Figure S1. Study flow chart. RNA-seq data were downloaded from the TCGA. DNA methylation data were downloaded from the UCSC-Xena database. Gene expression data were used for the differential expression analysis. Methylation data were used for the differential methylation analysis. Merged genes were obtained by identifying interactions between DEGs and methylated genes in glioblastoma. Genes were subjected to GO and KEGG pathway enrichment analyses and PPI network construction. Hub genes were identified by four local-based methods (DMNC,MNC,MCC and degree). Hub genes were subjected to survival analysis. TCGA, The Cancer Genome Atlas; UCSC, University of California Santa Cruz; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology; PPI, protein-protein interaction; MCC, maximal clique centrality; MNC, maximum neighborhood component; DMNC, density of MNC.

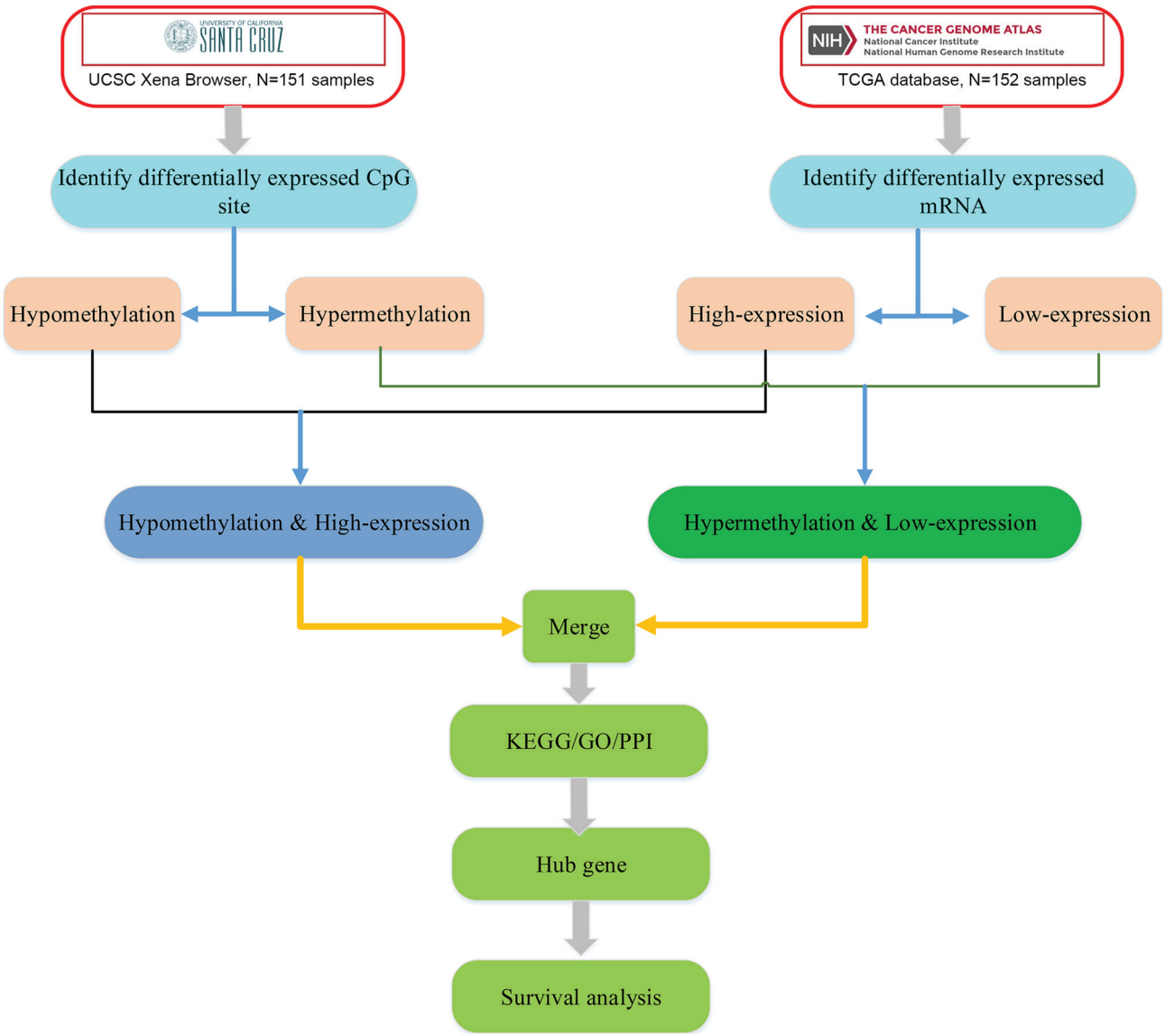

Figure S2. Differentially methylated CpG sites and differentially expressed genes. (A) Circos plot of the epigenome-wide association of DNA methylation in glioblastoma. Results are presented as CpG-specific association test results (logFC) ordered by genomic position. Blue represents hypomethylated CpG sites; red represents hypermethylated CpG sites; and chromosomal numbers are presented on the outer ring. (B) Heat map demonstrating the methylation of the top 50 CpG sites in patients who experienced long and short survival times, in descending order of the absolute value of logFC. logFC, log-fold change.

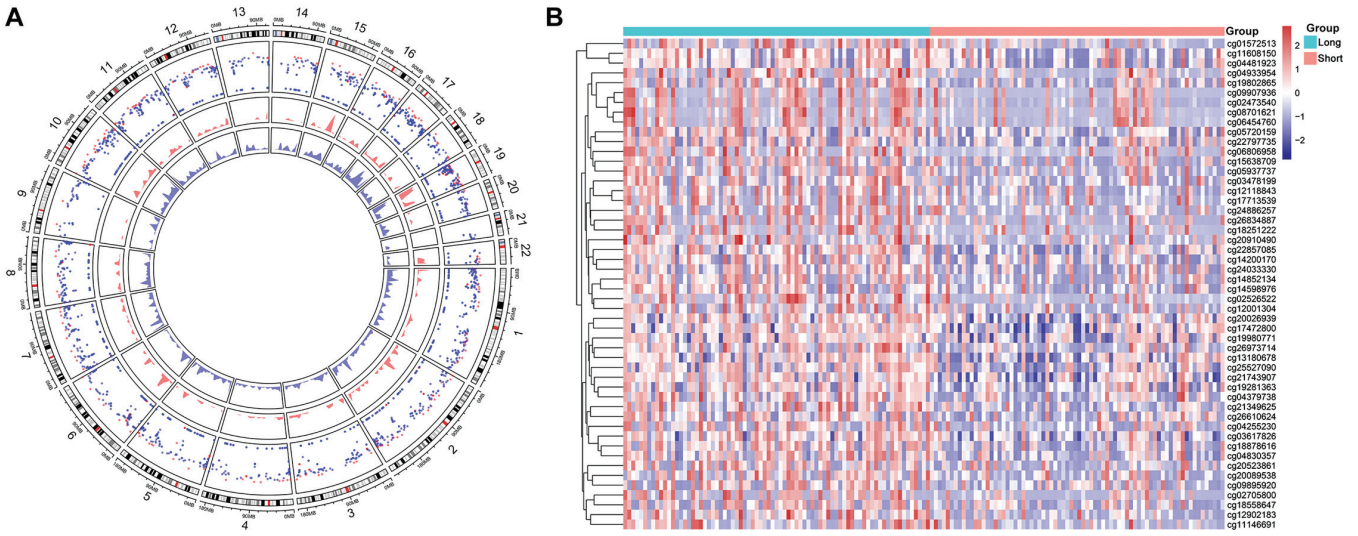

Figure S3. Heat maps of the hub genes in glioblastoma.