

### ***Supplemental Digital Content***

**FIGURE S1.** Purity of separated T cells of healthy donors. (A, B) CD3<sup>+</sup> as well as CD4<sup>+</sup> T cells, enriched from PBMCs of healthy donors, were stained for extracellular CD4 and CD8 or CD4 and CD3 expression, respectively, and were subsequently analyzed by flow cytometry. Representative plots, gated on “live” cells, as determined by forward/side scatter properties, are shown.

**FIGURE S2.** Gating strategy. CD4<sup>+</sup> T cells of healthy donors were stimulated with plate-bound anti-CD3 as well as soluble anti-CD28 for various time points and stained for extracellular CD4 and CD25 as well as intracellular SH2D1A (SAP) expression.

**FIGURE S3.** Total RNA was extracted from purified CD3<sup>+</sup> T cells of sepsis patients (n=23, Sepsis) within 48 hours after clinical diagnosis as well as from CD3<sup>+</sup> T cells of healthy donors (n=16, Control/black dots). Of the 23 sepsis patients, seven were diagnosed with early-stage sepsis (symptoms onset < 4 hours; labeled Early Sepsis/grey dots). In the remainder of patients (labeled Late Sepsis/white dots), the diagnosis was made up to 48 hours before blood samples were obtained. Relative expression of endogenous miR-31-5p was quantified by qPCR using U47 RNA as normalizing control. Scatter dot plot with each symbol representing data from one subject. Horizontal lines delineate means  $\pm$  SD. ns (not significant) Early vs. Late sepsis, \*  $p=0.0043$  Early sepsis vs. Control, \*\*  $p<0.0001$  Late sepsis vs. Control in one-way ANOVA with Tukey post test.

FIGURE S1

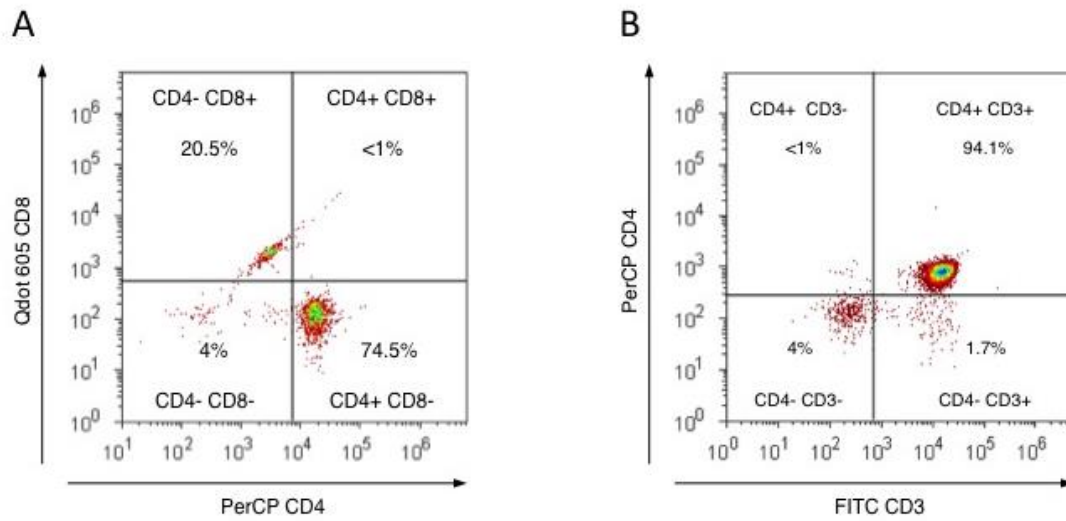


FIGURE S2

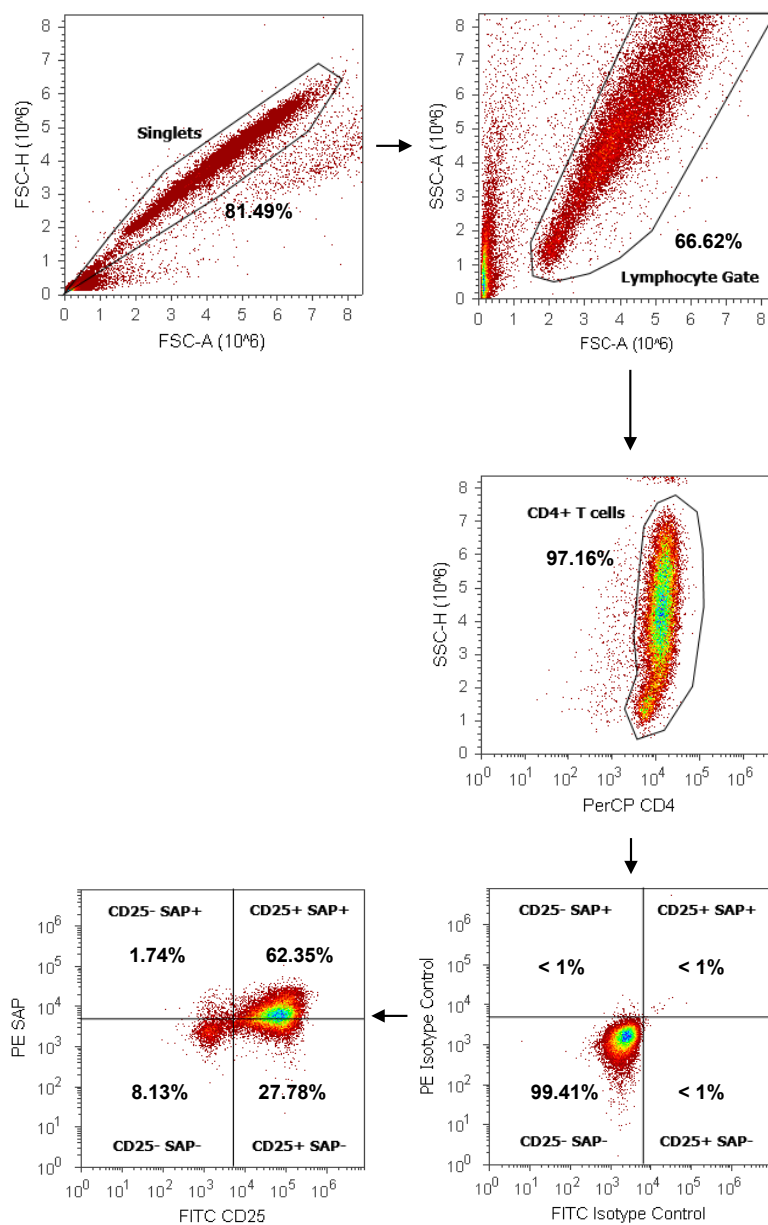
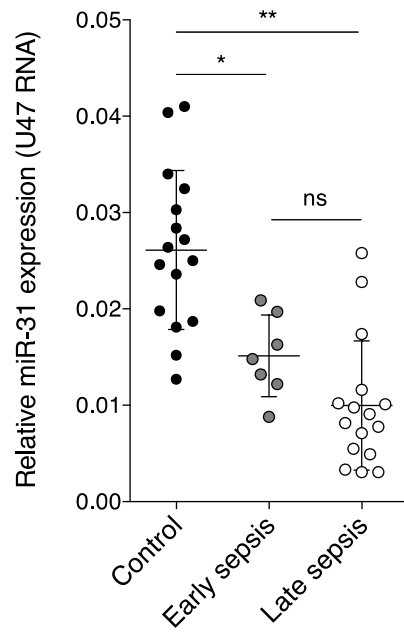


