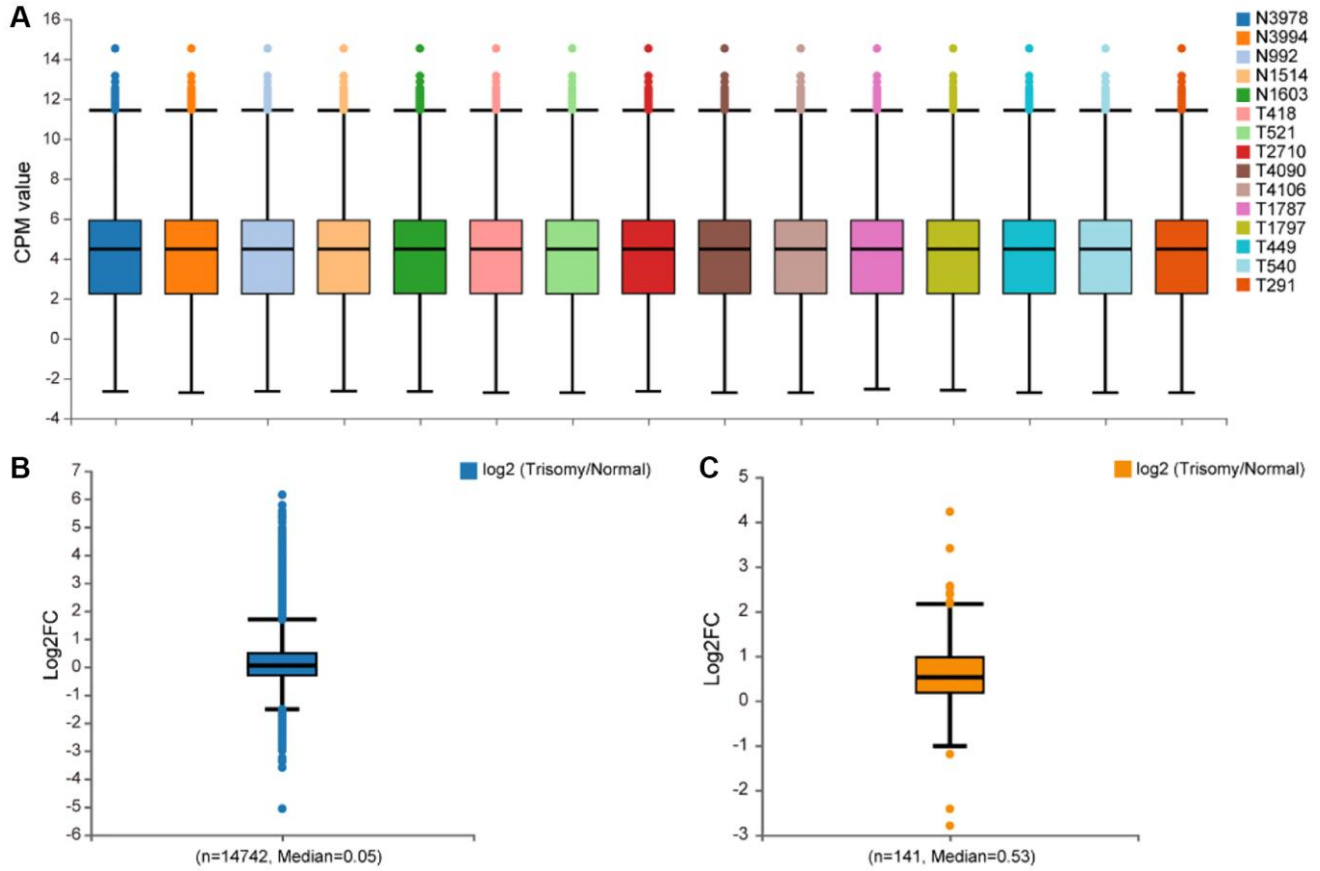
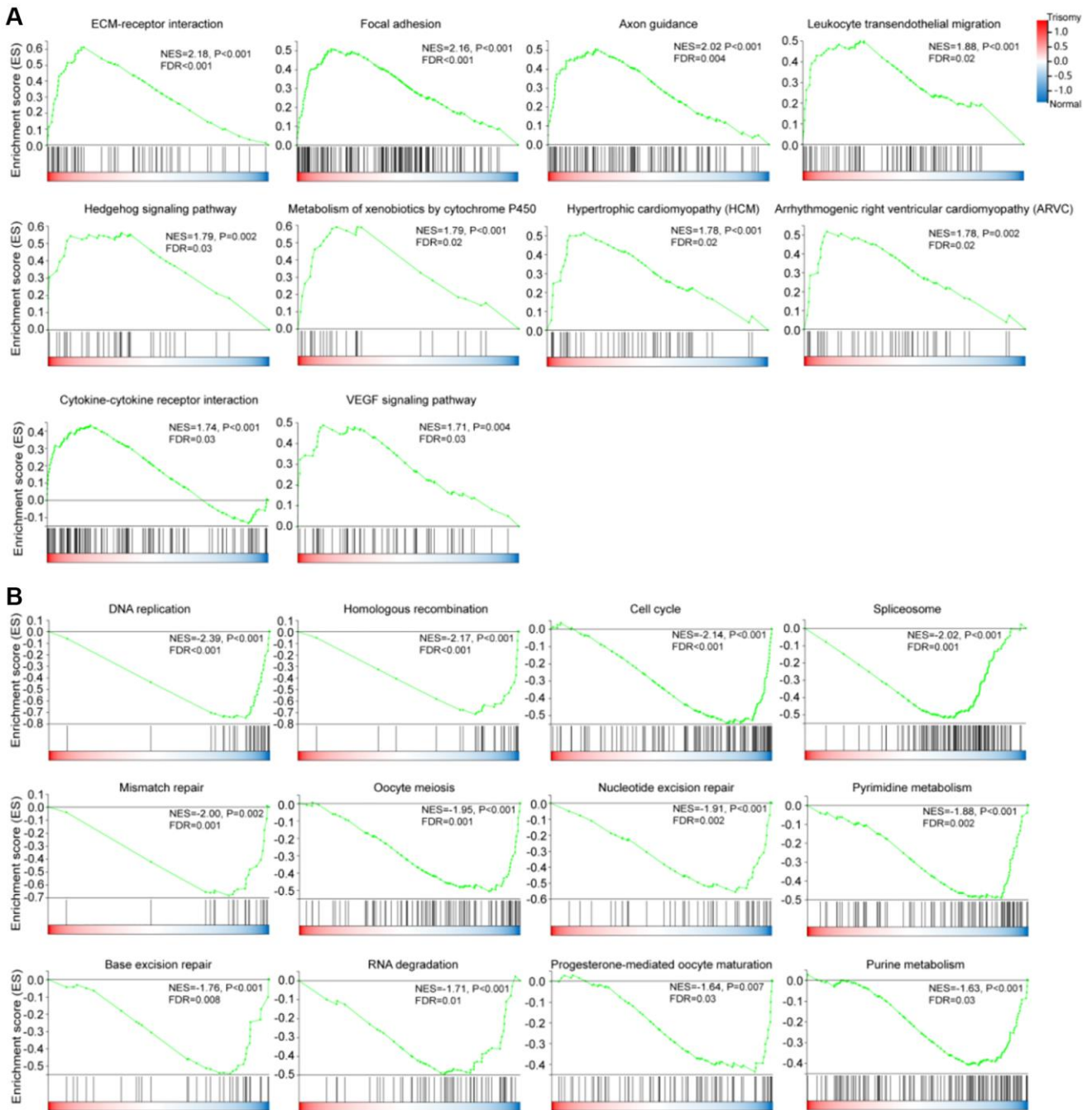


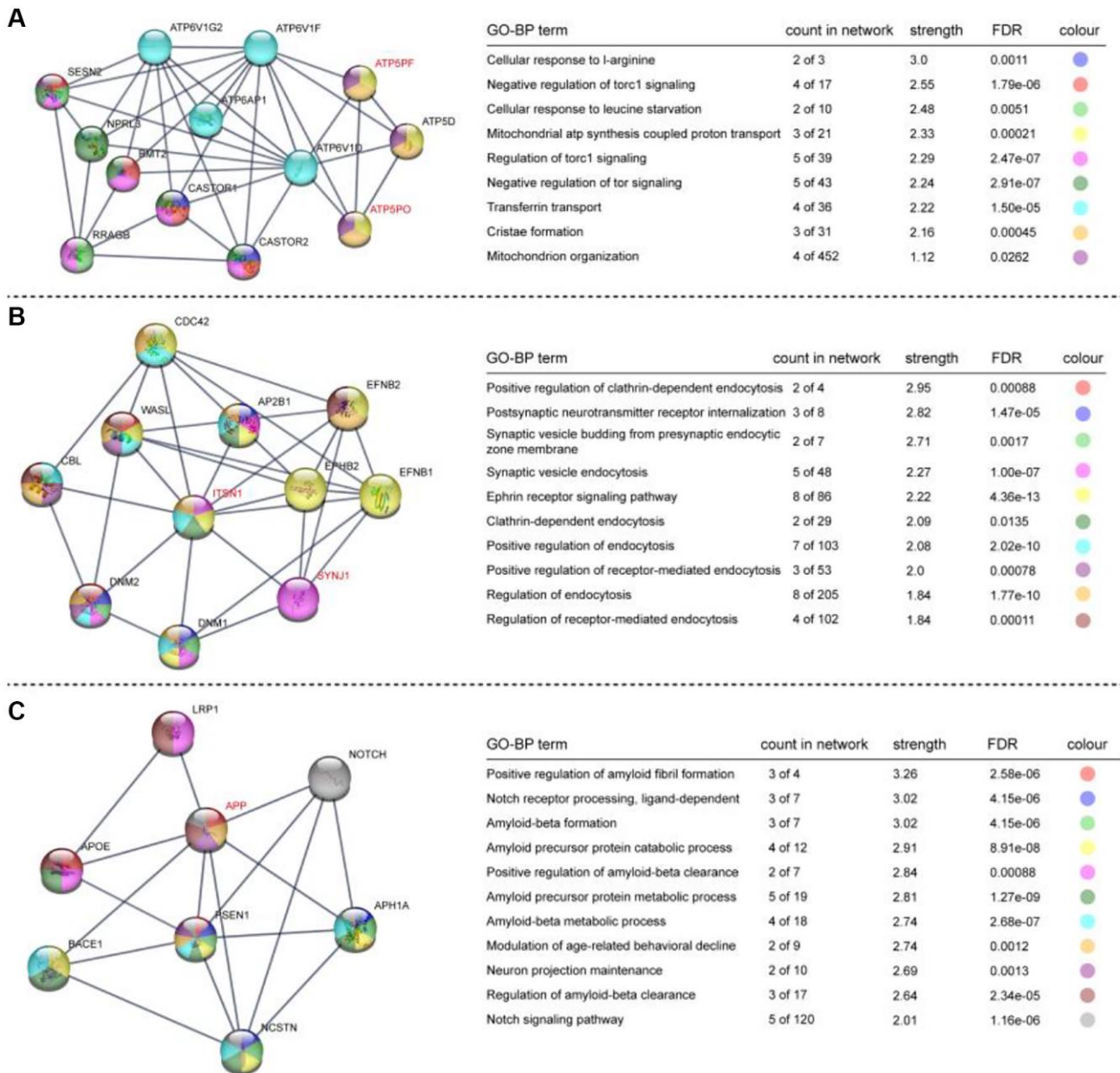
SUPPLEMENTARY FIGURES



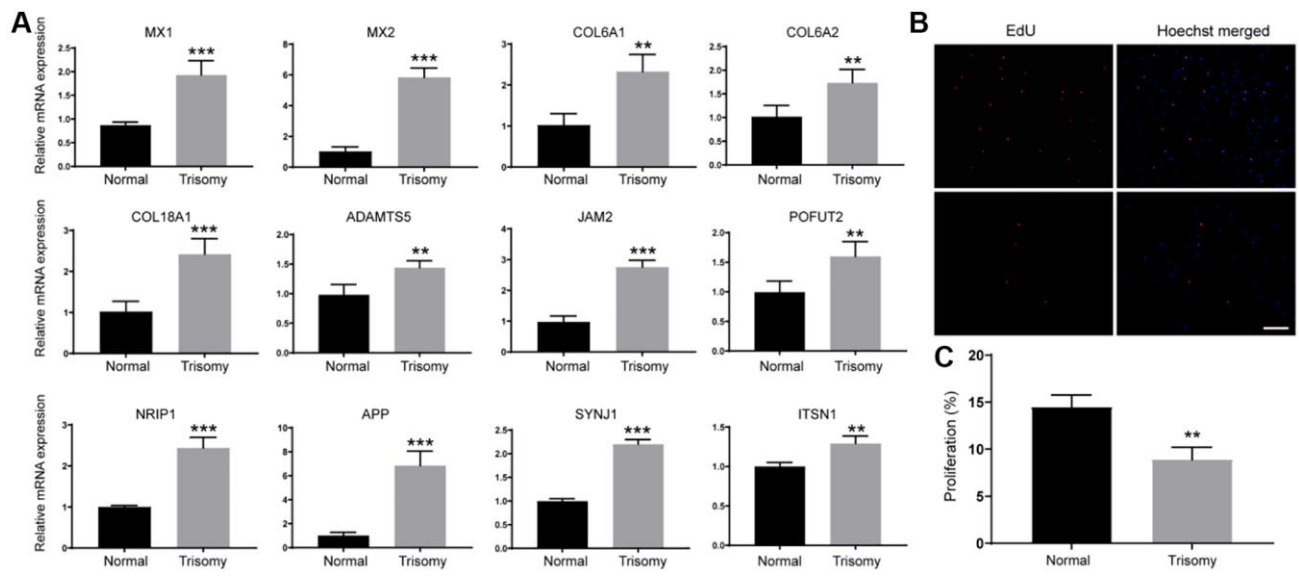
Supplementary Figure 1. Distribution of mRNA expression and fold change in Normal versus Trisomy. (A) Boxplot of mRNA expression in each sample from this study. (B) Boxplot of all the mRNA fold change distribution in Normal versus Trisomy. (C) Boxplot of HSA21 genes' fold change distribution in Normal versus Trisomy.



Supplementary Figure 2. Gene set enrichment analysis (GSEA) of all expressed genes in the “C2: curated gene sets” KEGG gene sets collection of MSigDB (Broad Institute). (A) Enriched GSEA KEGG pathways in Trisomy group. (B) Enriched GSEA KEGG pathways in Normal group.



Supplementary Figure 3. HSA21 up-regulated genes involved STRING protein network. (A–C) Secondary 3 networks clustered in the upregulated genes. The HSA21-related genes are marked in red.



Supplementary Figure 4. Gene expression validation and cell proliferation assay. (A) RT-qPCR validation of 12 HSA21 genes ($n = 4$, ** $p < 0.01$, *** $p < 0.001$). (B) Microscope images of EdU staining in amniocytes from Normal and Trisomy group (scale bar = 100 μm). (C) Quantitative results of proliferation ability in each group ($n = 3$, ** $p < 0.01$).