Figure S1. Comparison of gene expression levels between EC109 cells transfected with Lv-MEG3 or Lv-NC. (A) Scatter plot of mRNAs. Scatter plots were generated to assess variations in mRNA expression. Red and blue spots indicate differentially expressed unigenes, and black indicates unigenes that were not differentially expressed. The values corresponding to the x and y axes are the normalized signal values. (B) Volcano plots of mRNAs were constructed by fold change and P-values. Red and green spots indicate differentially expressed unigenes (red, upregulated; green, downregulated), and gray indicates unigenes that were not differentially expressed between the two groups. (C) Heatmap analysis of unigene expression level, in which each row represents a gene and each column corresponds to each sample. The normalized Z score of gene abundance is depicted by a pseudocolor scale, with red indicating positive expression, yellow equal expression and blue negative expression compared with the values of each gene, whereas the dendrogram displays the results of an unsupervised hierarchical cluster analysis placing similar genome profile values near each other. Visual inspection of the dendrogram and heat map demonstrates the ability of these genes to distinguish between EC109 cells transfected with Lv-MEG3 or Lv-NC. MEG3, maternally expressed gene 3; Lv, lentiviral vector; NC, negative control.
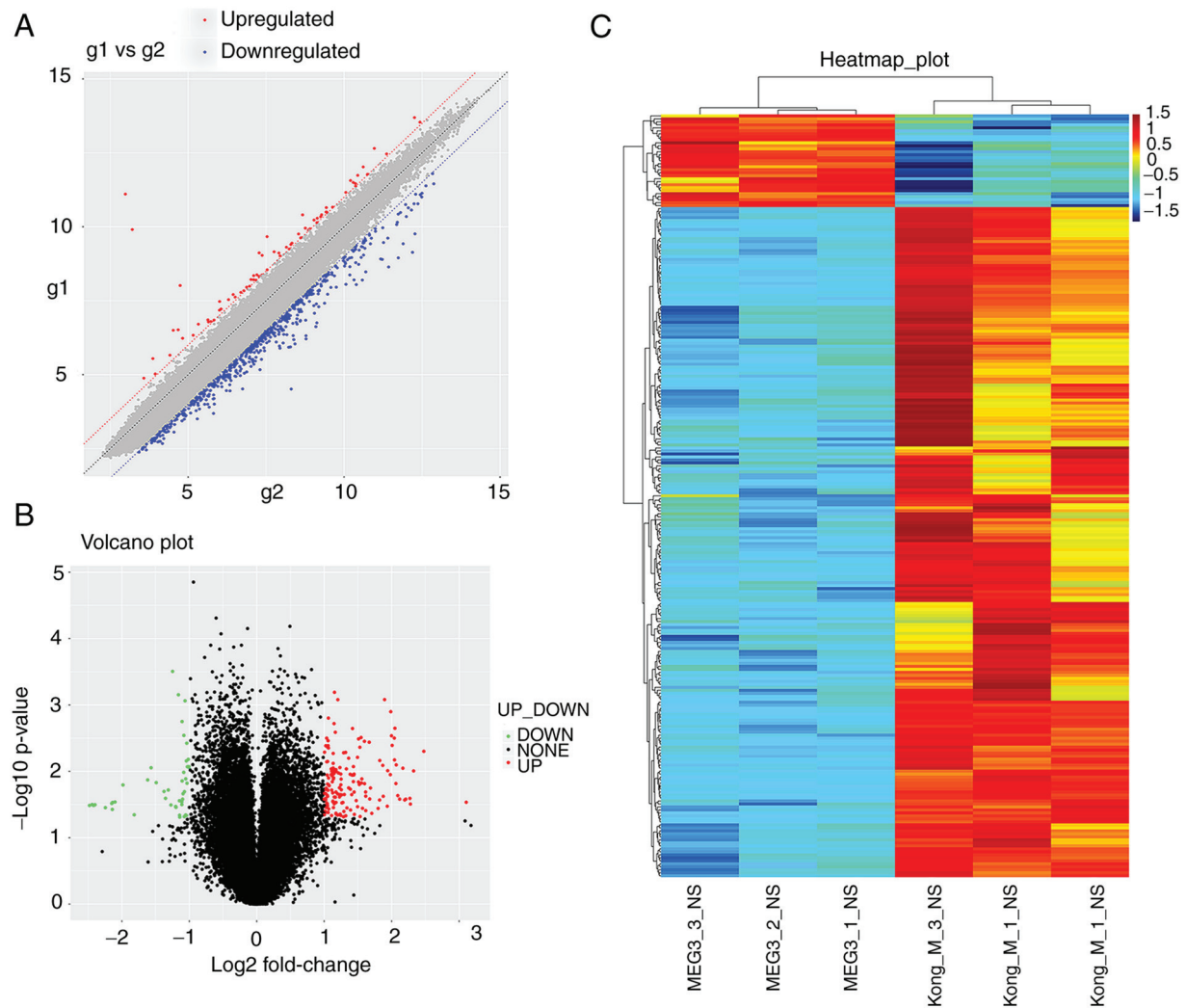
Figure S2. GO and KEGG pathway enrichment analyses for MEG3-related mRNAs. (A and B) Plot of the enriched GO terms. GO enrichment analysis for MEG3-related mRNAs. The y axis represents the enriched GO terms, while the x axis in panel (A) represents the number of MEG3-related mRNAs enriched in GO terms. The x axis in panel (B) represents the ratio of the MEG3-related mRNAs enriched in GO terms.
