

Supplementary Material

Table S1. Data cohort characteristics

Datasets	Patients (N)	Normal (N)
GSE49454 (whole blood)	157	20
GSE72509 (whole blood)	99	18
GSE110169 (whole blood)	82	77
GSE157103 (whole blood)	100	26
GSE161731(whole blood)	77	19
GSE163151 (whole blood)	7	20
GSE135779 (PBMC)	7(adult)	unused
GSE142016 (PBMC)	3	unused
GSE155222 (PBMC)	6	unused
GSE166992(PBMC)	6	unused
GSE163121(B cells)	3	unused
GSE164379(B cells)	7	unused

Table S2. Characteristics of the SLE patients and healthy controls

GSE72509	SLE (n=99)	HC (n=18)
Anti-ro		
high	24	NULL
med	23	NULL
none	52	NULL
Ism		
high	75	NULL
low	24	NULL
GSE49454	SLE (n=157)	HC (n=20)
Age (mean)	40.73	40.72
Gender		
Female	131	17
Male	26	3
Race		
White	141	19
Black	10	1
Asian	6	0
Country of origin		
China	1	NULL
Comorres	3	NULL
Cuba	5	NULL

France	92	12
North Africa	49	7
New Caledonia	1	NULL
Philippines	2	NULL
Vietnam	3	NULL
Zaire	1	NULL
French West Indies		1
Years since diagnosis of sle (mean)	11.11	NULL
SLEDAI (mean)	7.17	NULL
Skin		
N	124	NULL
Y	33	NULL
Joints		NULL
N	128	NULL
Y	29	NULL
Hemato		
N	147	NULL
Y	10	NULL
Renal		
N	93	NULL
Y	64	NULL
Cyp		
N	145	NULL
Y	12	NULL
Aza		
N	109	NULL
Y	48	NULL
Mmf		
N	133	NULL
Y	24	NULL
Csa		
N	153	NULL
Y	4	NULL
Iv cs		
N	153	NULL
Y	4	NULL
Oral cs		
N	17	NULL
Y	140	NULL
Cs mg/d (mean)	15.22	NULL
Cs mg/kg (mean)	0.22	NULL
Hcq		
N	67	NULL

Y	90	NULL
Hcq mg/d (mean)	200	NULL
a-dsd (mean)	66.62	NULL
Low c3		
N	88	NULL
Y	69	NULL
Low c4		
N	104	NULL
Y	53	NULL
Hb (mean)	13.075	NULL
Platelets (mean)	265.84	NULL
Leukocytes (mean)	6690.74	NULL
Neutrophils (mean)	4522.44	NULL
Lymphocytes (mean)	1632.40	NULL
CD4 Tcells (mean)	728.99	NULL
CD8 T cells (mean)	616.95	NULL
B cells (mean)	168.76	NULL
NK cells (mean)	109.88	NULL
Eosino (mean)	103.26	NULL
GSE110169	SLE (n=82)	HC (n=77)
Glucocorticoids		
False	31	1
True	45	NULL
NA	6	76
Sex		
Female	69	54
Male	13	23

Table S3. Characteristics of the COVID-19 patients and healthy controls

GSE157103	COVID-19 (n=100)	HC (n=26)
Anti-ro		
High	24	NULL
Med	23	NULL
None	52	NULL
Ism		
High	75	NULL
Low	24	NULL
Age (years)	61.23	62.8
Sex		
Female	74	13

Male	51	13
Icu		
No	60	10
Yes	66	16
Apacheii (mean)	20.95	19.64
Charlson score (mean)	3.5	4.34
Mechanical ventilation		
No	75	17
Yes	51	9
Ventilator-free days (mean)	20.34	22.42
Dm		
0	84	20
1	42	6
Hospital-free days post 45 day followup (days)	24.19	32.26
Ferritin (ng/ml)	833.51	250.5
Crp (mg/l)	131.17	73.75
Ddimer (mg/l_feu)	10.76	5.34
Procalcitonin (ng/ml)	3.07	2.11
Lactate (mmol/l)	1.46	2.09
Fibrinogen	516.51	362.28
GSE161731	COVID-19 (n=77)	HC (n=19)
Age (mean)	36.46	18.28
Gender		
Female	32	8
Male	45	11
Race		
Asian	8	7
Black/African American	9	NULL
Native Hawaiian/Pacific Islander	1	NULL
Unknown/Not reported	2	1
White	57	11
Time_since_onset		
late	22	NULL
early	19	NULL
middle	36	NULL
Hospitalized	12	NULL
GSE163151	COVID-19 (n=7)	HC (n=20)
Pathogen		
No pathogen	NULL	20
SARS-CoV-2, NP	7	NULL

Table S4: The expression difference of common genes among six cohorts.

