

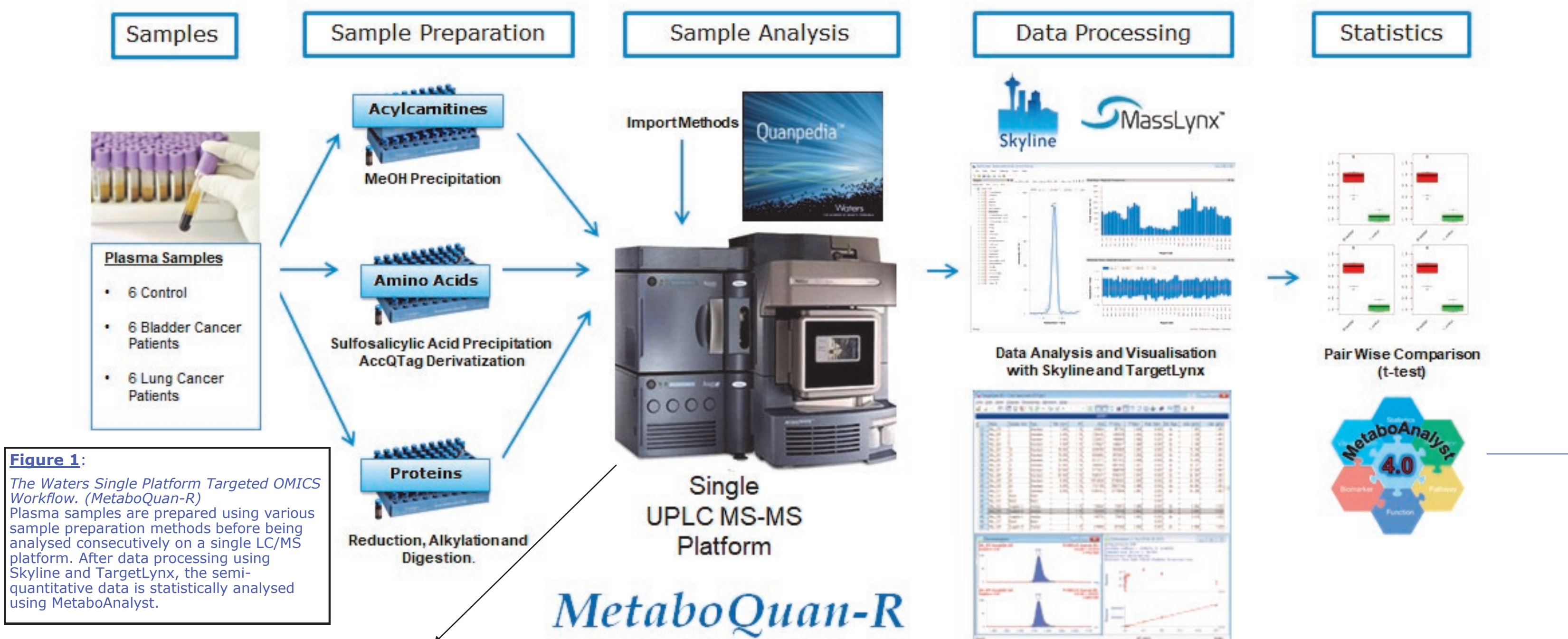
Targeted Multi-OMICS: Rapid Plasma Profiling of a Bladder and Lung Cancer Human Cohort

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TARGETED MULTI-OMICS WORKFLOW



