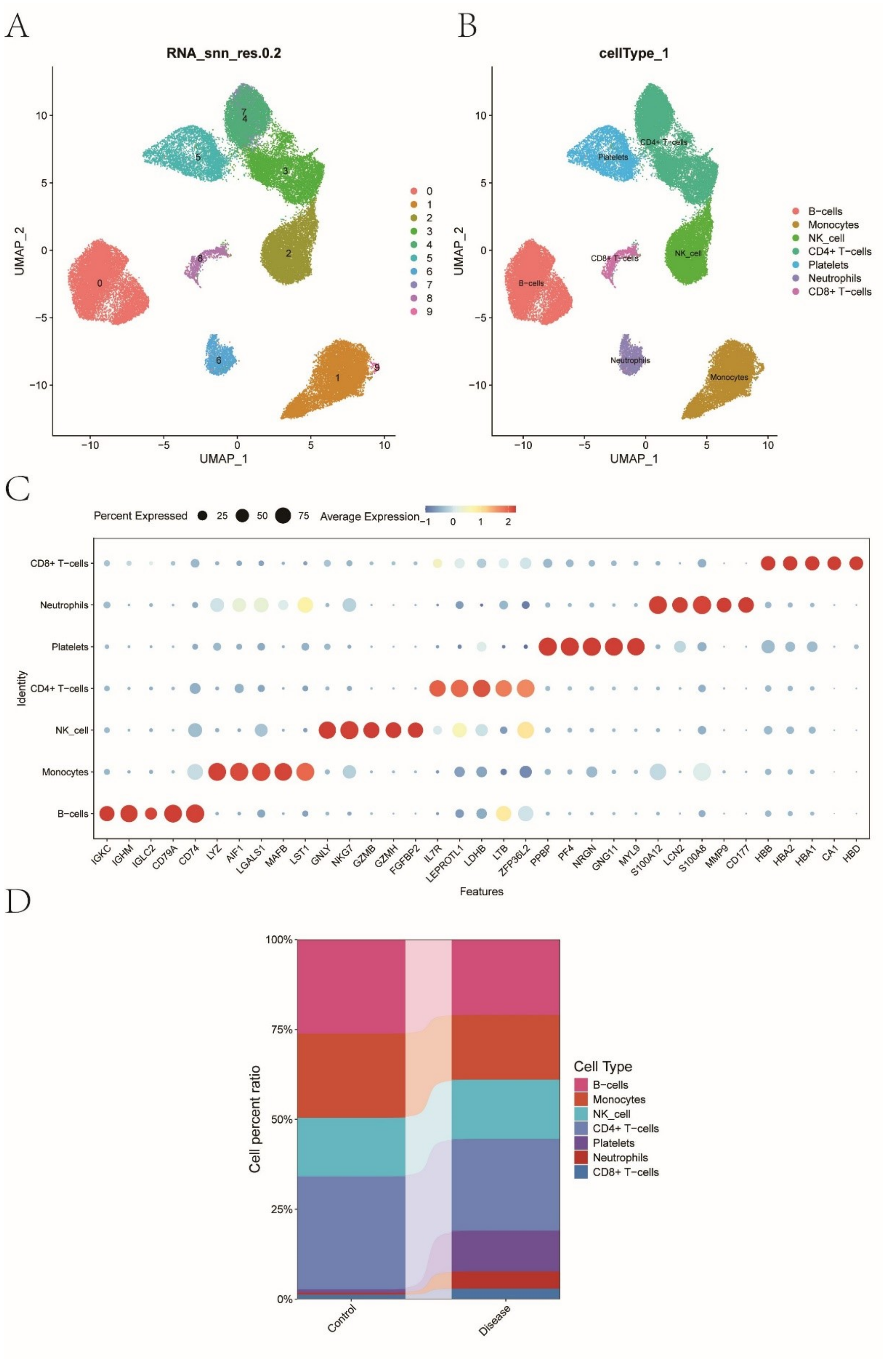
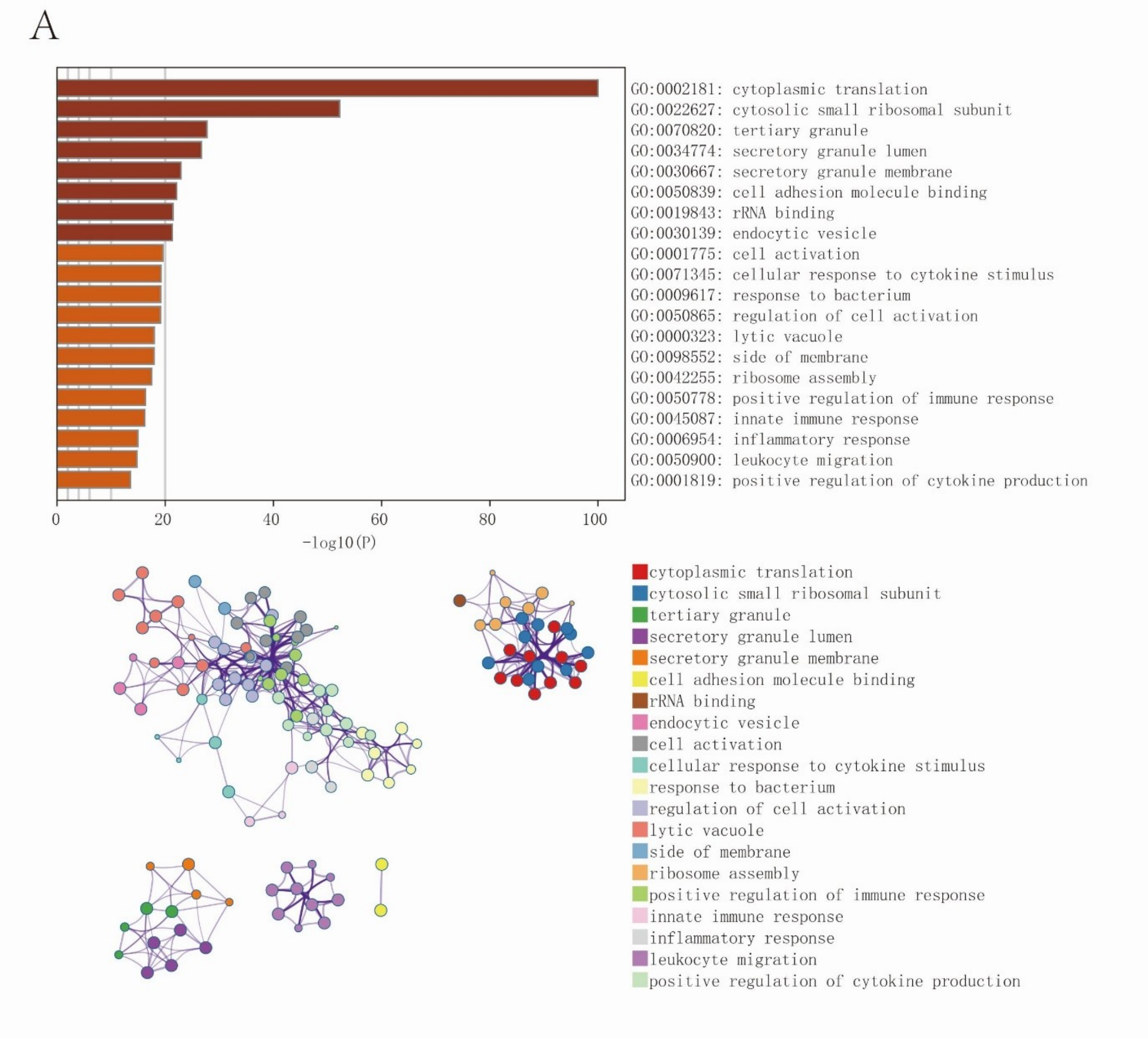
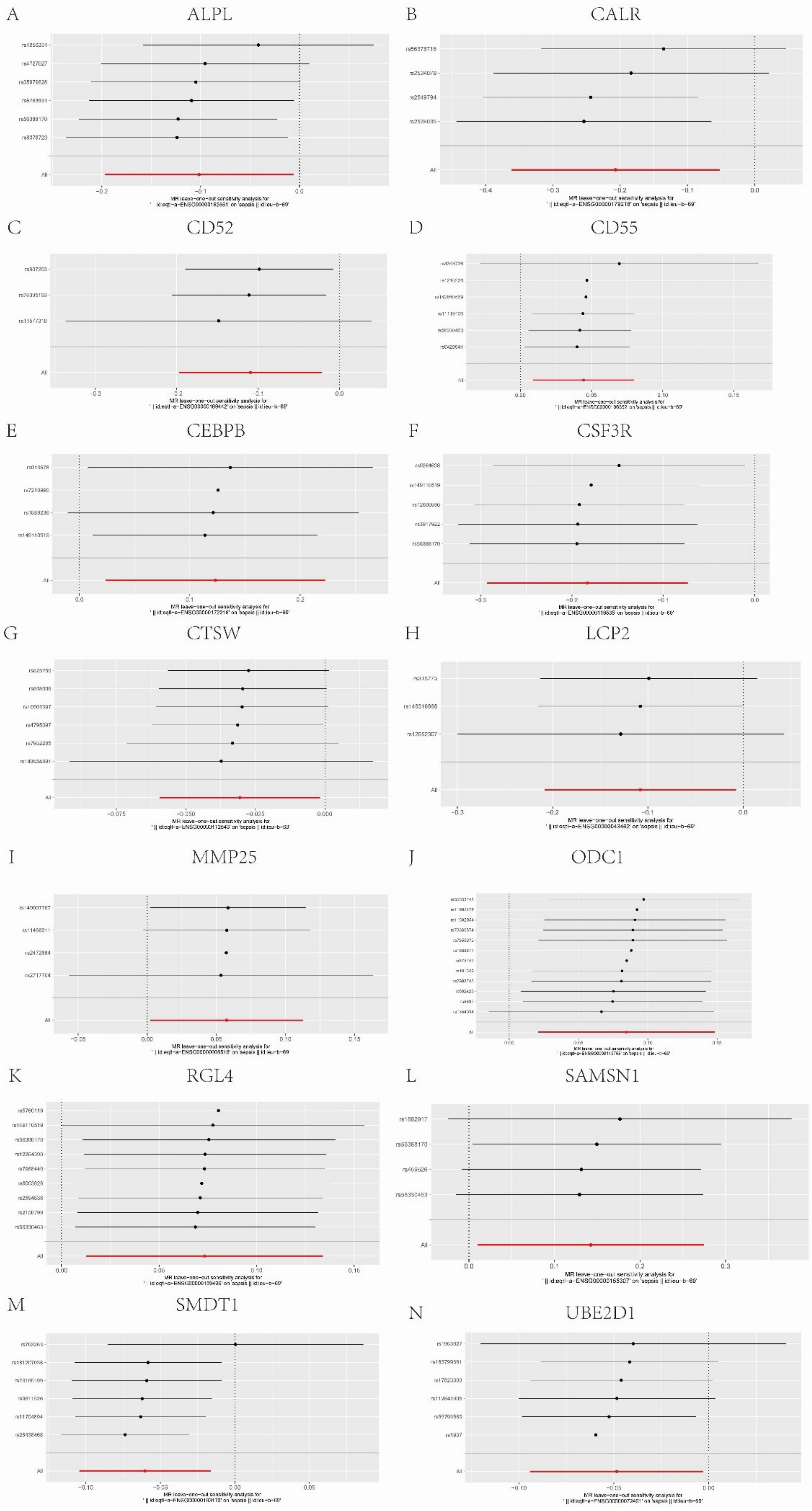
Supplementary Figure S1. Cell annotation. A – Based on the important components available in PCA, we divided the cells into 10 clusters using the UMAP algorithm. B – Annotation of the 10 clusters: the 10 clusters were annotated into 7 cell types, namely CD8+ T-cells, Neutrophils, Platelets, CD4+ T-cells, NK cells, Monocytes, and B-cells. C – Bubble plot of the 7 cell types and their cell markers using the Dotplot method. D – Differences in the proportions of the 7 cell types between the two sample groups