	GSE72509		GSE49454		GSE110169	
	logFC	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val
Immune						
CD3D			1.39	0.0180	1.06	0.0276
CXCL10			1.25	3.80E-06	1.45	8.65E-14
SH2D1A	1.59	0.0090	1.19	0.0339		
SH2D1B	1.55	0.0021	1.34	0.0054		
	GSE157103		GSE161731		GSE163151	
	logFC	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val
Immune						
CD3D	2.06	0.0057	1.91	4.45E-07		
CXCL10	1.23	0.0041	1.68	0.0001		
SH2D1A			1.25	7.52E-06	1.41	0.0308
SH2D1B			1.14	0.0445	1.64	0.0023

adjusted P<0.05 and |log2FC|>1

Figure S1

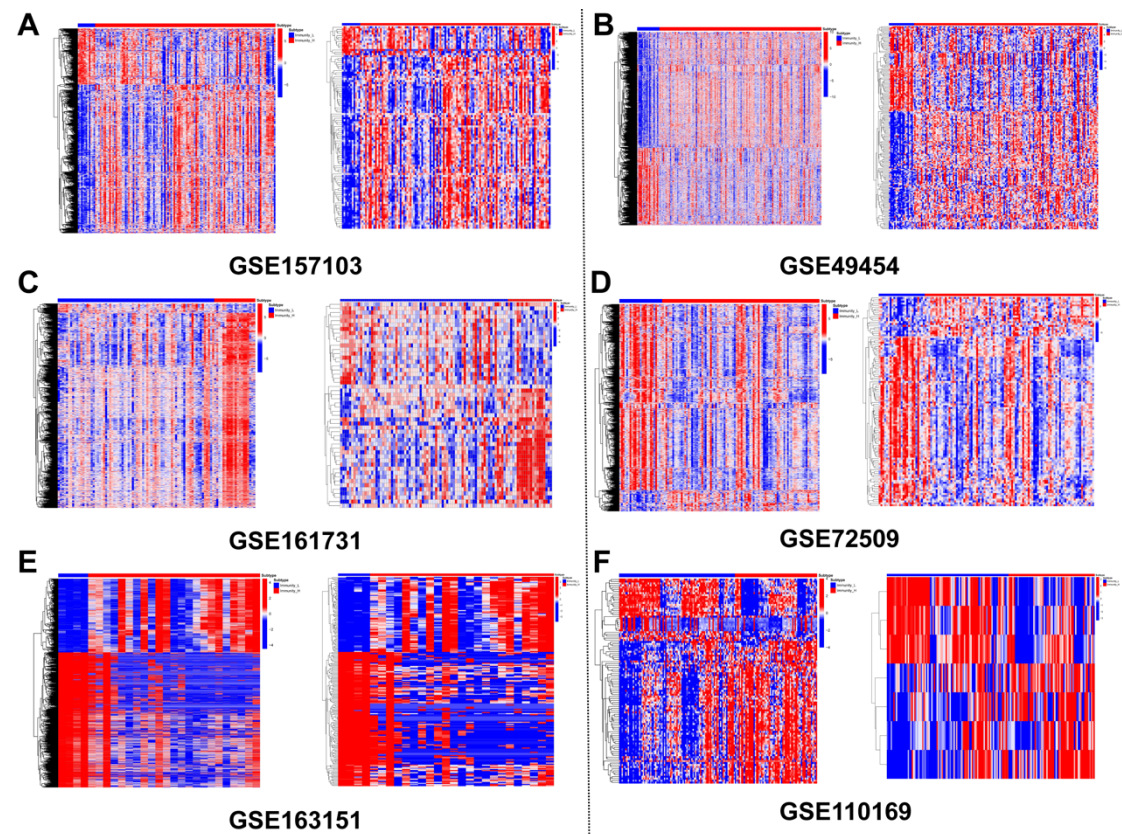


Figure S1. Immune-related genes were obtained by expression comparison between the high-immune and low-immune groups of COVID-19 and SLE cohorts. Heatmap showing the expression status of immune-related genes between the high-immune and low-immune groups of COVID-19 and SLE cohorts in (A) GSE157103, (B) GSE49454, (C) GSE161731, (D) GSE72509, (E) GSE163151, (F) GSE110169.