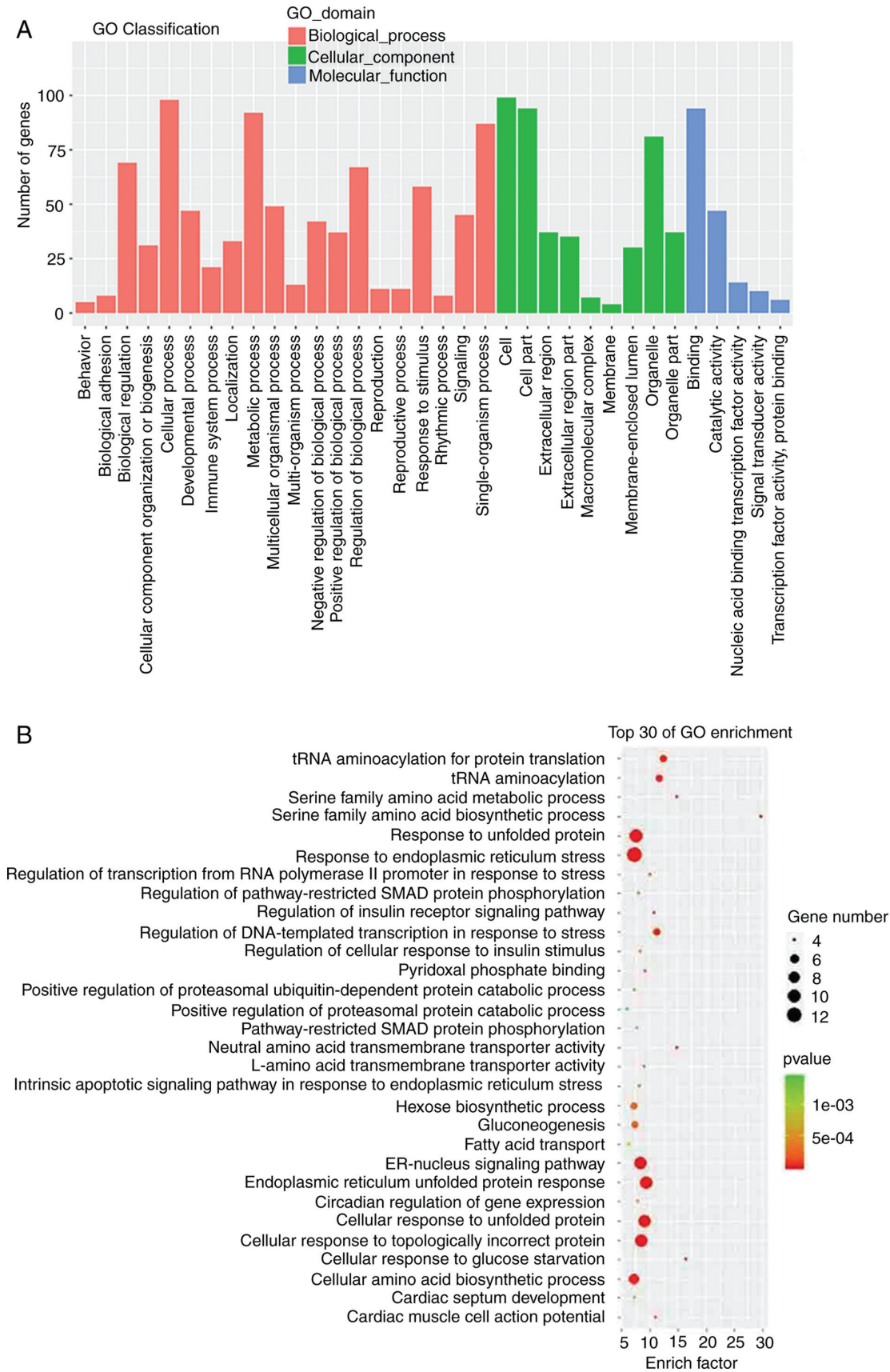
Figure S2. Continued. GO and KEGG pathway enrichment analyses for MEG3-related mRNAs. (C and D) Plot of KEGG pathways. KEGG pathway enrichment analysis for MEG3-related mRNAs. The y axis represents pathways, while the x axis in panel (C) represents the number of MEG3-related mRNAs enriched in KEGG pathways. In panel (D), the x axis represents the ratio of the MEG3-related mRNAs enriched in KEGG pathways. The color and size of each bubble represent enrichment significance and the number of MEG3-related mRNAs enriched in a GO term or pathway, respectively. $P<0.05$ was used as the threshold to select GO and KEGG terms. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; MEG3, maternally expressed gene 3.
