

Supplementary figure legends

Figure S1.

***ZDHHC1* inhibited growth, migration and invasion of MCF7 and HONE1 cells.**

(A). Representative images of colony-formation assays. (B). Flow cytometry analysis of cell cycle progression. (C). Flow cytometry analysis of cellular apoptosis. Vector and *ZDHHC1* transfected MCF7 and HONE1 cells were double stained with Annexin-V-FITC and PI for apoptosis measurement. (D). Morphology of MCF7 cells undergoing apoptosis were observed under electronic microscopy. (E). Representative images of wound-healing assays conducted with MCF7 and HONE1 overexpressing *ZDHHC1* or Vector. Photos were taken at 0h and 48h after the wound was made. (F). Representative images of Transwell assays measuring cell migration ability, using all two cells transfected with Vector or *ZDHHC1* 24h after seeding. (G). Representative images of Transwell assays measuring cell invasion ability, using MCF7 and HONE1 cells transfected with Vector or *ZDHHC1*.

Figure S2.

Knocked down *ZDHHC1* enhanced growth, migration and invasion of A549 cell.

(A-B). Knocked down *ZDHHC1* expression enhanced A549 cell growth. A549 cell transfected with sh*ZDHHC1* or empty vector were used for colony formation assay and CCK8 assay. (C). Flow cytometry analysis of cellular apoptosis. Vector and *ZDHHC1* knocked down in A549 cell were double stained with Annexin-V-FITC and PI for apoptosis measurement. (D). Flow cytometry analysis of cell cycle progression. (E). Transwell assays measuring cell migration and invasion ability, using A549 cell transfected with Vector or sh*ZDHHC1* 24h after seeding.

Figure S3.

Expression proteomic and metabolomic analyses of *ZDHHC1* overexpression in MCF7 cells.

(A). Enrichment of differential-expressed proteins categorized by function. (B). KEGG Pathway analysis showed the expression of proteins involved in multiple pathways, among which metabolic pathway are greatest altered by *ZDHHC1*. (C). Effects of ectopic expression of CYGB and *ZDHHC1* had on multiple proteins. (D). The Venn diagram showed an overlap of 18 proteins were regulated by both *ZDHHC1* and CYGB.

Figure S4.

Supplementary Figure 4. PPI network of protein interaction was constructed from bioinformatics.

Figure S5.

***ZDHHC1* promote *CYGB* expression and inhibit carbohydrate metabolites in MCF7 cells.**

(A).The positive correlation between *ZDHHC1* and *CYGB* was confirmed by bioinformatics (B). Verification of *CYGB* expression was increased in *ZDHHC1* cells by qPCR .(C).Pathway analysis of differential metabolites confirmed by gas chromatography-mass spectrometry metabolomics assay. Data was analyzed by MetaboAnalyst software. (D).Intracellular levels of glucose and its metabolites confirmed by GC-MS metabolomics analyses. (E). Expression of *ZDHHC1* decreased GLUT1, HXK2, and G6PD identified by Western blot in vector- and *ZDHHC1*- transfected MCF-7 and HONE1 cells.

