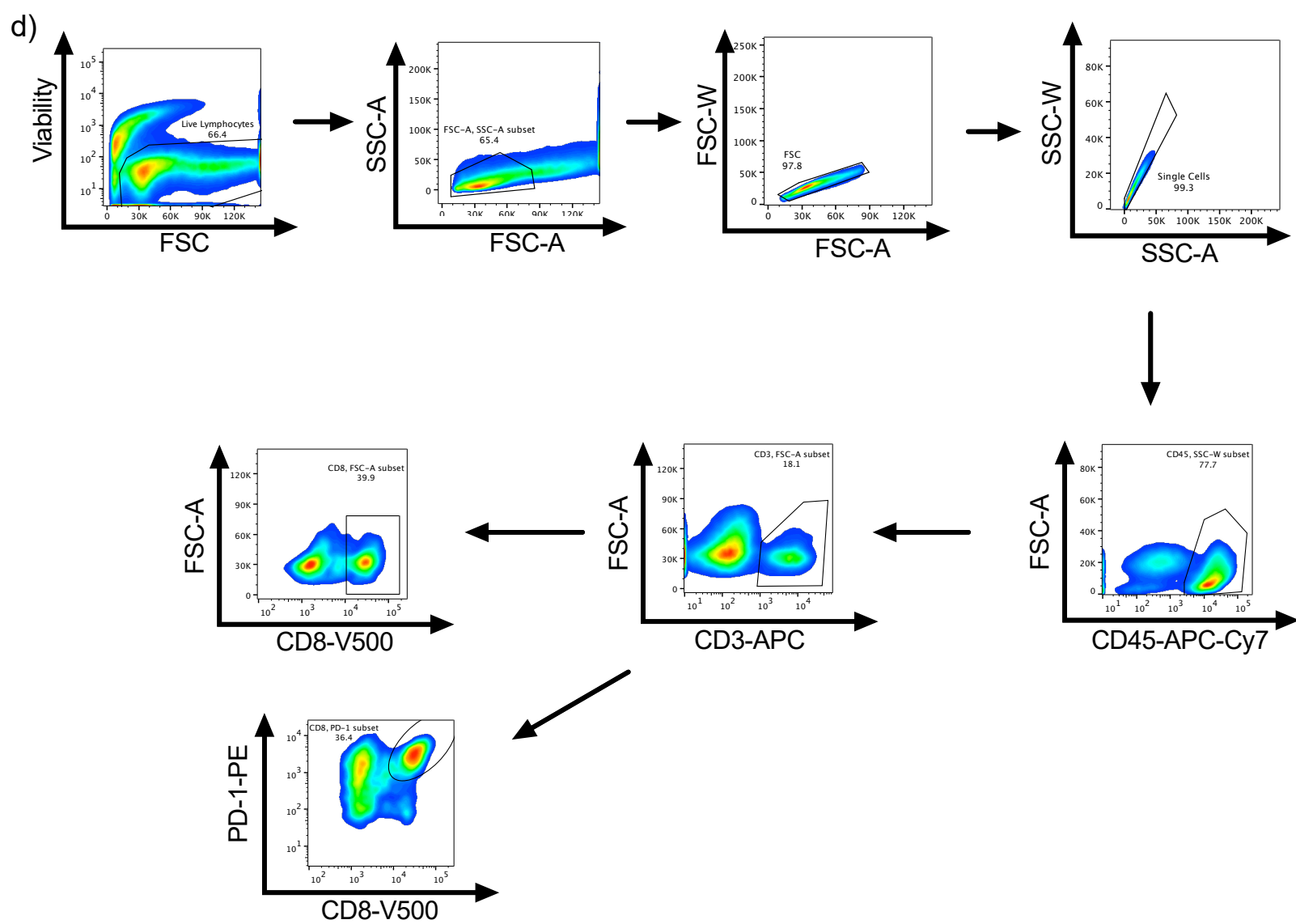
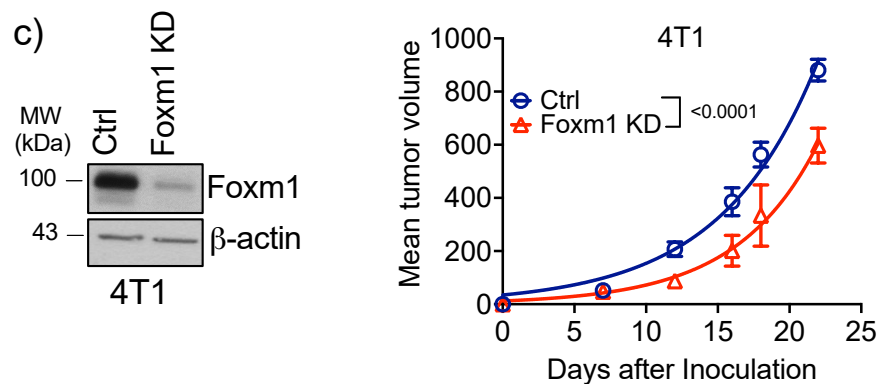
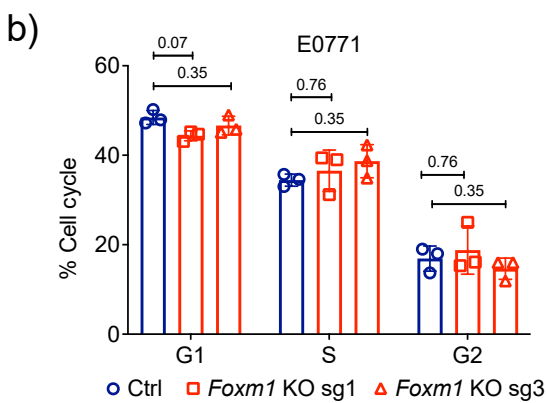
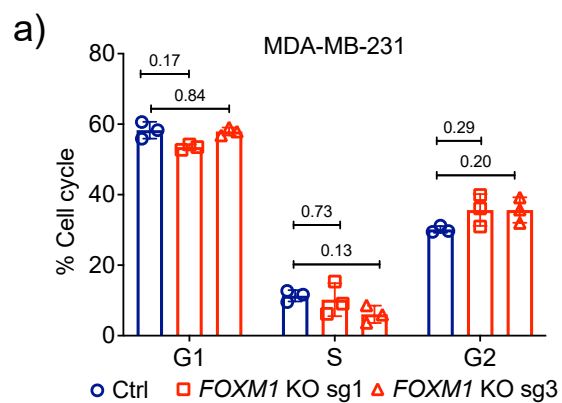
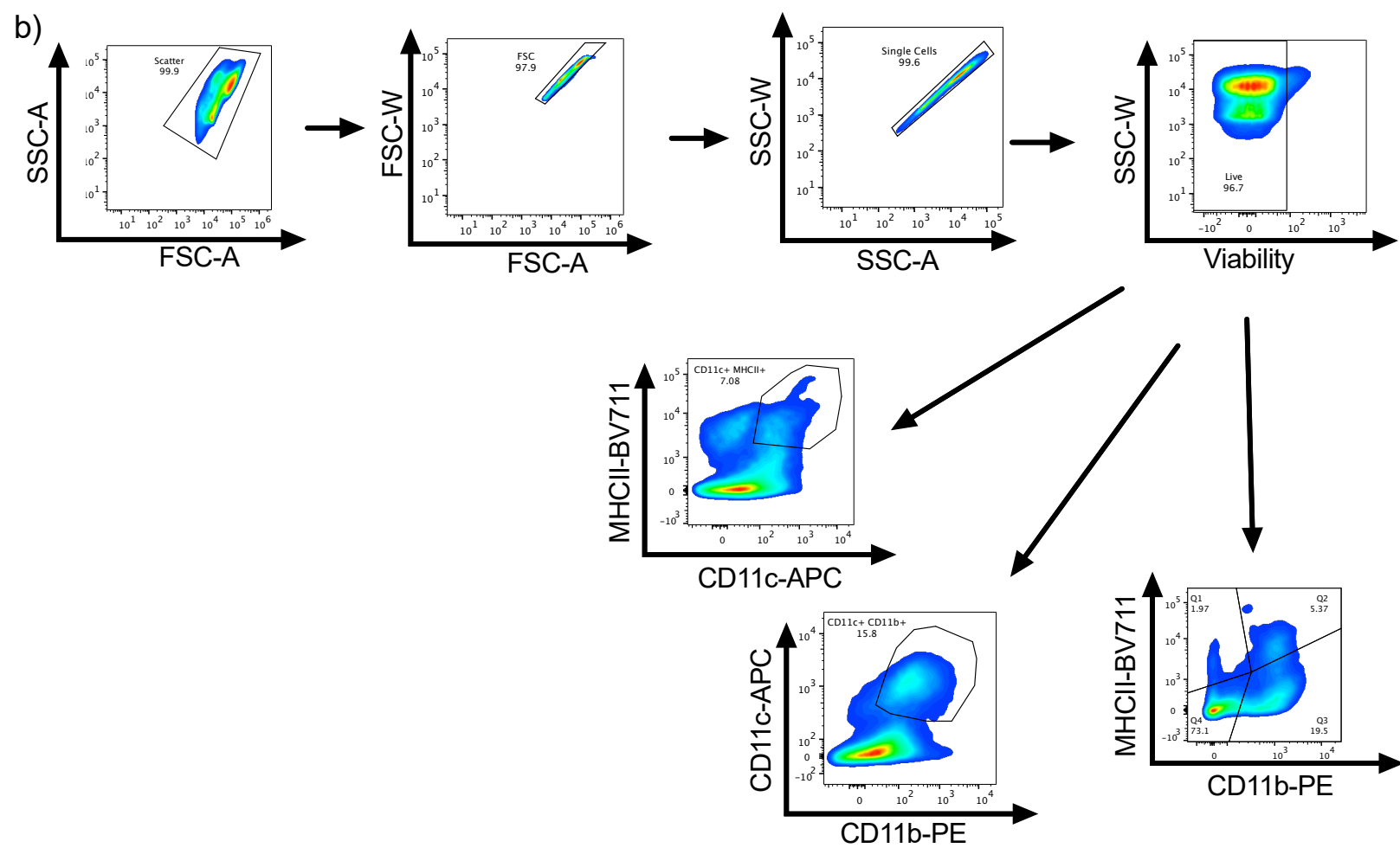
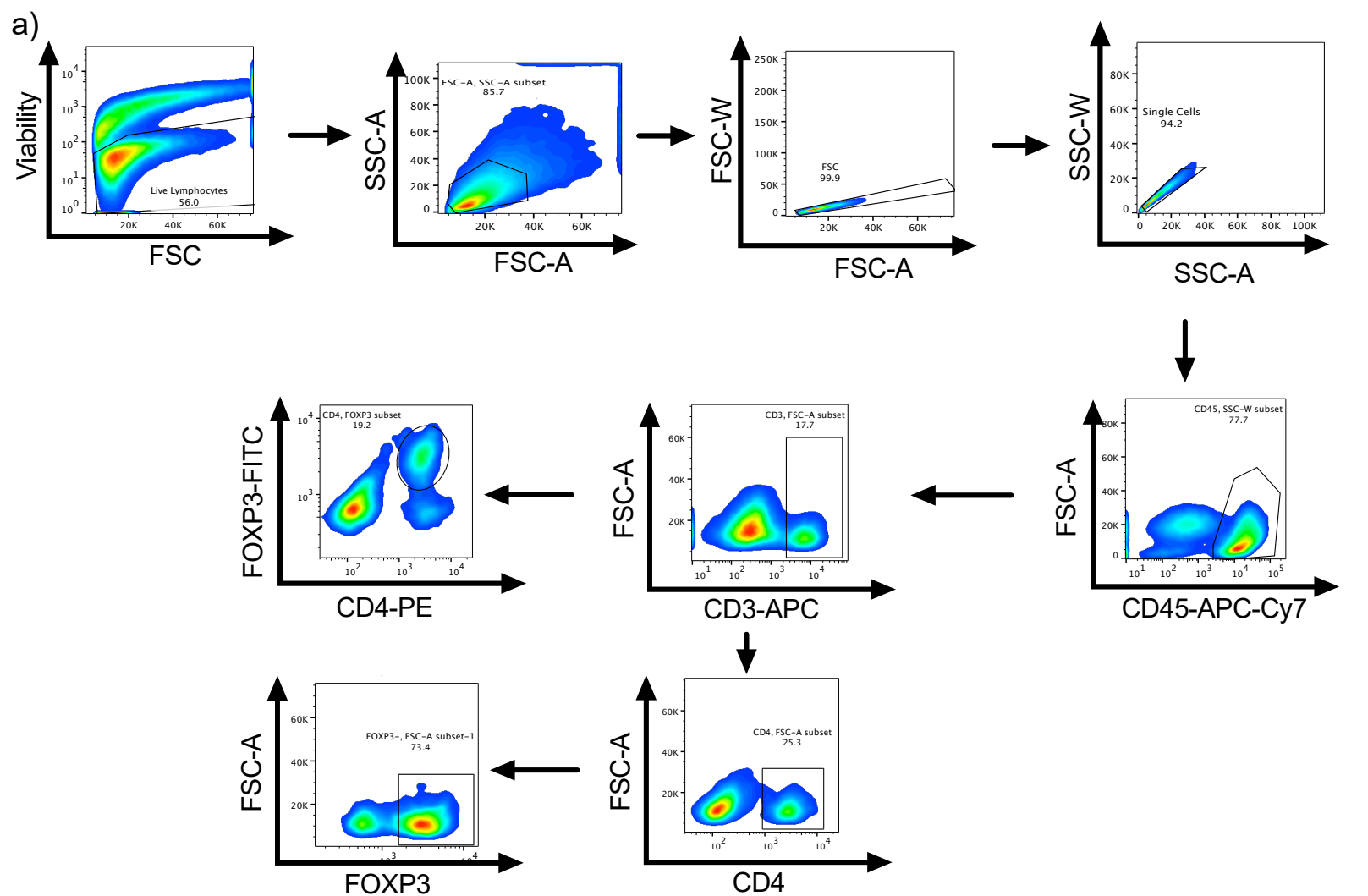




