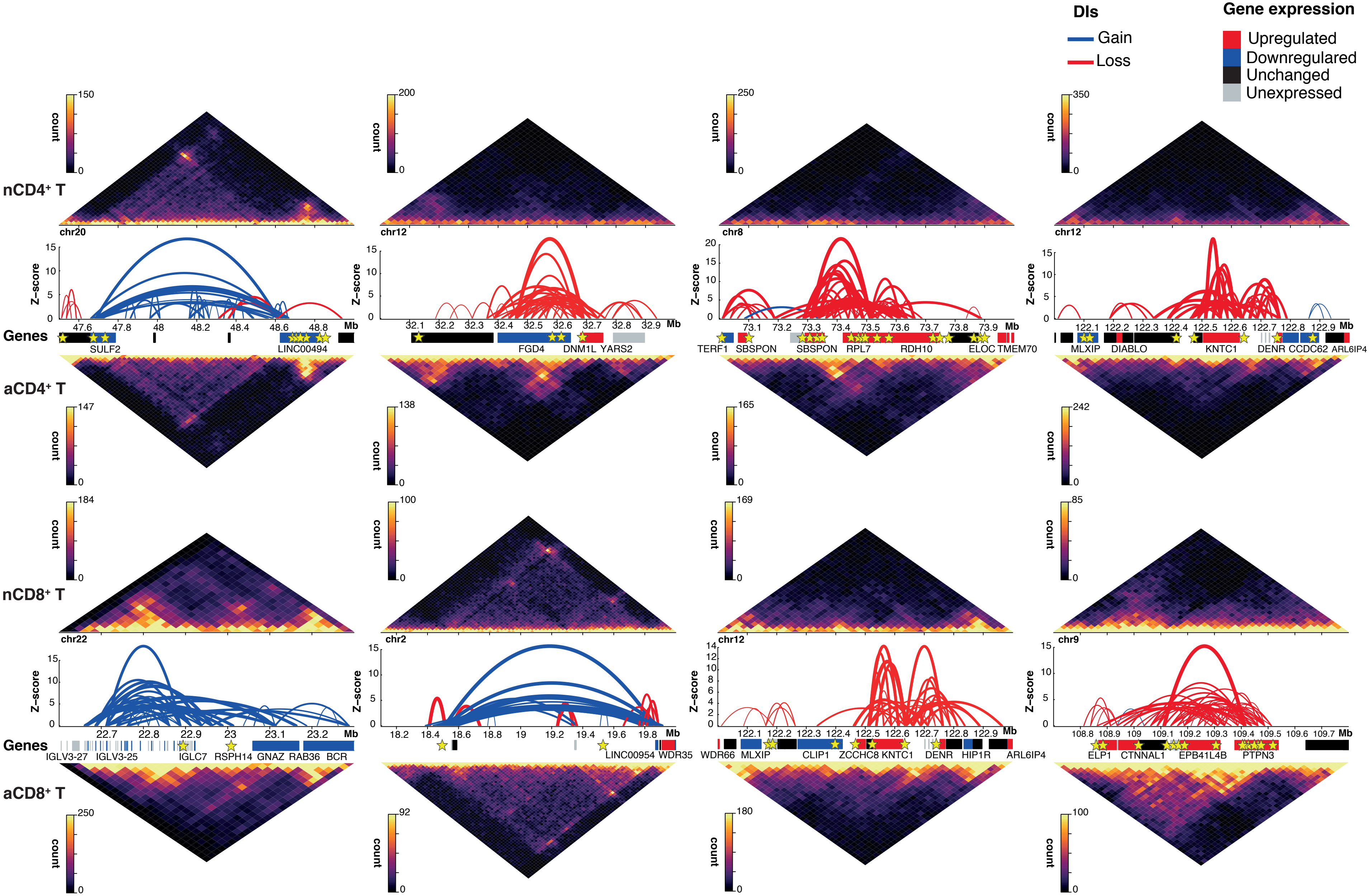

Figure S5. T cell activation induces extensive changes in gene-regulatory interactions. In-situ Hi-C contact matrices plotted at 25kbp resolution in resting (n) and activated (a) CD4+ (top rows) and CD8+ (bottom rows) T cells over highly ranked (by significance) activation-associated differential interactions (DI) as determined by the diffHic pipeline at 25 kbp (FDR<0.05). The colour scale indicates the number of reads per bin pair. DIs are represented by arcs in the centre where the vertical axis is the z-score (-log10 p-value as calculated by edgeR). Each arc connects the two interacting bins and therefore identifies the relevant bin pair. Red and blue arcs represent strengthened (logFC>0) and weakened (logFC<0) DIs, respectively, in response to activation. Genes are represented in squares and are coloured according to their expression changes upon activation: red, blue, black and grey represent up-regulated, down-regulated, unchanged and unexpressed genes, respectively. Only DE genes are named. Yellow stars represent activation-associated differentially accessible regions (FDR<0.05).