**Additional File 3**

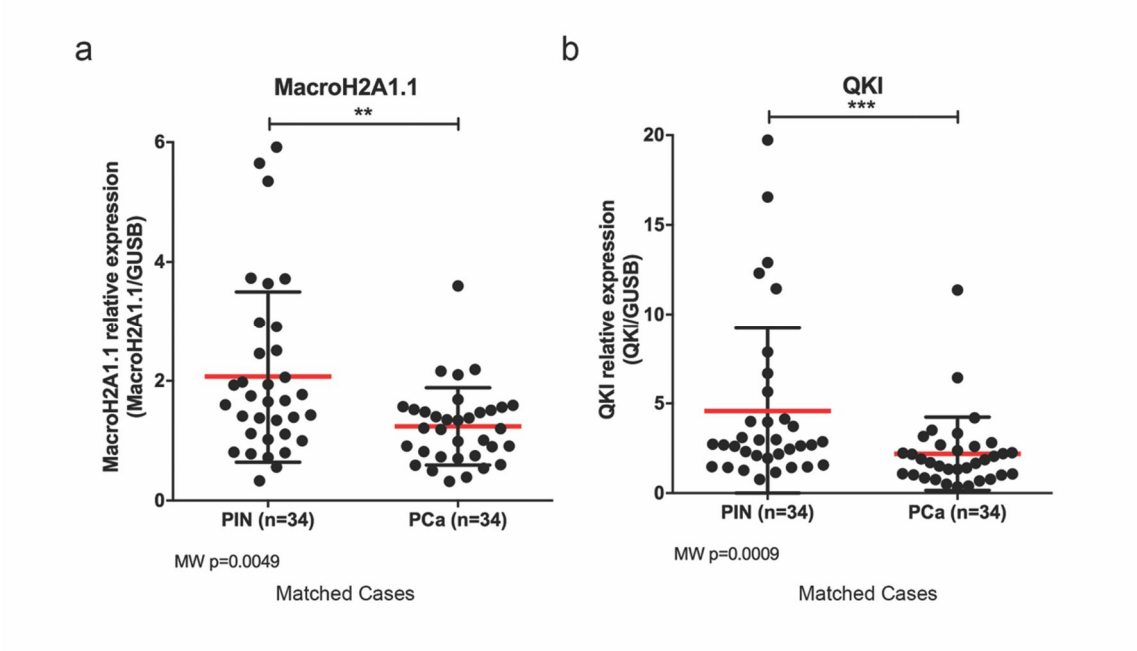


**Fig S1** Transcript levels of **(a)** macroH2A1.1 and **(b)** QKI in matched PIN and PCa (n=34) lesions from the same patients, assessed by RT-qPCR and normalized to GUSB mRNA levels. Mann-Whitney U-test: **p<0.01, ***p<0.001

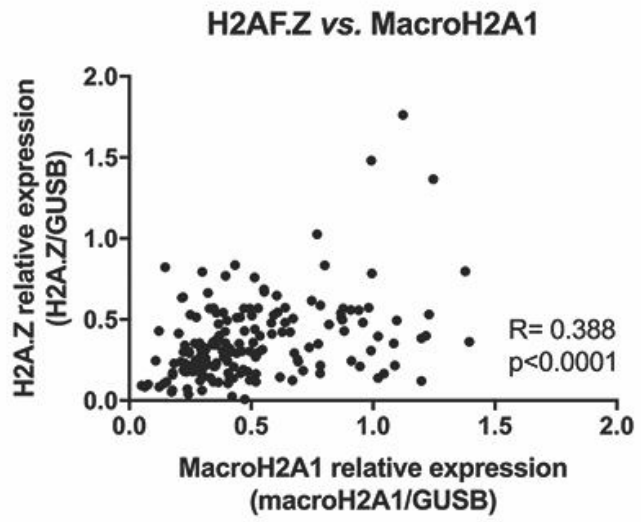


**Fig S2** Correlation between macroH2A1 and H2A.Z transcript levels (R=0.388, p<0.0001) in prostate cancer samples (n=197), assessed by RT-qPCR and normalized to GUSB. (R coefficient calculated by Spearman's rank correlation)

