

# COHORTS ANALYZED IN THE STUDY

Table 1 Characteristics of sepsis cohorts summarized from metadata and original publication.

Accession Number	Sepsis Source Type (And Disease Type)	Number of samples/ patients (And Organism)	Genders	Age	Mortality # died (%died)	Ancestry (And Country where study conducted)	Sample Source
E-MEXP-3567 [Irwin AD]	Bacterial (Pneumococcal Meningitis with some HIV co-infection)	15 samples ( <i>Homo sapiens</i> )	Male and Female	Infants	6 (40%)	No info (Malawi)	Blood (Total RNA)
E-MEXP-3850 [Kwan A]	Bacterial (Meningococcal Sepsis)	5 samples ( <i>Homo sapiens</i> )	Male and Female	Children	1 (20%)	No info (England)	Blood (Total RNA)
E-MTAB- 1548 [Almansa R]	General (Normal vs. Systemic Inflammatory response syndrome (SIRS) vs. Sepsis)	155 samples ( <i>Homo sapiens</i> )	Male and Female (some no info about gender)	42 - 88	17 (10.9%)	No info (Spain)	Blood
E-MTAB- 4421 [Davenport EE]	Bacterial (Gram positive & Gram Negative) & Viral	270 samples ( <i>Homo sapiens</i> )	Male and Female	18-89	58 (21.5%)	No info (United Kingdom)	Leukocyte Cells
E-MTAB- 4451 [Davenport EE]	Bacterial (Gram positive & Gram Negative) & Viral	114 Samples ( <i>Homo sapiens</i> )	Male and Female	31-91	57 (50%)	No info (United Kingdom)	Leukocyte Cells (Total RNA)
GSE 10474 [Howrylak JA]	Bacterial (Gram-positive and Gram Negative)	34 samples ( <i>Homo sapiens</i> )	No Info	No Info	12 (35.3%)	No info (United States of America)	Plasma (Total RNA)
GSE 110487 [Barcella M]	General	31 samples ( <i>Homo sapiens</i> )	No Info	No Info	7 (22.6%)	No info (Switzerland & Belgium)	Whole Blood (Total RNA)

GSE 13015 [Pankla R]	Bacterial & Fungal ( <i>B. pseudomallei</i> , <i>A.baumannii</i> , <i>Corynebacterium</i> <i>spp.</i> , <i>C. albicans</i> , <i>E. coli</i> , <i>Salmonella</i> <i>serotype B</i> , <i>S. aureus</i> , <i>Salmonella spp.</i> , <i>Streptococcus</i> infections)	92 Samples ( <i>Homo sapiens</i> )	Male and Female	18- 81	20 (21.7%)	Asian (Thailand)	Blood (Total RNA)
GSE 13904 [Wong HR]	Mainly Bacteria (Gram positive and gram negative) Other Pathogen	102 Samples ( <i>Homo sapiens</i> )	No Info	Children (Ages no info)	16 (15.6%)	No info (United States of America)	Whole Blood (Total RNA)
GSE 21802 [Bermejo- Martin JF]	Viral (H1N1; Some co-infected with Bacterial or Fungal superinfection)	19 samples ( <i>Homo sapiens</i> )	No Info	No Info	7 (36.8%)	No info (Spain)	Blood (Total RNA)
GSE 25504 [Smith CL]	Bacterial and viral ( <i>Staphylococcus</i> , <i>Enterovirus</i> , etc.)	170 samples ( <i>Homo sapiens</i> )	Female (68) and Male (102)	Neonates (Ages no info)	No info	No info (Scotland)	Whole Blood (Total RNA)
GSE 27131 [Berdal JE]	Viral (H1N1)	21 samples ( <i>Homo sapiens</i> )	Female (5) and Male (16)	28- 59	2 (9.5%)	No info (Norway)	Blood (Total RNA)
GSE 28750 [Sutherland A]	General (Sepsis vs Healthy vs Post- surgical)	41 samples ( <i>Homo sapiens</i> )	No info	No Info	No info	No info (Australia)	Whole Blood (Total RNA)
GSE 32707 [Dolinay T]	General ( Sepsis, SIRS, Sepsis + ARDS, No Sepsis ARDS, Untreated)	225 samples ( <i>Homo sapiens</i> )	No Info	No Info	62 (27.6%)	Asian/Pacific Islander, Black, White, Hispanic (United States of America)	Whole Blood (Total RNA)
GSE 33341 [Ahn SH]	Bacterial ( <i>Staphylococcus</i> <i>aureus</i> , <i>E coli</i> , <i>S</i> <i>Pneumonia</i> , Infection)	94 samples ( <i>Homo sapiens</i> )  227 samples ( <i>Mus musculus</i> )	Male- Human (53) Female- Human (41)  Male Mouse (227)	23- 91 (Humans)	2 (2.1%)	Asian, White, Black (United States of America)	Whole Blood (Total RNA)
GSE40586 [ Lill M ]	Bacterial ( <i>S. agalactiae</i> , <i>E. coli</i> , <i>S. pneumoniae</i> , <i>L. monocytogenes</i> , <i>N. meningitidis</i> )	39 samples ( <i>Homo sapiens</i> )	No info	No info	2 (5.1%)	No info (Estonia)	Peripheral Blood (Total RNA)

