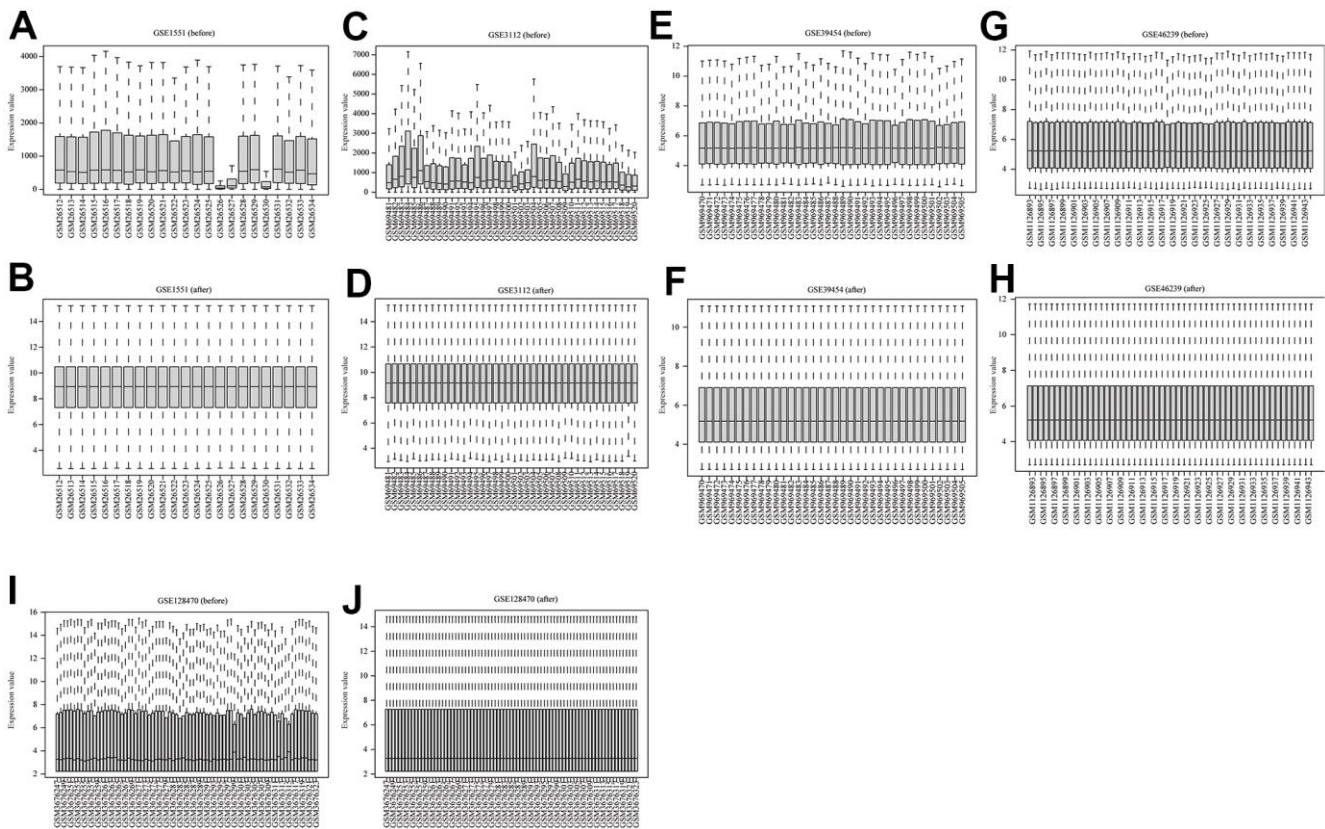
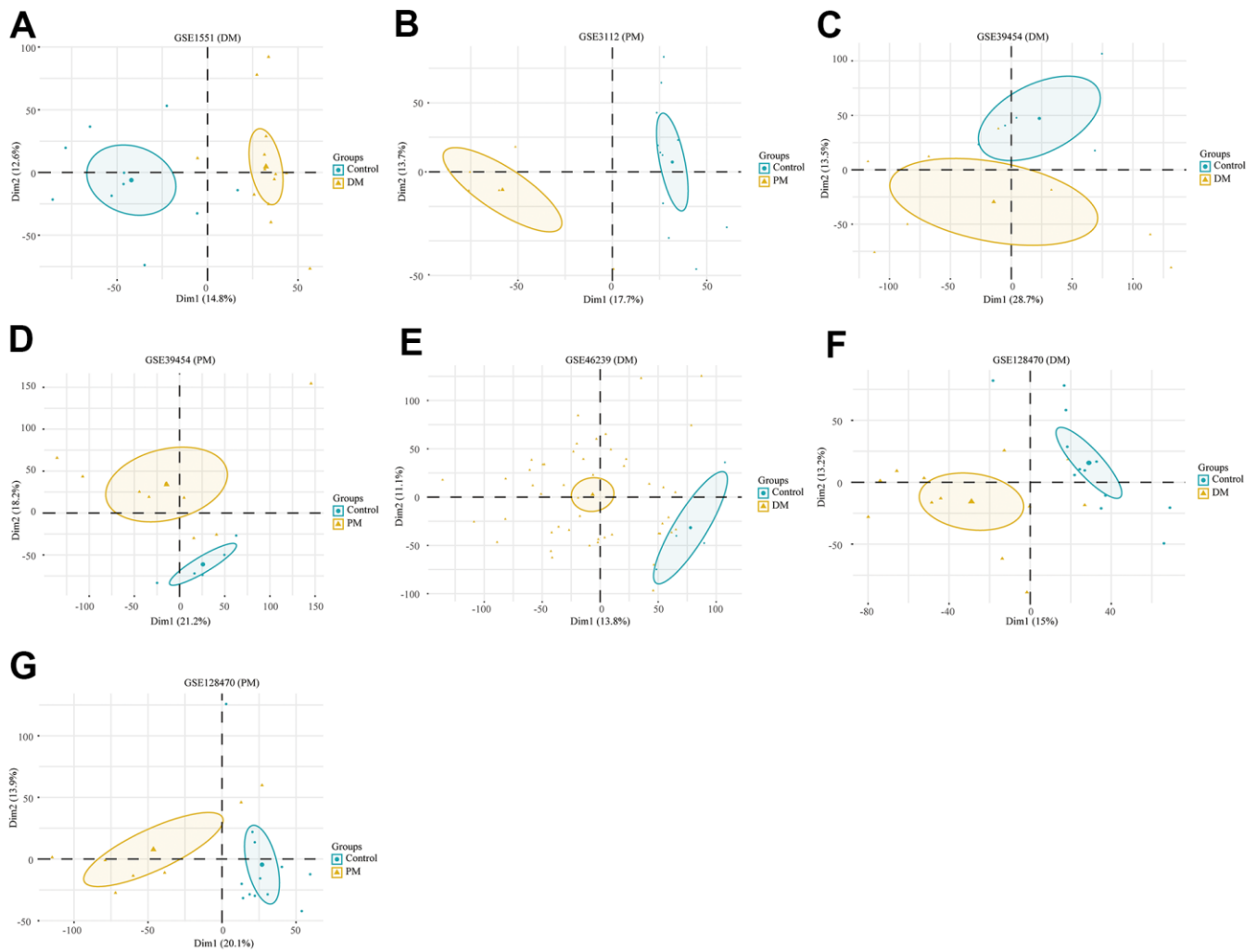


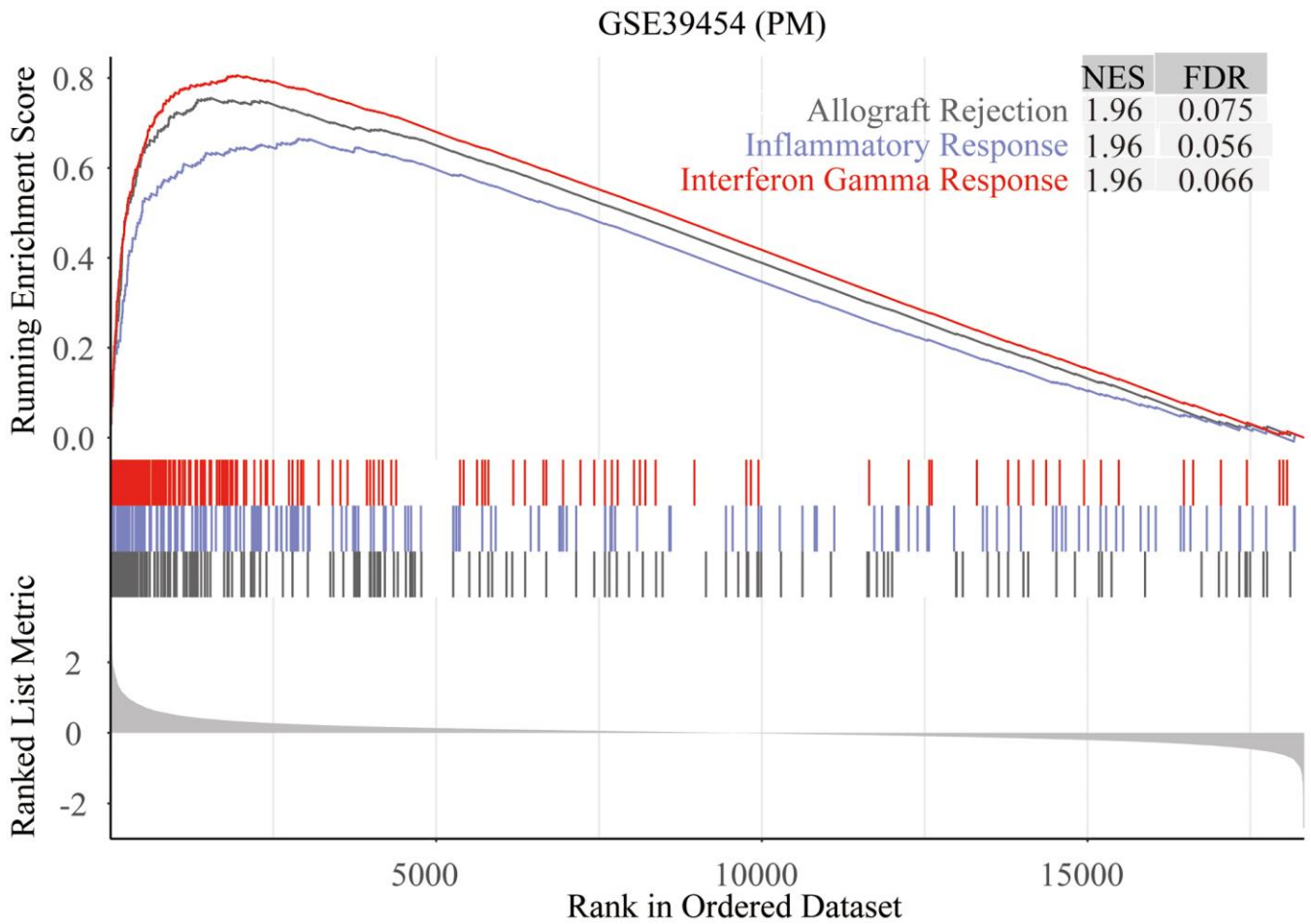
SUPPLEMENTARY FIGURES



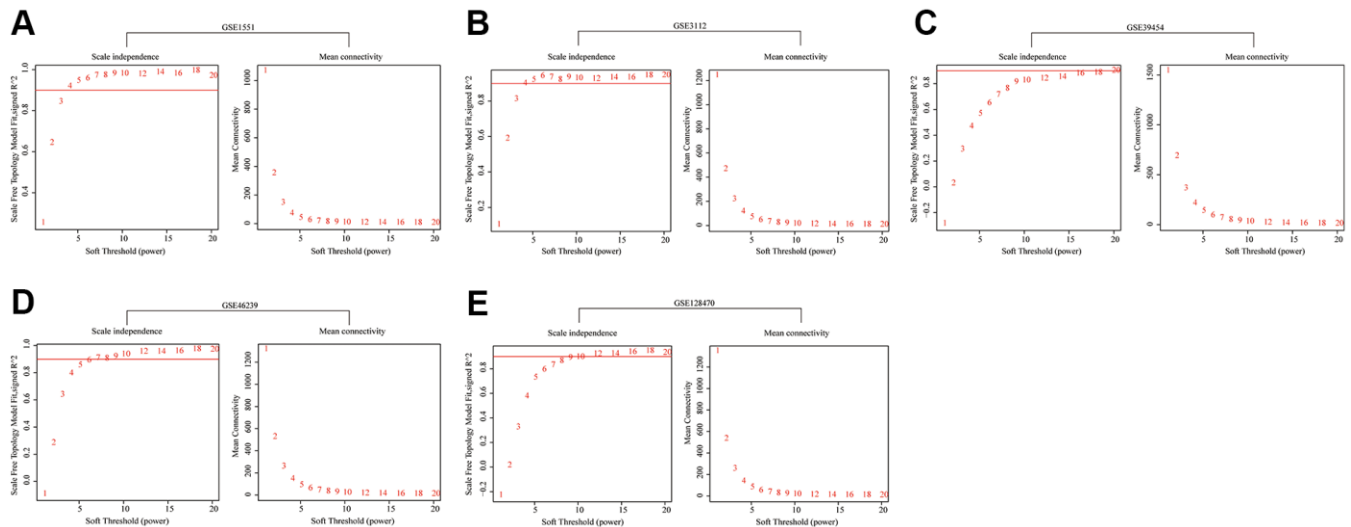
Supplementary Figure 1. Standardization of the five gene expressions. (A) Before