Functional regulations between genetic alteration-driven genes and drug target genes acting as prognostic biomarkers in breast cancer

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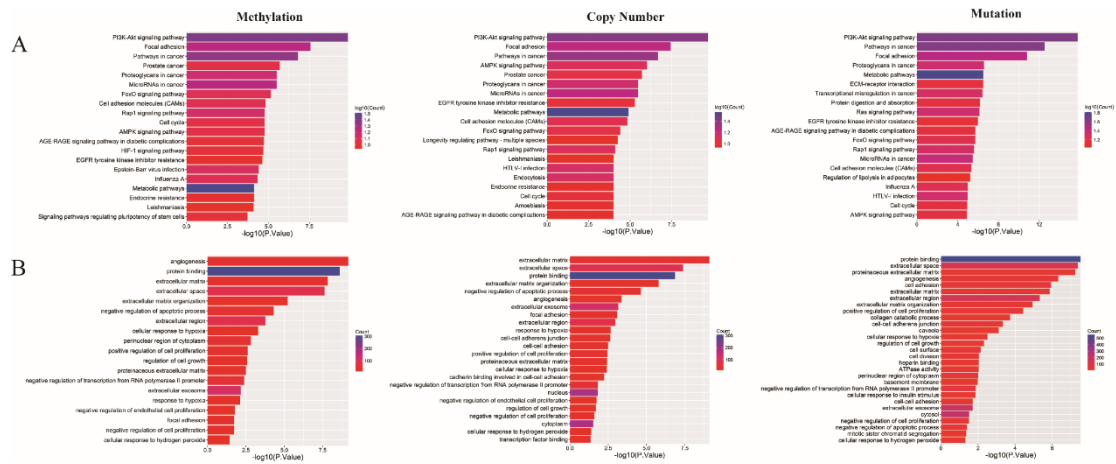
Figure S1. Identification of biological pathways and functions in breast cancer.

(A) Methylation, copy number, and mutation with significantly enriched pathways. (B) Methylation, copy number, and mutation with significantly enrichment functions.
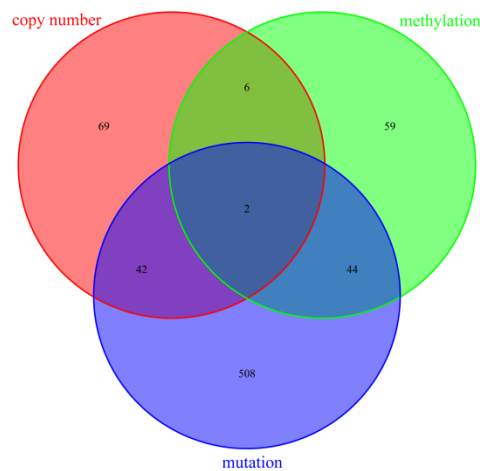

