Supplementary Table 1: Patient demographics and medications.

<table>
<thead>
<tr>
<th>NO.</th>
<th>Age</th>
<th>Gender</th>
<th>SLEDAI score</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLE1</td>
<td>29</td>
<td>F</td>
<td>8</td>
<td>None</td>
</tr>
<tr>
<td>SLE2</td>
<td>46</td>
<td>F</td>
<td>16</td>
<td>None</td>
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<tr>
<td>SLE3</td>
<td>48</td>
<td>F</td>
<td>4</td>
<td>None</td>
</tr>
<tr>
<td>SLE4</td>
<td>30</td>
<td>F</td>
<td>13</td>
<td>None</td>
</tr>
<tr>
<td>SLE5</td>
<td>44</td>
<td>F</td>
<td>10</td>
<td>None</td>
</tr>
<tr>
<td>SLE6</td>
<td>32</td>
<td>F</td>
<td>7</td>
<td>None</td>
</tr>
</tbody>
</table>

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

Supplementary Table 2: shRNA target sequence.

<table>
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<th>Target name</th>
<th>Target Seq</th>
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<tr>
<td>sh#1</td>
<td>CCCGTGGTCCAAGATCTATT</td>
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<tr>
<td>sh#2</td>
<td>GCTGAACATGCTCATCGTGTT</td>
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<tr>
<td>NC</td>
<td>TTCTCCGAACGTGTCAACGT</td>
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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).