Figure S1. Gene Set Enrichment Analysis of *SNF* using GO and KEGG pathway enrichment. (A-I) GO results of *SNF*; (J-L) KEGG pathway results of *SNF*. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; FDR, false discovery rate; NES, normalized enrichment score; SFN, stratifin.

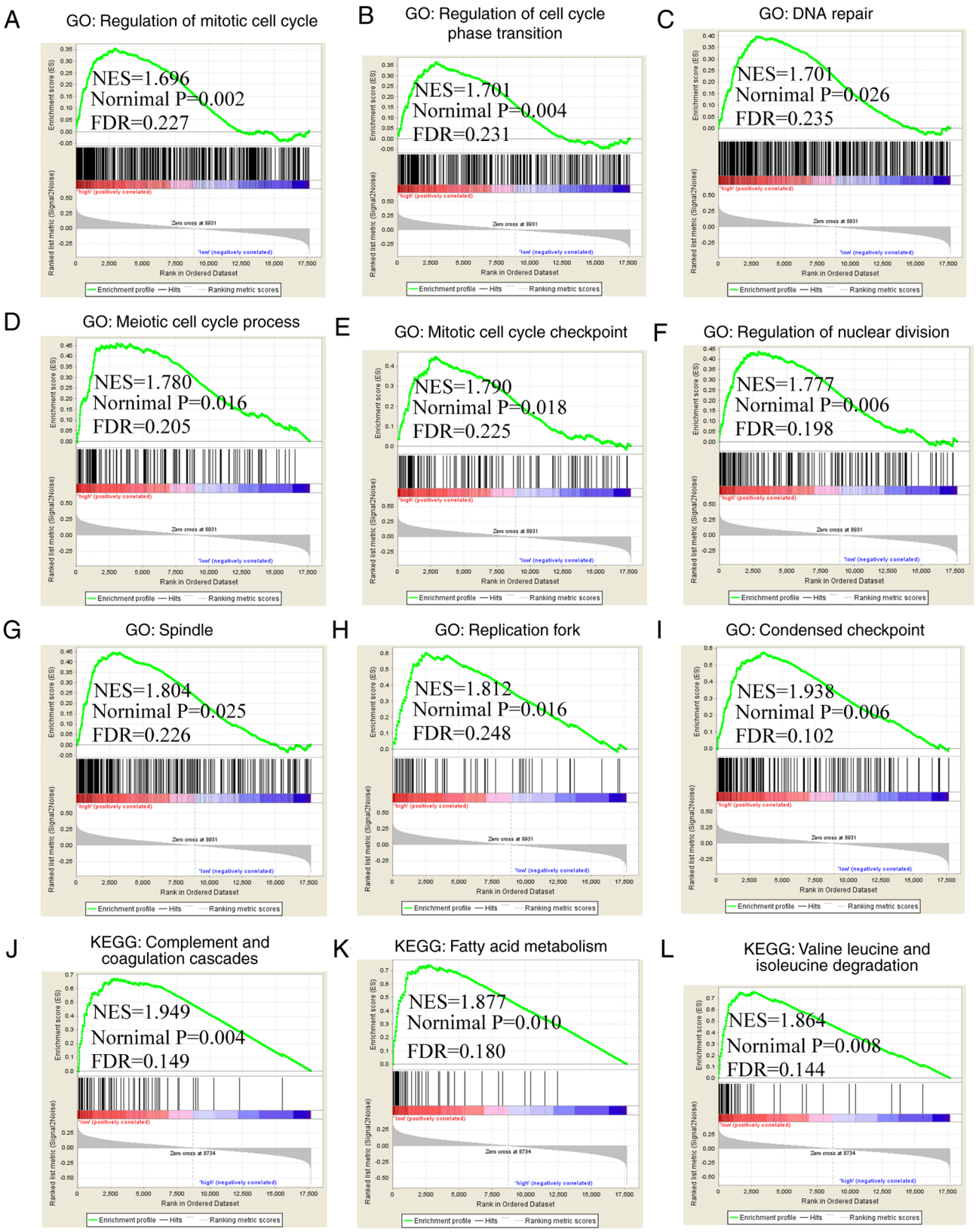

Figure S2. Gene Set Enrichment Analysis of *TDRD5* using GO and KEGG pathways. (A-I) GO results of *TDRD5*; (J-L) KEGG pathway results of *TDRD5*. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; FDR, false discovery rate; NES, normalized enrichment score; TDRD5, tudor domain containing 5.

