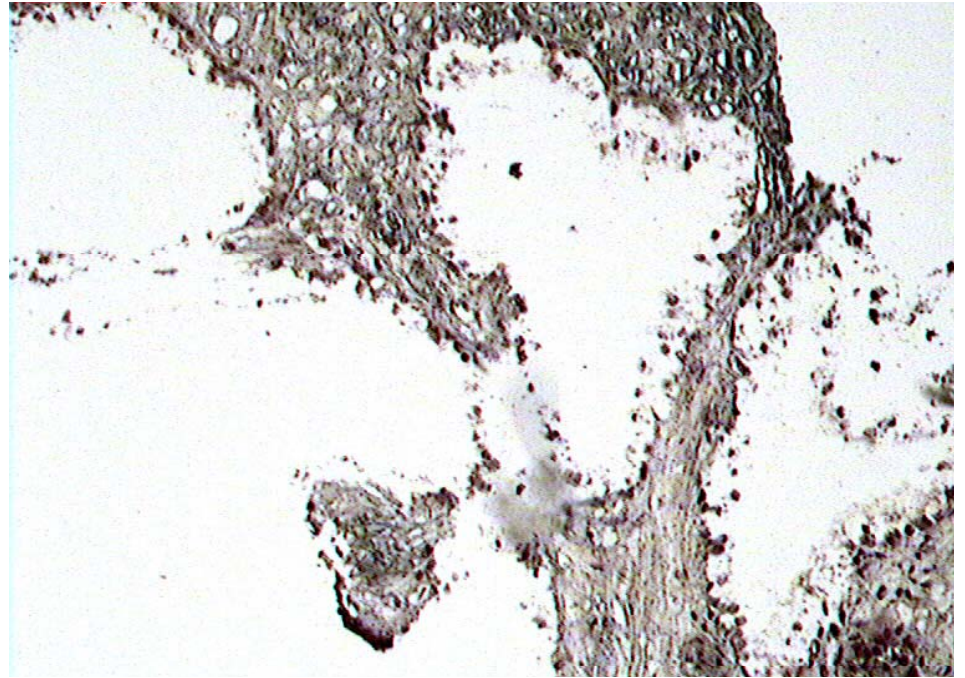
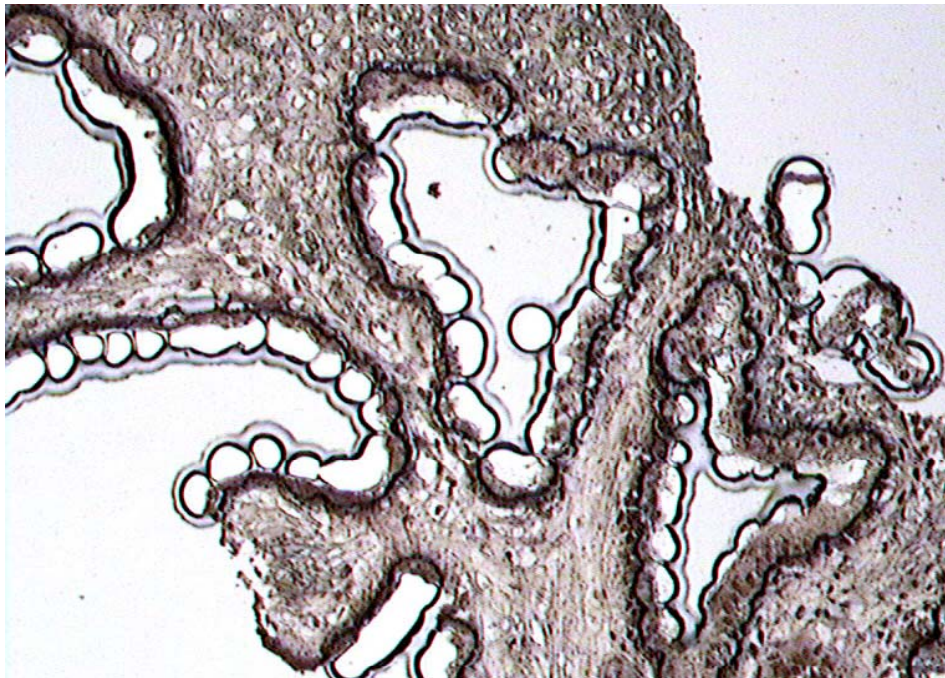


