Supplemental Figure 1. Selection of tumor-rich, immune cell-rich, and stroma-rich regions within PDAC tumors. (a) As part of the GeoMX workflow, FFPE slides of PDAC tumors from patients who received upfront surgical resection (*top*) or surgical resection following neoadjuvant therapy with either FOLFIRINOX alone (*middle*) or FOLFIRINOX + SBRT (*bottom*) were stained with fluorescently labeled anti-pan-cytokeratin (green), anti-CD45 (red), and anti-α-smooth muscle actin (αSMA, blue). These fluorescently labeled antibodies were used to manually define regions of interest with the intent being to select "tumor-rich regions" (rich in pan-cytokeratin staining but largely lacking CD45 and αSMA staining), "immune cell-rich regions" (rich in CD45 staining but largely lacking pan-cytokeratin and αSMA staining), and stroma-rich regions (rich in αSMA but largely lacking the other two markers). The white bar denotes 1mm.

Supplemental Figure 2. Networks of up and down regulated genes: F+SBRT vs. Surgery-alone. Interaction map of significantly differentially expressed genes when comparing F+SBRT treated patient tumors with those who received surgery-alone. Interaction map was generated with protein-protein interaction enrichment analysis and the Molecular Complex Detection (MCODE) algorithm, using the list of genes identified in figure 1.d. (a) Interaction map of genes with lower expression in F+SBRT treated patient tumors, compared to surgery alone. (b) Interaction map of genes with higher expression in F+SBRT treated patient tumors, compared to surgery alone.

Supplemental Figure 3. Networks of up and down regulated genes: F+XRT vs. Surgery-alone. Interaction map of significantly differentially expressed genes when comparing F+SBRT treated patient tumors with those who received surgery-alone. Interaction map was generated with protein-protein interaction enrichment analysis and the Molecular Complex Detection (MCODE) algorithm, using the list of genes identified in figure 1.e. (a) Interaction map of genes with lower expression in F+XRT treated patient tumors, compared to surgery alone. (b) Interaction map of genes with higher expression in F+XRT treated patient tumors, compared to surgery alone.

Supplemental Figure 4. Networks of up and down regulated genes: F+SBRT vs. FOLFIRINOX. Interaction map of significantly differentially expressed genes when comparing F+SBRT treated patient tumors with those who received FOLFIRINOX. Interaction map was generated with protein-protein interaction enrichment analysis and the Molecular Complex Detection (MCODE) algorithm, using the list of genes identified in figure 1.e. (a) Interaction map of genes with lower expression in F+SBRT treated patient tumors, compared to FOLFIRINOX. (b) Interaction map of genes with higher expression in F+SBRT treated patient tumors, compared to FOLFIRINOX.

Supplemental Figure 5. Networks of up and down regulated genes: F+XRT vs. FOLFIRINOX. Interaction map of significantly differentially expressed genes when comparing F+SRT treated patient tumors with those who received FOLFIRINOX. Interaction map was generated with protein-protein interaction enrichment analysis and the Molecular Complex Detection (MCODE) algorithm, using the list of genes identified in figure 1.e. (a) Interaction map of genes with lower expression in F+XRT treated patient tumors, compared to

FOLFIRINOX. (b) Interaction map of genes with higher expression in F+XRT treated patient tumors, compared to FOLFIRINOX.

Supplemental Table 1. Antibodies used in GeoMX analysis

Target	Conjugate ID (Nanostring)
AKT	CAB-962
B7-H3	CAB-959
BCL-2	CAB-960
β-2-Microglobulin	CAB-964
β-Catenin	CAB-963
CD14	CAB-397
CD19	CAB-993
CD3	CAB-1019
CD4	CAB-941
CD44	CAB-619
CD45	CAB-1018
CD45RO	CAB-389
CD56	CAB-1020
CD68	CAB-1023
CD8A	CAB-1022
FOXP3	CAB-840
Granzyme B	CAB-1044
Histone H3	CAB-498
Ki-67 (8D5)	CAB-689
Mouse IgG2a Isotype Control	CAB-891
MS4A1 (CD20)	CAB-943
Phospho-AKT	CAB-834
Pan-cytokeratin	CAB-886
PD-L1	CAB-833
PD-1	CAB-1024
PTEN	CAB-998
Rabbit IgG Isotype Control	CAB-836
S6	CAB-837
STAT3	CAB-957
Phospho-STAT3 (Y705)	CAB-958
VISTA	CAB-940

Supplemental Table 2. Differentially expressed genes.

DEGs shared by: FS vs. C, FS vs. F, FX vs. C, FX vs. F (26 genes)							
ATG7	ATM	CD164	CD47	CDKN1A	FAS	GAGE1	IKBKG
IL1A	IL25	IRF3	IRF5	ITCH	LAMP2	LILRB2	LILRB3
NOD2	NOTCH1	PSMB7	RELA	S100A7	SBNO2	TLR7	TNFRSF8
TPTE	YTHDF2						

DEGs shared by: FS vs. C, FS vs. F, FX vs. C (4 genes)	CD55	FLT3LG	ITGA2B	TFE3

DEGs shared by: FS vs C, FX vs C, FX vs F (10 genes)							
CD274	CEACAM8	IFNA7	IFNG	IL12B	IL5	JAK2	RAG1
SPANXB1	TNFAIP3						

