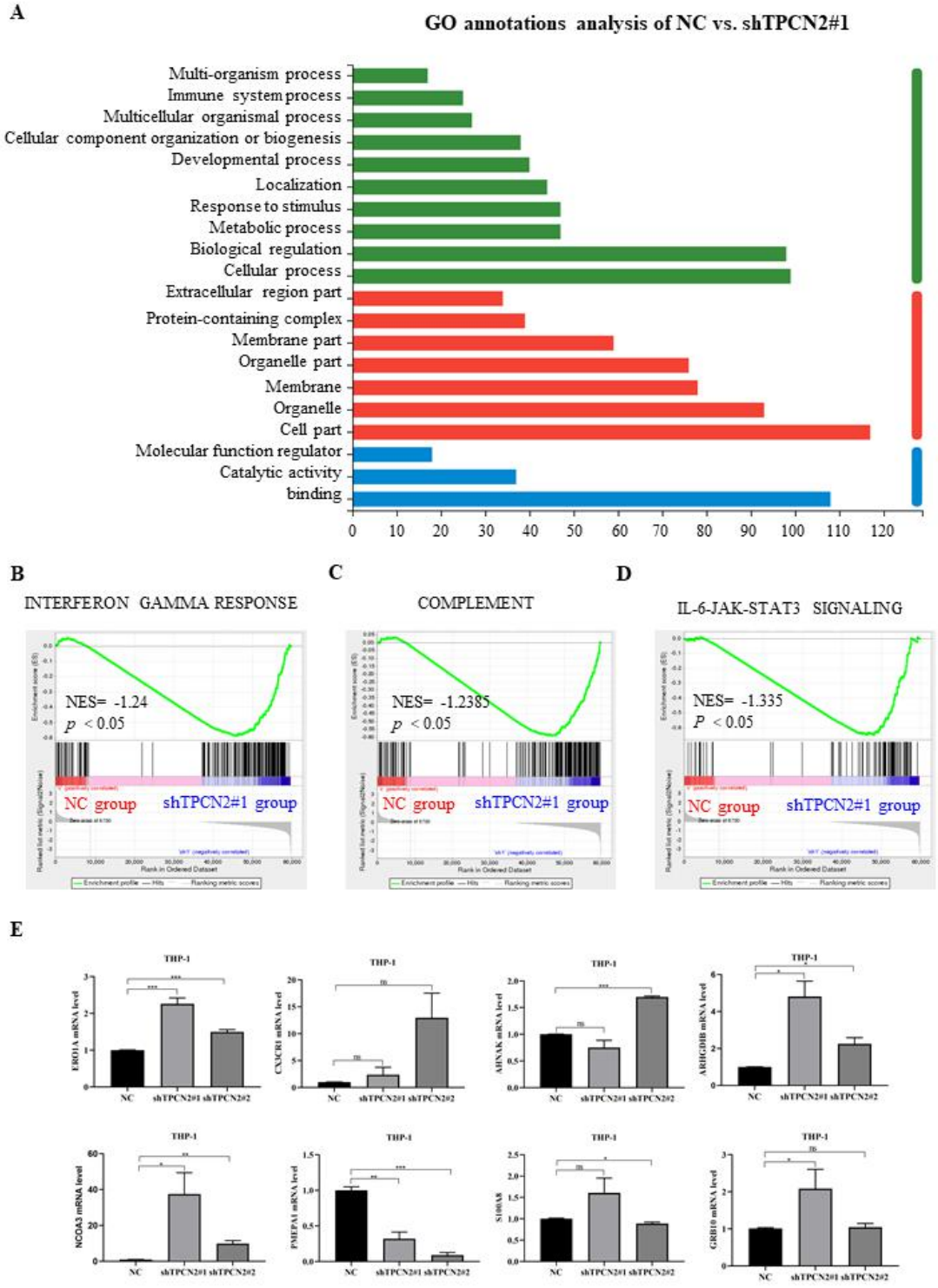
Supplementary Table 1: Patient demographics and medications.

NO.	Age	Gender	SLEDAI score	Teatment
SLE1	29	F	8	None
SLE2	46	F	16	None
SLE3	48	F	4	None
SLE4	30	F	13	None
SLE5	44	F	10	None
SLE6	32	F	7	None

F: Female; SLEDAI: Systemic Lupus Erythematosus Disease Activity Index.

Supplementary Table 2: shRNA target sequence.

Target name	**Target Seq**
sh#1	CCCGTGGTCCAAGATCTATTT
sh#2	GCTGAACATGCTCATCGTGTT
NC	TTCTCCGAACGTGTCACGT



Supplementary Figure 1. RNA-seq analyses of the effect of TPCN2-knockdown on the gene expression profile. (**A**) GO classification analysis of DEGs. NC group vs sh#1. Molecular function- blue; Cellular components- red; Biological process- green.

Representative enriched pathways in high-risk sh#1 through GSEA analysis. GSEA results showed that the IFN-γ response (**B**), complement (**C**) and IL-6-JAK-STAT3 (**D**) pathways were enriched in the sh#1 expression group. Top panels indicate the enrichment scores for each gene. Bottom panels show the ranking metrics of each gene. Y-axis: ranking metric values; X-axis: ranks for all genes. NES: normalized enrichment score. (**E**) The mRNA expression of some DEGs in THP-1 cells were detected by qRT-PCR. The RNA was extracted from cells knocked down of TPCN2 with two independent shRNA. The results were shown as the mean ±SD from 3 independent experiments. (**P*<0.05).