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.