Supplementary Materials

Figure Legend

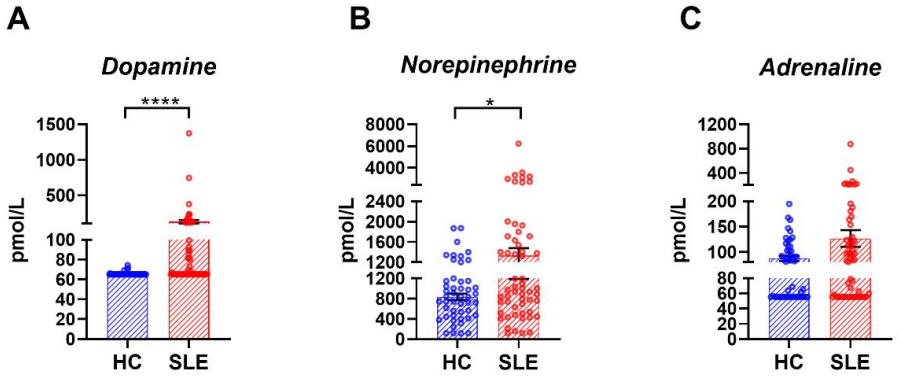

Fig. S1. Abnormally enhanced expression of catecholamine in the serum of SLE patients.
The serum concentration of (A) dopamine, (B) norepinephrine, (C) adrenaline in HCs (n=54) and SLE patients (n=57). (* p<0.05, **** p<0.01)

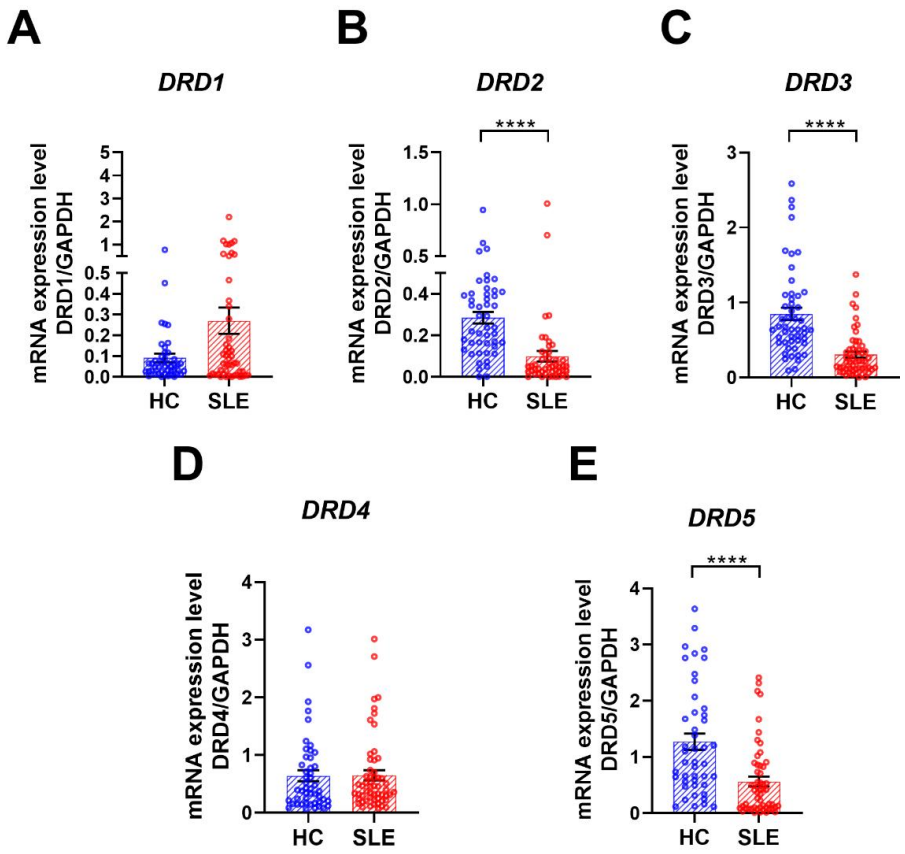

Fig. S2. Aberrant mRNA expression levels of DRDs in PBMCs of SLE patients.

