Figure S1. Cluster map of differential genes. Clustering is performed with log10 (Fragments Per Kilobase of transcript per Million mapped reads +1) values, red indicates high expression genes and blue indicates low expression genes. The color from blue to red indicates the gene expression higher. OE, overexpression; T24-CON, T24 control group; T24-EXP, T24 experimental group; OE-CON, T24-EGFR-OE control group; OE-EXP, T24-EGFR-OE experimental group. 1, 2, 3 present three biological replicates.

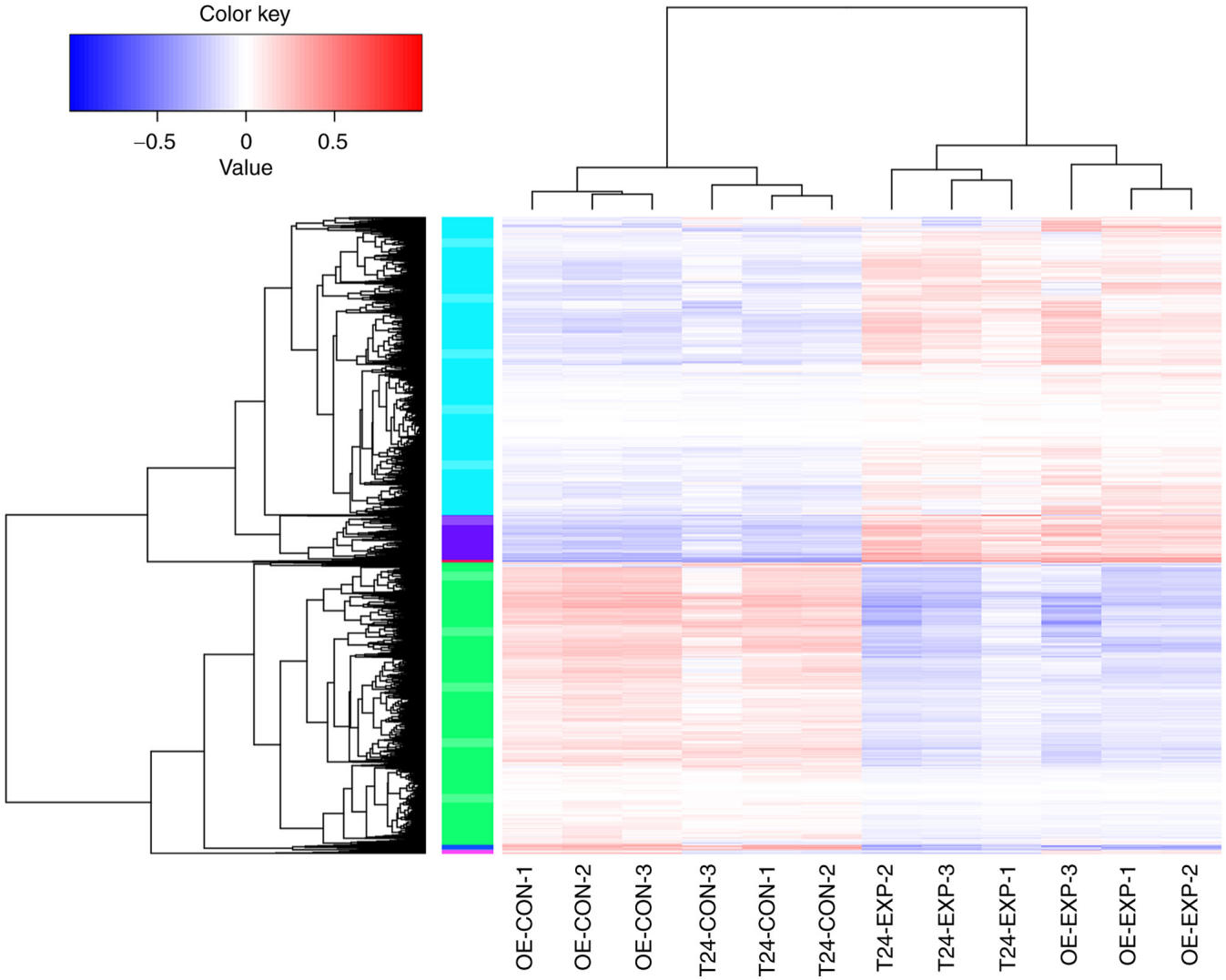

Figure S2. Histogram of GO enrichment in T24 cells. The vertical coordinate is enriched GO term and the horizontal coordinate is the number of differential genes in that term. Different colors are used to distinguish between biological processes, cellular components and molecular functions. GO, Gene Ontology.

