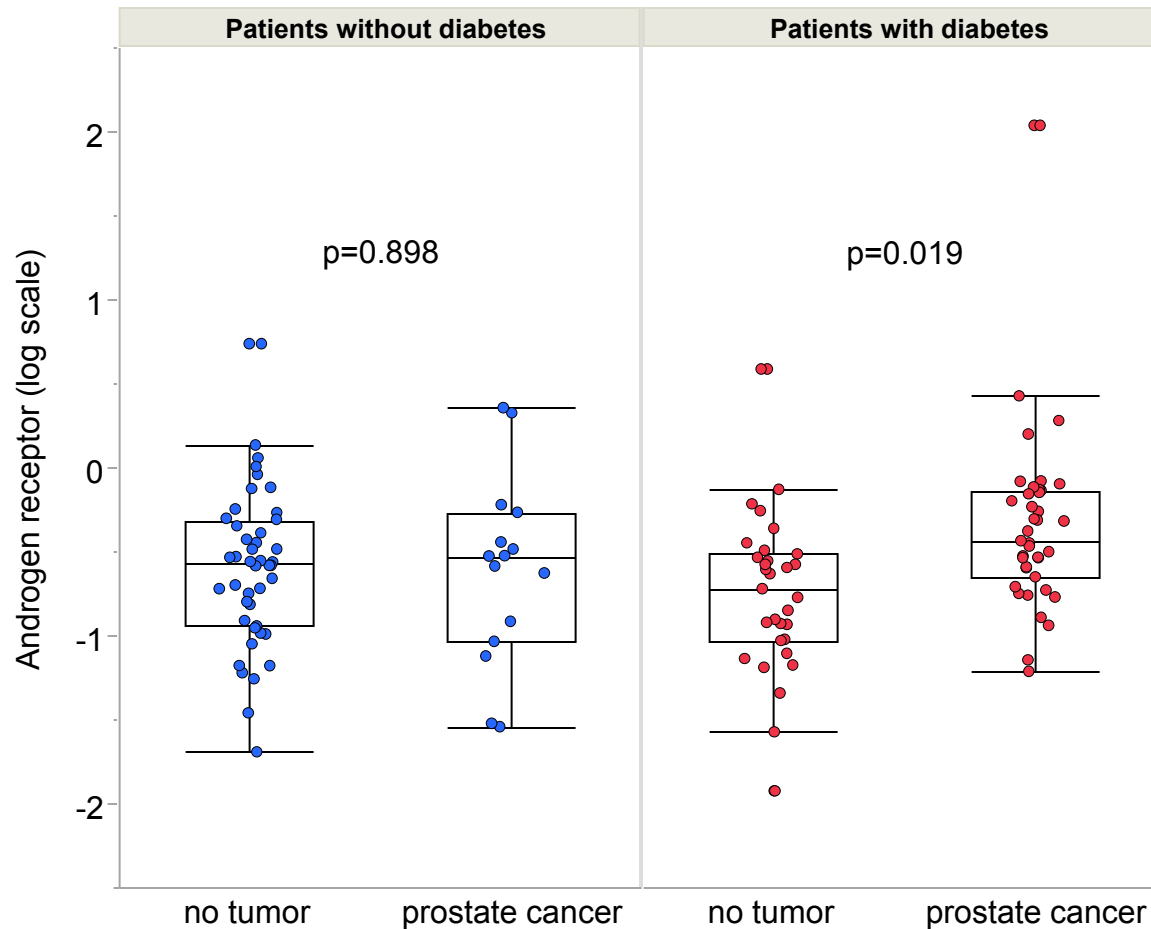
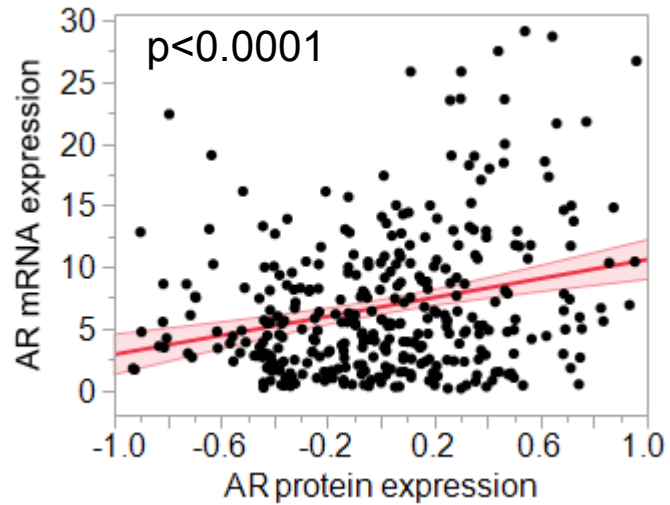


