

ORIGINAL RESEARCH ARTICLE

Dual roles of *FGF2* and *PGR* in lactate-driven metabolic reprogramming and immune evasion: Implications for prostate cancer outcomes

Supplementary File

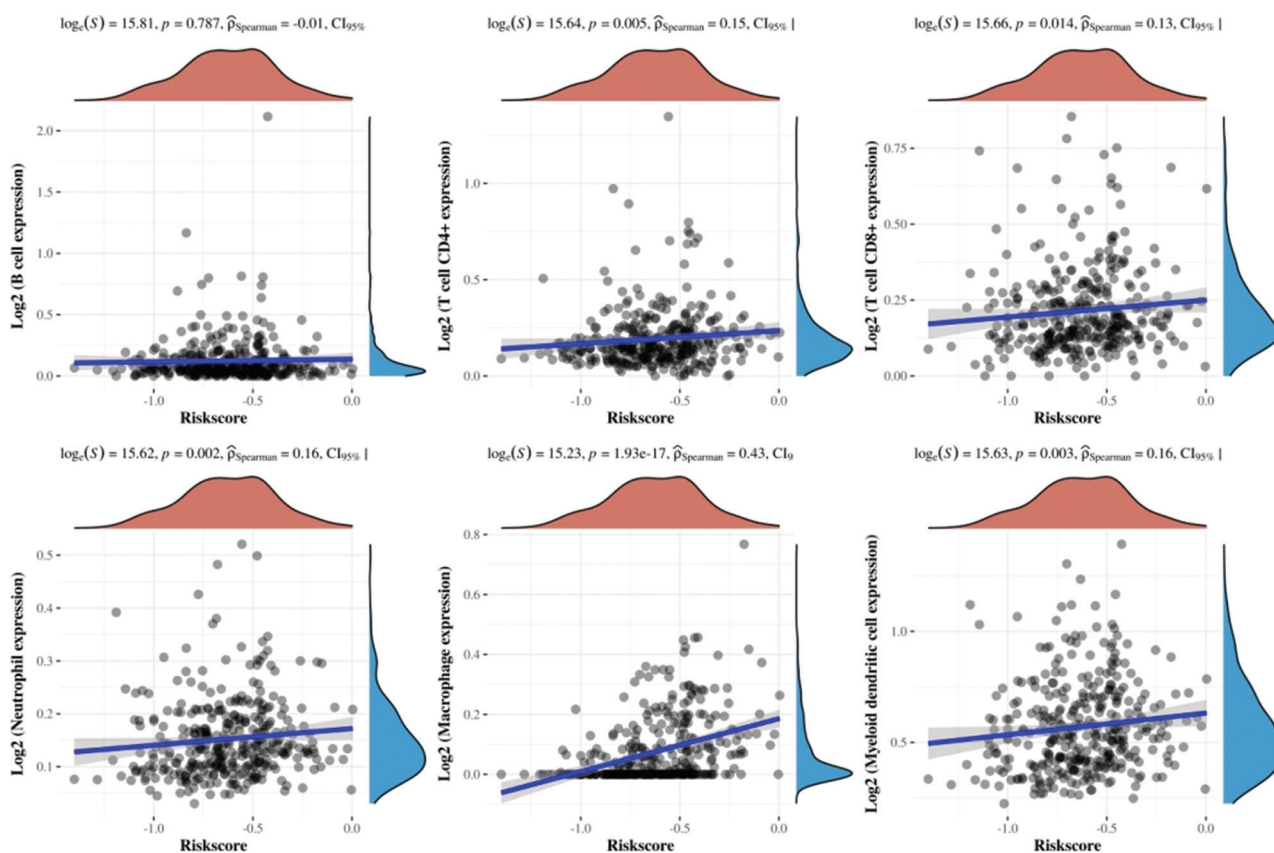


Figure S1. Scatter plot showing the risk score of model 1 versus the tumor immune estimation resource algorithm-based immune score
Abbreviation: CI: Confidence interval.

