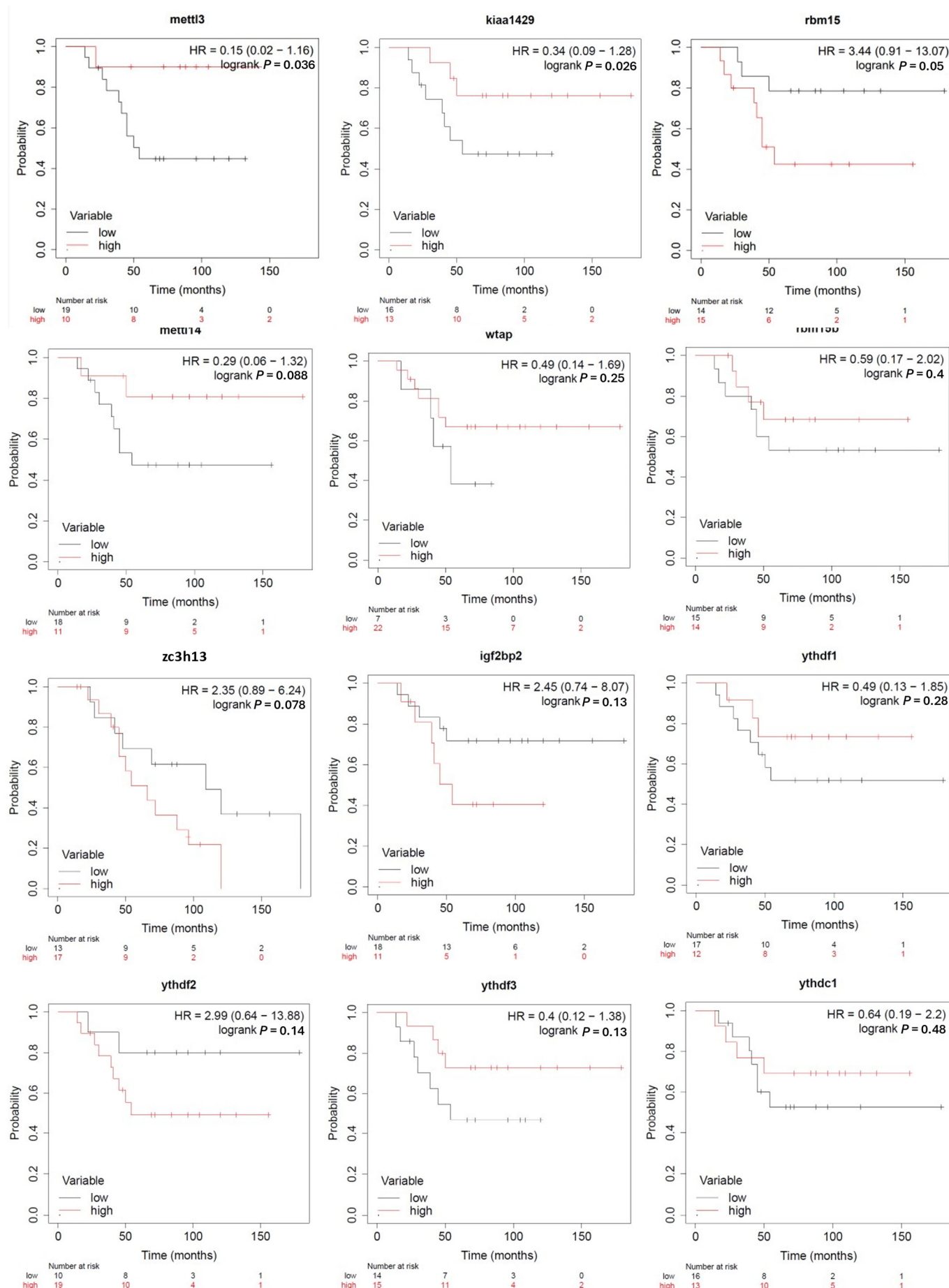


Supplementary Materials: RNA m6a Methylation Regulator Expression in Castration-Resistant Prostate Cancer Progression and its Genetic Associations

