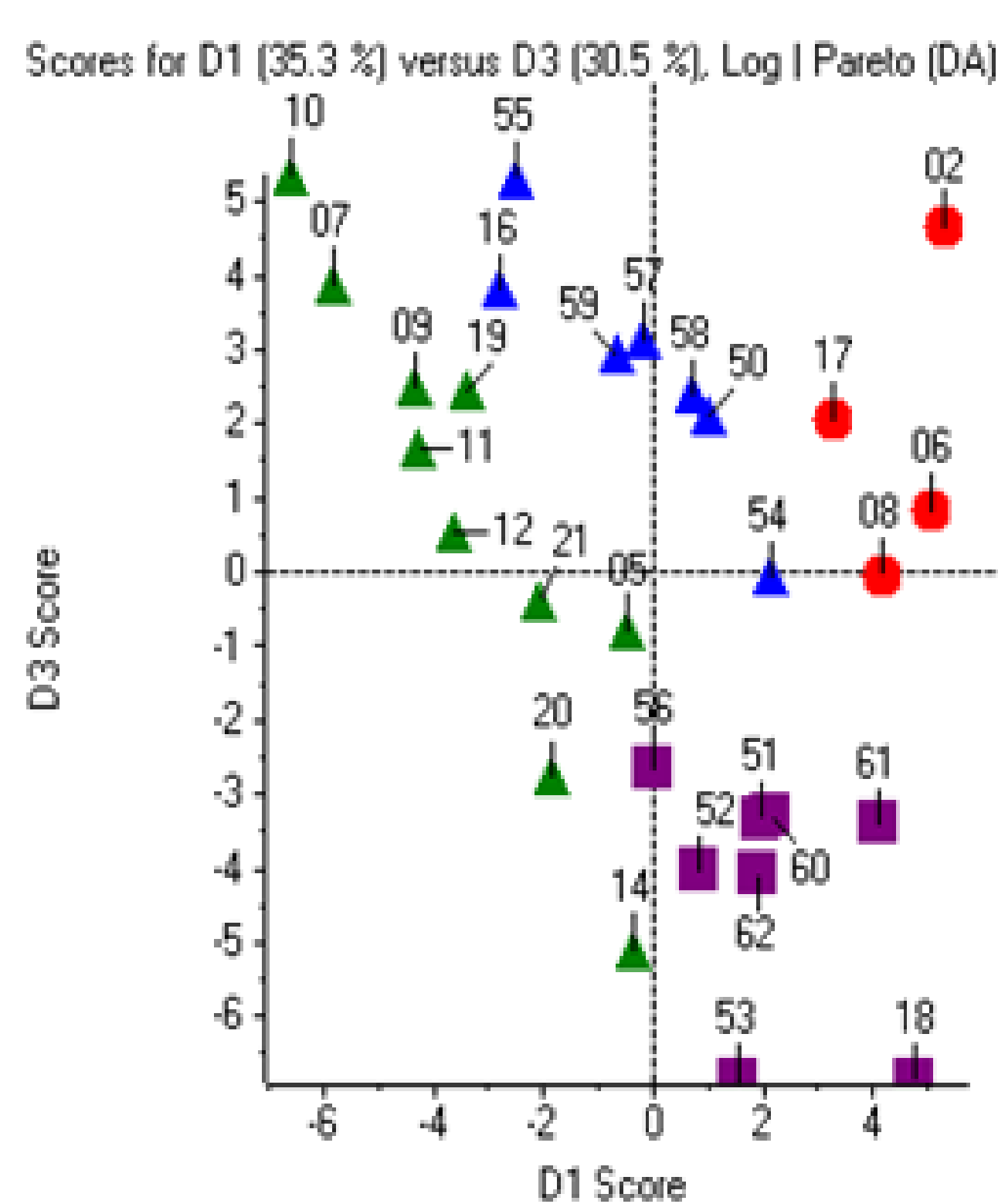
Run Metabolomics study on large group cancer patients and volunteers. Identify the most prominent biomarkers suitable for RCC diagnostic test development.

Method: Perform comprehensive profiling of urinary metabolites by GC-TOF-MS, RP-LC-ESI-MS and HILIC-LC-ESI-MS methods, analyzing urine samples from healthy volunteers and cancer patients. Apply multivariate statistics for data mining.