Figure S1

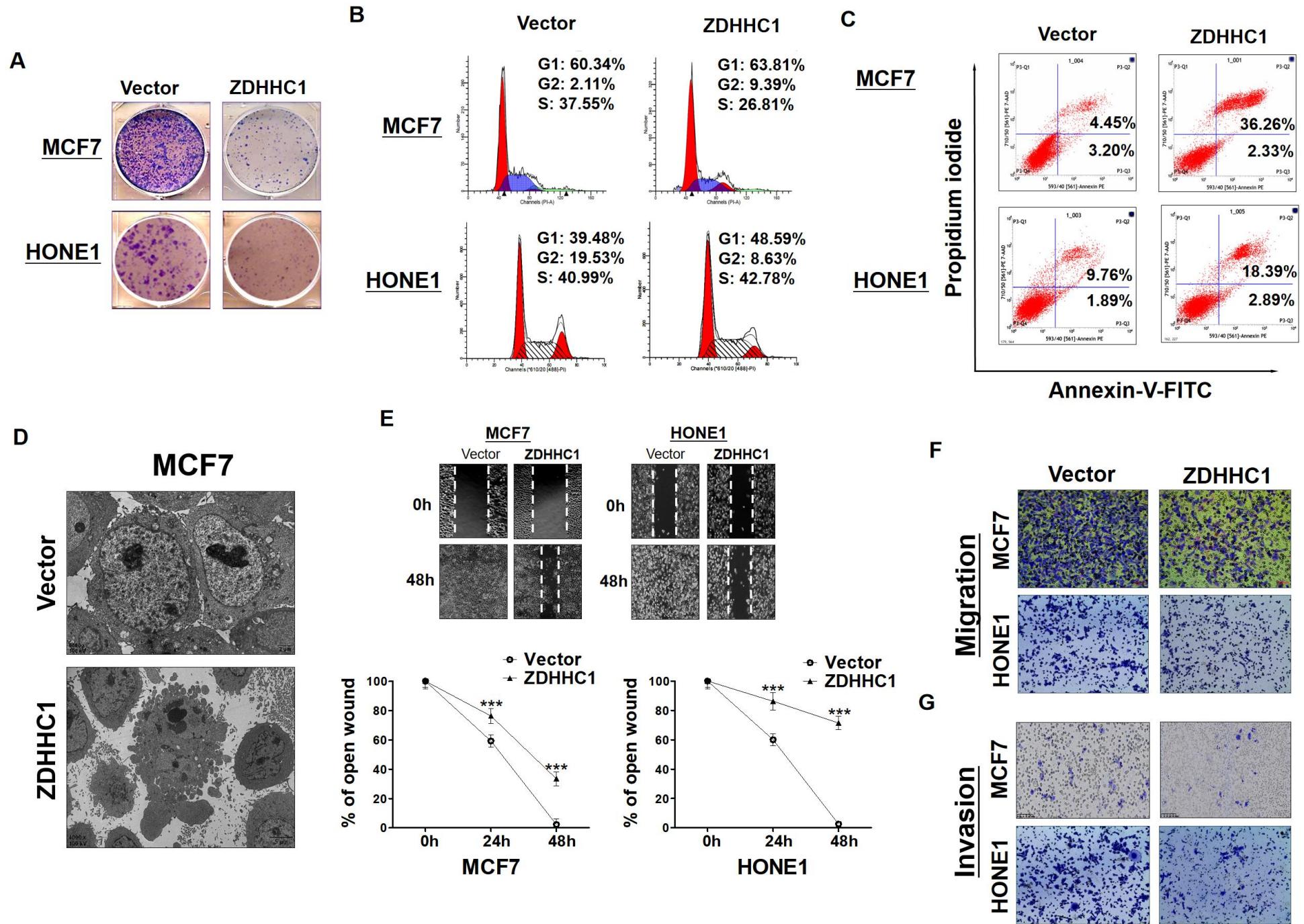


Figure S2