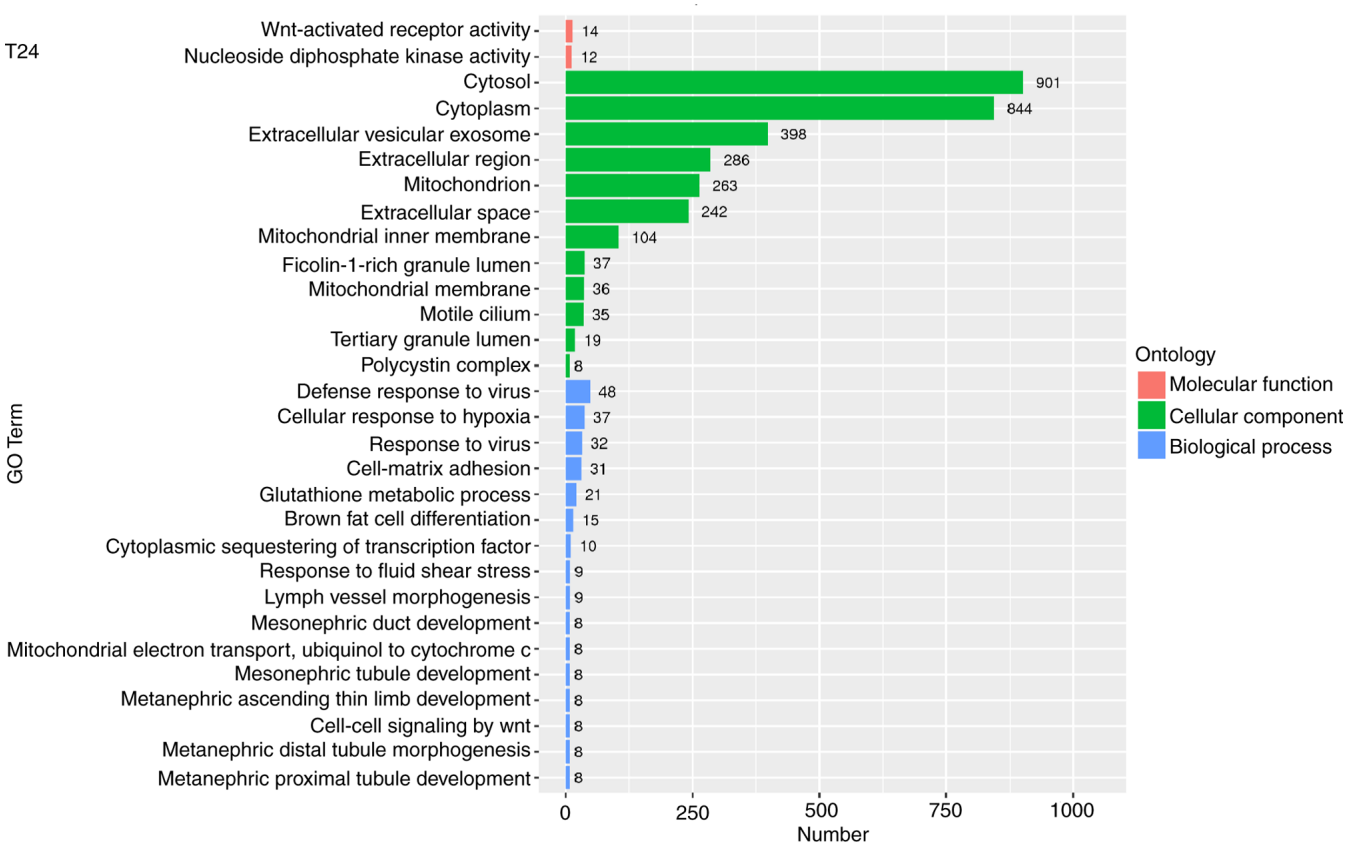

Figure S3. Histogram of GO enrichment in T24-EGFR-OE cells. The vertical coordinate is the enriched GO term and the horizontal coordinate is the number of differential genes in that term. Different colors are used to distinguish between biological processes, cellular components and molecular functions. GO, Gene Ontology; OE, overexpression.