Supplementary figure 1



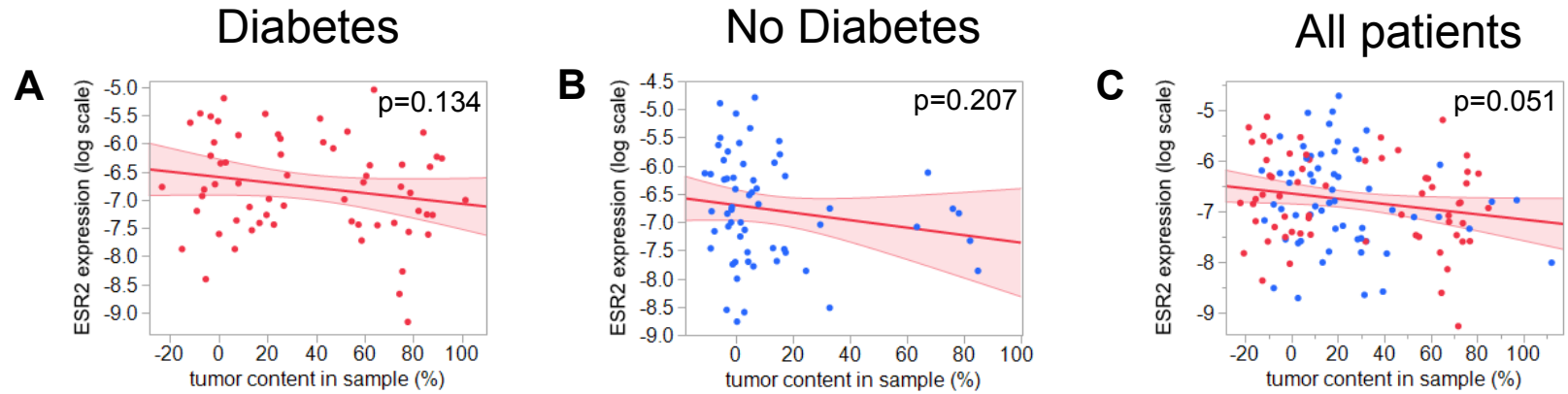
Supplementary figure 1. Androgen receptor gene expression in tumor adjacent benign tissue and prostate cancer in patients without diabetes (left panel) and with diabetes (right panel). In the box plots the box indicates the 25th and 75th percentiles, the horizontal black line is the median and the whiskers show 1.5 x IQR. Groups were compared by multiple linear regression analyses of log-transformed data, adjusting for age and BMI.