Figure S2

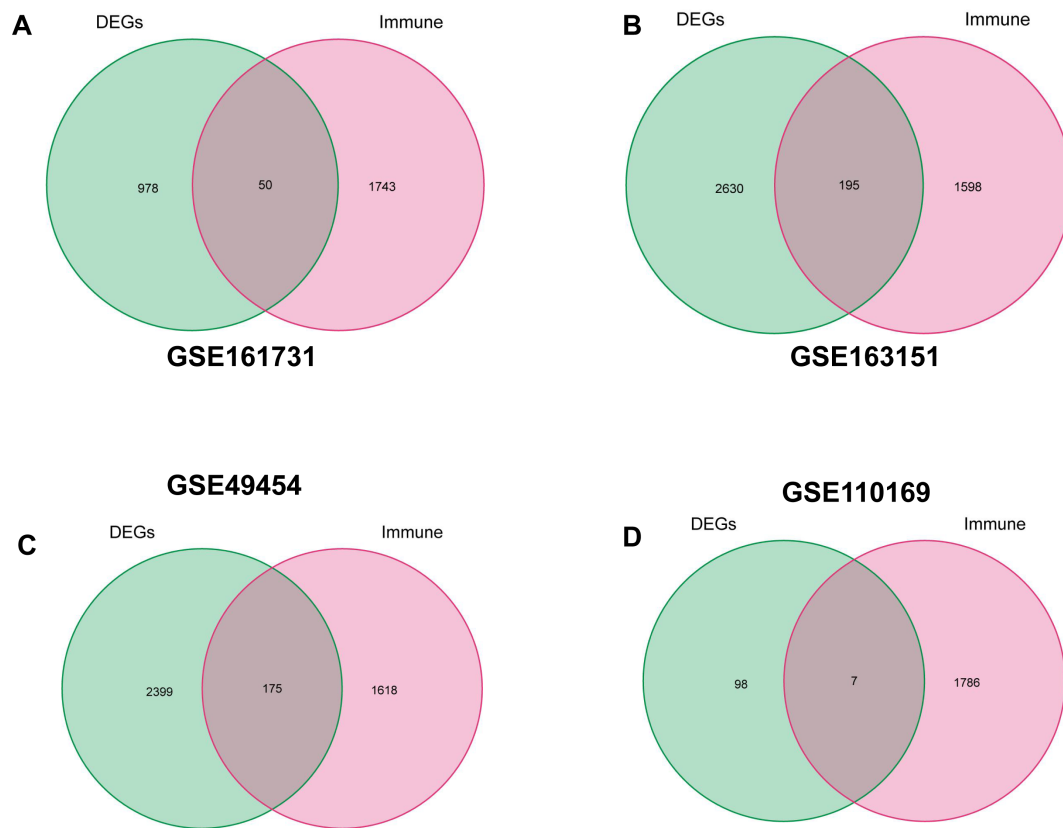


Figure S2. The overlapped genes between DEGs (differentially expressed genes) and immune genes. **(A)** GSE161731 **(B)** GSE163151 **(C)** GSE49454 **(D)** GSE110169.

Figure S3. GO and KEGG analysis were performed to get the biological behavior among the subgroups of COVID-19 cohorts. **(A)** GO and **(B)** KEGG analysis were performed to get the biological behavior among the subgroups of COVID-19 cohorts. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