DEGs shared by: FS vs. C, FS vs. F, FX vs. F (2 genes)	FEZ1	SPA17

DEGs shared by: FS vs. F, FX vs. C, FX vs. F (3 genes)	CLEC7A	KIR3DL1	PSEN2

DEGs shared by: FS vs. C, FX vs. C (61 genes)							
ABL1	ARG1	C8A	C9	CASP10	CCL1	CCL16	CCR3
CCR9	CD160	CD1E	CD207	CD8B	CLEC6A	CLU	COLEC12
CD45A1	CTAGE1	CTCFL	ELK1	FCGR1A	IFNA8	IFNA17	IFNB1
IFNL2	IL12RB1	IL18RAP	IL1RAPL2	IL21	IL22	IL24	IL26
IL5RA	ITGB1	KIR Activating Subgroup 2			KLRC2	LILRA1	LRRN3
MAGEA1	MAGEA3	MAGEB2	MAGEC3	MPPED1	NLRC5	PIN1	PRAME
PRM1	REPS1	SELE	SH2D1B	SMAD2	SSX1	SSX4	SYCP1
TANK	TAPBP	TMEFF2	ULBP2	XCL2	XCR1	ZNF205	

DEGs shared by: FS vs. C, FS vs. F (5 genes)				
AIRE	BAX	CASP3	IL11RA	SMAD3

DEGs shared by: FX vs. C, FX vs. F (8 genes)							
BST2	C2	CCRL2	CD80	HLA-DRB3	LAIR2	NLRP3	SEMG1

DEGs shared by FS vs. F, FX vs. F (7 genes)						
BID	CARD9	CD14	CX3CR1	IL7	MYD88	NRP1

DEGs unique to FS vs. C (24 genes)							
CD58	CD70	CFD	FADD	HLA-G	ICAM4	ICOSLG	IL3
IL3RA	IRGM	MAP2K4	NCAM1	NFKB1	PRG2	RRAD	S100A12
SIGIRR	SYK	TAP2	TFEB	TNFRSF10C	TNFSF13	TP53	TRAF6

DEGs unique to FX vs. C (9 genes)								
CCL14	CCR5	CD8A	IDO1	IFNA1	IL13RA2	IL23R	MEFV	ROPN1

DEGs unique to FS vs. F (3 genes)	LTA	MAP3K5	NOD1	

DEGs unique to FX vs. F (27 genes)								
BIRC5	C4BPA	CCL26	CD44	CD84	CXCL1	CYBB	ECSIT	HCK
IFIH1	IFIT1	IFIT2	IL17F	IL1B	IL1RN	ISG15	JAK3	LBP
LTB	MICB	NCF4	OAS3	PLAUR	RORC	SIGLEC1	TLR1	TLR4

Supplemental table 3. Top-ranked enriched gene sets based on up- and downregulated genes

F+SBRT vs. surgery-alone downregulated genes (22 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE SYSTEM PROCESS	15	4.10E-16	7.31E-12
REACTOME IMMUNE SYSTEM	11	1.31E-13	1.17E-09
GO REGULATION OF IMMUNE SYSTEM PROCESS	10	3.15E-10	1.42E-06
GO POSITIVE REGULATION OF RESPONSE TO STIMULUS	11	3.19E-10	1.42E-06
GO RECEPTOR BINDING	10	5.15E-10	1.84E-06
GO IMMUNE RESPONSE	9	9.39E-10	2.79E-06
GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	8	3.93E-09	1.00E-05
GO REGULATION OF CYTOKINE PRODUCTION	7	5.80E-09	1.29E-05
GO REGULATION OF CELL ADHESION	7	1.24E-08	2.14E-05
GO POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS	9	1.33E-08	2.14E-05

F+SBRT vs. surgery-alone upregulated genes (110 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE RESPONSE	67	5.64E-81	1.01E-76
GO IMMUNE SYSTEM PROCESS	75	5.52E-77	4.92E-73
GO DEFENSE RESPONSE	60	1.97E-65	1.17E-61
GO REGULATION OF IMMUNE SYSTEM PROCESS	51	4.64E-48	2.06E-44
KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION	30	3.39E-42	1.21E-38
GO RESPONSE TO CYTOKINE	38	3.52E-41	1.04E-37
GO CELLULAR RESPONSE TO CYTOKINE STIMULUS	36	1.21E-40	3.09E-37
REACTOME IMMUNE SYSTEM	40	9.96E-40	2.22E-36
GO INNATE IMMUNE RESPONSE	34	3.76E-37	7.45E-34
GO CELLULAR RESPONSE TO ORGANIC SUBSTANCE	47	7.83E-37	1.37E-33

F+XRT vs. surgery-alone downregulated genes (16 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE SYSTEM PROCESS	11	3.38E-12	6.02E-08
GO POSITIVE REGULATION OF RESPONSE TO STIMULUS	10	1.05E-10	9.39E-07
GO POSITIVE REGULATION OF DEFENSE RESPONSE	6	1.77E-09	1.05E-05
GO REGULATION OF DEFENSE RESPONSE	6	1.38E-07	6.16E-04
GO REGULATION OF RESPONSE TO STRESS	7	2.97E-07	8.63E-04
GO POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS	7	3.32E-07	8.63E-04
GO NEGATIVE REGULATION OF TYPE I INTERFERON PRODUCTION	3	3.39E-07	8.63E-04
GO POSITIVE REGULATION OF CELL COMMUNICATION	7	3.96E-07	8.82E-04
REACTOME IMMUNE SYSTEM	6	4.64E-07	9.18E-04
GO IMMUNE RESPONSE	6	1.21E-06	2.15E-03

Supplemental table 3 (cont.)