AMINO ACIDS

ACYLCARNITINES

PROTEINS

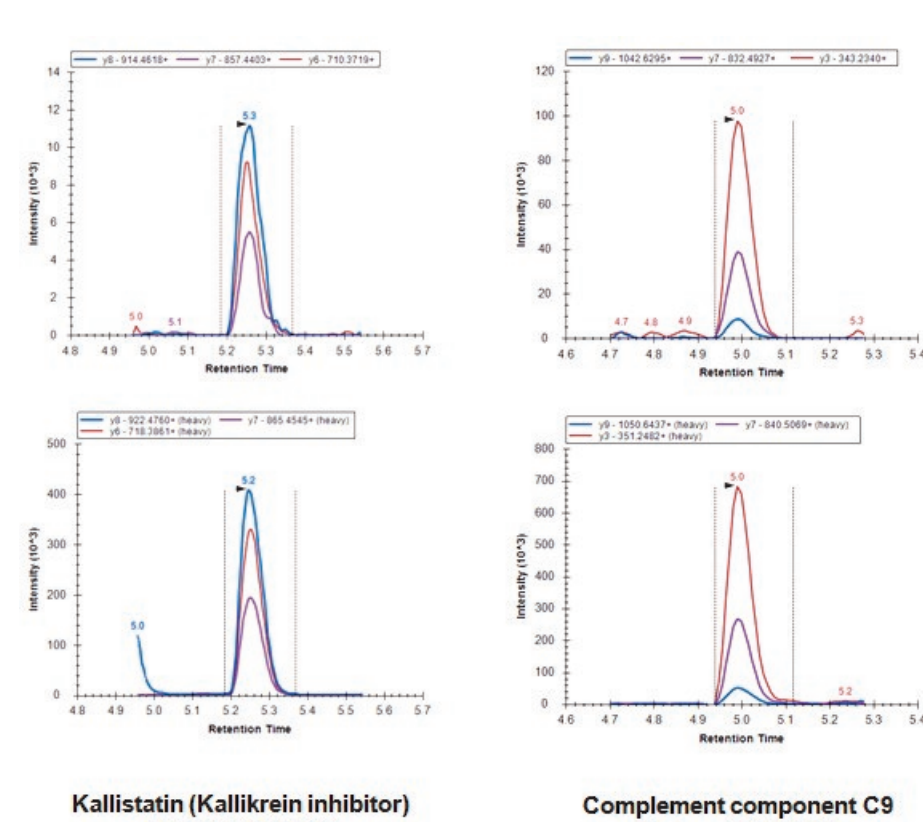
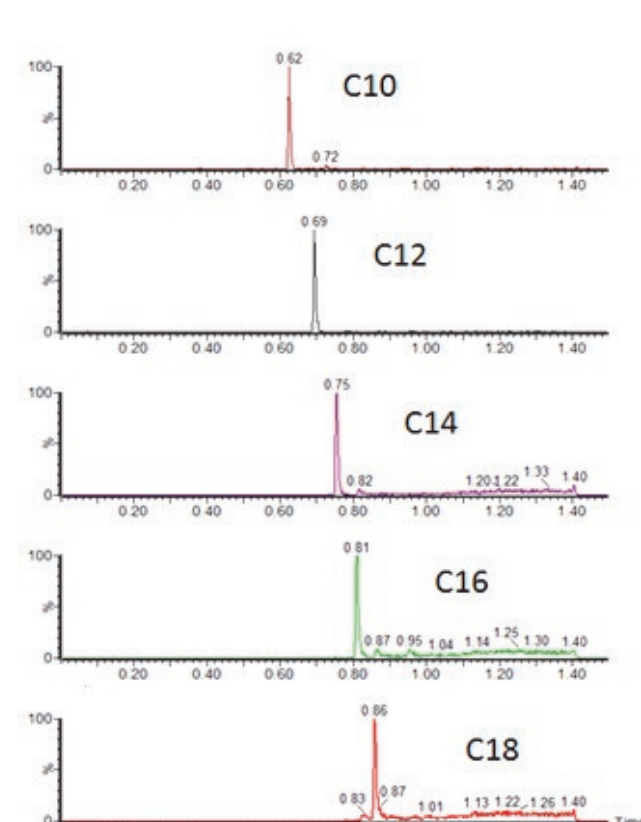
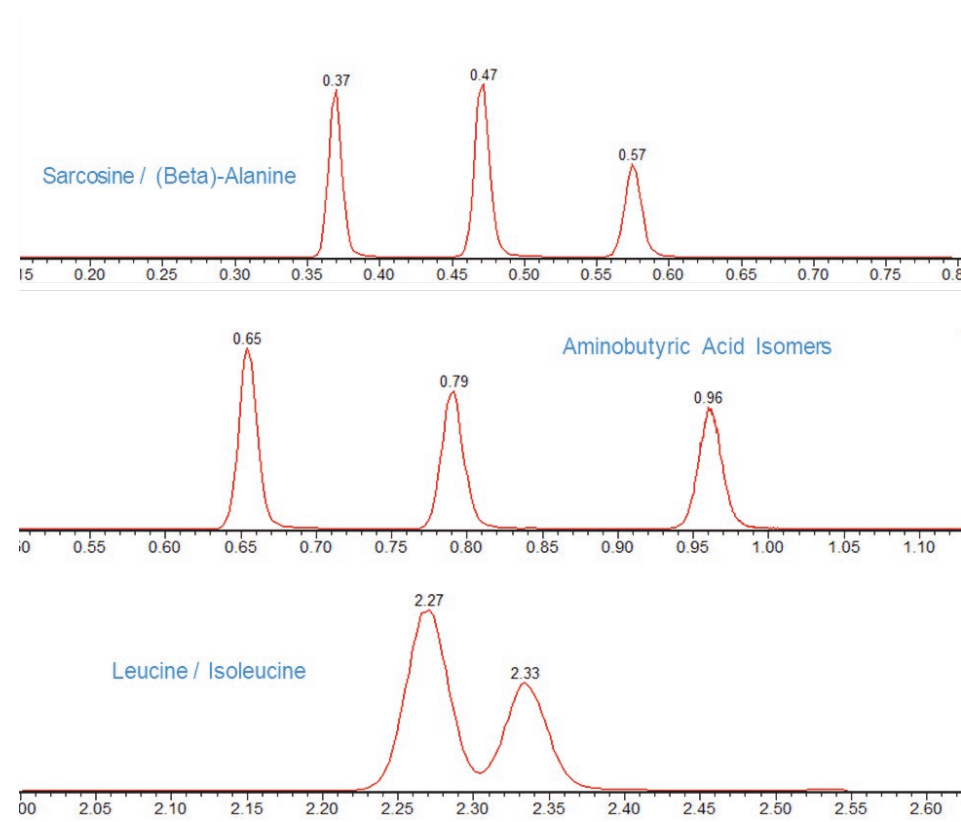