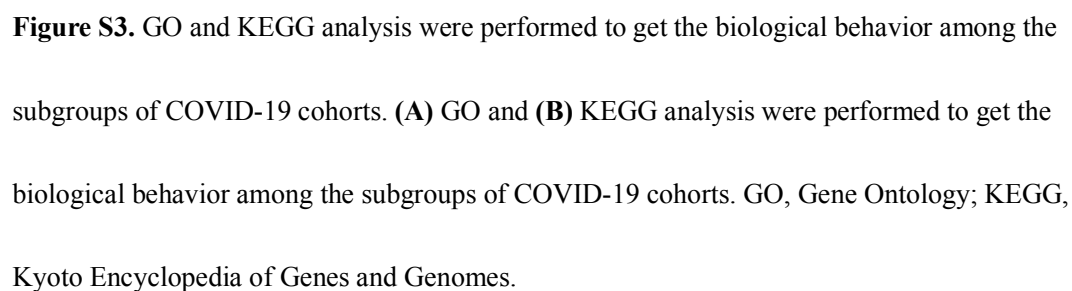


Figure S4

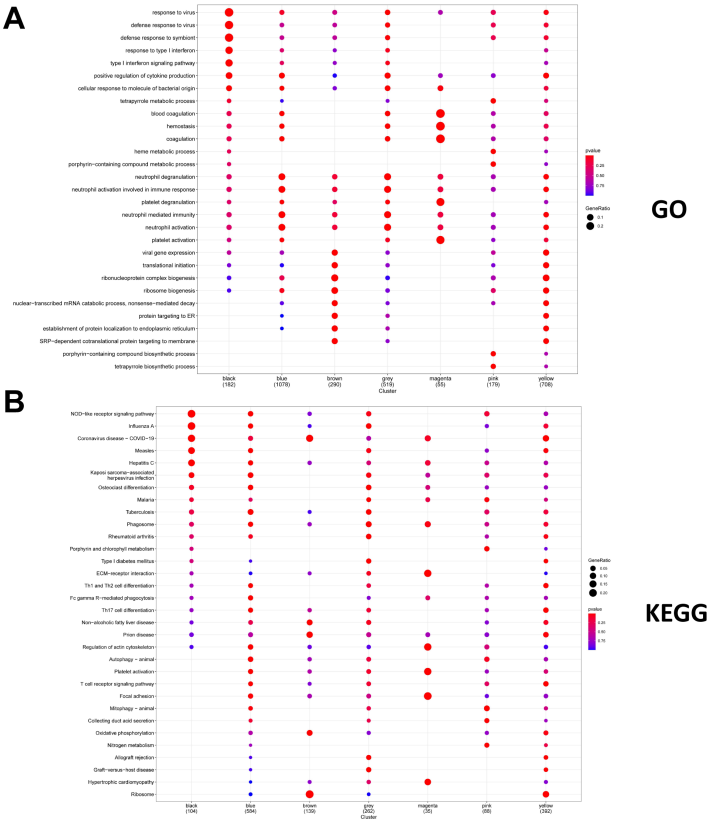


Figure S4. GO and KEGG analysis were performed to get the biological behavior among the subgroups of SLE cohorts. **(A)** GO and **(B)** KEGG analysis were performed to get the biological behavior among the subgroups of SLE cohorts. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Figure S5

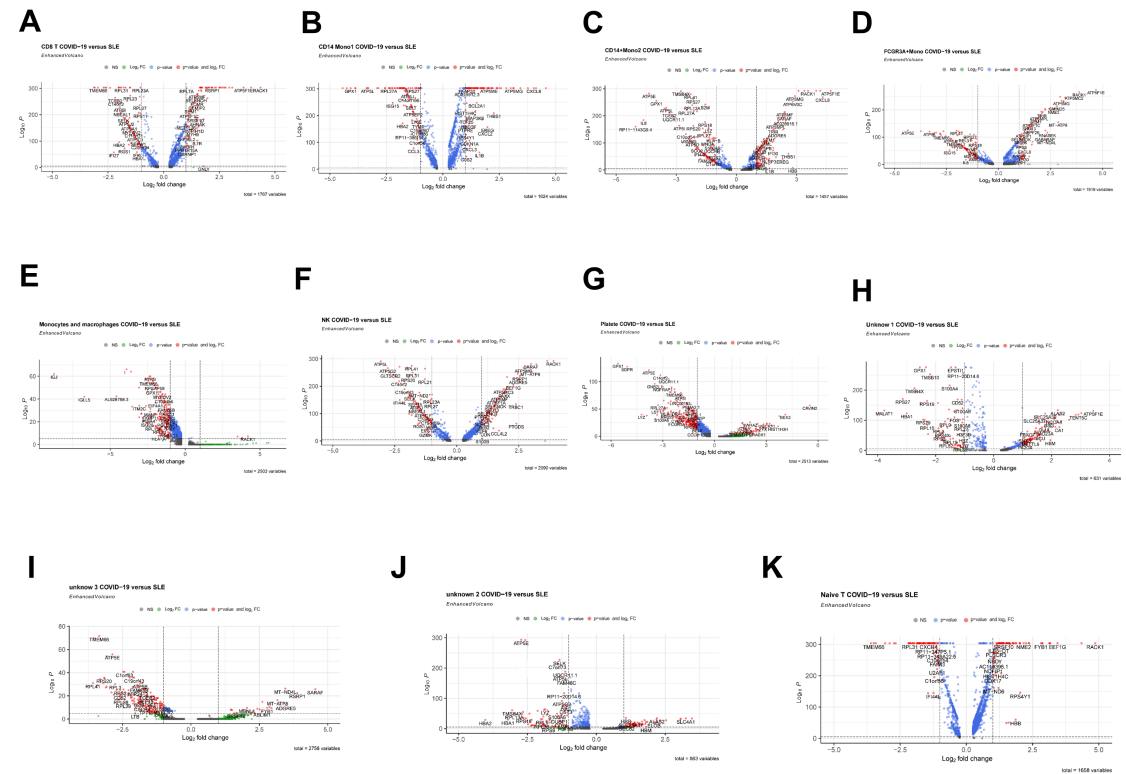


Figure S5. Volcano plot showing the differentially expressed genes in COVID-19 versus SLE. **(A)** CD8+ T, **(B)** CD14+ Mono1, **(C)** CD14+ Mono 2, **(D)** FCGR3A+ Mono, **(E)** Monocytes and macrophages, **(F)** NK, **(G)** platelets, **(H)** Unknown 1, **(I)** Unknown 3, **(J)** Unknown 2, **(K)** Naive T.