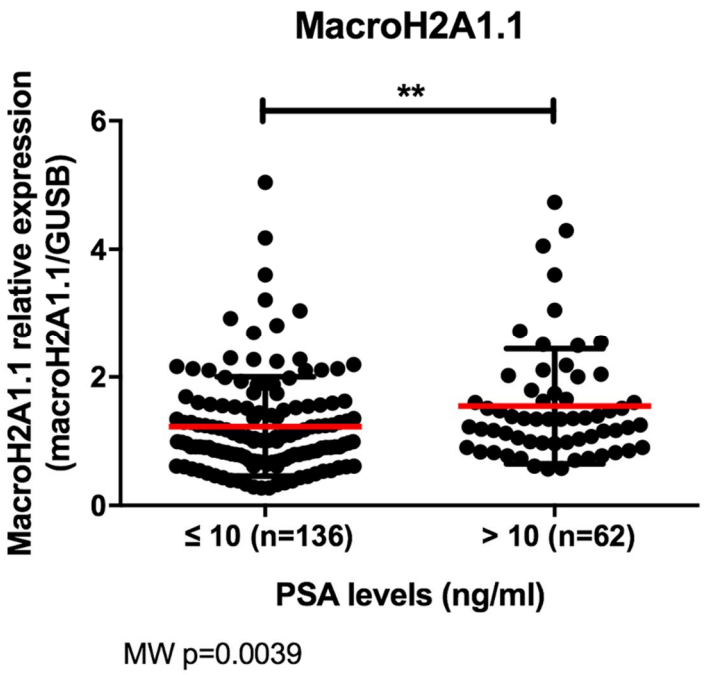


**Fig S3** Distribution of macroH2A1.1 mRNA levels in prostate cancer tissue samples, assessed by RT-qPCR and normalized to GUSB, according to categorized ≤10 ng/mL (n=136) and >10 ng/mL (n=62) PSA levels . Mann-Whitney U-test: **p<0.01

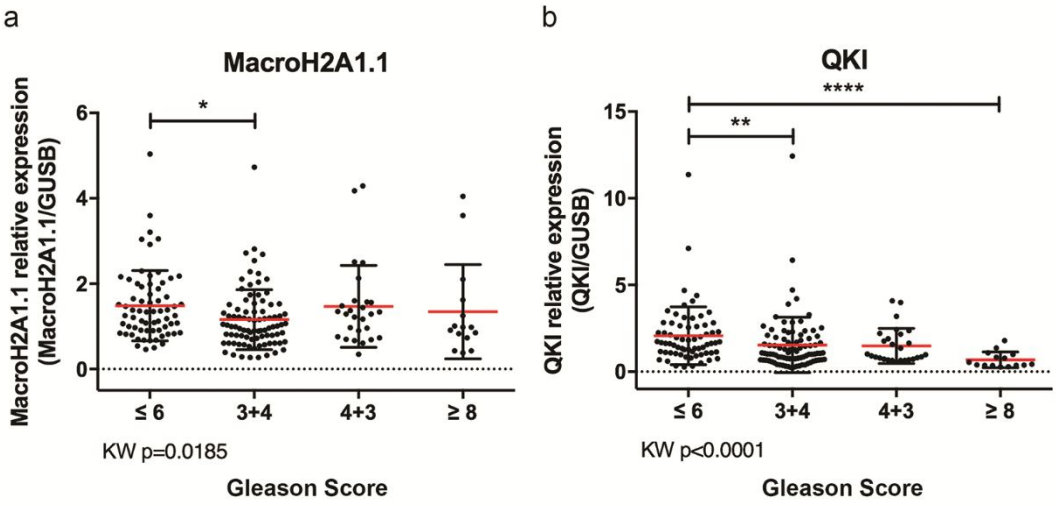


**Fig S4** Distribution of **(a)** MacroH2A1.1 and **(b)** QKI mRNA levels assessed by RT-qPCR and normalized to GUSB, among Gleason scores ≤6, 7 (3+4), 7 (4+3) and ≥8 prostate cancer tissue samples. Kruskal-Wallis Test: Adjusted *p<0.05, **p<0.01, ****p<0.0001.