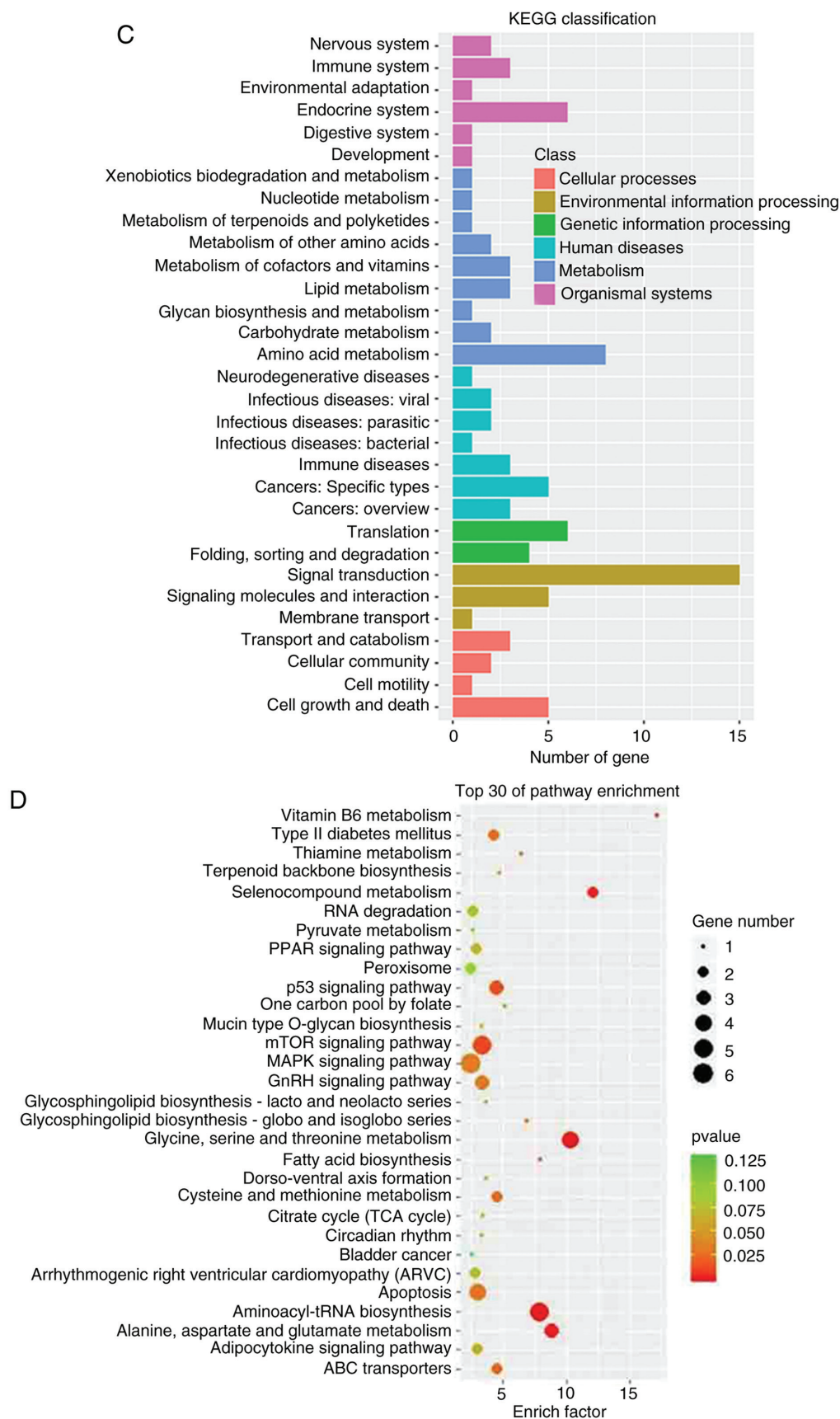
Figure S3. Protein-protein interaction networks of the proteins encoded by the top 50 differentially expressed genes. Each node represents the relevant gene. Analysis was performed with STRING75, utilizing the following settings: Minimum interaction score of 0.4; first shell of <10 interactors; and second shell with <5. Active interaction sources were text mining, experimental, databases, co-expression, neighborhood, gene fusion and co-occurrence. The line thickness indicates the strength of the data supporting the network edges.