



Supplementary Figure 4: Unfiltered metagenomic classifications including contaminants

Heatmap shows viral taxa identified in each sample type. Compared to Figure 3, this Figure shows all classified taxa without manually screening out contaminants. Rows are viral taxa, and columns are sample types, some with enhanced sequencing methods (HC and/or MDD). Only classifications with over 100 unique kmers, and at least 1 BLAST confirmed read are shown. Rows are grouped by whether they are RNA viruses vs DNA viruses (top vs bottom section). Color intensity corresponds to the RPM of the taxa. Red boxes correspond to detection in RNA libraries while blue boxes correspond to detection in DNA libraries. Stars represent the clinical diagnosis. Gray shaded columns represent samples that did not undergo DNA or RNA sequencing. The yellow bars indicate nucleated cell count in the CSF for each subject. The four groupings of columns from top left to bottom right correspond to infections diagnosed with a positive PCR, infections diagnosed by non-molecular techniques, subjects with unknown etiology, and negative controls including water.