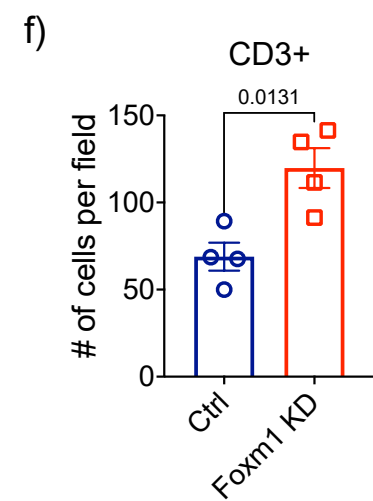
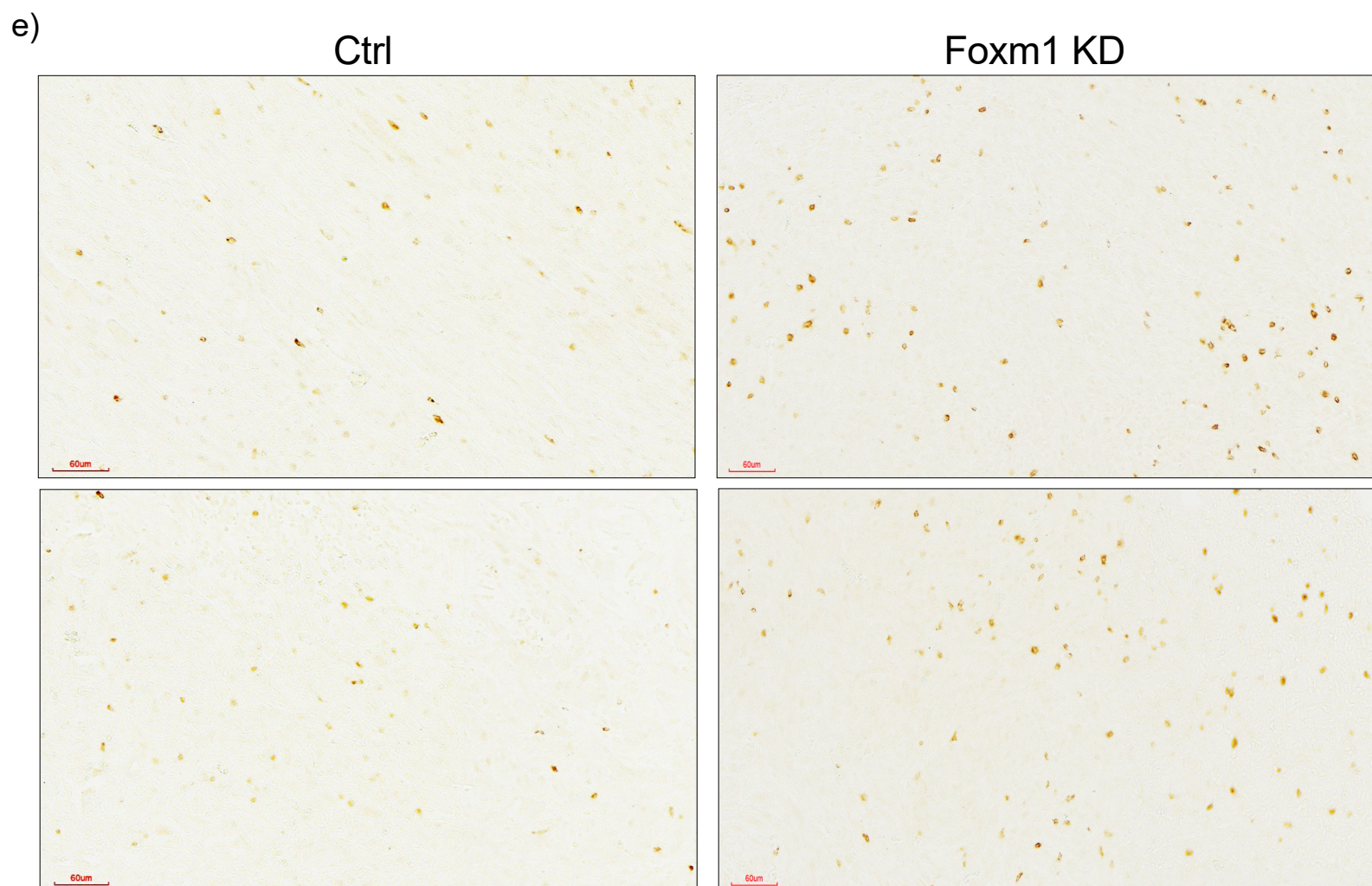
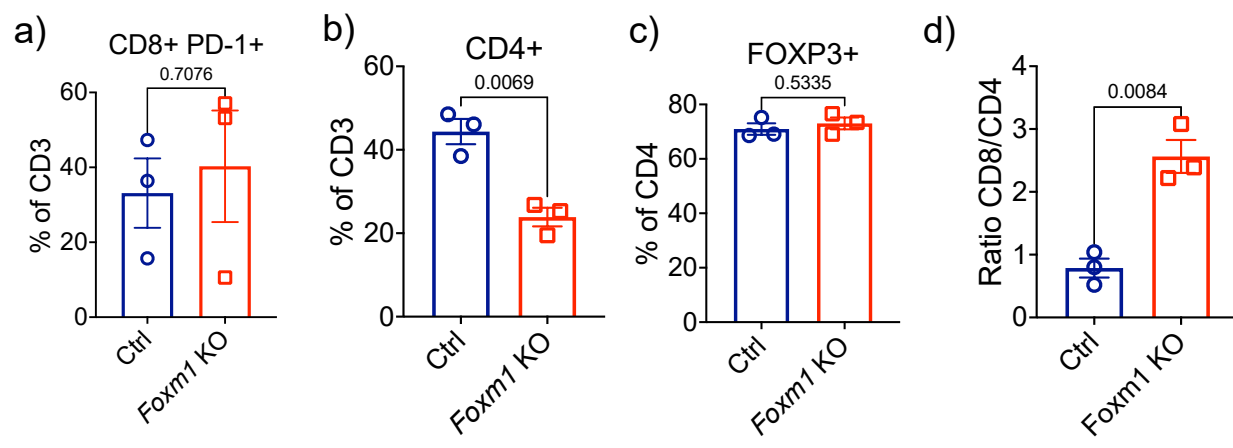
Supplementary Fig 1. FOXM1 is not essential for the growth/viability of breast cancer cells in vitro

(a-b) Propidium iodide-based cell cycle analyses for scrambled control (Ctrl) and *FOXMI* knockout in (a) MDA-MB-231 and E0771 cells using flow cytometry. Data represent mean + SEM of three independent biological experiments with multiple technical replicates for each experiment. Control and *FOXMI* knockout groups in all bar graphs are represented by dark blue circles and red squares or red triangles, respectively. **(c)** Left: Western blot analysis of 4T1 cells stably transfected with shRNA against Foxm1. Images are representative of three independent experiments. Right: Tumor growth in Balb/c mice orthotopically implanted with 4T1 cells expressing scrambled (n=4) and FoxM1 shRNA (n=4). Tumor volume was calculated using $V = \frac{1}{2} \times (w)^2 \times l$. Control and FOXM1 knockdown groups are represented by dark blue circles and red triangles, respectively **(d)** Gating strategy used for CD8 panel in flow cytometry experiments. p-values were calculated using multiple t test with Benjamini, Krieger, and Yekutieli correction (panel a-b) or non-linear regression with Malthusian growth (panel c, right). Results are displayed as mean +/- SEM from three independent experiments. Source data are provided as a Source Data file.



Supplementary Fig 2. Flow cytometry gating strategy for CD4 T cell and myeloid panel

(a) Gating strategy for flow cytometry of CD4 T cell panel. **(b)** Gating strategy for flow cytometry of myeloid cell panel.

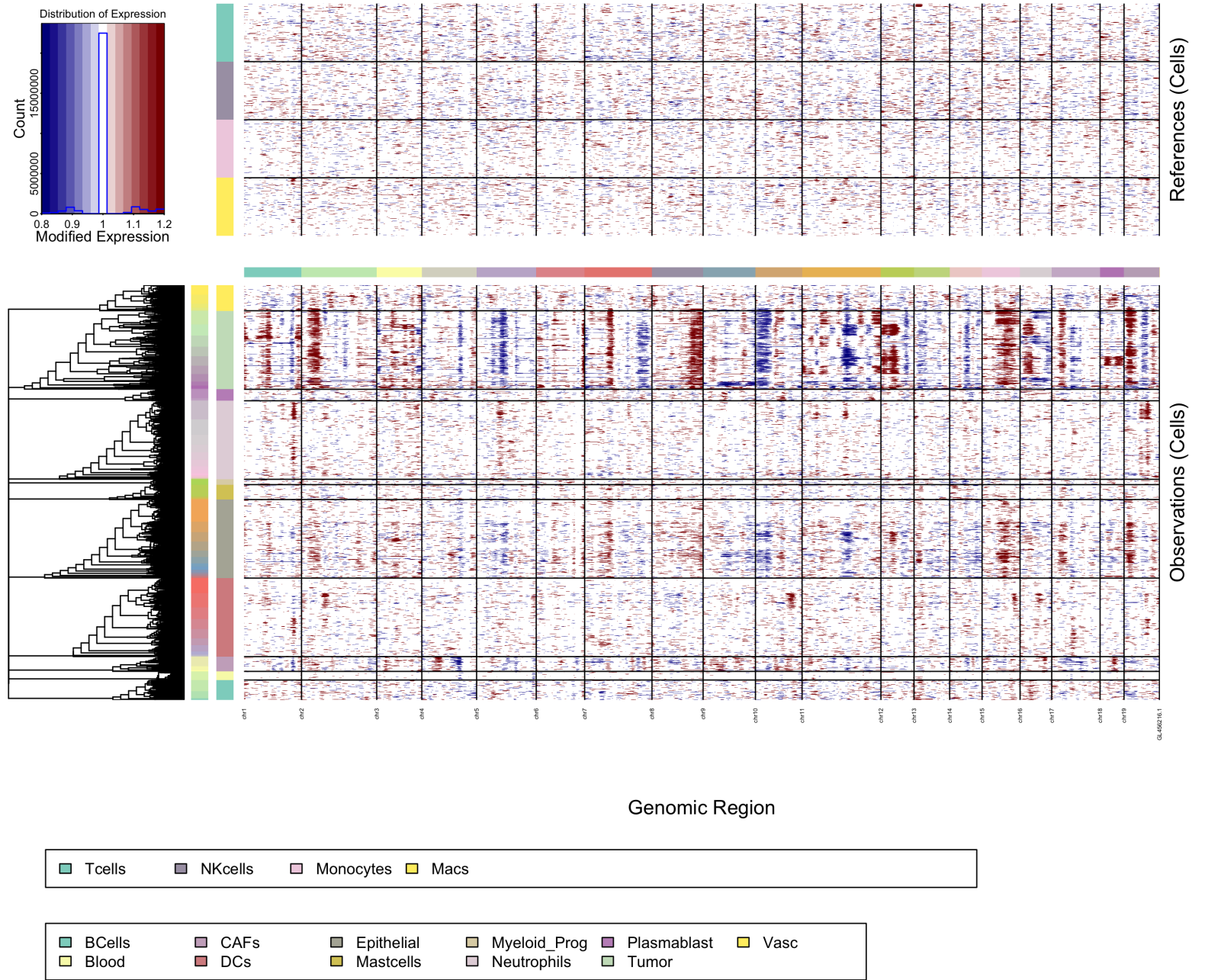


Supplementary Fig 3. FOXM1 depletion leads to increased infiltration of CD8+ cytotoxic T cells and reduced infiltration of CD4+ T cells into tumors

(a-c) Flow cytometry analysis showing the percentage of CD8+ PD-1+ (a), CD4+ T cells (b), and FOXP3+ cells gated out of CD4+ T cells (c) in Ctrl and Foxm1 KO E0771 tumor samples (n=3). (d) Flow cytometry analysis showing CD8/CD4 ratios in Ctrl and Foxm1 KO E0771 tumor samples (n=3). (e) Immunohistochemical analysis showing infiltration of CD3+ cells in the tumors from mice implanted with scrambled control (Ctrl, n=4 samples) and Foxm1 shRNA 4T1 cells (n=4 samples). Two representative images from 2 different tumor samples are shown per group. (f) Quantification of CD3+ T cell infiltration in 4T1 Ctrl and Foxm1 KD samples shown in (e). Mean values represent average number of CD3+ cells per field from n=4 mice per group. Error bars signify SEM for all panels. p values for all panels were determined using two-sided unpaired Welch's t-test. Control and FOXM1 knockout (or knockdown) groups in all bar graphs are represented by dark blue circles or red squares, respectively. Source data are provided as a Source Data file.

