SUPPLEMENTARY TABLES

Supplementary Table 1. Cox regression analysis.

	Univariate			Multivariate		
	Hazard_ratio	**CI95**	**p_values**	**Hazard_ratio**	**CI95**	**p_values**
Age	1.01	1-1.03	0.066			
Gender	0.82	0.58-1.17	0.284			
Race	1.14	0.95-1.37	0.166			
Family_History	1.16	0.81-1.68	0.418			
BMI	1	0.97-1.03	0.995			
Ethnicity	1.11	0.49-2.52	0.811			
Fibrosis_Stage	1.18	0.87-1.6	0.287			
Child_Pugh_Classification	1.52	0.84-2.77	0.17			
Tumor_Stage	**1.64**	**1.34-2.01**	**0**	**0.8**	**0.34-1.87**	**0.611**
Pathologic_T	**1.63**	**1.37-1.94**	**0**	**1.95**	**0.87-4.34**	**0.103**
Pathologic_N	**1.22**	**1.01-1.46**	**0.037**	**1.07**	**0.81-1.4**	**0.637**
Pathologic_M	**1.26**	**1.05-1.52**	**0.012**	**1.24**	**0.95-1.63**	**0.11**
Radiation_Therapy	0.84	0.21-3.42	0.808			
Vascular_Invasion	0.74	0.53-1.02	0.069			
BMS1P1	1.19	0.59-2.4	0.622			
C2orf27A	**2.13**	**1.51-2.99**	**0**	**1.5**	**0.99-2.27**	**0.057**
CFB	**0.85**	**0.75-0.97**	**0.017**	**1**	**0.85-1.18**	**0.979**
COL1A2	1.06	0.95-1.17	0.291			
CST3	1.2	0.97-1.48	0.091			
CYP4F30P	116840.6	0-4.11e13	0.245			
DEFB122	2384.77	0.03-2.03e8	0.179			
GPER1	0.96	0.81-1.13	0.6			
IGF2R	**1.28**	**1.01-1.63**	**0.041**	**1.08**	**0.83-1.4**	**0.565**
OR2A20P	5.13	0.3-86.48	0.256			
PFN1P2	0.33	0.07-1.45	0.141			
PON1	**0.85**	**0.79-0.92**	**0**	**0.88**	**0.8-0.97**	**0.01**
ZNF826P	1.35	0.99-1.83	0.057			
ZSCAN12P1	0.94	0.58-1.5	0.784			

Supplementary Table 2. Correlation between selected genes and infiltrating immune cells in GSE109211.

	CFB		IGF2R		PON1		C2orf27A	
	r	**p**	**r**	**p**	**r**	**p**	**r**	**p**
Activated.CD4.T.cell	-0.29	0.02	0.10	0.40	-0.16	0.19	0.19	0.12
Activated.CD8.T.cell	0.51	0.00	0.33	0.01	0.09	0.45	0.40	0.00
Activated.dendritic.cell	0.43	0.00	0.34	0.00	0.20	0.11	0.09	0.46
CD56bright.natural.killer.cell	0.68	0.00	0.56	0.00	0.33	0.01	0.35	0.00
Central.memory.CD4.T.cell	0.65	0.00	0.59	0.00	0.41	0.00	0.48	0.00
Central.memory.CD8.T.cell	0.44	0.00	0.50	0.00	0.48	0.00	0.09	0.46
Effector.memeory.CD4.T.cell	-0.18	0.13	-0.22	0.07	-0.48	0.00	0.02	0.89
Effector.memeory.CD8.T.cell	0.70	0.00	0.16	0.20	0.02	0.86	0.35	0.00
Natural.killer.cell	0.70	0.00	0.14	0.27	0.04	0.75	0.35	0.00
Natural.killer.T.cell	-0.40	0.00	-0.11	0.36	-0.01	0.96	-0.23	0.06
Type.1.T.helper.cell	0.56	0.00	0.26	0.03	0.21	0.08	0.44	0.00
Type.17.T.helper.cell	-0.52	0.00	-0.33	0.01	-0.30	0.01	-0.44	0.00
CD56dim.natural.killer.cell	0.61	0.00	0.13	0.28	0.14	0.26	0.23	0.06
Immature.dendritic.cell	0.24	0.05	0.50	0.00	0.48	0.00	0.30	0.01
Macrophage	-0.35	0.00	-0.30	0.01	-0.09	0.46	-0.06	0.62
MDSC	0.53	0.00	0.56	0.00	0.30	0.01	0.28	0.02
Neutrophil	-0.50	0.00	-0.33	0.01	-0.16	0.19	-0.21	0.09
Plasmacytoid.dendritic.cell	0.68	0.00	0.66	0.00	0.47	0.00	0.32	0.01
Regulatory.T.cell	0.56	0.00	0.13	0.31	0.01	0.95	0.38	0.00
Type.2.T.helper.cell	-0.46	0.00	-0.17	0.17	-0.15	0.22	0.02	0.86
Activated.B.cell	-0.42	0.00	-0.67	0.00	-0.60	0.00	-0.10	0.41
Eosinophil	0.16	0.18	0.34	0.00	0.34	0.01	0.12	0.33
Gamma.delta.T.cell	0.65	0.00	0.57	0.00	0.46	0.00	0.38	0.00
Immature..B.cell	-0.27	0.03	-0.27	0.03	-0.38	0.00	-0.04	0.74
Mast.cell	-0.16	0.20	0.02	0.86	0.02	0.85	0.00	0.99
Memory.B.cell	0.24	0.05	-0.00	0.97	-0.10	0.41	0.19	0.13
Monocyte	0.75	0.00	0.57	0.00	0.43	0.00	0.38	0.00
T.follicular.helper.cell	-0.22	0.08	0.32	0.01	0.16	0.19	-0.21	0.09

Supplementary Table 3. qRT-PCR primers.

Genes	Primers	Sequences (5’ to 3’)
Homo *β-actin*	Forward	CACCAACTGGGACGACAT
	Reverse	ACAGCCTGGATAGCAACG
Homo *C2orf27a*	Forward	TCACGCTGCTGTGGAATAGAA
	Reverse	ATCAGAGGCTGCTGGGGAA
Homo *IGF2R*	Forward	CACCAGGCGTTTGATGTTGG
	Reverse	TTTGGGAATGGTGCCCTCTC
Homo *CFB*	Forward	TCTCTGTGGCATGGTTTGGG
	Reverse	CCATACAGCTCTCGTGTCCC
Homo PON1	Forward	AGCGTGGTCGTATGTTGTCT
	Reverse	TGAGCCAGCAACTCAGCTAT

Supplementary Table 4. Target sequences of siRNAs and lncRNA smart silencer.

siRNAs	Target sequences
siR-*IGF2R*	GCATCAAGATATCGACTCT
siR-*CFB*	GTGGCAAGTTATGGTGTGA
siR-*PON1*	GTCGTATGTTGTCTACTAT
SmartSiliencer-*C2orf27A* (mix)	
ASO-h-C2orf27A_001	CCAAAGGTTTATGGCTGCAA
ASO-h-C2orf27A_001	GAGAGTAACTTTGTACCCAT
ASO-h-C2orf27A_001	ACCACAGTTACTTTATCCCT
si-h-C2orf27A_001	TCATCTGCGTTGCTCTAAA
si-h-C2orf27A_002	CCTCCAGGTTCAACAGTAT
si-h-C2orf27A_003	ACTGATTCCTTCCGAGACT