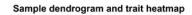
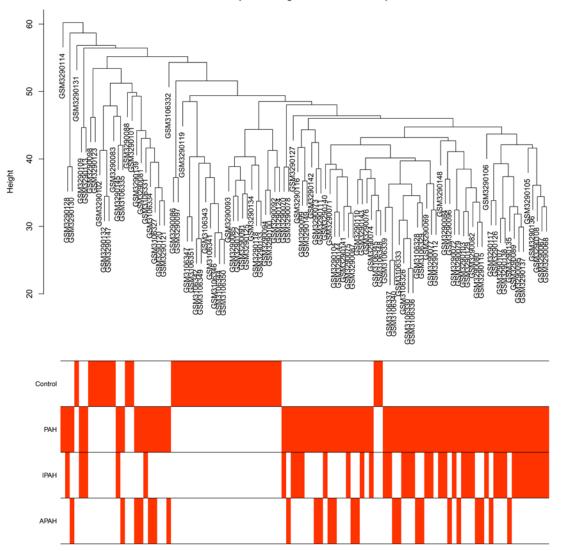
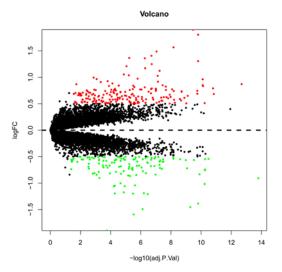
Bioinformatics analysis of the differentially co-expressed genes and immune cell infiltration features associated with pulmonary arterial hypertension

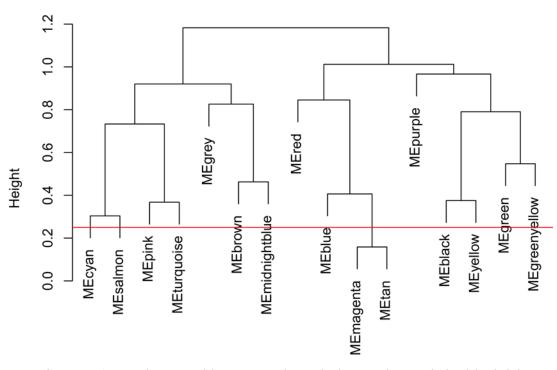




Supplementary Figure 1. Sample dendrogram and trait heatmap



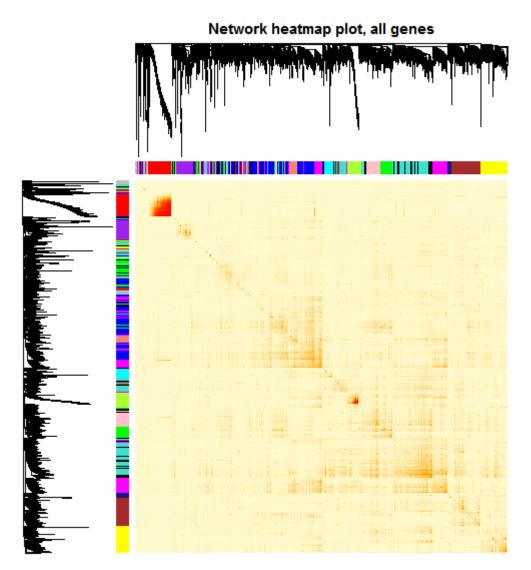
**Supplementary Figure 2.** Volcano plots of differentially expressed genes (DEGs) that have different expression between pulmonary arterial hypertension (PAH) lung tissues and normal lung tissues. Upper red dots: upregulated genes; lower green dots: down-regulated genes. Gray dots indicate the remaining genes that were not significantly changed



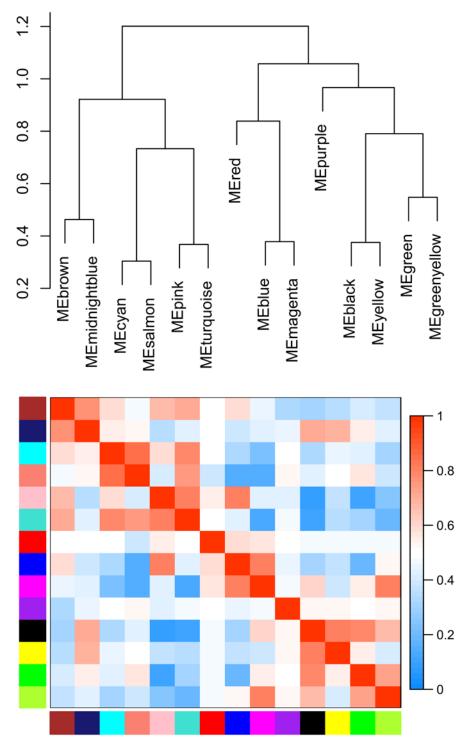
## Clustering of module eigengenes

**Supplementary Figure 3.** The gene modules were merged using the dynamic splicing method with height below 0.25.

Bioinformatics analysis of the differentially co-expressed genes and immune cell infiltration features associated with pulmonary arterial hypertension

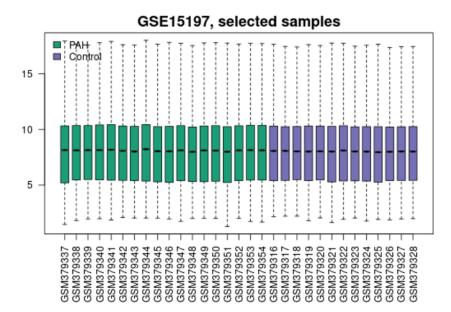


Supplementary Figure 4. Interactive relationship analysis of co-express genes. The light color indicates topological overlap, while the darker color indicates a high topological overlap



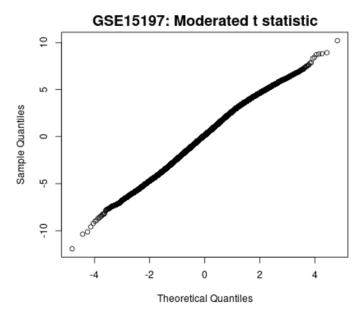
Supplementary Figure 5. Dendrogram and unsupervised hierarchical clustering heatmap of module eigengenes

Bioinformatics analysis of the differentially co-expressed genes and immune cell infiltration features associated with pulmonary arterial hypertension

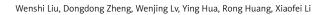


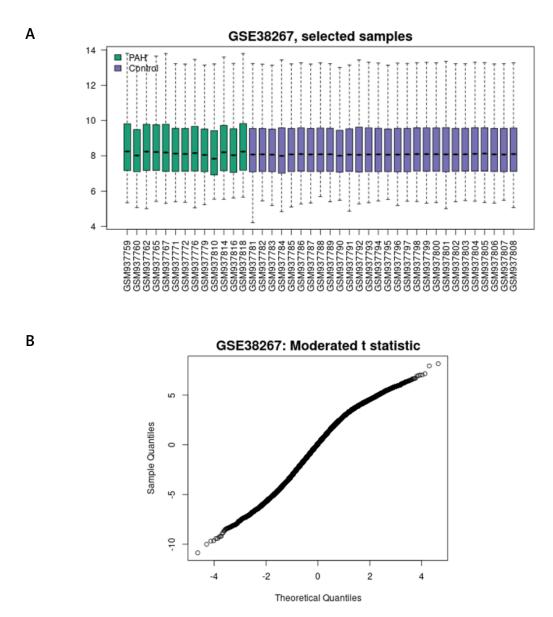
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Supplementary Figure 6. GEO2R online analysis of gene expression profile data GSE15197





Supplementary Figure 7. GEO2R online analysis of gene expression profile data GSE38267