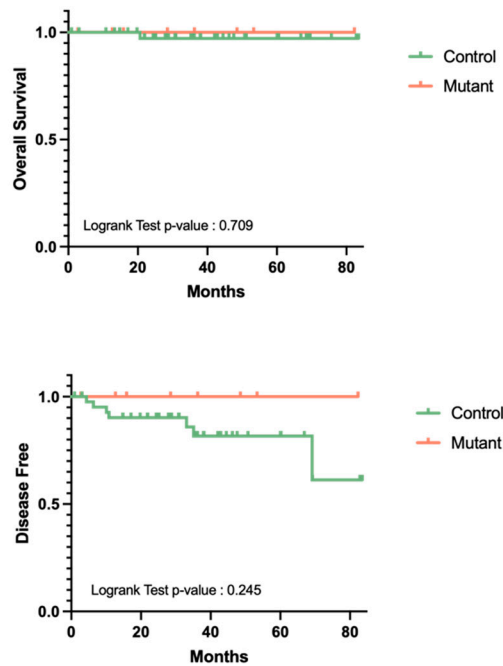


# Unveiling the Molecular Landscape of *FOXA1* Mutant Prostate Cancer: Insights and Prospects for Targeted Therapeutic Strategies

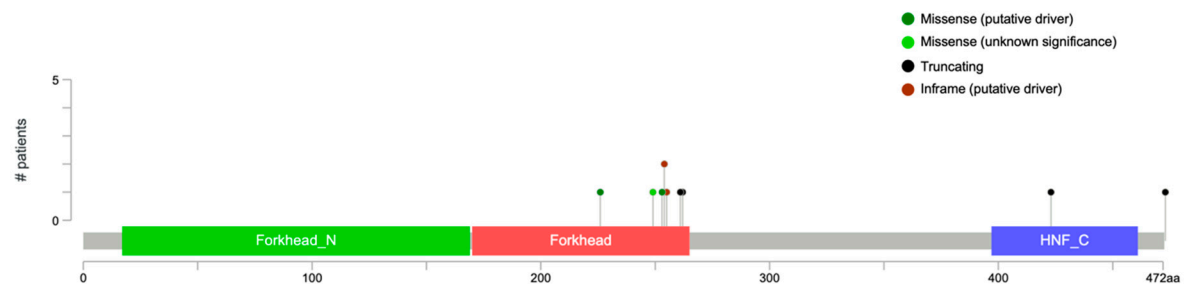
## Supplementary Data

**Supplementary Figure S1.** (A) Kaplan-Meier analysis plots comparing Overall Survival and Disease Free Months between *FOXA1* mutant and control groups. (B) A lollipop plot presenting the location of mutations and mutation types of *FOXA1* in *FOXA1* mutant prostate cancer. The plot was obtained from cBioportal.

