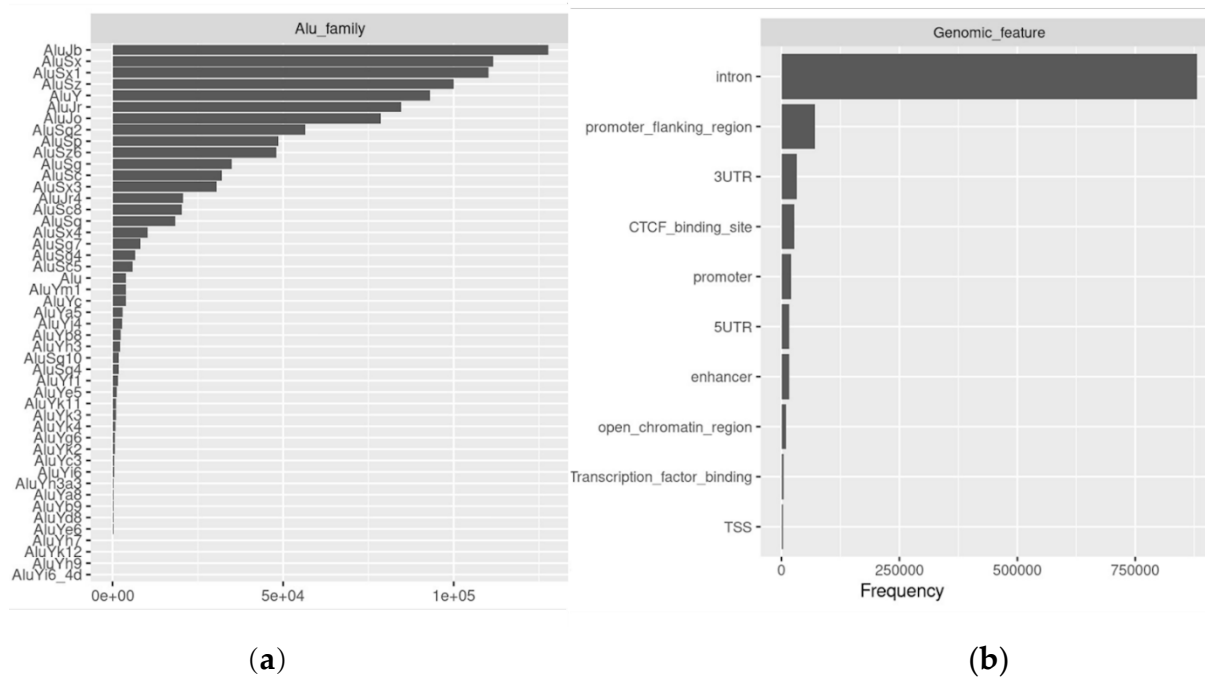


SUPPLEMENTARY FIGURES



Supplementary Figure S1. Genomic distribution of intragenic Alu elements. **(a)** Distribution of *Alu* subfamilies in all genes as defined by ensembl.org, and **(b)** position of *Alu* insertions in the gene body.

>C5aR1_3UTR_transcript

```
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GGGAGGCTCTGTCTCAAAAGCAAAGCAAAAACAAAAACAAAAACACCTAAAAAACCTGCAGTTTGTGTTGTACTTTGTTTTAAATTATG
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GGCAACATCTTGCAAACTACAATGTAGTCTCATAACCAGGATATTGACATTGATACAGTGAAGATACAGGACATTCTCATCACCACAGG
GATCCCCAGGATGCCACTTCCCTCCACCCCCACCCCCAGCCGTGTCCCTAACCCCTGGCAACCAGGAATCCACTCTCCATTTCTATAA
TGTGTGTCATTTCAAGAATGTTATTCAATGGAATCATATAGTATGTAACCTGTTTTGAGCTTAAAAAAAAGTATACATGACTTTAATGAG
GAAAATAAAAATGAATATTGAAATGT
```

Supplementary Figure S2. Gene sequence of C5aR1 3'UTR transcript. *AluSx1* element in bold letters.

