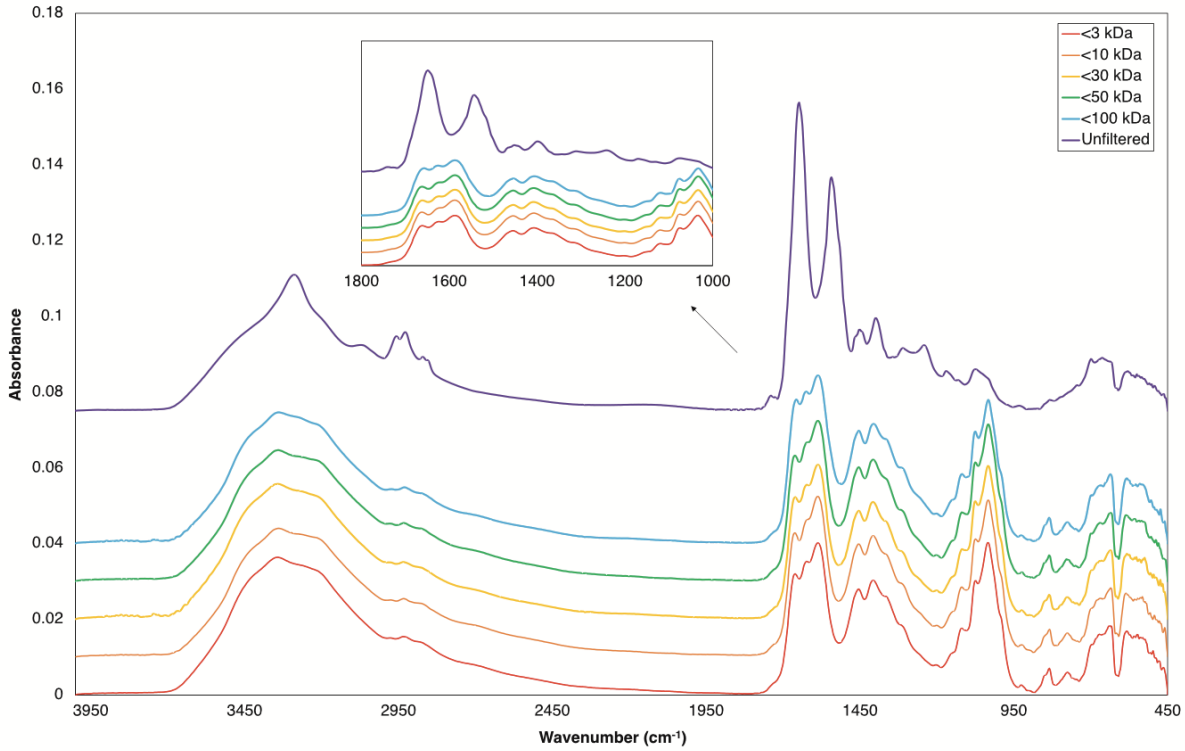

Fig 1. Example of patient serum spectra including unfiltered whole serum and each molecular weight region.
Average of the 30 GBM patients shown here. The inset is the wavenumber region between 1800 cm^{-1} and 1000 cm^{-1}, which was used for all chemometrics and machine learning analyses. Spectra is offset for clearer visualisation.

