

## Supplementary Material

### **$\alpha$ SMA<sup>+</sup> fibroblasts suppress Lgr5<sup>+</sup> cancer stem cells and restrain colorectal cancer progression**

Kathleen M. McAndrews<sup>1,†</sup>, Karina Vázquez-Arreguín<sup>1,†</sup>, Changsoo Kwak<sup>1,†</sup>, Hikaru Sugimoto<sup>1</sup>, Xiaofeng Zheng<sup>1</sup>, Bingrui Li<sup>1</sup>, Michelle Kirtley<sup>1</sup>, Valerie S. LeBleu<sup>1,2</sup>, and Raghu Kalluri<sup>1,3,4\*</sup>

<sup>1</sup>*Department of Cancer Biology, Metastasis Research Center, University of Texas MD Anderson Cancer Center, Houston, TX*

<sup>2</sup>*Feinberg School of Medicine, Northwestern University, Chicago, IL*

<sup>3</sup>*Department of Bioengineering, Rice University, Houston, TX*

<sup>4</sup>*Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX*

†Co-first authors

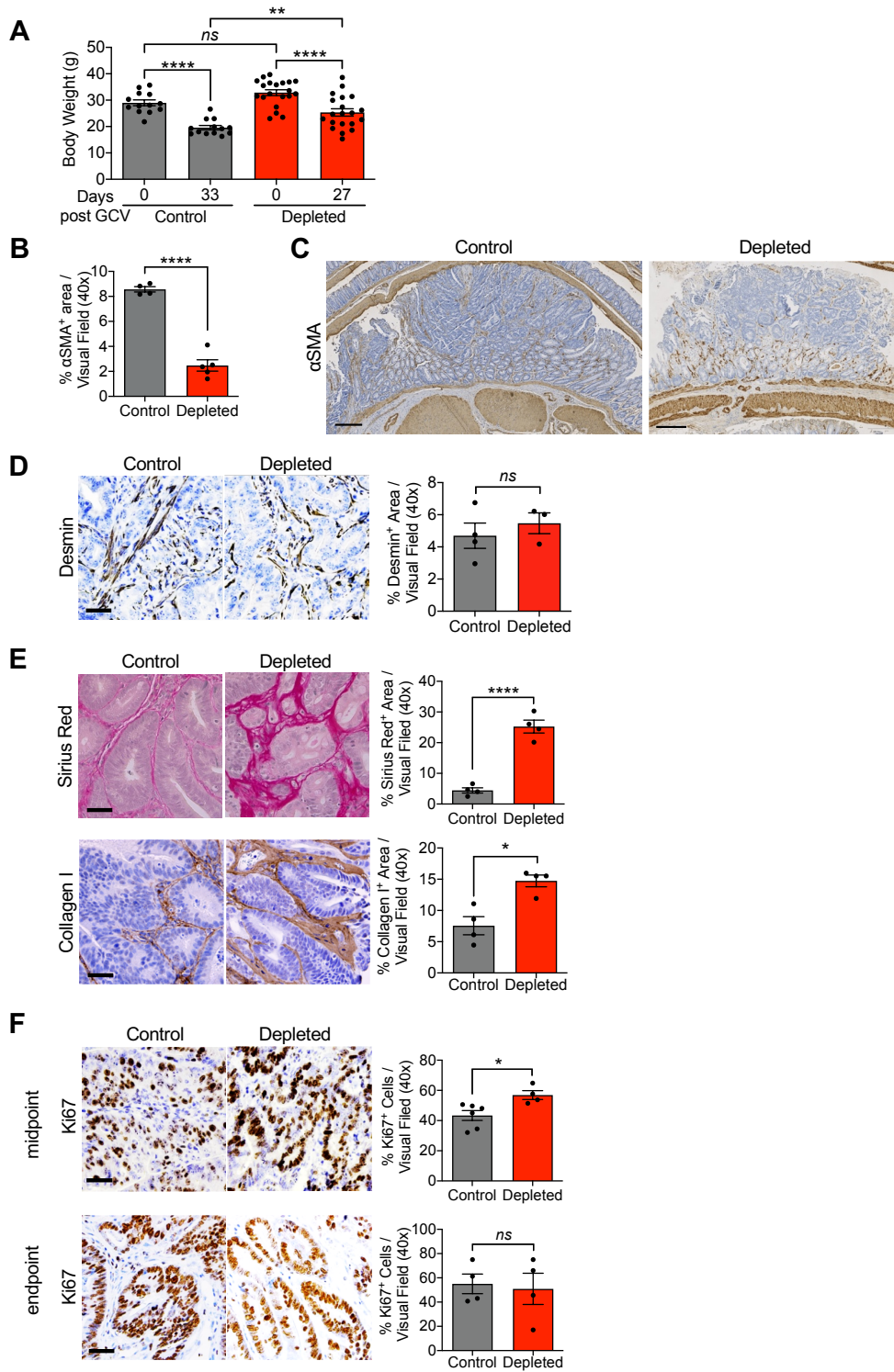
\*Corresponding author:

Raghu Kalluri, MD, PhD

Email: [rkalluri@mdanderson.org](mailto:rkalluri@mdanderson.org)

## Supplementary Figure Legends

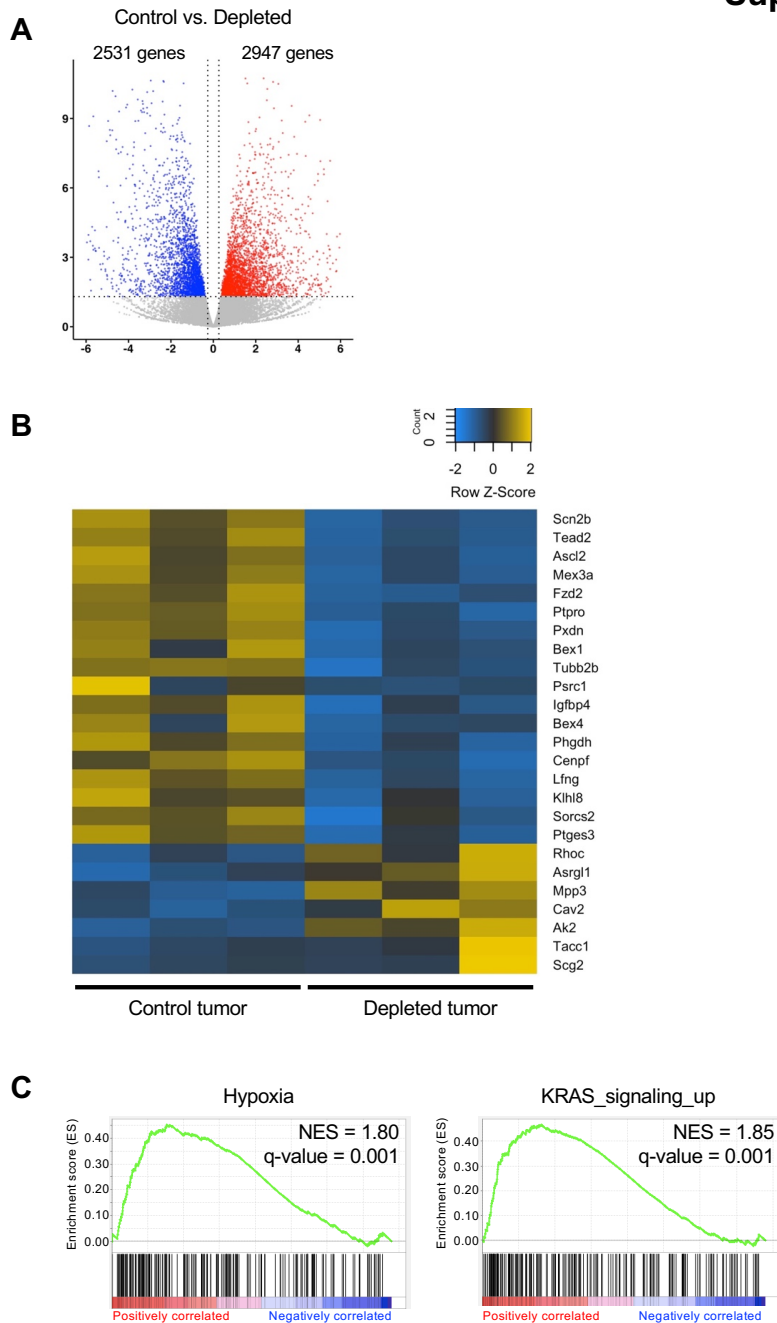
## Supplementary Figure 1



Supplementary Figure 1. Phenotypic characterization of  $\alpha$ SMA<sup>+</sup> CAF-depleted tumors.