F+XRT vs. surgery-alone upregulated genes (105 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE RESPONSE	64	1.81E-77	3.21E-73
GO DEFENSE RESPONSE	65	4.05E-76	2.77E-72
GO IMMUNE SYSTEM PROCESS	73	4.67E-76	2.77E-72
GO REGULATION OF IMMUNE SYSTEM PROCESS	53	1.64E-52	7.31E-49
GO REGULATION OF IMMUNE RESPONSE	41	9.81E-44	3.49E-40
GO INNATE IMMUNE RESPONSE	37	7.81E-43	2.32E-39
GO RESPONSE TO EXTERNAL STIMULUS	50	2.18E-42	5.53E-39
GO RESPONSE TO CYTOKINE	38	4.00E-42	8.91E-39
GO RESPONSE TO BIOTIC STIMULUS	40	1.28E-41	2.54E-38
GO CELLULAR RESPONSE TO CYTOKINE STIMULUS	35	6.73E-40	1.20E-36

F+SBRT vs. FOLFIRINOX downregulated genes (10 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE SYSTEM PROCESS	8	4.96E-10	8.83E-06
ABRAHAM ALPC VS MULTIPLE MYELOMA DN	3	7.18E-09	6.39E-05
GAVIN FOXP3 TARGETS CLUSTER P3	4	2.92E-08	1.74E-04
GO REGULATION OF RESPONSE TO STRESS	6	1.98E-07	6.75E-04
GO POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS	6	2.18E-07	6.75E-04
BIOCARTA HIVNEF PATHWAY	3	2.27E-07	6.75E-04
RUTELLA RESPONSE TO CSF2RB AND IL4 UP	4	5.83E-07	1.48E-03
PILON KLF1 TARGETS DN	6	1.12E-06	2.50E-03
RUTELLA RESPONSE TO HGF UP	4	1.36E-06	2.69E-03
TGCACTT MIR519C MIR519B MIR519A	4	1.79E-06	3.18E-03

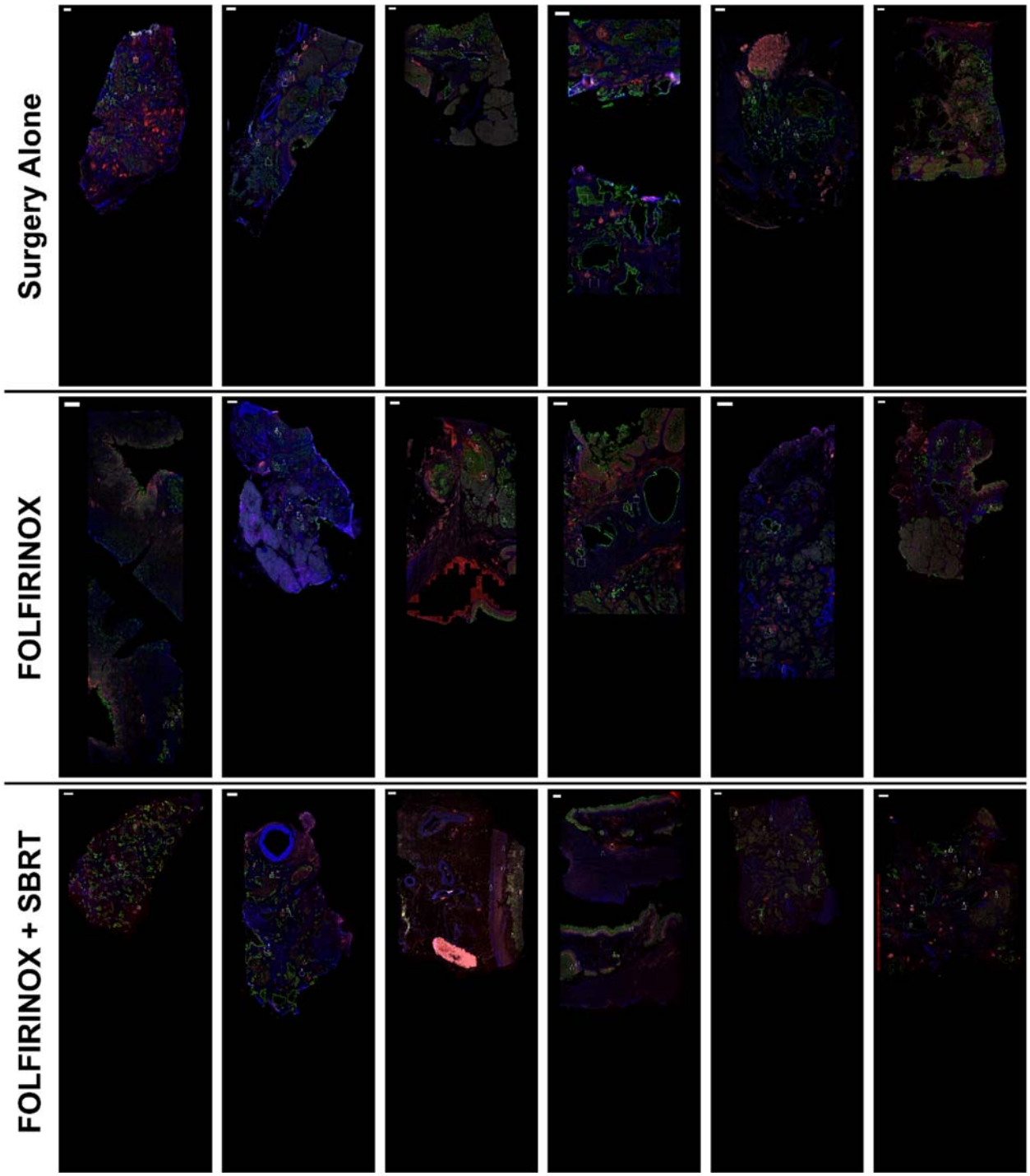
F+SBRT vs. FOLFIRINOX upregulated genes (40 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE SYSTEM PROCESS	31	7.34E-35	9.99E-31
GO IMMUNE RESPONSE	27	1.12E-34	9.99E-31
GO REGULATION OF IMMUNE SYSTEM PROCESS	26	4.92E-30	2.92E-26
GO DEFENSE RESPONSE	24	6.24E-28	2.78E-24
GO RESPONSE TO BIOTIC STIMULUS	21	7.14E-26	2.54E-22
GO RESPONSE TO EXTERNAL STIMULUS	24	6.61E-24	1.96E-20
GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	19	1.29E-22	3.28E-19
GO POSITIVE REGULATION OF MULTICELLULAR ORGANISMAL PROCESS	21	8.76E-22	1.95E-18
GO REGULATION OF CELL DEATH	21	2.64E-21	5.23E-18
GO RESPONSE TO BACTERIUM	16	3.59E-21	6.39E-18

Supplemental table 3 (cont.)

