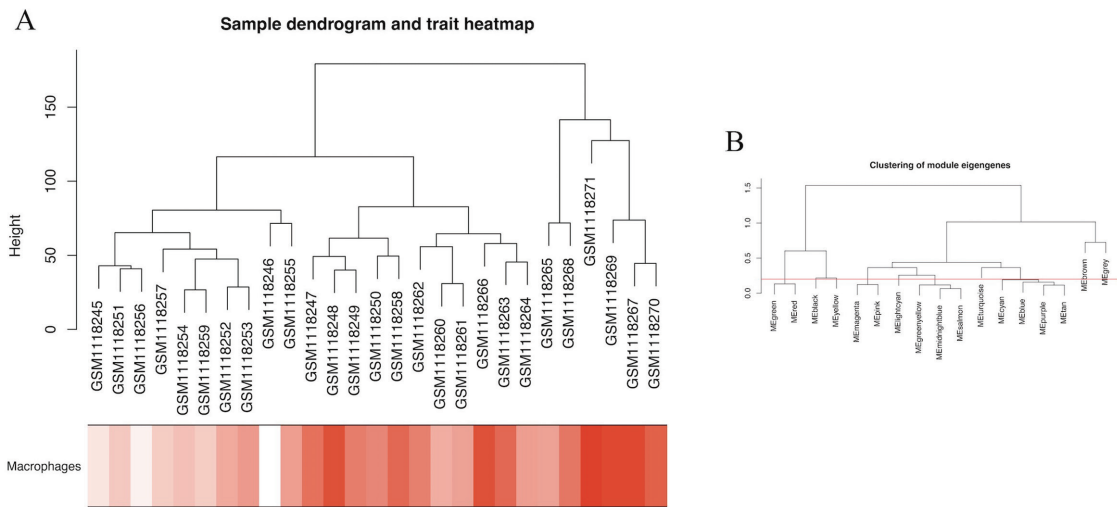
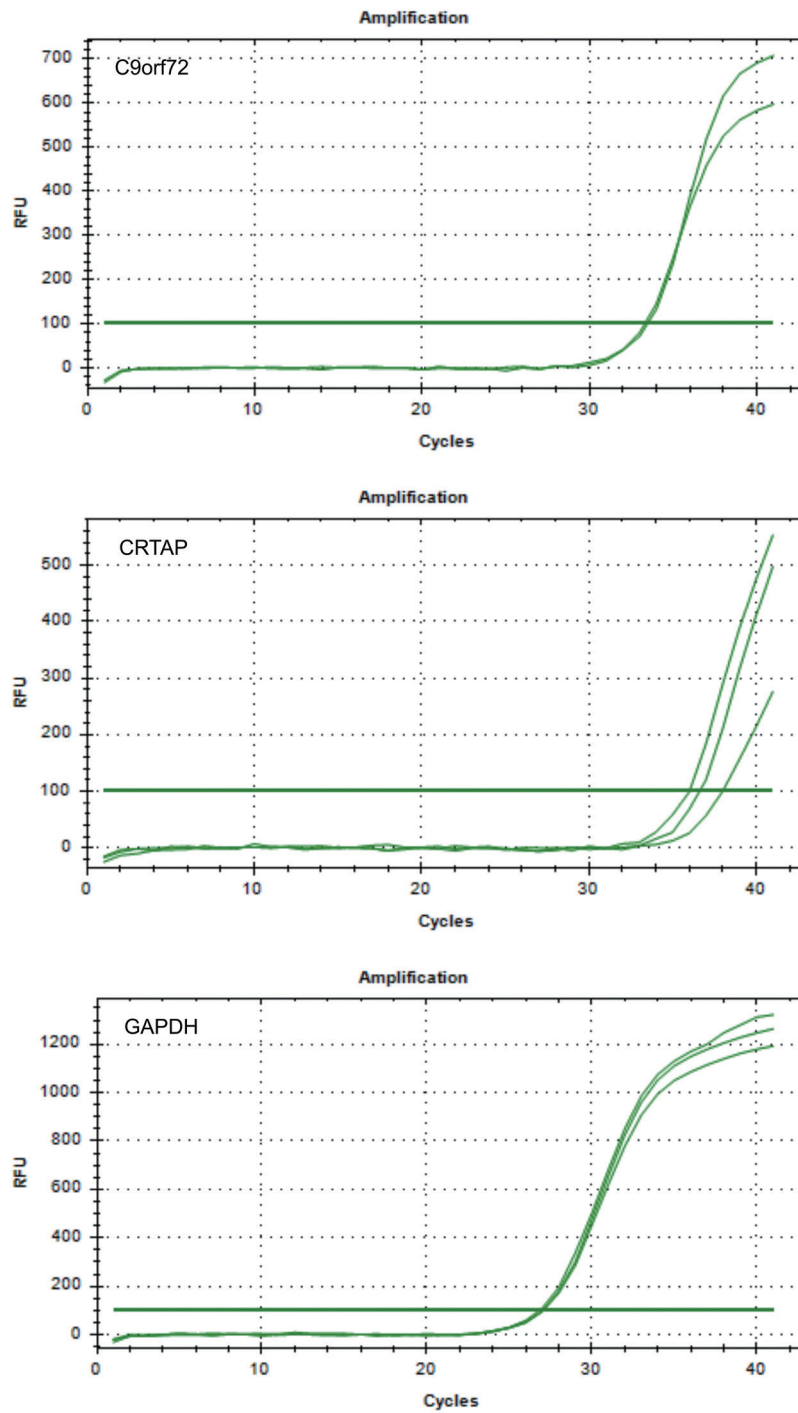