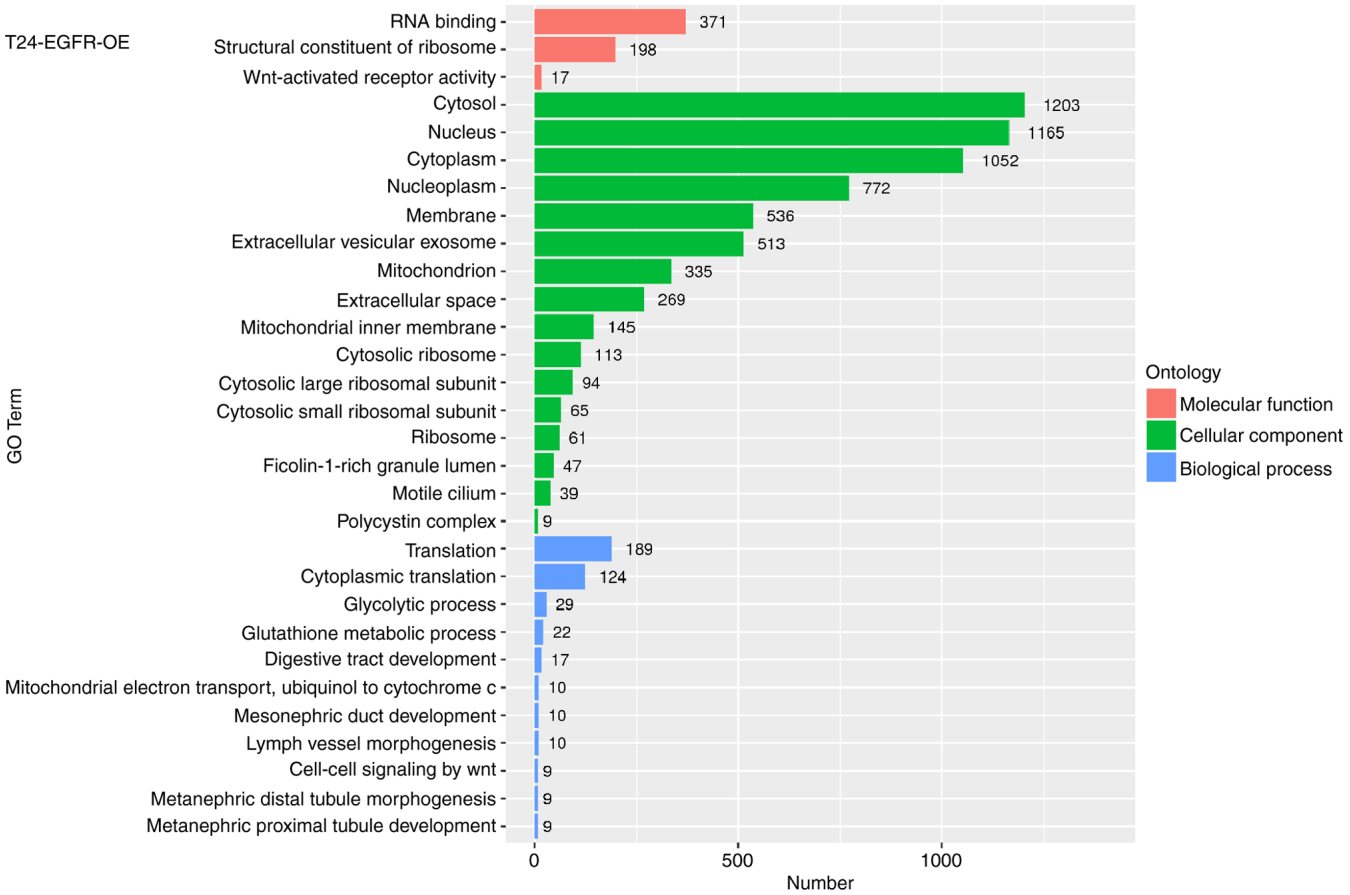

Figure S4. Annotated bar chart of T24 cells significantly enriched in KEGG. Vertical axis indicates pathway name; horizontal axis indicates number of genes. KEGG, Kyoto Encyclopedia of Genes and Genomes.