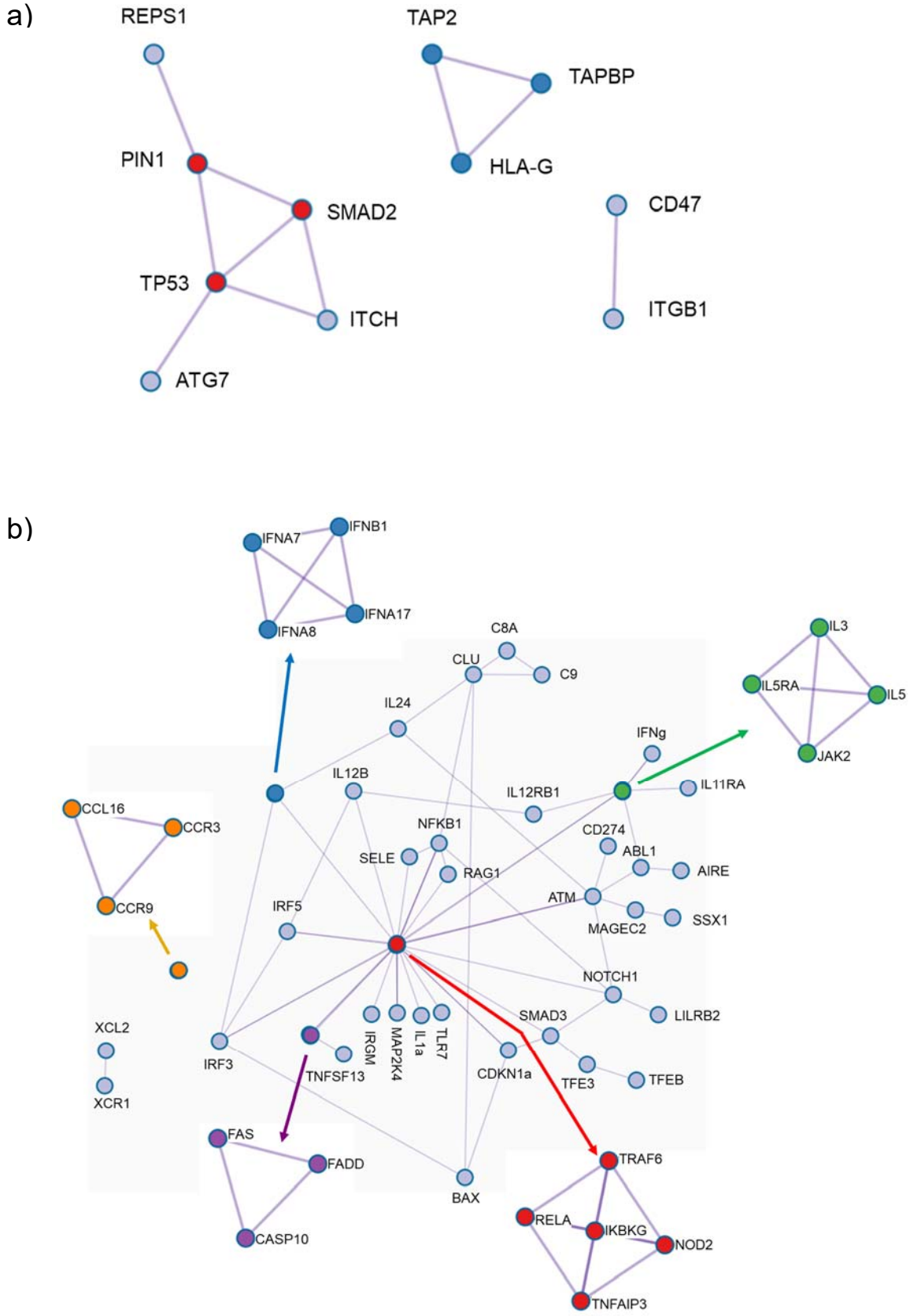
F+XRT vs. FOLFIRINOX downregulated genes (10 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE SYSTEM PROCESS	8	4.96E-10	8.83E-06
GO IMMUNE RESPONSE	5	1.78E-06	1.46E-02
GO IMMUNE EFFECTOR PROCESS	4	2.47E-06	1.46E-02
GSE14415 NATURAL TREG VS TCONV UP	3	4.02E-06	1.70E-02
GAVIN FOXP3 TARGETS CLUSTER P3	3	4.88E-06	1.70E-02
UEDA PERIFERAL CLOCK	3	5.75E-06	1.70E-02
ABRAHAM ALPC VS MULTIPLE MYELOMA DN	2	7.27E-06	1.70E-02
GSE19401 UNSTIM VS PAM2CSK4 STIM FOLLICULAR DC DN	3	9.53E-06	1.70E-02
GSE22886 NAÏVE TCELL VS DC DN	3	9.53E-06	1.70E-02
GSE37301 LYMPHOID PRIMED MPP VS PRO BCELL UP	3	9.53E-06	1.70E-02

F+XRT vs. FOLFIRINOX upregulated genes (73 genes)			
Gene Set Name	**Genes in Overlap**	**p-value**	**FDR q-value**
GO IMMUNE RESPONSE	55	6.75E-74	1.20E-69
GO DEFENSE RESPONSE	54	3.98E-69	3.55E-65
GO IMMUNE SYSTEM PROCESS	59	2.67E-67	1.58E-63
REACTOME IMMUNE SYSTEM	41	4.67E-50	2.08E-46
GO REGULATION OF IMMUNE SYSTEM PROCESS	45	1.75E-49	6.23E-46
GO RESPONSE TO BIOTIC STIMULUS	39	2.29E-47	6.79E-44
GO RESPONSE TO EXTERNAL STIMULUS	46	4.87E-46	1.24E-42
GO INNATE IMMUNE RESPONSE	35	6.60E-46	1.47E-42
GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	35	9.47E-41	1.87E-37
GO REGULATION OF CYTOKINE PRODUCTION	30	3.48E-38	6.20E-35

Supplemental Figure 1. Selection of tumor-rich, immune cell-rich, and stroma-rich regions within PDAC tumors.

