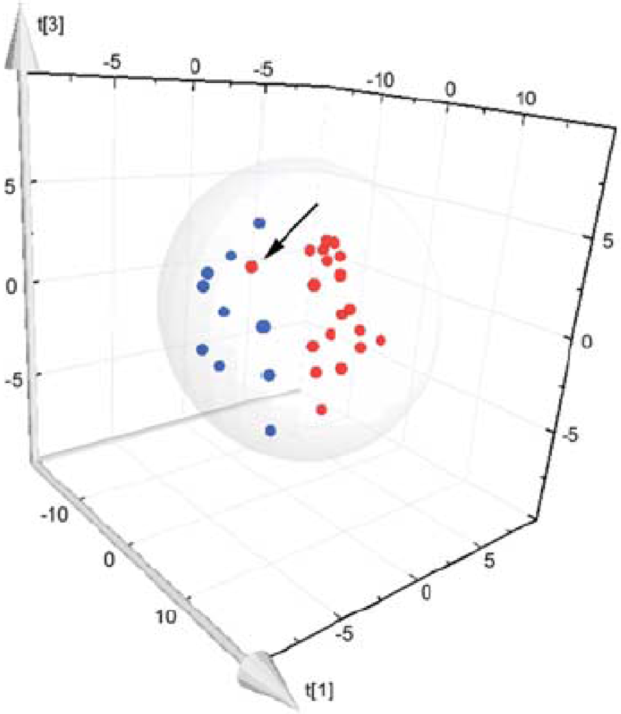

Figure 1. Partial least squares – discriminatory analysis (PLS-DA) model showing clear differences in the blood metabolic profiles of acute, poor outcome CLL patients (blue) and chronic, better outcome patients (red). The arrow indicates one patient clinically diagnosed as a better outcome patient yet whose metabolic profile was clearly more consistent with poor outcome patients.

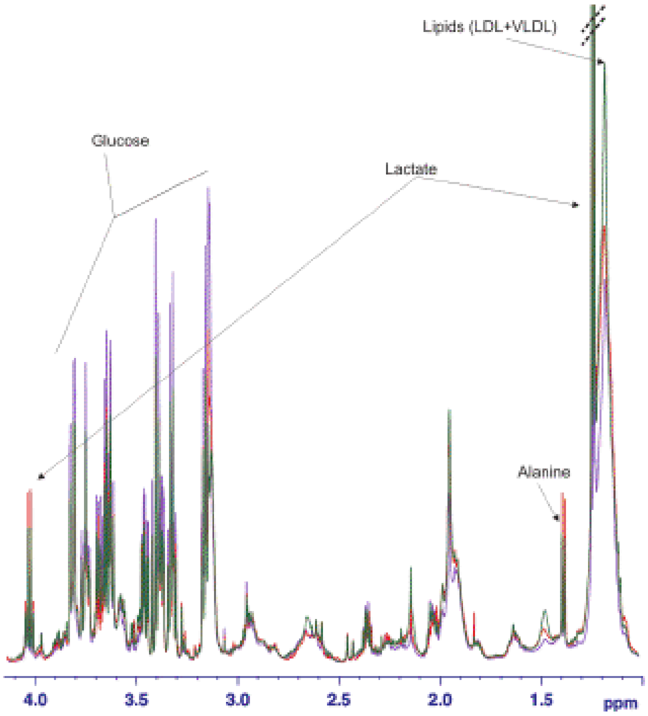

Figure 2. ^{1}H-NMR spectrum of blood serum from a representative control (green), cirrhotic patient without MHE (red) and with MHE (purple). A number of metabolites in the aliphatic region showing differences in concentration between the groups are labelled.

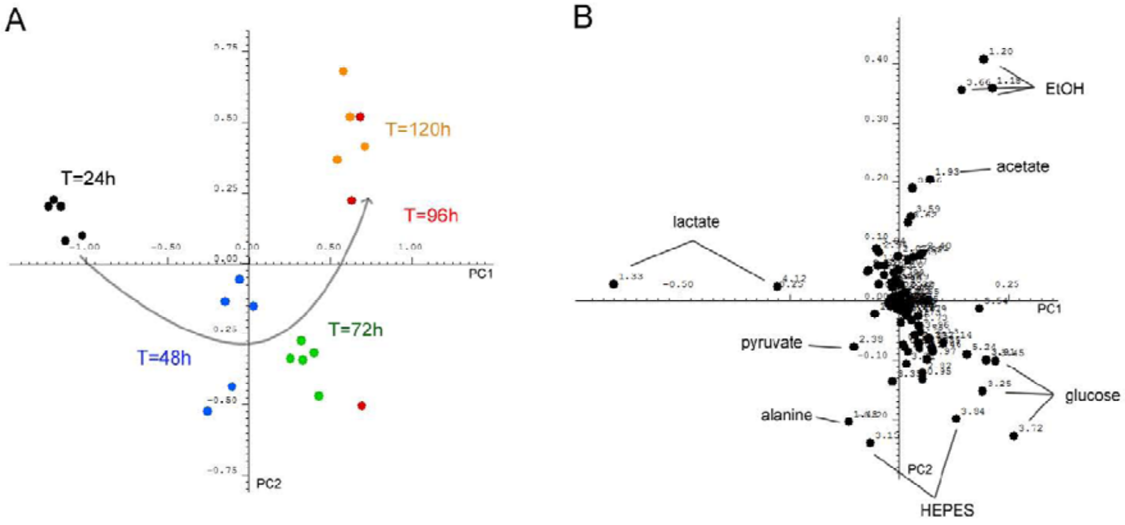

Figure 3. Metabonomics analysis of HFF conditioning media collected over a time course revealed important changes in the concentration of various metabolites and small compounds. The PLS-DA score plot (A) shows changes in the overall metabolic profile of individual samples over time whilst the PLS-DA loadings plot (B) reveals those metabolites changing most over time. Those metabolites present in the same vicinity as samples are present in high concentrations in these samples (eg lactate is present in high concentration in samples collected after 24h conditioning).