

**Supplementary Fig. 5: Sensitivity analysis of social network analysis of the representative sipuleucel-T treated patient. (A) Density plot of the clone frequency for all clones of the treated patient (red) and density plot of the clone frequency for subsampled clones of the treated patient (green)**. Subsampling was done by weighted clone frequency. **(B) Social network (V04 family gene) of the all clones of the treated patient.** **(C) Social network (V04 family gene) of the all clones of the naïve patient.** **(D) Social network (V04 family gene) of the subsampled clones of the treated patient.** Subsampling was done by weighted clone frequency.For each patient, social network analysis was first performed using R packages: Ape (24) and igraph (25). A convergent group was defined as the cluster that included the clones with the distance less than or equal to 1 (allowing maximum of 1 basepair mutation among clone sequences sharing the same V-gene, J-gene and CDR3 length). For all social network figures, each node represents a single clone colored by its first presenting time point, and the node size was attributed based on the corresponding abundance. The nodes connected by lines were within the same convergent group.