A

B

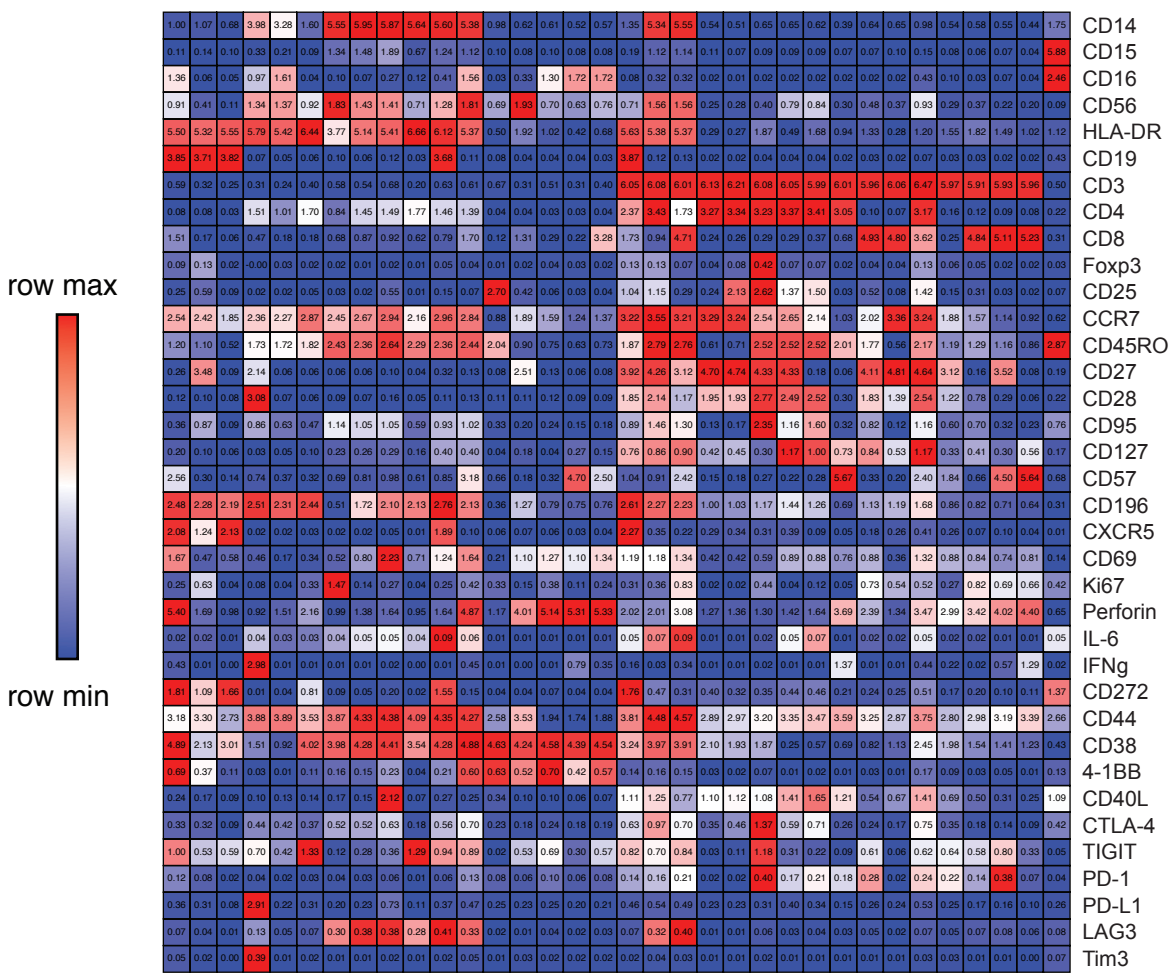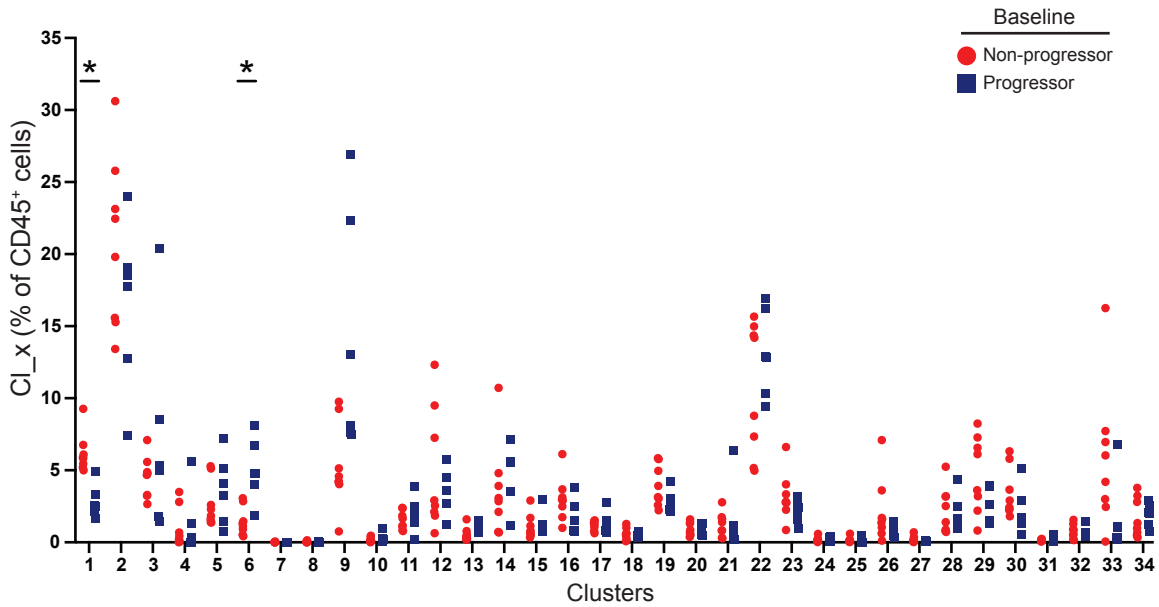**Supplementary Figure S1.**

Baseline PBMC samples were analyzed by high-dimensional single cell profiling using mass cytometry. **(A)** Heat map displaying relative expression values of CD45$^+$ Phenograph defined clusters. Numbers indicate mean CytofAsinh transformed expression values. **(B)** Quantification of CD45$^+$ Phenograph defined cluster frequencies between Progressors and Non-Progressors. Multiple *t*-tests were performed with Benjamini, Krieger and Yekutieli correction. *, q < 0.05.