

Supplemental Figure 2. Higher AURKA expression observed even in low-amplification tumors in TCGA

Breast tumor from the TCGA dataset were stratified based on the genomic AURKA copy number (low amplification – left, no amplification – right; high amplification excluded) and plotted against AURKA RNA expression. Higher AURKA RNA expression was observed in low AURKA-amplification compared to non-amplified tumors in these TCGA samples.