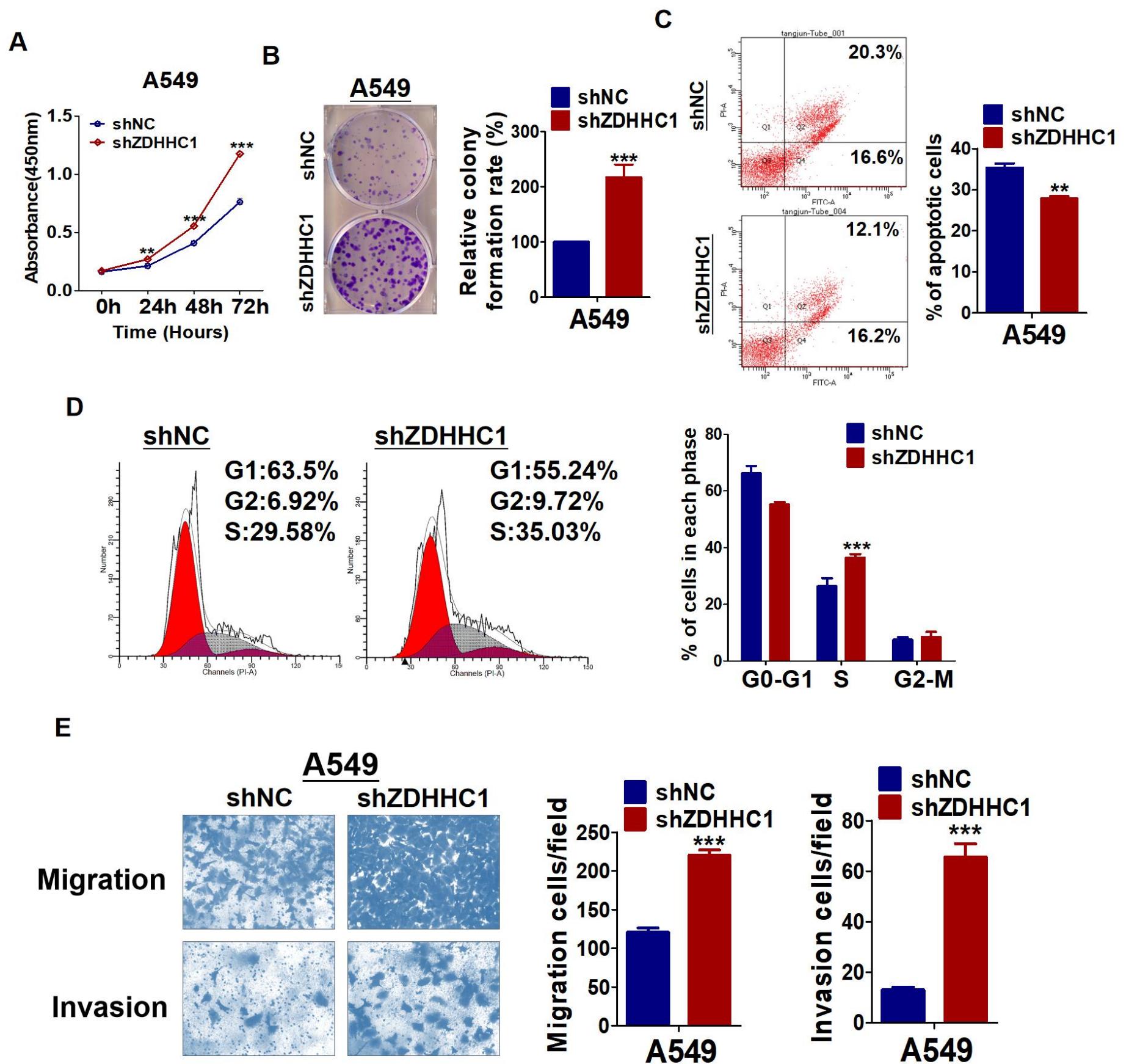


Figure S3

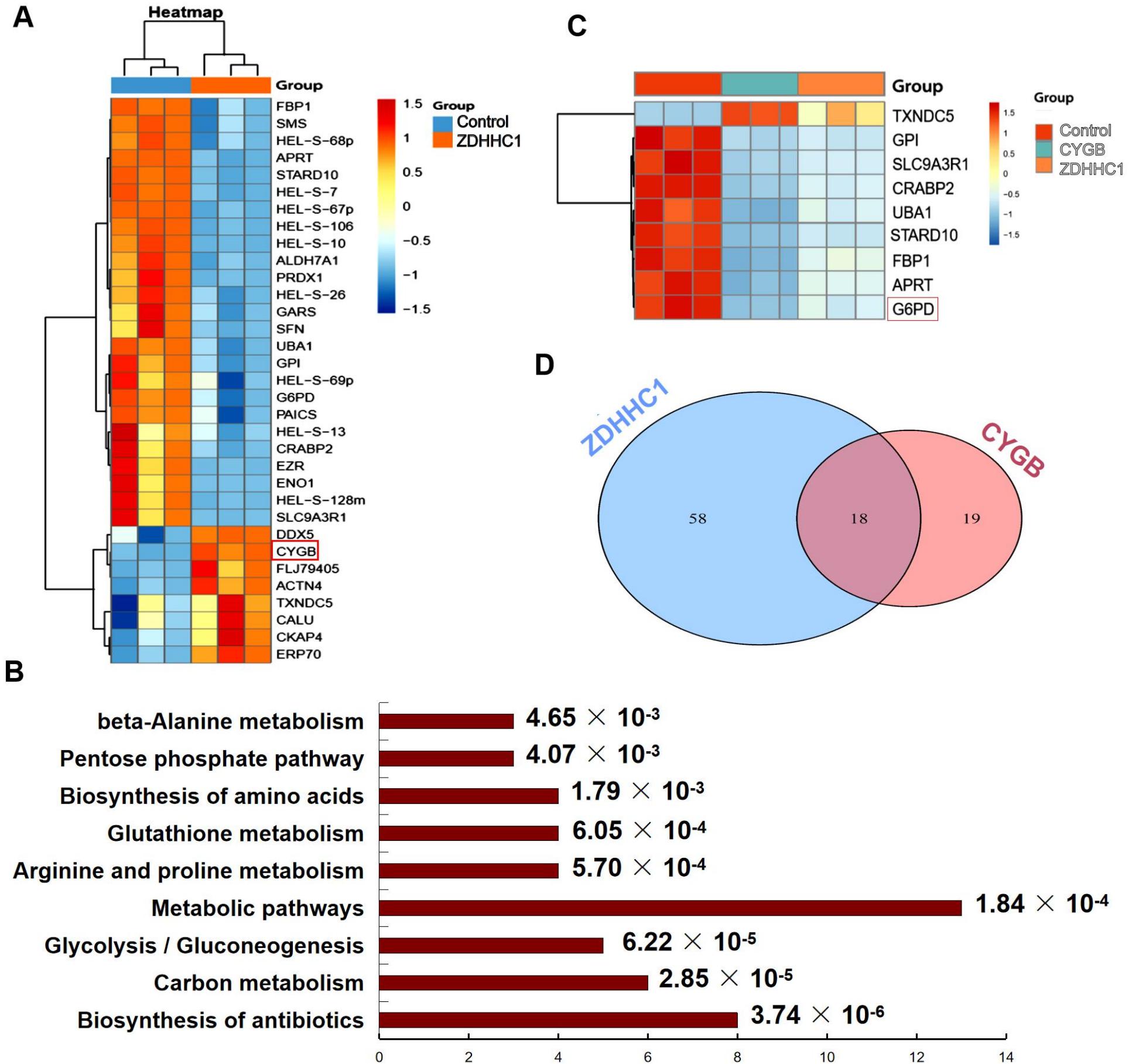


