

Exploring differential gene expression and biomarker potential in systemic lupus erythematosus

Supplementary Figure

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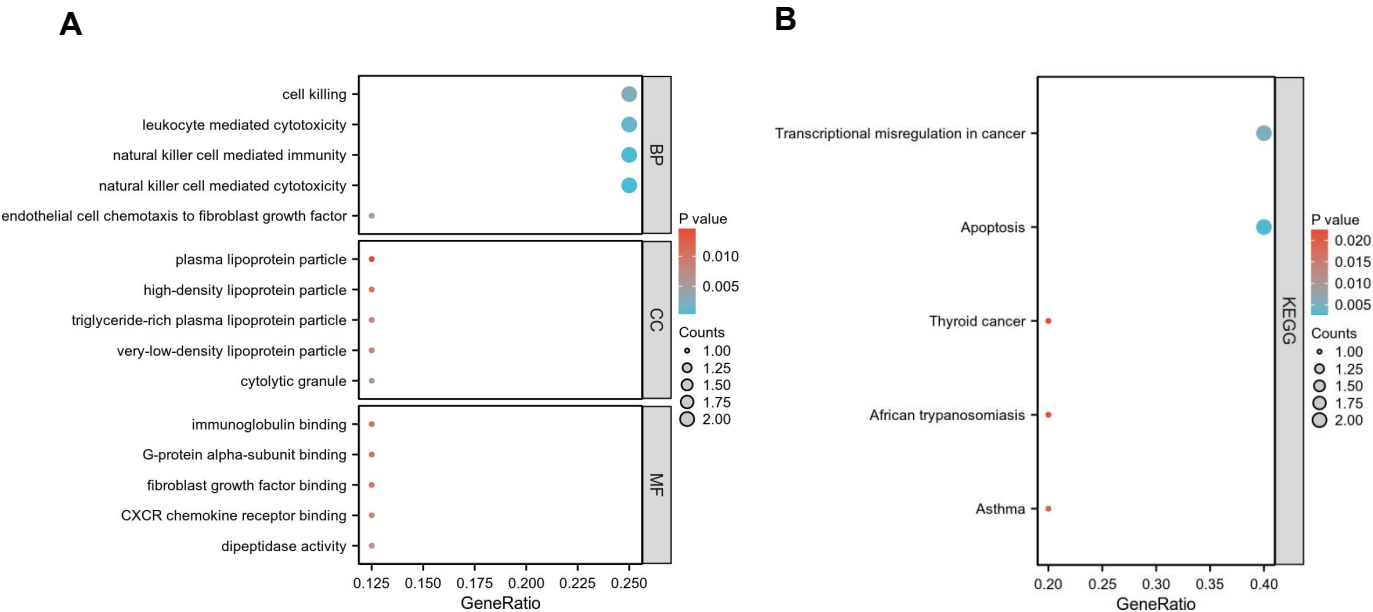
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Supplement Figure 1

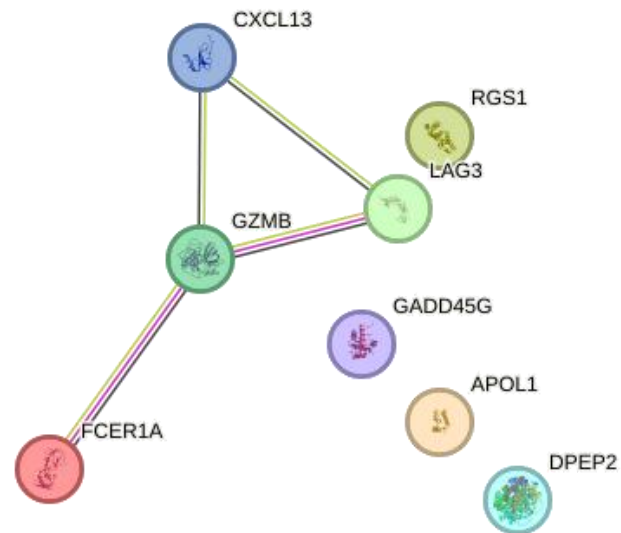
Bubble plots of GO and KEGG pathway enrichment analysis results.

(A) The bubble plot shows the top 5 processes enriched in EP-DEGs in BPs, CCs, and MFs. (B) The bubble plot visualizes the top 5 significantly enriched KEGG pathways in DEGs (co-DEGs). The size of the ball represents the number of genes, and the color change of the ball corresponds to different *p*-values.



Supplement Figure 2

Construction of a Protein-protein interaction (PPI) network.



