

Table S1. Information of the cell suspension.

Sample Name	Concentration (number/uL)	Viability (%)
C-1	2,846	92%
C-2	3,158	90%
T-1	3,351	91%
T-2	3,021	94%

Table S2. Comparison before and after data quality control.

Sample name	Cells number before filtration	Median genes before filtration	Cells number after filtration	Median genes after filtration
C-1	7,334	1,382	7,107	1,394
C-2	8,345	1,346	8,041	1,357
T-1	7,692	1,356	7,418	1,366
T-2	8,385	1,358	7,865	1,371

Table S3. Proportion of different types of cells.

Cell type	Proportion of control group 1(%)	Proportion of control group 2(%)	Average proportion of control group (%)	Proportion of infection group 1(%)	Proportion of infection group 2(%)	Average proportion of infection group (%)
B	38.55%	30.60%	34.57%	33.73%	25.97%	29.85%
CD4 T	31.23%	36.39%	33.81%	31.46%	39.39%	35.43%
CD8 T	11.43%	11.89%	11.66%	16.97%	15.15%	16.06%
Mono	9.78%	10.79%	10.29%	5.56%	5.38%	5.47%
NK	3.25%	4.75%	4.00%	6.57%	8.66%	7.61%
DCs	1.23%	1.17%	1.20%	0.83%	0.76%	0.80%
Platelet	2.72%	2.27%	2.49%	2.88%	2.47%	2.67%
Plasmablast	1.81%	2.15%	1.98%	1.99%	2.23%	2.11%

Table S4. Sequences of oligonucleotide primers.

Primer name	Gene name	Sequence (5'-3')
β-actin-F	β-actin	CACCACACCTTCTACAAC
β-actin-R		TCTGGGTCATCTTCTCAC
IL-4-F	IL-4	GTACCAGCCACTTCGTCCAT
IL-4-R		GCTGCTGAGATTCCTGTCAA
IL-5-F	IL-5	CTGCCTATGTTTGTGCCAATGCT
IL-5-R		TTCCCATCACCTATCAGCAGAGTTTC
IL-6-F	IL-6	CTTCTGCTTTCCTACCCCG
IL-6-R		AGTAGTCTGCTTGGGGTGGT
IL-10-F	IL-10	CCTTGTCGGAAATGATCCAG
IL-10-R		AGGGCAGAAAACGATGACAG
IL-13-F	IL-13	GTGTCATCCAAAGGACCAAGAGG
IL-13-R		TCGGATGTACTCACTGGAACATG

A

nFeature_RNA

nCount_RNA

percent_mito

C1 C2 T1 T2

Identity

nFeature_RNA

nCount_RNA

percent_mito

C1 C2 T1 T2

Identity

B

Standardized Variance

Average Expression

LOC102170870

LOC102176353

JHNAH

LOC102185461

MZB1

C1R

C1GA

C1GC

LOC102168148

THBS1

LOC102177287

LOC102186629

S105A9

LOC108632412

PSLYR9P1

S105A3

LOC102186681

TIME2C

LOC102170319

VCAN

SIXRAB

CFD

FCN1

S105A4

LOC102168428

ANKK1

OSG-F13A1

TYROBP

AP1

VM

CD309

LOC102170870

LOC102176353

JHNAH

LOC102185461

MZB1

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C1GA

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S105A3

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S105A9

LOC108632412

PSLYR9P1

S105A3

LOC102186681

TIME2C

LOC102170319

VCAN

SIXRAB

CFD

FCN1

S105A4

LOC10

Figure S1. Data filtering, dimensionality reduction and identification of highly variable genes (A) Number of genes, counts, and mitochondrial gene ratio before and after data filtering; (B) The top 2000 highly variable genes; (C) The elbow plot.

Figure S2 The proportion of cell subpopulations and changes in cell cycle

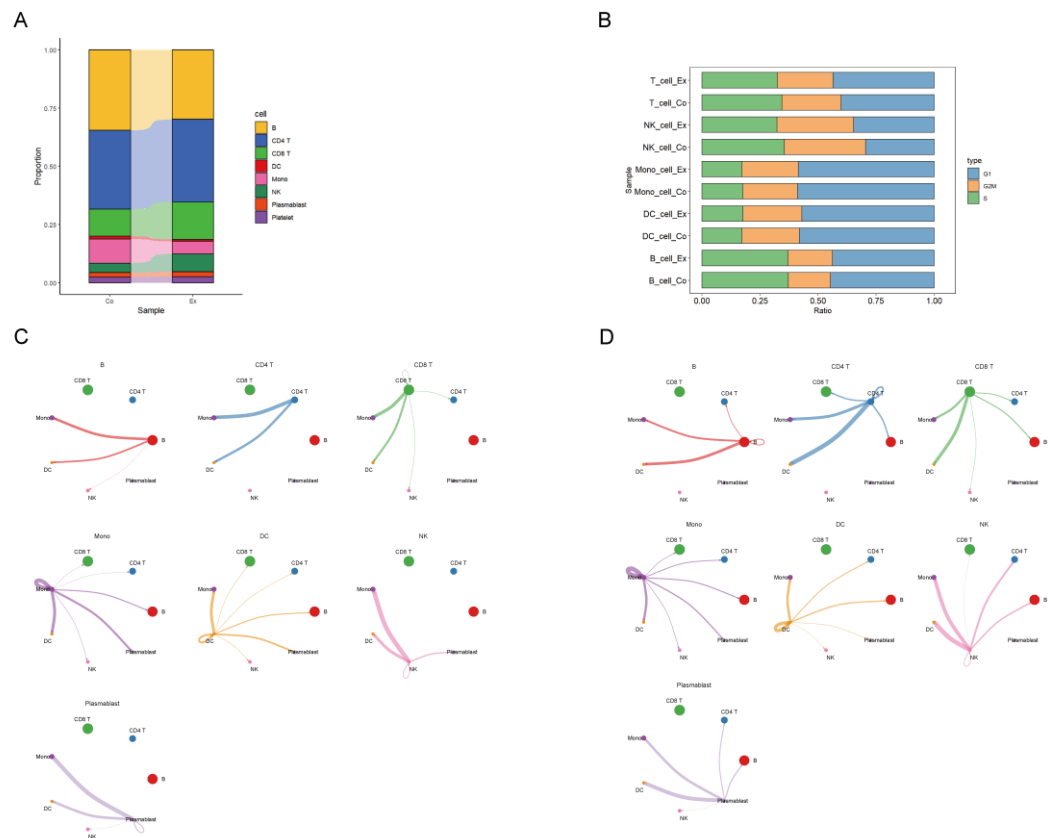


Figure S2. The proportion of cell subpopulations and changes in cell cycle. (A) Changes in the proportion of cell subpopulations; (B) The cell subpopulation cycle changes. (C) The number of cell communication in each subpopulation of the control group; (D) The number of cell communication in each subpopulation of the case group.