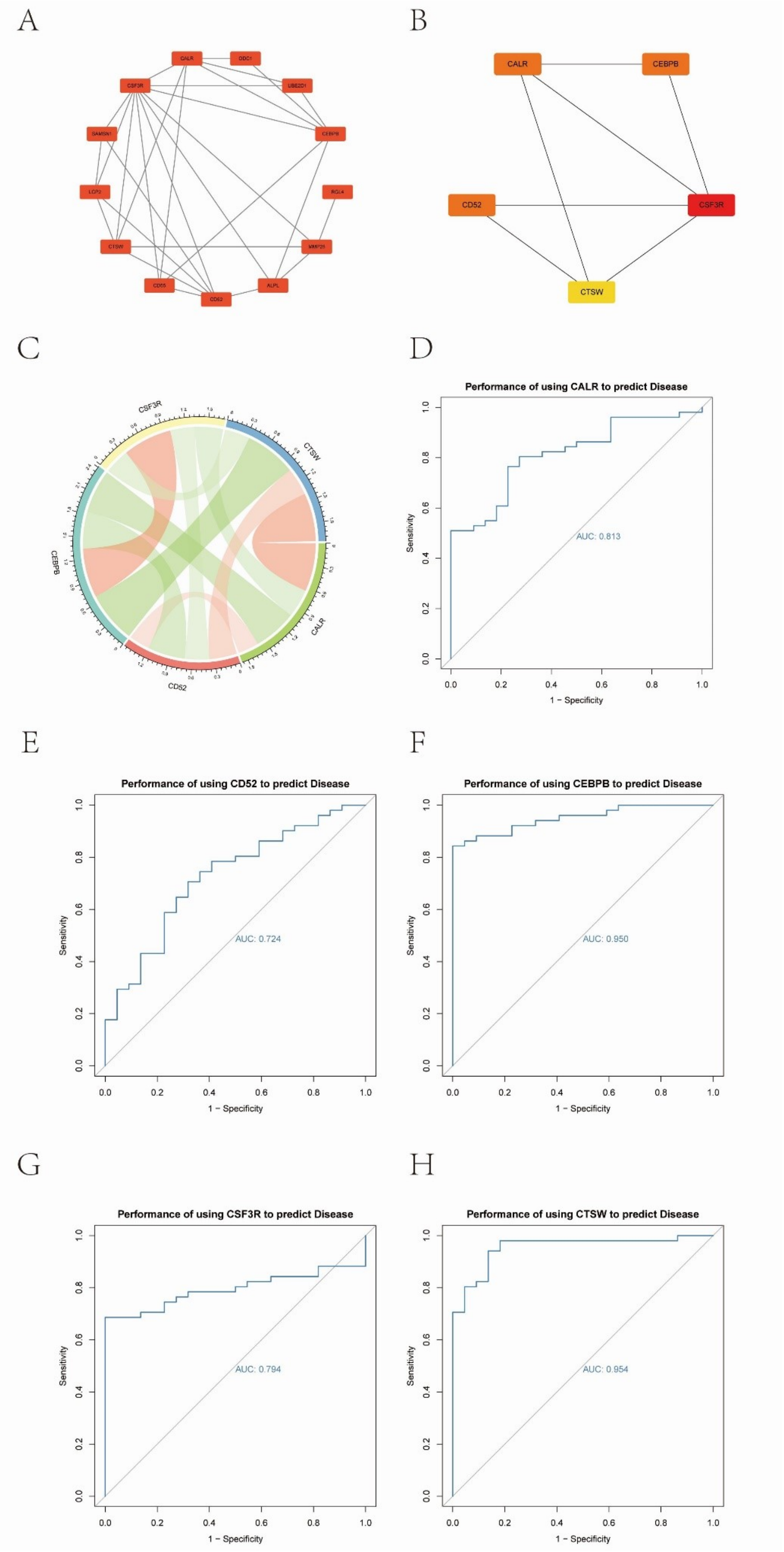
Supplementary Figure S2. Enrichment analysis. A – GO-KEGG enrichment analysis using the Metascape database