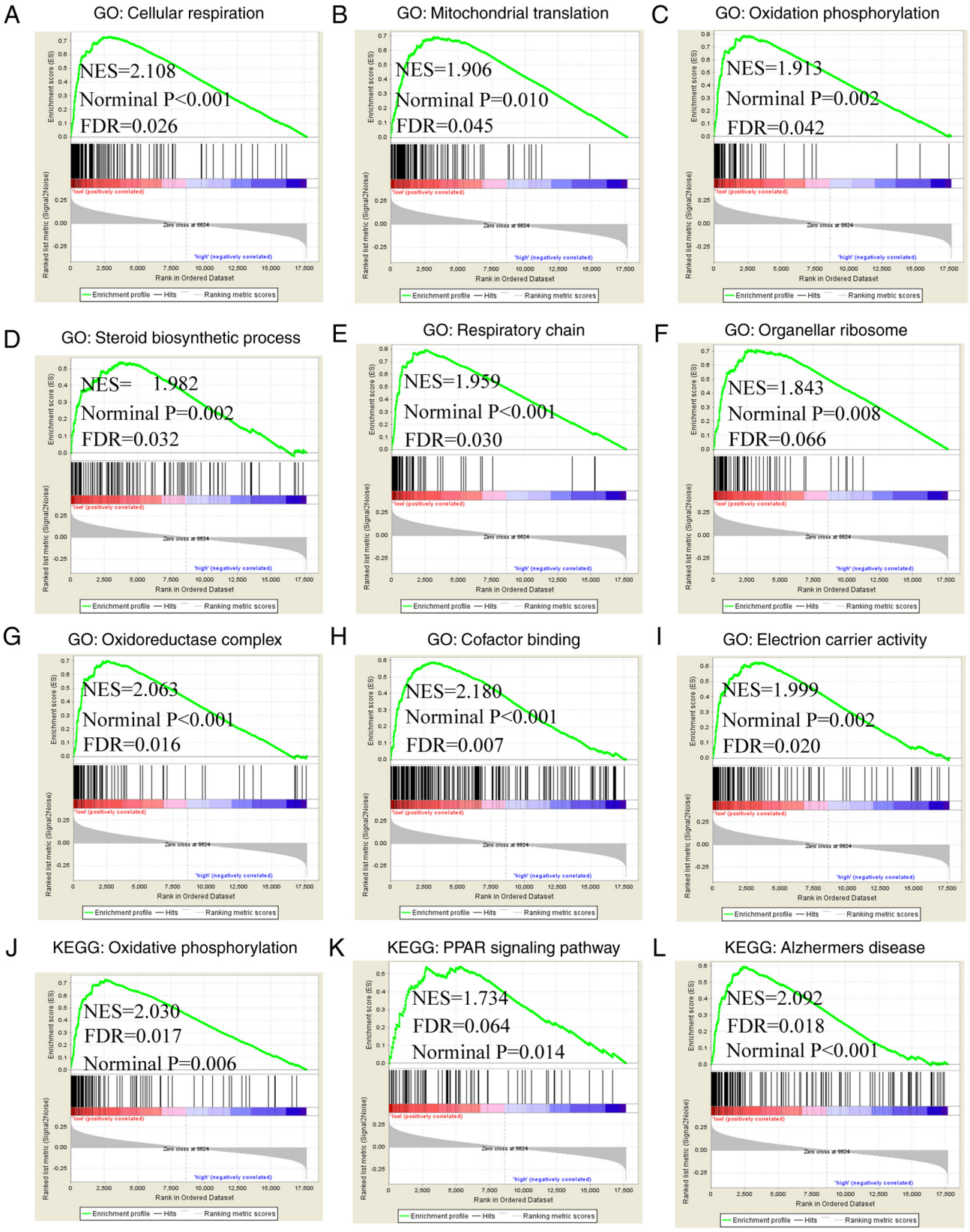

Figure S3. Gene Ontology results enriched by protein-coding genes. Yellow to orange indicates P-values from $5x10^{-2}$ to $<5x10^{-7}$.