Supplemental Figure 1

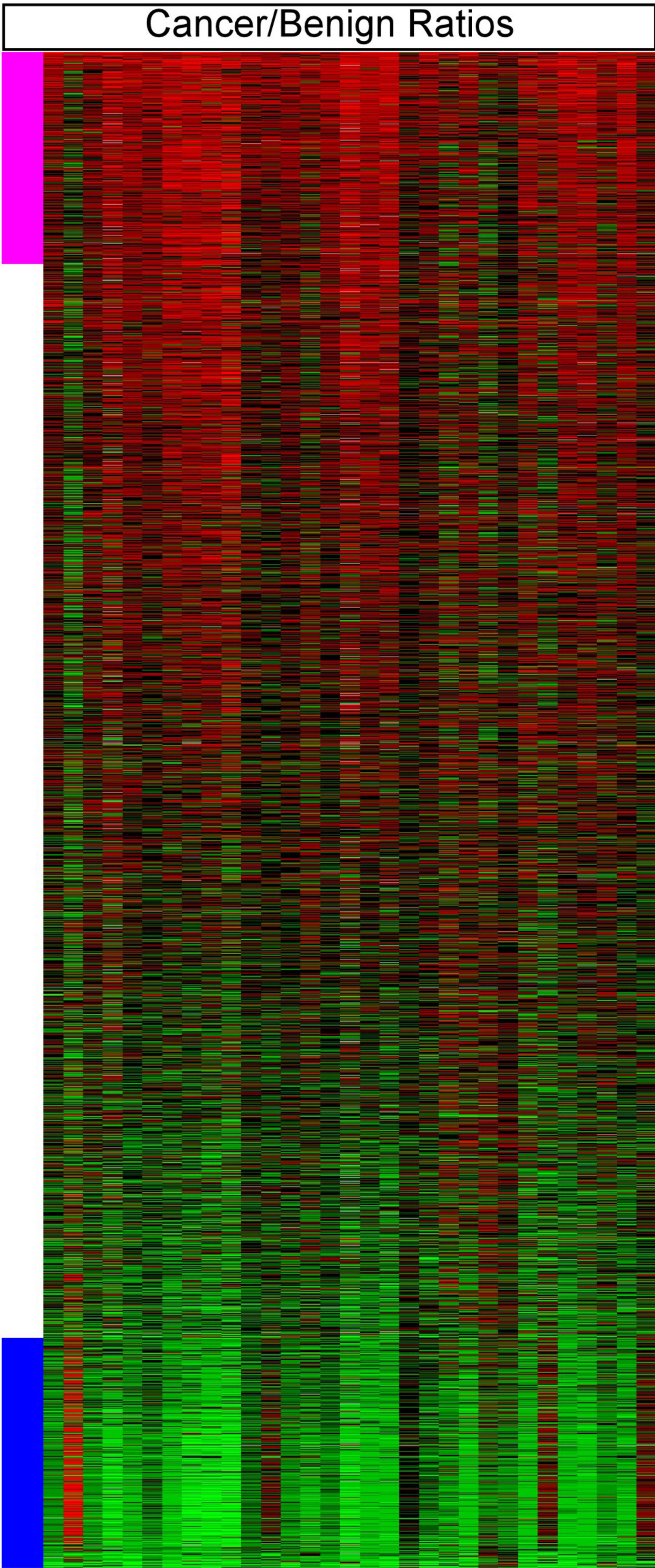


Supplemental Figure 2

Cancer/Benign Ratios

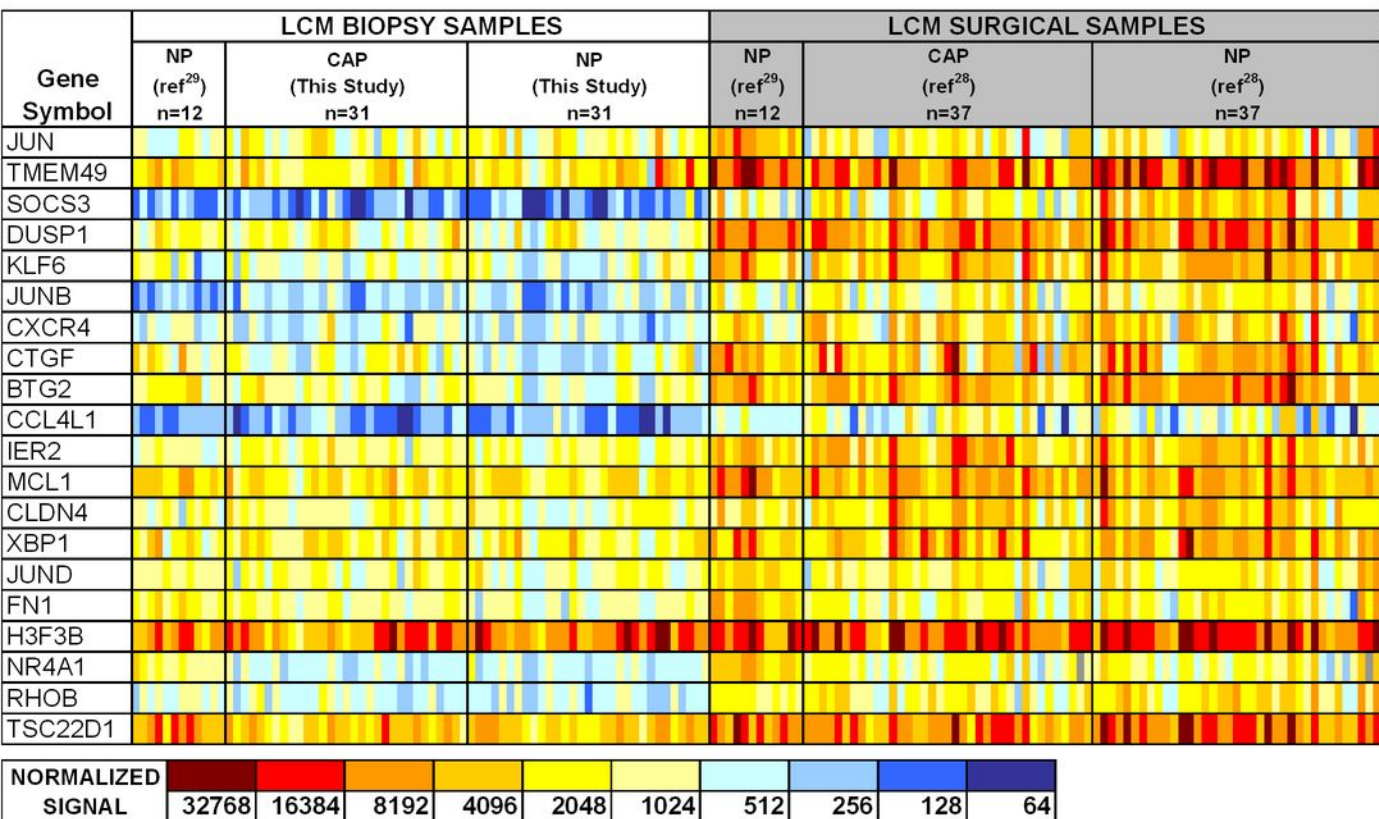
457 genes
up-regulated
q-value <0.01%

497 genes
down-regulated
q-value <0.01%



Supplemental Figure 3

A.



B.

		BIOPSY			SURGERY		
		NP (ref ²⁹) n=12	CAP (This Study) n=31	NP (This Study) n=31	NP (ref ²⁹) n=12	CAP (ref ²⁸) n=37	NP (ref ²⁸) n=37
BIOPSY	NP (ref ²⁹) n=12		7.16E-01	5.41E-01	2.73E-04	1.56E-03	2.67E-04
	CAP (This Study) n=31	7.16E-01		7.82E-01	4.63E-05	2.66E-04	4.28E-05
	NP (This Study) n=31	5.41E-01	7.82E-01		3.79E-05	2.07E-04	3.55E-05
SURGERY	NP (ref ²⁹) n=12	2.73E-04	4.63E-05	3.79E-05		3.57E-01	9.32E-01
	CAP (ref ²⁸) n=37	1.56E-03	2.66E-04	2.07E-04	3.57E-01		3.92E-01
	NP (ref ²⁸) n=37	2.67E-04	4.28E-05	3.55E-05	9.32E-01	3.92E-01	

