



Fig. S2. Effects of cell dissociation and the correlation between bulk RNA-seq and scRNA-seq data. **a**, Histogram showing the fraction of gene expression attributed to dissociation-associated genes in the 48,584 cells profiled in this study. The red dotted line corresponds to the threshold described by Van Oudenaerden *et al.*¹⁷ Their signature is based on detecting the upregulation of the expression of immediate-early genes (*FOS* and *JUN*) and stress-response genes (e.g., *HSPA1A* and *HSPA1B*). The plot shows that only a few cells (0.60%) are positive for the dissociation-response signature. Dissociation-associated artefacts were thus unlikely to be a major determinant of the cell subtypes identified in this study. **b**, tSNE plot of 48,584 cells colour coded for expression of the gene set (*FOS*, *JUN*, *HSPA1A*, and *HSPA1B*). **c**, Density dot plot and Pearson's correlation analysis (r) of the gene expression in the scRNA-seq and bulk mRNA-seq data of 12 NPC samples.