GC-TOF-MS

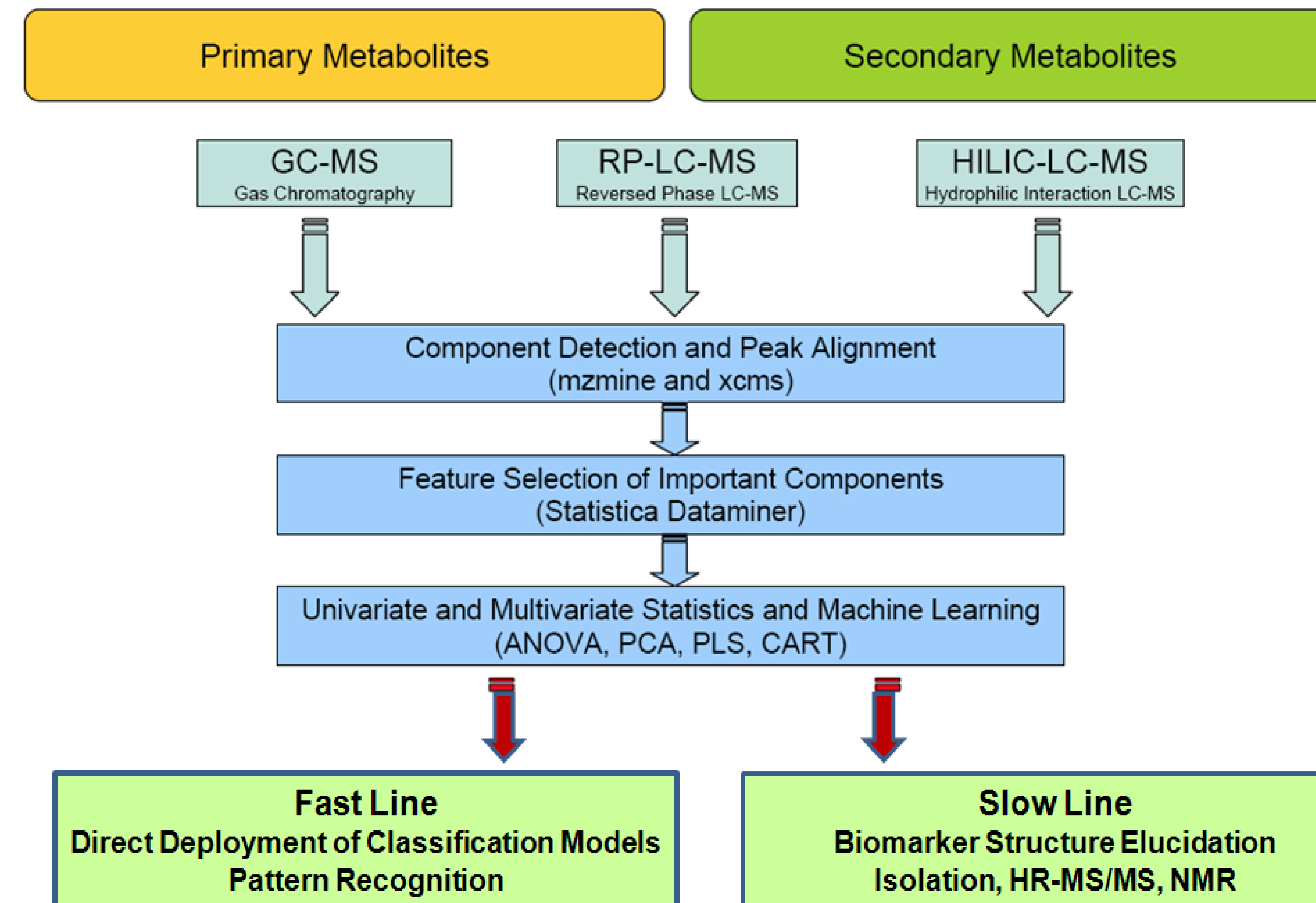
HILIC LC-MS

RP LC-MS



1-female RCC 2-male RCC 3-female control 4-male control

Small Molecule Biomarkers Workflow

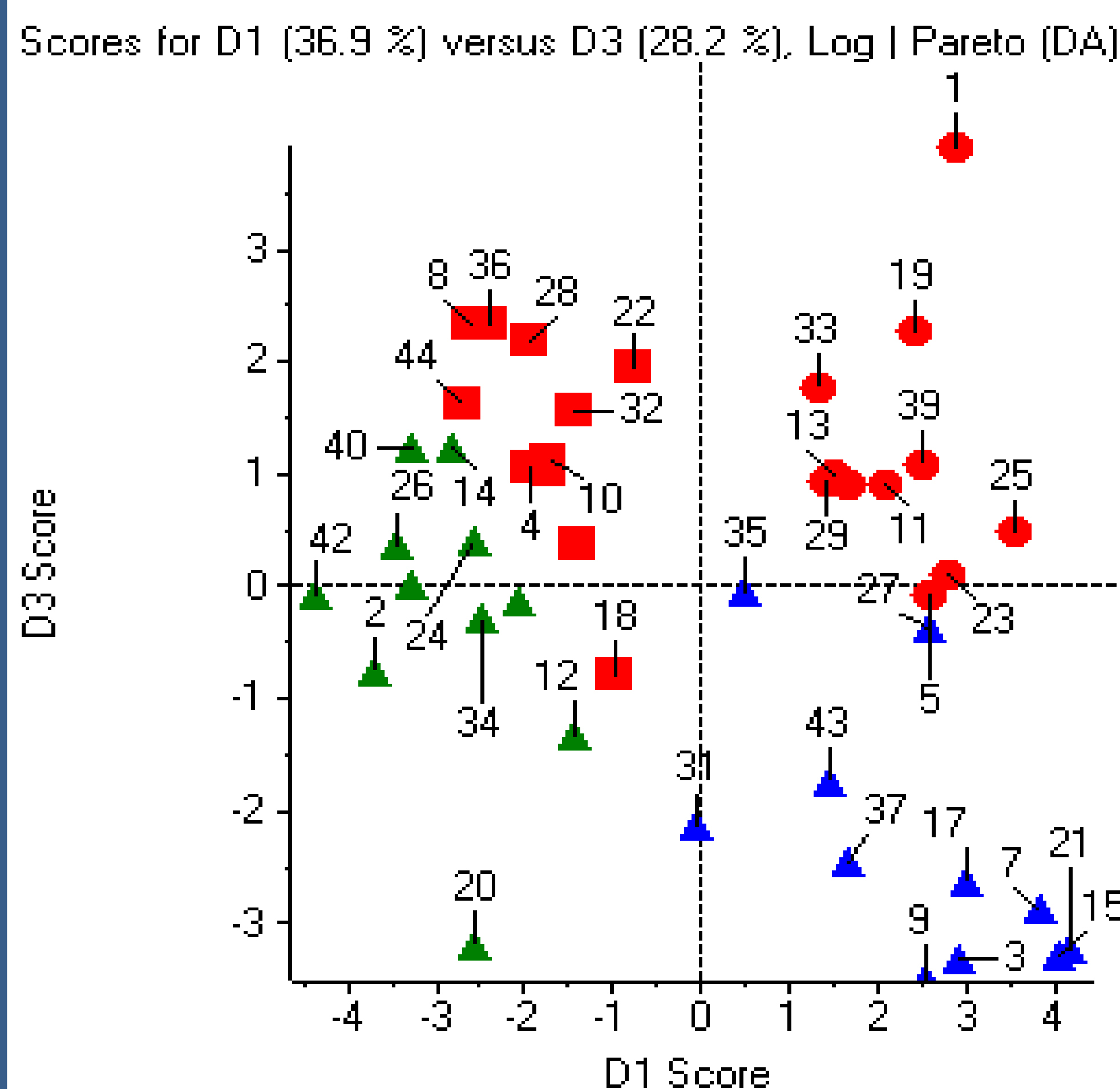


John W. Newman

USDA, ARS Western Human Nutrition Research Center (University of California, Davis)

Phase I **Aim:** Find potential differences between groups of individuals following high and low glycemic diet. Metabolomics pilot study. Proof of the concept.

