

Supplementary Table S1. Summary of report output from XCMS for a list of features identified in plasma and CSF from 10 male individuals. XCMS output includes fold change for each feature (calculated by average peak areas), the p-value associated with the fold change (Welch's t-test), the *m/z* for the feature, the retention time in minutes, the number samples the feature was found in for both sample groups, and the integrated peak area of the feature in each individual sample. Features are identified by MS/MS spectral matching using the METLIN database.

Supplementary Figure S1. **A)** Library match of a pure standard (left) to the endogenous metabolite tyrosine in CSF (right) using MS/MS spectra. **B)** Box plot illustrating the variation of tyrosine in biological replicates of human plasma and CSF from 10 male individuals.