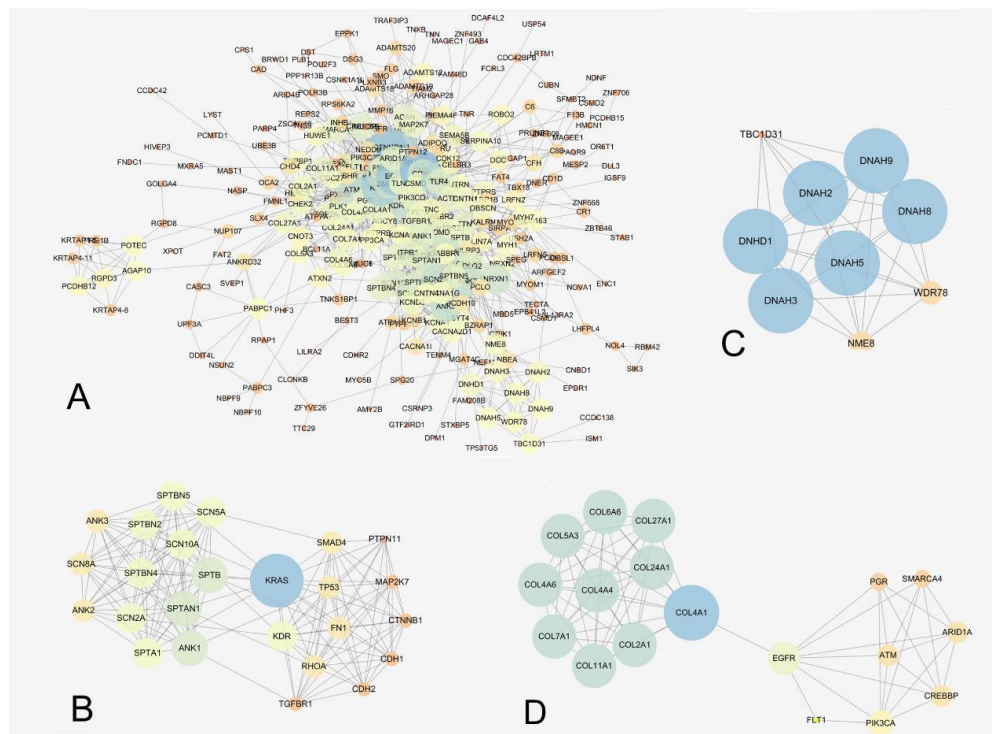
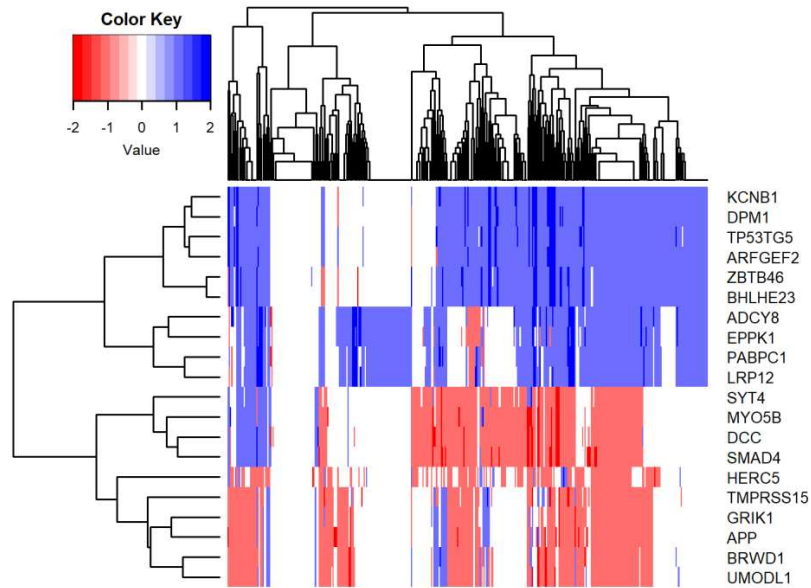


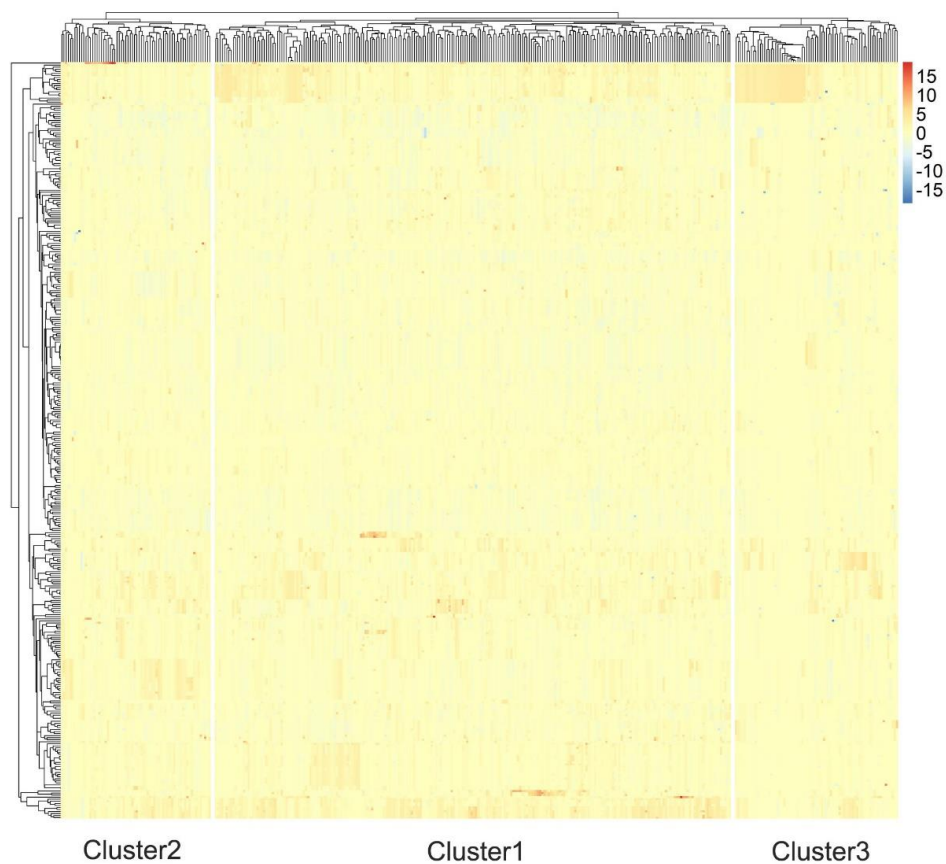
Supplementary figure1. Hierarchical clustering results of co-expression modules in the 415 STAD patients. Genes in modules are marked with different colors (blue and turquoise), with grey color representing no genes in any modules.



Supplementary figure 2. The PPI network of driver genes (A) and the top three clustering modules with highest MCODE scores (B, C, D). Network nodes and edges denote proteins and protein-protein interactions respectively. Of note, proteins which have no connection with other proteins were disabled in the PPI network.



Supplementary figure3. Unsupervised hierarchical clustering of the 20 driver genes with the most frequent copy-number alterations. Notably, dark red, red, white, blue, and dark blue represent high level amplification, amplification, copy-neutral, deletion and high level deletion respectively.



Supplementary figure4. Unsupervised hierarchical clustering of the 369 driver genes in STAD patients. The right bar shows the copy number variation values of 369 driver genes, with red and blue representing amplification and deletion respectively.