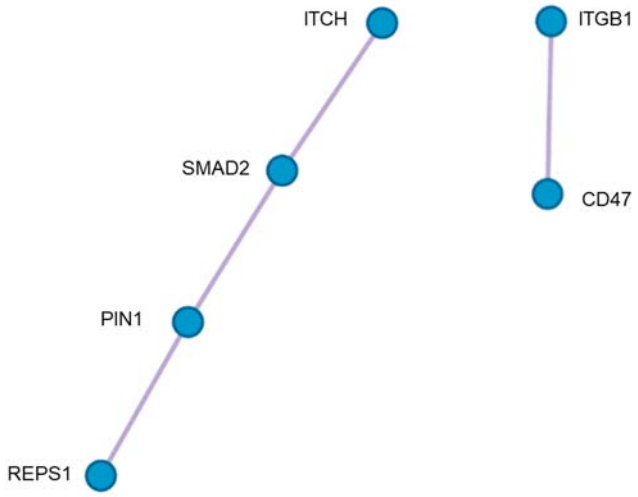


Supplemental Figure 2. Networks of up and down regulated genes: F+SBRT vs. Surgery-alone



Supplemental Figure 3. Networks of up and down regulated genes: F+XRT vs. Surgery-alone

a)



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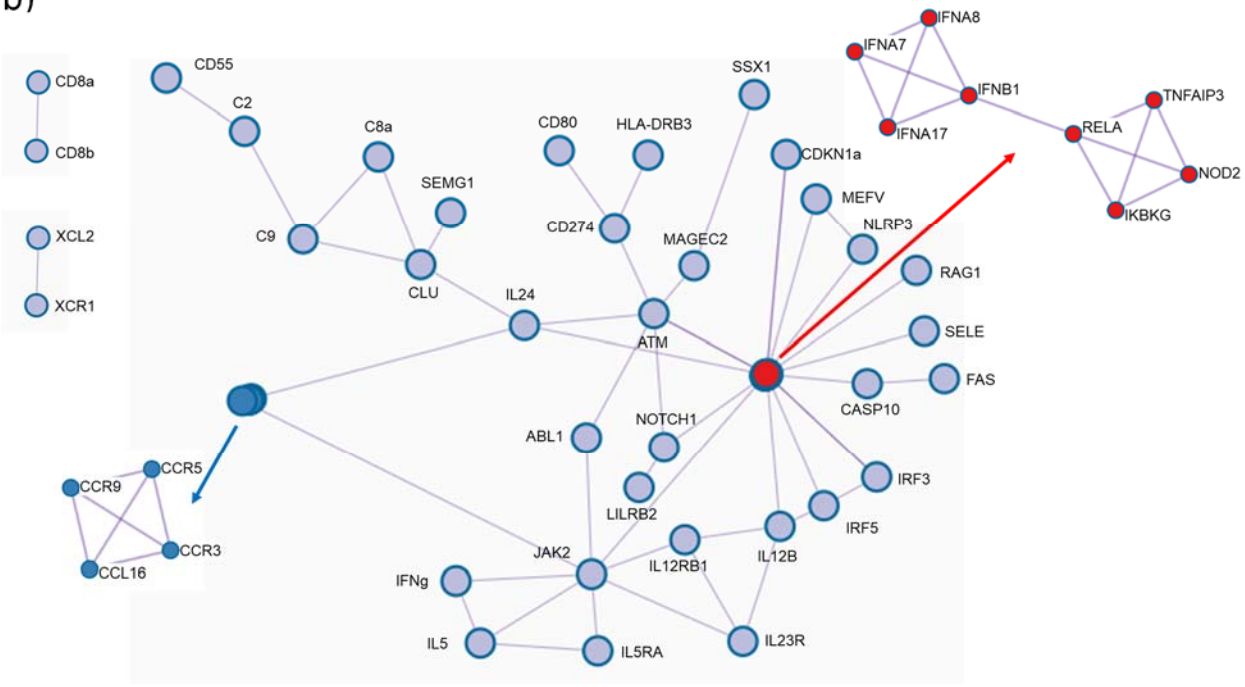
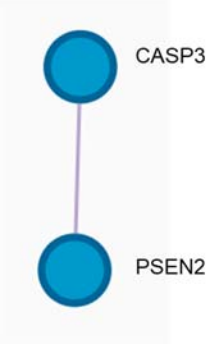
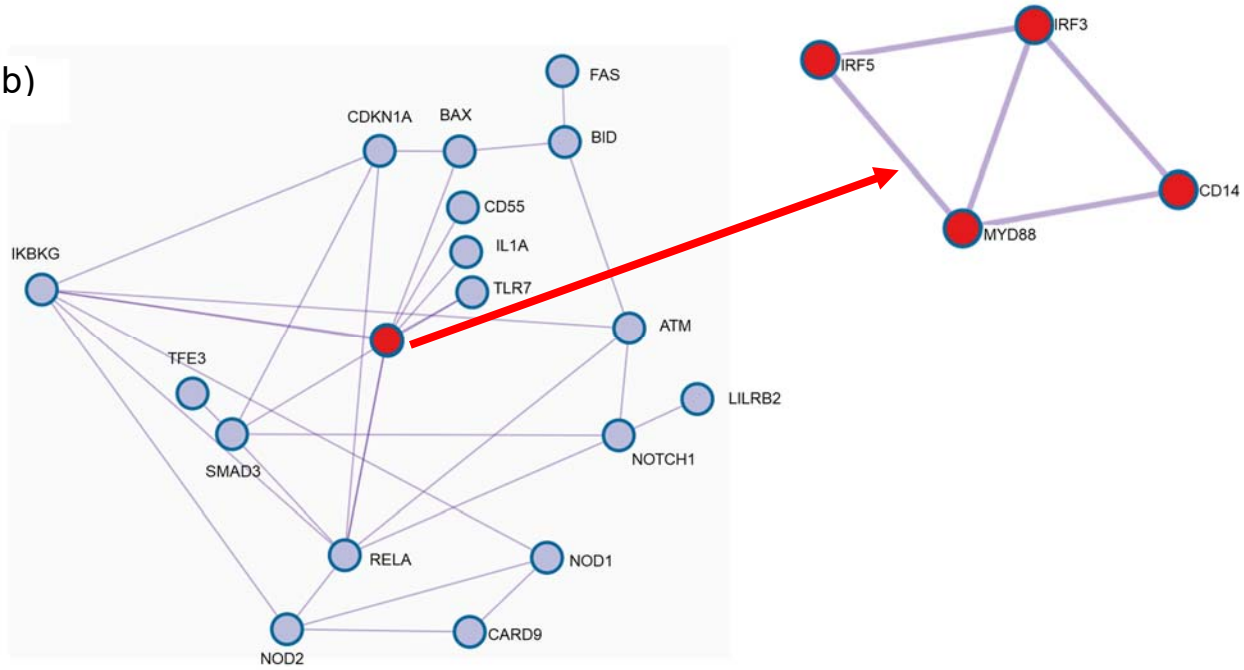