**A.** Body weight of control and depleted mice following GCV treatment to deplete  $\alpha$ SMA<sup>+</sup> CAFs. Control, n=13; depleted, n=20. **B.** Quantitation of  $\alpha$ SMA staining in CAF-depleted (n = 5) and control (n = 4) tumors (representative images in Figure 1H). **C.** Representative immunohistochemistry for  $\alpha$ SMA<sup>+</sup> CAF-depleted and control tumors, Scale bar: 200  $\mu$ m. **D.** Representative immunohistochemistry and quantification for desmin in  $\alpha$ SMA<sup>+</sup> CAF-depleted (n = 3) and control (n = 4) tumors, Scale bar: 50  $\mu$ m. **E.** Representative picrosirius red staining and immunohistochemistry for type I collagen in control (n = 4) and (n = 4) depleted tumors, and quantification of staining. Scale bar: 50  $\mu$ m. **F.** Midpoint: Representative immunohistochemistry and quantification for Ki67 in  $\alpha$ SMA<sup>+</sup> CAF-depleted (n = 4) and control (n = 6) tumors at 20 days post GCV. Endpoint: Representative immunohistochemistry and quantification for Ki67 in  $\alpha$ SMA<sup>+</sup> CAF-depleted (n = 4) and control (n = 4) tumors at endpoint. Scale bar: 50  $\mu$ m. GCV: ganciclovir. The data are presented as mean  $\pm$  SEM. **A**, one-way ANOVA with Sidak's multiple comparison test performed; **B, D, E top panel, F**, unpaired t-test performed; **E bottom panel**, Mann-Whitney test performed. \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*\*  $P < 0.0001$ , *ns*: not significant.