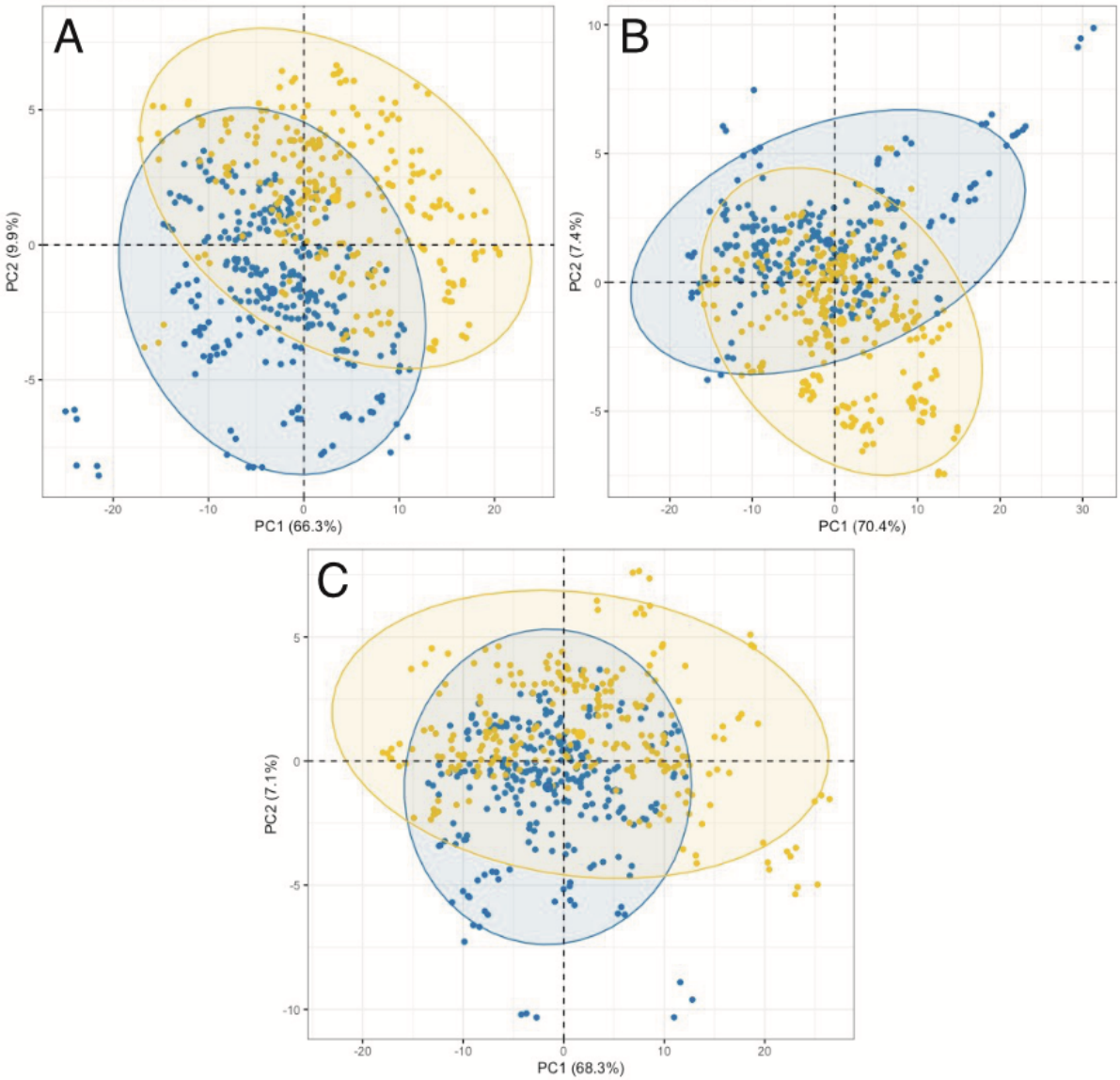

Fig 2. Principal component analysis scores plots for the unfiltered whole serum of the first and second dimensions.

The three figures represent (A) GBM in blue and non-cancer in yellow, (B) lymphoma in blue and non-cancer in yellow and (C) GBM in blue and lymphoma in yellow. The eclipses in each class represent a 95% confidence interval. Values in parentheses within the axes legends are the total explained variance (TEV) for each principal component (PC).

