

**Supplementary material for "DNA methylation status is more reliable than gene expression at detecting cancer in prostate biopsy"**

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**Supplementary Table S1. Expression changes of genes selected for methylation-based classifier observed on microarrays.** Fold change (FC) and adjusted *p*-values are given for comparison of combined cancerous and non-cancerous samples from cancer bearing prostates with BPH. DGKZ and mir10B probes were filtered-out in data preparation steps so the adjusted *p*-values are unavailable.

<b>Gene name</b>	<b>Gene symbols</b>	<b>Adjusted <i>p</i>-value</b>	<b>FC</b>
hairy and enhancer of split 5 (Drosophila)	HES5	0.344967386	0.94
integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ITGB2	0.363337043	0.69
integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ITGB2	0.404614672	0.71
retinoic acid receptor, beta	RARB	0.926476998	1.01
<b>retinoic acid receptor, beta</b>	<b>RARB</b>	<b>0.00372112</b>	<b>0.78</b>
retinoic acid receptor, beta	RARB	0.176002584	0.93
transforming, acidic coiled-coil containing protein 2	TACC2	0.016793631	1.31
transforming, acidic coiled-coil containing protein 2	TACC2	0.021926906	1.27
gene name	gene symbols	<i>p</i> -value (not adjusted)	FC
diacylglycerol kinase, zeta	DGKZ	0.240383004	1.09
diacylglycerol kinase, zeta	DGKZ	0.593016866	1.01
diacylglycerol kinase, zeta	DGKZ	0.304895273	1.03
microRNA 10b	MIR10B	0.240383004	1.05

## **Titles and legends to supplementary figures**

**Supplementary Figure S1. qRT-PCR validation of genes with the highest magnitude of changes between BPH and PCa by microarray profiling.** Relative mRNA levels were measured in RNA extracted from 19 BPH samples, 20 cancerous prostate samples with low dysplastic cell content (< 10%), 22 cancerous prostate samples with high dysplastic cell content (30-90%), and 27 adjacent non-cancerous prostate samples. Geometric mean expression of UBC and RPLP0 was used for normalization. The horizontal line is the median. Statistical significance was assessed by the Mann-Whitney test.  $p$ -values < 0.05 were considered significant (\*). (\*\*)  $p$ -value < 0.001; (\*\*\*)  $p$ -value < 0.0001.

**Supplementary Figure S2. Gene expression measurement in core biopsies by qRT-PCR.** RNA was isolated from core biopsies taken from 131, 59 and 37 patients with histologically diagnosed PCa, BPH, and high-grade PIN, respectively. The horizontal line is the median. Statistical significance was assessed by the Mann-Whitney test.  $p$ -values < 0.05 were considered significant (\*). (\*\*)  $p$ -value < 0.001; (\*\*\*)  $p$ -value < 0.0001.

**Supplementary Figure S3. MS-qPCR validation of differentially methylated regions between BPH and PCa.** DNA (1  $\mu$ g) extracted from 14 BPH samples, 15 cancerous prostate samples with low dysplastic cell content (< 10%), 15 cancerous prostate samples with high dysplastic cell content (30-90%), and 26 adjacent non-cancerous prostate samples was bisulfite-converted and subjected to MS-qPCR. Results are expressed as percentages of the methylation level of fully methylated DNA from an EpiTect PCR Control DNA Set normalized to input DNA. The horizontal line is the median. Statistical significance was assessed by the Mann-Whitney test.  $p$ -values < 0.05 were considered significant (\*). (\*\*)  $p$ -value < 0.001; (\*\*\*)  $p$ -value < 0.0001.

**Supplementary Figure S4. Validation of differentially methylated regions in core biopsies by MS-qPCR.** DNA (1  $\mu$ g) was isolated from core biopsies taken from 131, 59 and 37 patients with histologically diagnosed PCa, BPH, and high-grade PIN, respectively. The horizontal line is the median. Statistical significance was assessed by the Mann-Whitney test.  $p$ -values < 0.05 were considered significant (\*). (\*\*)  $p$ -value < 0.001; (\*\*\*)  $p$ -value < 0.0001.

