Table SI. Characteristics and preprocessing information of the GEO datasets used in the present study.

GEO accession	Sample type	Disease context/stage	Cohort structure	Platform	Preprocessing/ normalization
GSE46955	Blood monocytes and total RNA	Gram-negative sepsis during the acute sepsis phase, recovery phase and healthy donor control. Cells were further analyzed under basal or *ex vivo* LPS-stimulated conditions	Blood monocytes from patients with sepsis and recovered patients and healthy donors, with samples including basal and LPS-treated conditions: Sepsis basal and sepsis + LPS, recovery basal and recovery + LPS and healthy basal and healthy + LPS	GPL6104; Illumina humanRef-8 (version 2.0) expression beadchip and expression profiling by array	Probe-level data were background-corrected using Illumina BeadStudio software and quantile-normalized in R software
GSE57065	Whole blood/blood leukocyte transcriptome and total RNA	Septic shock dynamic sampling cohort. Blood samples were collected within 30 min, 24 h and 48 h after septic shock onset, with healthy volunteers used as controls	28 patients in the ICU enrolled at septic shock onset with serial blood sampling at H0, H24 and H48, compared with 25 healthy volunteers	GPL570; Affymetrix Human Genome U133 Plus (version 2.0) Array; expression profiling by array	RMA normalization
GSE28750	Whole blood collected in PAX gene tubes for leukocyte RNA isolation	Early sepsis diagnostic cohort: Sepsis patients who met the 1992 Consensus Statement criteria and had microbiological evidence of systemic infection; post-surgical systemic inflammation and healthy controls were included for comparison	GEO microarray subset included 41 samples: Sepsis (n=10), post-surgical systemic inflammation (n=11) and healthy controls (n=20)	GPL570; Affymetrix Human Genome U133 Plus (version 2.0) Array; expression profiling by array	Processed GEO Series Matrix data were used for downstream analysis
GSE69528	Whole blood and total RNA	Culture-determined sepsis cohort focused on septicemic melioidosis and sepsis caused by other	29 patients with septicemic melioidosis caused by *Burkholderia pseudomallei*, 54 patients	GPL10558; Illumina HumanHT-12 (version 4.0) expression beadchip; expression profiling by	Quantile normalization, flooring of intensities <10 to 10, $\log_2$ transformation and PALO filtering

	pathogens; uninfected healthy and type 2 diabetes mellitus controls were included	with sepsis caused by other pathogens, 28 healthy controls and 27 subjects with type 2 diabetes mellitus	array

Preprocessing and normalization information was obtained from the 'Sample data processing' or associated preprocessing fields in the original GEO Series Matrix files. H0, H24 and H48 indicate blood sampling within 30 min, 24 h and 48 h after septic shock onset, respectively. LPS, lipopolysaccharide; RMA, robust multi-array average; PALO, present or absent likelihood of outlier; ICU, intensive care unit; GEO, Gene Expression Omnibus; GPL, GEO platform accession; PAX, PreAnalytiX.