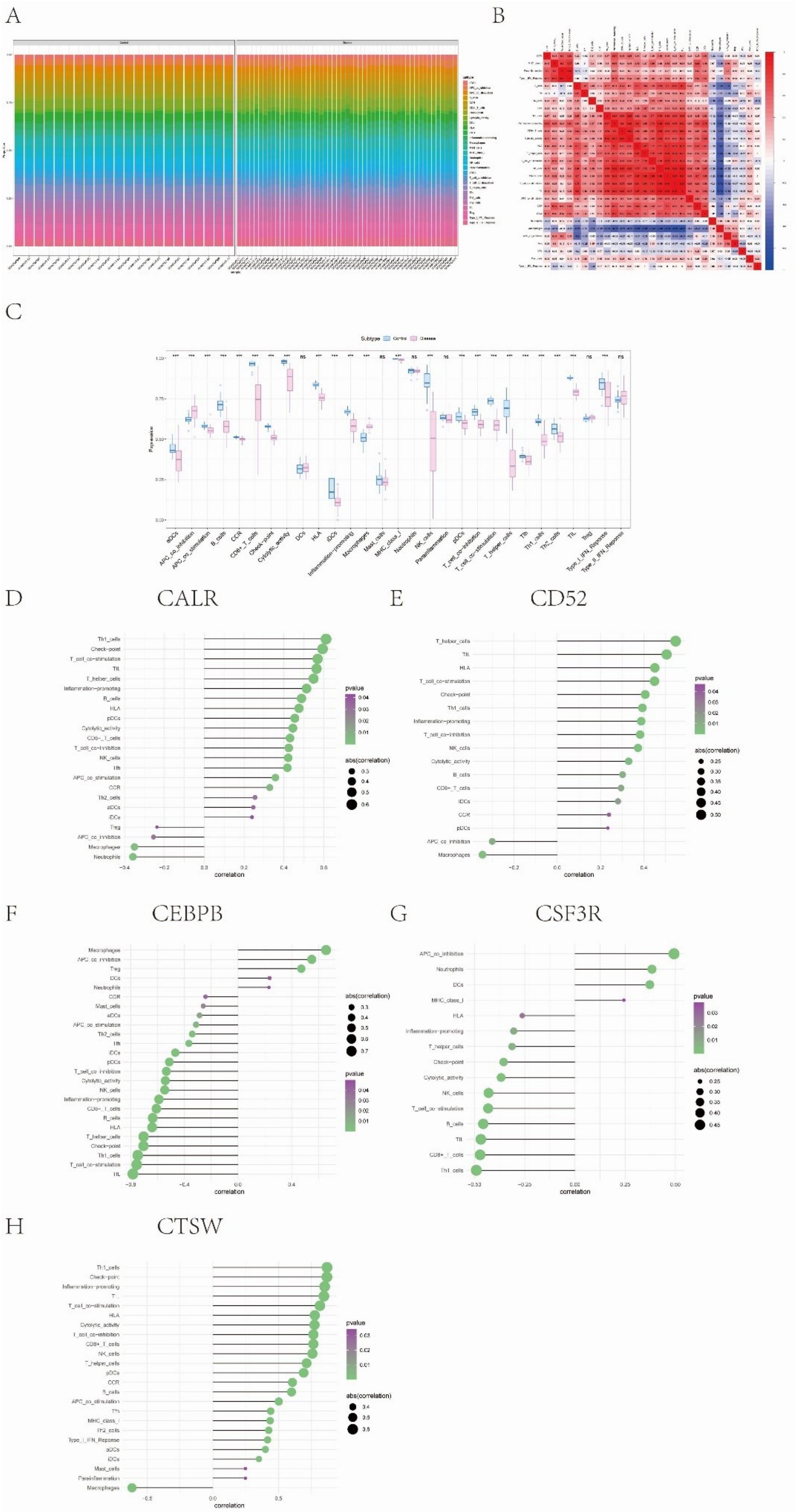
Supplementary Figure S3. Leave-out Test. A–N – Forest plots of the leave-out test for SNPs corresponding to key genes



