Supplemental figure S1 Generation of gene expression profile for Her2+/TN phenotype in the training cohort (n=149). (A). First screening of Her2+/TN related genes. 44 Her2+/TN breast cancers were used as the group to distinguish the gene expression from the other 105 tumors. 1428 probes were selected at a level of the Bonferroni corrected P value less than 0.01. By using the 1428-probe set in a hierarchical clustering pattern, 39 tumors that were mostly Her2+/TN formed group 3 with two other subgroups emerging on the heat map, groups 1 and 2. (B) Second screening for the most differentially expressed genes between the three groups. By ANOVA test, 1349 probes were selected at a level of P value less than 0.001 among the three groups. A three-cluster pattern was apparent on the heat map based on hierarchical clustering analysis using the 1349-probe set. The tumors with Her2+/TN status were 2.4% (1/42) in group 1, 10.3% (7/68) in group 2 and 92.3% (36/39) in group 3. The bottom color bars: deep pink, Her2+; blue, TN.