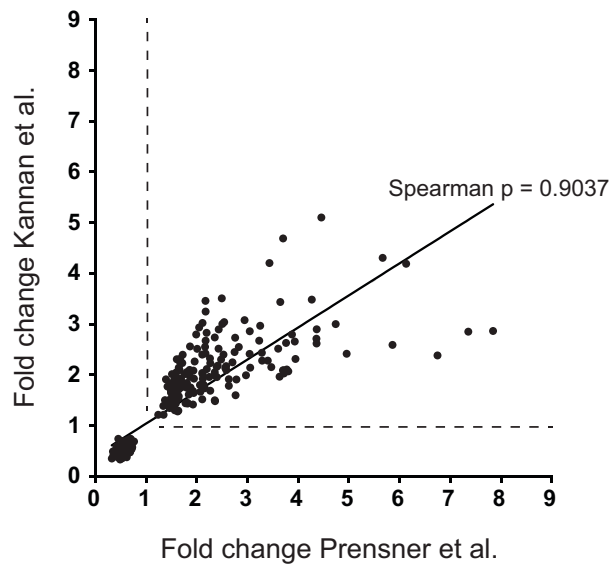
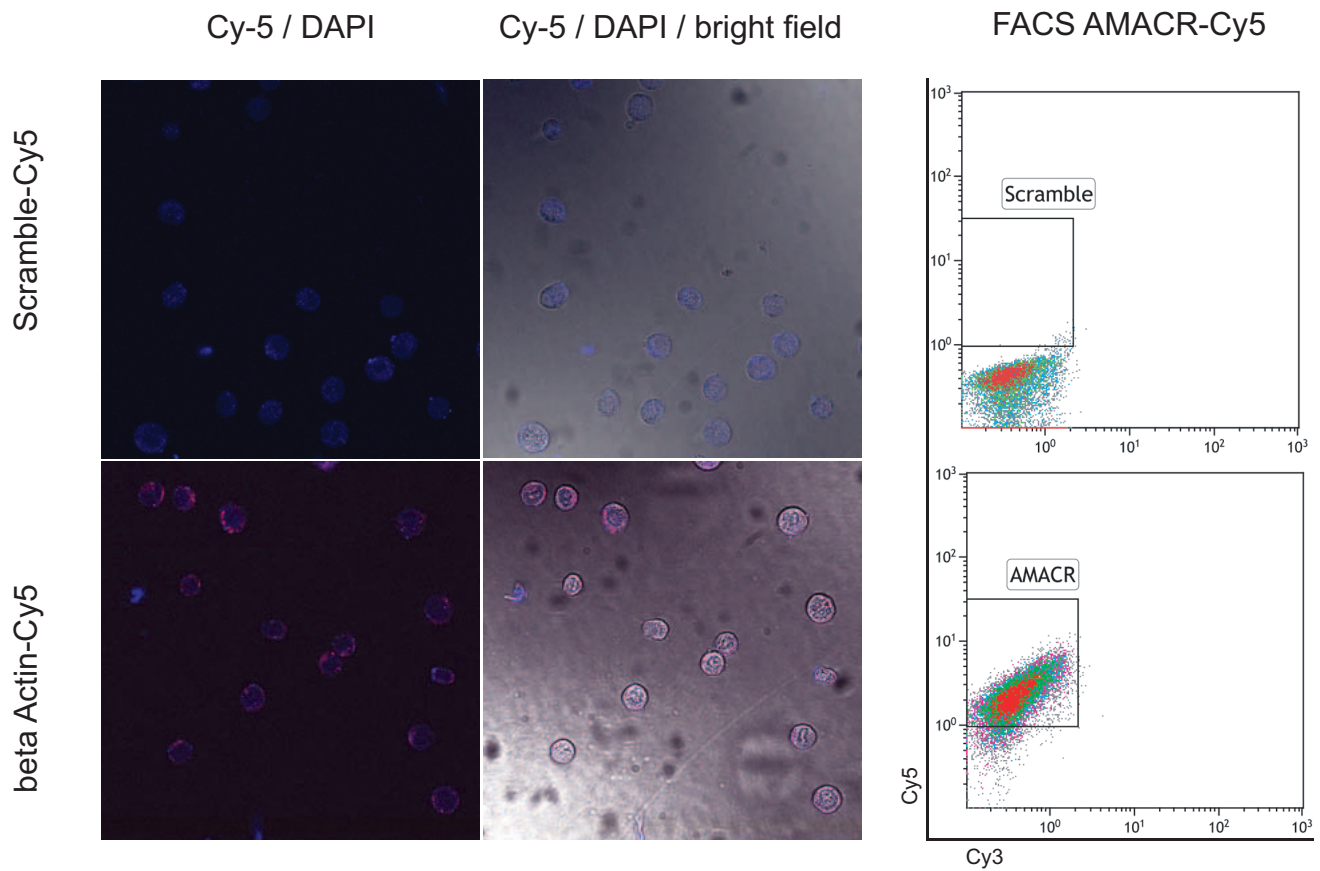


SUPPLEMENTARY FIGURES AND TABLE

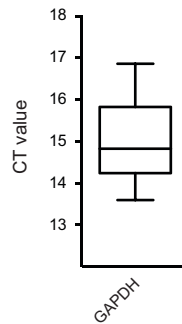


Supplementary Figure S1: Fold changes of the 322 significantly differentially expressed genes at a FDR of 0.1 from the indicated RNA-seq data sets. The change in gene expression strongly correlates (Spearman's correlation coefficient $\rho = 0.9037$).



Supplementary Figure S2: Intracellular uptake of beta Actin SmartFlare in LNCAP cells. Upper panel: scramble-Cy5 control, lower panel: beta Actin-Cy5, left panel: Cy5/ DAPI overlay, right panel: Cy5/DAPI and bright field overlay. Signal is only detected within the cellular borders determined in bright field; confocal microscopy, bar = 50µm.

single cell (LNCAP)



Supplementary Figure S3: Single cell gene expression analysis for GAPDH of 23 LNCAP cells shows strong variation between cells.

Supplementary Table S4: Cellular distribution of CD45 positive lymphocytes, CD45/Epcam-Stromal cells and Epcam + epithelial cells in examined needle biopsies. Cell types were gated from living cells. AMACR high and low expressing cells were gated from epithelial cells. Cell type “other” did not show conclusive marker expression of either of the above groups.

Cell type distribution in biopsy samples

Figure 3	% of living cells			
	Biopsy			
Lymphocytes	9,0			
Stromal cells	30,45			
Epithelial cells	17,30			
Other	43,25			
	% of epithelial cells			
AMACR high	22,34			
AMACR low	21,28			
Figure 4	% of living cells			
	Biopsy R1	Biopsy R2	Biopsy L1	Biopsy L2
Lymphocytes	1,08	0,0	0,0	2,48
Stromal cells	17,63	14,79	14,36	12,16
Epithelial cells	56,14	53,33	53,46	55,15
Other	25,15	31,88	32,18	30,21
	% of epithelial cells			
AMACR high	16,78	26,69	30,03	21,77
AMACR low	37,19	24,96	18,18	28,23