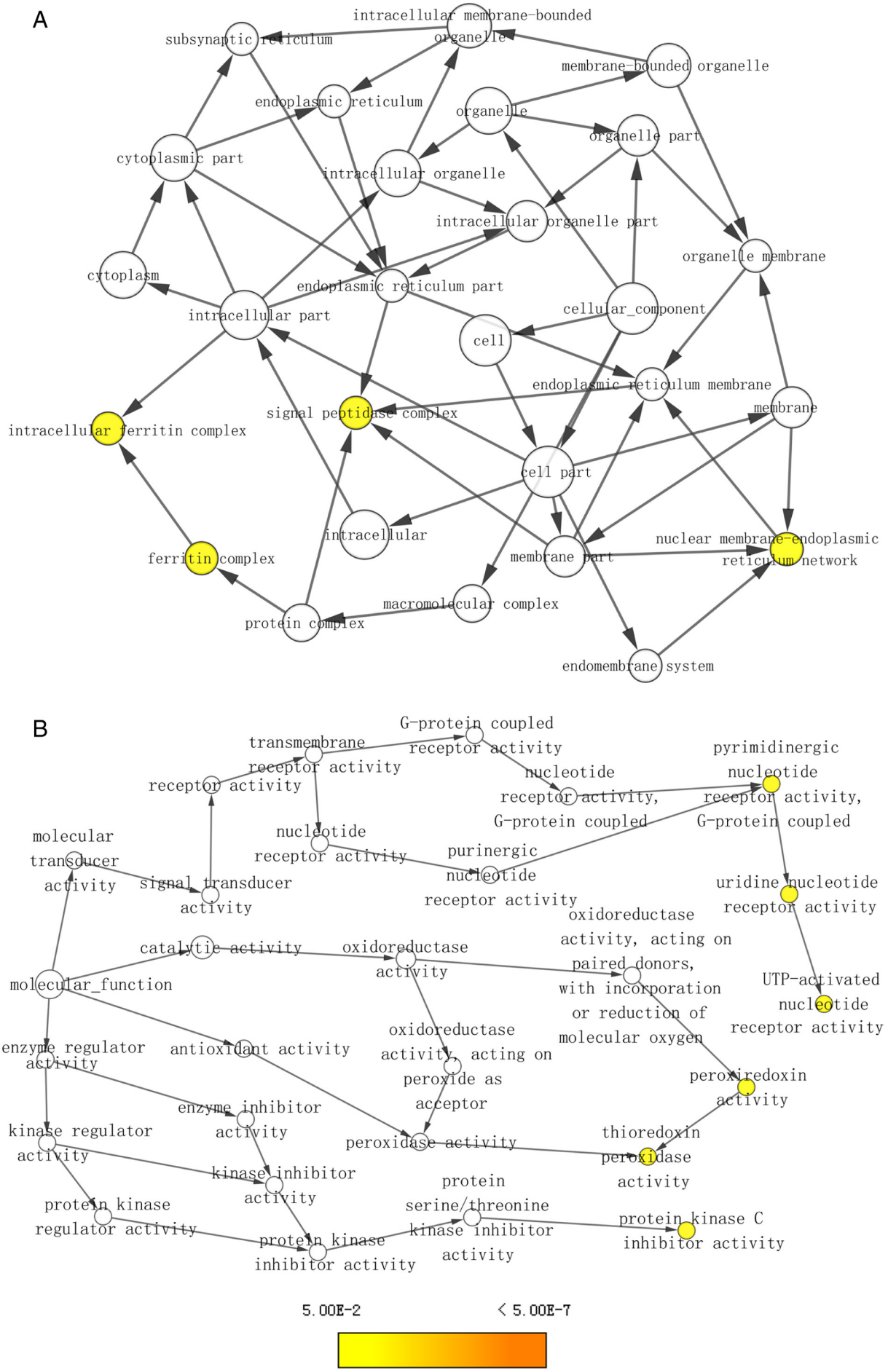

Figure S4. Heatmap and volcano plot of differentially expressed genes. (A) Heatmap of differentially expressed genes; (B) volcano plot of differentially expressed genes. Green to red indicates changes in expression from -4 to 4.