Method: Perform blood plasma metabolite profiling by UPLC-RP-ESI-ITMS. Apply multivariate statistics for data mining.



Results: Data obtained demonstrates the presence of the blood plasma metabolites capable of discrimination between samples from individuals being on high and low glycemic diet for 3 days and sampled in the fasting time or post-prandially. Phase I is completed. Four groups were sampled.

Phase II: **Aim:** Use Phase I proof of concept methodology to carry out next set of studies:

Methods: a) Identify the most prominent biomarkers suitable for tests development.

b) Perform validation the most prominent biomarkers.

PCA score plot for UPLC-RP-LC-MS metabolic profiling analysis data is illustrating samples discrimination and groups clustering.

Yale University

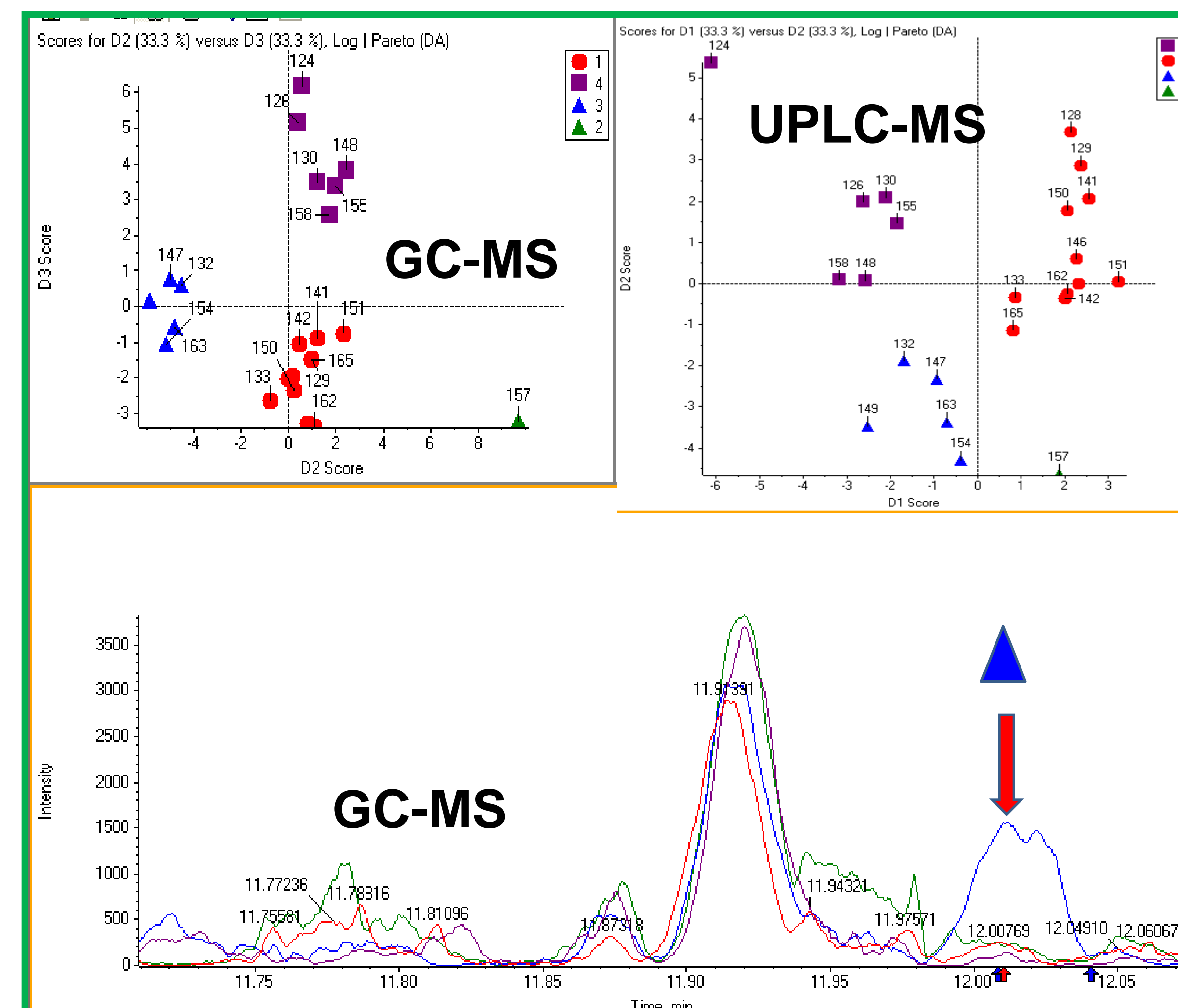
Yale School of Public Health

Kathleen M. McCarty

