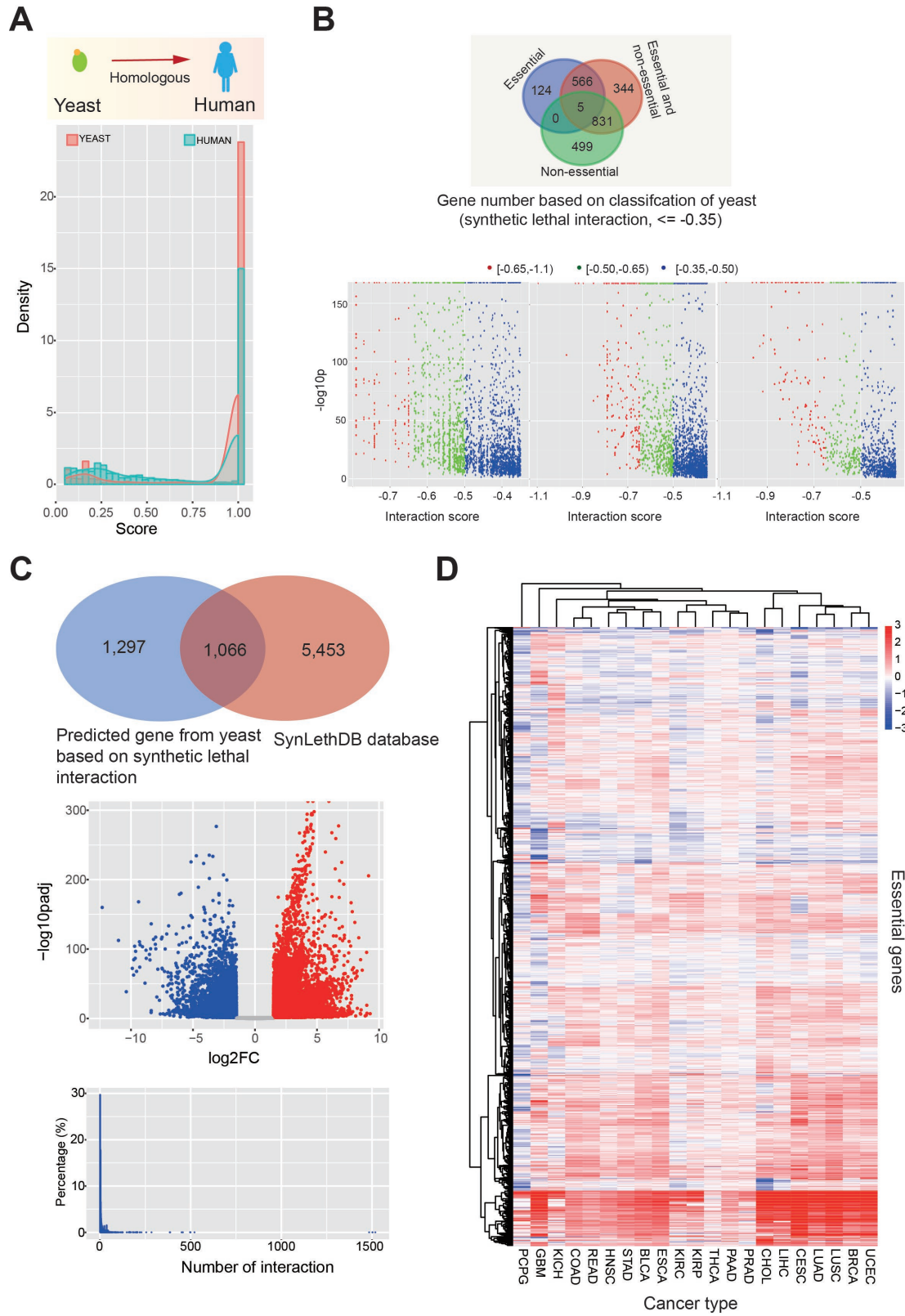
