Figure S1. Workflow for the bioinformatics analysis strategy. KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction; lnc, long noncoding; GO, gene ontology; TCGA, the Cancer Genome Atlas.

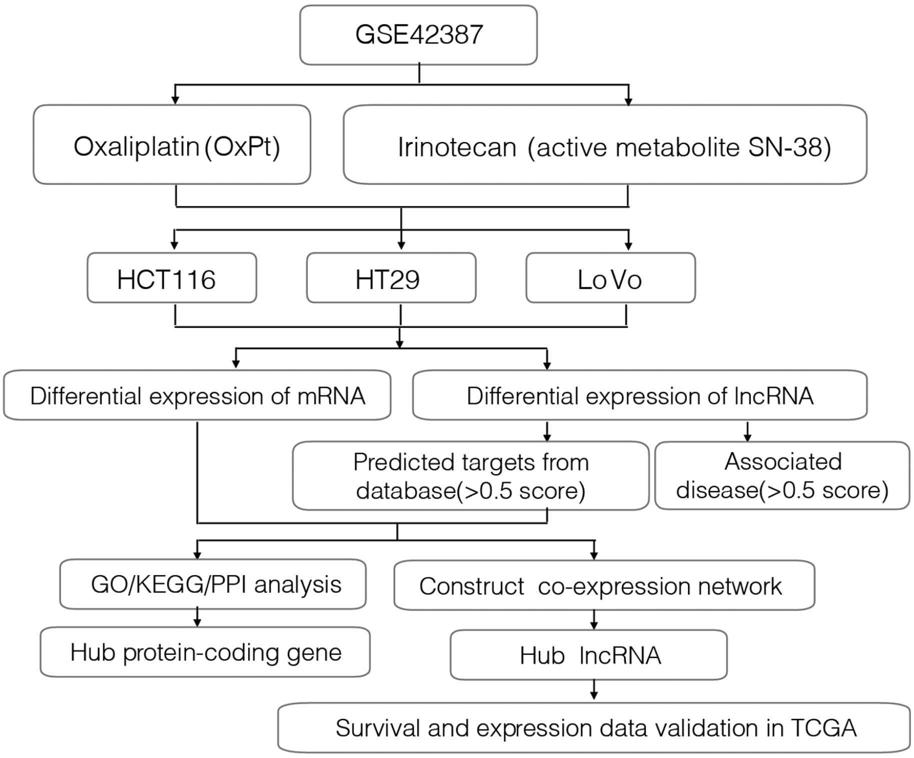

Figure S2. Distribution analysis of gene expression. (A) Distribution of gene expression levels in each group, where the x-axis indicates the relative intensity value and the y-axis shows the proportion of genes. (B) Distribution of genes based on the expression level of each sample, where x-axis shows each analyzed sample and y-axis shows the gene value distribution in each sample. (C) Principle component analysis of each sample in the nine groups: Component 1 vs. component 2. Dots represent the PC value of each sample. (D) Number of screened DEGs in six groups. (E) Volcano graph displaying pairs of expressed genes, where the x- and y-axis represent the log-transformed threshold values. Dots represent DEGs; red dots indicate significantly upregulated DEGs and blue dots indicate significantly downregulated DEGs that passed the screening threshold. Black dots represent non-significant DEGs. DEGs, differentially expressed genes.

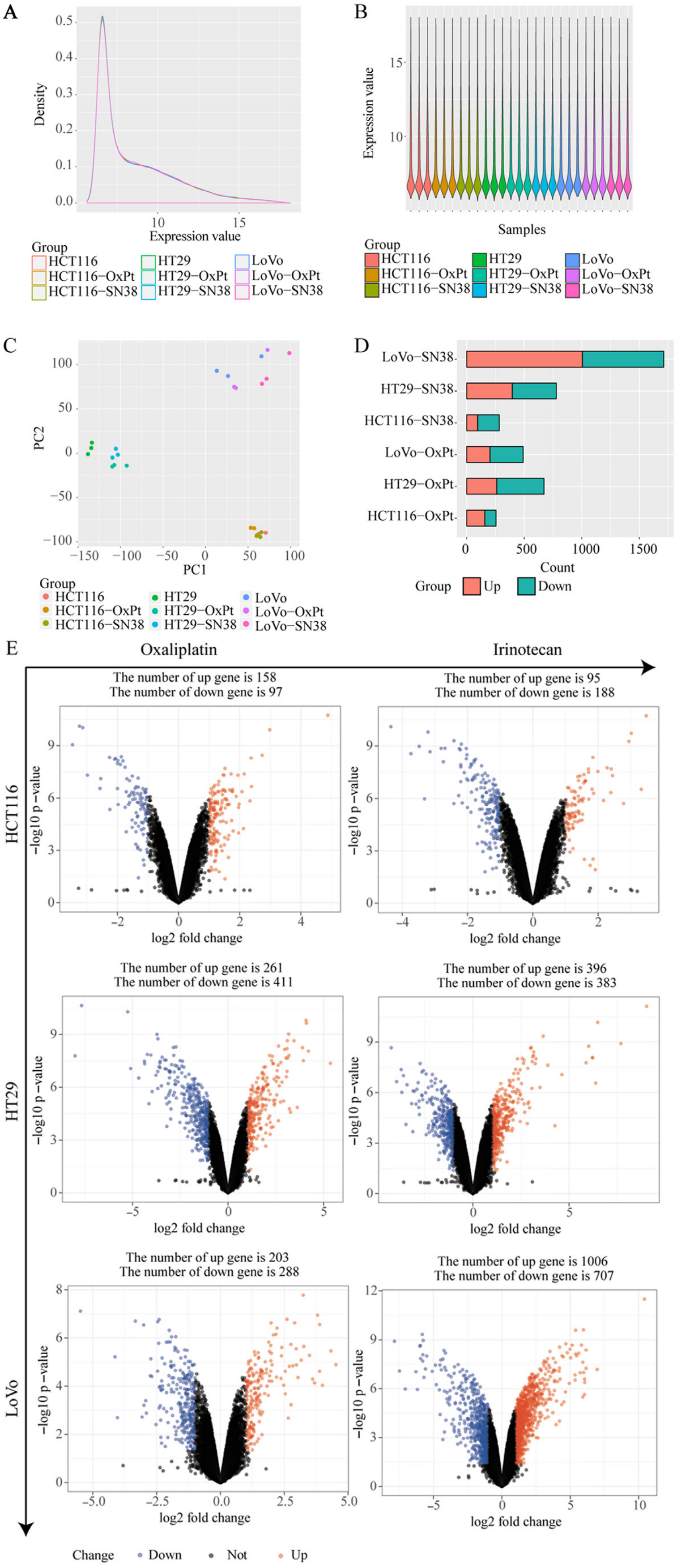

Figure S3. Cancer Hallmarks Analytics Tool text mining analysis. The value on the x-axis indicates npmi. Different-colored bars indicate specific cancer hallmarks. Npmi, normalized point-wise mutual information.