A MDACC PCR Data

B Landi Microarry Data

Figure S10. Scatter plots showing the correlations of NR gene expression between tumor and adjacent normal samples taken from either the MDACC (A) or Landi et al. (B) datasets.
The x- and y-axes represent the log2 transformed expression values for normal and tumor samples, respectively. The figures show that the NR expression in tumor samples is significantly correlated with that in the adjacent normal tissue. Pearson correlations were 0.87 ($P < 0.001$) for the MDACC dataset and 0.92 ($P < 0.001$) for the Landi et al. dataset (28).