SUPPLEMENTAL FIGURE AND TABLE LEGENDS

Supplemental Figure 1. Pharmacokinetic evaluation of paclitaxel delivery. Paclitaxel drug concentrations were measured by mass spectroscopy and samplings of MMTV-Neu tumors and plasma. The results show significant systemic delivery of this drug when administered using intraperitoneal injections, both in the tumor and in the plasma.

Supplemental Figure 2. Hierarchical clustering analysis of the untreated and responding murine chemotherapy signature using 337 human breast tumors. A) The 348 genes highly expressed in untreated C3(1)-T-antigen tumors versus carboplatin/paclitaxel treated tumors was used to cluster the human breast tumor data set from Prat et al. 2010. B) The highlighted dendrogram node identifies the 30 genes that were selected for additional analyses, for which 26 orthologs were found in the other human data sets (missing genes are identified by underlining) and used to evaluate correlations with pathological complete response. C) The 74 genes highly expressed in those C3(1)-T-antigen tumors that responded to carboplatin/paclitaxel treatment versus those tumors that did not respond was used to cluster the human breast tumor data set from Prat et al. 2010. D) The highlighted dendrogram node identifies the 12 genes that were selected for additional analyses and were used to evaluate correlations with pathological complete response on other data sets.

Supplemental Figure 3. Kaplan-Meier analyses for the prediction of Distant Relapse Free Survival. Using the Hatzis et al. data set, Kaplan-Meier plots were performed for A) pCR vs. residual disease (RD), B) the five PAM50-defined intrinsic subtypes, C) pCR vs. RD within just Basal-like subtype patients, D) high versus low expression of the RESP-HUM 12-gene signature, E) high versus low expression of the UNTREATED-HUM 26-gene signature, and F) high versus low expression of an 11-gene proliferation signature taken from Nielsen et al. 2010.

Supplemental Table 1. List of mouse C3(1)-T-antigen gene expression microarrays used to derive the murine gene lists.
Supplemental Table 2.  A) UNTREATED gene list obtained from a Significance Analysis of Microarray (SAM) study of untreated (n=7) versus carboplatin/paclitaxel treated (n=12) mouse C3(1)-T-antigen tumors using a 1% FDR.  B) RESP-HIGH gene list obtained from a SAM study of carboplatin/paclitaxel treated non-responder (n=9) versus responder (n=3) mouse C3(1)-T-antigen tumors using a 1% FDR.

Supplemental Table 3. Modules/expression signatures analysis of carboplatin/paclitaxel treated C3(1)-T-antigen mouse tumors. A collection of 302 gene expression modules/signatures were tested for differences in expression on the treated versus untreated C3(1)-T-antigen tumors. The ANOVA p-value and multiple-hypothesis corrected p-values are shown, as is the publication for the initial description of each signature. The “direction” shows in which class the signature was highest.

Supplemental Table 4. Univariate and Multivariate Analysis for pCR using clinical and genomic features including the UNTREATED-HUM and RESP-HUM signatures on the Miyake et al. data set. Univariate and multivariate analyses were performed using the clinically HER2-normal subset of patients sets taken from Miyake et al. 2012.

Supplemental Table 5. Summary of drugs used in this study, their doses, and utilized schedules of administration.