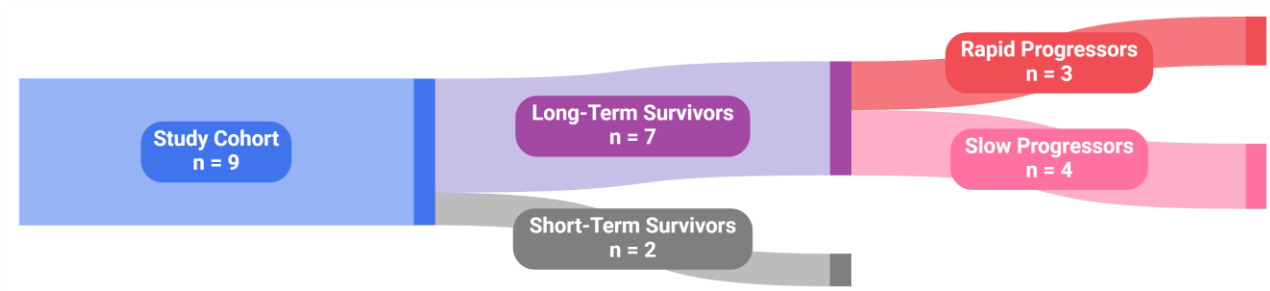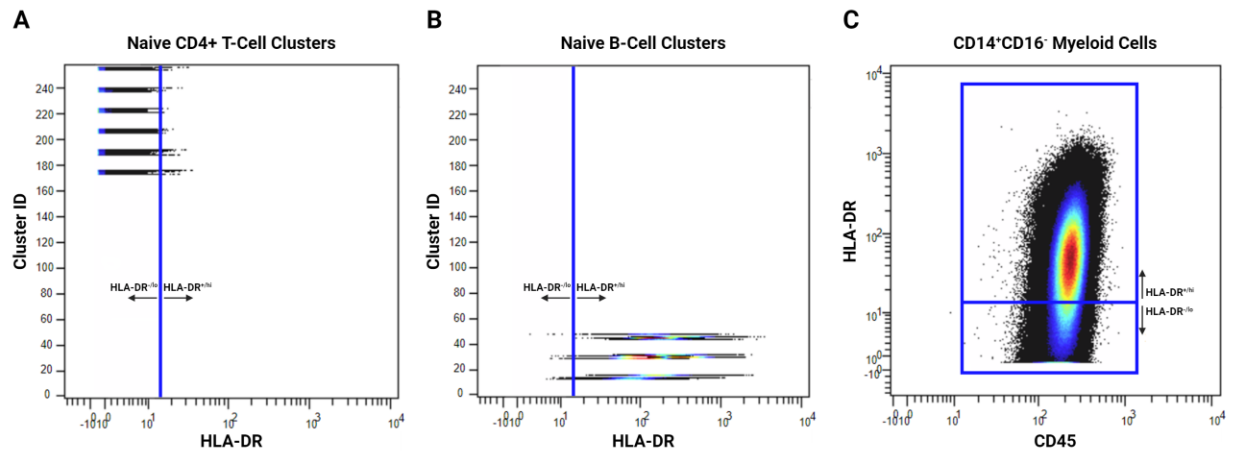**Supplementary Fig. S1**   Cleanup gating workflow used for the refinement of the raw cytometry by time-of-flight (CyTOF) data into intact single cells (singlets).

Supplementary Fig. S2 Sankey diagram of study patient grouping. Study patients (n=9) were grouped according to duration of survival and progression-free survival. Patients who survived for up to 16 weeks after the start of treatment were considered short-term survivors (n=2), while patients who survived for longer than 16 weeks after the start of treatment were considered long-term survivors (n=7). Long-term survivors for whom disease progression was confirmed during the first 16 weeks following treatment initiation were categorized as rapid progressors (n=3), while long-term survivors for whom disease progression was confirmed after more than 16 weeks following treatment initiation were categorized as slow progressors (n=4).

Supplementary Fig. S3 Determination of the cutoff of HLA-DR expression for the separation of classical monocytes and monocytic myeloid-derived suppressor cells (M-MDSCs). (A) The subset of naïve CD4+ T cells was used as a negative control for HLA-DR expression. (B) The subset of naïve B cells was used as a positive control for HLA-DR expression. (C) The cutoff of HLA-DR expression for the separation of the cells of the CD14+CD16- myeloid cell subset into HLA-DR$^{+/hi}$ classical monocytes and HLA-DR$^{-/lo}$ M-MDSCs was set according to the expression cutoffs in the negative and positive control subsets.