



Fig. S7. Associations of gene signatures with survival in NPC and HNSCC. **a**, Prognostic values of the NPC signatures in 128 patients in NPC Cohort B. Forest plots show HRs (blue/red squares) and CIs (horizontal ranges) derived from multivariate Cox regression survival analyses for disease-free survival adjusted for age, sex, smoking history, disease stage, and pretreatment EBV DNA copy number in NPC; the corresponding Cox regression *P*-values are also shown. Significant results are indicated with red squares. **b**, Prognostic values of the HNSCC signatures in 366 patients in a TCGA HNSCC cohort (all samples and stratification by primary site). The corresponding prognostic signatures in NPC (i.e., cell cycling, macrophages, pDCs, *CLEC9A*⁺ DC1, NK cells, and plasma cells) were obtained from two HNSCC scRNA-seq studies (Supplementary information, Table S7). As *CLEC9A*⁺ DC1 was not identified in HNSCC studies, the NPC DC1 signature was used instead to infer its prognostic value in HNSCC. Forest plots show HRs (blue/red squares) and CIs (horizontal ranges) derived from multivariate Cox regression survival analyses for disease-free survival adjusted for age, sex, smoking history and disease stage; the corresponding Cox regression *P*-values are also shown. Significant results are indicated with red squares.