## Supplementary Figure 2

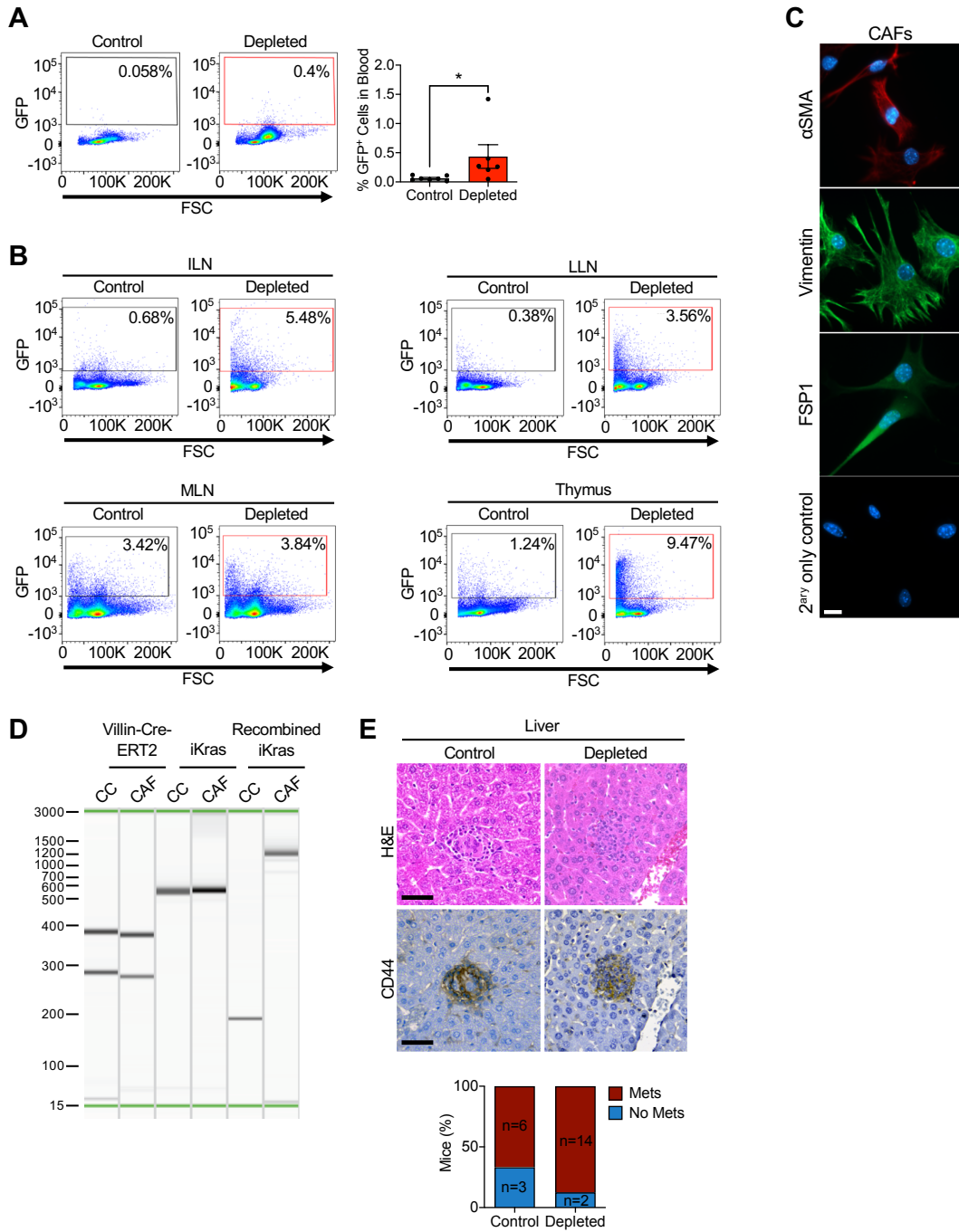


**Supplementary Figure 2. Depleted tumors are associated with malignancy-related gene signatures.**

**A.** Volcano plots showing downregulated and upregulated genes identified by RNA sequencing in control vs. depleted tumors. **B.** Heatmap of genes associated with CRC recurrence in control compared to depleted tumors. **C.** Selected GSEA enrichment plots associated with malignancy

from the RNA analysis comparing control and depleted tumors. FDR: false discovery rate; NES: normalized enrichment score.

### Supplementary Figure 3

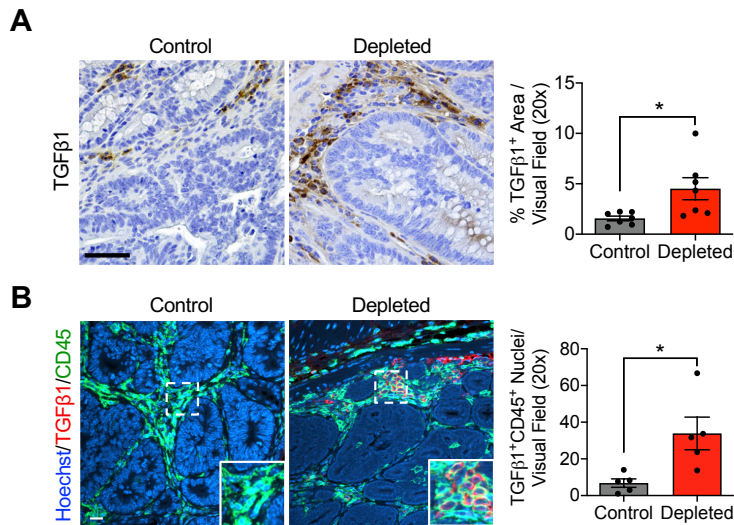


### Supplementary Figure 3. Depletion of $\alpha$ SMA<sup>+</sup> CAFs increases liver metastasis.

**A.** Representative FACS dot plots and quantification of the percentage GFP<sup>+</sup> CTCs in the blood of control (n = 7) and depleted (n = 6) mice at endpoint. **B.** Representative FACS dot plots for data presented in Figure 2B. **C.** Immunostaining of iKAP CAFs for  $\alpha$ SMA (red), vimentin (green),

