



**Supplementary Fig. S9. Gene expression landscape of EBV-related cHL.** **A**, Volcano plot showing differential expression of 750 genes in Epstein-Barr virus (EBV) positive ( $n=7$ ) versus EBV-negative ( $n=25$ ) tumors. Genes with top 20  $p$ -adjusted ( $p\text{-adj}$ ) and  $p\text{-adj} < 0.05$  in the four significantly different LM22 gene sets (by EBV status) are labeled. See also **Supplementary Table S11**. **B**, Heatmap showing gene set specificity of differentially expressed genes ( $p\text{-adj} < 0.05$ ) in the four LM22 gene sets. **C**, Box plot indicating (minimum, first quartile, median, third quartile, and maximum) the CIBERSORT imputed fraction of 22 immune cell types over all immune cells by EBV status (two-sided Wilcoxon test). Abbreviations: natural killer (NK), plasma cell (PC), memory (mem.), resting (rest.), activated (act.). **D**, Pearson correlation of immune cell fraction by CIBERSORT versus multiplexed immunofluorescence.