**A)**



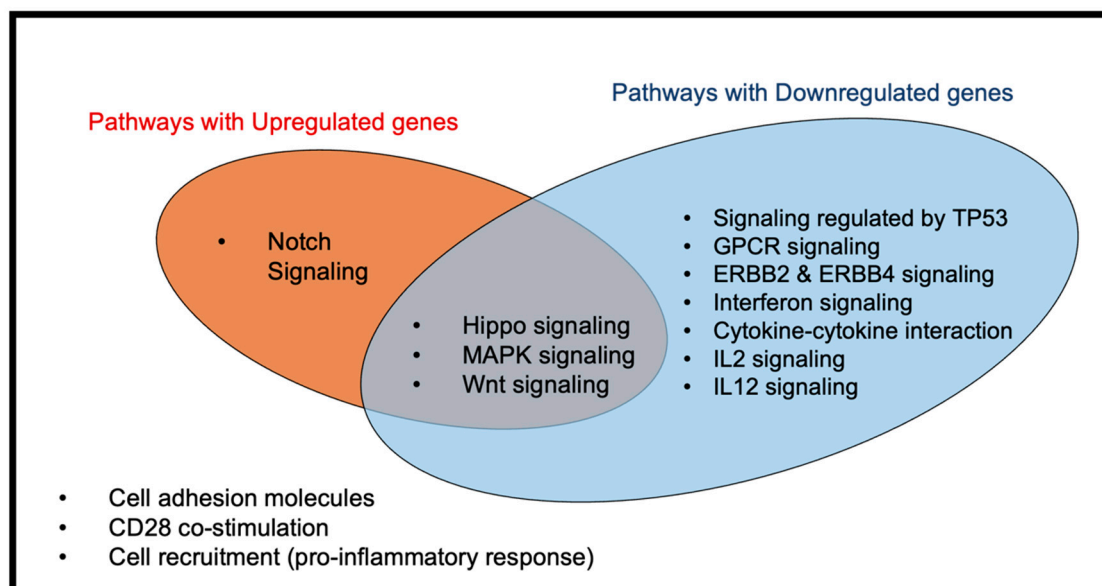
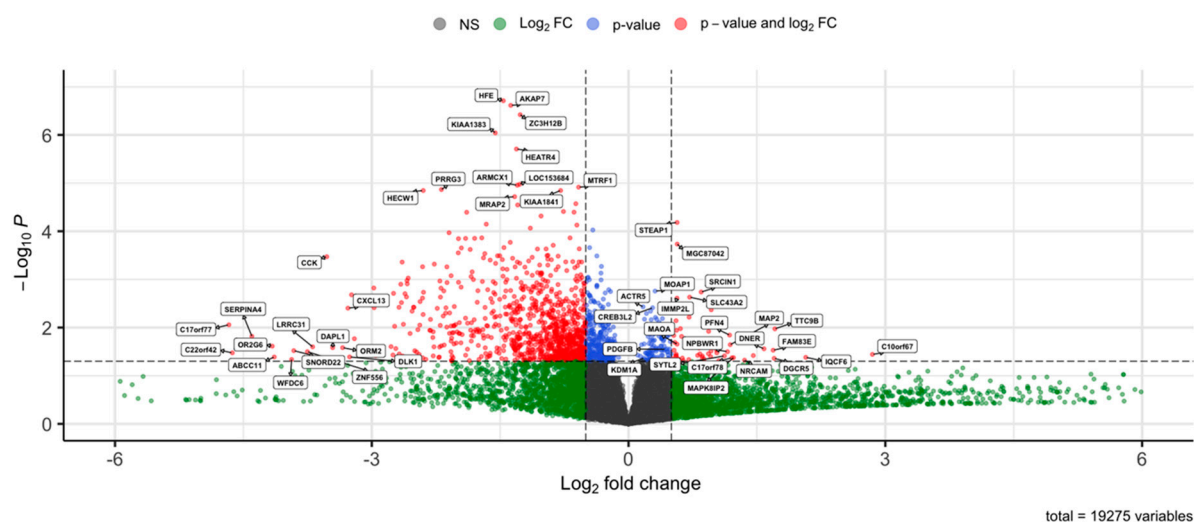
**B)**