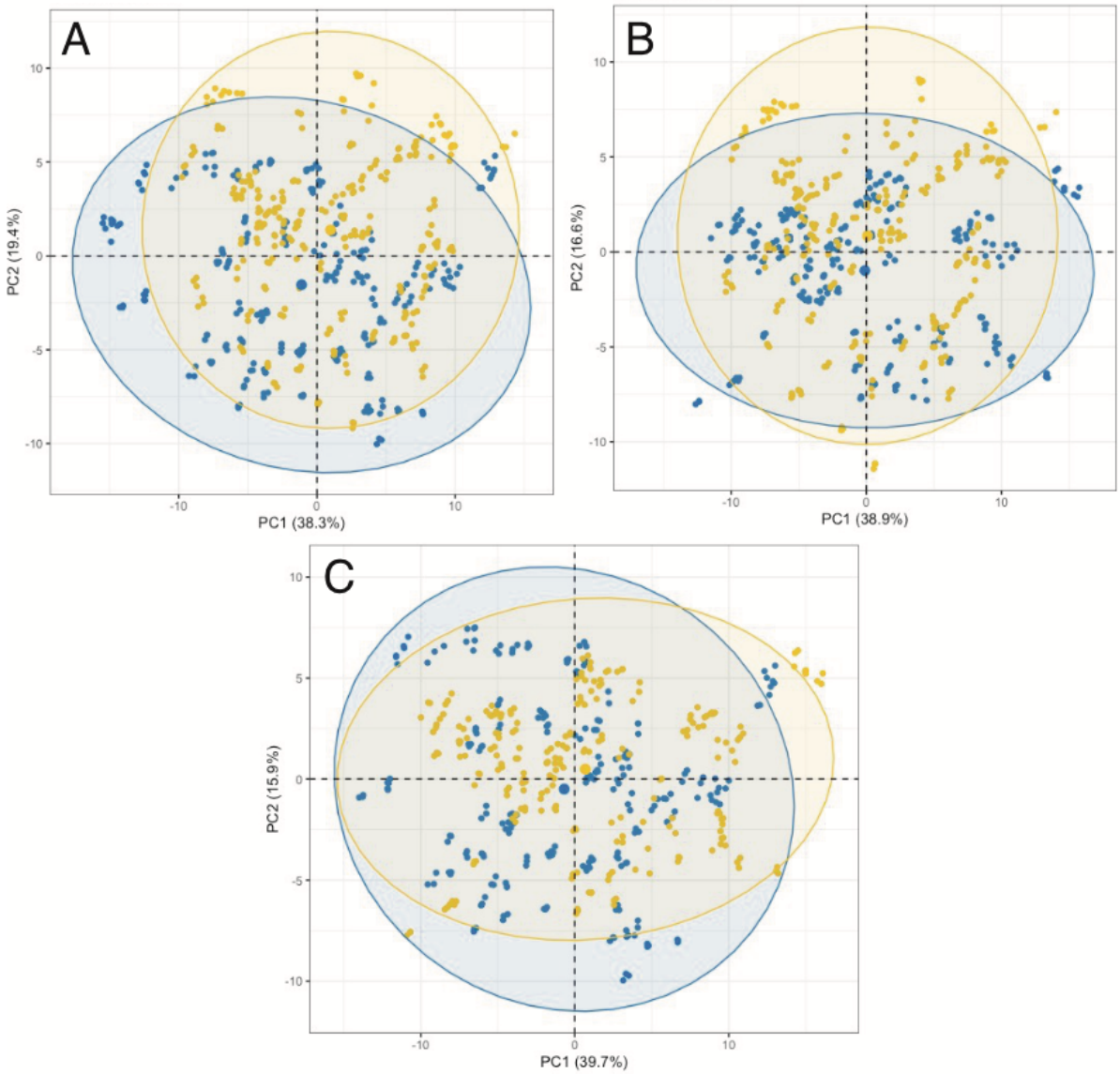

Fig 3. PCA scores plots for the filtered serum (<100 kDa) of the first and second dimensions. The three figures represent (A) GBM in blue and non-cancer in yellow, (B) Lymphoma in blue and non-cancer in yellow and (C) GBM in blue and lymphoma in yellow. The eclipses in each class represent a 95% confidence interval. Values in parentheses are the TEV for each PC.