Supplemental Figure 4

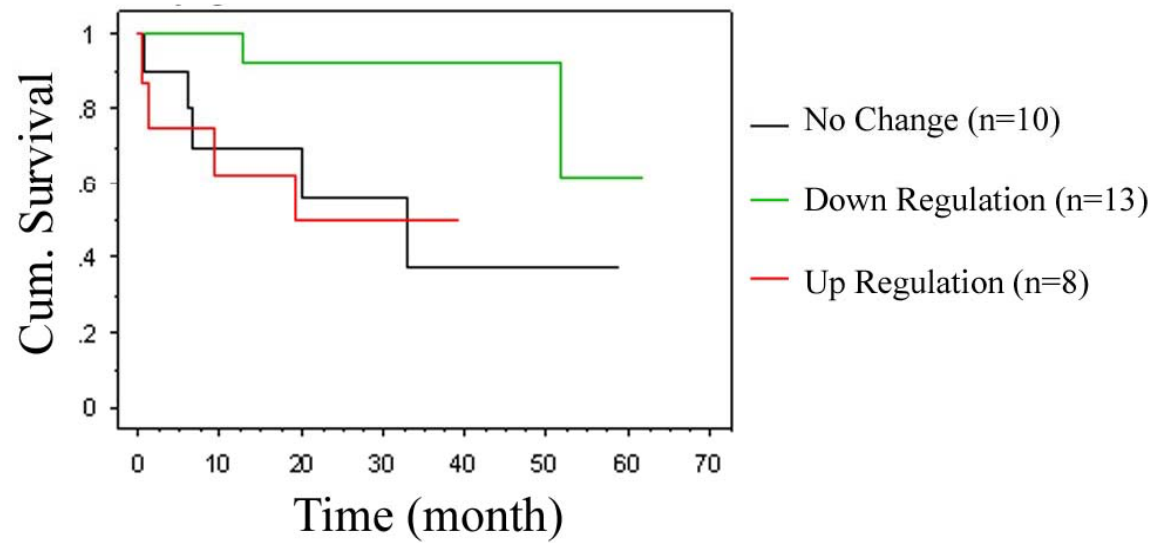


Figure Legends

Supplemental Figure 1. Frozen section of prostate needle biopsy after laser pulsing of benign luminal epithelial cells before (a) and after (b) removal of the cells from the section for RNA extraction. The refractile circles (a) show the sites that the 5 micron diameter laser beam targeted the cells.

Supplemental Figure 2. cDNA microarray gene expression analysis from prostate needle biopsies. Normal and neoplastic epithelium was microdissected individually from needle core biopsies from 31 patients. Following 2 rounds of linear amplification, transcript levels were measured by microarray hybridization. A total of 5910 genes were tested. The heatmap of differentially expressed genes (cancer *vs.* benign) is shown. 457 genes were upregulated, and 497 genes were downregulated, q -values $< 0.01\%$. Red: upregulated in tumor; Green: downregulated in tumor. Row: genes; Column: patients.

Supplemental Figure 3. Comparison of expression levels of ischemia-associated genes identified in Lin, et al. (29) in biopsy and surgical samples. A. Heatmap of expression levels of samples from three different studies. Expression levels are denoted by colors corresponding to signal intensity. Most genes are consistently upregulated in radical prostatectomy samples relative to needle biopsy samples. B. T-tests between groups demonstrate insignificant differences overall comparing only needle biopsy samples, or only surgical samples, and significant differences between needle biopsy samples and surgical samples.

Supplemental Figure 4. The correlation between each patient's pretreatment androgen receptor (AR) mRNA and his biochemical relapse (serum PSA) was analyzed by Kaplan-Meier Plot. No change: there was not any difference in AR mRNA level between benign and cancer epithelium. Downregulation: the patient's benign AR mRNA was 2 fold less than cancer AR. Upregulation: the patient's benign AR mRNA was 2 fold more than cancer AR. X-axis: time to biochemical relapse, Y-axis: % of relapse free survival.