GSE 4607 [Wong HR]	Viral Fungal Bacterial ( <i>C. albicans</i> , <i>E. coli</i> <i>Varicella</i> , etc., vs Healthy)	57 Samples ( <i>Homo sapiens</i> )	No info	Children	9 (15.8%)	No info (No info)	Whole Blood (Total RNA)
GSE 54514 [Parnell GP]	Bacterial (Type of Bacteria not specified for the affected)	163 samples ( <i>Homo sapiens</i> )	Male and female	18-86	31 (19%)	No info (Australia)	Whole Blood (Total RNA)
GSE 63042 [Langley]	Bacterial ( <i>S. pneumoniae</i> , <i>Staphylococcus</i> , <i>Enterobacteriaceae</i> )	129 Samples ( <i>Homo sapiens</i> )	No info	No info	28 (21.7%)	No info (United States of America)	Blood (Total RNA)
GSE 63311 [Pena OM]	General (Sepsis vs no sepsis)	83 Samples ( <i>Homo sapiens</i> )	No info	No info	No info	No info (Canada)	Whole Blood (Total RNA)
GSE64457 [Demaret J]	Bacteria ( <i>Bacilli</i> gram negative, <i>Cocci</i> gram positive), Fungal and Other	23 Samples ( <i>Homo sapiens</i> )	No Info	No Info	No info	No info (United States of America)	Purified Neutrophils (Total RNA)
GSE65682 [Scicluna BP]	Bacterial ( <i>Streptococcus pneumoniae</i> , <i>Staphylococcus aureus</i> , etc., Unknown)	802 Samples ( <i>Homo sapiens</i> )	Male and female	17-93	114 (14.2%)	No info (Netherlands)	Whole Blood (Total RNA)
GSE66099 [Wong]	General (Septic shock vs SIRS vs healthy)	276 Samples ( <i>Homo sapiens</i> )	No info	No info	No Info	No info	Blood (Total RNA)
GSE66890 [Kangelaris]	General (Sepsis vs Sepsis with ARDS)	62 Samples, ( <i>Homo sapiens</i> )	Male and Female	18-91	14 (22.6%)	No info	Blood (Total RNA)
GSE74224 [Mchugh L]	Bacterial (Gram- positive isolations, Gram-negative isolations), Fungal & Mixed infections	105 Samples ( <i>Homo sapiens</i> )	No info	No info	No info	White, East Indian/Asian, Aboriginal and Torres Strait Islander(Austr alia)	Peripheral Blood (Total RNA)
GSE8121 [Shanley TP]	Viral Fungal Bacterial ( <i>C. albicans</i> , <i>E. faecalis</i> <i>E. coli</i> <i>Varicella</i> , etc)	45 Samples ( <i>Homo sapiens</i> )	No info	Children	5 (11.1%)	Asian, Black, Caucasian, unreported (United States of America)	Whole Blood (Total RNA)

GSE95233 [Venet F]	Bacterial (Gram-positive, Gram-negative), Fungal and other	125 Samples, ( <i>Homo sapiens</i> )	Homosexual, Male and Female	25-85	34 (27.2%)	No info (France)	Whole Blood (Total RNA)
GSE9960 [Tang BM]	Bacterial (Gram Positive, Gram-negative and mixed)	70 Samples, ( <i>Homo sapiens</i> )	No info	No info	No info	No info (Australia)	Circulating mononuclear cells (Total RNA)

Table 2 Characteristics of patients included in the logistic regression analysis.

Accession ID	Cohort description and Sepsis Type	Number of samples and Organism	Genders	Age
E-MTAB-4421 [Davenport EE]	Bacterial/ Viral	270 samples ( <i>Homo sapiens</i> )	Male and Female	18-89
E-MTAB-4451 [Davenport EE]	Bacterial/Viral	114 Samples ( <i>Homo sapiens</i> )	Male and Female	31-91
GSE27131 [Berdal JE]	Viral	21 samples ( <i>Homo sapiens</i> )	Female (5) and Male (16)	28- 59
GSE33341 [Ahn SH]	Bacterial	94 samples ( <i>Homo sapiens</i> )	Male- Human (53) Female- Human (41)	23-91 (Humans)
GSE54514 [Parnell GP]	Bacterial	163 samples ( <i>Homo sapiens</i> )	Male (64) and female (99)	18-86
GSE65682 [Scicluna BP]	Bacterial	802 Samples ( <i>Homo sapiens</i> )	Male and female	17-93
GSE95233 [Venet F]	Bacterial, Fungal and other	125 Samples ( <i>Homo sapiens</i> )	Homosexual, Male and Female	25-85