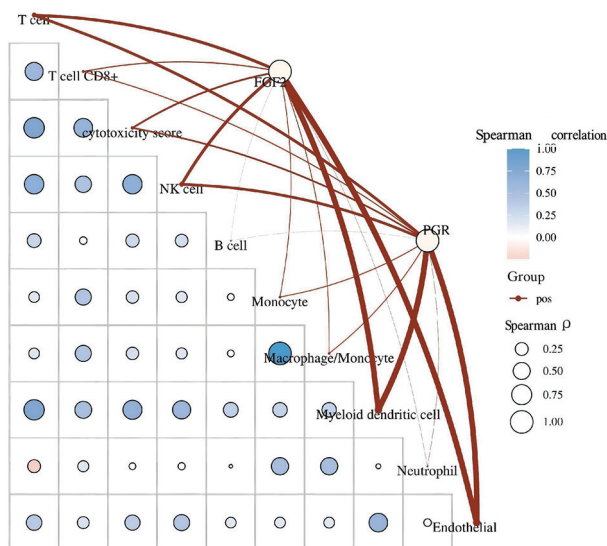


Figure S2. Network diagram showing the correlation between progesterone receptor and fibroblast growth factor 2, and immune cell infiltration

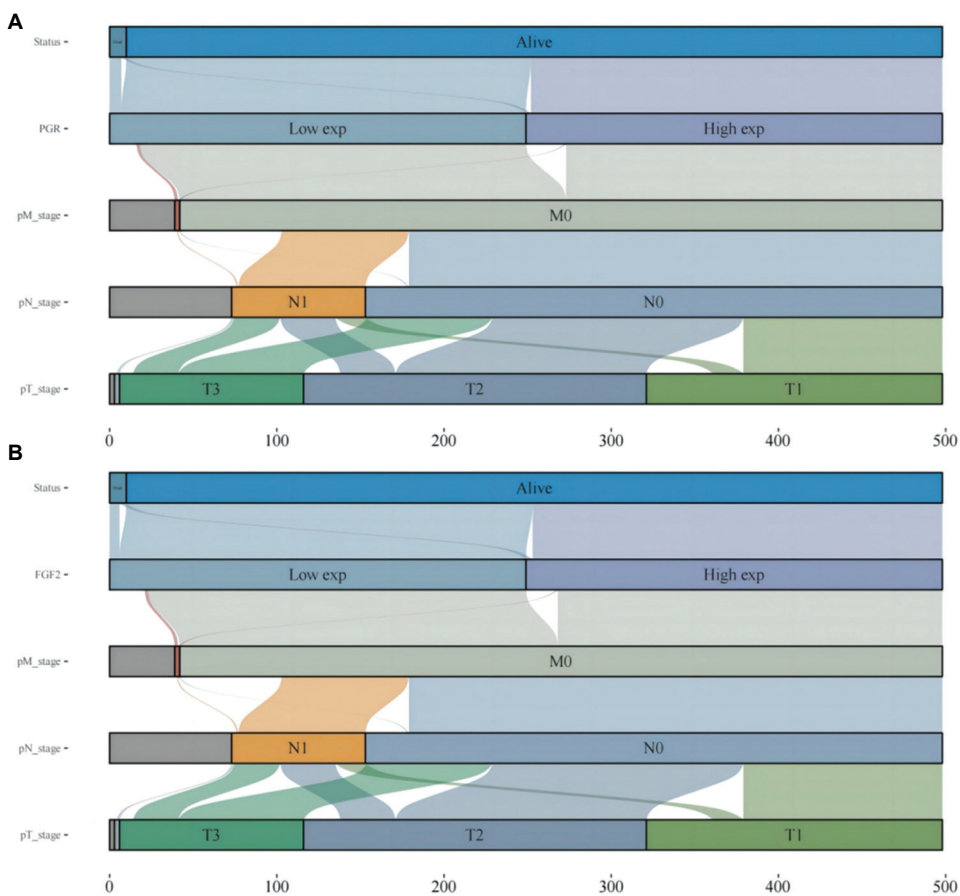


Figure S3. Sankey diagrams showing the association between gene expression and TNM stage in clinical prostate cancer: (A) progesterone receptor expression and (B) fibroblast growth factor 2 expression
Abbreviations: exp: Expression; TNM: Tumor–node–metastasis.