Figure 2: representative chromatograms demonstrating separations achieved for MetaboQuan-R methods using the same Mobile Phase and UPLC Column

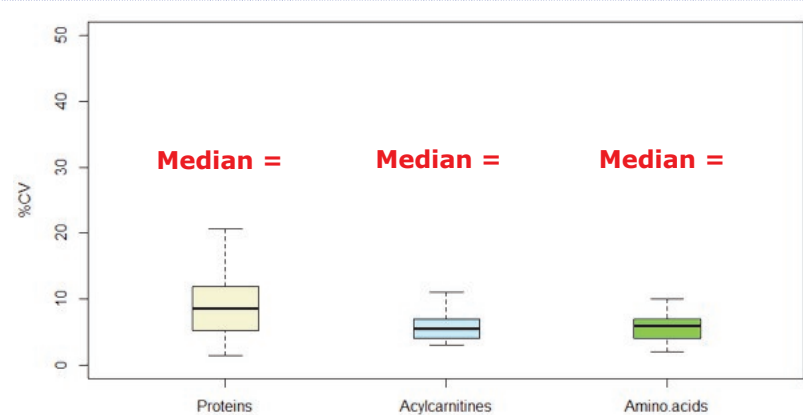


Figure 3: Box and whisker plot representing the distribution of the peak area coefficients of variation (%CV) across the quality control samples for the 128 detected compounds in plasma.

