

Supplementary Table S4: ORA for 216 differentially expressed genes. Abbreviations: DN:

downregulation of 112 genes in progressive tumors; FDR: false discovery rate; IL2: interleukin 2, IL6:

interleukin 6; JAK: Janus kinase; mTORC1: mammalian/mechanistic target of rapamycin complex1;

KRAS: Kirsten rat sarcoma virus; ORA; over representation analysis; PI3K: phosphoinositide 3-kinase;

TGF: transforming growth factor; TNFA: tumor necrosis factor alpha; UV: ultraviolet; UP: upregulation

of 104 genes in responsive tumors; WNT: Wingless Int-1

UP/DN	Hallmark	Hypergeometric p-value	Hypergeometric FDR	Matched Symbol
UP	ANDROGEN RESPONSE	0.002	0.096	GUCY1A1, KRT19, INSIG1
UP	APICAL JUNCTION	0.021	0.237	TMEM8B, WNK4, INSIG1
UP	ESTROGEN RESPONSE EARLY	0.022	0.237	RETREG1, TOB1, KRT19
UP	ESTROGEN RESPONSE LATE	0.022	0.237	TOB1, TSPAN13, KRT19
UP	APICAL SURFACE	0.024	0.237	TMEM8B
UP	UV RESPONSE DN	0.043	0.335	DBP, INSIG1
UP	XENOBIOTIC METABOLISM	0.093	0.335	XDH, ESR1
UP	MYOGENESIS	0.094	0.335	CACNA1H, HRC
UP	GLYCOLYSIS	0.094	0.335	GNE, CACNA1H
UP	E2F TARGETS	0.094	0.335	UBR7, DONSON
UP	P53 PATHWAY	0.094	0.335	TOB1, WWP1
UP	KRAS SIGNALING UP	0.094	0.335	TSPAN13, GUCY1A1
UP	KRAS SIGNALING DN	0.094	0.335	COL2A1, PDK2
UP	MTORC1 SIGNALING	0.094	0.335	ACACA, INSIG1

UP	PI3K AKT MTOR SIGNALING	0.112	0.372	ACACA
UP	UNFOLDED PROTEIN RESPONSE	0.126	0.394	LSM1
UP	NOTCH SIGNALING	0.162	0.450	
UP	SPERMATOGENESIS	0.168	0.450	GSG1
UP	ANGIOGENESIS	0.180	0.450	
UP	HEDGEHOG SIGNALING	0.180	0.450	
UP	PANCREAS BETA CELLS	0.198	0.465	
UP	WNT BETA CATENIN SIGNALING	0.207	0.465	
UP	UV RESPONSE UP	0.214	0.465	COL2A1
UP	REACTIVE OXYGEN SPECIES PATHWAY	0.237	0.494	
UP	TGF BETA SIGNALING	0.258	0.516	
UP	MYC TARGETS V2	0.274	0.518	
UP	ADIPOGENESIS	0.300	0.518	TOB1
UP	OXIDATIVE PHOSPHORYLATION	0.300	0.518	MRPS30
UP	G2M CHECKPOINT	0.300	0.518	SLC38A1
UP	CHOLESTEROL HOMEOSTASIS	0.336	0.561	
UP	IL6 JAK STAT3 SIGNALING	0.383	0.618	
UP	PROTEIN SECRETION	0.413	0.631	
UP	INTERFERON ALPHA RESPONSE	0.417	0.631	
UP	PEROXISOME	0.439	0.646	
UP	BILE ACID METABOLISM	0.464	0.663	

