Figure S3: Quantitative real-time RT-PCR verification of RAI2 expression and Correlative analysis of RAI2 mRNA expression in primary breast tumors

(A) Quantitative real-time RT-PCR verification of RAI2 expression. Quantitative analysis of RAI2 transcript expression in an independent set of primary breast tumors with known DTC status by quantitative RT-PCR. Box plots show the median fold change in RAI2 transcript expression normalized to RPLP0 and UHR in the two groups. P-value is calculated by two-sided student’s t-test (*, p<0.05). (B) Correlative analysis of RAI2 mRNA expression in primary breast tumors. RAI2 expression was determined in one large published expression data set (Curtis et al., Breast #6) and correlated to the indicated clinico-pathological parameters.