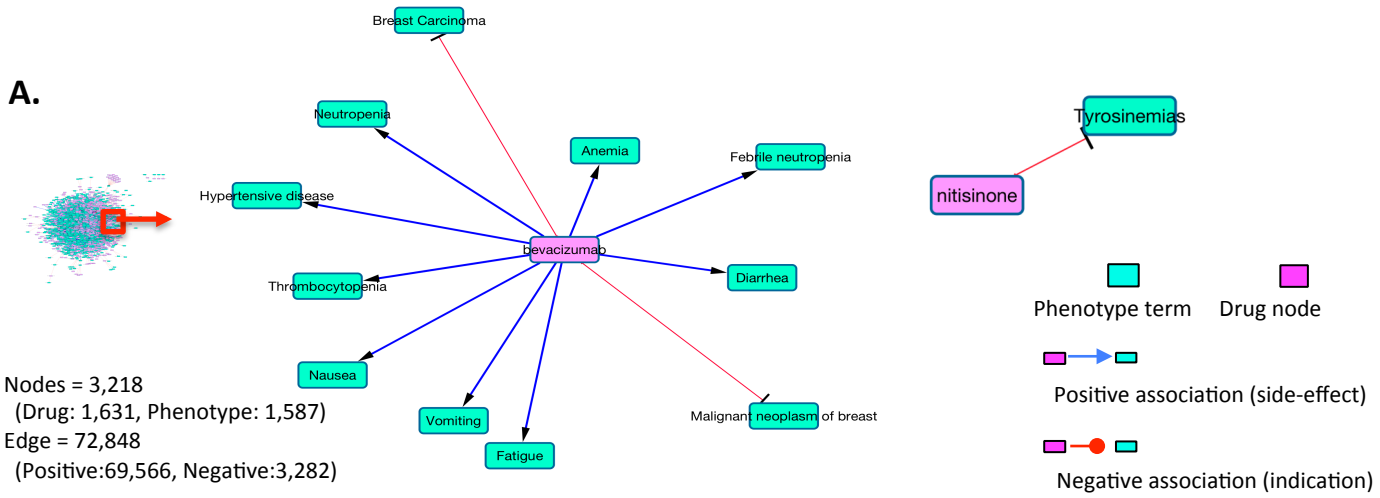
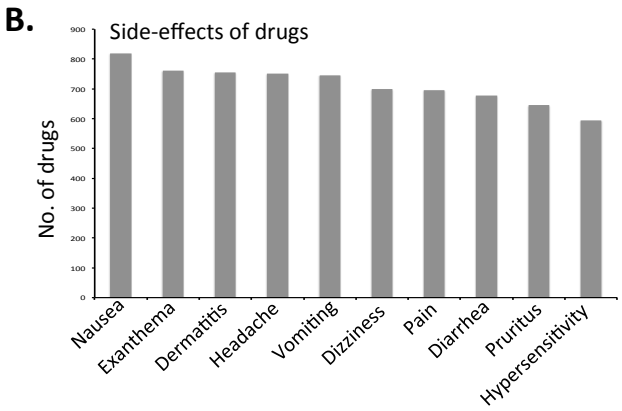
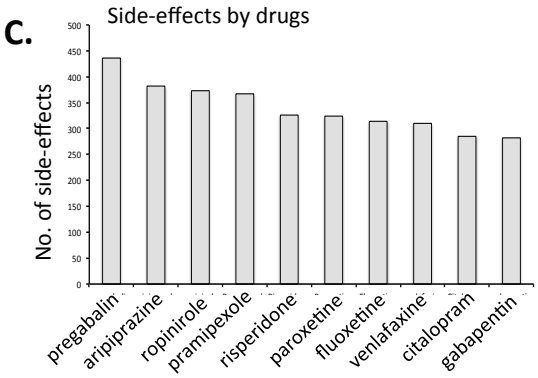
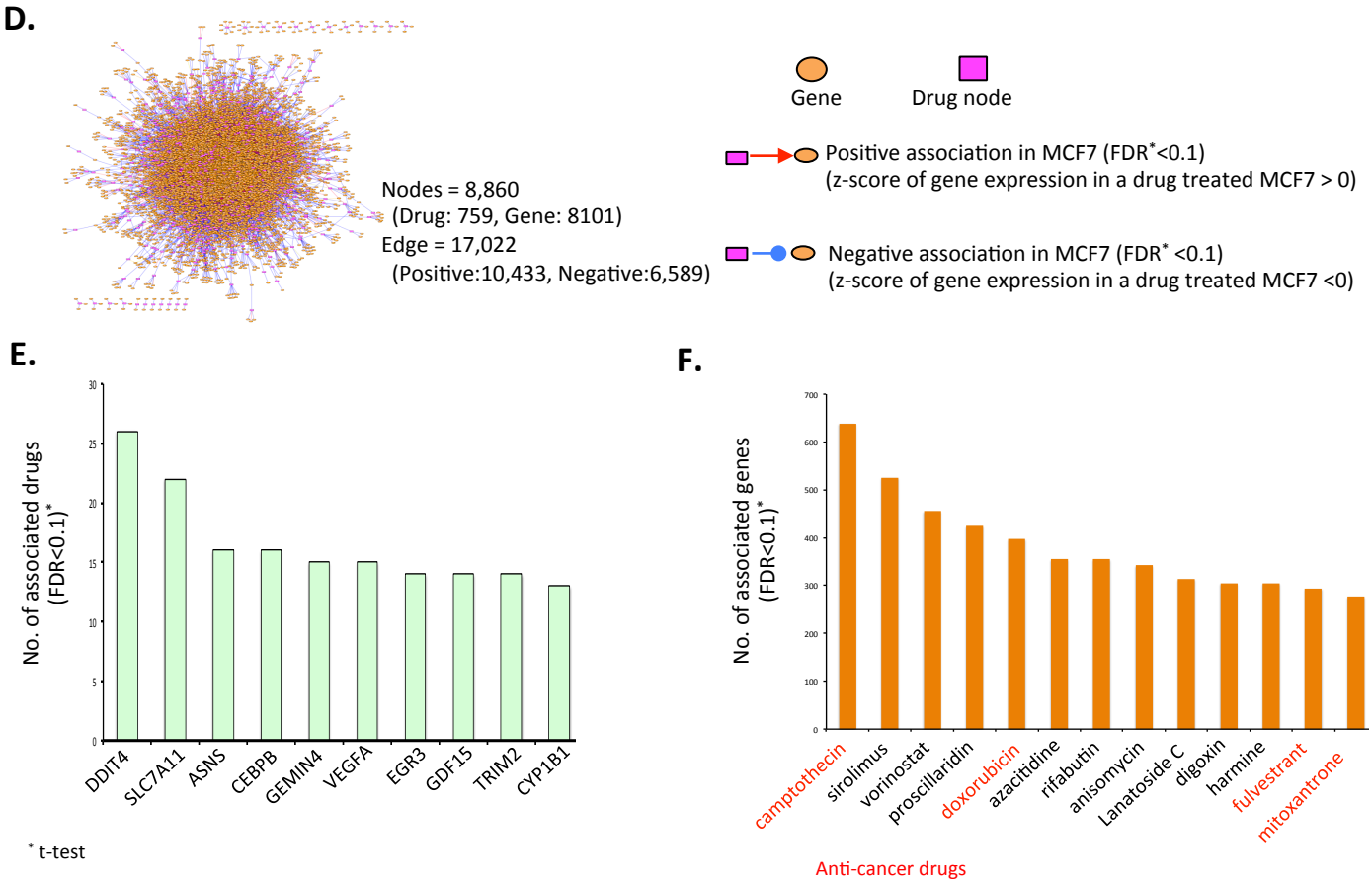


