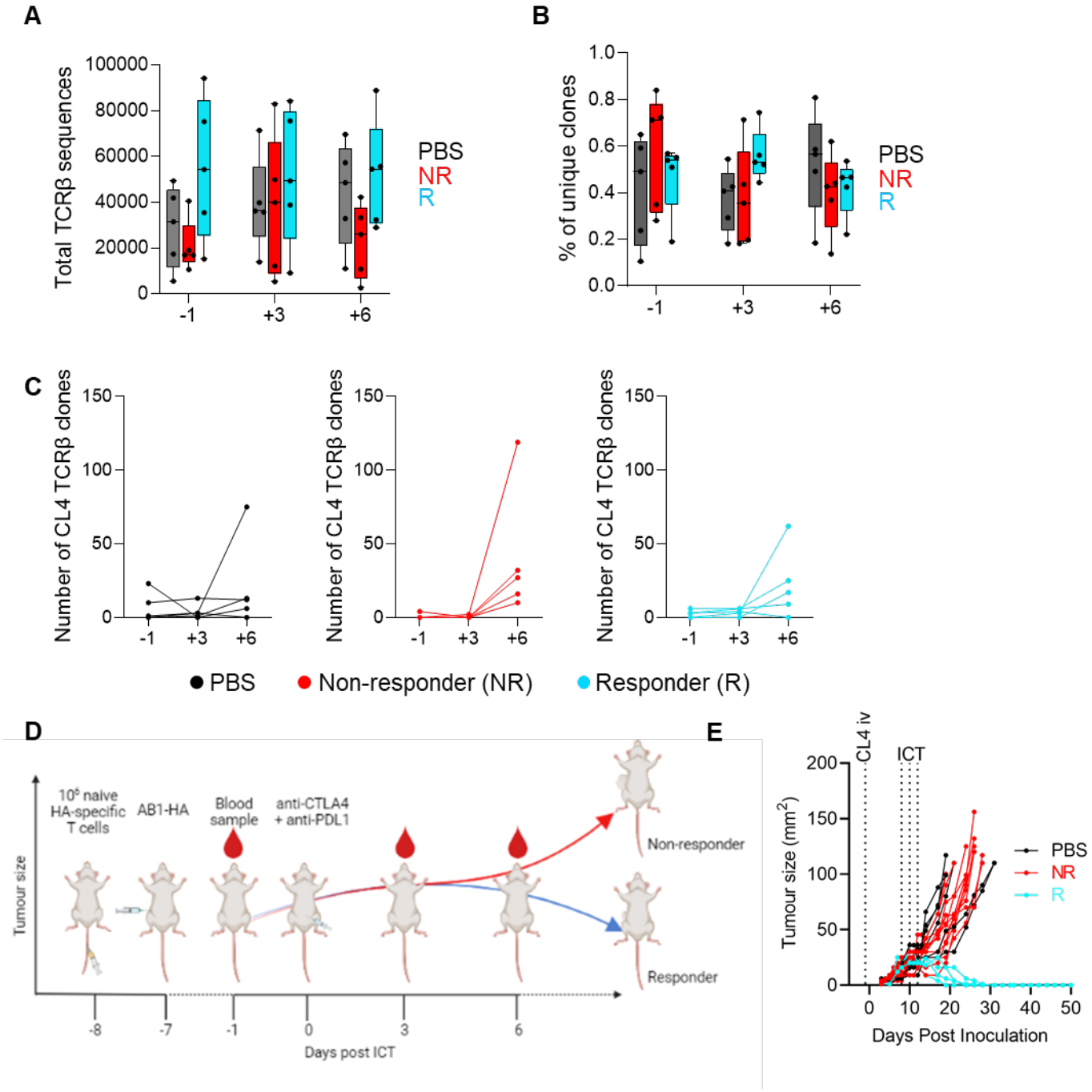

Fig. S1. Blood TCRβ repertoire metrics. (**A**) Total, (**B**) unique number of TCRβ sequences, and (**C**) number of endogenous CL4 clones from sequential blood samples of PBS treated, ICT non-responding, and responding animals. (**D**) Timeline and (**E**) tumor growth curves of experiment setup to track TCR transgenic tumor-antigen specific T cells in ICT treated animal. Each dot represents one animal, mean ± SEM represented in dot plots. Dots connected by line represents sequential samples from an individual animal. One-way ANOVA with Kruskal-Wallis tests were used to compare between groups at each time-point.