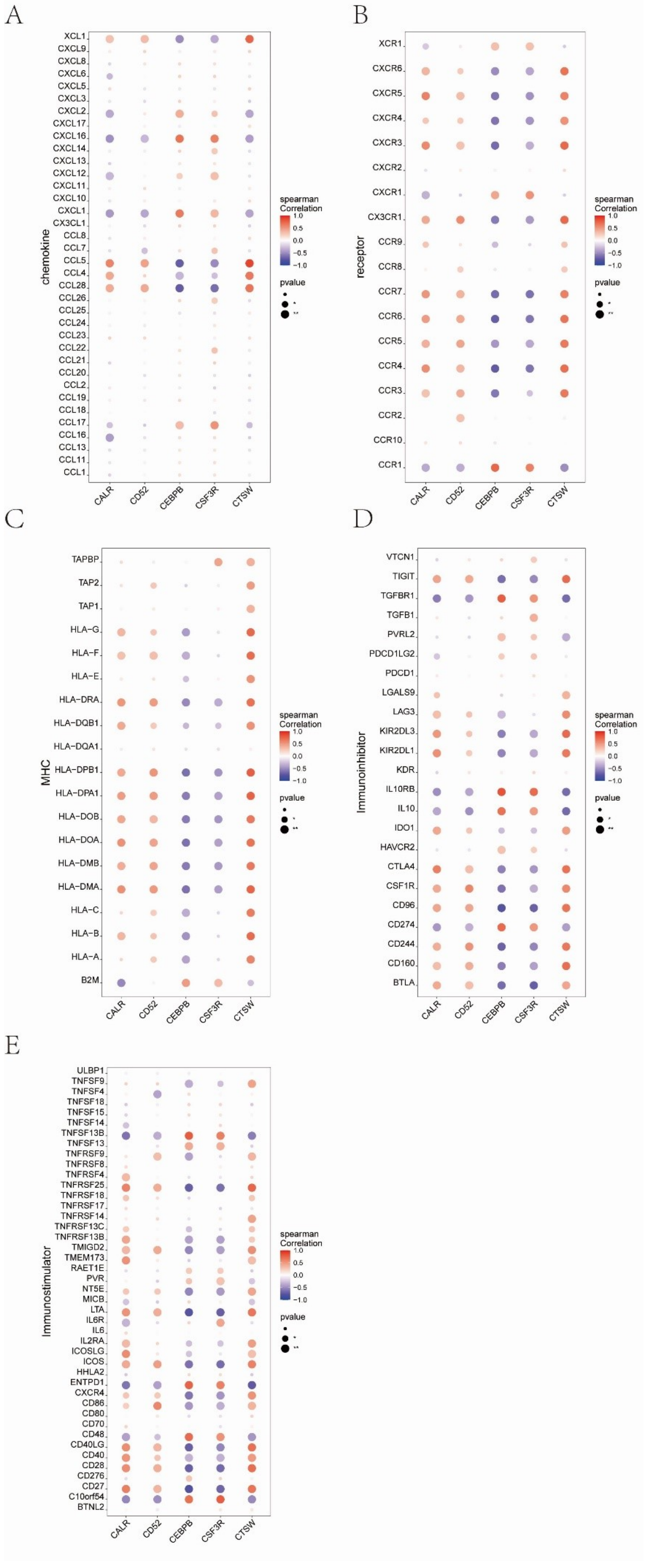
Supplementary Figure S4. PPI Network and ROC of Key Genes. A – Cytoscape network diagram showing the interactions of important genes. B – Top five genes ranked by degree. C – Circos plot showing the correlation among the five key genes. D–H – ROC curves for the five key genes



