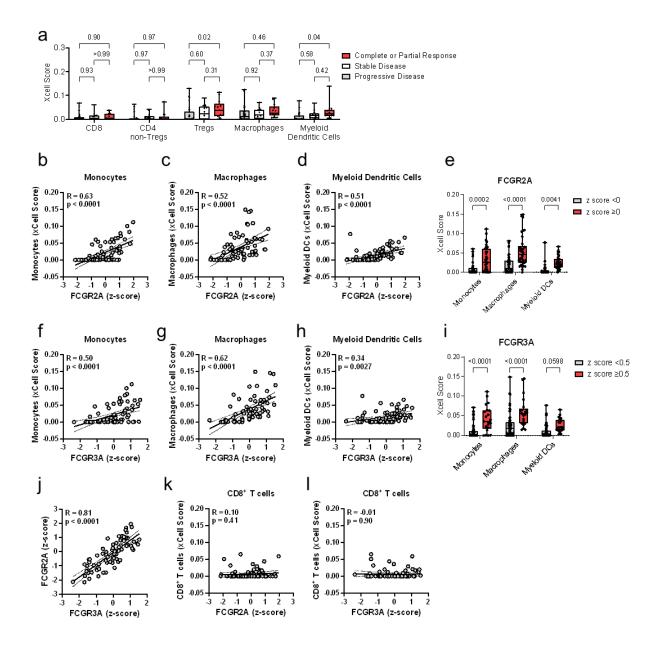
1 Supplementary Figure S17



Supplementary Figure S17. FCGR2A and FCGR3A bulk RNA-seq expression z-scores correlation with immune cell type enrichment scores. (a) Intratumoral cell type fraction of macrophages, myeloid dendritic cells, monocytes, CD8+ T cells, CD4+ non-Tregs and Tregs in pre-treatment tumor biopsies from patients with a variety of solid cancers treated with botensilimab ± balstilimab (n=55), as determined from gene set enrichment analysis of bulk RNA-

seg data by xCell. In violin plots, the center line represents the median. (b-d) Intratumoral (b) monocyte, (c) macrophage and (d) myeloid dendritic cell type enrichment scores from pretreatment tumor biopsies obtained by xCell gene set enrichment analysis of bulk RNA-seq data (y-axis) plotted against FCGR2A bulk RNA-seq gene expression z-scores (x-axis) (n=74). (e) xCell enrichment score for monocytes, macrophages and myeloid DCs cell types by FCGR2A (n= 40 with z-score <0 and n=34 with z-score ≥0) high versus low expression. (f-h) Intratumoral (f) monocyte, (g) macrophage and (h) myeloid dendritic cell type enrichment scores plotted against FCGR3A bulk RNA-seq gene expression z-scores (x-axis) (n=74). (i) xCell enrichment score for monocytes, macrophages and myeloid DCs cell types by FCGR3A (n= 53 with z-score <0.5 and n=21 with z-score ≥0.5) high versus low expression. (j) FCGR2A (y-axis) plotted against FCGR3A (x-axis) bulk RNA-seg gene expression z-scores (n=74). (k) FCGR2A and (l) FCGR3A correlation with CD8⁺ T cells from pre-treatment tumor biopsies obtained by xCell gene set enrichment analysis of bulk RNA-seg data (n=74). Data were analyzed with a two-way ANOVA followed by (a) Tukey's multiple comparisons test or (e, i) Šídák's multiple comparisons test. The correlation coefficient R, and the p-value (p) of the simple linear regression is indicated on the graph (b-d, fh, j-l).

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