Supplemental Figure 4. Networks of up and down regulated genes: F+SBRT vs. FOLFIRINOX

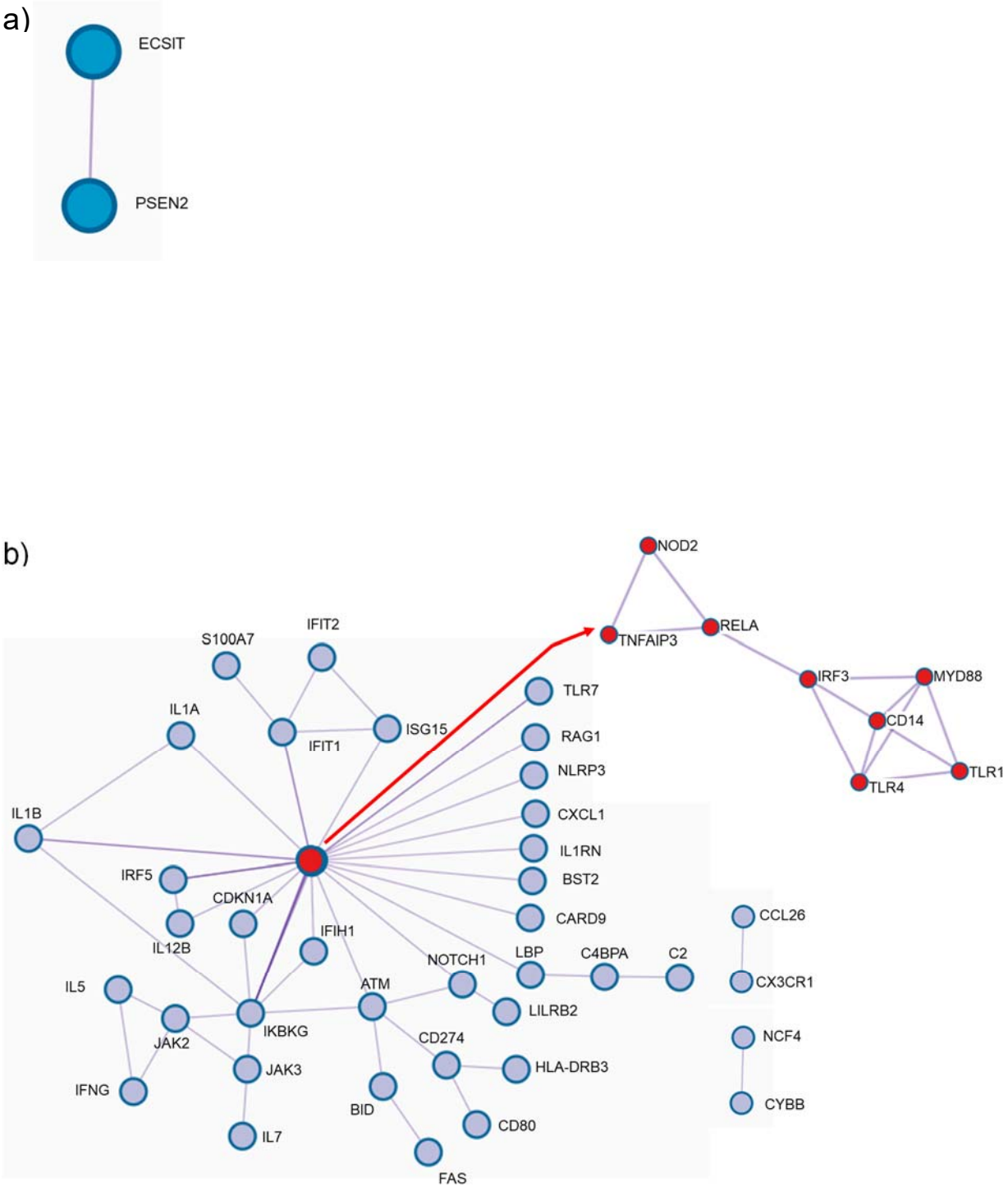
a)



b)



Supplemental Figure 5. Networks of up and down regulated genes: F+XRT vs. FOLFIRINOX



Supplemental table 4. Transcription factor target motifs enriched within gene sets altered by FOLFIRINOX + SBRT compared to surgery alone.