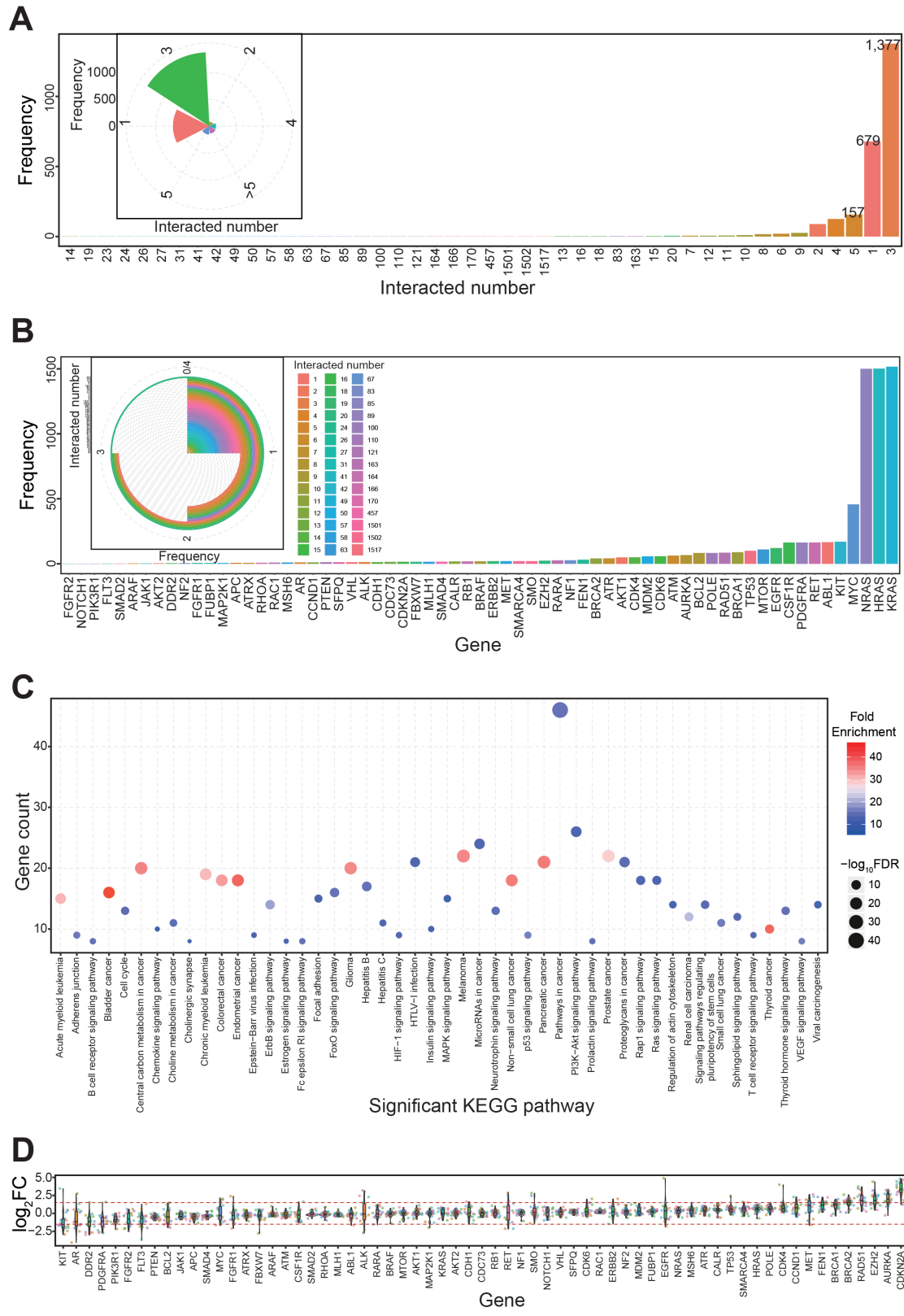