Supplementary figure 2



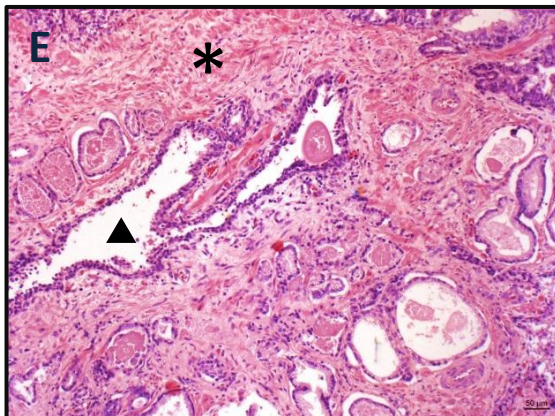
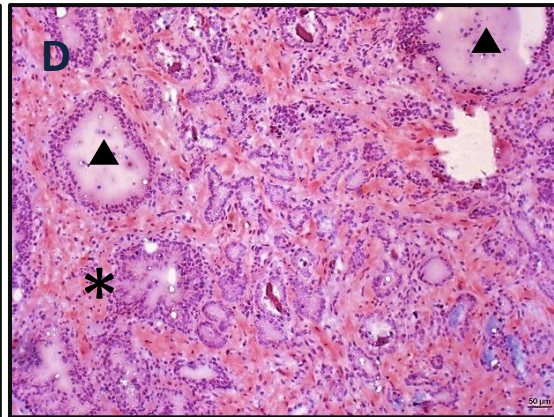
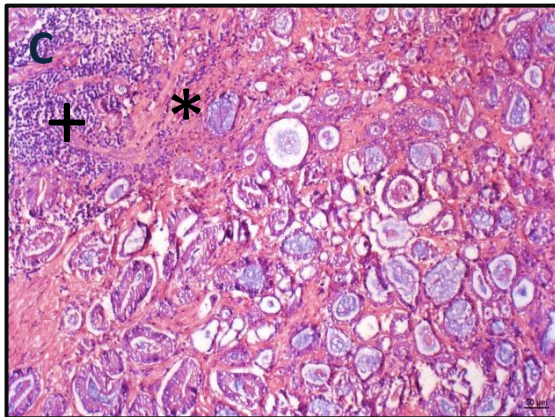
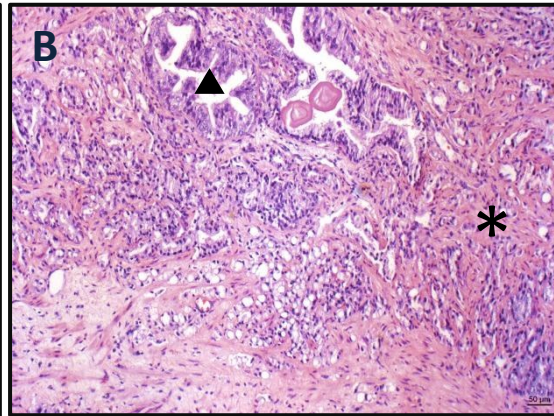
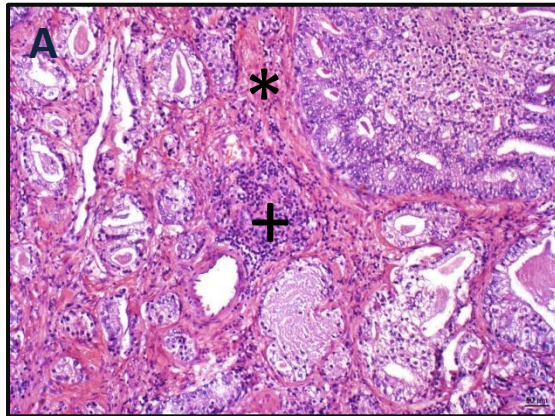
Supplementary figure 2. There is a significant correlation between mRNA and protein expression for the AR in prostate cancer in data from the Cancer Genome Atlas Research Consortium (TCGA).

Supplementary figure 3



Supplementary figure 3. Correlation between the *ESR2* mRNA expression (encoding estrogen receptor beta) and tumor content in sample in diabetes (left panels, red dots), no diabetes (middle panels, blue dots) and all patients combined (right panels). Samples of men with and without type 2 diabetes, who underwent a radical prostatectomy, were included in the study. Tumor content was quantified by an experienced pathologist. mRNA expression of target genes was analyzed by RT-qPCR and normalized to *UBC* mRNA in duplicate. Red line represents fit line \pm 95% CI. Data was log-transformed where indicated and associations were tested by multiple linear regression analyses with adjustment for age and BMI.

Supplementary figure 4



* = fibromuscular stroma

+ = inflammatory cells

▲ = benign prostatic glands

Supplementary figure 4. A-E: Exemplary demonstration of interindividual heterogeneity in prostate cancer histology. All samples from the study collective. A,C and E from patients with diabetes, B and D from patients without. Gleason scores: A 4+4, B 4+5, C and D 3+4, E 3+3. Hematoxylin-Eosin stained slides, 100x Magnification, bar = 50µm.