a)

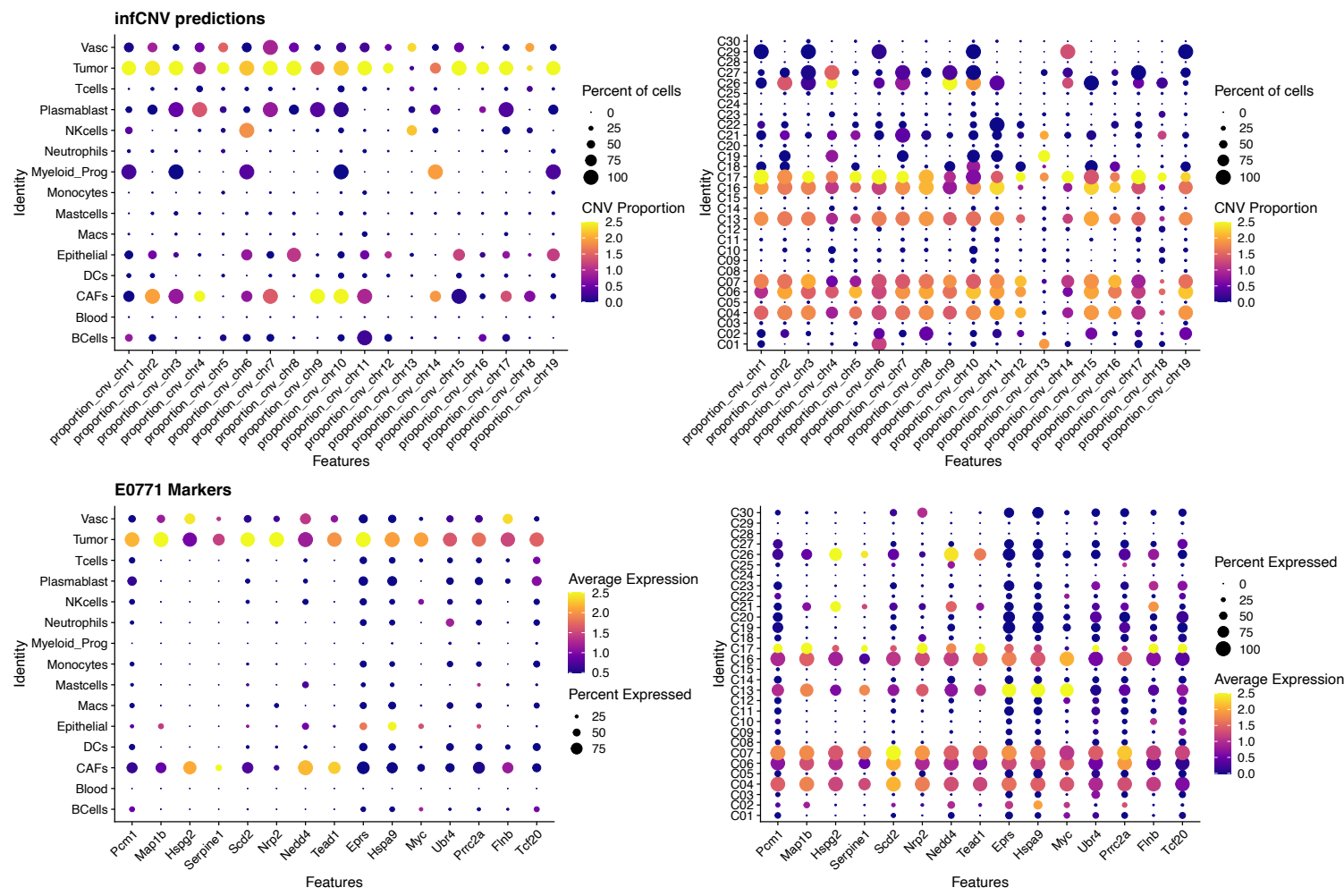
inferCNV



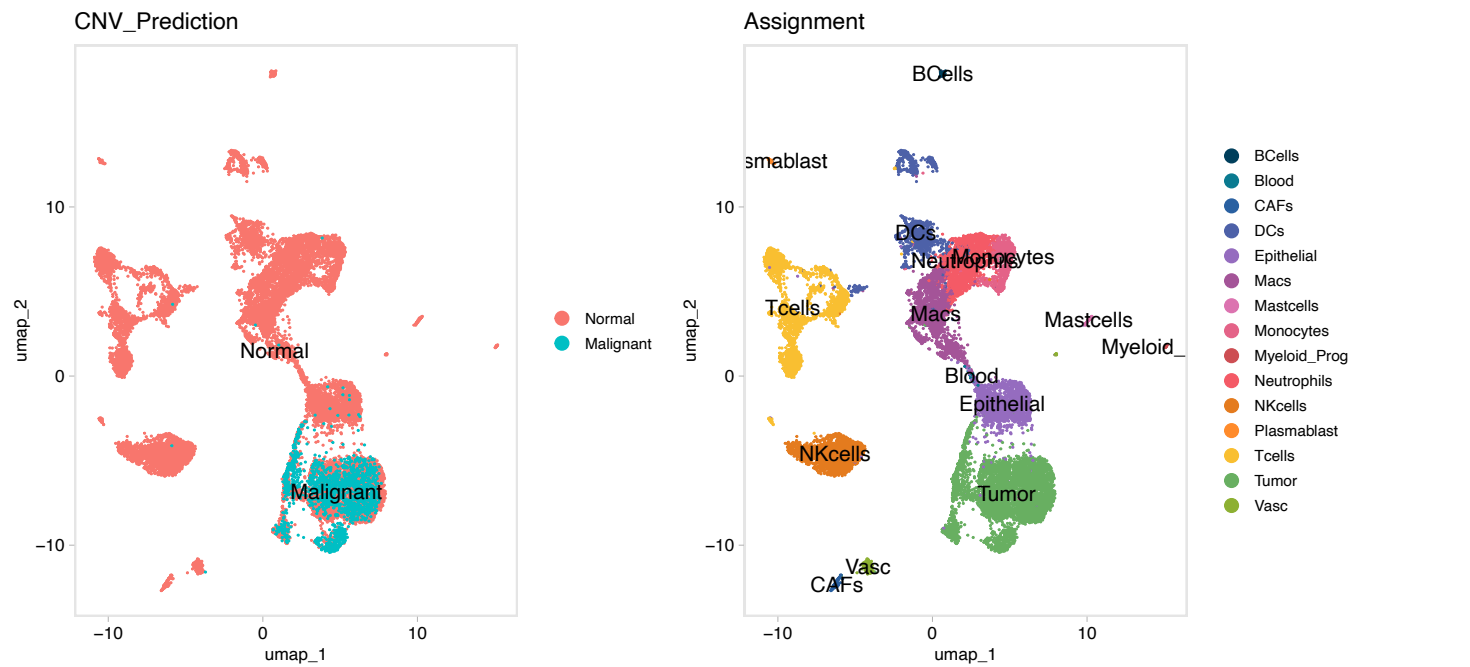
Supplementary Fig 4. InferCNV analysis indicates significant copy number variations in E0771 cancer cells

InferCNV heatmap of copy number variations in the genome of reference cells (top) and our scRNA-seq samples (bottom). InferCNV was performed on a subset of all normal cells (both epithelial and immune types) and cancer cells. Columns represent different chromosomes; rows represent the cell population of interest. Reference cells consisted of normal immune cells including T cells, NK cells, monocytes, and macrophages. Copy number variations are represented on a spectrum from blue to red, with dark blue representing inferred deletions and dark red representing inferred copy number gain.

a)

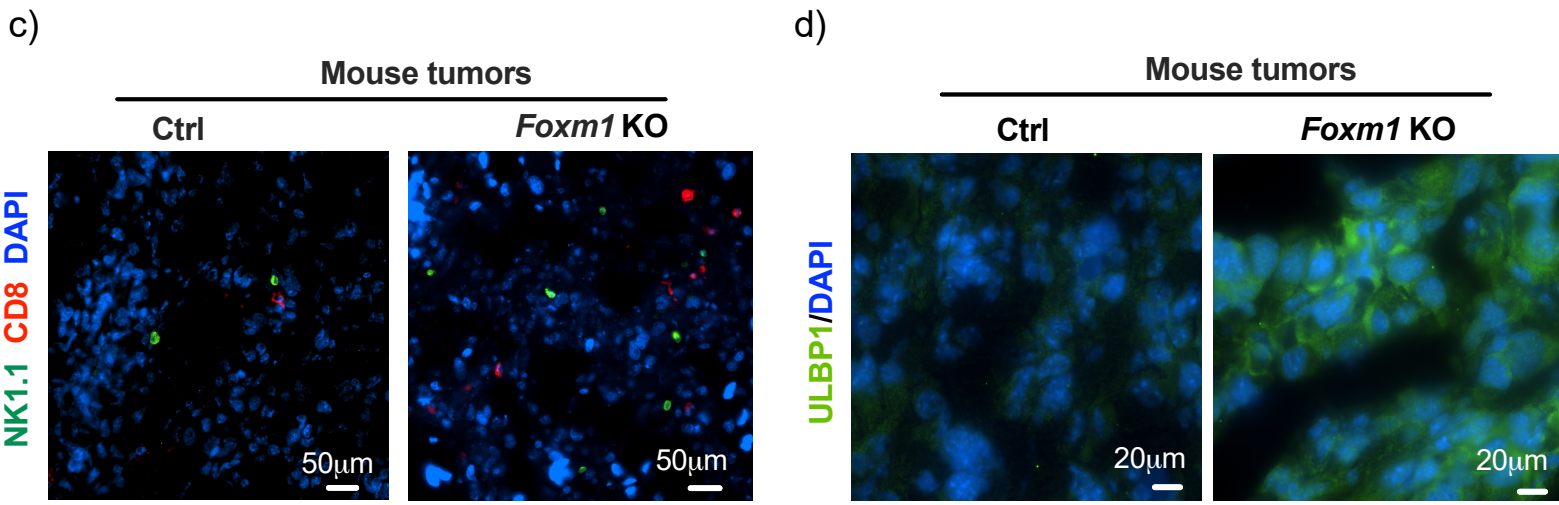
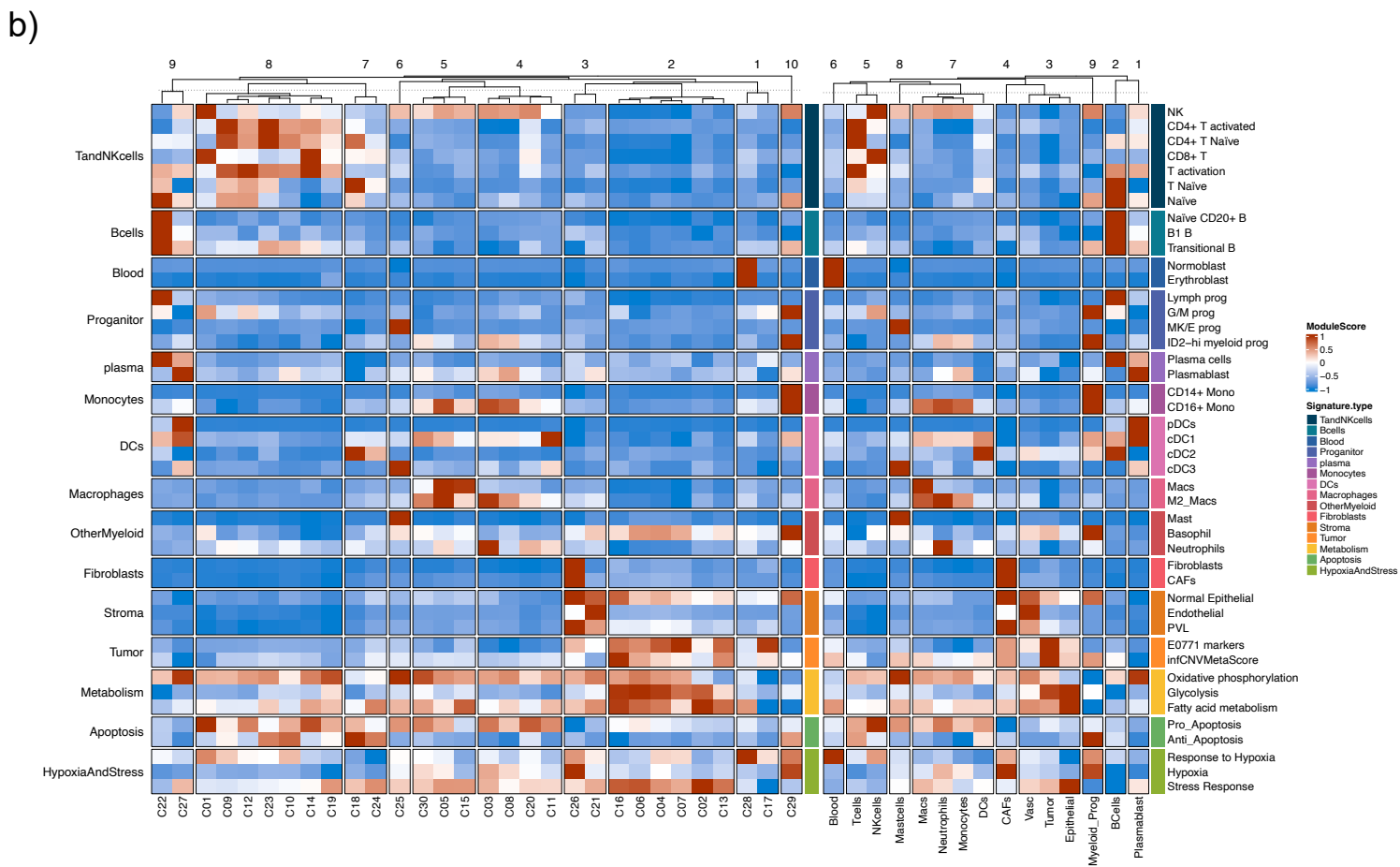
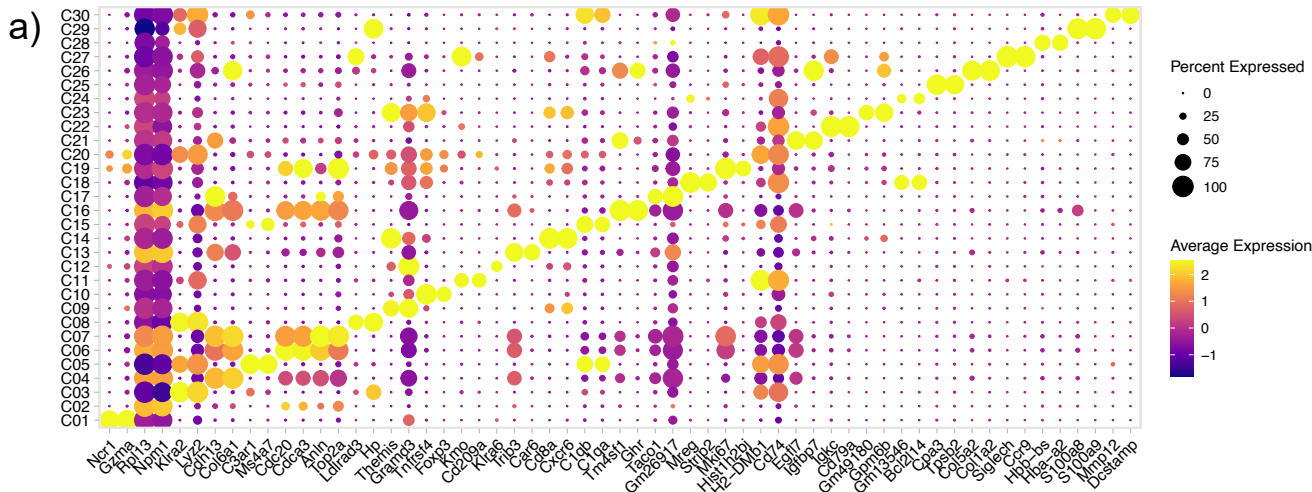