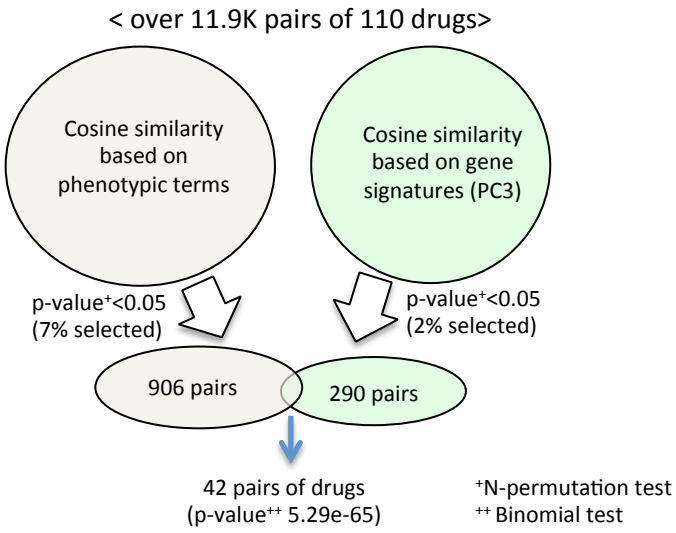




Supplemental figure 1. Distribution of phenotype and gene signatures for drugs.
A. Drug and associated hybrid phenotypes, such as side-effects and therapeutic effects (indications). This directional network consists of two types of nodes (drugs and phenotypes), and directional edges for positive (side-effect) and negative (therapeutic effect) associations between drugs and phenotypes. Cyan: phenotypes; pink: drugs. Edge directionality is denoted by distinct color and shapes. **B-C.** B. Phenotype distribution for each drug. The overall distribution of phenotypic terms, including side-effects and indications, was power-law like. The side-effects associated with the largest number of drugs were nausea, dermatitis, and headache. C. Highly ranked drugs with many side-effects. The drugs with the most diverse side-effects were in the psychiatric and neurodegeneration categories (schizophrenia, epilepsy, and Parkinsonism).



Supplemental figure 1. Distribution of phenotype and gene signatures for drugs.
D. Bipartite directional network of drug-gene signatures based on drug treated expression profiles of MCF7 cells in the Connectivity map. Orange nodes: gene signatures; pink nodes: treated drugs. Red and arrow-ended edges: positive associations between drug and gene signatures (FDR of t-test < 0.1 and gene expression z-score >0). Blue and blunt-ended edges: negative associations (FDR of t-test <0.1 and gene expression z-score <0). **E-F.** Sample distributions between drugs and associated genes. E. Analyzed gene signatures and associated drugs displayed n-by-n relationships within scale-free network. Anti-cancer drugs, such as camptothecin and doxorubicin, had larger numbers of associated gene signatures in MCF7 cells. F. Known anti-cancer drugs. As in E, the overall distribution for the number of associated genes for each drug was power-law like.



Supplemental figure 2. Selection of similar drugs based on gene signatures in PC3 and phenotypic terms