normalization of GSE1551 microarray; (B) After normalization of GSE1551 microarray; (C) Before normalization of GSE3112 microarray; (D) After normalization of GSE3112 microarray; (E) Before normalization of GSE39454 microarray; (F) After normalization of GSE39454 microarray; (G) Before normalization of GSE46239 microarray; (H) After normalization of GSE46239 microarray; (I) Before normalization of GSE128470 microarray; (J) After normalization of GSE128470 microarray.



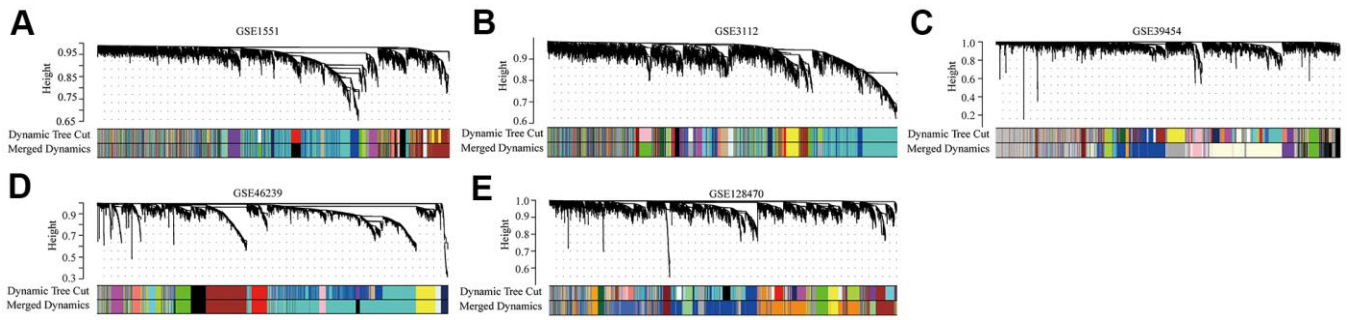
Supplementary Figure 2. Principal component analyses (PCA) performed on of seven data series. (A) GSE1551 (dermatomyositis, DM); **(B)** GSE3112 (polymyositis, PM); **(C)** GSE39454 (DM); **(D)** GSE39454 (PM); **(E)** GSE46239 (DM); **(F)** GSE128470 (DM); **(G)** GSE128470 (PM).