Supplementary Table S1. Patient characteristics prior to therapy

Number	57
Age	
Median	63
Range	49-74
ECOG PS	
0	52
1	3
PSA	
Median	12.2
Range	1.4-58.6
Clinical Stage (AJCC 2002 criteria)	
T1c	7
T2a	7
T2b	10
T2c	19
T3a	11
T3b	2
T4	1
Biopsy Gleason Score	
6	5
7	22
8	17
9	12
10	1

Supplementary Table S2. Clinical data characteristics of patient samples on microarrays (n=31)

ID	Age	Clinical Stage	Surgical margin status	Nodal status at surgery	Gleason Sum Score			Censored for progression (PSA > 0.4)	Time (months) to progression (PSA > 0.4)
					Biopsy	Surgical	LCM		
6082-02	62	T2b	Negative	Positive	8	9	4+4	0	6.8
6082-03	66	T3a	Negative	Positive	7	7	3+3	0	15.4
6082-04	69	T3a	Positive	Negative	6	7	3+3	1	39.2
6082-07	69	T3a	Negative	Negative	7	7	3+4	1	35.5
6082-08	59	T2c	Negative	Negative	7	6	3+3	1	38.8
6082-10	66	T1c	Negative	Negative	8	6	3+3	1	36.0
6082-13	74	T2b	Negative	Negative	8	8	3+3	0	13.6
6082-14	72	T2a	Negative	Negative	9	8	4+3	1	32.5
6082-15	52	T2a	Positive	Negative	6	7	3+3	1	16.6
6082-16	65	T2a	Negative	Negative	8	7	3+4	1	30.0
6082-19	52	T3a	Negative	Negative	7	7	3+3	1	24.1
6082-22	59	T3a	Negative	Negative	7	7	3+3	1	24.1
6082-23	56	T3a	Negative	Negative	7	8	3+3	1	22.9
6082-24	69	T2a	Positive	Negative	8	8	4+4	1	23.5
6082-25	63	T1c	Negative	Negative	9	7	3+3	0	6.4
6082-28	63	T2b	Positive	Negative	9	7	3+4	1	23.2
6082-31	57	T2c	Negative	Negative	7	7	3+3	1	19.7
6082-32	65	T2c	Negative	Negative	8	6	3+3	1	11.6
6082-34	66	T2c	Negative	Negative	9	9	4+4	0	0.7
6082-36	63	T2c	Positive	Positive	8	9	3+4	1	6.3
KP-01	56	T2c	Negative	Negative	7	6	4+4	1	13.0
KP-02	62	T3b	Negative	Negative	7	7	4+4	1	6.4
KP-03	56	T2b	Negative	Negative	7	7	3+3	1	7.5
KP-04	71	T1c	Positive	Negative	7	7	3+3	1	4.8
KP-05	68	T2b	Positive	Negative	10	10	4+5	1	2.8
UW-01	60	T2c	Positive	Positive	7	7	4+4	0	1.4
UW-03	54	T2c	Positive	Positive	9	9	4+4	0	0.6
UW-05	64	T2c	Negative	Negative	8	7	4+3	1	20.1
UW-09	59	T3b	Negative	Positive	7	NA	4+4	0	10.1
UW-10	58	T2b	Negative	Negative	7	8	3+4	1	10.4
UW-11	63	T2c	Negative	Negative	7	8	3+3	1	9.8

Supplementary Table S3. Comparison of gene expression changes differentiating neoplastic from normal prostate epithelium across four different microarray data sets.

This Study*	True et al, ²⁸ 2006	Lapointe et al, ¹⁵ 2004	Glinsky et al, ^y 2004
top 1% (21 genes)	top 1% 10 (48%)	top 1% 7 (33%)	top 1% 4 (19%)
	top 5% 17 (81%)	top 5% 12 (57%)	top 5% 10 (48%)
	top 10% 19 (90%)	top 10% 15 (71%)	top 10% 13 (62%)
top 5% (107 genes)	top 1% 13 (12%)	top 1% 9 (8%)	top 1% 8 (7%)
	top 5% 36 (34%)	top 5% 23 (21%)	top 5% 19 (18%)
	top 10% 57 (53%)	top 10% 35 (33%)	top 10% 34 (32%)
top 10% (214 genes)	top 1% 14 (7%)	top 1% 14 (7%)	top 1% 8 (4%)
	top 5% 50 (23%)	top 5% 36 (17%)	top 5% 29 (14%)
	top 10% 81 (38%)	top 10% 56 (26%)	top 10% 54 (25%)

*Top unique genes (among the 2140 common to all four datasets) identified in this study between normal epithelium and cancer as ranked by SAM t-test score(d).