Figure S1

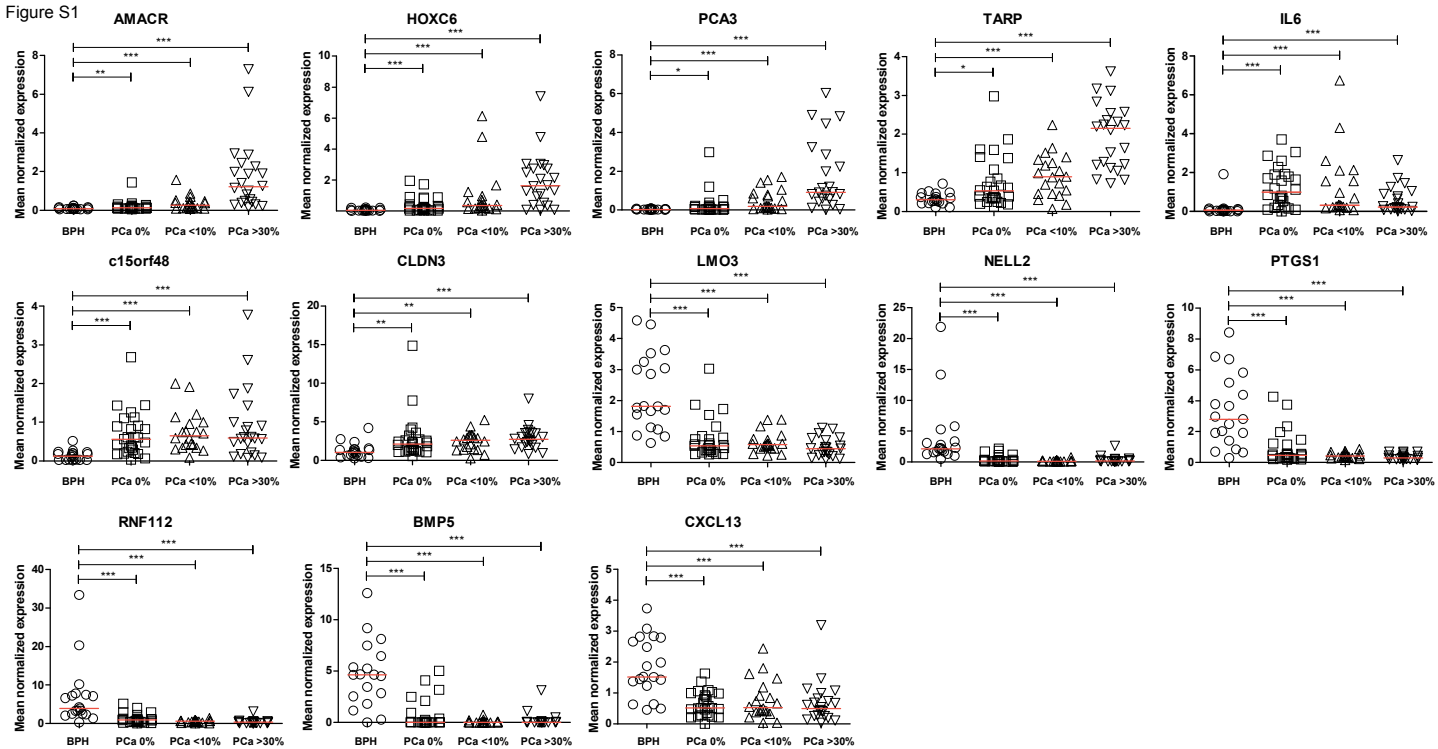


Figure S2

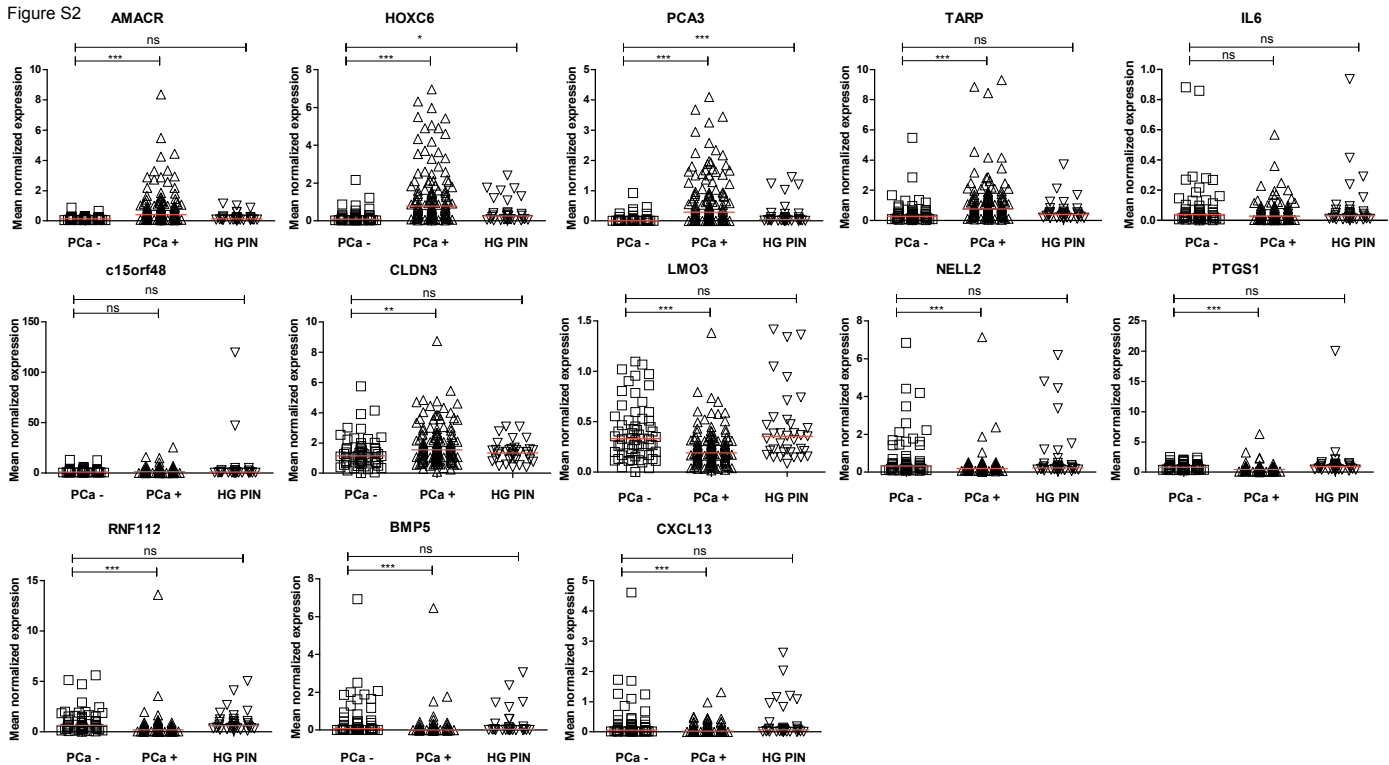