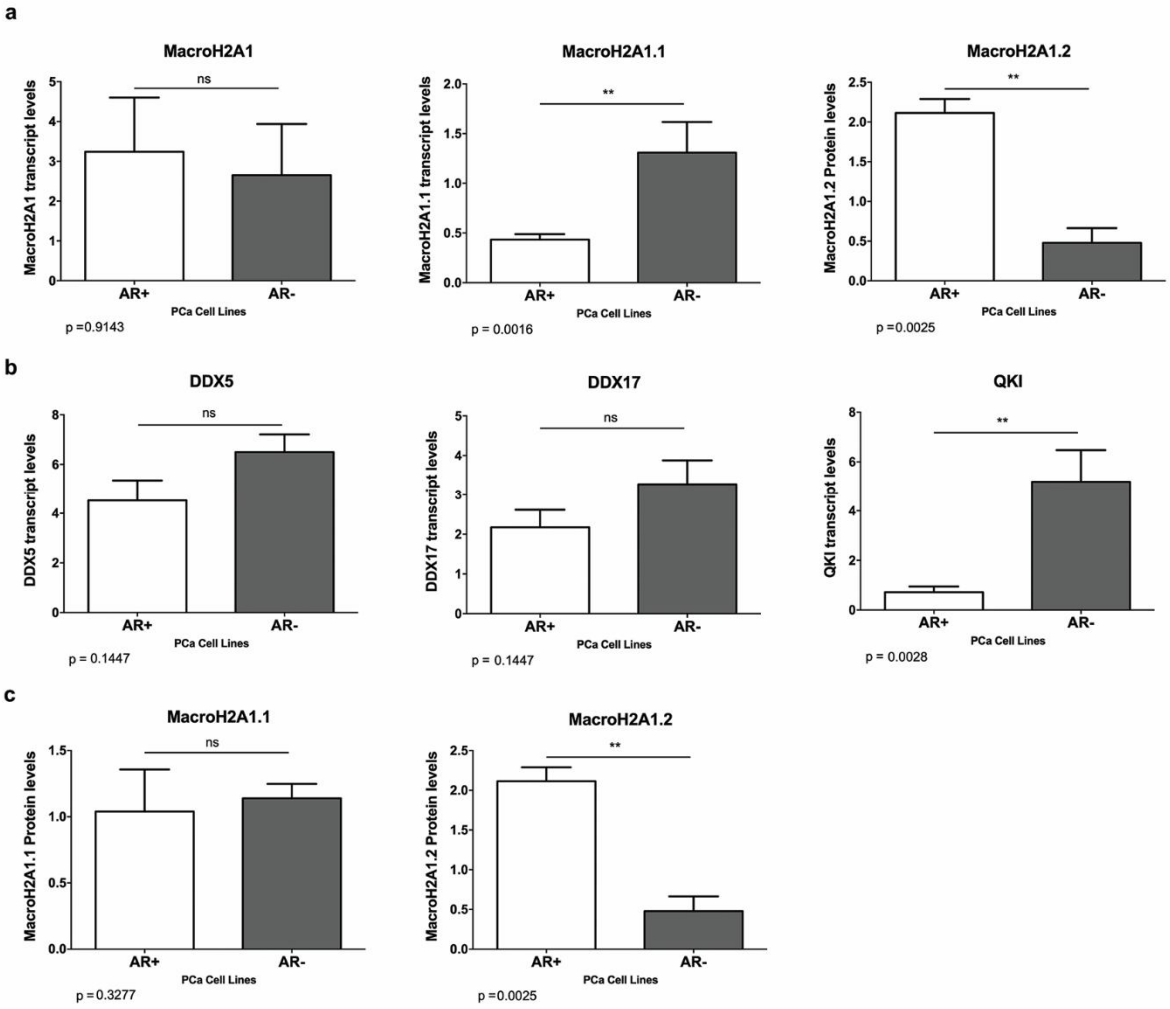


**Fig S5 (a)** Distribution of transcript levels of total macroH2A1, macroH2A1.1 and macroH2A1.2, assessed by RT-qPCR and normalized to GUSB mRNA levels, in androgen-receptor positive prostate cancer cell lines (22Rv1, LNCaP and VCaP), and in androgen-receptor negative prostate cancer cell lines (DU145 and PC-3). **(b)** Distribution of transcript levels of splicing regulators DDX5, DDX17 and QKI, assessed by RT-qPCR and normalized to GUSB, in androgen positive and negative prostate cancer cell lines. **(c)** Distribution of macroH2A1.1 and macroH2A1.2 protein levels, normalized to β-actin, in androgen positive and negative prostate cancer cell lines. Mann-Whitney U-test: **p<0.01, ***p<0.001. ns – non significant.