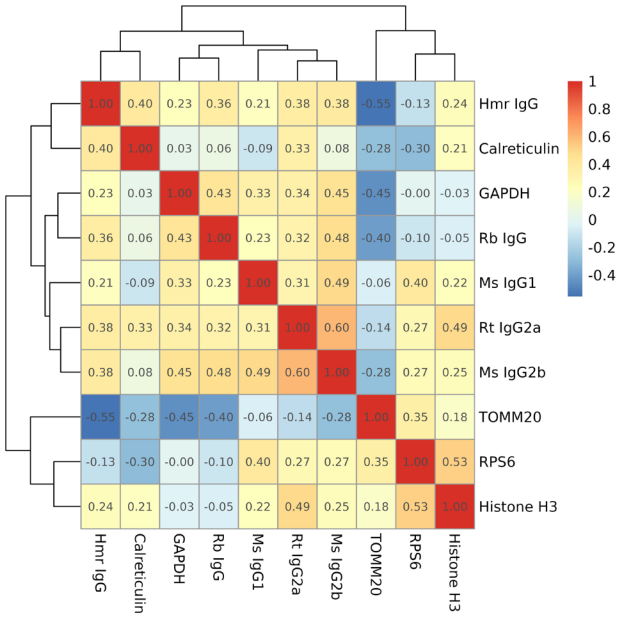
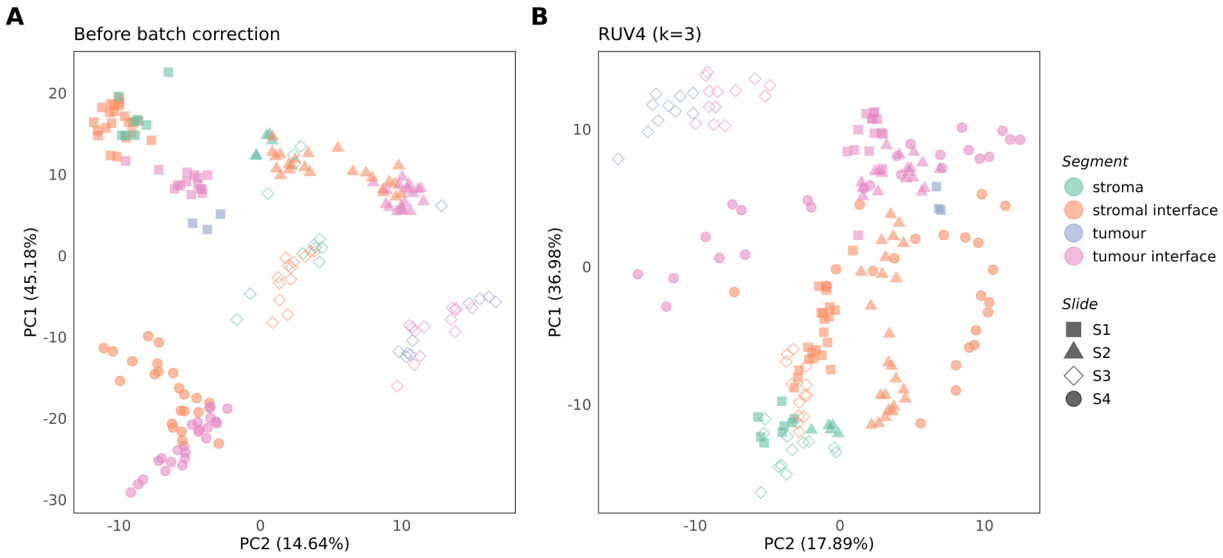
Supplementary Information

Supplement to: Rahul L & Meg LD et al. Resolving tissue-level proteomic complexity in cutaneous squamous cell carcinoma (cSCC) with ultra high-plex spatial profiling