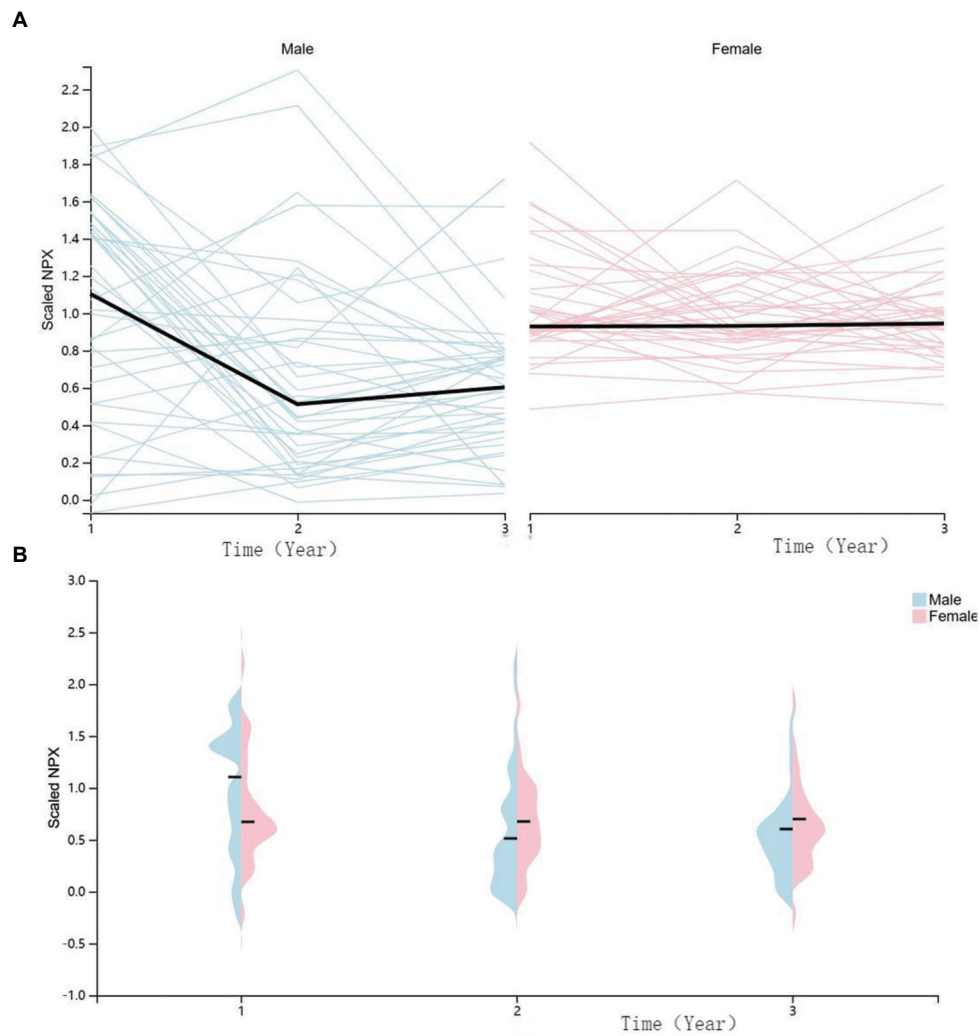


Figure S4. The expression of fibroblast growth factor 2 in plasma proteins using proximity extension assay technology. (A) Overall trend within three years. (B) Analysis of differences within three years. Abbreviation: NPX: Normalized protein expression.

Table S1. Results of univariate and multivariate regression analyses for the six genes

Genes	Total (n)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	p-value	Hazard ratio (95% CI)	p-value
CD40	501	0.994 (0.801–1.234)	0.960	-	-
FGF2	501	0.727 (0.568–0.930)	0.011	0.874 (0.556–1.375)	0.561
INPP5D	501	1.132 (0.885–1.448)	0.323	-	-
PGR	501	0.689 (0.520–0.913)	0.010	0.784 (0.467–1.318)	0.359
PRKCB	501	0.803 (0.633–1.019)	0.072	-	-
PTGER2	501	0.875 (0.715–1.072)	0.198	-	-

Abbreviation: CI: Confidence interval.