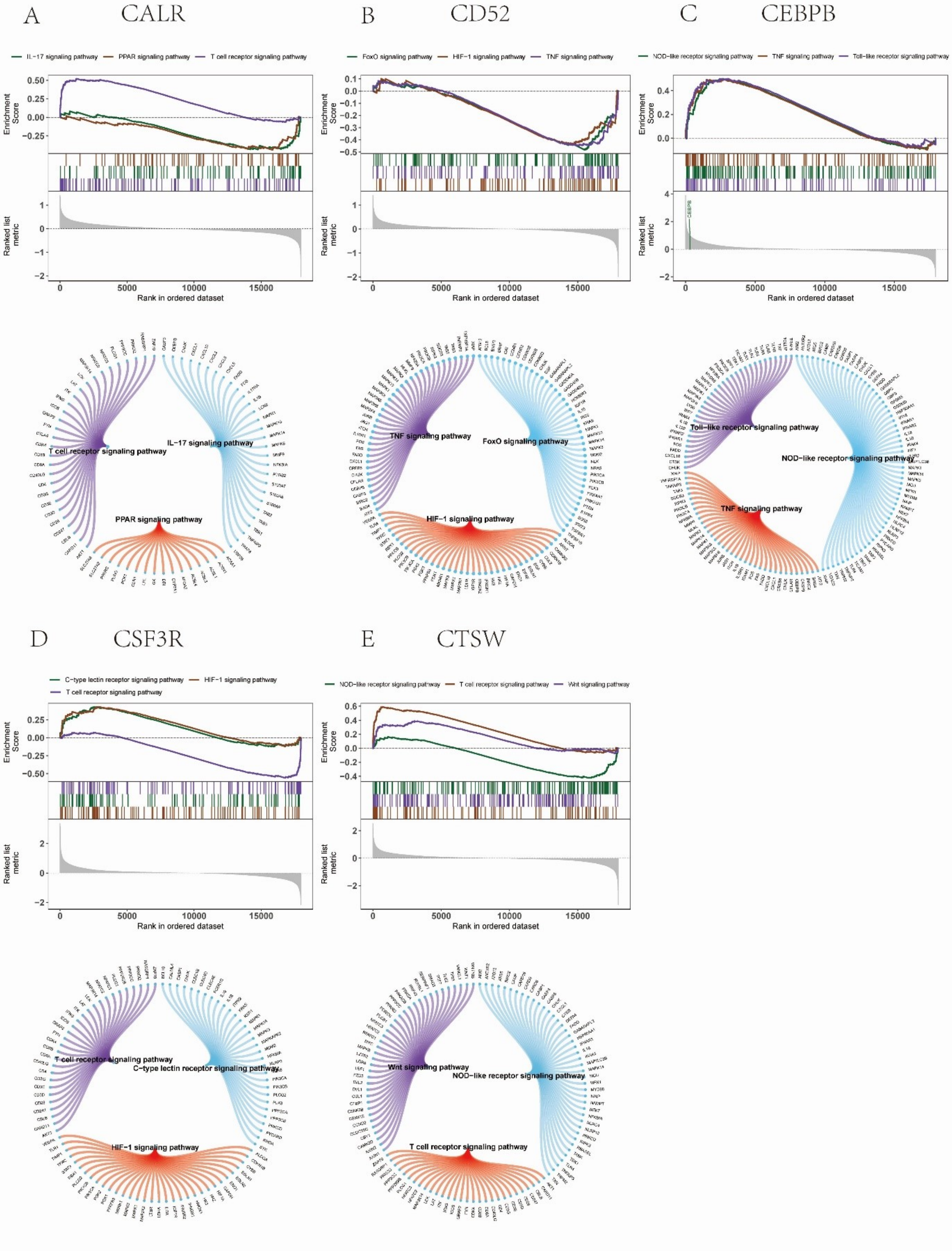
Supplementary Figure S5. Immune Infiltration Analysis. A – Relative percentages of 29 immune cell subpopulations. B – Pearson correlation among the 29 immune cells, with blue indicating negative correlation and red indicating positive correlation. C – Differences in immune cell content between control and disease samples. D–H – Correlation between the five key genes and immune cells