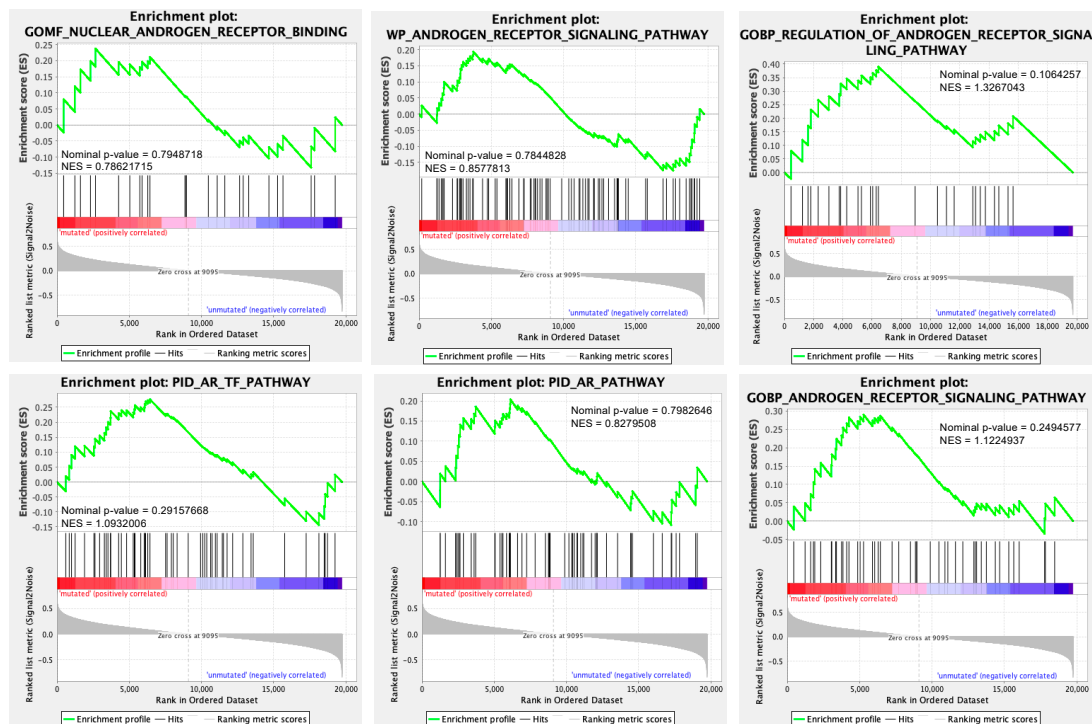


**Supplementary Table S1.** Detailed information of *FOXA1* mutations

Sample ID	Protein Change	Mutation Type	Variant Type
TCGA-YL-A9WI-01	D226N	Missense_Mutation	Single Nucleotide Polymorphism
TCGA-KK-A8IB-01	M253K	Missense_Mutation	Single Nucleotide Polymorphism
TCGA-CH-5737-01	E255_N256del	In_Frame_Deletion	Deletion
TCGA-HC-7210-01	F254_G257delinsC	In_Frame_Deletion	Deletion
TCGA-KK-A8IG-01	Q263Afs*60	Frame_Shift_Insertion	Insertion
TCGA-EJ-5494-01	*473Eext*34	Nonstop_Mutation	Single Nucleotide Polymorphism
TCGA-EJ-5494-01	A423Dfs*17	Frame_Shift_Deletion	Deletion

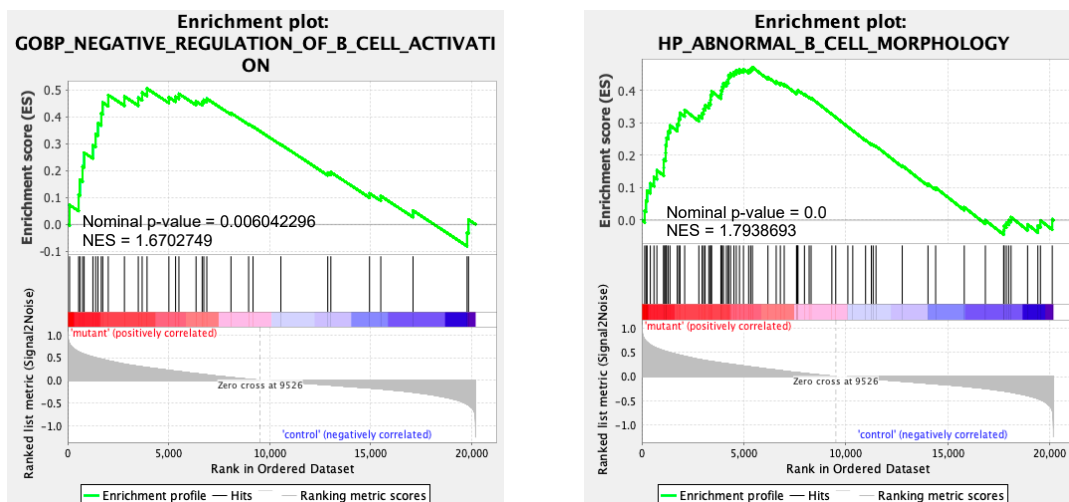
TCGA-J9-A8CP-01	R262Sfs*57	Frame_Shift_Deletion	Deletion
TCGA-HC-8265-01	D249V	Missense_Mutation	Single Nucleotide Polymorphism
TCGA-EJ-7789-01	F254V	Missense_Mutation	Single Nucleotide Polymorphism





**Supplementary Figure S3.** GSEA analysis for AR signaling. GSEA analysis shows no significant difference in AR signaling in *FOXA1* mutant and control group.

\*NES=Normalized Enrichment Score.



**Supplementary Figure S4.** GSEA analysis related to B cell. Negative regulation of B cell activation and abnormal B cell morphology were upregulated in *FOXA1* mutant group.

\*NES=Normalized Enrichment Score.