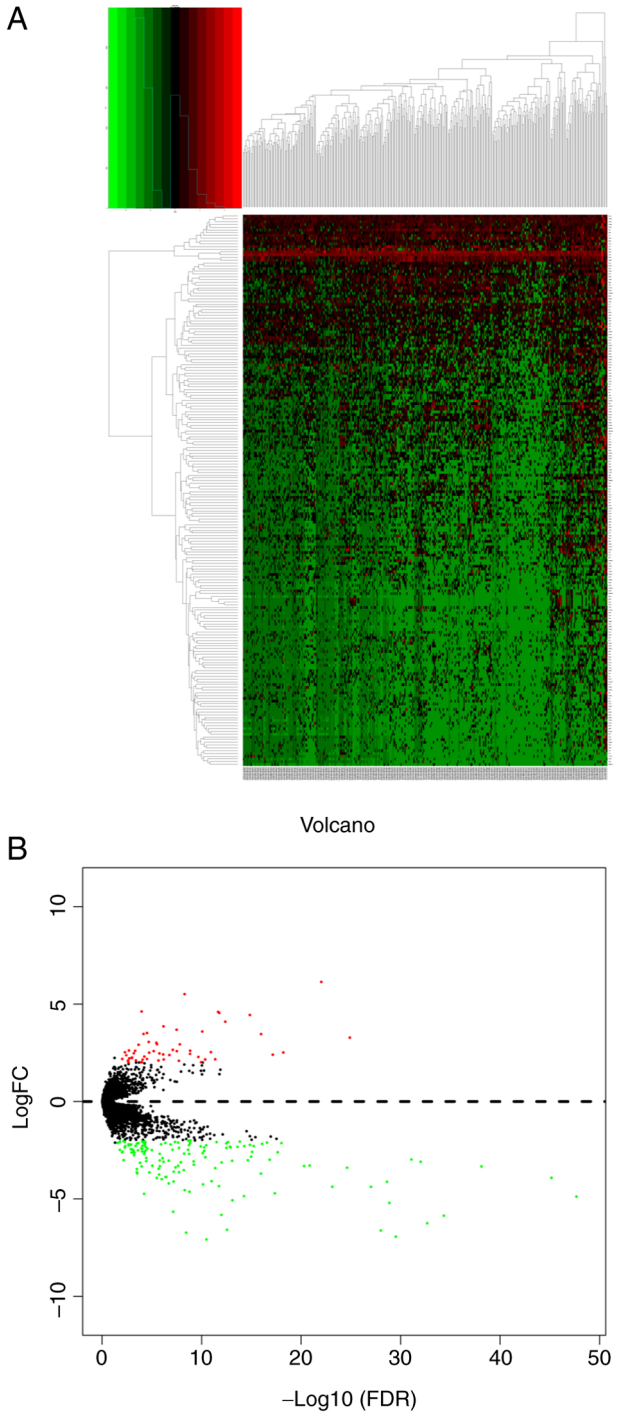

Figure S5. Chemical composition of seven target drugs. (A-G) Chemical composition of, indolylheptylamine, mimosine, disopyramide, lidocaine, NU-1025, bumetanide and DQNLAOWBTJPFKL-PKZXCIMASA-N.

