A

B

Principal component analysis

C

D

NanoString immune cell abundance signatures

Cell type	Genes
B cells	**Blk, Cd19, Fcrlb,** Ms4a1, Pnoc, **Spib, Tcl1, Tnfrsf17**
CD45	**Ptprc**
CD8 T cells	**Cd8a, Cd8b1**
Cytotoxic cells	Ctsw, **Gzma, Gzmb, Klrb1, Klrd1, Klrk1, Nkg7, Prf1**
DC	Ccl2, **Cd209e, Hsd11b1**
Exhausted CD8	Cd244, **Eomes, Lag3, Ptger4**
Macrophages	Cd163, **Cd68, Cd84,** Ms4a4a
Mast cells	**Cpa3, Hdc,** Ms4a2
Neutrophils	Ceacam3, **Csf3r, Fpr1**
NK CD56dim cells	Il21r, **Kir3dl1, Kir3dl2**
NK cells	**Ncr1, Xcl1**
T cells	Cd3d, Cd3e, Cd3g, **Cd6, Sh2d1a,** Trat1
Th1 cells	**Tbx21**
Treg	**Foxp3**

E

CD8 T effector and stromal signatures

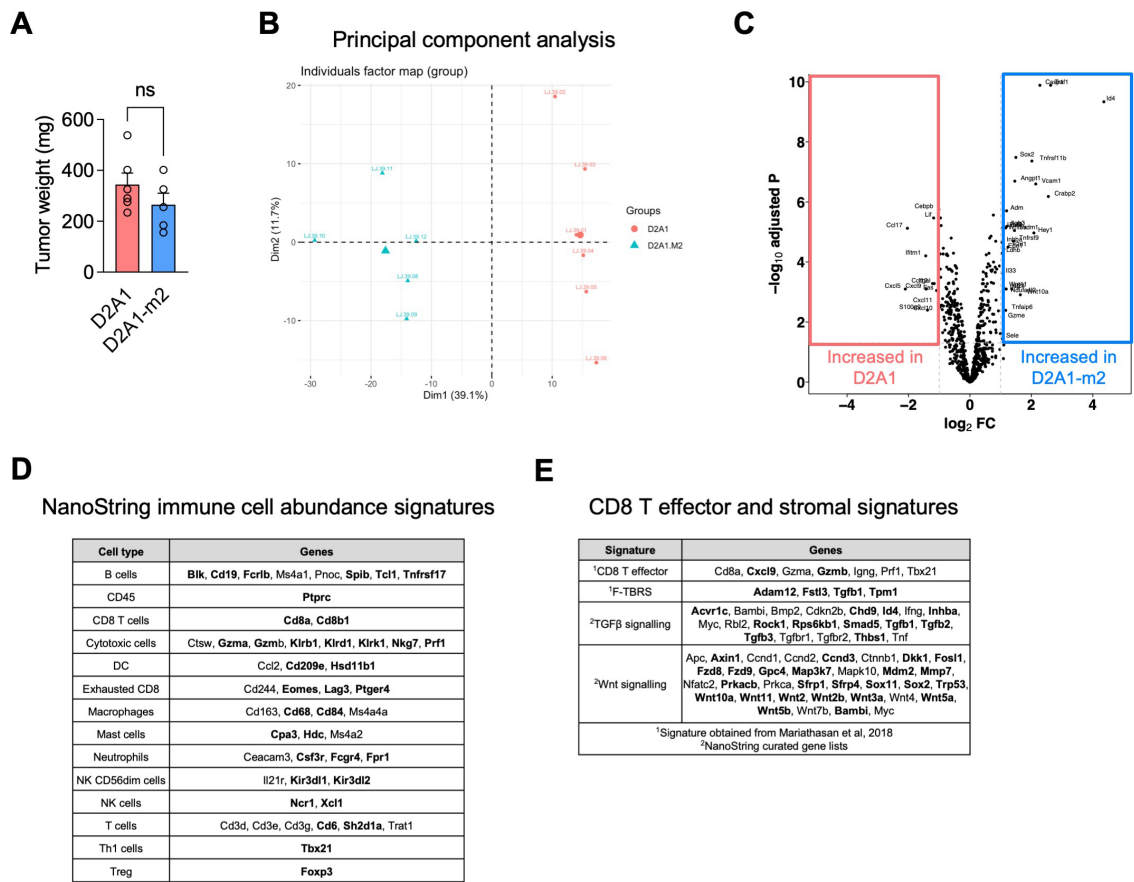| Signature	Genes
[1]CD8 T effector	Cd8a, **Cxcl9,** Gzma, **Gzmb,** Igng, Prf1, Tbx21
[1]F-TBRS	**Adam12, Fstl3, Tgfb1, Tpm1**
[2]TGFβ signalling	**Acvr1c,** Bambi, Bmp2, Cdkn2b, **Chd9, Id4,** Ifng, **Inhba,** Myc, Rbl2, **Rock1, Rps6kb1, Smad5, Tgfb1, Tgfb2, Tgfb3,** Tgfbr1, Tgfbr2, **Thbs1,** Tnf
[2]Wnt signalling	Apc, **Axin1,** Ccnd1, Ccnd2, **Ccnd3,** Ctnnb1, **Dkk1, Fosl1, Fzd8, Fzd9, Gpc4, Map3k7,** Mapk10, **Mdm2, Mmp7,** Nfatc2, **Prkacb,** Prkca, Sfrp1, **Sfrp4,** Sox11, **Sox2,** Trp53, **Wnt10a, Wnt11, Wnt2, Wnt2b, Wnt3a,** Wnt4, **Wnt5a, Wnt5b,** Wnt7b, **Bambi,** Myc
	[1]Signature obtained from Mariathasan et al, 2018
	[2]NanoString curated gene lists

Supplementary Figure S2

NanoString profiling of D2A1 and D2A1-m2 tumors. Associated with Fig. 3. **A,** D2A1 and D2A1-m2 tumor weights at necropsy (mean values per mouse ± SEM, unpaired *t*-test). **B,** Principal component analysis (PCA) plots of D2A1 and D2A1-m2 tumor NanoString data. Large symbols indicate centroids for each group. **C,** Volcano plot showing differentially expressed genes between D2A1 and D2A1-m2 tumors. Genes with an absolute $\log_2$ fold change of >1 and an adjusted *P* value of <0.05 are considered significant. **D,** NanoString immune cell population abundance signatures were analyzed by hierarchical clustering on Spearman's correlation distance, followed by identification of optimal clusters using Silhouette score. Genes within signatures that were significantly correlated are indicated in bold in the panel lists. **E,** 'CD8 T effector' and stromal signatures were analyzed as described in panel D.