

Figure S2

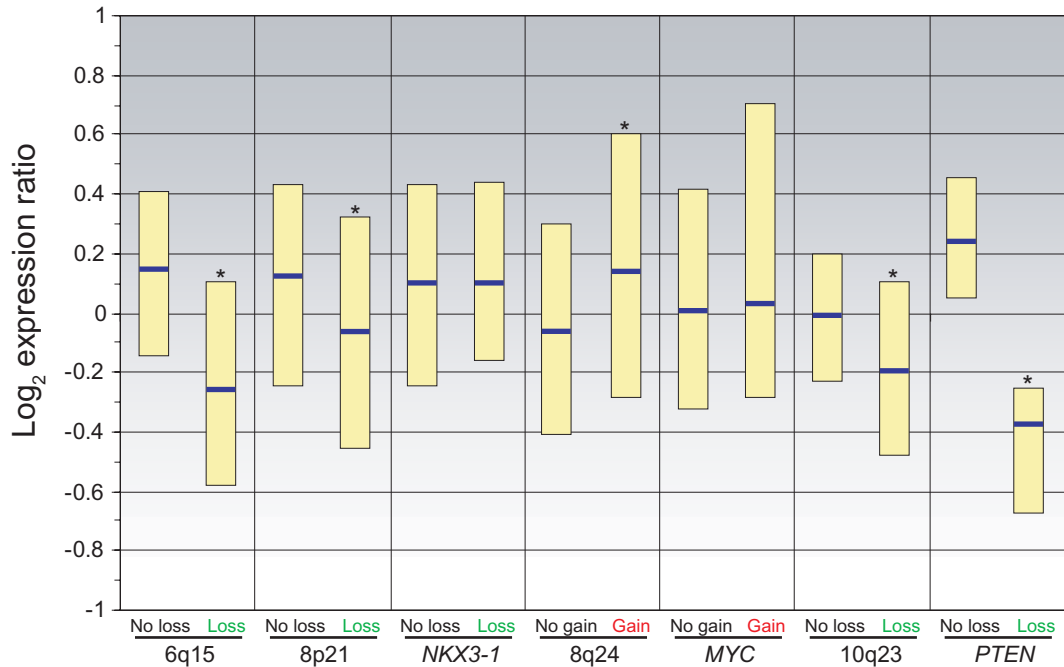


Figure S2. Impact of CNAs on gene expression. Box plots display 25th, 50th (median) and 75th percentiles of gene-expression (log₂ ratio) for genes within selected cytobands or for selected genes, for the 64 prostate tumor samples stratified by CNA (change vs. no change, as indicated). Number of genes within cytobands are 23 (6q15), 69 (8p21), 145 (8q24), and 69 (10q23). * indicates P<0.001 (Student's t-test). Findings indicate a general concordance between CNA and gene expression, as previously documented in breast cancer (1).

REFERENCES

1. Pollack, J. R., Sorlie, T., Perou, C. M., Rees, C. A., Jeffrey, S. S., Lonning, P. E., Tibshirani, R., Botstein, D., Borresen-Dale, A. L., and Brown, P. O. Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. *Proc Natl Acad Sci U S A*, 99: 12963-12968, 2002.