UP	COAGULATION	0.537	0.675	
UP	DNA REPAIR	0.568	0.675	
UP	FATTY ACID METABOLISM	0.585	0.675	
UP	APOPTOSIS	0.594	0.675	
UP	MITOTIC SPINDLE	0.673	0.675	
UP	IL2 STAT5 SIGNALING	0.673	0.675	
UP	EPITHELIAL MESENCHYMAL TRANSITION	0.675	0.675	
UP	ALLOGRAFT REJECTION	0.675	0.675	
UP	COMPLEMENT	0.675	0.675	
UP	INTERFERON GAMMA RESPONSE	0.675	0.675	
UP	INFLAMMATORY RESPONSE	0.675	0.675	
UP	HEME METABOLISM	0.675	0.675	
UP	HYPOXIA	0.675	0.675	
UP	MYC TARGETS V1	0.675	0.675	
UP	TNFA SIGNALING VIA NFKB	0.675	0.675	
DN	MTORC1 SIGNALING	0.004	0.194	ME1, PIK3R3, PHGDH, GLA, NFIL3
DN	XENOBIOTIC METABOLISM	0.017	0.210	AQP9, CROT, SLC6A12, TGFB2
DN	ESTROGEN RESPONSE LATE	0.018	0.210	GJB3, PPIF, TRIM29, GLA
DN	UV RESPONSE DN	0.024	0.210	CACNA1A, PIK3R3, KIT
DN	NOTCH SIGNALING	0.025	0.210	FZD7
DN	UV RESPONSE UP	0.033	0.210	PPIF, ICAM1, SLC6A12

DN	APICAL SURFACE	0.045	0.210	SCUBE1
DN	PI3K AKT MTOR SIGNALING	0.047	0.210	PIK3R3, ADCY2
DN	BILE ACID METABOLISM	0.055	0.210	AQP9, CROT
DN	APICAL JUNCTION	0.066	0.210	PIK3R3, ICAM1, CDH3
DN	ALLOGRAFT REJECTION	0.067	0.210	ICAM1, TGFB2, CDKN2A
DN	COMPLEMENT	0.067	0.210	ME1, MMP12, CASP1
DN	INFLAMMATORY RESPONSE	0.067	0.210	AQP9, P2RX7, ICAM1
DN	HYPOXIA	0.067	0.210	PLIN2, EFNA3, NFIL3
DN	ESTROGEN RESPONSE EARLY	0.067	0.210	ZNF185, PPIF, GLA
DN	KRAS SIGNALING DN	0.067	0.210	TGFB2, TENM2, TCF7L1
DN	CHOLESTEROL HOMEOSTASIS	0.112	0.329	NFIL3
DN	APOPTOSIS	0.128	0.354	TGFB2, CASP1
DN	PROTEIN SECRETION	0.170	0.359	GLA
DN	INTERFERON ALPHA RESPONSE	0.173	0.359	CASP1
DN	PEROXISOME	0.193	0.359	ALB
DN	IL2 STAT5 SIGNALING	0.199	0.359	PLIN2, NFIL3
DN	ADIPOGENESIS	0.201	0.359	ME1, PLIN2
DN	INTERFERON GAMMA RESPONSE	0.201	0.359	ICAM1, CASP1
DN	GLYCOLYSIS	0.201	0.359	ME1, EFNA3
DN	P53 PATHWAY	0.201	0.359	CDKN2A, CASP1
DN	KRAS SIGNALING UP	0.201	0.359	CROT, SCG5
DN	TNFA SIGNALING VIA NFKB	0.201	0.359	ICAM1, NFIL3

DN	ANGIOGENESIS	0.245	0.409	
DN	HEDGEHOG SIGNALING	0.245	0.409	
DN	PANCREAS BETA CELLS	0.269	0.427	
DN	WNT BETA CATENIN SIGNALING	0.280	0.427	
DN	SPERMATOGENESIS	0.282	0.427	SCG5
DN	REACTIVE OXYGEN SPECIES PATHWAY	0.319	0.469	
DN	TGF BETA SIGNALING	0.345	0.480	
DN	FATTY ACID METABOLISM	0.346	0.480	ME1
DN	MYC TARGETS V2	0.366	0.494	
DN	EPITHELIAL MESENCHYMAL TRANSITION	0.465	0.553	COL7A1
DN	MYOGENESIS	0.465	0.553	TNNI2
DN	HEME METABOLISM	0.465	0.553	SLC25A37
DN	E2F TARGETS	0.465	0.553	CDKN2A
DN	G2M CHECKPOINT	0.465	0.553	MEIS2
DN	IL6 JAK STAT3 SIGNALING	0.496	0.576	
DN	ANDROGEN RESPONSE	0.545	0.620	
DN	UNFOLDED PROTEIN RESPONSE	0.590	0.656	
DN	COAGULATION	0.665	0.722	
DN	DNA REPAIR	0.696	0.740	
DN	MITOTIC SPINDLE	0.795	0.797	
DN	OXIDATIVE PHOSPHORYLATION	0.797	0.797	
DN	MYC TARGETS V1	0.797	0.797	