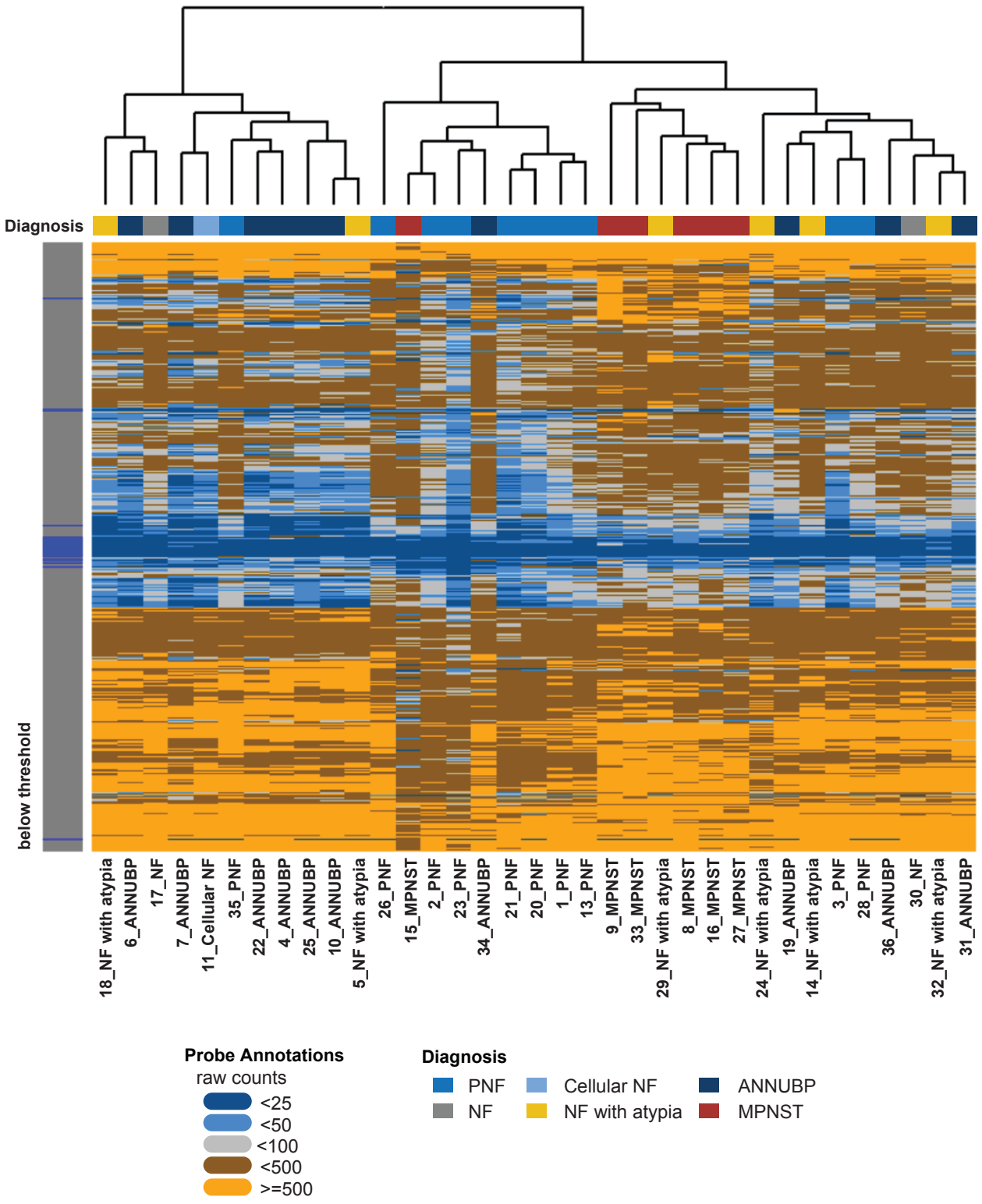

Supplemental Figure 1

Supplemental Figure 1. Heatmap of raw counts. Hierarchically clustered heatmap showing raw counts of all genes. Rows represent individual genes and their respective raw counts in each sample according to the colors specified on the legend below. Columns represent individual samples with tumor subtype annotated above and sample ID below. Blue bars at left denote genes with low counts below threshold that were dropped from subsequent analysis.