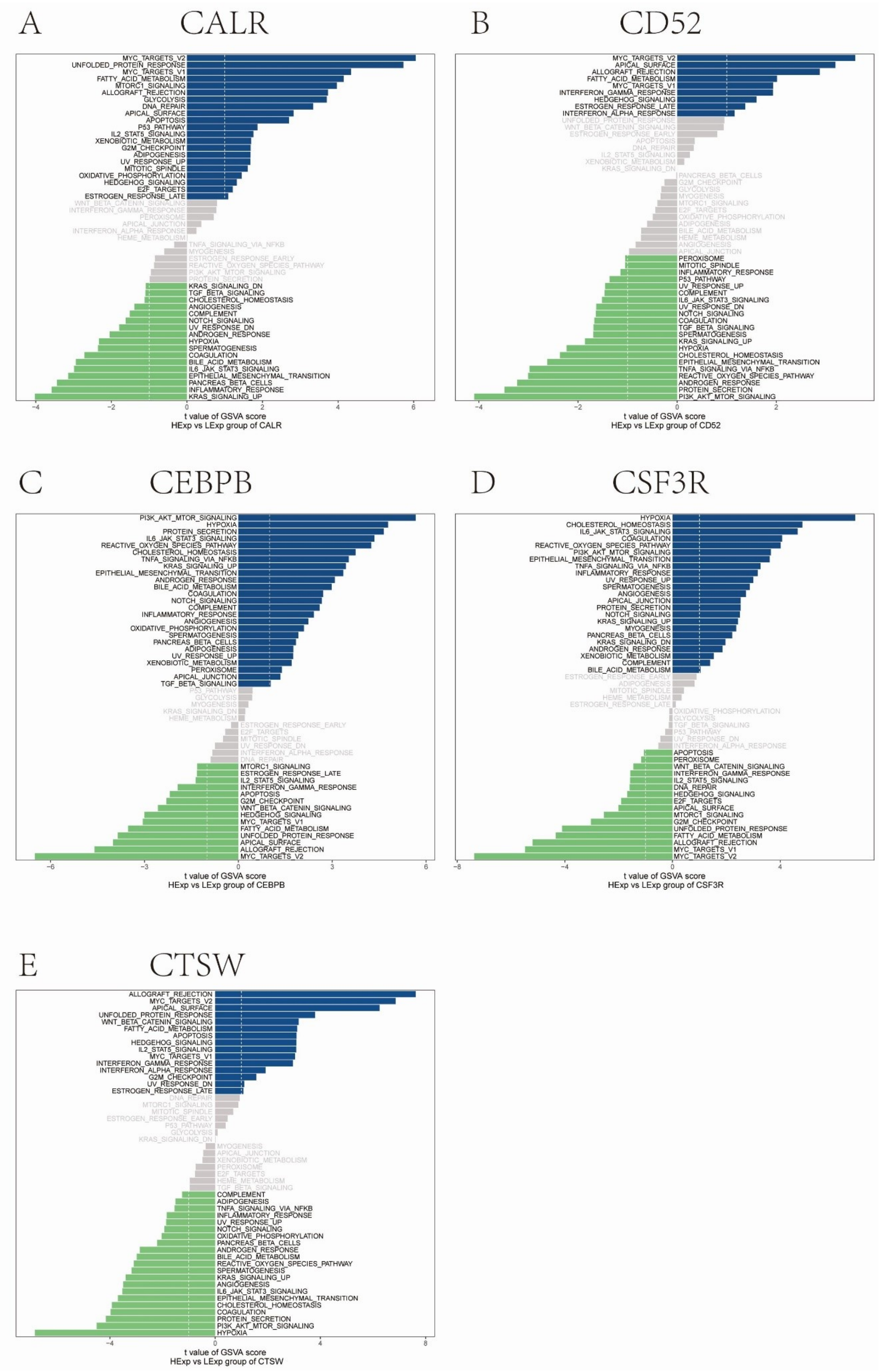
Supplementary Figure S6. Relationship Between Key Genes and Immune Factors. A –E – Correlation between key genes and chemokines, immunoinhibitors, immunostimulators, MHC, and receptors



Supplementary Figure S7. GSEA Analysis of Key Genes. A–E – KEGG signaling pathways involving key genes, including pathway regulation and involved genes

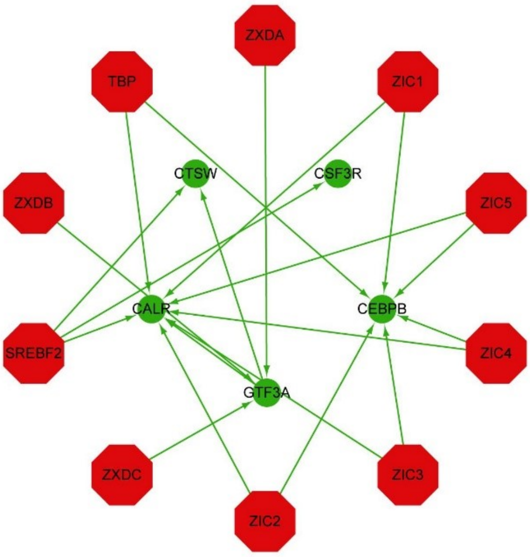


Supplementary Figure S8. GSVA Analysis of Key Genes. A–E – GSVA analysis of key genes, with blue indicating pathways associated with high gene expression and green indicating pathways associated with low gene expression. The background gene set is hallmark

