



Legend supplementary Figure 1:

Top:

Venn Mapping of the merged prostate/breast data sets: Hierarchical clustering of the z -value profiles. **a**, dendograms indicating similar clusters. **b**, clinical parameters. column **B**: Breast cancer data set: black indicates ER positive and grey ER negative tumours. column **P**: Prostate cancer data set: light grey indicates normal (NAP/BPH), dark grey prostate tumour (PCA) and black indicates metastatic prostate sample (MET). The coloured column **R**: indicates whether the genes are up (yellow) or down (blue) as compared to the reference in the particular array.

c, z -value profiles. Each row and column represents a microarray experiment. Similarity is determined by calculating the z -value for the number of commonly shared, differentially expressed genes in any of two microarray experiments. Cut-off value for fold differential gene expression was set at 2. Distinction is made between more (red colour) or less (green colour) than the expected number of overlapping genes. Data is shown with z -value > 2.58 (p -value < 0.01), black indicates a z -value ≤ 2.58 (p -value ≥ 0.01).

Left:

Hierarchical tree after standard expression ratio clustering of the merged prostate/breast data sets. Clinical parameters are depicted in columns B and P and are similarly coded as the top panel.