and FSP-1 (green). Blue nuclei stained with Hoechst. Scale bar: 20  $\mu\text{m}$ .  $2^{\text{ary}}$  only control: no primary antibody, Alexa Fluor 488 secondary antibody only. **D.** Electrogram of PCR products from cancer cells (CC) and CAFs for the indicated alleles. PCR was performed for the Villin-Cre-ERT2 allele (300 and 400 bp), iKras allele (600 bp), and Cre-mediated recombined iKras allele (unrecombined allele: 1000 bp, recombined allele: 180 bp). **E.** Representative images of H&E and CD44 immunohistochemistry in liver sections and quantification of mice with liver metastasis (identified by CD44 staining). Control, n = 9 mice; depleted, n = 16 mice. Scale bars: 100  $\mu\text{m}$ . The data are presented as mean  $\pm$  SEM. **A,** Mann-Whitney test performed. \*  $P < 0.05$ , *ns*: not significant.

## Supplementary Figure 4



**Supplementary Figure 4.  $\alpha$ SMA<sup>+</sup> CAF-depleted tumors show increased TGFβ1 in immune cells.**

**A.** Representative immunohistochemistry for TGFβ1 in control (n = 7) and depleted (n = 7) tumors and quantification of staining. Scale bar: 50  $\mu$ m. **B.** Costaining for CD45 (green) and TGFβ1 (red) in control (n = 5) and depleted (n = 5) tumors. Scale bar, 20  $\mu$ m. **A, B,** unpaired t-test with Welch's correction performed. \*  $P < 0.05$ , \*\*  $P < 0.01$ , ns: not significant.



## Supplementary Tables

**Supplementary Table 1: Mouse genotypes.**

						Villin-Cre <sup>ERT2</sup> ; LSL-KrasG12D/+; Apc F/F; Trp53 F/F; rtTA		
ID	Tamoxifen start date	Doxycycline start date	GCV start date	DOD	GCV treatment (days)	αSMA-TK/0	αSMA-RFP/0	Luc/0
G894	9/4/15	9/4/15	10/26/15	11/17/15	22	0	RFP	0
M26	9/4/15	9/4/15	10/26/15	11/12/15	17	0	RFP	0
M129	10/28/15	10/28/15	1/9/16	1/28/16	19	0	0	L
M144	10/28/15	10/28/15	1/9/16	1/24/16	15	0	0	L
M148	10/28/15	10/28/15	1/9/16	1/16/16	7	0	0	L
V226	12/8/15	12/8/15	2/2/16	2/21/16	19	0	RFP	n.d.
V202	12/8/15	12/8/15	2/2/16	3/2/16	29	0	RFP	0
M196	12/8/15	12/8/15	2/2/16	3/30/16	57	0	0	0
V218	12/8/15	12/8/15	2/2/16	3/26/16	53	0	0	n.d.
M200	12/8/15	12/8/15	2/2/16	3/10/16	37	0	0	n.d.
V227	12/8/15	12/8/15	2/2/16	6/6/16	125	0	RFP	n.d.
159F	12/8/15	12/8/15	2/2/16	3/23/16	50	0	RFP	n.d.
V212	12/8/15	12/8/15	2/2/16	3/13/16	40	0	0	n.d.
V215	12/8/15	12/8/15	2/2/16	3/15/16	42	0	0	0
V232	12/8/15	12/8/15	2/2/16	5/5/16	93	0	RFP	n.d.
V264	1/3/16	1/3/16	2/19/16	4/10/16	51	0	0	L
V271	1/3/16	1/3/16	2/19/16	4/29/16	70	0	0	L
V269	1/3/16	1/3/16	2/19/16	3/23/16	33	0	0	L
V282	1/3/16	1/3/16	2/19/16	3/17/16	27	0	0	L
V275	1/3/16	1/3/16	2/19/16	6/25/16	127	0	RFP	L
V276	1/3/16	1/3/16	2/19/16	6/11/16	113	0	0	L
V325	1/3/16	1/3/16	2/19/16	4/9/16	50	0	RFP	L
V299	1/3/16	1/3/16	2/19/16	7/25/16	157	0	0	L
V302	1/3/16	1/3/16	2/19/16	3/21/16	31	0	RFP	L