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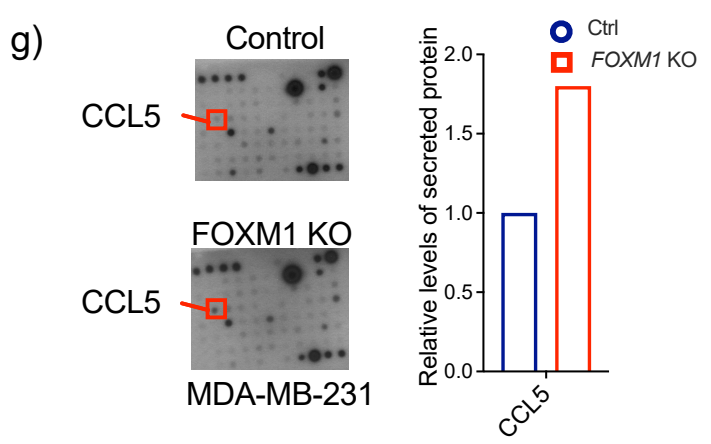
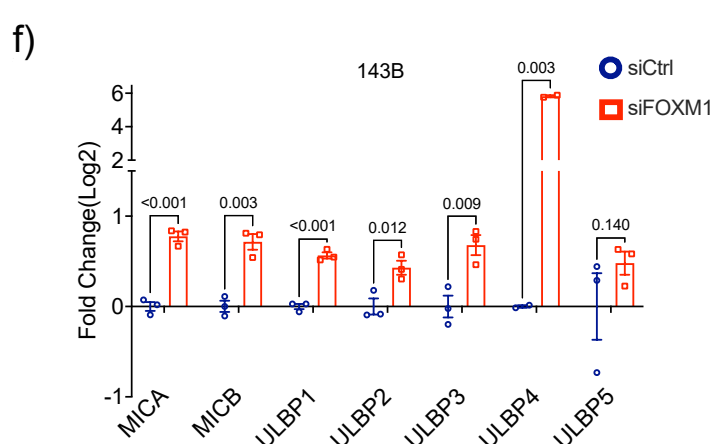
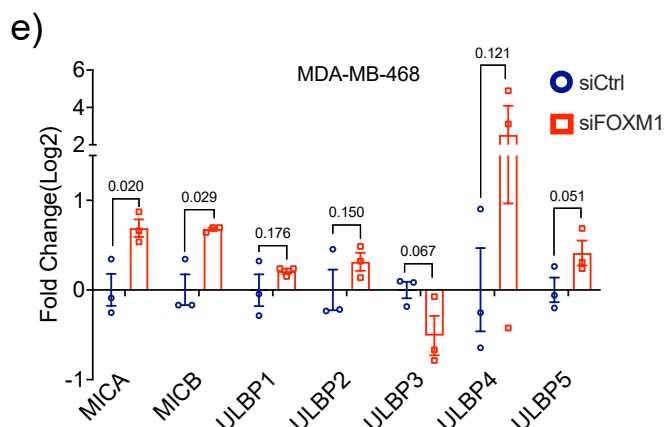
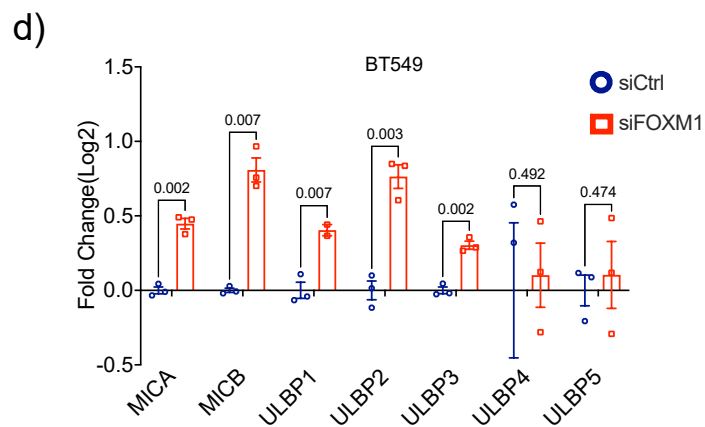
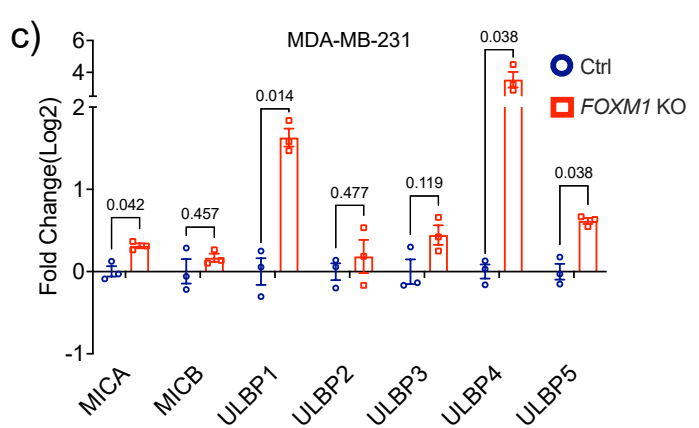
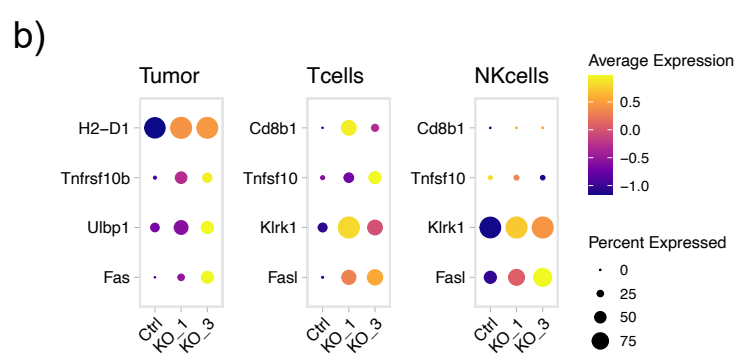
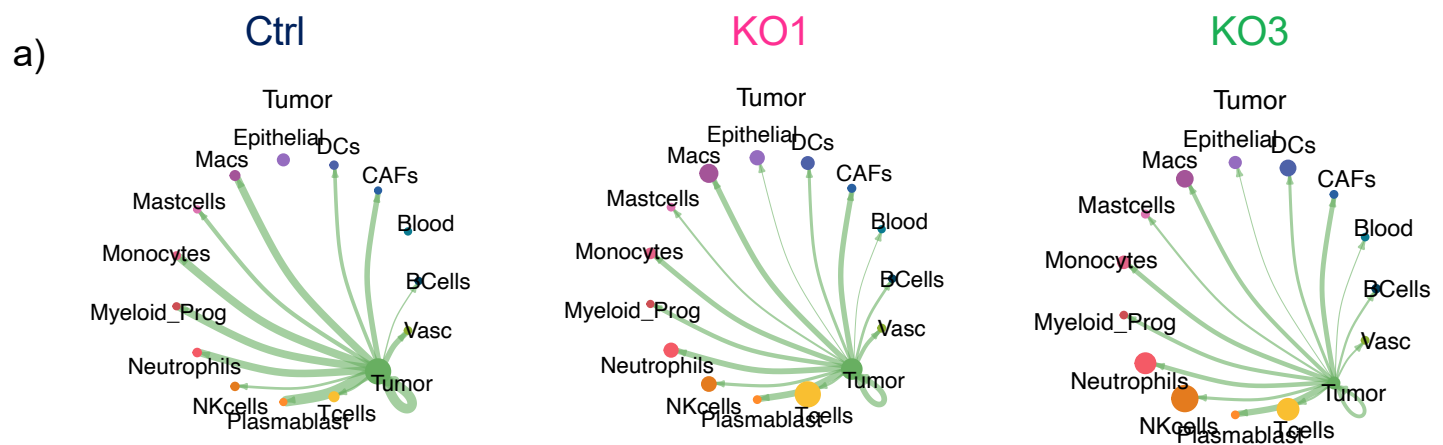
Supplementary Fig 5. InferCNV analysis distinguishes cancer cell populations from normal cells in the tumor microenvironment

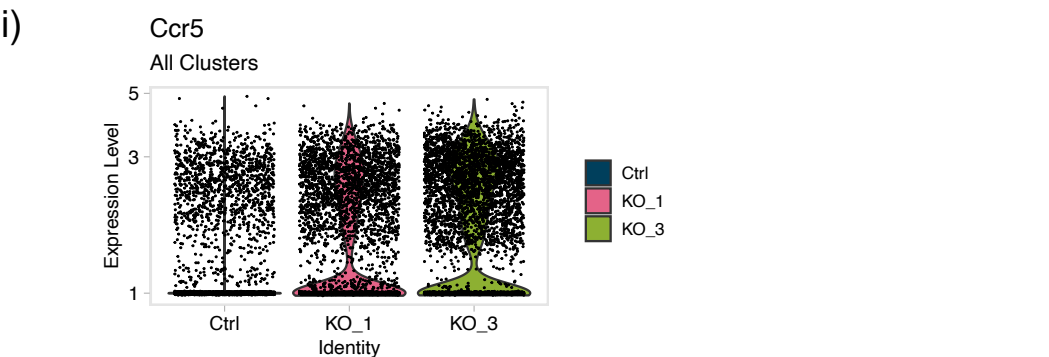
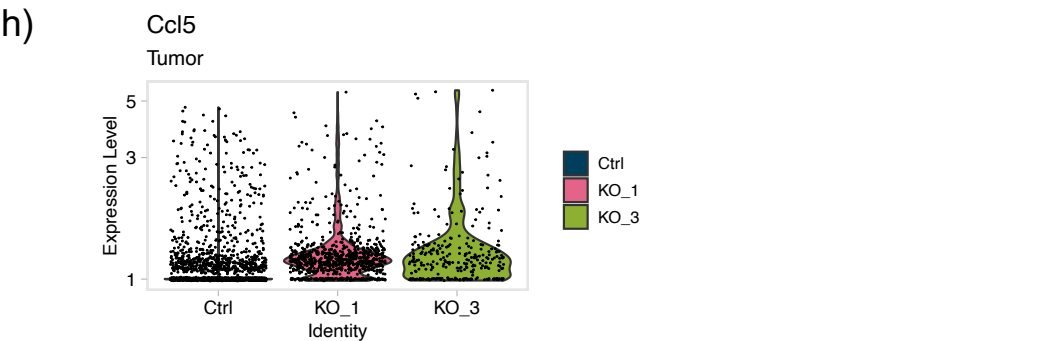
(a) Top panels: InferCNV analysis based on clusters and cell types. Colors of dots represent the proportion of copy number variations in each chromosome for each cell type; size of dots represents % of cells with copy number variations. Bottom panels: E0771 cancer cell-specific marker genes. **(b)** Clustering and assignment of normal and malignant cancer cells based on prediction of copy number variations (n=5 samples).