F+SBRT vs. surgery-alone			
Enriched in upregulated genes		**Enriched in upregulated genes (cont.)**	
Transcription Factor	**FDR-adjusted p-value**	**Transcription Factor**	**FDR-adjusted p-value**
KLF13	*0.000123*	*SNAI2*	*0.016068*
LEF1	*0.000123*	*TCF3*	*0.016068*
SNF1	*0.000952*	*TP53*	*0.016243*
SRF	*0.000952*	*RUNX2*	*0.017725*
POU2F1	*0.00145*	*ZFHX3*	*0.022552*
NR5A2	*0.001511*	*USF2*	*0.024764*
TCF4	*0.003412*	*ZBTB7A*	*0.026002*
POU2F2	*0.004727*	*HNF4A*	*0.032677*
RUNX1	*0.007633*	*FOXO3A*	*0.038192*
SAMD9L	*0.008882*	*FOXA1*	*0.038192*
JUN	*0.008882*	*PRDM1*	*0.038192*
YY1	*0.008951*	*RELB*	*0.038192*
CEBPD	*0.012103*	*RELA*	*0.038310*
MIB2	*0.012103*	*FOXJ1*	*0.038919*
NFKB1	*0.122820*	*ATF2*	*0.045132*
POU1F1	*0.016068*	*FOXF1*	*0.046137*
NFIA	*0.016068*	*SMARCA2*	*0.047039*
SNAI1	*0.016068*		

Enriched in downregulated genes	
Transcription Factor	**FDR-adjusted p-value**
SRF	*0.003532*

Supplemental table 5. Transcription factor target motifs enriched within gene sets altered by FOLFIRINOX + XRT compared to surgery alone.

F+XRT vs. surgery-alone			
Enriched in upregulated genes		**Enriched in upregulated genes (cont.)**	
Transcription Factor	**FDR-adjusted p-value**	**Transcription Factor**	**FDR-adjusted p-value**
LEF1	*0.000006*	*CRTC3*	*0.020796*
TCF4	*0.000204*	*FOXJ1*	*0.020796*
SRF	*0.000351*	*ZFHX3*	*0.020796*
JUN	*0.001511*	*ETS1*	*0.031622*
POU1F1	*0.003149*	*ELF3*	*0.040872*
KLF13	*0.003779*	*HNF1A*	*0.040872*
SND1	*0.0037900*	*GATA1*	*0.040872*
POU2F1	*0.005689*	*CBEPB*	*0.040872*
POU2F2	*0.005689*	*RUNX1*	*0.040872*
SAMD9L	*0.005779*	*FOXF1*	*0.045304*
YY1	*0.007127*	*GATA1*	*0.045304*
NR5A2	*0.011655*	*IRF8*	*0.048165*
RUNX2	*0.019098*	*HNF4A*	*0.048731*

Enriched in downregulated genes	
Transcription Factor	**FDR-adjusted p-value**
None	*n/a*

Supplemental table 6. Transcription factor target motifs enriched within gene sets altered by FOLFIRINOX + SBRT compared to FOLFIRINOX alone.

F+SBRT vs. FOLFIRINOX	
Enriched in upregulated genes	
Transcription Factor	**FDR-adjusted p-value**
RUNX1	*0.000418*
SND1	*0.003836*
NR3C1	*0.022453*
TP53	*0.022453*
LEF1	*0.022453*
NFYA	*0.026683*
KLF13	*0.030524*
MAX	*0.040325*
NR5A2	*0.047903*

Enriched in downregulated genes	
Transcription Factor	**FDR-adjusted p-value**
None	*n/a*

Supplemental table 7. Transcription factor target motifs enriched within gene sets altered by FOLFIRINOX + XRT compared to FOLFIRINOX.

F+XRT vs. FOLFIRINOX	
Enriched in upregulated genes	
Transcription Factor	**FDR-adjusted p-value**
SND1	*0.013709*
JUN	*0.013709*
RELA	*0.015582*
RUNX1	*0.015582*
REL	*0.029124*
LTF	*0.030045*
SPI1	*0.030045*
POU1F1	*0.030045*
TCF4	*0.030045*
NFKB1	*0.042192*
HIF1A	*0.049391*
NR3C1	*0.049391*
SREBF1	*0.049391*
SRF	*0.049391*

Enriched in downregulated genes	
Transcription Factor	**FDR-adjusted p-value**
None	*n/a*

Supplemental Table 8. Statistics describing protein expression.