Figure S3

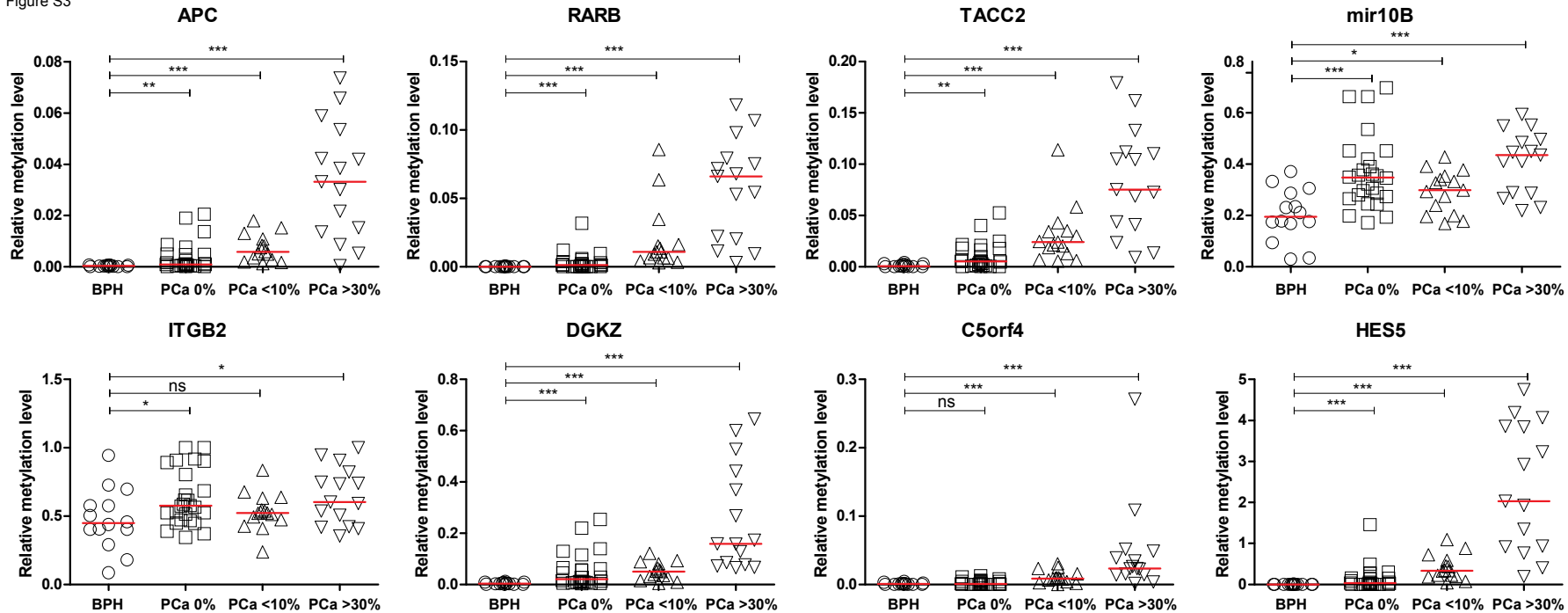


Figure S4

