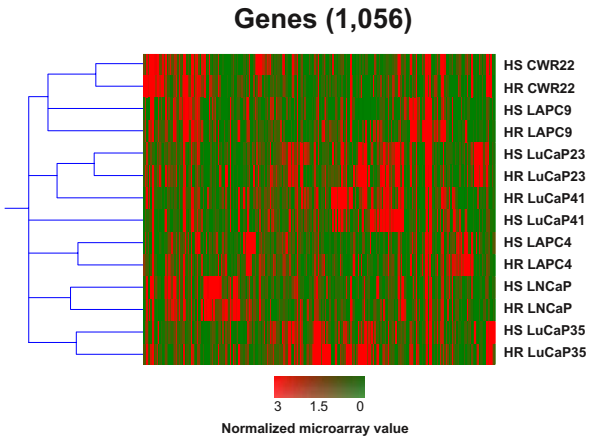
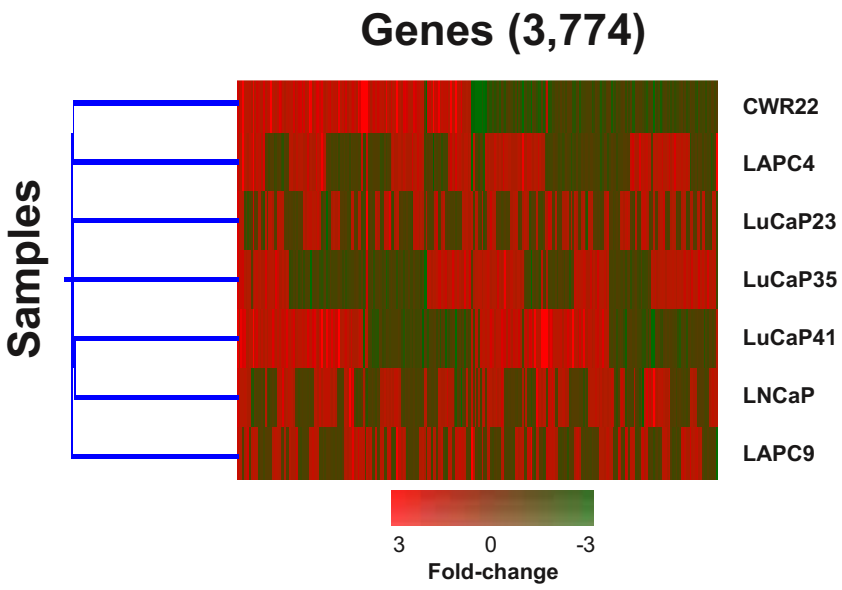
Supplementary Figure 1

a



Supplementary Figure 1

b



Supplementary Figure 1

c

Gene Name (Acc. No.)	CWR22	LuCaP23	LuCaP35	LuCaP41	LNCaP	LAPC4	LAPC9	Score
Androgen receptor (M23263)	2.5 (I)	3.1 (I)	3.1 (I)	3.6 (I)	2.7 (I)	2.3 (I)	2.2 (I)	7.0
Androgen receptor (M23263)	2.0 (I)	3.1 (I)	2.7 (I)	6.0 (I)	2.0 (I)	1.3 (NC)	1.4 (NC)	5.0
Carbonic anhydrase precursor (AF037335)	1.8 (I)	1.4 (NC)	-1.2 (NC)	4.7 (I)	3.7 (I)	1.1 (NC)	1.5 (I)	4.0
Elongation factor 1 alpha-2 (X70940)	-1.1 (I)	-1.2 (NC)	1.7 (I)	1.1 (I)	1.0 (NC)	1.3 (I)	-1.3 (NC)	4.0
HLA class I locus C heavy chain (X58536)	1.9 (I)	1.1 (NC)	1.1 (NC)	2.5 (I)	1.7 (I)	1.1 (NC)	4.4 (I)	4.0
Platelet-type Phosphofructokinase (D25328)	-3.3 (MD)	-1.8 (D)	-2.7 (D)	-2.4 (D)	-2.2 (D)	1.7 (NC)	1.2 (NC)	-4.5
Secreted cement gland Protein XAG-2 homolog (AF038451)	-10.7 (D)	-1.7 (D)	1.7 (NC)	-2.0 (D)	-2.5 (D)	-3.2 (D)	1.9 (I)	-4.0
Slow MyBP-C (X73114)	-4.1 (D)	-3.8 (D)	-1.5 (NC)	-3.7 (D)	-1.2 (NC)	-1.8 (D)	-1.2 (NC)	-4.0

Supplementary Fig. 1 – Expression profiling of seven hormone sensitive/hormone refractory xenografts (**a)** Seven 0.5 cm^3 tumors from each xenograft, grown in either intact (hormone sensitive) or castrated (hormone refractory) mice, were pooled and total RNA was extracted to generate a single sample. After processing, the cRNA was hybridized to the Affymetrix U95A chip and the microarray data was analyzed by Microarray Suite. Background elements which did not significantly vary (standard deviation < 1000 and coefficient of variation < 1) or were not detected in any of the samples (defined as perfect match hybridization not significantly different than mismatch control signal intensity) were filtered out. The remaining elements, representing 1,056 genes, were then used by an unsupervised learning algorithm to generate a hierarchical clustering diagram. (**b)** The microarray data, obtained as described in **a**, was reanalyzed using Microarray Suite whereby each pair was condensed into a single dataset that represents the ratio in expression between each hormone sensitive xenograft and its hormone refractory counterpart. In addition, using a number of parameters as defined by Microarray Suite software such as fold-change, absolute signal intensity and the confidence in each probe set given by perfect match/mismatch ratios, elements from the condensed dataset were assigned an independent designation of increase (I), marginal increase (MI), no change (NC), marginal decrease (MD) or decrease (D). Elements assessed as NC in all of the xenograft pairs were filtered out to generate a list of 3,774 genes that was then used by an unsupervised learning algorithm to generate a hierarchical clustering diagram. (**c)** Each of the designations described in **b** was assigned a value ranging from +1 (I) to -1 (D) and a score for each element was produced by summing the values across each of the seven hormone sensitive/hormone refractory xenograft pairs. Elements with the highest absolute scores are shown.