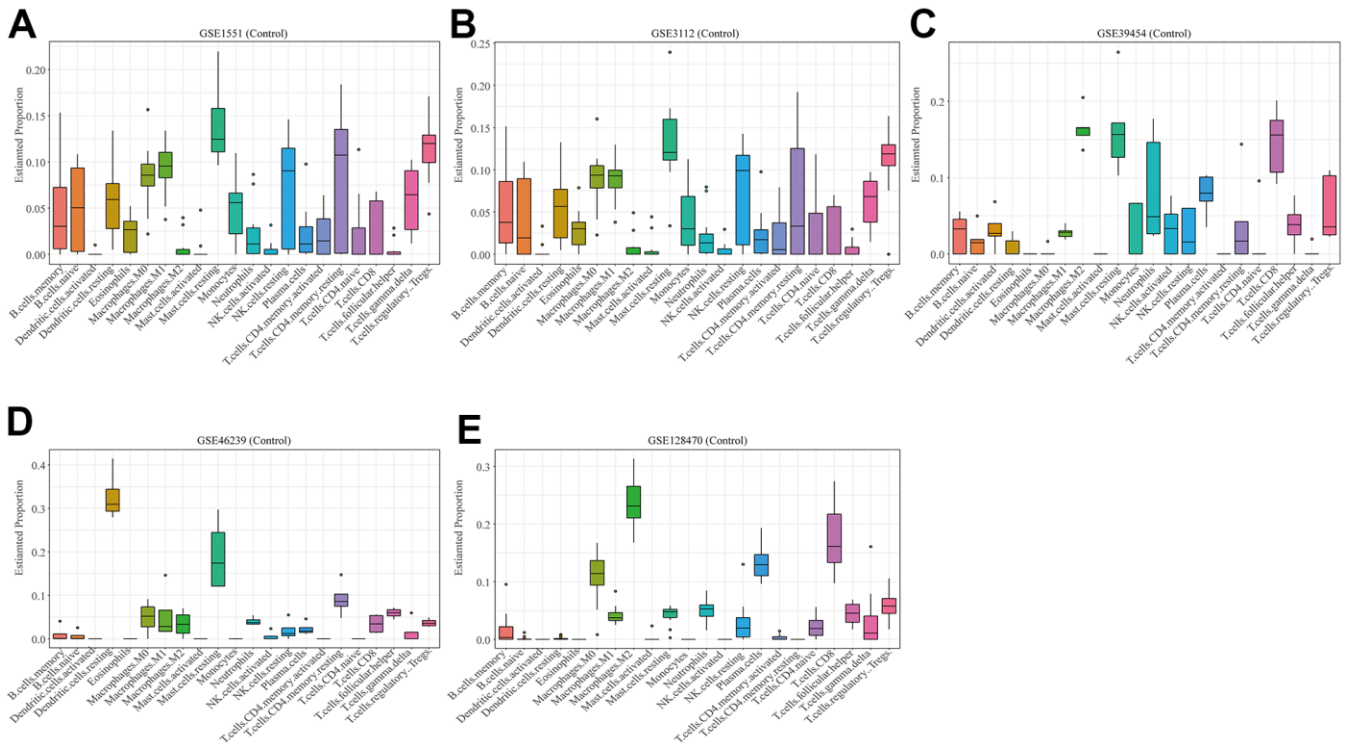
Supplementary Figure 3. Gene set enrichment analysis (GSEA) result of GSE39454 (PM).