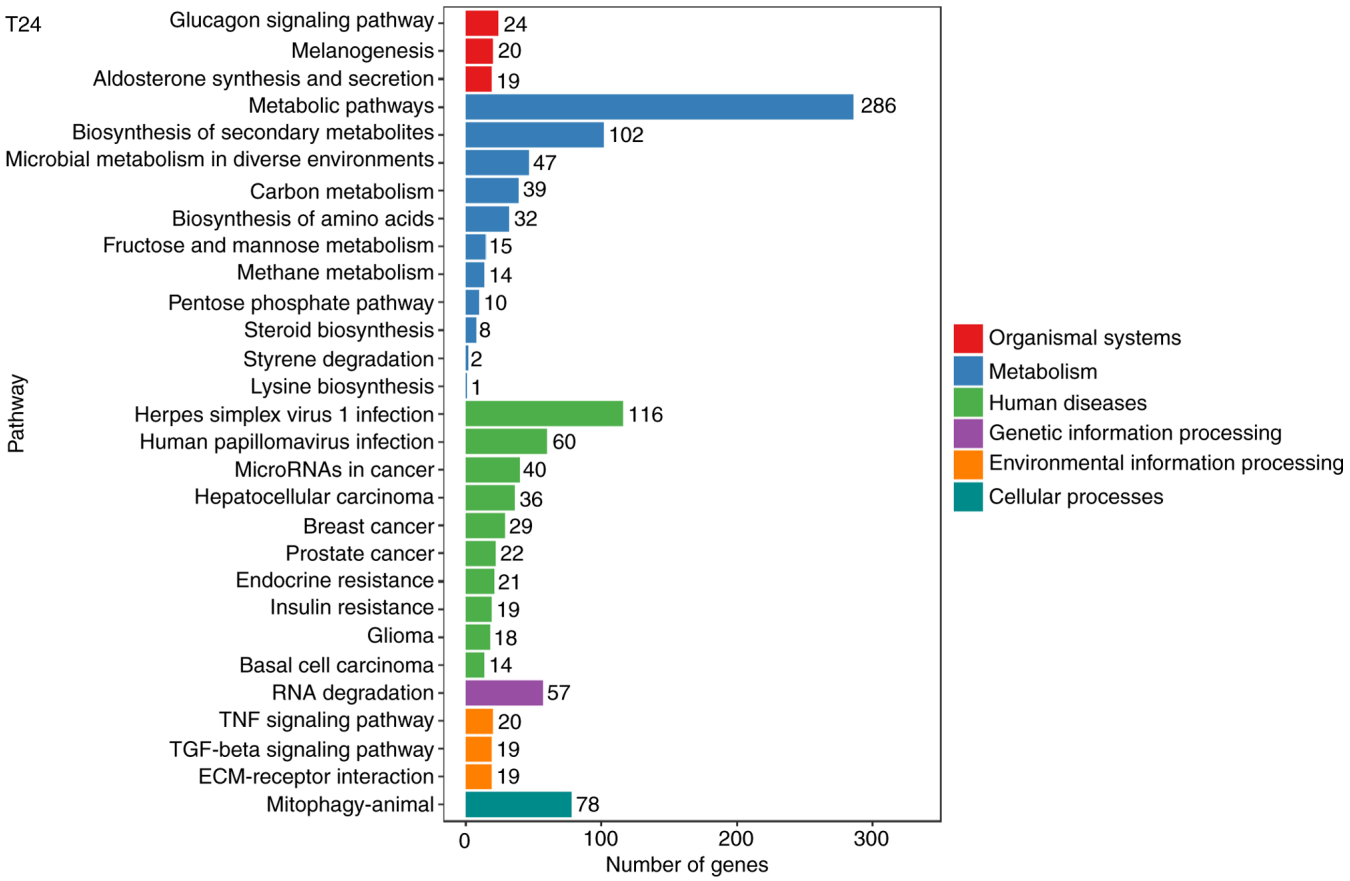

Figure S5. Annotated bar chart of T24-EGFR-OE cells significantly enriched in KEGG. Vertical axis indicates pathway name; horizontal axis indicates number of genes. KEGG, Kyoto Encyclopedia of Genes and Genomes; OE, overexpression.