Figure S2. Intersection diagram of genes which methylation alteration-driven, CNV alteration-driven and Mutation alteration-driven.
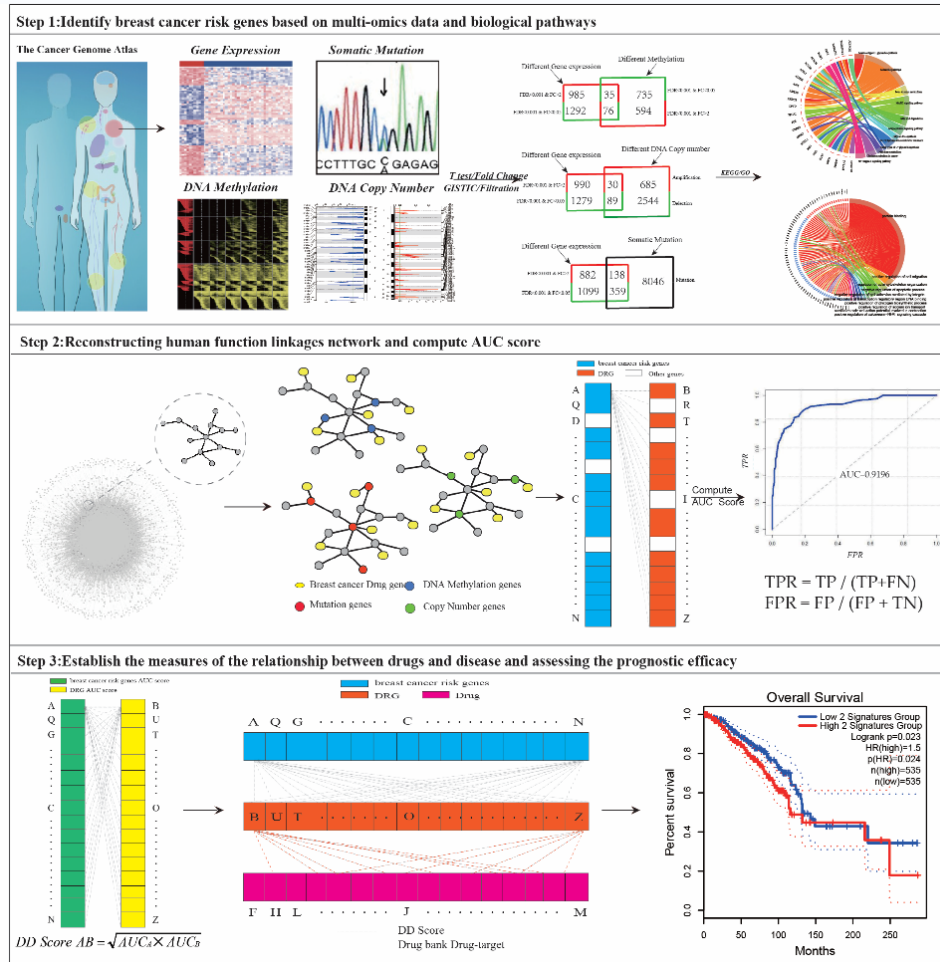
Figure S3. Flowchart of the strategy to identify functional regulations between genetic alteration-driven genes and drug target genes. Mapping the methylation, copy number, and mutation risk genes to the human functional linkage network. mutual predictability method was used to identified functional correlation between genetic alteration-driven genes and drug response genes in breast cancer. The potentially prognostic value of functional regulations between genetic alteration-driven genes and drug target genes were calculated.
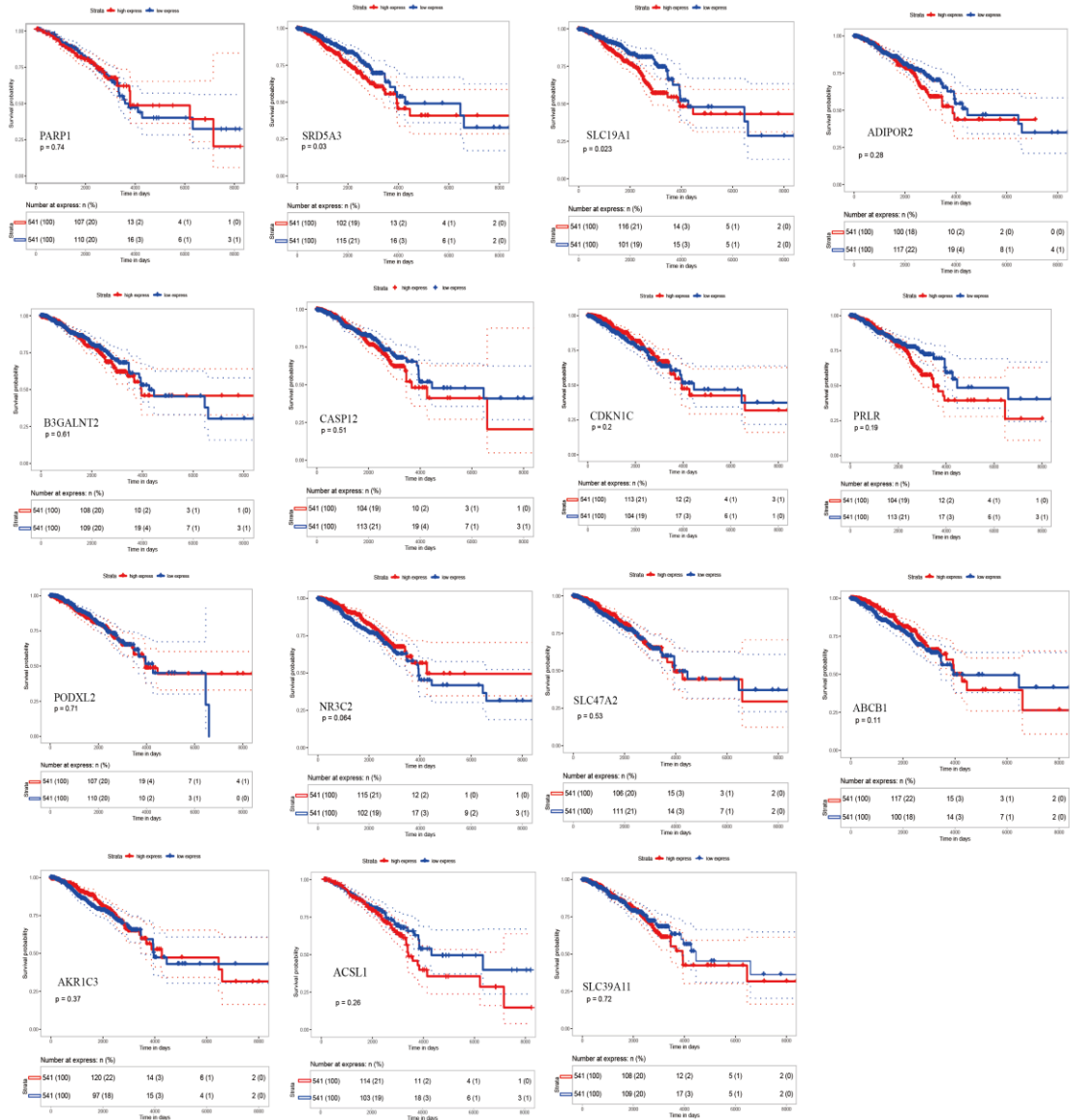
Figure S4. Survival analysis of individual genes of genetic alteration-driven gene pairs in the TCGA cohort. Comparison of the survival rates of two groups with respect to individual genes, which are involved in prognostic genetic alteration-driven gene pairs.