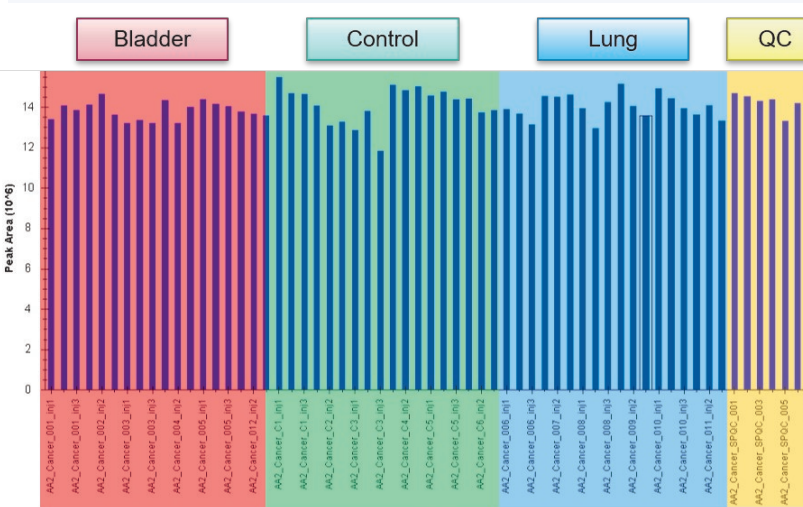


Figure 4: Peak areas for the spiked amino acid standard (valine d8) for all samples. The overall median coefficient of variation was observed to be 5%.

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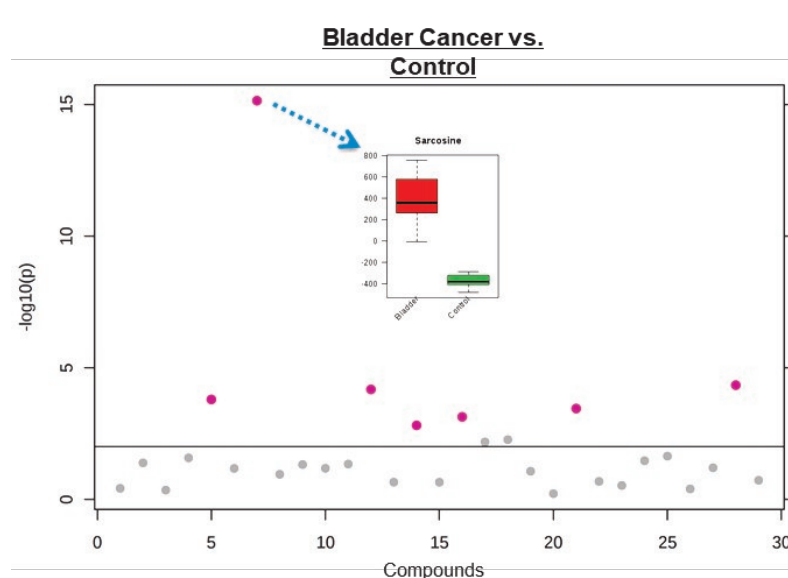


Figure 5: Pair-wise comparisons of 28 amino acids (t-test, FDR cut-off value = 0.01). The pink dots represent significantly different amino acids between the two conditions. Sarcosine was found to be over expressed for both bladder and lung cancer subjects.