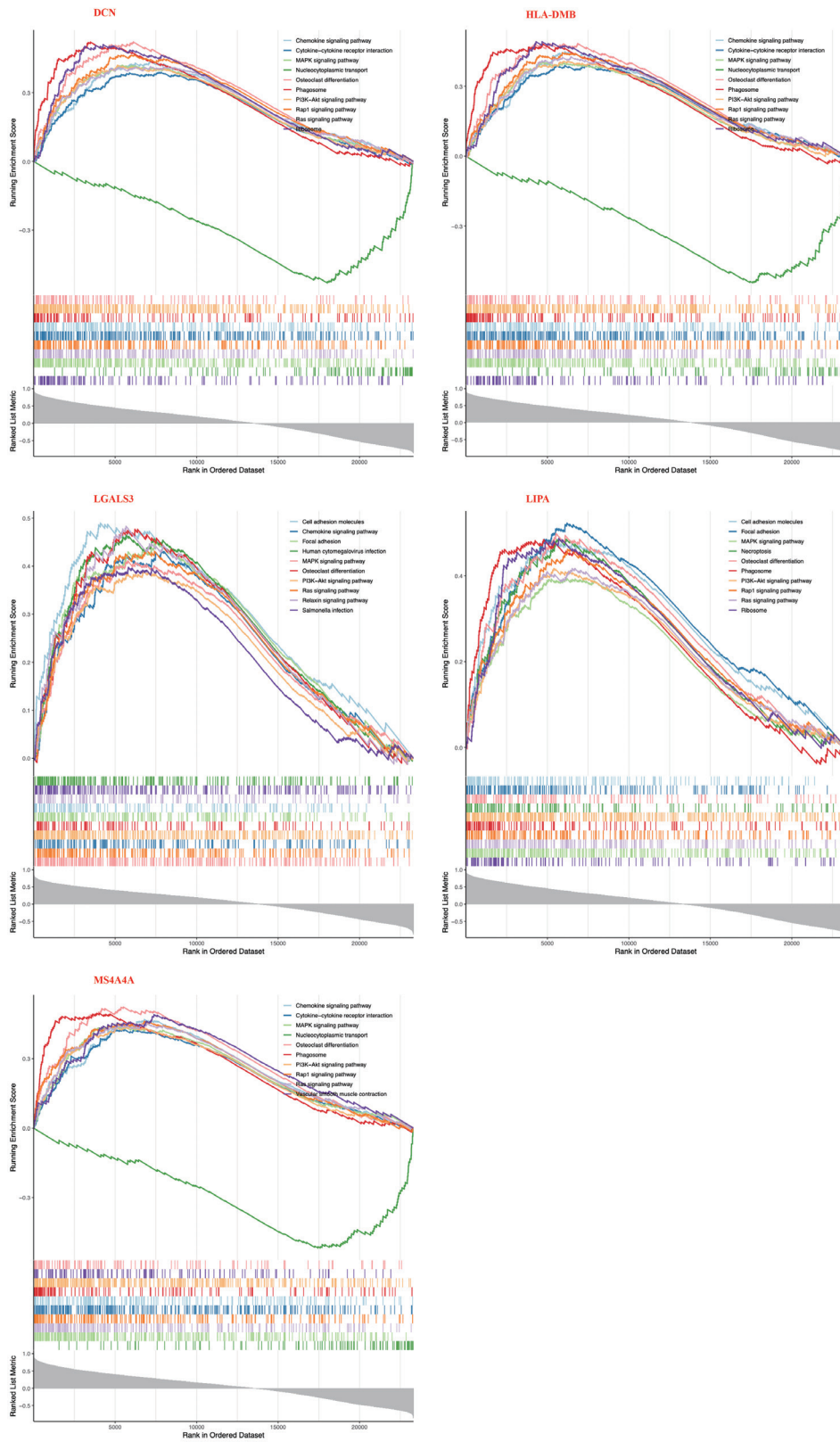
Figure S1 The violin plot of the 18 cell clusters (Clusters 0-17).



**Figure S2** WGCNA data set preprocessing. (A). Sample clustering and outlier checking, and sample clustering heat map based on macrophage scores. (B). The merged dynamic shear-tree algorithm was used to analyze similar modules by setting MEDissThres to 0.2. WGCNA module selection by the soft threshold.



**Figure S3** The amplification curves of *C9orf7*, *CRTAP*, and *GAPDH* in RT-qPCR. RFU, relative fluorescence units.



**Figure S4** Single-gene enrichment analyses of *DCN*, *HLA-DMB*, *LGALS3*, *LIPA*, and *MS4A4A*.