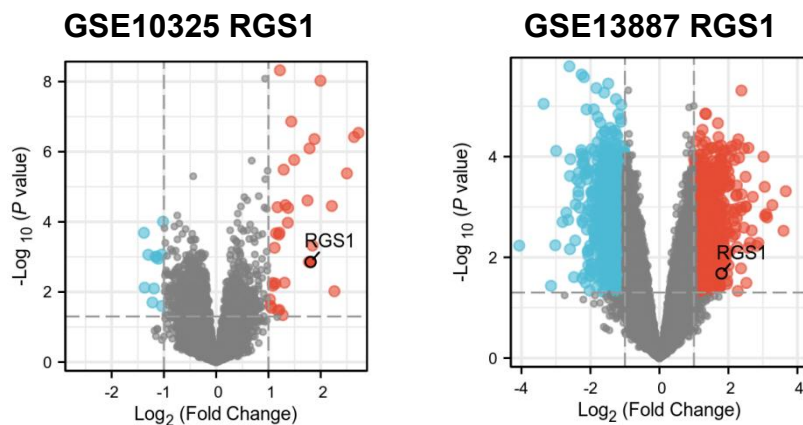
Supplement Figure 3

Gene validation in GSE10325 and GSE13887 datasets.

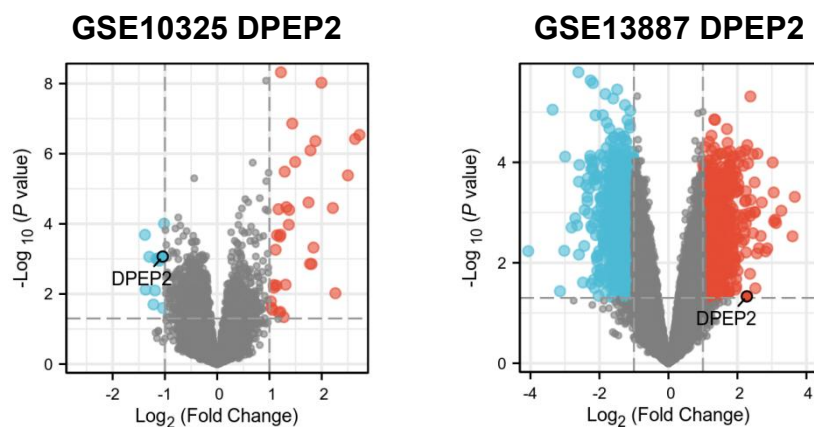
(A-G) Volcano plots of hub genes expressed in GSE10325 and GSE13887 datasets.

(H) Volcano plot of *FCER1A* and *RGS1*, genes with consistent expression levels in GSE10325 and GSE13887.