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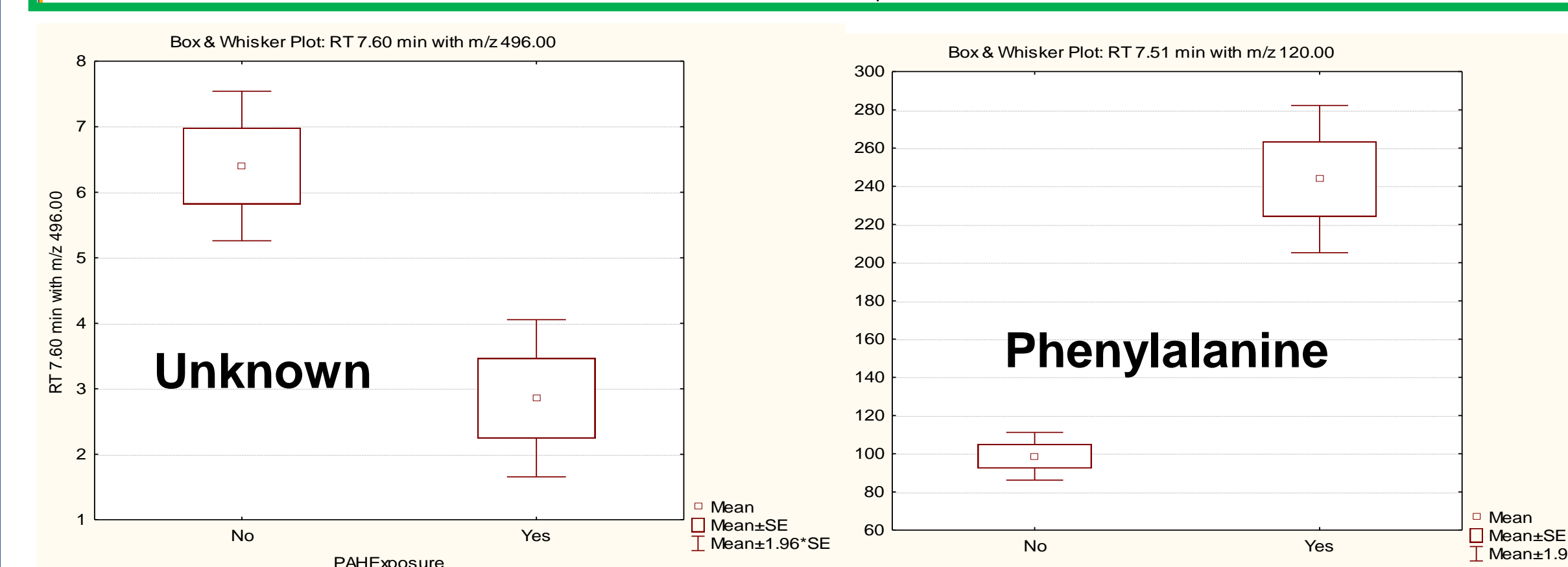
Phase I **Aim:** Find potential differences between groups of individuals with PAH exposure and without it. Among these subjects PAH-DNA adducts detected and not detected. Four groups of subjects are defined for data mining.

Method: Perform blood plasma metabolite profiling by GC-TOF-MS and UPLC-ITMS. Apply multivariate statistics for data mining



Results: Data obtained demonstrates the presence of the blood plasma metabolites capable of discrimination between defined groups of samples. Potential biomarkers are detected. Phase I is completed.

Phase II: **Aim:** Large scale experiments: **Methods:** a) Identify the most prominent biomarkers suitable for the tests development. b) Perform validation the most prominent biomarkers.



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<http://metabolomics-core.ucdavis.edu/>