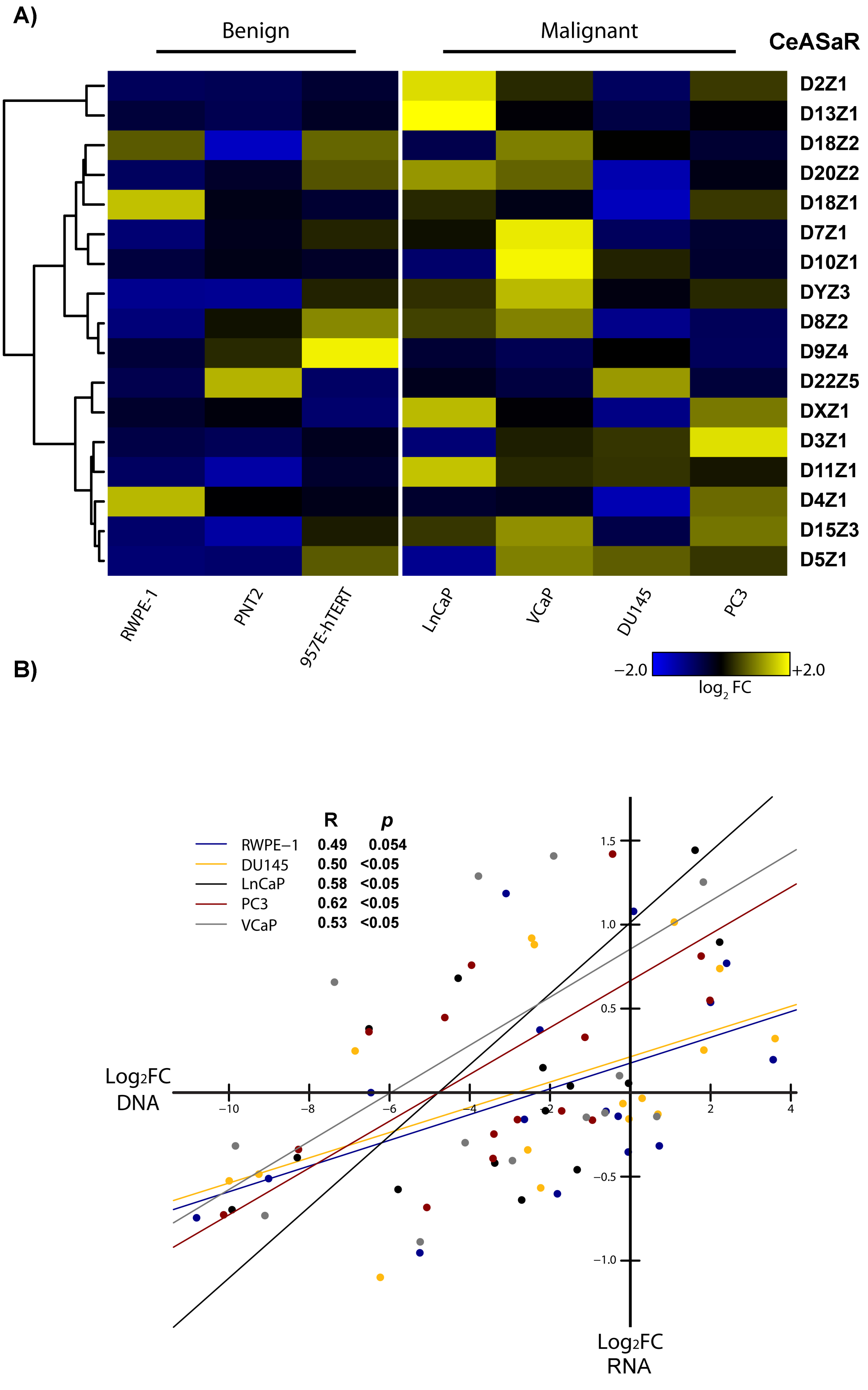
A)
Benign
Malignant
CeASaR
D2Z1
D13Z1
D18Z2
D20Z2
D18Z1
D7Z1
D10Z1
DYZ3
D8Z2
D9Z4
D22Z5
DXZ1
D3Z1
D11Z1
D4Z1
D15Z3
D5Z1
RWPE-1
PNT2
957E-hTERT
LnCaP
VCaP
DU145
PC3
−2.0
+2.0
$\log_2$ FC
B)
R
p
RWPE−1 0.49 0.054
DU145 0.50 <0.05
LnCaP 0.58 <0.05
PC3 0.62 <0.05
VCaP 0.53 <0.05
1.5
1.0
0.5
−0.5
−1.0
−10
−8
−6
−4
−2
2
4
Log2FC DNA
Log2FC RNA

Figure S10. Centromere Transcript Abundance. A) Heat map showing Centromere α-repeat Satellite RNA **(**CeASaR). We quantitated RNA expression in the prostate epithelial cell lines RWPE-1, PNT2, and 957E-hTERT and the prostate cancer cell lines DU145, LnCaP, PC3, and VCaP using the qPCR assays designed in this study, but including an extra RT step. RNA isolated from these cells was treated with DNAse to eliminate DNA contamination. A PCR reaction without the RT step confirmed the elimination of genomic DNA. Quantitative Real-time RT-PCR analysis indicated that specific CeASaRs are transcribed at varying levels. Differences in expression are indicated by log2 values. B) Levels of RNA expression of alpha repeats of centromere arrays generally, but not always, correlate with the genomic size of the arrays. Statistical analysis using the Pearson correlation coefficient indicated that the log2 FC values of array transcript levels correlated with the log2 FC values of genomic alpha repeat content with significant *p* values (left legend). Thus, it would appear that there is differential expression of at least some centromeric sequences.