

Grieve *et al.*

Supplementary Figure Legends

Table S1: Correlation of genes scores in the SJRH cohort

Table S2: Association of biomarkers with clinicopathological parameters in the SJRH cohort.

Table S3: Prognostic significance of biomarkers in stage I-III patients in the SJRH cohort

Table S4: Correlation between mRNA-protein in the JBR.10 cohort

Figure S1: IHC staining of biomarkers on the SJRH TMAs. Representative images demonstrating low and high nuclear staining of HEXIM1 (a, b), cytoplasmic staining of UMPS (c, d), and cytoplasmic staining of FAM64A (e, f), respectively.

Figure S2: Prognostic evaluation of individual biomarkers in SJRH cohort. The OS and RFS curves according to HEXIM1 (a, b), UMPS (c, d), and FAM64A (e, f), respectively.

Table S1: Correlation of gene scores in the SJRH cohort

	FOSL2	ATP1B1	STMN2	TRIM14	HEXIM1	UMPS	FAM64A
FOSL2		-0.32 (<i>p</i> < 0.0001)	0.23 (<i>p</i> = 0.003)	-0.11 (<i>p</i> =0.301)	0.19 (<i>p</i> = 0.017)	0.06 (<i>p</i> =0.417)	0.01 (<i>p</i> =0.943)
ATP1B1			-0.1 (<i>p</i> =0.216)	0.03 (<i>p</i> =0.749)	-0.06 (<i>p</i> =0.469)	-0.09 (<i>p</i> =0.245)	0.16 (<i>p</i> = 0.034)
STMN2				0.31 (<i>p</i> = 0.003)	0.13 (<i>p</i> =0.093)	0.19 (<i>p</i> = 0.014)	0.185 (<i>p</i> = 0.017)
TRIM14					0.11 (<i>p</i> =0.285)	0.30 (<i>p</i> = 0.004)	0.18 (<i>p</i> =0.091)
HEXIM1						0.061 (<i>p</i> =0.432)	0.087 (<i>p</i> =0.258)
UMPS							0.265 (<i>p</i> = 0.0005)
FAM64A							

Table S2: Association of biomarkers with clinicopathological parameters in the SJRH cohort

Characteristics	HEXIM1			UMPS			FAM64A		
	High (n=44)	Low (n=129)	p-value	High (n=123)	Low (n=47)	p-value	High (n=143)	Low (n=27)	p-value
Age			0.71			0.58			1
<61	12 (27.3%)	41 (31.8%)		40 (32.5%)	13 (27.7%)		46 (32.2%)	8 (29.6%)	
≥61	32 (72.7%)	88 (68.2%)		83 (67.5%)	34 (72.3%)		97 (67.8%)	19 (70.4%)	
Sex			0.6			0.12			0.09
Male	21 (47.7%)	68 (52.7%)		59 (48.0%)	29 (61.7%)		67 (46.9%)	18 (66.7%)	
Female	23 (52.3%)	61 (47.3%)		64 (52.0%)	18 (38.3%)		76 (53.1%)	9 (33.3%)	
TNM stage			0.11			0.9			0.26
I	31 (70.5%)	77 (59.7%)		76 (61.8%)	30 (63.8%)		88 (61.5%)	17 (63.0%)	
II	11 (25.0%)	30 (23.3%)		30 (24.4%)	10 (21.3%)		34 (23.8%)	7 (25.9%)	
III	2 (4.5%)	22 (17.0%)		17 (13.8%)	7 (14.9%)		21 (14.7%)	3 (11.1%)	
Histology			0.638			0.72			0.16
Adeno	23 (52.3%)	66 (51.2%)		61 (49.6%)	25 (53.2%)		75 (52.4%)	12 (44.4%)	
SCC	16 (36.4%)	41 (31.8%)		40 (32.5%)	16 (34.0%)		44 (30.8%)	13 (48.2%)	
Other	5 (11.3%)	22 (17.0%)		22 (17.9%)	6 (12.8%)		24 (16.8%)	2 (7.4%)	
Type of Surgery			0.1			0.18			0.22
Pneumectomy	6 (13.6%)	7 (5.4%)		11 (8.9%)	1 (2.1%)		12 (8.4%)	0 (0%)	
Lesser surgery	38 (86.4%)	122 (94.6%)		112 (91.9%)	46 (97.9%)		131 (91.6%)	27 (100%)	
Chemotherapy			0.44			0.28			0.87
Post	11 (25.0%)	44 (34.1%)		41 (33.3%)	13 (27.7%)		45 (31.5%)	9 (33.3%)	
None	31 (70.5%)	77 (59.7%)		73 (59.3%)	33 (70.2%)		89 (62.2%)	17 (63.0%)	
Other	2 (4.5%)	8 (6.2%)		9 (7.4%)	1 (2.1%)		9 (6.3%)	1 (3.7%)	
KRAS Mutation			0.57			0.71			0.25
Present	14 (31.8%)	35 (27.1%)		37 (30.1%)	12 (25.5%)		43 (30.1%)	5 (18.5%)	
Absent	30 (68.2%)	94 (72.9%)		86 (69.9%)	35 (74.5%)		100 (69.9%)	22 (81.5%)	

Abbreviation: Adeno, adenocarcinoma; SCC, squamous cell carcinoma

Table S3: Prognostic significance of biomarkers in SJRH cohort

Biomarker	OS		RFS	
	HR (CI)	<i>p</i> -value	HR (CI)	<i>p</i> -value
FOSL2	0.50 (0.30-0.84)	0.0089	0.56 (0.35-0.91)	0.0184
ATP1B1	0.66 (0.39-1.14)	0.138	0.66 (0.38-1.12)	0.1216
STMN2	1.35 (0.85-2.14)	0.2004	1.53 (1.00-2.33)	0.0493
TRIM14	1.18 (0.63-2.22)	0.6045	1.07 (0.61-1.91)	0.8269
HEXIM1	0.72 (0.45-1.16)	0.1787	0.81 (0.53-1.25)	0.3454
UMPS	0.52 (0.31-0.86)	0.0109	0.62 (0.39-0.99)	0.0439
FAM64A	0.90 (0.49-1.66)	0.7381	1.16 (0.67-2.01)	0.6022

Abbreviations: CI, 95% confidence interval; HR, hazard ratio; OS, overall survival; RFS, recurrence-free survival

Table S4: Correlation between mRNA-protein in JBR.10 cohort

	Correlation coefficient	(p-value)
FOSL2 (n=126)	0.1012	0.2594
ATP1B1 (n=126)	0.2064	0.0226
STMN2 (n=126)	-0.0191	0.8315
TRIM14 (n=117)	0.0549	0.5583

Figure S1

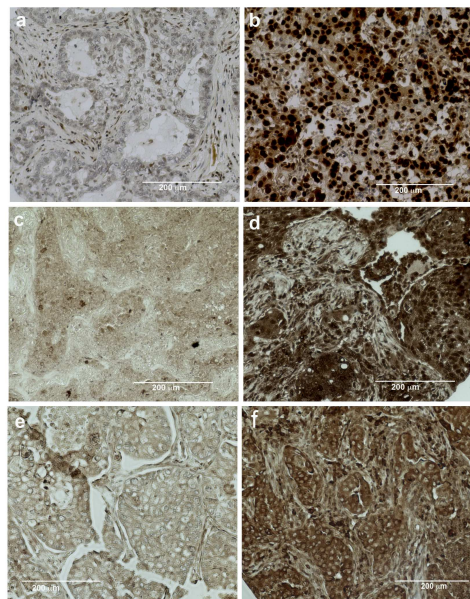


Figure S2