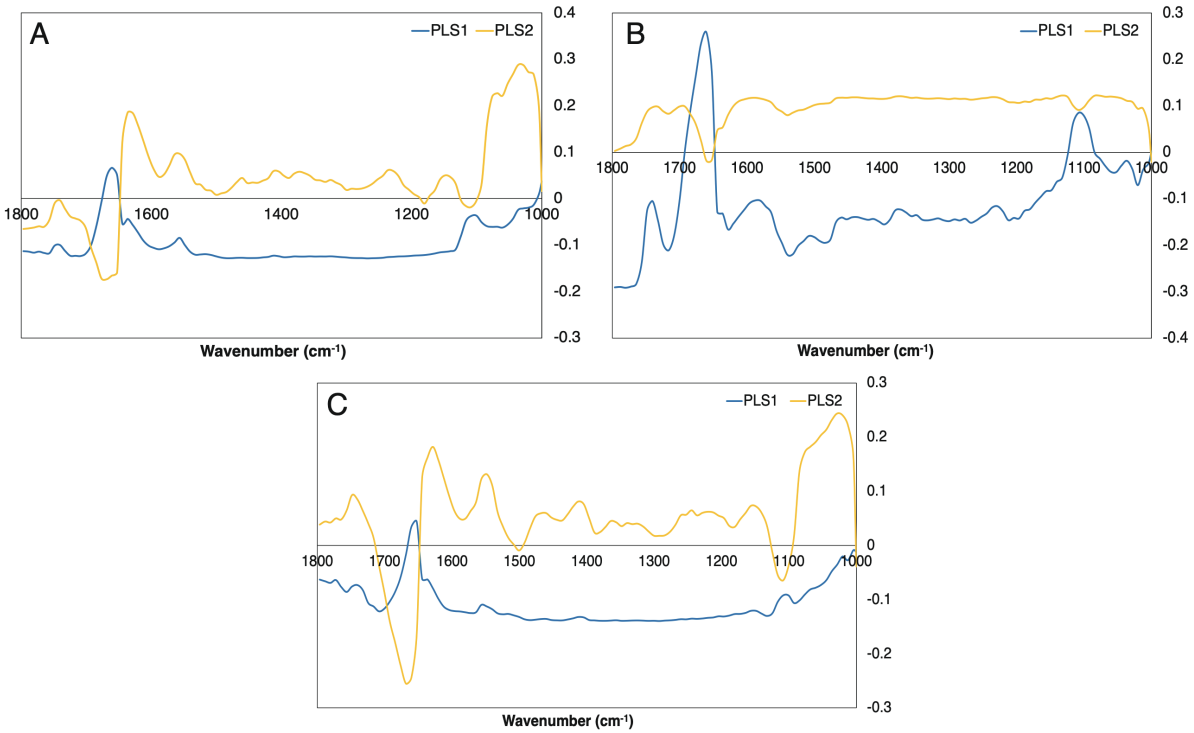

Fig 4. PLS loadings plots for the 1st and 2nd latent variables (LVs) for the unfiltered whole serum.
(A) GBM *versus* non-cancer, (B) Lymphoma *versus* non-cancer and (C) GBM *versus* lymphoma.

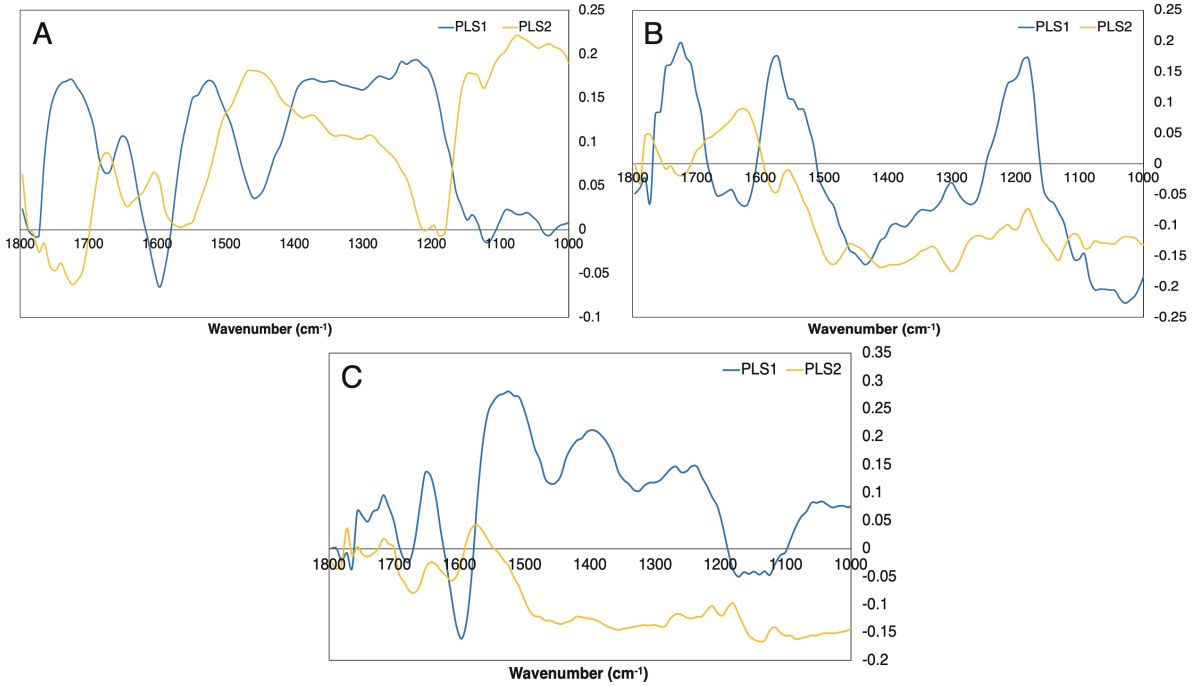

Fig 5. PLS loadings plot for the 1st and 2nd LVs for the filtered serum (<100 kDa).
(A) GBM *versus* non-cancer, (B) Lymphoma *versus* non-cancer and (C) GBM *versus* lymphoma.