

Supplementary Table 1 Primers designed for validation of commonly expressed genes in four dataset by quantitative real-time PCR.

Primer name	Forward sequence (5'-3')	Reverse sequence (5'-3')	Tm(F/R)	Amplicon size
CEACAM1-human	AACTTTGAAGCCCAGCAAC C	GCAGGACAGGTTTCATTAC TGC	59.3/59.8	108
PFKFB3-human	AAAGTCCGGAAGCAATGTG C	ATTGGTGGCATCGAAAACC G	59.4/59.5	96
PSTPIP2-human	CTGAAATCAACACCCTGAA GCG	CCTGGCCTCTTCTCTTAAA CTC	60.1/58.1	107
SOCS3-human	AGTACGATGCCCCGCTTTAA G	TTGGCTTCTTGTGCTTGTG C	60.5/59.9	107
IL18RAP-human	AGTGAGAACCATTGTGGGA GAC	AGCCAAATCGTGCTTTGCA G	60.0/60.0	119
LILRA5-human	AGGTGTCAGATGTGTCTCT GC	TTTTTCAGCCCTGGAGATG C	59.7/58.5	84
TNFAIP6-human	AAGCACGGTCTGGCAAATA C	ATGGCCGCCTTCAAATTCA C	58.8/59.5	71
GK-human	ACTTCGTCCCAGCATTTCG	TCCACAGATTATCCCTCTTG CG	58.8/59.9	71
RPS18-human	ATCCTCAGTGAGTTCTCCCG	CTTTGCCATCACTGCCATTA	58.5/56.4	106

Note: CEACAM1: carcinoembryonic antigen related cell adhesion molecule 1; GK: glycerol kinase; PFKFB3: 6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 3; TNFAIP6: TNF alpha induced protein 6; IL18RAP: interleukin 18 receptor accessory protein; LILRA5: leukocyte immunoglobulin like receptor A5; PSTPIP2: proline-serine-threonine phosphatase interacting protein 2; SOCS3: suppressor of cytokine signaling 3; RPS18: ribosomal protein S18.

Supplementary Table 2 Summary of DEGs selected from each dataset using $|\log_2$ Fold Change $|\geq 1.5$ and FDR < 0.05 as cut-off criteria.

Dataset accession number	Upregulated gene in <i>Staphylococcus aureus</i>-induced sepsis	Downregulated gene in <i>Staphylococcus aureus</i>-induced sepsis	Upregulated gene in <i>Escherichia coli</i>-induced sepsis	Downregulated gene in <i>Escherichia coli</i>-induced sepsis
GSE4607	320	177	389	108
GSE25504	132	34	204	156
GSE33341	220	165	154	141
GSE65088	335	116	367	61

Note: FDR: false discovery rate.

Supplementary Table 3 The common genes in any three datasets.

Upregulated gene in <i>Staphylococcus</i> <i>aureus</i> -induced sepsis	Downregulated gene in <i>Staphylococcus</i> <i>aureus</i> -induced sepsis	Upregulated gene in <i>Escherichia</i> <i>coli</i> -induced sepsis	Downregulated gene in <i>Escherichia</i> <i>coli</i> -induced sepsis
ACSL1	CCR7	ANXA3	ABLIM1
ANXA3	CD247	ARG1	AUTS2
B4GALT5	CD96	BASP1	BCL11B
CEACAM1	FCMR	CA4	CCR7
CST7	ID3	CD177	CD52
DRAM1	IL7R	CEACAM1	CD96
FCGR1B	ITM2A	CLEC5A	FAM102A
FFAR2	LEF1	FFAR2	FCMR
GK	LRRN3	FLOT1	LEF1
GYG1	LY9	FPR1	LRRN3
HK3	NELL2	GK	NELL2
HP		GPR84	PASK
IL18R1		GYG1	RASGRP1
IL1RN		HK3	
LCN2		HP	
MMP9		IL18R1	
OLFM4		IL18RAP	
PFKFB3		LILRA5	
PLSCR1		LIMK2	
PSTPIP2		MMP8	
RETN		MMP9	
S100A12		OLFM4	
SAMSN1		ORM1	
SERPINB1		PFKFB2	
SERPING1		PFKFB3	
SLC2A3		PGS1	
SOCS3		PLSCR1	
SORT1		PSTPIP2	
STOM		RETN	
TNFAIP6		SAMSN1	
TXN		SERPINB1	

SERPING1

SMPDL3A

SOCS3

SORT1

STOM

TLR5

TNFAIP6

TNFSF10

UPP1

VPS9D1

Note: The bold font represents emerged in both *Staphylococcus aureus* and *Escherichia coli* groups.