Supplementary Fig 6. Single cell transcriptome analysis of tumor and immune cells from control and Foxm1 KO tumors

(a) Top differentially expressed genes per cluster used to differentiate cell types in our single cell dataset. **(b)** Module score heatmap for all clusters. Each cell was scored using Seurat::AddModuleScore function with a set of known gene signatures associated with the annotated cell types (right had side row annotations). Columns represent averaged expression per cluster (left heatmap) or Assigned cell type (right heatmap) **(c)** Immunofluorescent staining showing infiltrated CD8⁺ T cells and NK cells in E0771 Ctrl and *Foxm1* KO tumors. CD8⁺ and NK1.1⁺ cells are green and red, respectively; DAPI staining is blue. Scale bar = 50 μ m. **(d)** Immunofluorescent staining of ULBP1 in E0771 control and *Foxm1* knockout tumor xenografts. Green indicates mouse ULBP1; blue indicates DAPI staining. Scale bar = 20 μ m. Images are representative of three biological samples per group.





j) Mouse Cytokine Array plate map

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	POS	POS	NEG	NEG	BLANK	Axl	BLC (CXCL13)	CD30 Ligand (TNFSF8)	CD30 (TNFRSF8)	CD40 (TNFRSF5)	CRG-2	CTACK (CCL27)	CXCL16	Eotaxin-1 (CCL11)
2	Eotaxin-2 (CCL24)	Fas Ligand (TNFSF6)	Fractalkine (CX3CL1)	G-CSF	GM-CSF	IFN-gamma	IGFBP-3	IGFBP-5	IGFBP-6	IL-1 alpha (IL-1 F1)	IL-1 beta (IL-1 F2)	IL-2	IL-3	IL-3 R beta
3	IL-4	IL-5	IL-6	IL-9	IL-10	IL-12 p40/p70	IL-12 p70	IL-13	IL-17A	KC (CXCL1)	Leptin R	Leptin	LIX	L-Selectin (CD62L)
4	Itln (CXCL1)	MCP-1 (CCL2)	MCP-5	M-CSF	MIG (CXCL9)	MIP-1 alpha (CCL3)	MIP-1 gamma	MIP-2	MIP-3 beta (CCL19)	MIP-3 alpha (CCL20)	PF-4 (CXCL4)	P-Selectin	RANTES (CCL5)	SCF
5	SDF-1 alpha	TARC (CCL17)	I-309 (TCA-3/CCL1)	TECK (CCL25)	TMF-P-1	TNF alpha	TNF RI (TNFRSF1A)	TNF RII (TNFRSF1B)	TPO	VCAM-1 (CD106)	VEGF-A	BLANK	BLANK	POS

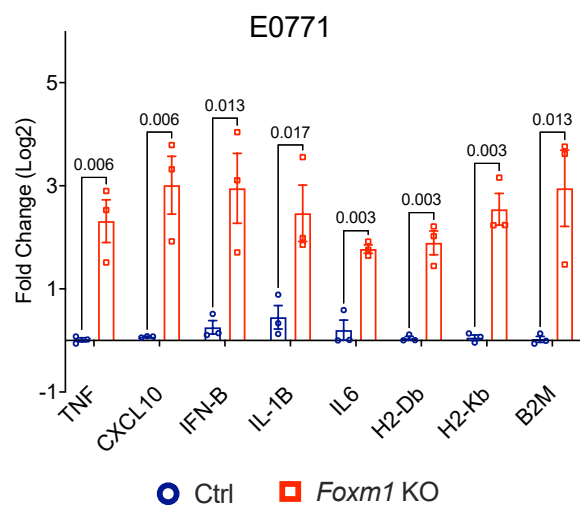
k) Human Cytokine Array plate map

	A	B	C	D	E	F	G	H	I	J	K
1	POS	POS	POS	POS	NEG	NEG	ENA-78 (CXCL5)	G-CSF	GM-CSF	GRO a/b/g (CXCL8)	GRO alpha (CXCL1)
2	I-309 (CCL1)	IL-1 alpha (IL-1 F1)	IL-1 beta (IL-1 F2)	IL-2	IL-3	IL-4	IL-5	IL-6	IL-7	IL-8 (CXCL8)	IL-10
3	IL-12 p40/p70	IL-13	IL-15	IFN-gamma	MCP-1 (CCL2)	MCP-2 (CCL8)	MCP-3 (CCL7)	M-CSF	MDC (CCL22)	CXCL9	MIP-1 beta (CCL4)
4	MIP-1 delta	RANTES (CCL5)	SCF	SDF-1 alpha	TARC (CCL17)	TGF beta 1	TNF alpha	TNF beta (TNFSF1B)	EGF	IGF-1	Angiogenin
5	OSM	TPO	VEGF-A	PDGF-BB	Leptin	BDNF	BLC (CXCL13)	Ck beta 8-1 (CCL23)	Eotaxin-1 (CCL11)	Eotaxin-2 (CCL24)	Eotaxin-3 (CCL26)
6	FGF-4	FGF-6	FGF-7 (KGF)	FGF-9	FLT-3 Ligand	Fractalkine (CX3CL1)	GCP-2 (CXCL6)	GDNF	HGF	IGFBP-1	IGFBP-2
7	IGFBP-3	IGFBP-4	IL-16	IP-10 (CXCL10)	LIF	LIGHT (TNFSF14)	MCP-4 (CCL13)	MIF	MIP-3 alpha	NAP-2 (CXCL7)	NT-3
8	NT-4	OPN (SPP1)	OPG (TNFRSF11)	PARC	PLGF	TGF beta 2	TGF beta 3	TIMP-1	TIMP-2	POS	POS

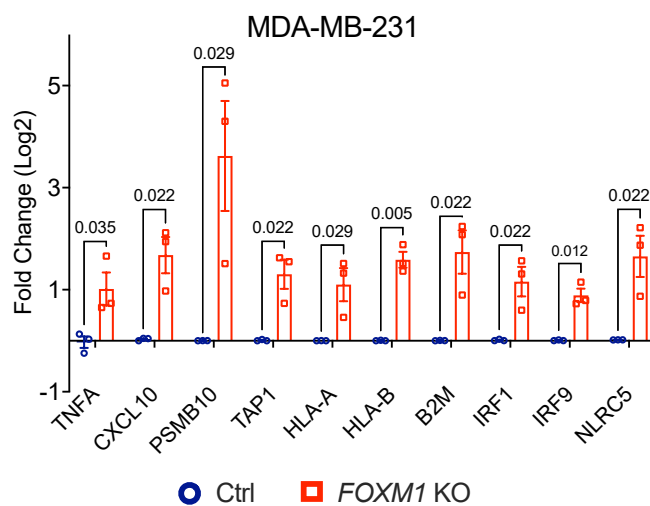
Supplementary Fig 7. Foxm1 depletion alters cell-cell communication and cytokine secretion in tumor microenvironment

(a) CellChat communication network showing outgoing signals from tumors to different cell populations in scrambled control (Ctrl) and Foxm1 knockout (KO1 and KO3) cells. Intensity of signals and interactions are indicated by thicknesses of lines and size of dots, respectively. (b) Expression of ligand-receptor pairs in corresponding cell types for CellChat pathways involved in cell death signaling (FAS, TRAIL), antigen presentation (MHC I), and NK cell activation (NKG2DL). (c-f) qRT-PCR analysis of human ULBP1 and other NKG2DL levels in MDA-MB-231, BT549, MDA-MB-468, and 143B cells (n = 3 biological replicates/group). (g) Cytokine array analysis of differentially secreted factors in media collected from scrambled control (Control) and FOXM1 knockout MDA-MB-231 cells. Red box indicates highly altered levels of the cytokine CCL5 in FOXM1 KO cells compared to control cells. Bar graphs show quantification of bands in the red box, reflecting levels of differentially expressed CCL5 normalized to negative control. (h - i) Expression of CCL5 in tumor cells and corresponding receptor CCR5 on all clusters in Ctrl and Foxm1 KO E0771 samples from scRNA- seq dataset. (j-k) Cytokine array plate map for mouse and human cytokines assessed in this study. All qRT-PCR data presented in panels c-f represent the mean $\pm$ SEM of the log₂ of fold change values from three biological replicates, with each replicate containing two technical replicates. Panel g represents data from one experiment with three pooled biological replicates. p values in panels c, d, and f were calculated using multiple t test with Benjamini, Krieger, and Yekutieli correction. p values in panel e were calculated using one-way unpaired Welch's t test. Control and FOXM1 knockout groups in all bar graphs are represented by dark blue circles or red squares, respectively. Source data are provided as a Source Data file.

