

Figure S1 Comparison of *SPARC* and *SPP1* expression data obtained from real-time RT-PCR and microarray experiments.

Gene expression in RT-PCR experiments was normalized to the expression level of *PPIA* (cyclophilin A) in the sample and centralized by subtracting median expression value across samples. Gene expression data from microarray were also centralized by subtracting median expression value across samples.

(A) Scatter plots of normalized *SPARC* expression levels between two experiments from 24 EAC tissues. Pearson correlation coefficient between two experiments and significance of correlation coefficient is indicated at the top of plots.

(B) Scatter plots of normalized *SPP1* expression levels between two experiments from 24 EAC tissues.