Key Genes Identified in Nonsyndromic Microtia by Analysis of Transcriptomics and Proteomics

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Supplementary Figures

Figure S1. KEGG analysis for TFs and their target genes enriched in the blue, dark red, and dark turquoise modules.

Figure S2. Distribution features of gene expression before and after normalization of data among CS and NSM samples.
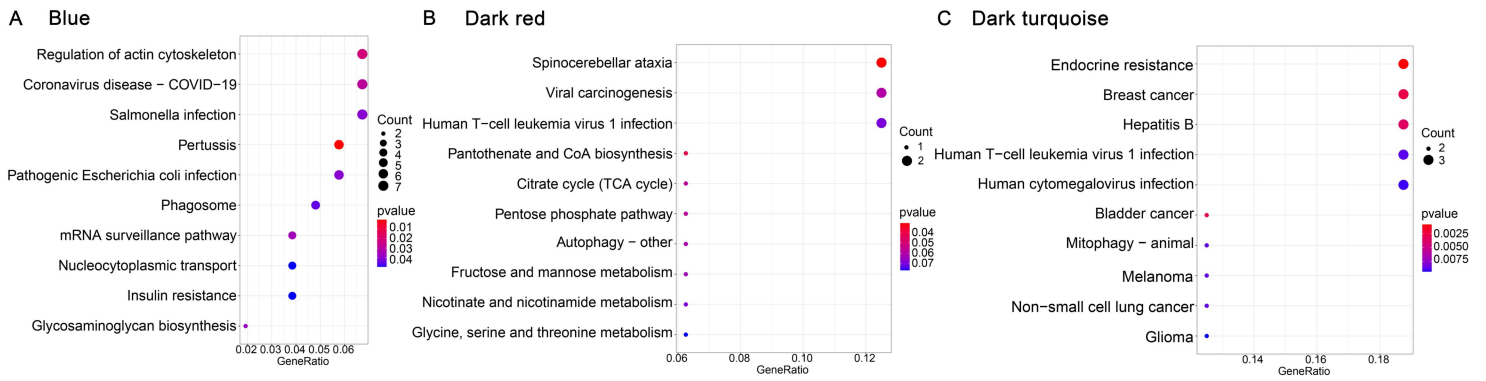
Figure S1.

Figure S1. KEGG analysis for TFs and their target genes enriched in the blue, dark red, and dark turquoise modules. The size of the dot represents gene count, and the color represents the P value. P < 0.05 is considered to be statistically significant.
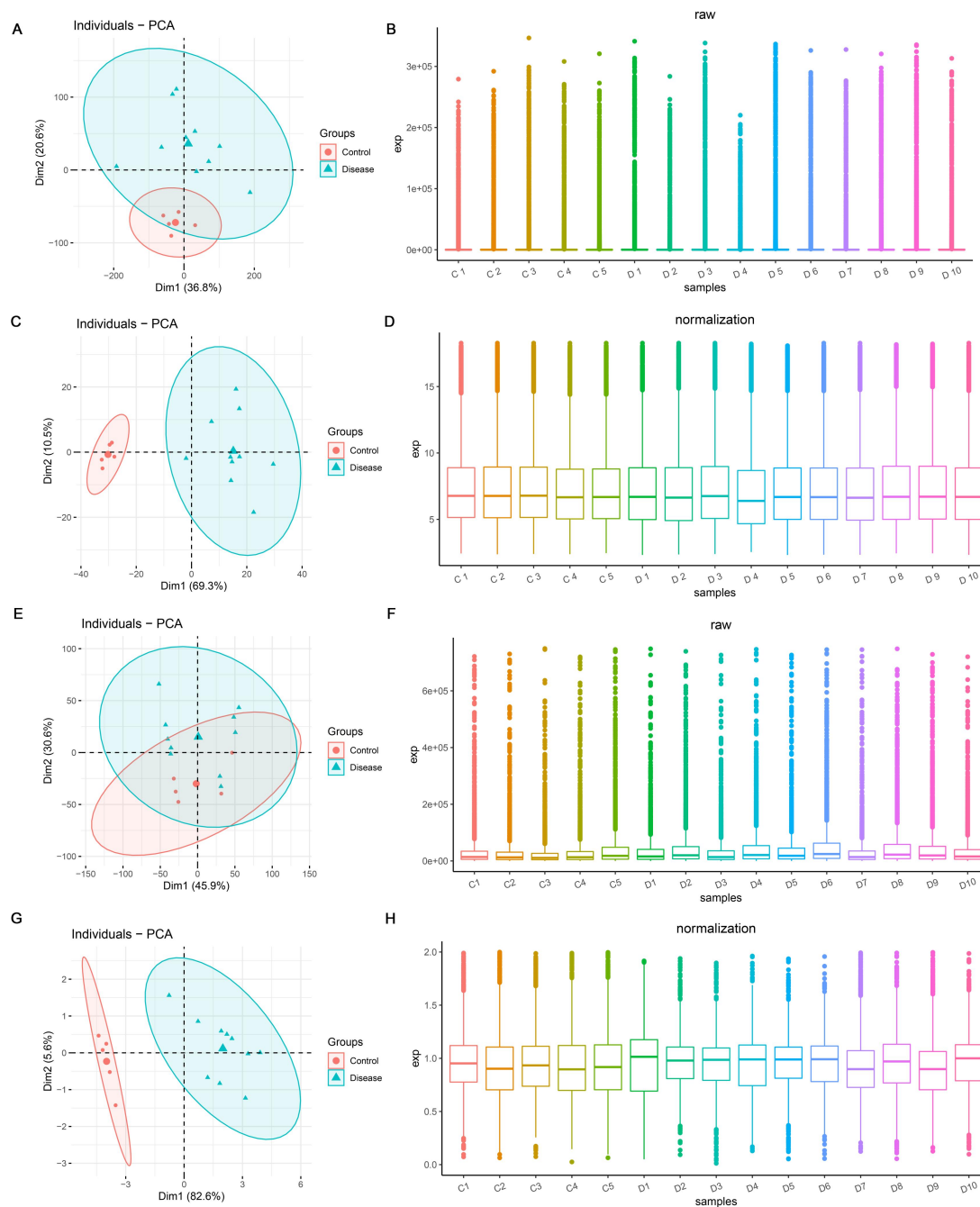
Figure S2.

Figure S2. Distribution features of gene expression before and after normalization of data among CS and NSM samples. A-B. Transcriptomics data before normalization. C-D. Transcriptomics data after normalization. E-F. Proteomics data before normalization. G-H. Proteomics data after normalization. A, C, E, G. PCA. The red dots represent the CS group and the blue dots represent the NSM group. B, D, F, H. Box plot. The horizontal axis stands for different samples, while the vertical axis represents expression value. The horizontal line within each box represents the median, and the top and bottom of each box indicate the 75th and 25th percentile.