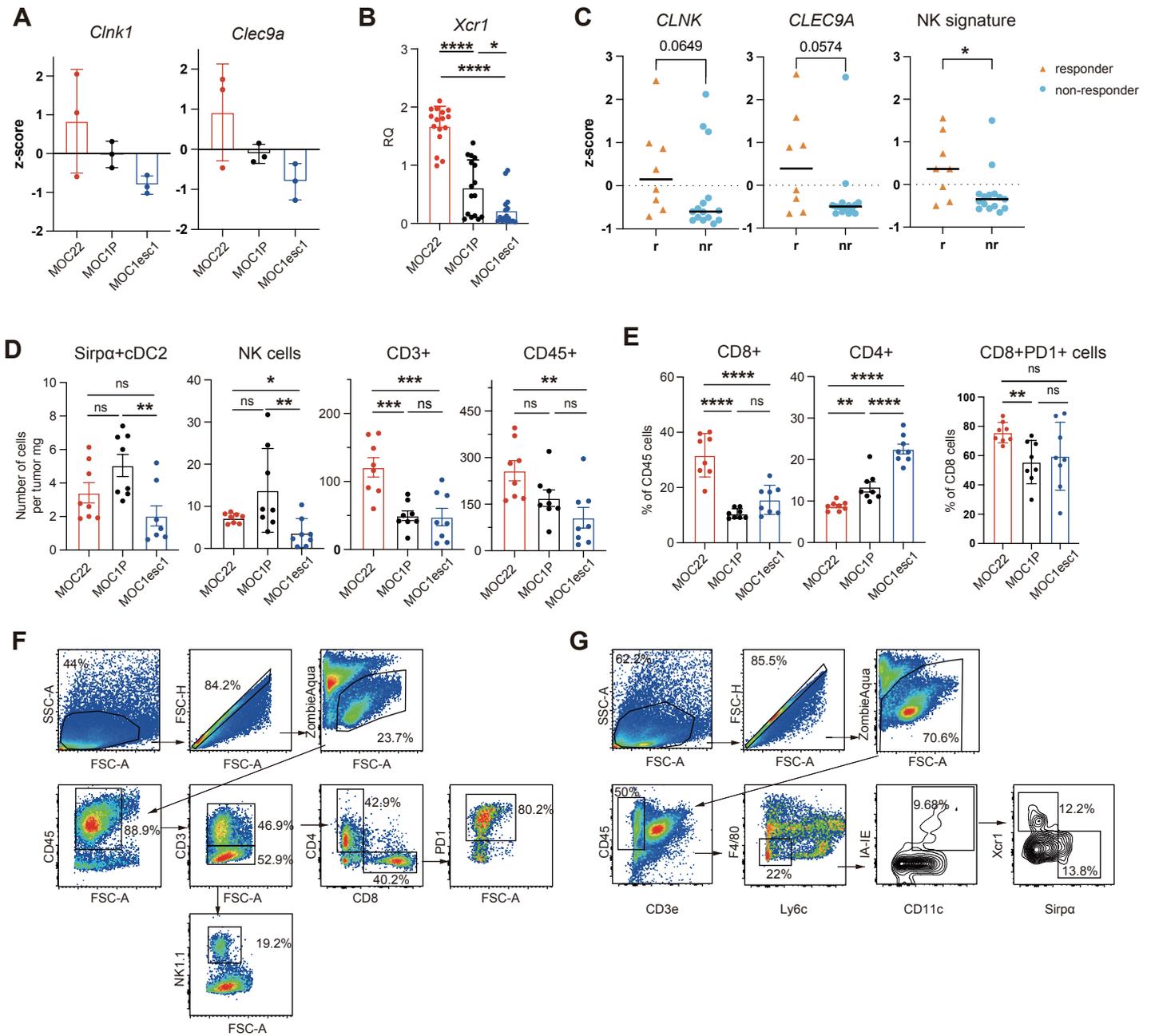


# Figure S2



**Figure S2**

**A.** Bulk RNA-sequencing data from MOC22 tumors harvested on day 17, and MOC1 and MOC1-esc1 tumors harvested on day 14 post implantation are shown for indicated genes as z-score. (n=3 for each model.)

**B.** qPCR data of *Xcr1* from in vivo established tumors harvested on day 12 post-inoculation. n=16, pooled data from two independent experiments.

**C.** Bulk RNA-seq data of indicated genes in pretreatment tumor samples from patients who received subsequent aPD1 therapy shown as z-score. “NK signature” represents the average z-score of *GNLY*, *KLRC3*, *KLRD1*, *KLRF1*, and *NCR1* (10). (n=8 responders, n=15 non-responders.)

**D, E.** Flow cytometric analysis of MOC22, MOC1P and MOC1esc1 tumors harvested on day 12 post-inoculation. (n=8 tumors each, representative data of two independent experiments.)

**F, G.** Representative gating strategies for T and NK cells (F) and DCs (G) used throughout the paper.

Individual data with mean  $\pm$  SD are plotted in Figure S2A, B, D, E, and individual data with mean are plotted in Figure S2C.

Data were analyzed using the Mann-Whitney U Test to generate two-tailed P values in Figure S2C, and one-way ANOVA followed by Tukey’s multiple comparison for Figure S2B, D, E.