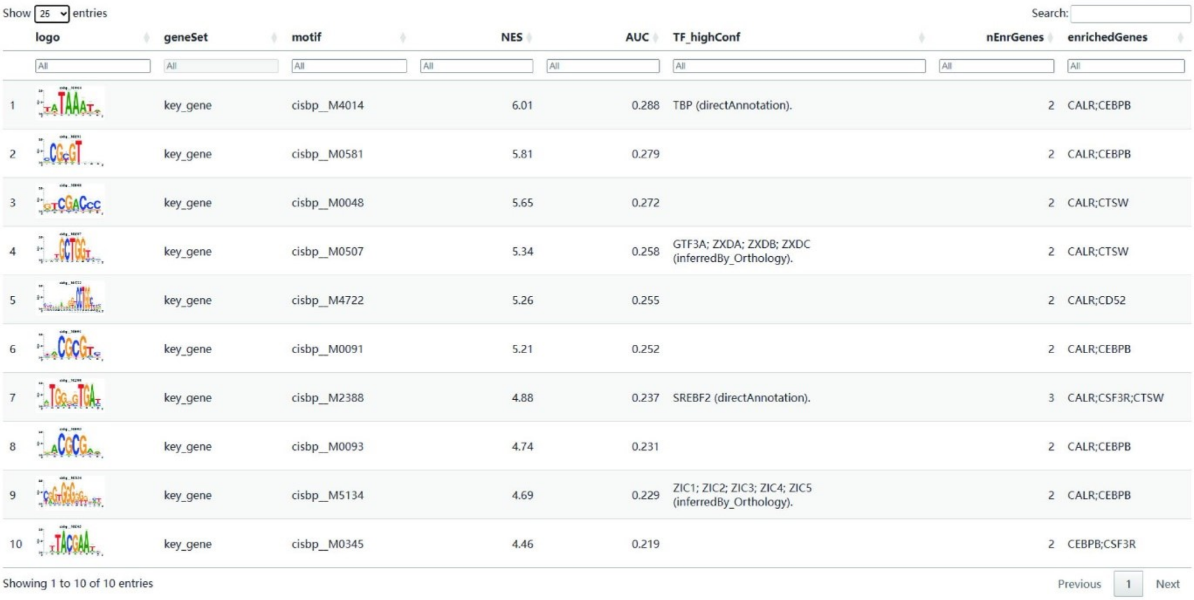


Supplementary Figure S9. Transcriptional Regulatory Network of Key Genes. A – Transcriptional regulatory network of key genes, with green representing key genes and red representing transcription factors. B – All motifs and corresponding transcription factors enriched for the key genes are displayed