						Villin-Cre <sup>ERT2</sup> ; LSL-KrasG12D/+; Apc F/F; Trp53 F/F; rTA		
ID	Tamoxifen start date	Doxycycline start date	GCV start date	DOD	GCV treatment (days)	α-SMA-TK/0	α-SMA-RFP/0	Luc/0
G826	9/4/15	9/4/15	10/26/15	11/2/15	7	TK	0	n.d.
G846	9/4/15	9/4/15	10/26/15	11/27/15	32	TK	0	L
G862	9/4/15	9/4/15	10/26/15	12/1/15	36	TK	0	L
G876	9/4/15	9/4/15	10/26/15	10/30/15	4	TK	RFP	L
G877	9/4/15	9/4/15	10/26/15	12/3/15	38	TK	RFP	L
G893	9/4/15	9/4/15	10/26/15	11/24/15	29	TK	0	L
M2	9/4/15	9/4/15	10/26/15	11/27/15	32	TK	0	L
M9	9/4/15	9/4/15	10/26/15	11/6/15	11	TK	0	0
M11	9/4/15	9/4/15	10/26/15	12/3/15	38	TK	0	L
M80	10/28/15	10/28/15	1/9/16	1/26/16	17	TK	0	0
M126	10/28/15	10/28/15	1/9/16	1/27/16	18	TK	0	0
M169	12/8/15	12/8/15	2/2/16	3/4/16	31	TK	RFP	L
V204	12/8/15	12/8/15	2/2/16	2/15/16	13	TK	RFP	n.d.
V225	12/8/15	12/8/15	2/2/16	2/28/16	26	TK	0	n.d.
V228	12/8/15	12/8/15	2/2/16	3/4/16	31	TK	RFP	0
V234	12/8/15	12/8/15	2/2/16	3/4/16	31	TK	0	0
160F	12/8/15	12/8/15	2/2/16	3/4/16	31	TK	RFP	0
V213	12/8/15	12/8/15	2/2/16	3/8/16	35	TK	0	0
V265	1/3/16	1/3/16	2/19/16	3/25/16	35	TK	RFP	L
V277	1/3/16	1/3/16	2/19/16	3/25/16	35	TK	0	L
V297	1/3/16	1/3/16	2/19/16	3/17/16	27	TK	RFP	L
V284	1/3/16	1/3/16	2/19/16	3/13/16	23	TK	0	L
V324	1/3/16	1/3/16	2/19/16	3/20/16	30	TK	RFP	L
V295	1/3/16	1/3/16	2/19/16	3/17/16	27	TK	0	0
V305	1/3/16	1/3/16	2/19/16	3/20/16	30	TK	0	L
V304	1/3/16	1/3/16	2/19/16	3/25/16	35	TK	0	L
V319	1/3/16	1/3/16	2/19/16	3/17/16	27	TK	0	L
V327	1/21/16	1/21/16	3/9/16	3/26/16	17	TK	0	L
V336	1/21/16	1/21/16	3/9/16	3/22/16	13	TK	0	0
V350	1/21/16	1/21/16	3/9/16	3/25/16	16	TK	0	L
V356	1/21/16	1/21/16	3/9/16	4/5/16	27	TK	0	L
V382	1/21/16	1/21/16	3/9/16	3/29/16	20	TK	RFP	0

