



Supplementary Figure 2. Single-Cell RNA Sequencing Classification. (A) UMAP plot showing the clustering of single-cell CD11b+Ly6Chigh myeloid cells from sham-operated and sepsis-surviving (CLP) mice. Each point represents an individual cell, colored by cluster identity. 13 clusters were determined. Corresponding (predicting) cell type annotated based on known cell-type-specific marker genes: classical monocytes (clusters 0, 2, 3, 6), dendritic-like cells (cluster 1), M1-like macrophages (cluster 4), non-classical monocytes (clusters 5, 10), M2-like macrophage (cluster 7), monocyte-derived dendritic-like cells (cluster 9), proliferating monocytic myeloid-derived suppressor cells (M-MDSCs) (clusters 8, 11, 12). (B) Frequency maps indicate the distribution of 13 clusters between sham and CLP groups.

DEGs: B6 CLP vs. sham

CL#0

Up (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
4.777	1.1953	0	Lamc1
3.3617	1.0696	0.004	Cped1
3.0356	0.9464	0.0011	Clmn
2.9642	1.4916	0.0014	Arg2
2.9002	1.546	0.0019	Tgm1
2.8725	0.3623	0.0053	Pole2
2.5422	5.8171	5.43E-10	Pbx1
2.3801	3.2279	0.0005	Tacstd2
2.3461	1.1925	0.0042	Mctp2
2.3374	1.6699	0.0043	Oas1g
2.2894	0.886	0.0074	Ly6a
2.2331	3.5525	0.0004	Aig1
2.2158	1.5461	0.0057	Nnmt
2.1495	2.8753	0.0003	Nrg1
2.1392	3.6358	0.0002	Tarm1

Down (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
-1.9952	4.1836	4.41E-07	Mtss1
-2.1043	4.6271	0	Ehd1
-2.1557	0.8668	0.0075	Cers4
-2.1832	1.2257	0.0071	Inpp4b
-2.1954	0.4518	0.0082	Sult1a1
-2.2202	3.3618	8.98E-06	Adam19
-2.2972	3.5221	6.54E-06	Cd83
-2.3121	1.3889	0.0023	Itga8
-2.356	1.0182	0.0042	Cbr2
-2.6771	0.7386	0.0018	Pdgfb
-3.5745	5.5382	0.0003	Lpl

CL#1

Up (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
3.8726	3.2098	4.50E-07	Spon1
3.6149	0.8552	0.0002	Nrg1
3.6035	0.4719	0.0004	Lbp
3.1705	4.8863	1.46E-06	F11r
3.1296	2.0067	0.0002	Tarm1
2.9741	3.3027	0	Ly6a
2.9143	0.8895	0.0044	Morn2
2.617	2.2621	0.0006	C4b
2.5744	1.0072	0.0082	Mapk13
2.5191	5.5631	5.81E-13	Pbx1
2.1232	3.1511	0.0014	Il21r
2.0735	4.1188	9.09E-07	Cd300lf
2.0119	1.943	0.0097	Fam234b
1.8941	5.623	2.22E-11	Vcan
1.8559	3.1998	0.0033	Ccr5
1.8556	4.0041	7E-06	Aig1
1.6223	3.0803	0.0015	Zdhhc23
1.6026	7.495	3.66E-14	Ms4a6d
1.571	4.766	4.50E-07	Jaml

Down (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
-1.8234	3.753	6.95E-06	Tnip3
-1.963	3.5662	2.45E-06	Mrc1
-1.966	2.2208	0.0016	Chn2
-2.0625	4.6	0	Ehd1
-2.1214	2.883	0.0001	Heg1
-2.6888	2.0637	0.0002	Cd36
-2.814	4.455	0.0001	Cd209a
-2.9262	0.8033	0.0014	Alox5
-2.9482	0.5298	0.0011	Gstp3
-3.0996	0.2052	0.0014	Efnb2
-3.4948	0.2128	0.0002	Gdf15
-3.8682	0.2142	0	Ndnf

CL#2

Up (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
4.0239	0.8911	0.0004	Cd38
3.136	3.7687	5.3E-06	F11r
2.9911	1.6696	0.0008	Lamc1
2.4742	3.4678	0.0001	Tarm1
2.4694	2.1374	0.0049	Elane
2.469	1.8779	0.0055	Gpld1
2.4601	5.5327	4.26E-10	Pbx1
2.3253	5.3156	4.86E-06	Ier3
2.2754	3.7728	0	Aig1
2.2352	3.5881	0.0019	Ifitm1
2.0736	2.9833	0.0007	Ptgfrn
2.0579	7.99	4.86E-06	Vcan
2.0227	2.6928	0.0058	Hebp1
1.973	5.6687	6.36E-08	Gcnt2
1.9444	4.1567	0.0049	Al506816
1.898	6.8224	7.10E-11	Camk2d
1.8852	4.928	0	Atp11a
1.8851	5.8334	6.59E-09	Fcgr1

Down (P<0.01)

logFC	AveExpr	p_val_adj	gene_names
-1.936	3.979	4.42E-06	Mtss1
-1.965	4.1792	0.0001	Ehd1
-1.9853	1.839	0.0058	Hcar2
-2.0009	3.5654	0	Adam19
-2.0833	1.5694	0.0067	Il12rb2
-2.1613	1.6026	0.0066	Cgnl1
-2.3008	1.7468	0.0028	Zbtb16
-2.4374	2.0967	0.0019	Upb1
-2.5382	1.4765	0.003	Chn2
-2.626	0.7817	0.0073	Layn
-2.8217	5.5416	0	Lpl
-2.9898	2.6693	0	Cd83
-3.2036	2.7795	0.0002	Cd209a

Supplementary Figure 3. Highly upregulated and downregulated DEGs (P<0.01) of Clusters 0, 1, and 2 (CLP surviving group vs. Sham control group).

Supplementary Table 1. Raw lipidomics data from 6 sham (S1-S6) and 6 CLP-surviving mice (C1-C6) after 2 hours of fasting. S1'-S6' and C1'-C1' samples are non-fasted plasma from the same animals and NIST SRM 1950 plasma QC samples. The table includes an internal standard and a reference for calculating concentration. TG, triacylglycerols, DG, diacylglycerols, and MAG, monoacylglycerols. PC, phosphatidylcholine; LPC, lyso-PC; PI, phosphatidylinositol; PS, phosphatidylserine; LP, PE, phosphatidylethanolamine; SM, sphingomyelin; FFA, free fatty acid; Cer, ceramide; H Cer, hexosylceramide.

Supplementary Table 2. Raw concentration data of lipidomics used for Figure 4. An "A" or "B" following the name of each lipid denotes its isomeric form.