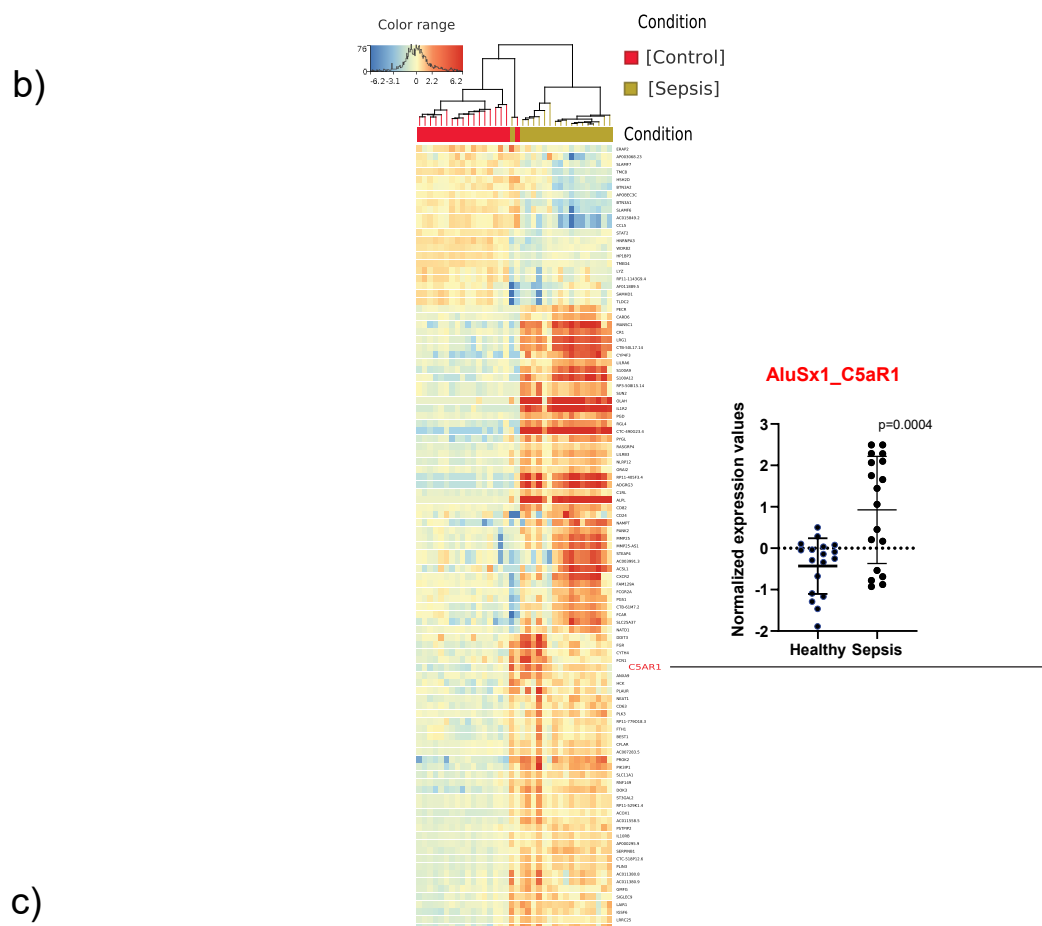
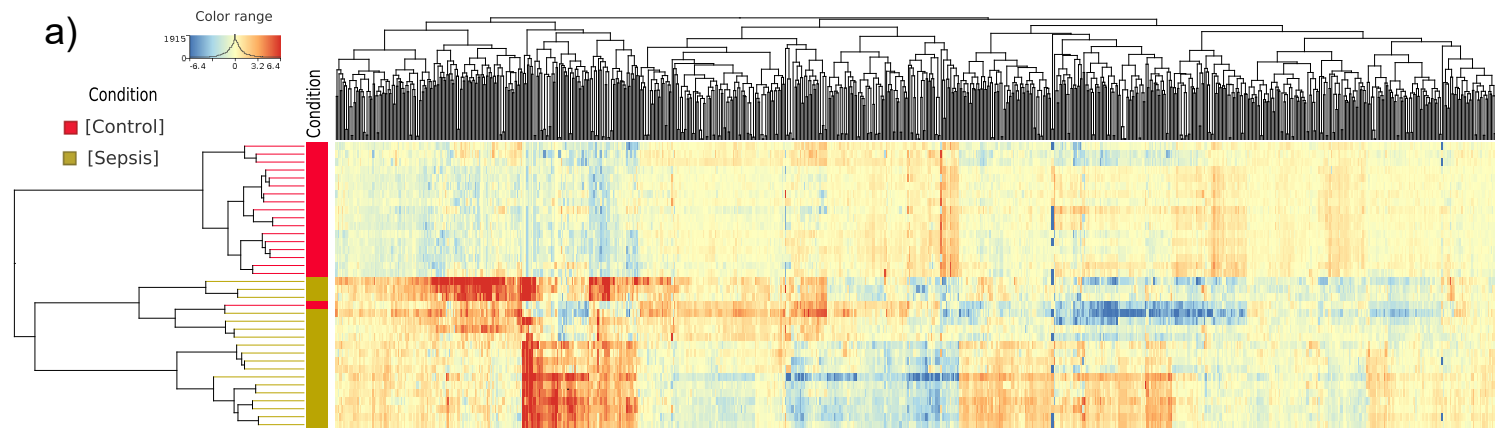


Figure S3. Expressed *Alu* elements transcribed from intragenic regions, RNA-seq dataset from peripheral blood mononuclear cells (PBMC) of sepsis patients including healthy controls at Taizhou Hospital (PRJNA607653). (a) Hierarchical clustering of normalised values of intragenic *Alu* containing transcripts, with a cut-off of 400 transcripts in at least one participant. This threshold produced 850 *Alu* transcripts (based on Table S3). (b) Heatmap of *Alu* containing transcripts with the highest expression (>1000 raw reads in one or more samples) and highest fold change (threshold 2.5) between patients with sepsis and healthy controls. *Alu* transcripts from within the same genes are. Line connected to *AluSx1* C5aR1 (red letters) shows p -value of $p \leq 0.004$. (c) IGV presentation of the structure of the C5aR1 gene with RNA-seq data from the Taizhou study. One alignment from sepsis patient (SRR11118030) and one healthy control (SRR11118016).