Supplementary Figure 4. Unsupervised hierarchical clustering heatmaps of viral and bacterial protein data: Unsupervised clustering of viral (top) and bacterial (bottom) proteins observed in ≥ 24 total patient samples. Complete linkage clustering was used with Euclidean distance measures. Cells show $\log_{10}$ normalised TMT-label intensity with blue and red indicating reduced and increased intensity, respectively, relative to the experimental reference sample. Black cells indicate missing values. Column labels represent either healthy NAT (blue labels) or tumour OSCC (red labels) patient samples. Protein UniProt accession numbers are shown for each row. For the bacterial heatmap, 6 patient samples, "C3N-03619_H","C3N-01754_H", "C3N-03619_T", "C3N-01754_T", "C3N-03226_TO" and "C3N-00871_TO", were excluded from this analysis due to a high number of missing values that prevented hierarchical analysis.