## Supplementary files (Figure S1-S3)



**Figure S1. Distribution and expression patterns of involved genes.**

- A. Gene pairs in human are predicted from yeast according to the feature of homologous.
- B. Gene distributions of genes based on classification of essential genes in yeast, and interacted scores are also presented.
- C. Expression pattern and number of interaction of involved gene.
- D. A heat map indicates expression distribution of all classified essential genes.



**Figure S2. Distributions of interacted numbers and further functional analysis.**

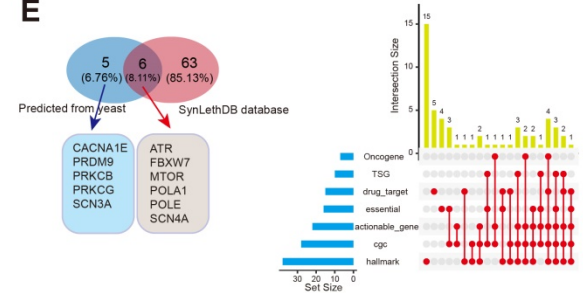
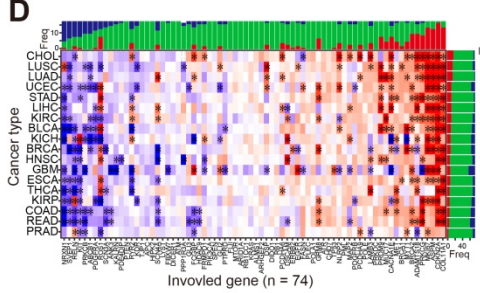
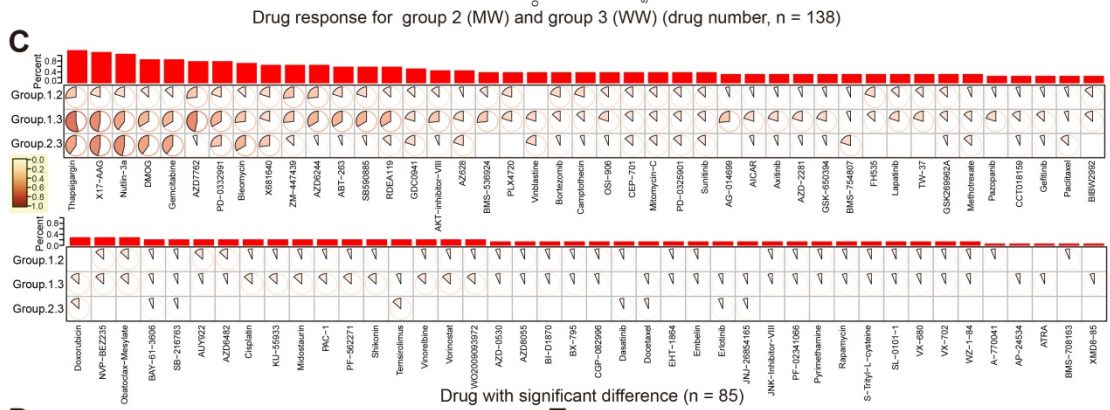
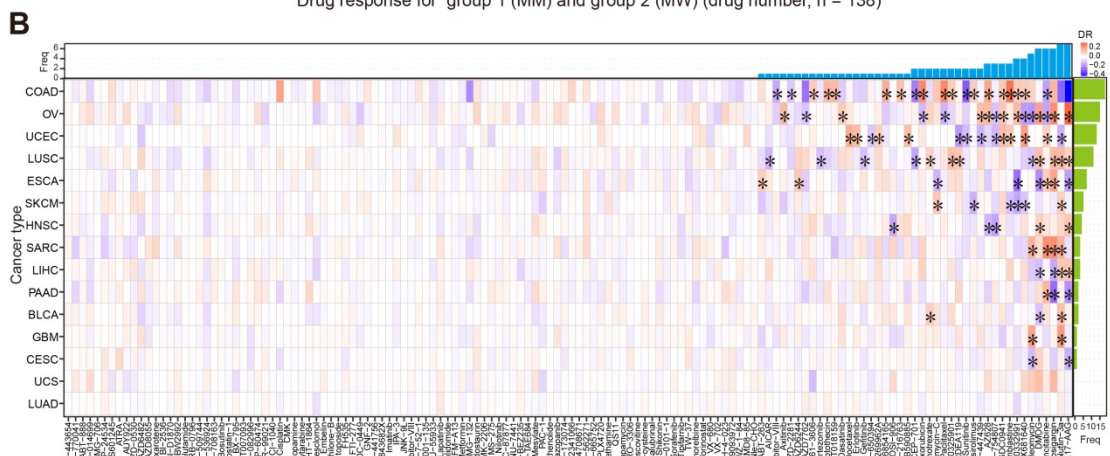
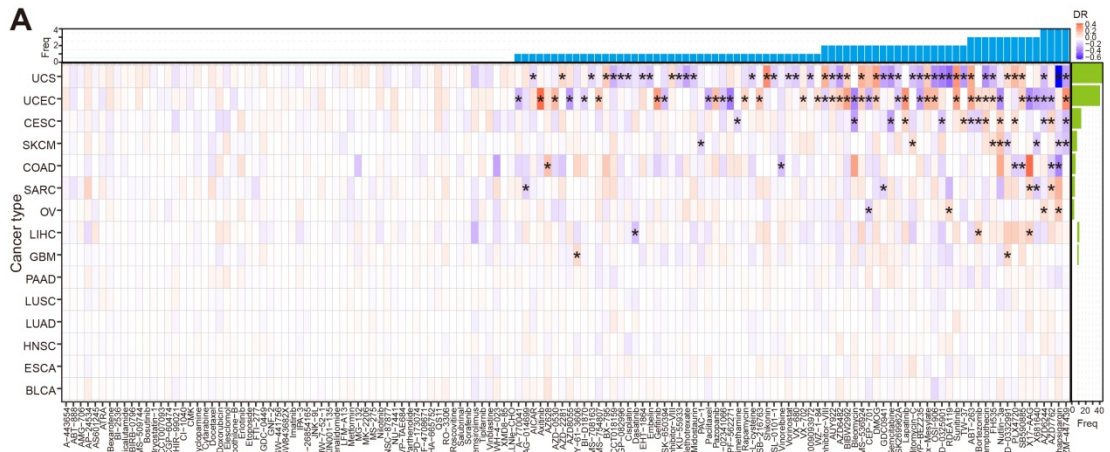
A. Distribution of interacted number based on all gene pairs (each gene pair