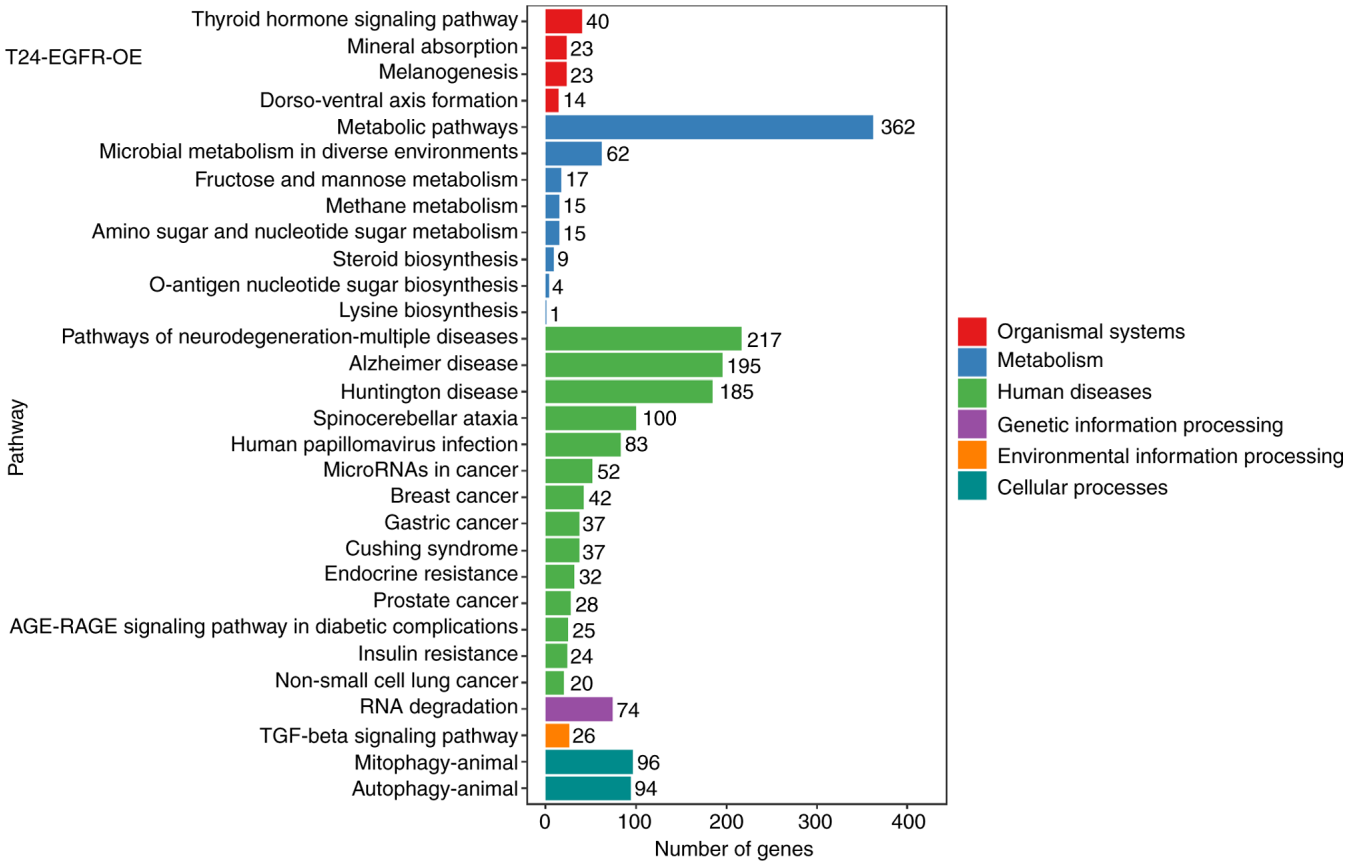

Figure S6. RNA-Seq correlation check. The Pearson correlation Coefficient presents correlation coefficient that indicates the degree and direction of correlation between two variables, which indicates the closeness and direction of correlation between two variables. The larger the absolute value of this coefficient, the more intimate the relationship between the two variables, and its absolute value is between 0 and 1. RNA-Seq, RNA Sequencing; T24-CON, T24 control group; T24-EXP, T24 experimental group; OE-CON, T24-EGFR-OE control group; OE-EXP, T24-EGFR-OE experimental group. 1, 2, 3 present three biological replicates; OE, overexpression.

