

Supplementary Figure S1.

Electropherogram obtained from the Agilent Bioanalyzer showing the integrity of a representative RNA sample extracted from soft bone metastatic sample. A RIN number here indicates the RNA integrity with a value of 10 being the most intact and a value of 4 being acceptable.

Supplementary Figure S2.

Validation of the microarray analysis using quantitative PCR analysis for the genes upregulated in the soft bone metastatic samples. Each transcript was normalized to the level of GAPDH in the sample. All the samples were compared to the level of the respective transcript in the prostate pool obtained from Clontech (CPP).

Supplementary Table S1.

672 differentially expressed genes in the bone metastatic samples compared to the matched soft tissues samples. A two fold increase in the level of the transcript across the 5 matched samples analyzed was considered as upregulated and a ratio of 0.5 was considered as down regulated.

Supplementary Table S2.

Primer sequences used for quantitative PCR analysis.