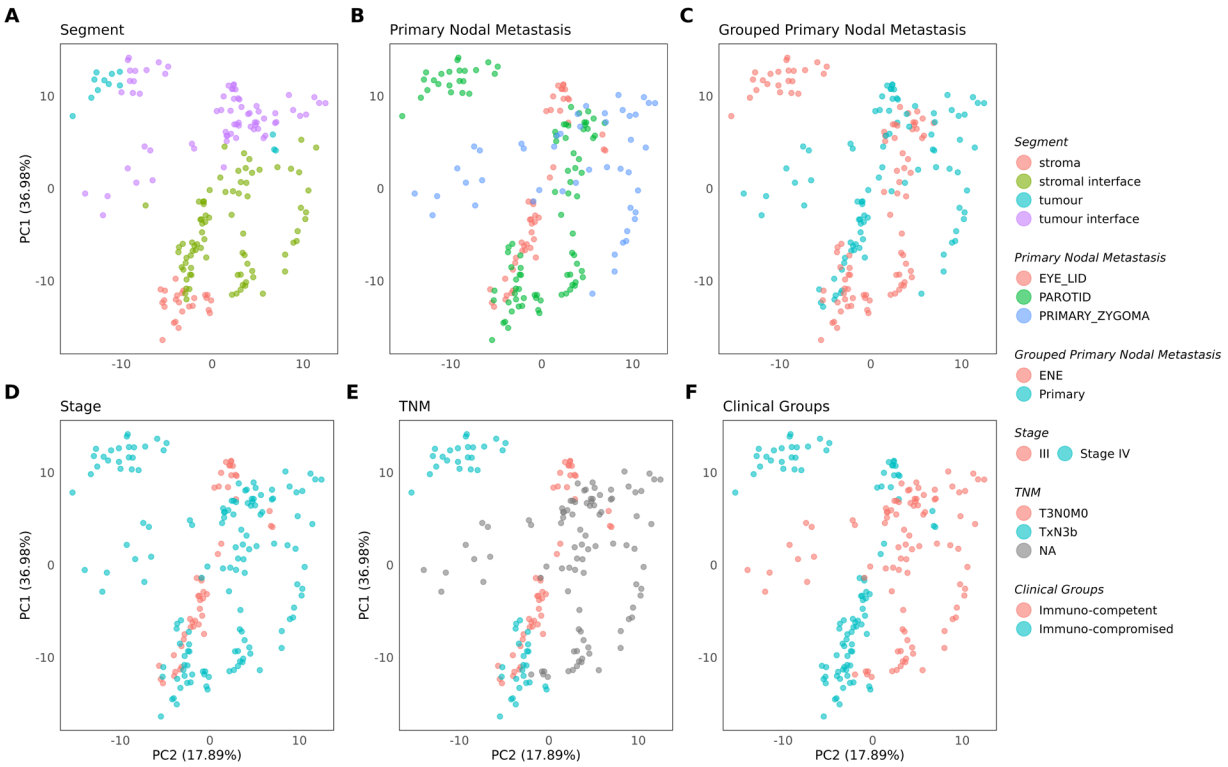
Supplementary Figures



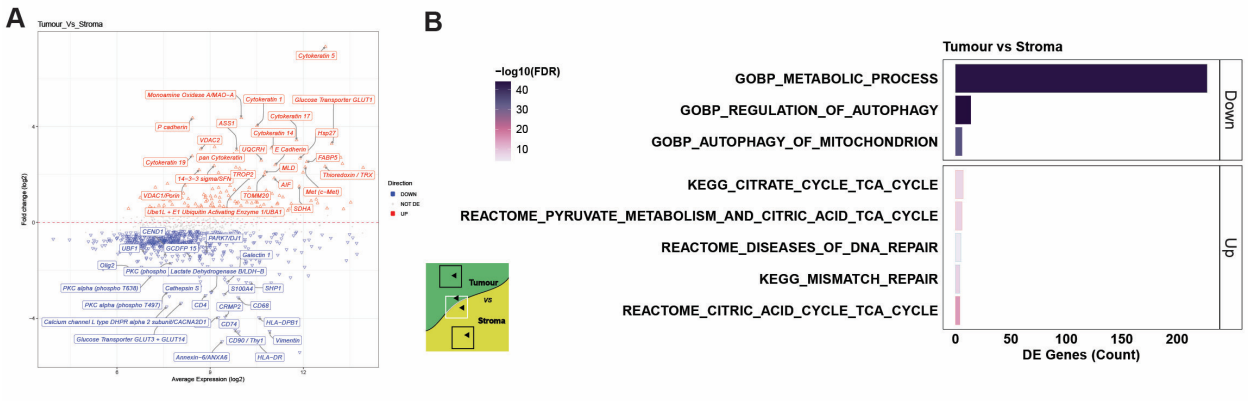
Supplemental Figure 1: Data quality assessment. Correlation matrix for the housekeeping and background control proteins in the assay.



Supplemental Figure 2: Batch effect correction. PCA plots stratified by ROI 'SegmentLabel' and 'Slide' before (A) and after (B) batch correction for slide (i.e. patient).



Supplemental Figure 3. Quality control assessment. PCA plots stratified by different factors of interest including ROI 'label', 'Primary Nodal Metastasis', 'Grouped Mets', disease 'Stage', 'TNM' and 'Progress'.



Supplemental Figure 4. (A) DE analysis results presented as M (log ratio)-A (mean average) plots and (B) top enrichment pathways bar plots for tumour vs stroma samples. Limma-voom eBayes pipeline used in the DE analysis with DE markers identified using a cutoff based on an adjusted p-value of ≤ 0.05 using the Benjamini Hochberg procedure. Limma::fry function used for the pathway enrichment analysis, providing the gene counts in each gene-set and associated FDR.