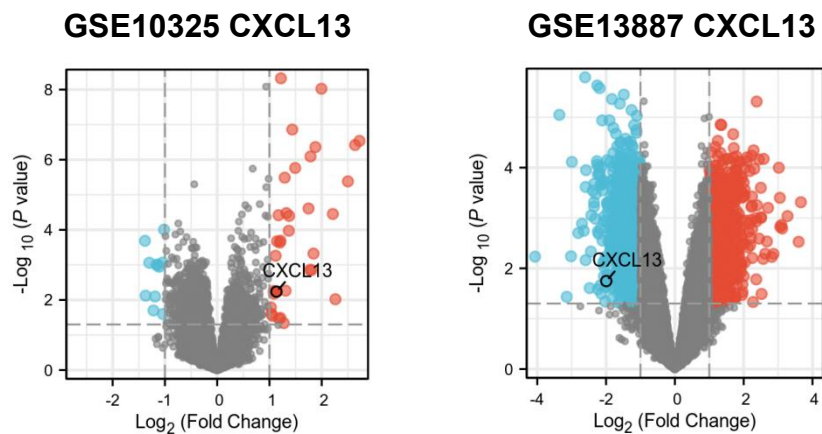
A

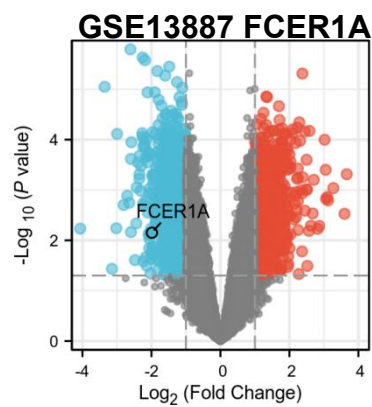
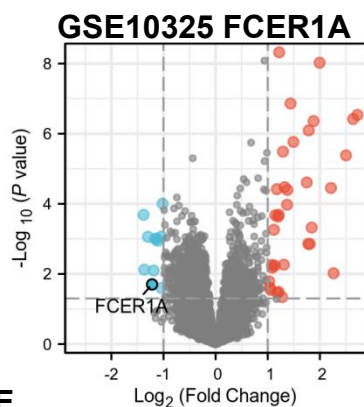
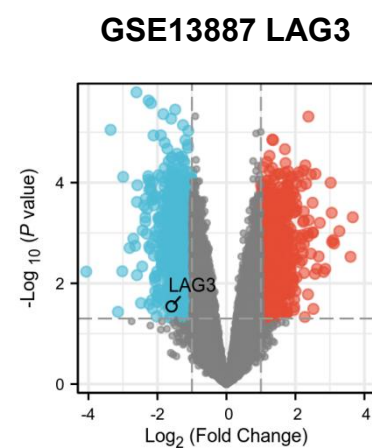
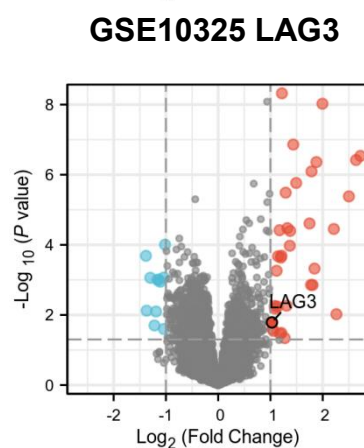
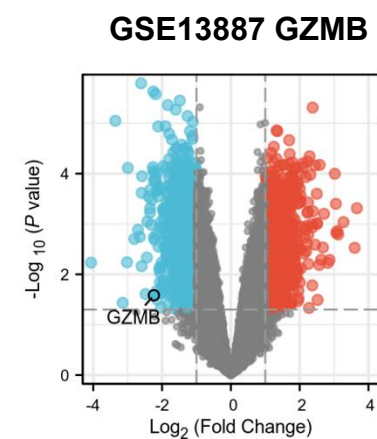
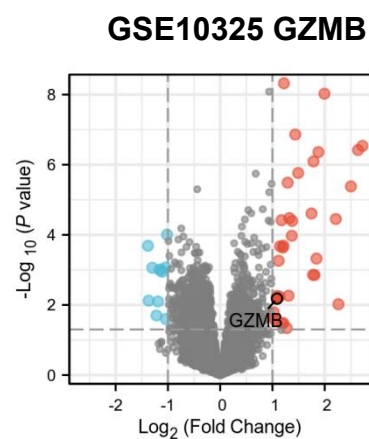
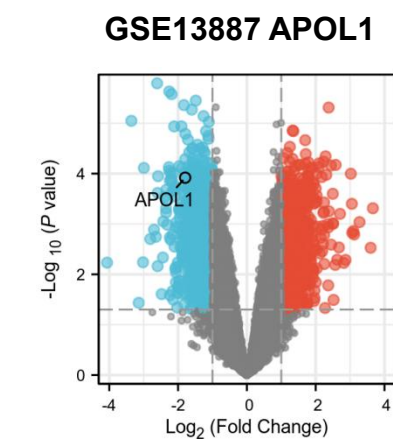
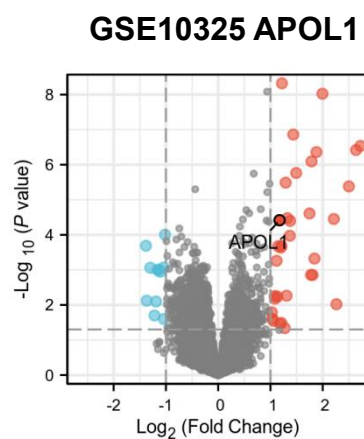


B



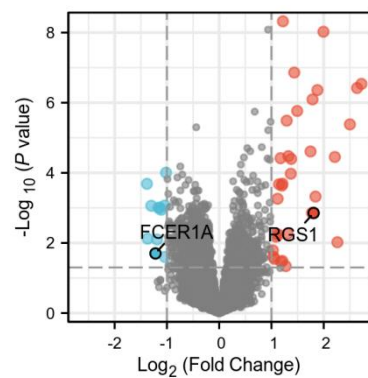
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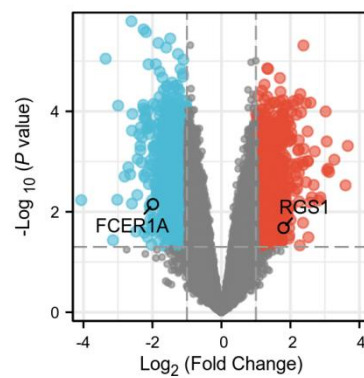
D**E****F****G**

H

GSE10325



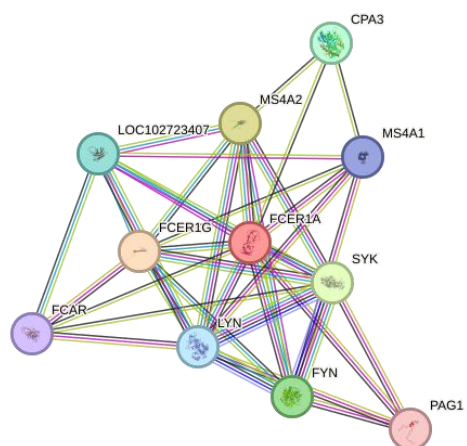
GSE13887



Supplement Figure 4

Construction of the FCER1A and RGS1 PPI network.

A



B