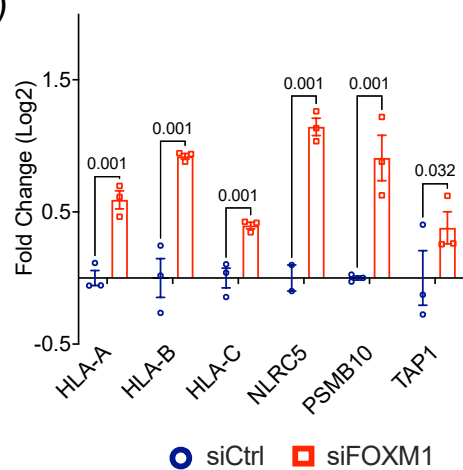
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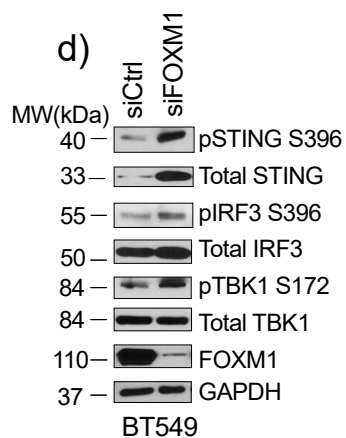
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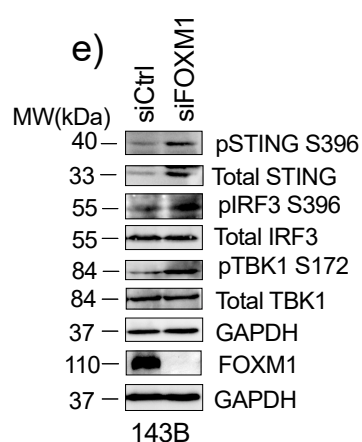
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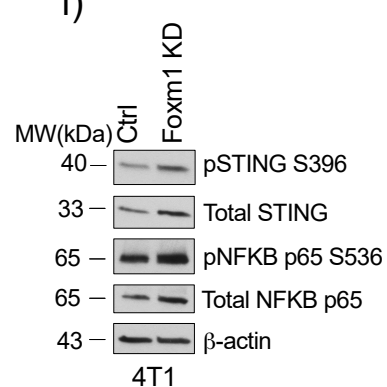
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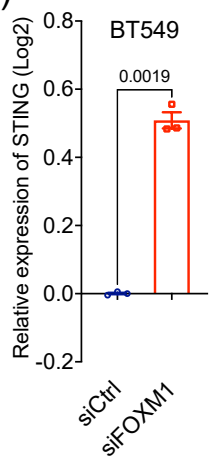
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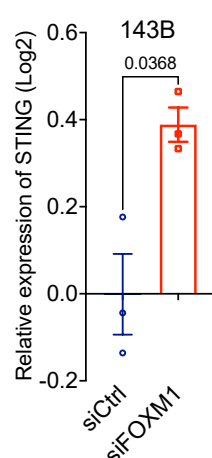
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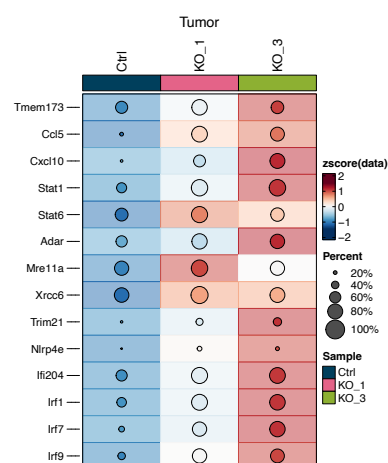
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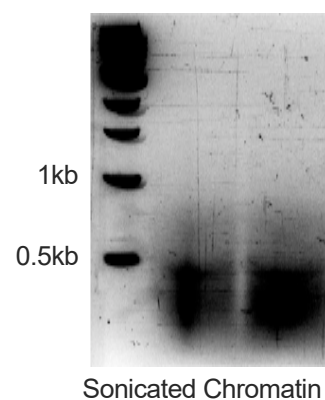
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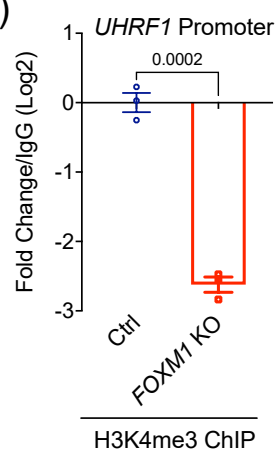
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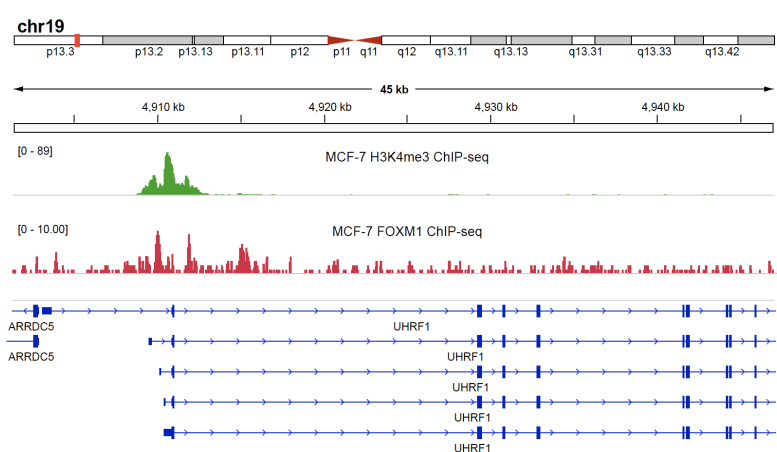
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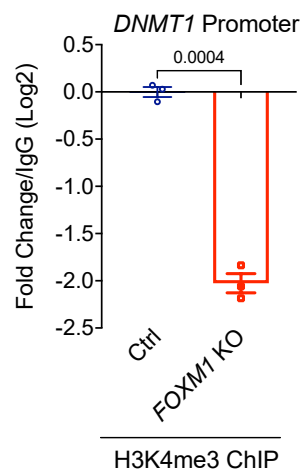
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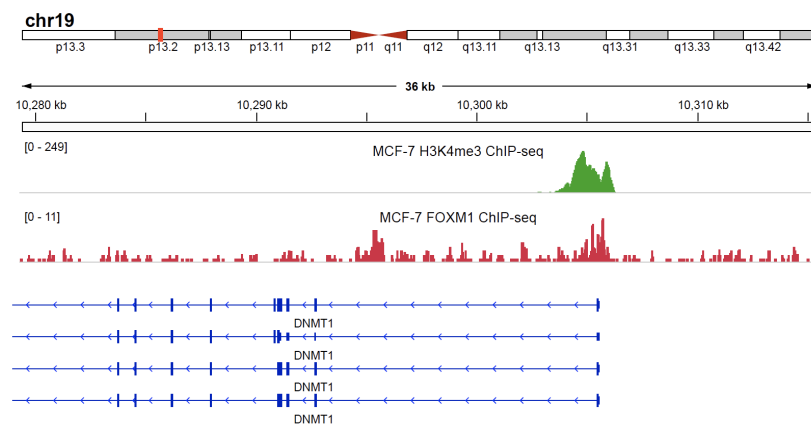
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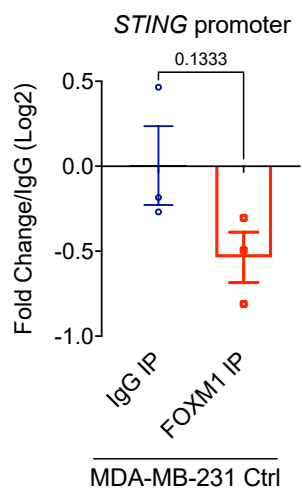
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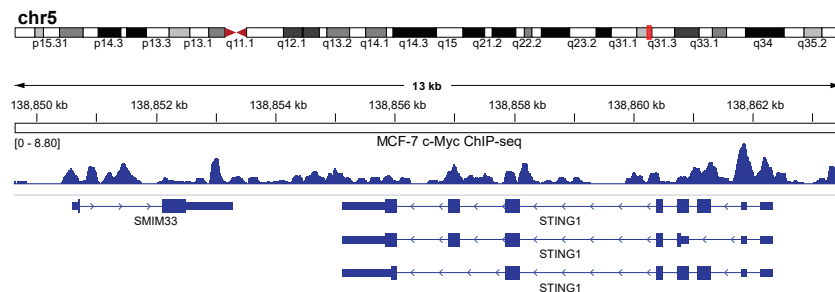
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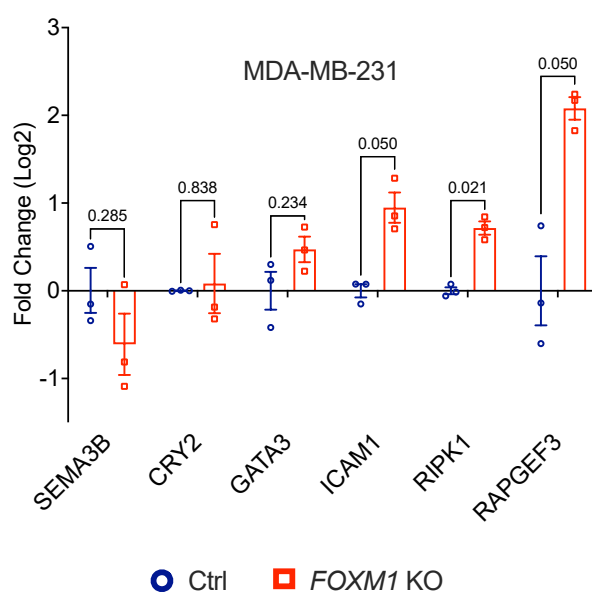
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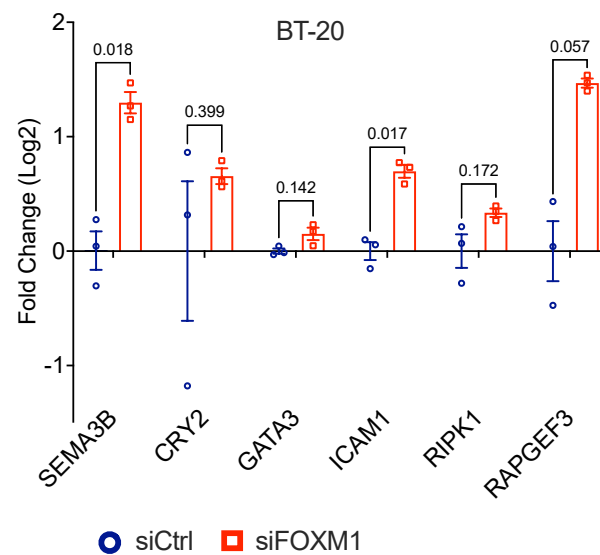
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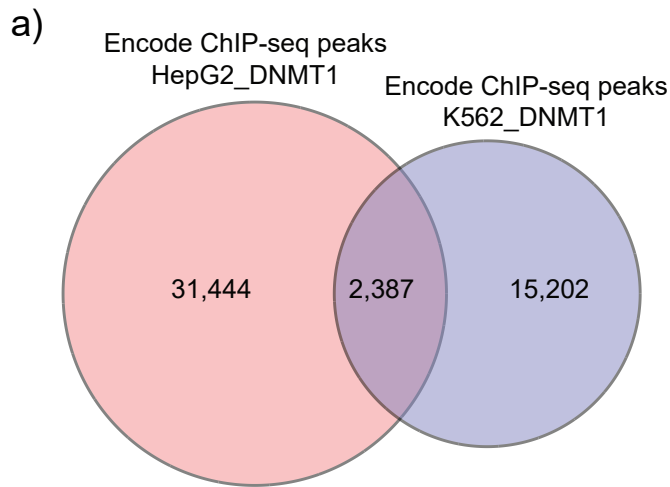


r)

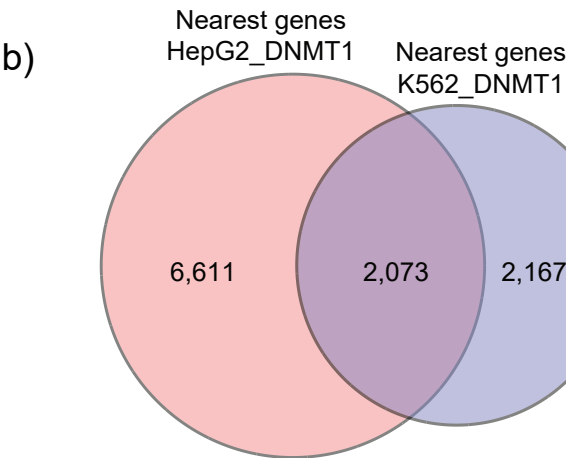
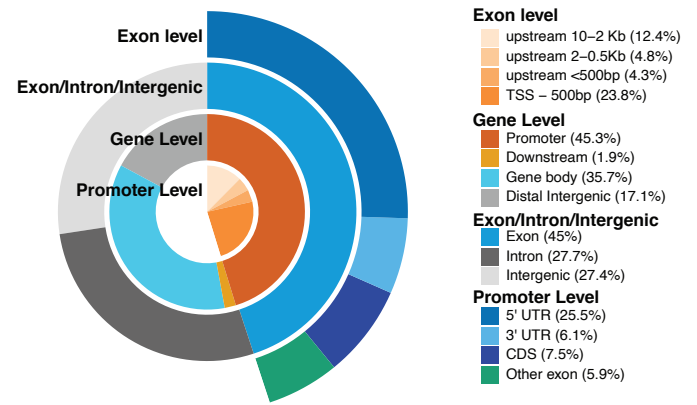


Supplementary Fig 8. FOXM1 depletion results in increased cGas-STING and reduced DNMT1-UHRF1 activation

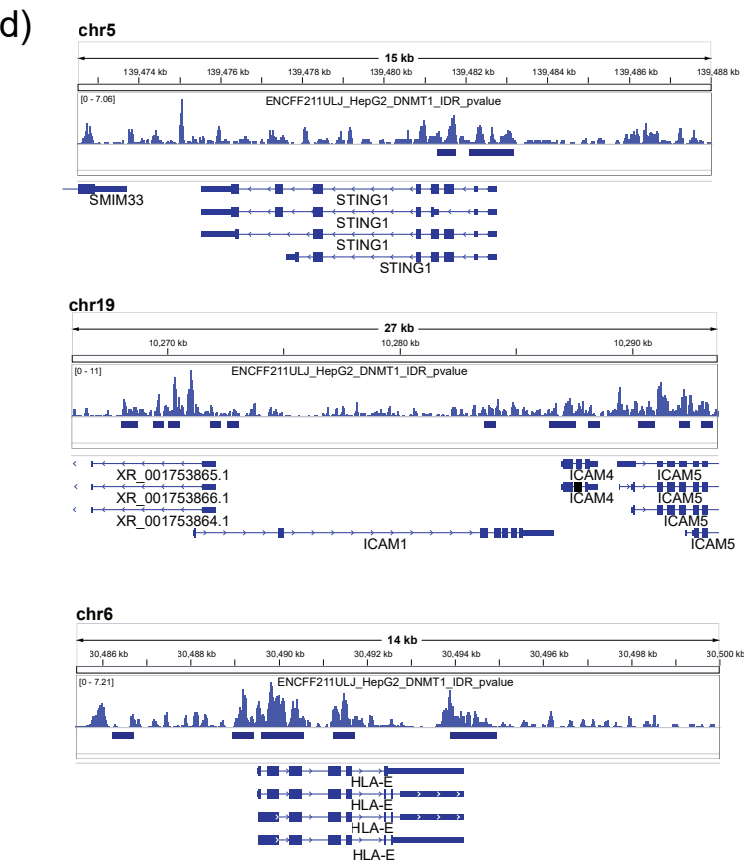
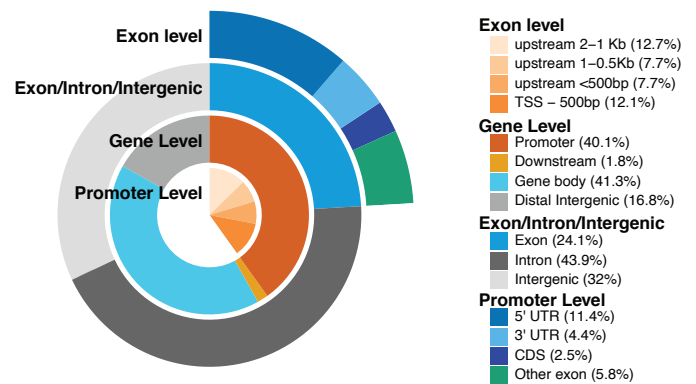
(a-b) qRT-PCR analysis of immune activating genes involved in cytokine signaling inflammation, antigen presentation, and interferon signaling in scrambled Control and FOXM1 KO E0771, MDA-MB-231 (c) qRT-PCR analysis of immune activating genes in siCtrl and siFOXM1 transfected BT549 cells. (d-e) Western blot analysis for activation of cGas-STING pathway in siCtrl and siFOXM1 transfected BT549 and 143B cells. (f) Western blot analysis on stable scrambled Ctrl and Foxm1 KD 4T1 cells using antibodies against STING pathway proteins. (g-h) qRT-PCR levels of STING in siCtrl and siFOXM1 transfected BT549 and 143B cells. (i) mRNA levels of STING (TMEM173) and other downstream molecules in the cGas/STING pathway in the E0771 Ctrl and Foxm1 KO tumor population from the scRNA-seq data. (j) Picture showing sheared chromatin used for ChIP experiments. (k,m) ChIP-qPCR analyses for enrichment of H3K4me3 on UHRF1(k) and DNMT1(m) promoter in MDA-MB-231 Ctrl and FOXM1 KO cells. (l,n) ENCODE ChIP-seq analysis of FOXM1 and H3K4me3 enrichment in the promoter region of UHRF1(l) and DNMT1(n) in MCF7 cells. (o) ChIP-qPCR assay in MDA-MB-231 cells using IgG and FOXM1 antibody and primers spanning STING promoter region. (p) ENCODE ChIP-seq analysis of MYC enrichment in the promoter region of STING in MCF7 cells. (q-r) qRT-PCR analysis of known DNMT1 target genes in Ctrl and FOXM1 KO MDA-MB-231 and siCtrl and siFOXM1 transfected BT20 cells. All qRT-PCR and qPCR data represent the mean $\pm$ SEM of the log2 of fold change values from three biological replicates, with each replicate containing two technical replicates. Western blot images are representative of three independent experiments. p values for panel a-c, q, and r were calculated using multiple t test with Benjamini, Krieger, and Yekutieli correction. p values in panel g,h,k,m,o were calculated using a two-sided Welch's t test. Control and FOXM1 knockout groups in all bar graphs are represented by dark blue circles or red squares, respectively. Source data are provided as a Source Data file.