contain one or two in screened 65 genes), and pie distribution shows several dominant class (>5 shows number of genes with more than 5 interactions).

B. Distribution of interacted number based on all gene pairs, and the detailed distributions are also presented.

C. Based on the screened 65 genes, significant enriched KEGG pathways are presented (FDR < 0.05).

D. A pan-cancer analysis shows expression patterns of these involved genes. The two red dotted lines shows the 1.5 and -1.5 (the cutoff values of deregulated genes), and each point shows the relevant value in one cancer type.



**Figure S3. Drug responses for synthetic lethal interactions at mutation level.**

A. Drug response of gene pairs across cancer types based on GDSC between group 1 (MM) and group 2 (MW). \* indicates drug with significant statistical difference between the two groups ( $DR > 0.1$  or  $DR < -0.1$  and simultaneously  $p < 0.05$  ( $FDR < 0.1$ )).

B. Drug response of gene pairs across cancer types based on GDSC between group 2 (MW) and group 3 (WW). \* indicates drug with significant statistical difference between the two groups ( $DR > 0.1$  or  $DR < -0.1$  and simultaneously  $p < 0.05$  ( $FDR < 0.1$ )).

C. The distribution of significant drug responses based on pairwise comparison. The pie distribution indicates significant cancer types in 15 total cancers.

D. Expression patterns of involved genes ( $n = 74$ ) across different cancer types. Significantly abnormally expressed genes are screened based on  $p_{adj} < 0.05$ , and  $\log_2FC > 1.5$  (up-regulated) or  $\log_2FC < -1.5$  (down-regulated), or the gene is thought as stably expressed in tumor samples.

E. Gene distribution based on the source and specific gene.