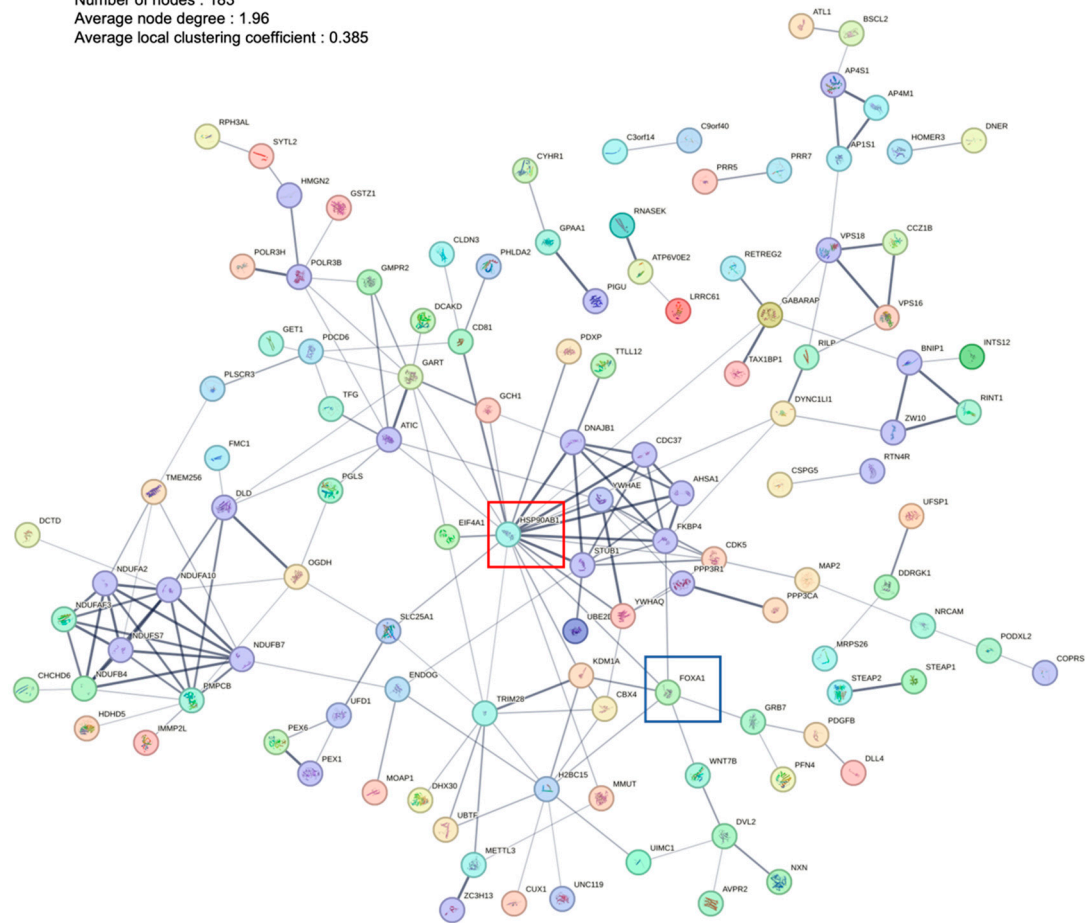
**Supplementary Table S2.** *FOXA1* mutation-associated signaling pathways in TCGA and GEO datasets.

Pathways	<i>p</i> -value	
	TCGA	GSE123619
Hippo signaling pathway	0.007	0.018835332
ERBB signaling pathway	0.00229186	4.62334E-05
Interferon signaling	0.014055387	0.028836313
Notch signaling	0.01188312	0.046089423
Cell adhesion	0.04769012	0.000230778
Wnt signaling	0.00767968	0.045312137
Signaling regulated by TP53	0.00113	2.89E-07
MAPK signaling	0.03439121	7.65E-05
IL2 signaling	0.012385331	0.000129847

**Supplementary Table S3.** Monoamine neurotransmitter related pathways.

Pathways	<i>p</i> -value	
	TCGA	GSE123619
Dopamine beta-hydroxylase deficiency	0.000605401	0.038811814
Monoamine oxidase-a deficiency (MAO-A)	0.000605401	0.038811814
Serotonin	0.019527612	0.048104587

PPI enrichment p-value = 0.000271  
 Number of nodes : 183  
 Average node degree : 1.96  
 Average local clustering coefficient : 0.385



**Supplementary Figure S5.** Protein-protein interaction presented by STRING. The results displayed connected nodes representing proteins encoded by the 168 upregulated genes and other proteins mediating their interactions. The lines connecting proteins indicate both functional and physical protein associations, and the line thickness indicates the strength of data support. HSP90AB1 protein was marked by the red box and FOXA1 protein was marked by the blue box.