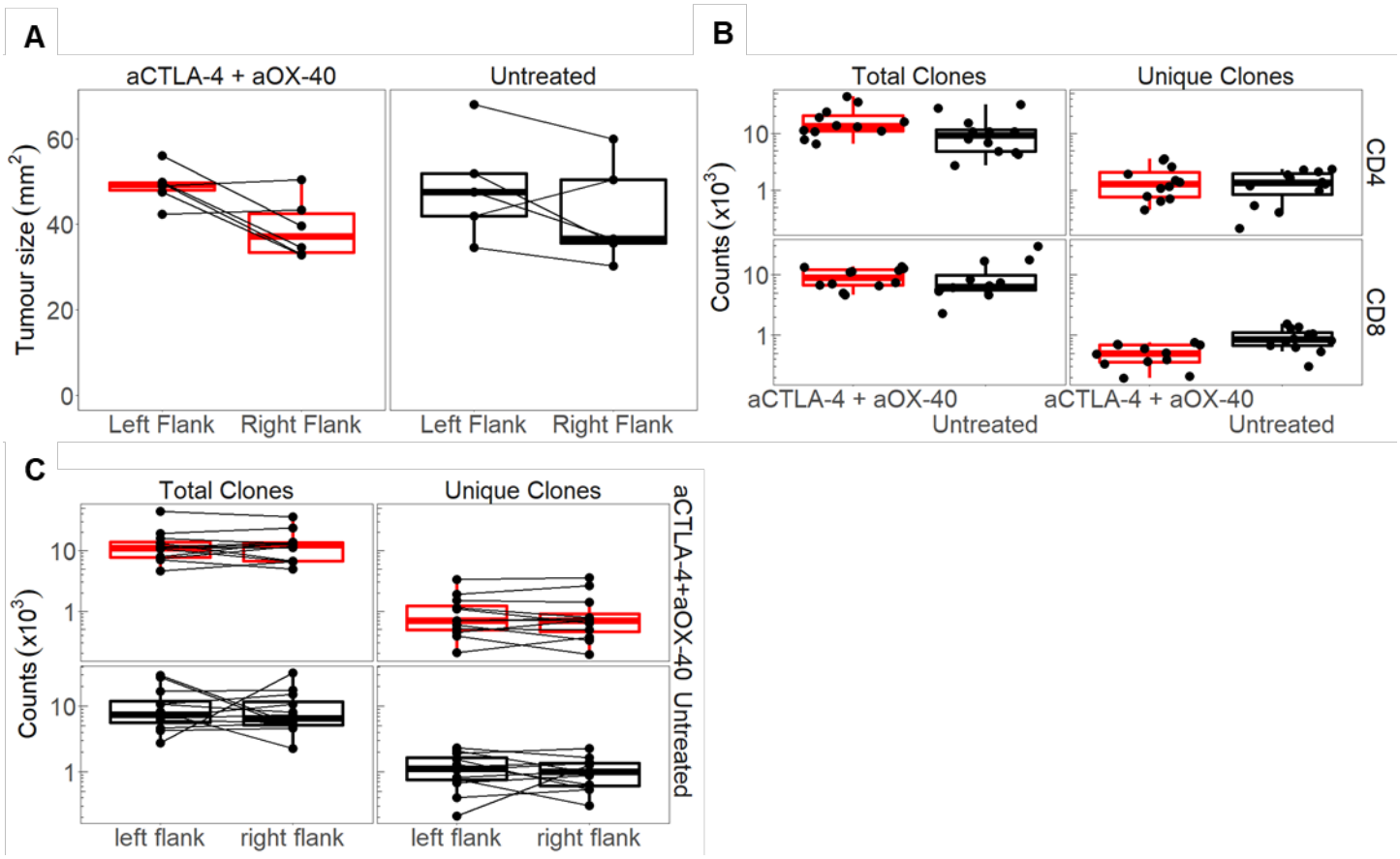

Fig. S2. TCRβ repertoire features in bilateral tumors. (**A**) Tumor sizes, total and unique number of TCRβ clonotypes in ICT (anti-CTLA-4 + anti-OX-40) and PBS treated animals, plotted by (**B**) cell type and (**C**) flanks. Each dot represents one sample, mean ± SEM represented in dot plots. Dots connected by line represents bilateral, paired samples from an individual animal. Wilcoxon-matched-pairs signed rank test used to compare paired samples.