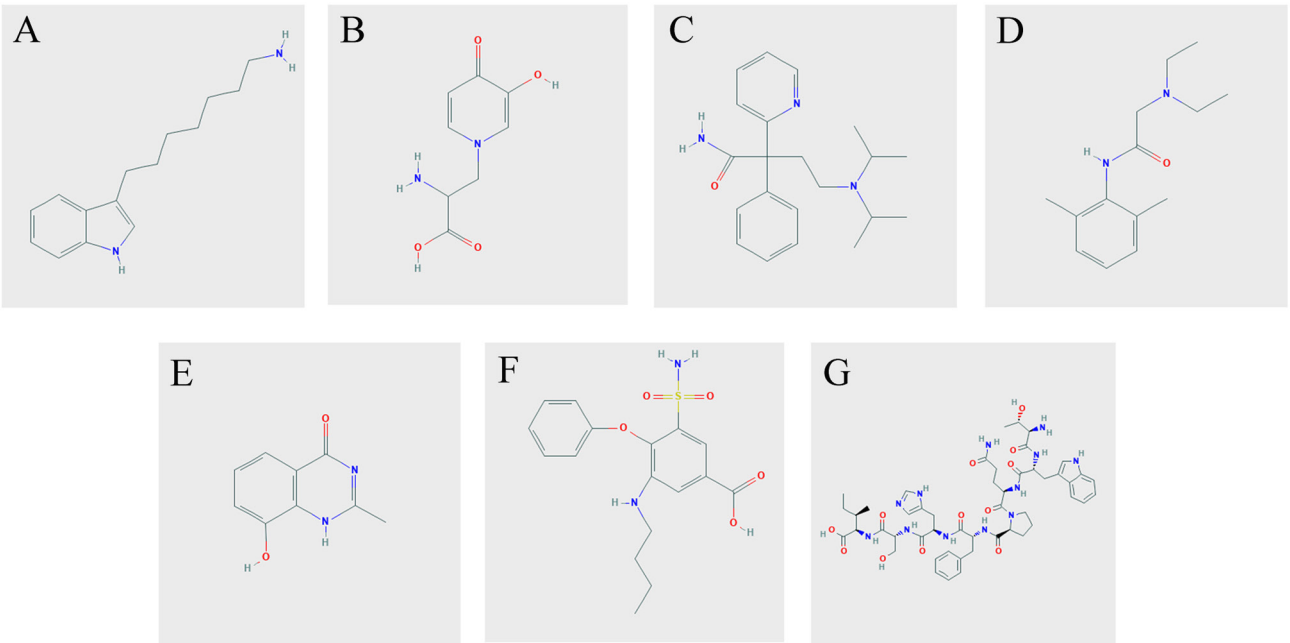
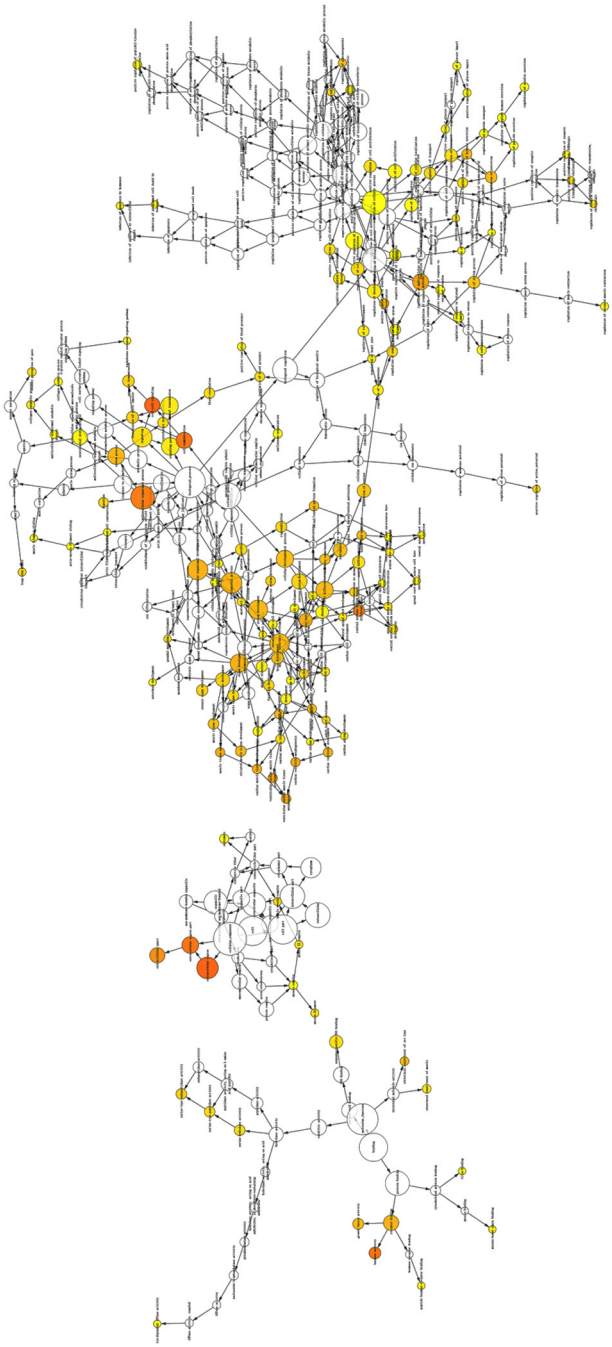
Figure S6. Gene Ontology results enriched from differentially expressed genes. Yellow to orange indicates P-values from $5x10^{-2}$ to $<5x10^{-7}$.