Table S2. Results of systematic analysis of the relationship between PGR and clinical baseline data

Characteristics	Low expression of PGR	High expression of PGR	p-value
N	250	251	-
Pathologic T stage (n [%])			
T2	89 (18)	100 (20.2)	0.433
T3	151 (30.6)	143 (28.9)	
T4	7 (1.4)	4 (0.8)	
Pathologic N stage (n [%])			
N0	162 (37.9)	186 (43.5)	0.006
N1	51 (11.9)	29 (6.8)	
Clinical T stage (n [%])			
T1 and T2	176 (43.2)	176 (43.2)	0.380
T3 and T4	31 (7.6)	24 (5.9)	
Primary therapy outcome (n [%])			
PD	14 (3.2)	15 (3.4)	0.317
SD	18 (4.1)	12 (2.7)	
PR	22 (5)	18 (4.1)	
CR	154 (35)	187 (42.5)	
Clinical M stage (n [%])			
M0	231 (50.2)	226 (49.1)	1.000
M1	2 (0.4)	1 (0.2)	
Age (n [%])			
≤60	108 (21.6)	117 (23.4)	0.442
>60	142 (28.3)	134 (26.7)	
Gleason score (n [%])			
6 and 7	138 (27.5)	156 (31.1)	0.114
8, 9, and 10	112 (22.4)	95 (19)	
Prostate-specific antigen (ng/mL) (n [%])			
<4	199 (44.8)	218 (49.1)	0.245
≥4	16 (3.6)	11 (2.5)	
Overall survival event (n [%])			
Alive	243 (48.5)	248 (49.5)	0.335
Dead	7 (1.4)	3 (0.6)	
Progression-free interval event (n [%])			
No	194 (38.7)	213 (42.5)	0.037
Yes	56 (11.2)	38 (7.6)	
DSS event (n [%])			
No	244 (48.9)	250 (50.1)	0.362
Yes	4 (0.8)	1 (0.2)	
Residual tumor (n [%])			
R0	147 (31.3)	169 (36)	0.042
R1 and R2	87 (18.5)	67 (14.3)	

Abbreviations: CR: Complete response; DSS: Disease-specific survival; M: Metastasis; N: Node; PD: Progressive disease; PR: Partial response; SD: Stable disease; T: Tumor; PGR: Progesterone receptor.

Table S3. Results of systematic analysis of the relationship between *FGF2* and clinical baseline data

Characteristics	Low expression of <i>FGF2</i>	High expression of <i>FGF2</i>	<i>p</i> -value
N	250	251	-
Pathologic T stage (<i>n</i> [%])			
T2	90 (18.2)	99 (20)	0.692
T3	151 (30.6)	143 (28.9)	
T4	6 (1.2)	5 (1)	
Pathologic N stage (<i>n</i> [%])			
N0	167 (39)	181 (42.3)	0.258
N1	44 (10.3)	36 (8.4)	
Clinical T stage (<i>n</i> [%])			
T1 and T2	164 (40.3)	188 (46.2)	0.009
T3 and T4	36 (8.8)	19 (4.7)	
Primary therapy outcome (<i>n</i> [%])			
PD	13 (3)	16 (3.6)	0.300
SD	15 (3.4)	15 (3.4)	
PR	25 (5.7)	15 (3.4)	
CR	160 (36.4)	181 (41.1)	
Clinical M stage (<i>n</i> [%])			
M0	226 (49.1)	231 (50.2)	0.988
M1	2 (0.4)	1 (0.2)	
Age (<i>n</i> [%])			
≤60	106 (21.2)	119 (23.8)	0.260
>60	144 (28.7)	132 (26.3)	
Gleason score (<i>n</i> [%])			
6 and 7	138 (27.5)	156 (31.1)	0.114
8, 9, and 10	112 (22.4)	95 (19)	
Prostate-specific antigen (ng/mL) (<i>n</i> [%])			
<4	199 (44.8)	218 (49.1)	0.245
≥4	16 (3.6)	11 (2.5)	
Overall survival event (<i>n</i> [%])			
Alive	244 (48.7)	247 (49.3)	0.745
Dead	6 (1.2)	4 (0.8)	
Progression-free interval event (<i>n</i> [%])			
No	191 (38.1)	216 (43.1)	0.006
Yes	59 (11.8)	35 (7)	
DSS event (<i>n</i> [%])			
No	245 (49.1)	249 (49.9)	0.366
Yes	4 (0.8)	1 (0.2)	
Residual tumor (<i>n</i> [%])			
R0	149 (31.7)	167 (35.5)	0.102
R1 and R2	85 (18.1)	69 (14.7)	

Abbreviations: CR: Complete response; DSS: Disease-specific survival; M: Metastasis; N: Node; PD: Progressive disease; PR: Partial response; SD: Stable disease; T: Tumor; FGF2: Fibroblast growth factor 2.