A



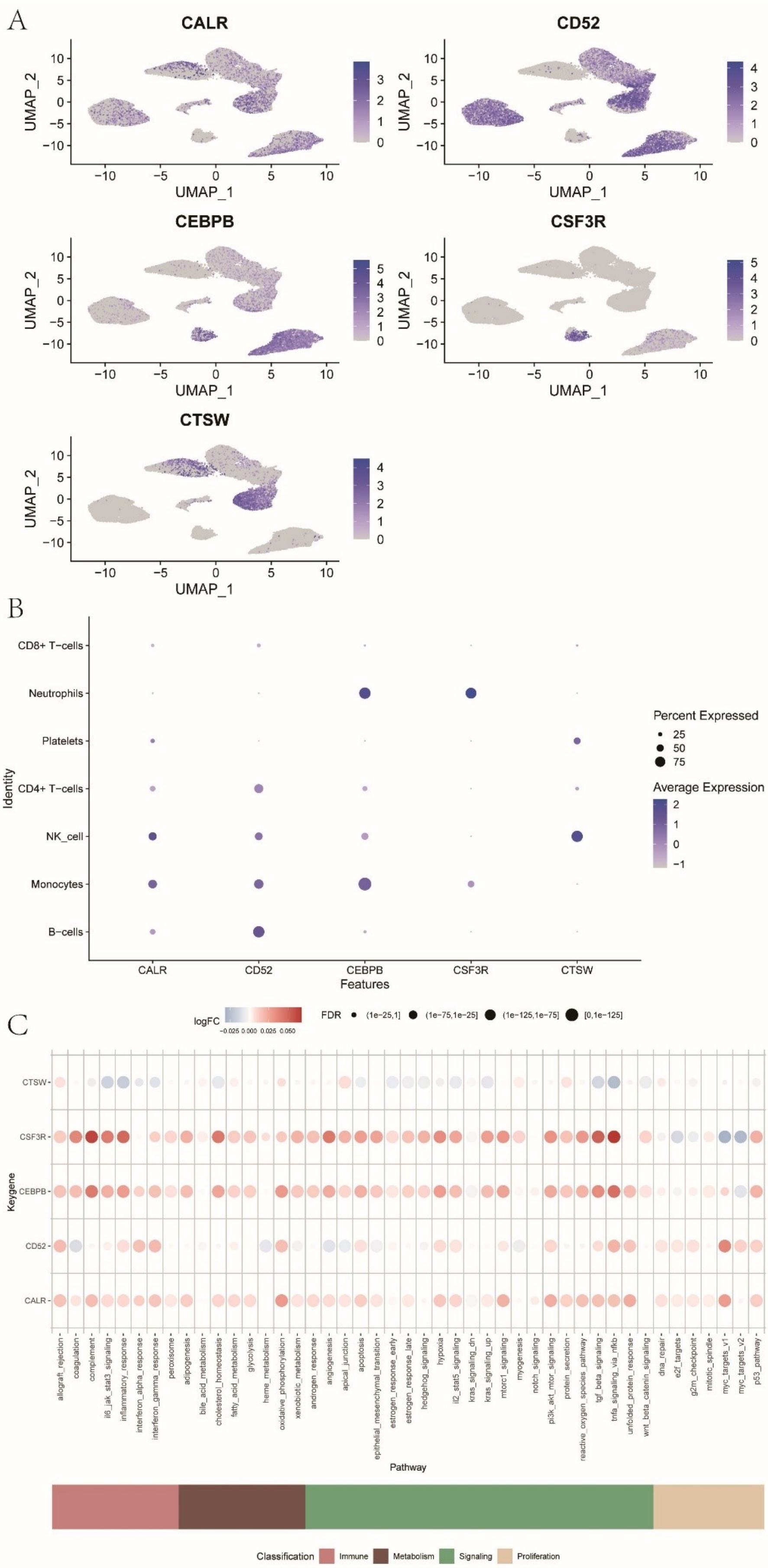
B



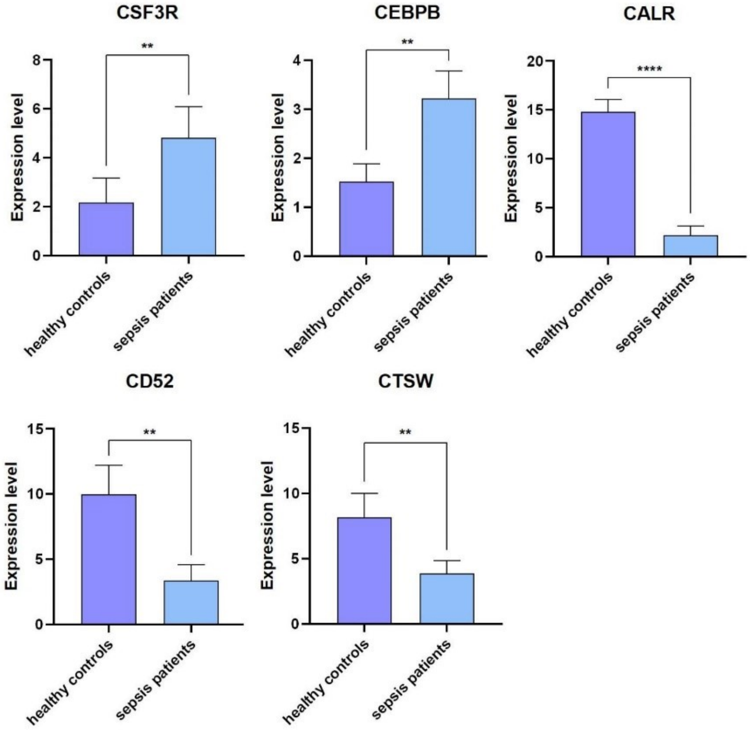
	logo	geneSet	motif	NES	AUC	TF_highConf	nEnrGenes	enrichedGenes
	All	All	All	All	All	All	All	All
1		key_gene	cisbp__M4014	6.01	0.288	TBP (directAnnotation).	2	CALR;CEBPB
2		key_gene	cisbp__M0581	5.81	0.279		2	CALR;CEBPB
3		key_gene	cisbp__M0048	5.65	0.272		2	CALR;CTSW
4		key_gene	cisbp__M0507	5.34	0.258	GTF3A; ZXDA; ZXDB; ZXDC (inferredBy_Orthology).	2	CALR;CTSW
5		key_gene	cisbp__M4722	5.26	0.255		2	CALR;CD52
6		key_gene	cisbp__M0091	5.21	0.252		2	CALR;CEBPB
7		key_gene	cisbp__M2388	4.88	0.237	SREBF2 (directAnnotation).	3	CALR;CSF3R;CTSW
8		key_gene	cisbp__M0093	4.74	0.231		2	CALR;CEBPB
9		key_gene	cisbp__M5134	4.69	0.229	ZIC1; ZIC2; ZIC3; ZIC4; ZIC5 (inferredBy_Orthology).	2	CALR;CEBPB
10		key_gene	cisbp__M0345	4.46	0.219		2	CEBPB;CSF3R

Showing 1 to 10 of 10 entries

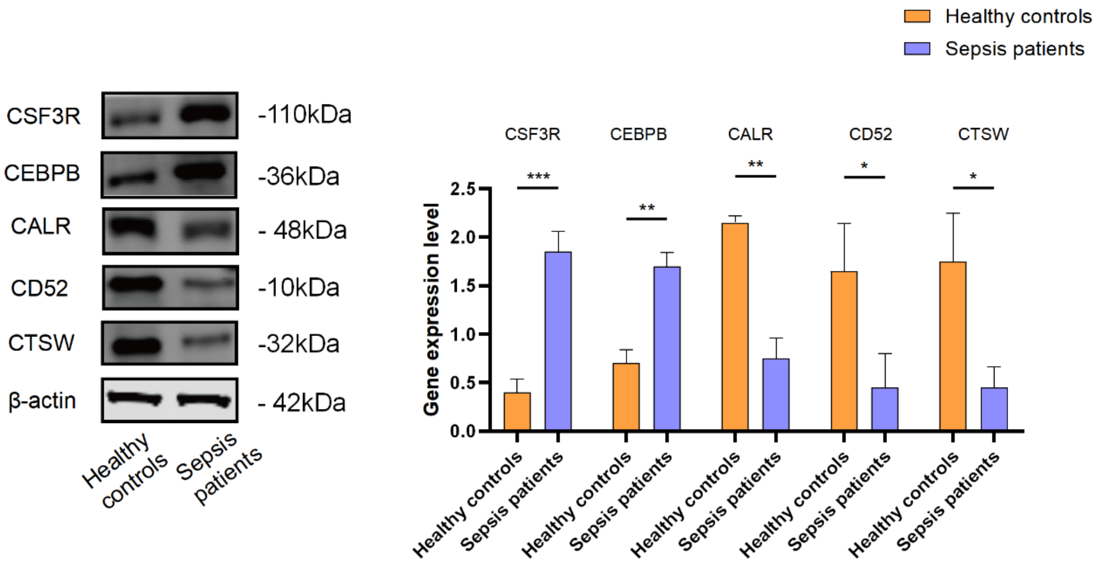
Supplementary Figure S10. Overview of Single-Cell Expression. A, B – Overview of the expression of key genes in single cells. (C) Correlation between key genes and immune metabolic pathways



Supplementary Figure S11. qRT-PCR Results. The expression levels of five key genes (CALR, CD52, CEBPB, CSF3R, CTSW)



Supplementary Figure S12. Western Blot Results. The protein expression of five key genes: CALR, CD52, CEBPB, CSF3R, and CTSW



Supplementary Table SI. Sense and antisense primers for real-time reverse transcription polymerase chain reaction

Primer name	Sequences (5’-3’)
hsa-GADPH F	GGAGCGAGATCCCTCCAAAAT
hsa-GADPH R	GGCTGTTGTCATACTTCTCATGG
hsa-CD52 F	GCATCCAGCAACATAAGCGG
hsa-CD52 R	GCTGAGACGTGTCACCTCAA
hsa-CALR F	AGTTCCGGCAAGTTCTACGG
hsa-CALR R	ACAGAGCATAAAAGCGTGCAT
hsa-CEBPB F	GGGAATCTTTTCCGTTTCAAGCA
hsa-CEBPB R	TGCCCCCAAAAGGCTTTGTA
hsa-CSF3R F	TGAAAAGAGGCTTAGGGCCG
hsa-CSF3R R	GGCTGGGTGCCATCCTTATG
hsa-CTSW F	AGATCCAGTTCAACCGGAGTT
hsa-CTSW R	TGTGAGGTCACTGAATGGAGT