c) Peak position HepG2_DNMT1

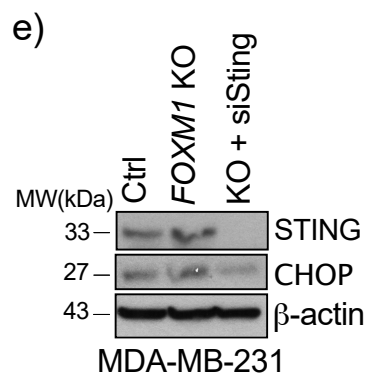
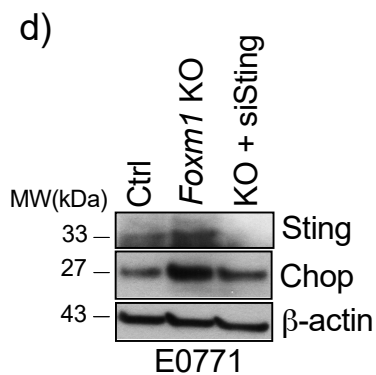
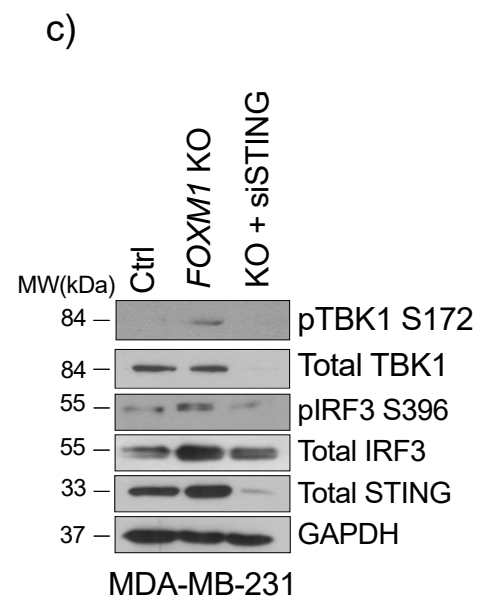
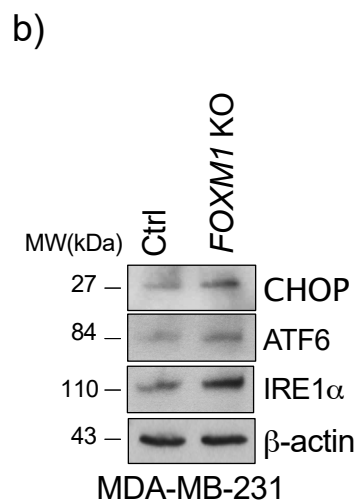
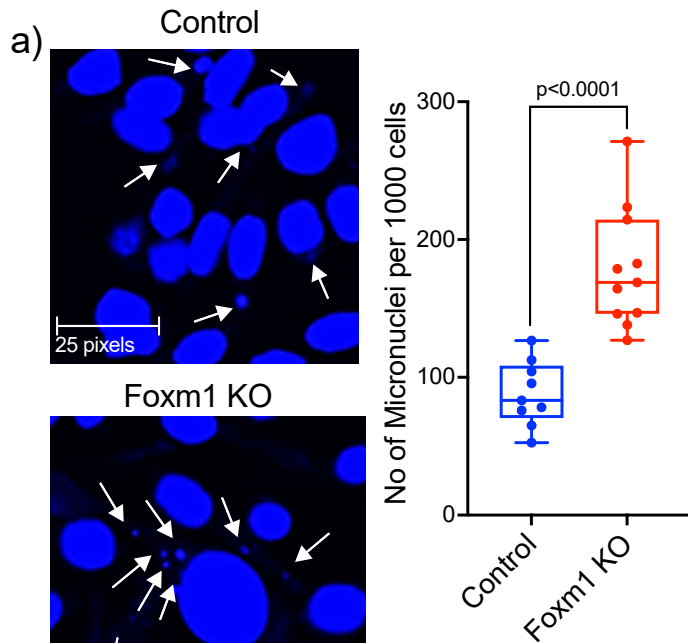


Peak position K562_DNMT1



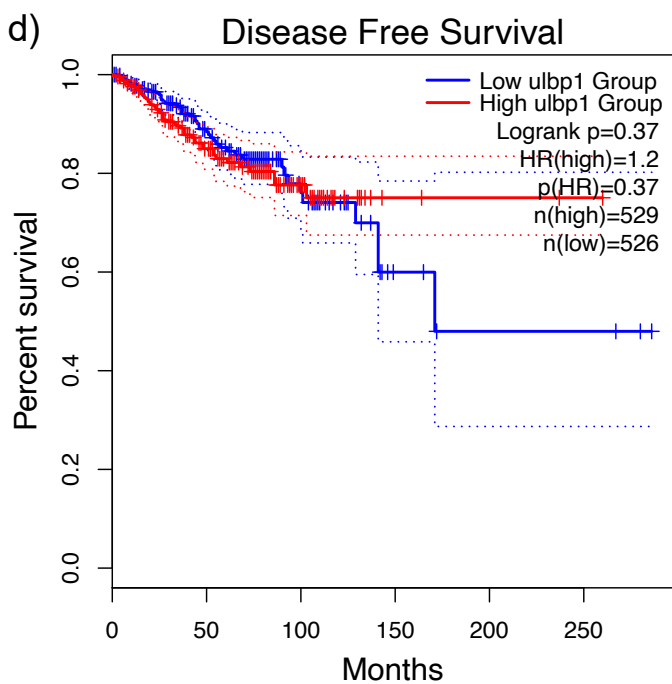
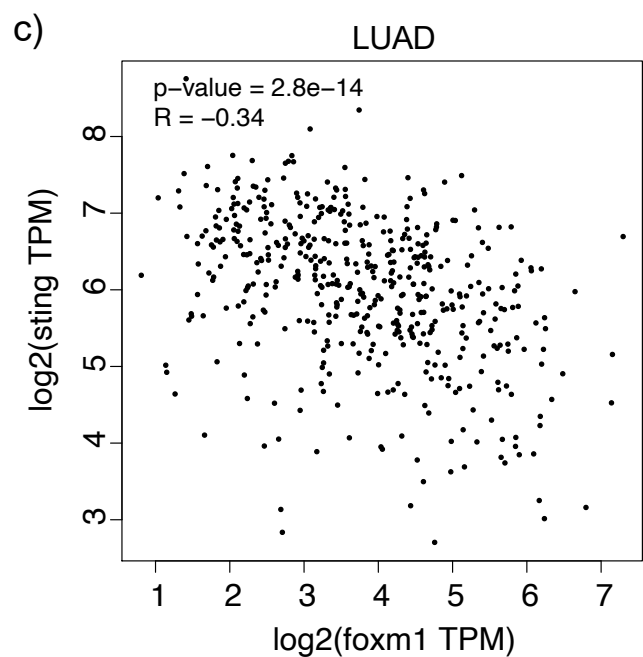
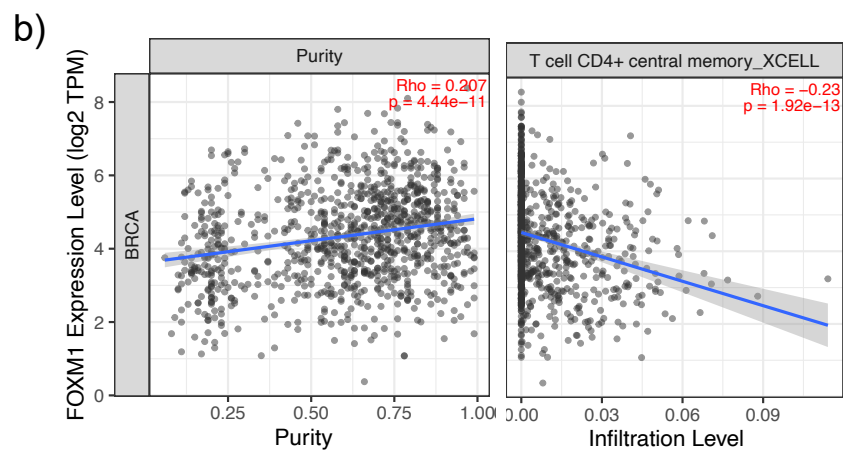
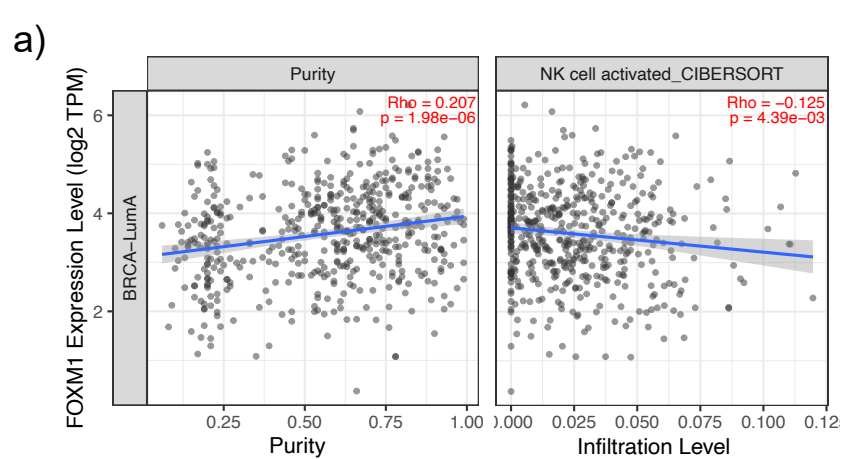
Supplementary Fig 9. ChIP-seq analysis displays binding of DNMT1 on STING and other immune gene promoters

ChIP-seq data of DNMT1 from HepG2 and K562 cell lines were downloaded from ENCODE website (<https://www.encodeproject.org/>). We selected p-value (bigwig file) and IDR ranked peaks (bed file) from combined 2 repeats for each cell line was extracted. The peaks were further filtered with scores less than 200 removed. **(a)** Venn diagram (top) of binding peaks from HepG2 and K562 and their overlapping peaks (2,387 peaks); **(b)** Venn diagram (bottom) number of unique genes with binding peaks at their promoter regions, with 2,073 common genes detected with DNMT1 binding at their promoter regions. **(c)** peaks in different regions (promoter, exon, intron, etc) for two cell lines. **(d)** binding peaks (p-value track of HepG2) in promoter regions of STING1, ICAM1, and HLA-E, and **(e)** no binding peaks observed in the promoter regions of ADCY9, TIAM2, and PARD3 from HepG2 cell line.