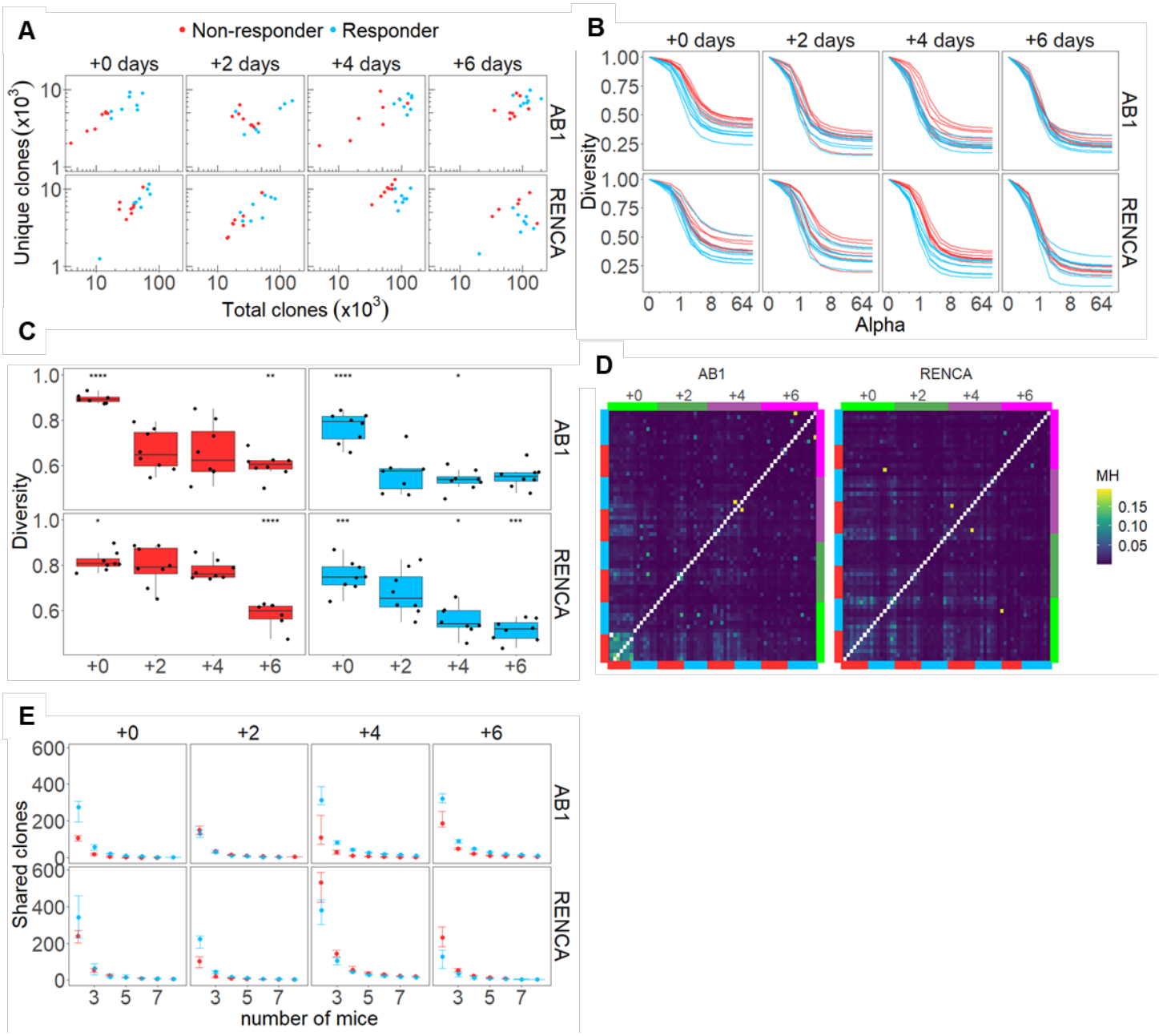

Fig. S3. Dynamic tumor TCRβ repertoire features in ICT responders and non-responders. (A) Total and unique number of TCRβ clonotypes, (B) Renyi entropy curves representing tumor TCRβ diversity. (C) TCRβ diversity of responding and non-responding tumors depicted over time. Wilcoxon's ranked test was used to compare the mean diversity index in each group against the global mean *p < 0.05, ***p < 0.005, ****p< 0.001. (D) Heatmap comparing TCRβ repertoire overlap in all samples. Morisita-Horn Overlap index between all tumors for both models, ICB response and all time-points represented. (E) Mean number of clones shared by the number of different animals in responding and non-responding groups.