Figure S4

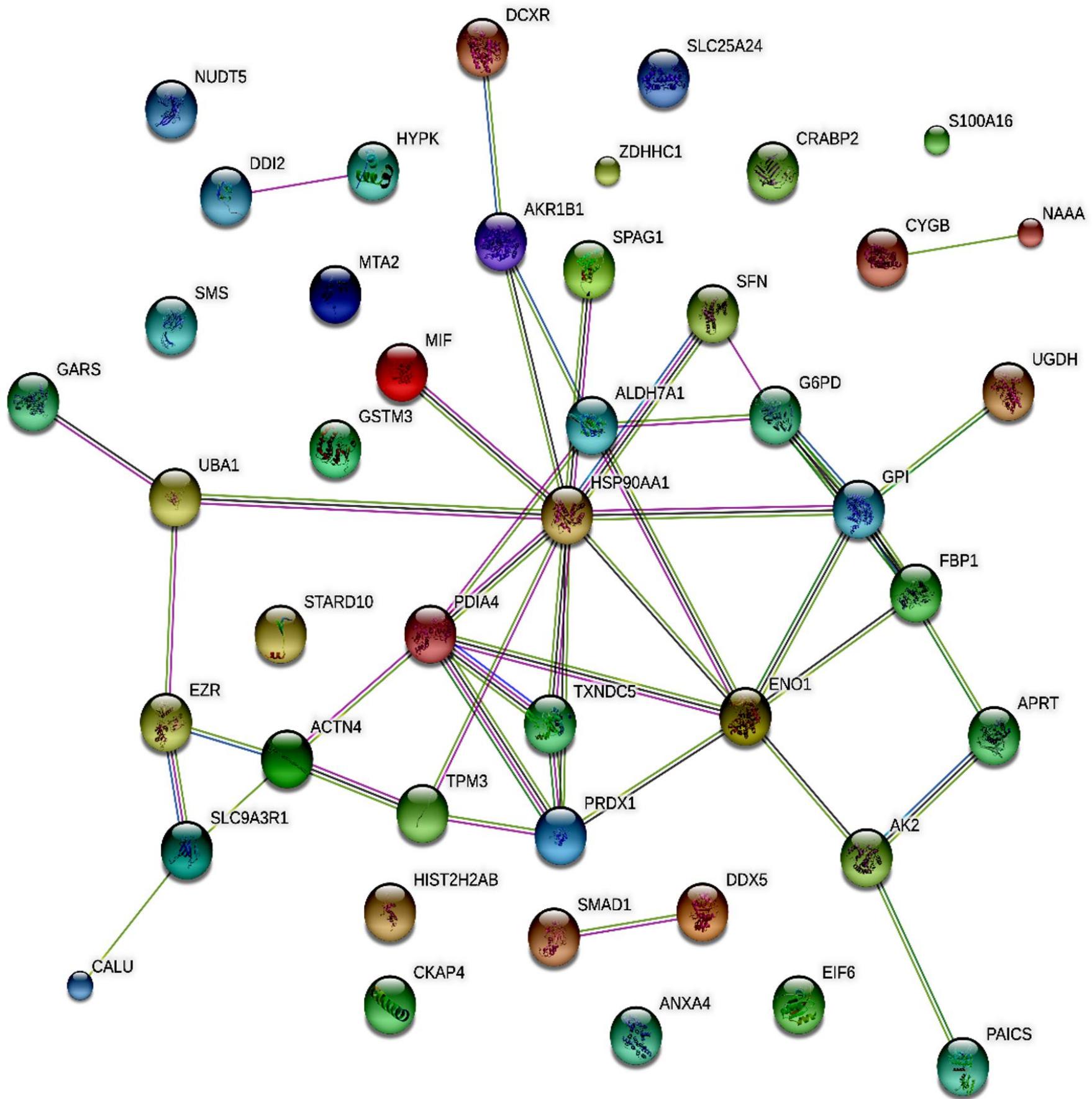


Figure S5