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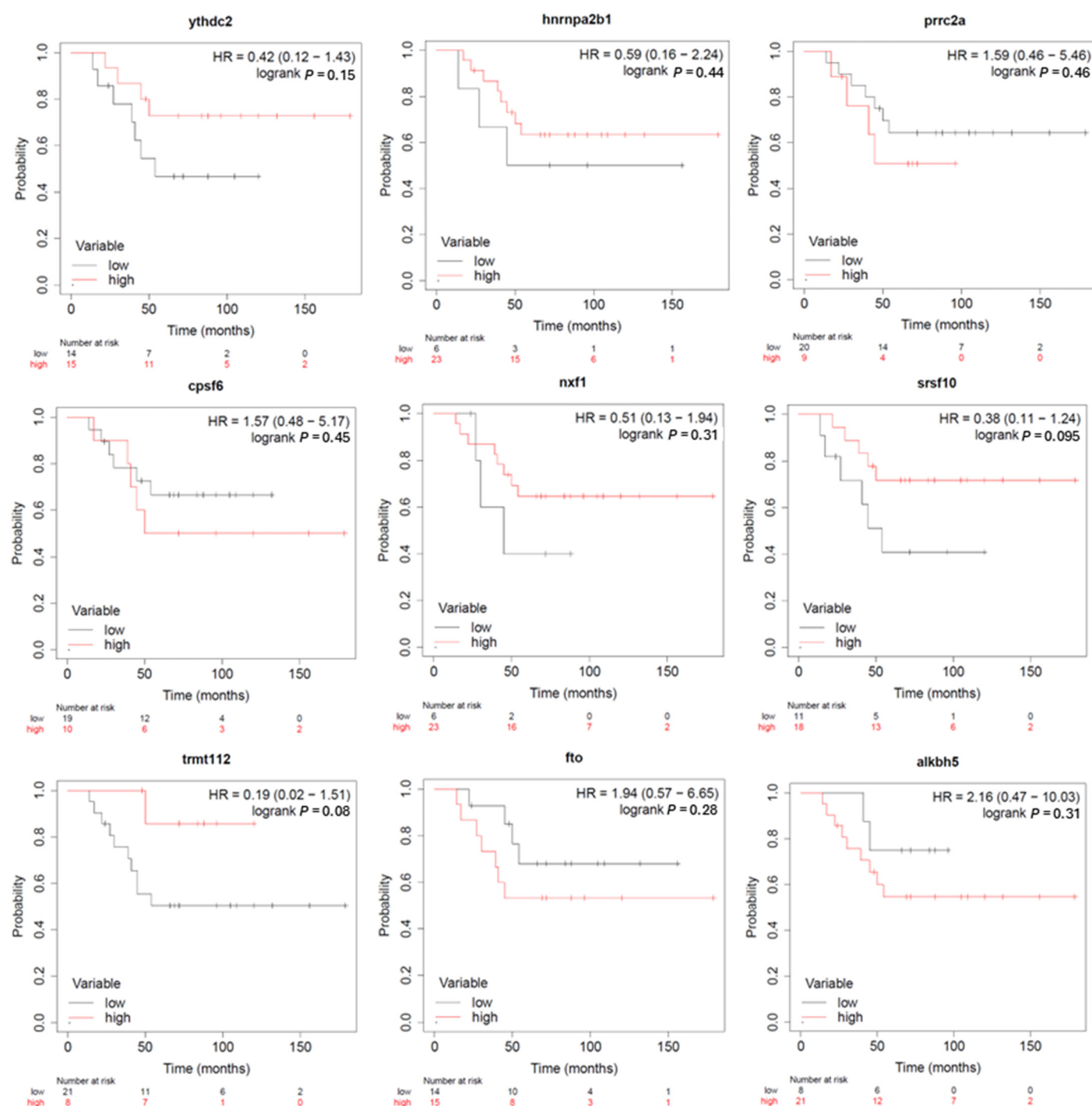


Figure S1. Univariate Kaplan-Meier Survival analysis of m6A methylation regulators for overall survival of CRPC patients after the first hormone refractory therapy. Based on the univariate cox regression analysis performed using the Kaplan-Meier Plotter, 18 m6A regulators showed no significant correlation between their expression and overall survival of CRPC patients. HR: hazard ratio; low: low expression of the m6A regulator; high: high expression of the m6A regulator.

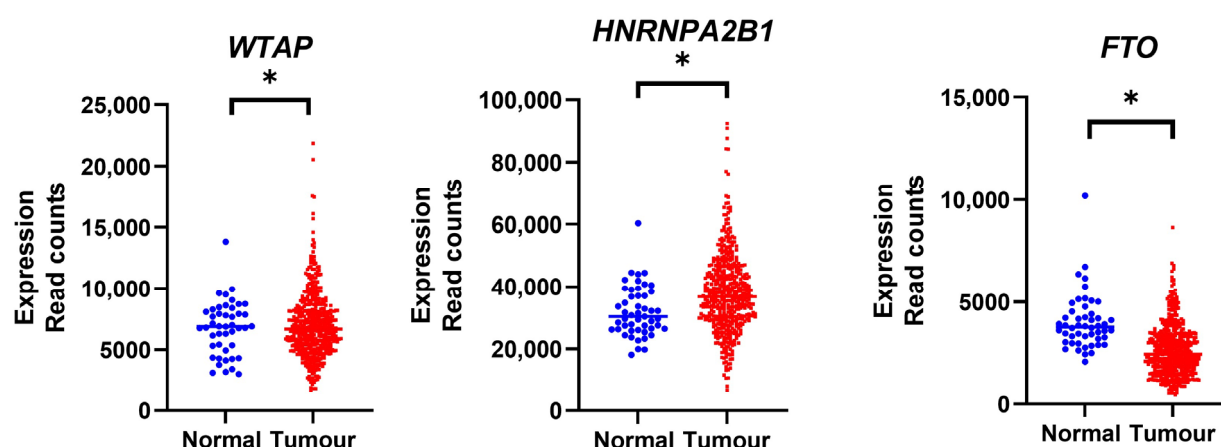


Figure S2. Three m6A regulator genes were found to be differentially expressed in primary PCa ($n = 450$) tissue compared to healthy controls ($n = 49$) using The Cancer Genome Atlas Program (TCGA) RNAseq data, * $p < 0.05$.

Table S1. SWATH-MS label-free quantification of m6A regulator expression in prostate cancer cell lines.

Table S2. SWATH-MS label-free quantification of m6A regulator expression in androgen- and anti-androgen-treated LNCaP cell line.

Table S3. RNA sequencing transcriptomic analysis of m6A regulator expression in androgen- and anti-androgen-treated LNCaP cell line.

Table S4. RNA sequencing analysis of m6A regulator expression in prostate cancer tumor and adjacent normal tissues.

Table S5. Log₂ median expression data for m6A regulatory genes recruited from the Grasso dataset (N = Normal Tissue, T = Localized Prostate Cancer, WA = CRPC).

Table S6. Survival data of CRPC patients after first hormone therapy from the Grasso dataset (survival event at 5 years 1 = Dead, 0 = Alive).

Table S7. PCa risk loci association with m6A regulator genes.

Table S1–S7. are attached separately as an Excel file.