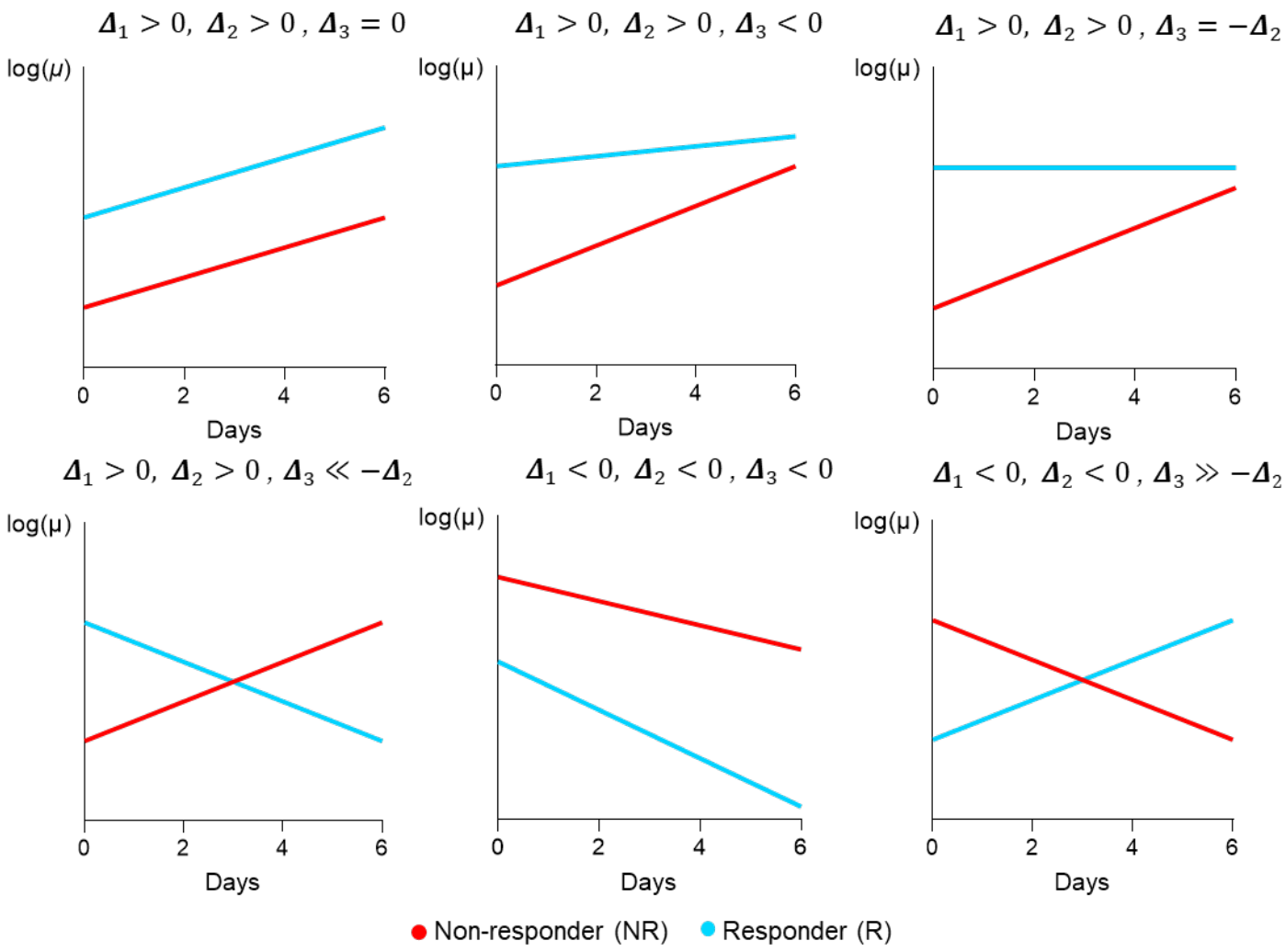

Fig. S4. Generalized linear model of dynamic change. Dynamic changes of individual TCRβ clusters were modelled based on coefficients that measured different dynamic features. Graphs represent some patterns of change associated with different combinations of coefficient values.