n.d.: not determined

**Supplementary Table 2: GSEA of differentially regulated pathways in depleted compared to control tumors.**

**Positively regulated pathways**

Pathway name	Size	ES	NES	Nom p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
HALLMARK_TNFA_SIGNALING_VIA_NFKB	191	0.5698	2.2740	0.0000	0.0000	0.0000	3083	tags=47%, list=20%, signal=58%
HALLMARK_INFLAMMATORY_RESPONSE	191	0.5229	2.0725	0.0000	0.0000	0.0000	2203	tags=32%, list=14%, signal=37%
HALLMARK_KRAS_SIGNALING_UP	192	0.4662	1.8504	0.0000	0.0014	0.0040	3262	tags=40%, list=21%, signal=49%
HALLMARK_PANCREAS_BETA_CELLS	39	0.5808	1.8070	0.0000	0.0013	0.0050	1629	tags=33%, list=10%, signal=37%
HALLMARK_HYPOXIA	185	0.4520	1.7988	0.0000	0.0012	0.0060	3062	tags=36%, list=20%, signal=44%
HALLMARK_INTERFERON_GAMMA_RESPONSE	181	0.4500	1.7595	0.0000	0.0020	0.0120	4257	tags=42%, list=27%, signal=57%
HALLMARK_IL6_JAK_STAT3_SIGNALING	83	0.4830	1.7322	0.0000	0.0024	0.0160	4377	tags=46%, list=28%, signal=63%
HALLMARK_APOPTOSIS	152	0.3810	1.4768	0.0066	0.0490	0.3360	3243	tags=32%, list=21%, signal=39%
HALLMARK_KRAS_SIGNALING_DN	175	0.3619	1.4254	0.0090	0.0751	0.4930	2313	tags=33%, list=15%, signal=38%
HALLMARK_SPERMATOGENESIS	119	0.3644	1.3698	0.0234	0.1175	0.7050	1911	tags=24%, list=12%, signal=27%
HALLMARK_P53_PATHWAY	181	0.3377	1.3437	0.0240	0.1367	0.7870	4082	tags=36%, list=26%, signal=48%
HALLMARK_IL2_STAT5_SIGNALING	188	0.3298	1.3095	0.0395	0.1725	0.8810	4031	tags=36%, list=26%, signal=48%
HALLMARK_COMPLEMENT	172	0.3302	1.3021	0.0452	0.1698	0.8950	3865	tags=37%, list=25%, signal=49%
HALLMARK_BILE_ACID_METABOLISM	107	0.3486	1.2952	0.0749	0.1682	0.9110	4249	tags=35%, list=27%, signal=47%
HALLMARK_MYOGENESIS	190	0.3246	1.2839	0.0529	0.1729	0.9410	3167	tags=28%, list=20%, signal=35%
HALLMARK_ESTROGEN_RESPONSE_EARLY	189	0.3220	1.2723	0.0651	0.1779	0.9540	3720	tags=34%, list=24%, signal=44%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	188	0.3194	1.2667	0.0661	0.1753	0.9580	5781	tags=48%, list=37%, signal=76%