Tumor-rich regions	Mean ± S.D. (counts)		
	Surgery-alone	FOLFIRINOX	F+SBRT
AKT	11316 ± 5632	11443 ± 3743	7515 ± 3830
B7-H3	2949 ± 1925	2774 ± 3116	2027 ± 1030
BCL2	466 ± 226	937 ± 473	544 ± 253
B-2-Microglobulin	18929 ± 13725	13142 ± 12483	13342 ± 12448
B-Catenin	74809 ± 48524	51511 ± 33442	38820 ± 29988
CD3	1610 ± 1669	2248 ± 1900	928 ± 664
CD4	2032 ± 1585	2045 ± 1132	1107 ± 712
CD8A	997 ± 902	1381 ± 1463	904 ± 786
CD14	1303 ± 762	2425 ± 4493	965 ± 906
CD19	269 ± 143	297 ± 134	273 ± 171
CD20	389 ± 257	486 ± 553	246 ± 118
CD44	2365 ± 1483	5215 ± 5026	1342 ± 1311
CD45	796 ± 563	1536 ± 1336	529 ± 332
CD45RO	584 ± 352	969 ± 967	238 ± 145
CD56	959 ± 1052	2832 ± 4251	753 ± 730
CD68	14134 ± 13181	9205 ± 10630	4705 ± 2336
FOXP3	177 ± 102	169 ± 85	181 ± 98
GZMB	1454 ± 690	1506 ± 839	1078 ± 429
Ki-67	3147 ± 3021	1164 ±1548	1252 ± 1145
p-AKT	562 ± 281	596 ± 203	537 ± 262
PD-1	277 ± 134	273 ± 141	298 ± 183
PD-L1	1538 ± 834	1428 ± 712	1664 ± 1005
PTEN	530 ± 290	712 ± 338	337 ± 131
S6	5634 ± 2157	6596 ± 3113	6069 ± 2997
STAT3	8456 ± 5070	8061 ± 2495	5559 ± 2280
p-STAT3	311 ± 163	351 ± 157	330 ± 153
VISTA	1255 ± 630	1161 ± 805	547 ± 424

Supplemental Table 8 (cont.)

Immune-rich regions	Mean ± S.D. (counts)		
	Surgery-alone	FOLFIRINOX	F+SBRT
AKT	6978 ± 3830	8499 ± 3730	5231 ± 4485
B7-H3	1750 ± 1226	3389 ± 4429	2035 ± 1504
BCL2	2924 ± 3631	1886 ± 930	927 ± 699
B-2-Microglobulin	14896 ± 7126	15761 ± 10250	11004 ± 6065
B-Catenin	9489 ± 7125	12220 ± 7837	6734 ± 11580
CD3	24767 ± 16522	19663 ± 14206	8940 ± 8058
CD4	15070 ± 9736	11286 ± 4901	6366 ± 5361
CD8A	6012 ± 4493	7655 ± 7325	3506 ± 2296
CD14	2433 ± 1300	4587 ± 4667	1453 ± 780
CD19	2829 ± 3115	641 ± 582	502 ± 961
CD20	32520 ± 31208	9572 ± 12645	6027 ± 10992
CD44	8344 ± 5106	10422 ± 8389	3264 ± 2241
CD45	19457 ± 13769	12728 ± 12770	4687 ± 4804
CD45RO	4721 ± 2702	6037 ± 6359	1507 ± 1085
CD56	2317 ± 2820	3039 ± 4002	1902 ± 2735
CD68	10343 ± 10726	15110 ± 15091	6953 ± 6333
FOXP3	187 ± 84	237 ± 160	129 ± 84
GZMB	1184 ± 703	2065 ± 1572	787 ± 484
Ki-67	2918 ± 3363	1763 ± 1751	3007 ± 8136
p-AKT	355 ± 126	511 ± 252	343 ± 209
PD-1	682 ± 443	708 ± 483	190 ± 113
PD-L1	1262 ± 597	1927 ± 1281	1181 ± 651
PTEN	482 ± 259	708 ± 416	253 ± 134
S6	3695 ± 1278	4809 ± 2269	3038 ± 1568
STAT3	5918 ± 3555	6114 ± 2117	3418 ± 2476
p-STAT3	223 ± 84	361 ± 209	238 ± 143
VISTA	1940 ± 1211	2067 ± 1006	721 ± 842

Supplemental Table 8 (cont.)

Stroma-rich regions	Mean ± S.D. (counts)		
	Surgery-alone	FOLFIRINOX	F+SBRT
AKT	15106 ± 5700	17598 ± 10011	11345 ± 6251
B7-H3	5728 ± 2956	4790 ± 4371	5189 ± 3207
BCL2	1122 ± 559	1832 ± 960	630 ± 215
B-2-Microglobulin	9662 ± 4885	9428 ± 5619	5944 ± 2403
B-Catenin	24877 ± 12649	21421 ± 13465	11831 ± 5965
CD3	5753 ± 4479	3606 ± 3307	1066 ± 690
CD4	5963 ± 3661	3456 ± 1781	1716 ± 848
CD8A	2357 ± 1895	1886 ± 2125	792 ± 661
CD14	4437 ± 2332	5410 ± 4756	2285 ± 133
CD19	468 ± 327	481 ± 302	177 ± 52
CD20	1344 ± 1390	1080 ± 1725	338 ± 293
CD44	4358 ± 2513	5954 ± 4515	1249 ± 967
CD45	1937 ± 1235	2054 ± 2113	488 ± 350
CD45RO	1406 ± 967	1239 ± 1051	285 ± 152
CD56	4343 ± 6227	5953 ± 6873	2592 ± 3756
CD68	12771 ± 6636	9282 ± 9390	4799 ± 2665
FOXP3	243 ± 183	293 ± 221	106 ± 39
GZMB	4088 ± 3495	3758 ± 3492	1458 ± 624
Ki-67	1631 ± 1312	576 ± 480	396 ± 523
p-AKT	828 ± 482	1102 ± 684	638 ± 261
PD-1	404 ± 235	469 ± 321	194 ± 62
PD-L1	2241 ± 1569	3002 ± 1809	1569 ± 632
PTEN	1126 ± 609	1171 ± 526	567 ± 188
S6	5039 ± 1498	6708 ± 3768	4601 ± 1232
STAT3	9294 ± 5156	10478 ± 5920	5929 ± 2929
p-STAT3	322 ± 213	476 ± 256	338 ± 154
VISTA	2881 ± 1879	1744 ± 869	663 ± 442