Many cancer-associated somatic copy number alterations (SCNAs) are known. Currently, one of the challenges is to identify the molecular downstream effects of these variants. Although several SCNAs are known to change gene expression levels, it is not clear whether each individual SCNA affects gene expression. We reanalyzed 77,840 expression profiles and observed a limited set of 'transcriptional components' that describe well-known biology, explain the vast majority of variation in gene expression and enable us to predict the biological function of genes. On correcting expression profiles for these components, we observed that the residual expression levels (in 'functional genomic mRNA' profiling) correlated strongly with copy number. DNA copy number correlated positively with expression levels for 99% of all abundantly expressed human genes, indicating global gene dosage sensitivity. By applying this method to 16,172 patient-derived tumor samples, we replicated many loci with aberrant copy numbers and identified recurrently disrupted genes in genomically unstable cancers.