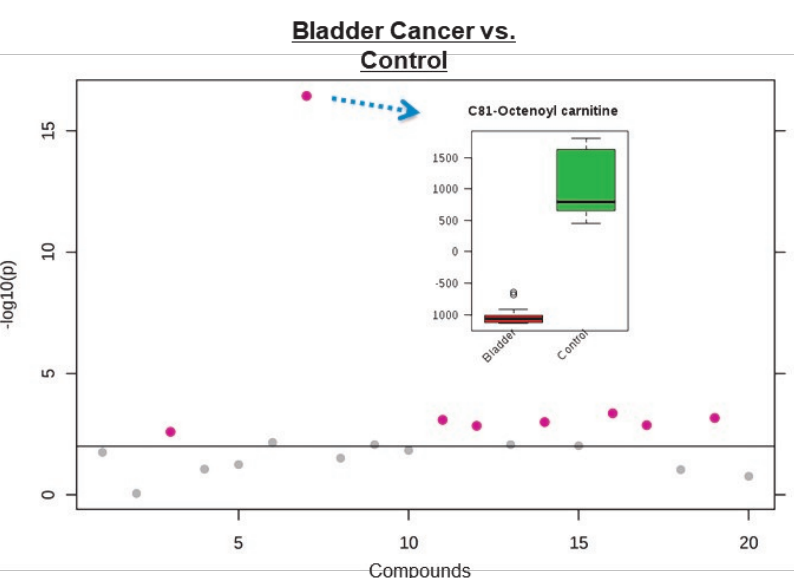


Figure 6: Pair-wise comparisons of 20 acylcarnitines (t-test, FDR cut-off value = 0.01). The pink dots represent significantly different acylcarnitines between the two conditions. Octenoyl carnitine (C8:1) was shown to be under-expressed in bladder cancer subjects. The statistical differentiation of acylcarnitine markers for lung cancer was less conclusive.

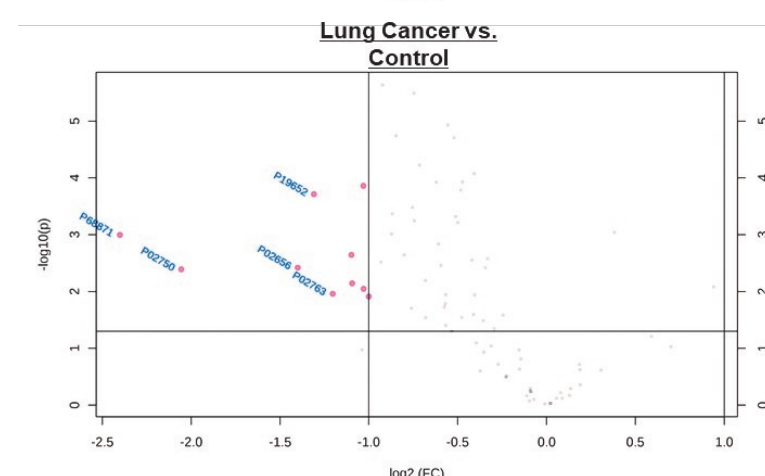
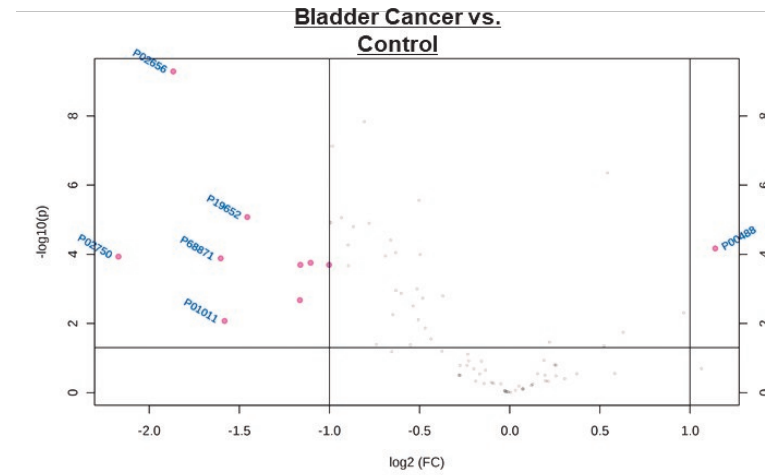


Figure 7: Volcano plot highlighting potential proteins of interest (pink dots) when comparing bladder cancer vs. control and lung cancer vs. control.

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