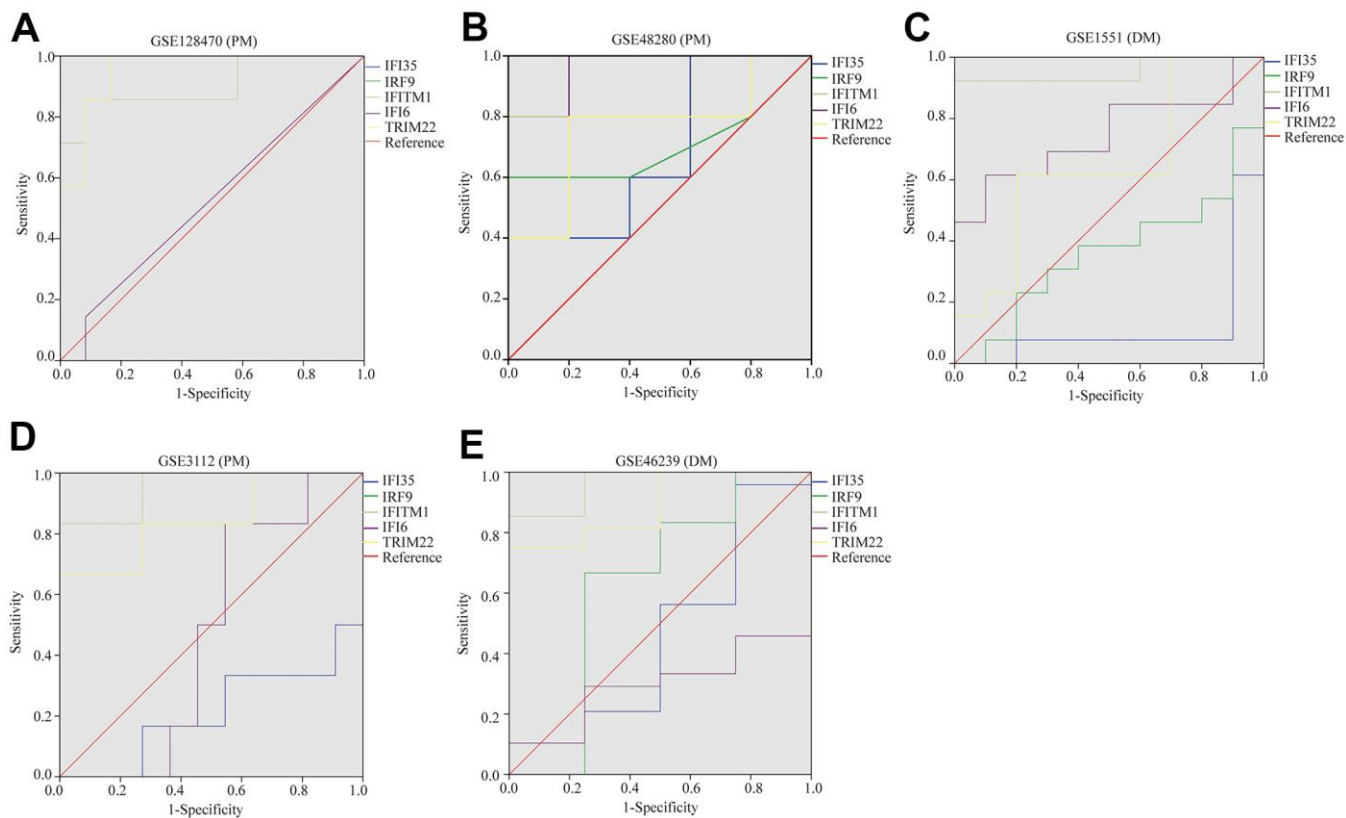
Supplementary Figure 4. Weighted gene co-expression network analysis (WGCNA) soft thresholds of the five microarrays. (A) GSE1551; (B) GSE3112; (C) GSE39454; (D) GSE46239; (E) GSE128470.



Supplementary Figure 5. WGCNA cluster dendrograms of the five microarrays. (A) GSE1551; (B) GSE3112; (C) GSE39454; (D) GSE46239; (E) GSE128470.



Supplementary Figure 6. Boxplots of the proportion of 22 immune cell sorts in healthy controls of the five microarrays. (A) GSE1551 (Control); (B) GSE3112 (Control); (C) GSE39454 (Control); (D) GSE46239 (Control); (E) GSE128470 (Control).



Supplementary Figure 7. Receiver operating characteristics of five hub genes. (A) GSE128470 (PM); (B) GSE48280 (PM); (C) GSE1551 (DM); (D) GSE3112 (PM); (E) GSE46239 (DM).