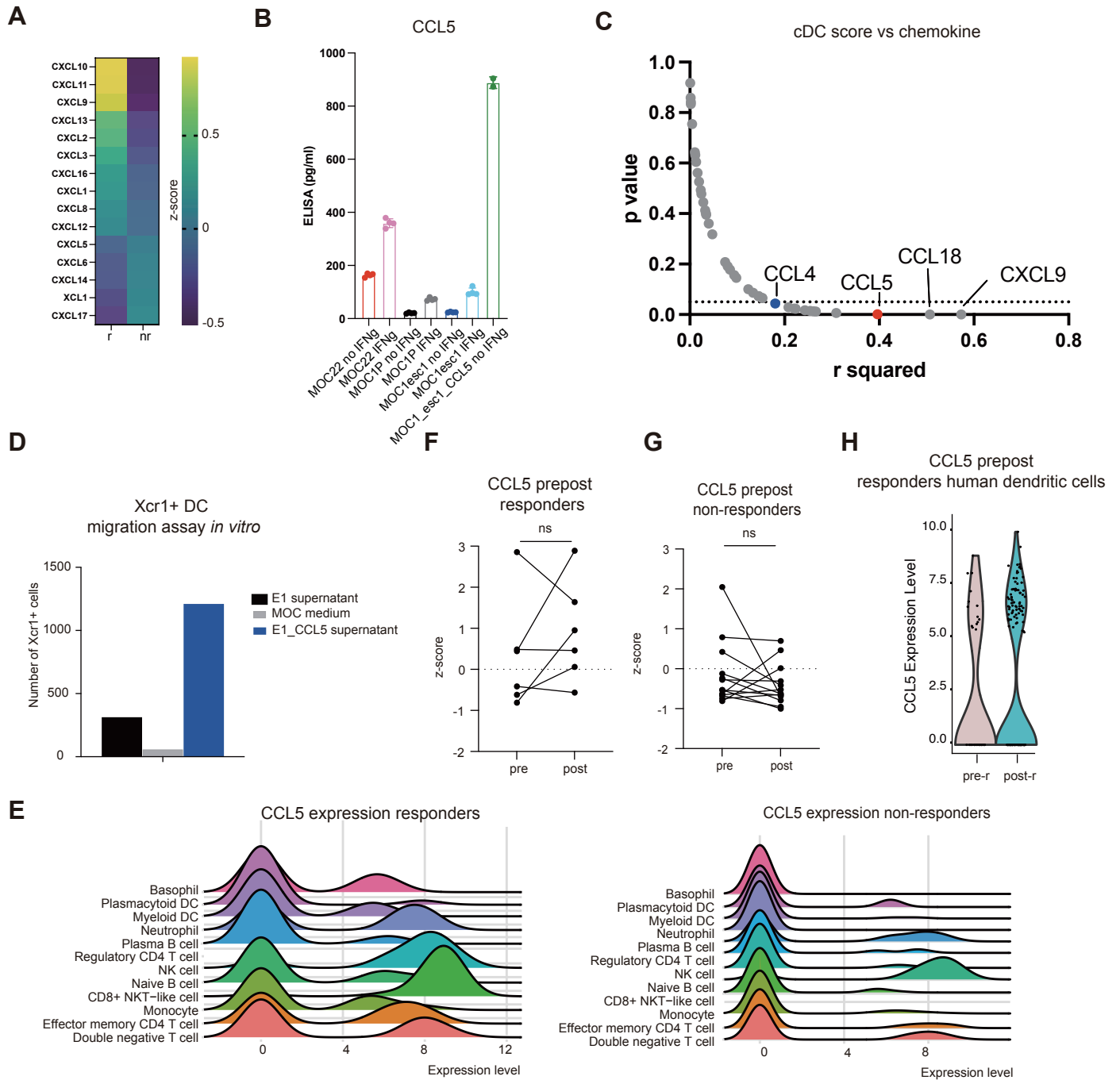# Figure S4

Figure S4.

A. Heatmap of CXC chemokines ligands (CXCL) based on pretreatment bulk RNA-seq data between responders and non-responders.

B. CCL5 expression in each MOC model cultured media with or without IFN-γ stimulation (100U/ml for 48 hours) were analyzed by CCL5-ELISA. n=2-3.

C. p value and r squared value calculated from Pearson correlation coefficient of cDC score and chemokine RNA expression are plotted. Broken line represents a p value of 0.05.

D. Number of Xcr1+ DCs migrated using the migration assay described in Methods.

E. Distribution plots showing cumulative expression levels of CCL5 in various immune subtypes other than CD8+ T cells, based on scRNA-seq of HNSCC patients prior to pembrolizumab. Left panel responders, right panel non-responders.

F, G. Comparison of CCL5 expression in bulk RNA-seq data from pre and post treatment samples in responders (F) and non-responders (G), shown as z-score. n=6.

H. Violin plot showing CCL5 expression level in human dendritic cells between responders pre- and post-treatment based on scRNA-seq data.

Individual data and mean are plotted in Figure S4B, D. Data were analyzed using the Mann–Whitney U Test to generate two-tailed P values in Figure S4F, G.