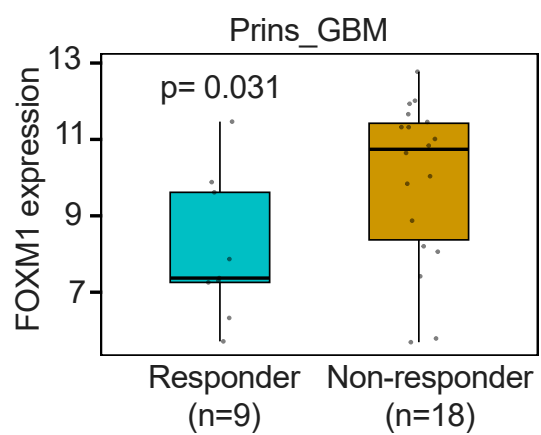


Supplementary Fig 10. STING mediates the effects of FOXM1 on cGas-STING pathway and UPR signaling activation

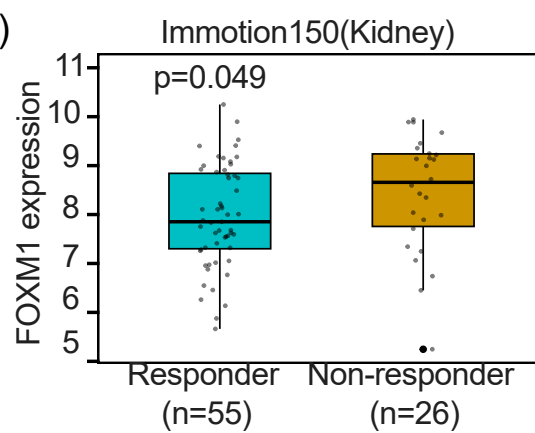
(a) (left) Representative pictures of immunofluorescence showing increased number of micronuclei in *Foxm1* KO cells compared to scrambled control. Arrows indicate micronuclei. Right: Quantification of numbers of micronuclei per 1000 cells counted from immunofluorescence pictures (n = 9 for ctrl and n = 10 for *Foxm1* KO). All data points are displayed on the box and whiskers plot, with the 25th to 75th quartile being represented inside the box, while error bars represent outliers. Data are derived from three biological replicates, with each replicate containing two technical replicates. **(b)** Western blot analysis of Ctrl and *FOXMI* KO MDA-MB-231 using antibodies against indicated UPR proteins. **(c)** Western blot analysis of STING pathway activation in MDA-MB-231 cells transfected with STING siRNA in *FOXMI* KO cells. **(d-e)** Western blot analysis of Ctrl, *Foxm1* KO, and KO cells transfected with STING siRNA in mouse E0771 **(d)** or human MDA-MB-231 **(e)** using antibodies against STING and CHOP. β -actin was used as a loading control. Western blot images are representative of three independent experiments. p value for panel a was calculated using an unpaired two-sided Welch's t test. Source data are provided as a Source Data file.



e)



f)



Supplementary Fig 11. Effect of FOXM1-STING-ULBP1 signaling on immune infiltration and patient survival

(a-b) Spearman correlation of tumor purity and FOXM1 RNA levels with immune cell infiltration in breast cancer patients from the TIMER2.0 database. Cell populations of interest include activated NK cells and CD4⁺ central memory cells. (c) Pearson correlation analysis between FOXM1 and STING RNA levels in patients (n = 483) with lung adenocarcinoma (LUAD) from the GEPIA2 database. (d) Kaplan-Meier curve showing associations between disease-free survival and ULBP1 levels from the GEPIA2. Samples were divided into those with low (n=526) and high ULBP1 levels (n=529). (e-f) FOXM1 levels (high versus low) in GBM patients treated with pembrolizumab (Prins_GBM_2019 study) and patients with kidney cancer treated with atezolizumab (IMmotion150 study), divided into those who did and did not respond to therapy. The number of patients is indicated at the bottom. p values for panels a-b were calculated by TIMER2.0 database using Spearman correlation coefficient. The p value for panel c was calculated by GEPIA2 using Pearson correlation coefficient and a two-tailed t distribution. p values for panels e-f were calculated using two-sided Wilcoxon rank-sum test.

Supplementary Table 1- Sequence and location of FOXM1 sgRNAs

Name	Sequence	Genomic Location
Mouse FOXM1 sg1	GGGCCCCTGCAGCGTTAAGC	Chr 6+:128367369-128367388
Mouse FOXM1 sg3	CTACAGGTTGAGGAGCCCTC	Chr 6+: 128369284-128369307
Human FOXM1 sg1	TCTCCCGTTTCTGCTCGCAA	Chr12+: 2873982-2874002
Human FOXM1 sg3	ATAGCCTATCCAACATCCAG	Chr12+: 2872195-2872214
Scrambled sgRNA	GCACTACCAGAGCTAACTCA	

Supplementary Table 2- qPCR primers and siRNA sequences

Primer/siRNA	F(5' -3')	R(5' -3')
Mouse IFNb	CCAGCTCCAAGAAAGGACGA	CGCCCTGTAGGTGAGGTTGAT
Mouse IL-1B	GCAACTGTTCTGAACTCAACT	ATCTTTTGGGGTCCGTCAACT
Mouse CXCL10	ATCATCCCTGCGAGCCTATCCT	GACCTTTTTTGGCTAAACGCTTT C
Mouse TNFa	ATGGCCTCCCTCTCATCAGT	GTTTGCTACGACGTGGGCTA
Mouse ULBP1	CTAACACAACCGGAAAGCCCCT	CAGTGCTTGTGTCAACACGGA
Mouse B2M	ACAGTTCCACCCGCCTCACATT	TAGAAAGACCAGTCCTTGCTGAA G
Mouse H2-Db	GTAAAGCGTGAAGACAGCTGC	CTGAACCCAAGCTCACAGG
Mouse H2-Kb	CGGCGCTGATCACCAAACA	AGCGTCGCGTTCCCGTT
Mouse DNMT1	AGAGACCAGGATAAGAAACGCA	CTCCTTTGATTTCCGCCTCAAT
Mouse UHRF1	CCACACCGTGAAGTCTCTGTC	AGGCGCACATCATAATCGAAG
Human TNFa	CTCTTCTGCCTGCTGCACTTTG	ATGGGCTACAGGCTTGTCACTC
Human CXCL10	GGTGAGAAGAGATGTCTGAATCC	GTCCATCCTTGGAAGCACTGCA
Human PSMB10	TCCTTCGAGAACTGCCAAAGA	ATCGTTAGTGGCTCGCGTATC
Human TAP1	TCCTGGTGGTCCTCTCCTCTCTT	GTGTTGTTATAGATCCCGTCACC C
Human HLA-A	ACCCTCGTCTGCTACTCTC	CTGTCTCCTCGTCCCAATACT
Human HLA-B	CAGTTCGTGAGGTTTCGACAG	CAGCCGTACATGCTCTGGA
Human B2M	GAGGCTATCCAGCGTACTCCA	CGGCAGGCATACTCATCTTTT
Human IRF1	CTGTGCGAGTGTACCGGATG	ATCCCCACATGACTTCCTCTT
Human IRF9	GCCCTACAAGGTGTATCAGTTG	TGCTGTCGCTTTGATGGTACT
Human NLRC5	ACCTTAAGCCTGTGTCCACG	CTGTGAACCTGCCACAGCA
Human DNMT1	CGTGGTGGTGGATGACAAG	GGCTCCCCGTTGTAGGAGAT
Human UHRF1	GACAAGCAGCTCATGTGCGATG	AGTACCACCTCGCTGGCATCAT
Human ULBP1	GGATCCAACAAAACACCCT CTC	GGACCCAGACCAGGCTAA CAG
Human ULBP2	AGCAACTGCGTGACATTCAG	GCCATCCTATACAGTCTCCCA
Human ULBP3	TCTATGGGTACCTAGAAGAGC	TCCACTGGGTGTGAAATCCTC
Human ULBP4	GCACTTGGGGAGAATTGACCC	ACATCTCGACTTGCAGAGTGG
Human ULBP5	GACAGCTACCAAATAGCGAAGC	GGTAAGGAGTGTGAGTCGTCT
Human MICA	CTTCAGAGTCATTGGCAGACAT	TGTGGTCACTCGTCCCAACT
Human MICB	TCTTCGTTACAACCTCATGGTG	TCCCAGGTCTTAGCTCCCAG
Human CRY2	AACCACGACGAGACCTACG	GAGTTGGCGTTCATTCCGG
Human GATA3	GCCCCTCATTAAGCCCAAG	TTGTGGTGGTCTGACAGTTCTG
Human ICAM1	ATGCCAGACATCTGTGTCC	GGGGTCTCTATGCCCAACAA
Human RIPK1	GGGAAGGTGTCTCTGTGTTTC	CCTCGTTGTGCTCAATGCAG
Human RAPGEF3	GACCGGAAGTACCACCTTAGG	AGATTCCCACAACCTTGCTCC
ALU-C4-QC1(for bisulfite)	GGTTAGGTATAGTGGTTTATATTTGT AATTTTAGTA	ATTAATAAATAATCTTAAACTC CTAACCTCA
Human Methylated STING	TTAGGTTGGAGTGTAAATGGTACG	AAATTAATAAACGTAATAACGCA
Human Unmethylated STING	TAGGTTGGAGTGTAAATGGTATGA	AAAAATTAATAAACATAATAACA CAT

Human STING promoter ChIP	CCAAACCTAGGGCCCCTGG	CCACCAAGACCCAGGGAGAC
Human DNMT1 promoter ChIP	AGGGGATGTACCAAACGGAGAG	TGCTTTATCCCCATCACACCTG
Mouse STING siRNA	AACAUUCGAUUCCGAGUAU	UAUCUCGGAAUCGAAUGUU
Human STING siRNA	CGAACUCUCUCAAUGGUAU	AUACCAUUGAGAGAGUUCG
Human FOXM1 siRNA	GGACCACUUUCCCUACUUU	AAAGUAGGGAAAGUGGUCC
Control siRNA	CGUACGCGGAUACUUCGA	UCGAAGUAUUCCGCGUACG
Human DNMT1 siRNA	Sigma pre-designed siRNA SiRNA ID: SASI_Hs01_00204021 Sequence start: 2818	

Supplementary Table 3- Antibodies used for western blot, flow cytometry, and ChIP assay

Description	Catalog #	Reactivity	Isotype	Company
FOXM1(C-20)	SC-502	H Ms R	Rabbit IgG	Santa Cruz Biotechnology
FoxM1 (D3F2B) Rabbit mAb #20459	20459S	H	Rabbit IgG	Cell signaling
STING (D2P2F) Rabbit mAb 13647	13647	H Ms	Rabbit IgG	Cell signaling
Phospho-STING (Ser366) (E9A9K) Rabbit mAb 50907	50907	H	Rabbit IgG	Cell signaling
TBK1/NAK (D1B4) Rabbit mAb 3504	3504	H Ms R Mk	Rabbit IgG	Cell signaling
Phospho-TBK1/NAK (Ser172) (D52C2) XP® Rabbit mAb 5483	5483	H Ms	Rabbit IgG	Cell signaling
STING (D1V5L) Rabbit mAb (Rodent Preferred) 50494	50494	H Ms R	Rabbit IgG	Cell signaling
Phospho-STING (Ser365) (D8F4W) Rabbit mAb 72971	72971	Ms	Rabbit IgG	Cell signaling
TBK1/NAK (D1B4) Rabbit mAb 3504	3504	H Ms R Mk	Rabbit IgG	Cell signaling
Phospho-TBK1/NAK (Ser172) (D52C2) XP® Rabbit mAb 5483	5483	H Ms	Rabbit IgG	Cell signaling
ATF-6 (D4Z8V) Rabbit mAb #65880	65880S	H Ms	Rabbit IgG	Cell signaling
IRE1α (14C10) Rabbit mAb #3294	3294S	H Ms R	Rabbit IgG	Cell signaling
CHOP (L63F7) Mouse mAb 2895	2895S	H Ms R	Mouse IgG	Cell Signaling
DNMT1 (D63A6) XP® Rabbit mAb #5032	5032S	H Ms R Mk	Rabbit IgG	Cell Signaling
UHRF1 Antibody (H-8)	sc-373750	H Ms R	Mouse IgG	Santa Cruz Biotechnology
Tri-Methyl-Histone H3 (Lys4) (C42D8) Rabbit mAb #9751	9751S	H M R Mk Dm Sc	Rabbit IgG	Cell Signaling
mouse anti-rabbit IgG-HRP	sc-2357	Rbt	Mouse IgG	Santa Cruz Biotechnology
m-IgGk BP-HRP	sc-516102	Ms		Santa Cruz Biotechnology
Anti-rabbit IgG, HRP-linked Antibody 7074	7074	R	Goat IgG	Cell signaling
β-actin-HRP	A3854	H Ms R	Mouse IgG	Sigma
GAPDH-HRP	HRP-60004	H Ms R	Mouse IgG	Proteintech
BV711 Rat Anti-Mouse I-A/I-E	563414	Ms	Rat IgG	BD Biosciences
PE Rat Anti-CD11b	557397	Ms	Rat IgG	BD Biosciences
APC Hamster Anti-Mouse CD11c	550261	Ms	Rat IgG	BD Biosciences
APC/Cyanine7 anti-mouse CD45.2 Antibody	560694	Ms	Hamster IgG	BD Biosciences
BV711 Rat Anti-Mouse CD8a	563046	Ms	Rat IgG	BD Biosciences
APC Hamster Anti-Mouse CD3e	553066	Ms	Hamster IgG	BD Biosciences
PE Rat Anti-Mouse CD4	561837	Ms	Rat IgG	BD Biosciences
FOXP3-FITC	35-5773-U025	Ms	Rat IgG	Cytek Biosciences
NK1.1- FITC	35-5941-U025	Ms	Rat IgG	Cytek Biosciences

CD8-V500	85-1886-U025	Ms	Rat IgG	Cytek Biosciences
PD-1-PE	50-9985-U025	Ms	Rat IgG	Cytek Biosciences
CD4,FITC, clone GK1.5	35-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, PE, clone GK1.5	50-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, APC, clone GK1.5	20-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, PE-Cy7, clone GK1.5	60-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, Percp-Cy5.5, clone GK1.5	65-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, Violet Fluor 450, clone GK1.5	75-0041-U025	Ms	Rat IgG	Cytek Biosciences
CD4, Violet Fluor 500, clone GK1.5	85-0041-U025	Ms	Rat IgG	Cytek Biosciences
Purified Rat Anti-Mouse CD16/CD32 (Mouse BD Fc Block™)	553141	Ms	Rat IgG	BD Biosciences