FIGURE S3



**Table S1. Primer Sequences**

<b>Cloning</b>	
SH2D1A 3'-UTR	
for	5'-CTCGAGCCTGATGTCTGCCTGAAAGC-3'
rev	5'-GTTTAAACAACCTCCAGGTTGGTCTGTGG-3'
<b>Mutagenesis</b>	
SH2D1A 3'-UTR mut1	
for	5'-GGATTAATGTCAATTCC <u>GG</u> CCAAATATAAATAATCCTCAG-3'
rev	5'-CTGAGGATTTTTATTTATATTTGGCC <u>GG</u> AATIGACATTAATCC-3'
SH2D1A 3'-UTR mut2	
for	5'-CTGAAAGCAACCTTCC <u>GG</u> CCCTAGTGTCTGATATTGG-3'
rev	5'-CCAATATCAGAACACTAGGCC <u>GG</u> AAGGTTGCTTTCAG-3'
<b>Real-time PCR</b>	
EZH2	for 5'-CTGGGTGAGGTCAATCCTG-3' (UPL probe #38) rev 5'-CGCTTTTCTGTAGGCGATGT-3' (UPL probe #38)
FIH	for 5'-ACCCTGTTTCATCACCCATGT-3' (UPL probe #21) rev 5'-TCTCGTAGTCGGGATTGTCA-3' (UPL probe #21)
IFN- $\gamma$	for 5'-GGCATTTTGAAGAATTGGAAAG-3' (UPL probe #21) rev 5'-TTTGGATGCTCTGGTCATCTT-3' (UPL probe #21)
IL-2	for 5'-AAGTTTTACATGCCCAAGAAGG-3' (UPL probe #65) rev 5'-AAGTGAAAGTTTTTGCTTTGAGCTA-3' (UPL probe #65)
IL-4	for 5'-TGCTCACATTGTCACCTGC-3' (UPL probe #38)

rev 5'-GCACATGCTAGCAGGAAGAAC-3' (UPL probe #38)

NIK

for 5'-TGCGCTGTCAAAAAGGTG-3' (UPL probe #17)

rev 5'-CTGGGTGAGGTCAATCCTG-3' (UPL probe #17)

SDHA

for 5'-GAGGCAGGGTTTAATACAGCA-3' (UPL probe #80)

rev 5'-CCAGTTGTCCTCCTCCATGT-3' (UPL probe #80)

SH2D1A

for 5'-CCTCTGCAGTATCCAGTTGAGA-3' (UPL probe #73)

rev 5'-GCTTTCAGGCAGACATCAGG-3' (UPL probe #73)

SUZ12

for 5'-ACATGGGAGACTATTCTTGATGG-3' (UPL probe #16)

rev 5'-GCAACGTAGGTCCCTGAGAA-3' (UPL probe #16)

TBP

for 5'-GAACATCATGGATCAGAACAACA-3' (UPL probe #87)

rev 5'-ATAGGGATTCCGGGAGTCAT-3' (UPL probe #87)

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UTR, untranslated region; for, forward; rev, reverse. Base exchanges are highlighted.

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**Table S2. Correlation between miR-31 expression and laboratory parameters**

<b>Parameter</b>	<b>Correlation coefficient r</b>	<b>p-value</b>
<i>SOFA</i> score	-0.48 (Pearson)	* $p=0.04$
Interleukin-6	-0.30 (Spearman)	ns, $p=0.19$
C-reactive protein	-0.38 (Pearson)	ns, $p=0.074$
WBC	-0.04 (Pearson)	ns, $p=0.87$

*SOFA*, sequential organ failure score assessment; WBC, white blood cell count; ns, not significant