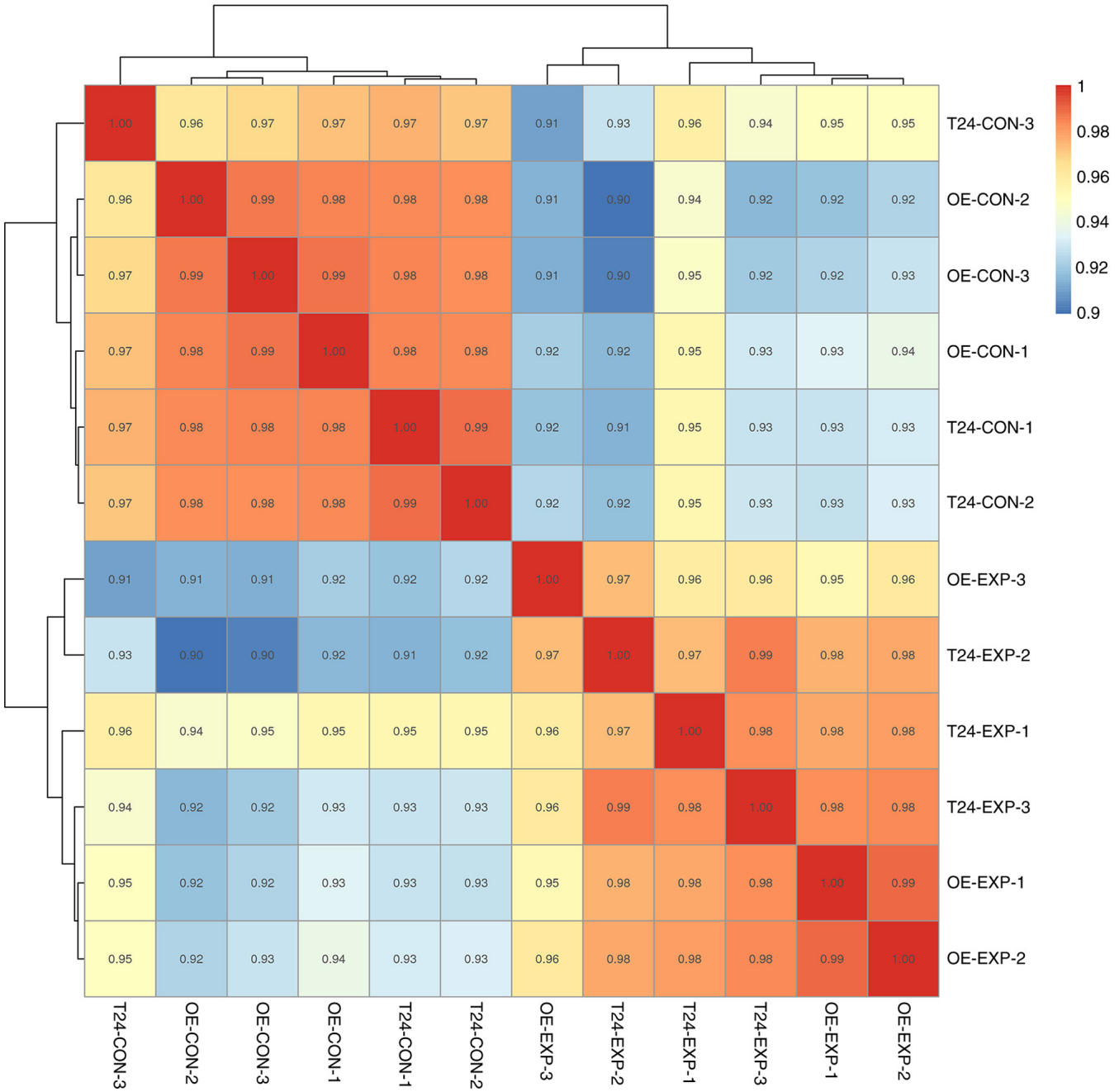

Figure S7. Protein expression of the constructed cell lines. Compared with ordinary T24 cells, the expression of EGFR and p-EGFR in the group of overexpressed EGFR cells are shown in supplement Fig. 7. Data are presented as the mean ± SEM from three independent experiments. ***P<0.001 vs. control. p-, phosphorylated; OE, overexpression.