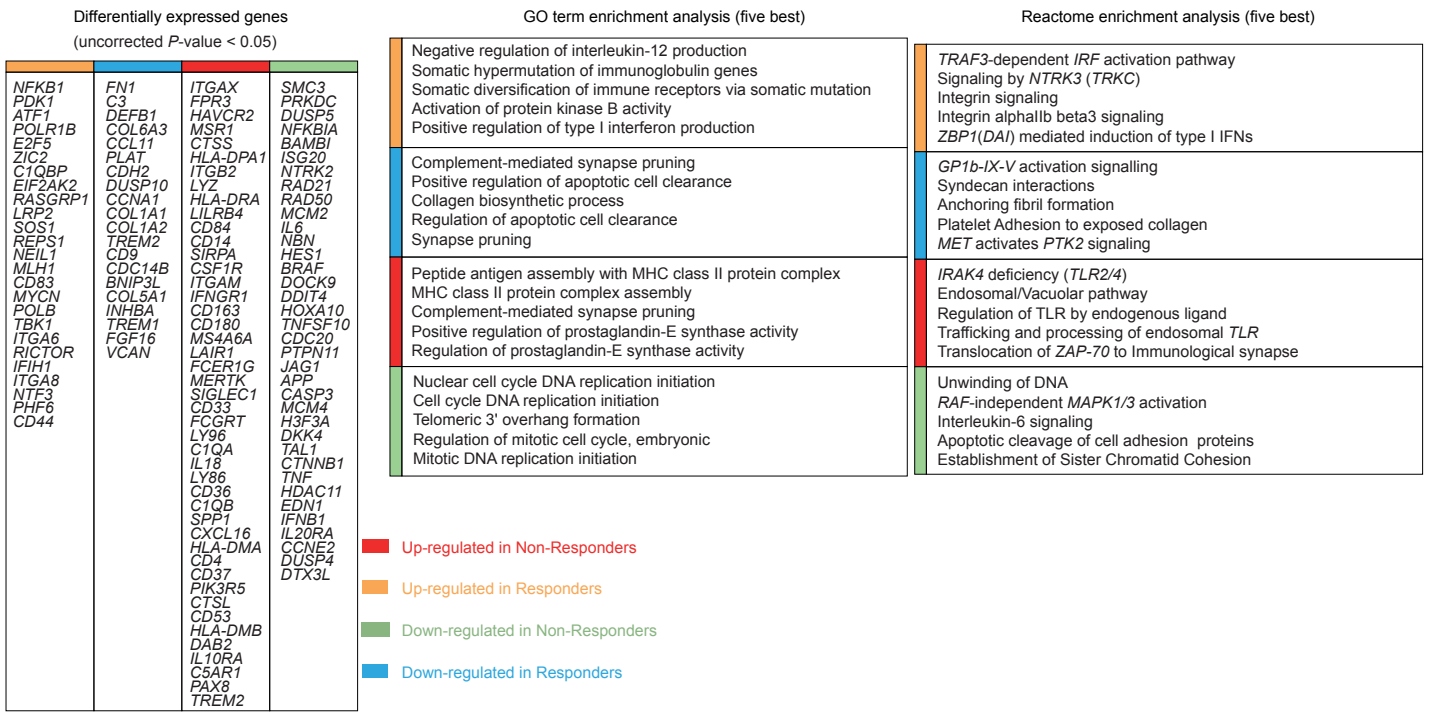
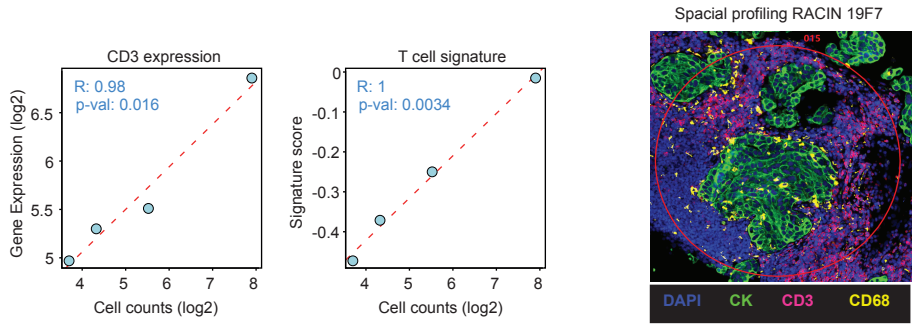


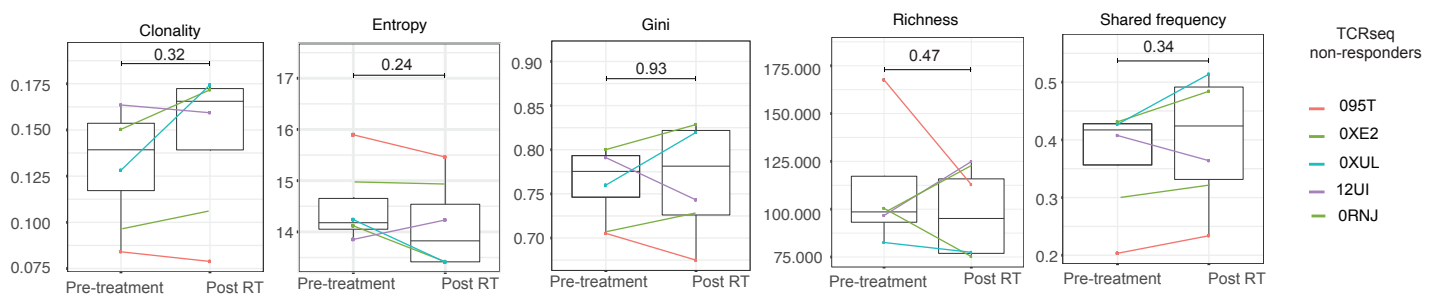
A



B



C



Supplementary Fig. S5

Supplementary Fig. S5. Evaluation of effects of RACIN. (A) Full list of differentially expressed genes (unadjusted P -value < 0.05) between baseline and post-irradiation biopsy in responding vs. non-responding tumors, as shown in Figure 6B (left table). A Gene Ontology (GO) term (middle table) and Reactome enrichment analysis of these genes was performed, and the five most significant pathways are shown for each list of genes. (B) Significantly positive correlation between CD3 cell quantification by immune fluorescence imaging (x-axis) and by NanoString GeoMx (y-axis) measuring *CD3E* gene expression (left plot) or the T cell signature score (right plot). (C) Comparison of TCR CDR3 diversity by clonality, Shannon diversity entropy, the Gini coefficient, richness and TCR shared frequency in patients with non-responding tumors.