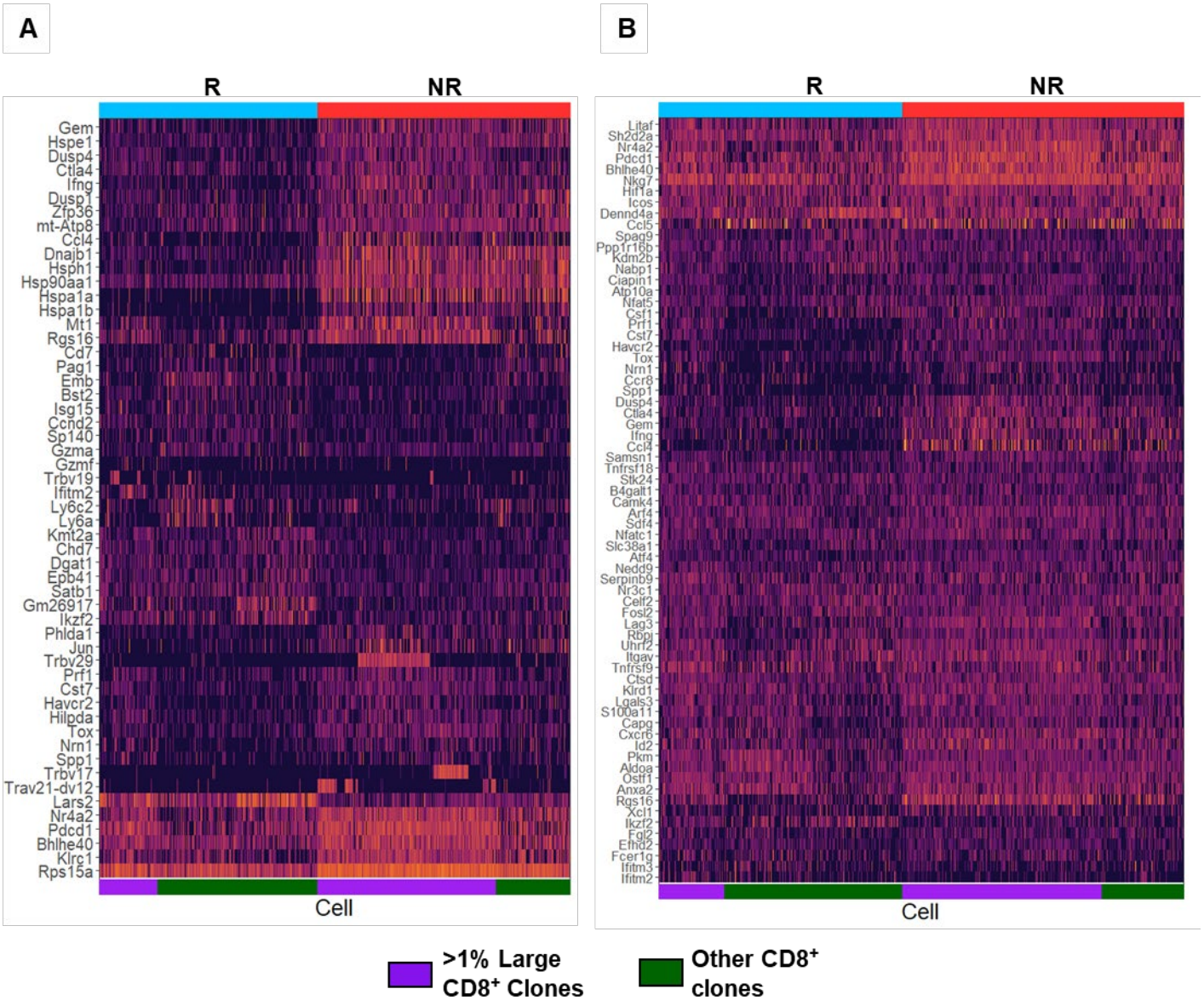

Fig. S5. Differentially expressed gene expression of individual CD8$^+$ TILs. (A) Heatmap of significant differentially expressed genes and (B) T cell exhaustion geneset in CD8$^+$ TILs from the large clones, other clones, ICT responders and non-responder groups.