HALLMARK_UV_RESPONSE_UP	147	0.3237	1.2483	0.0950	0.1910	0.9770	3667	tags=31%, list=24%, signal=40%
HALLMARK_HEME_METABOLISM	181	0.3180	1.2378	0.0846	0.1971	0.9840	4902	tags=42%, list=31%, signal=61%
HALLMARK_ALLOGRAFT_REJECTION	180	0.3104	1.2270	0.0904	0.2046	0.9890	2729	tags=25%, list=18%, signal=30%
HALLMARK_XENOBIOTIC_METABOLISM	180	0.3020	1.1947	0.1089	0.2516	0.9940	4393	tags=43%, list=28%, signal=60%
HALLMARK_ADIPOGENESIS	188	0.2933	1.1585	0.1680	0.3073	0.9990	5339	tags=44%, list=34%, signal=66%
HALLMARK_COAGULATION	121	0.3051	1.1490	0.2025	0.3153	0.9990	3806	tags=40%, list=24%, signal=52%
HALLMARK_ANDROGEN_RESPONSE	93	0.3146	1.1391	0.2122	0.3216	0.9990	4471	tags=37%, list=29%, signal=51%
HALLMARK_HEDGEHOG_SIGNALING	36	0.3694	1.1254	0.2825	0.3384	0.9990	3567	tags=36%, list=23%, signal=47%
HALLMARK_PROTEIN_SECRETION	93	0.2960	1.0696	0.3314	0.4584	1.0000	6099	tags=48%, list=39%, signal=79%
HALLMARK_ESTROGEN_RESPONSE_LATE	189	0.2607	1.0437	0.3718	0.5086	1.0000	3286	tags=26%, list=21%, signal=33%
HALLMARK_UV_RESPONSE_DN	135	0.2702	1.0384	0.3808	0.5038	1.0000	4642	tags=37%, list=30%, signal=52%
HALLMARK_CHOLESTEROL_HOMEOSTASIS	71	0.2855	0.9909	0.4703	0.6101	1.0000	4582	tags=38%, list=29%, signal=54%
HALLMARK_INTERFERON_ALPHA_RESPONSE	86	0.2671	0.9339	0.5741	0.7486	1.0000	4257	tags=36%, list=27%, signal=49%
HALLMARK_APICAL_JUNCTION	193	0.2301	0.9176	0.6845	0.7691	1.0000	4332	tags=29%, list=28%, signal=40%
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	45	0.2732	0.8774	0.6769	0.8487	1.0000	5686	tags=44%, list=36%, signal=70%
HALLMARK_GLYCOLYSIS	193	0.2187	0.8625	0.8048	0.8588	1.0000	4090	tags=27%, list=26%, signal=37%
HALLMARK_TGF_BETA_SIGNALING	52	0.2534	0.8450	0.7504	0.8726	1.0000	3706	tags=23%, list=24%, signal=30%
HALLMARK_FATTY_ACID_METABOLISM	148	0.2178	0.8364	0.8302	0.8656	1.0000	5167	tags=35%, list=33%, signal=52%
HALLMARK_PEROXISOME	100	0.2221	0.8060	0.8818	0.8962	1.0000	5401	tags=43%, list=35%, signal=65%
HALLMARK_PI3K_AKT_MTOR_SIGNALING	99	0.2140	0.7784	0.9032	0.9130	1.0000	5465	tags=36%, list=35%, signal=56%

**Negatively regulated pathways**

Pathway name	Size	ES	NES	Nom p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
HALLMARK_E2F_TARGETS	186	-0.6553	-2.9231	0.0000	0.0000	0.0000	3513	tags=69%, list=23%, signal=88%
HALLMARK_G2M_CHECKPOINT	185	-0.5678	-2.5512	0.0000	0.0000	0.0000	3138	tags=50%, list=20%, signal=62%
HALLMARK_MYC_TARGETS_V1	183	-0.5155	-2.3179	0.0000	0.0000	0.0000	4648	tags=57%, list=30%, signal=80%
HALLMARK_MITOTIC_SPINDLE	196	-0.4308	-1.9542	0.0000	0.0000	0.0000	4419	tags=41%, list=28%, signal=56%
HALLMARK_MYC_TARGETS_V2	54	-0.5144	-1.9091	0.0000	0.0000	0.0000	4044	tags=65%, list=26%, signal=87%
HALLMARK_WNT_BETA_CATENIN_SIGNALING	39	-0.4885	-1.6423	0.0118	0.0032	0.0190	1550	tags=28%, list=10%, signal=31%
HALLMARK_DNA_REPAIR	138	-0.3401	-1.4742	0.0000	0.0178	0.1190	4204	tags=39%, list=27%, signal=53%
HALLMARK_ANGIOGENESIS	34	-0.3474	-1.1690	0.2282	0.2272	0.8400	1968	tags=24%, list=13%, signal=27%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	189	-0.2557	-1.1540	0.1159	0.2261	0.8650	2086	tags=23%, list=13%, signal=26%
HALLMARK_APICAL_SURFACE	41	-0.2813	-1.0056	0.4548	0.5691	0.9990	3360	tags=39%, list=22%, signal=50%
HALLMARK_NOTCH_SIGNALING	32	-0.2834	-0.9359	0.5924	0.7451	1.0000	1550	tags=19%, list=10%, signal=21%
HALLMARK_MTORC1_SIGNALING	188	-0.1998	-0.9095	0.7416	0.7652	1.0000	3855	tags=28%, list=25%, signal=36%
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	107	-0.1958	-0.8088	0.9018	0.9054	1.0000	3872	tags=29%, list=25%, signal=38%