The relative mRNA expression of (A) *DRD1*, (B) *DRD2*, (C) *DRD3*, (D) *DRD4*, (E) *DRD5* in PBMCs from HCs (n=50) and SLE patients (n=58). (**** $p < 0.0001$)

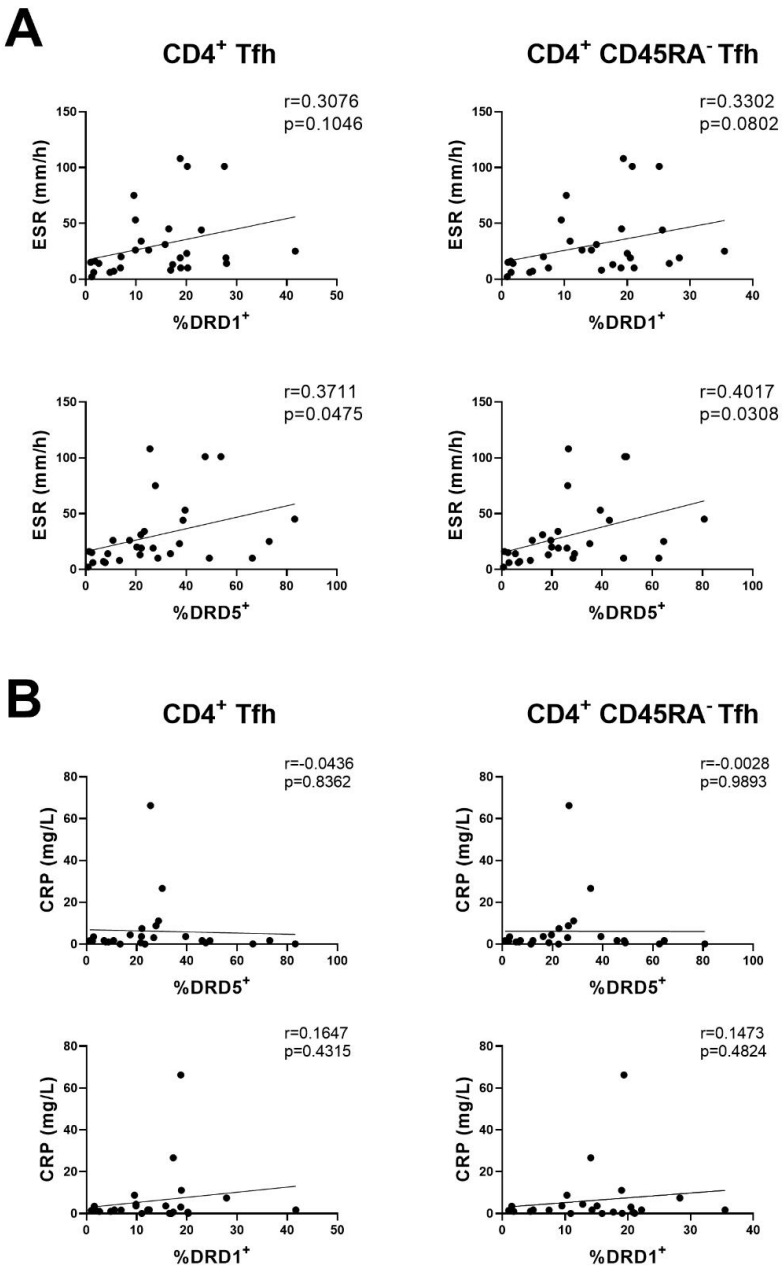

Fig. S3. Correlation analysis of D1-like receptors in CD4$^+$ Tfh and CD4$^+$ CD45RA$^-$ Tfh cells with the inflammatory indicators of SLE patients.
The correlation analysis of D1-like receptors in Tfh cells with (A) ESR (n=29), (B) CRP (n=25).

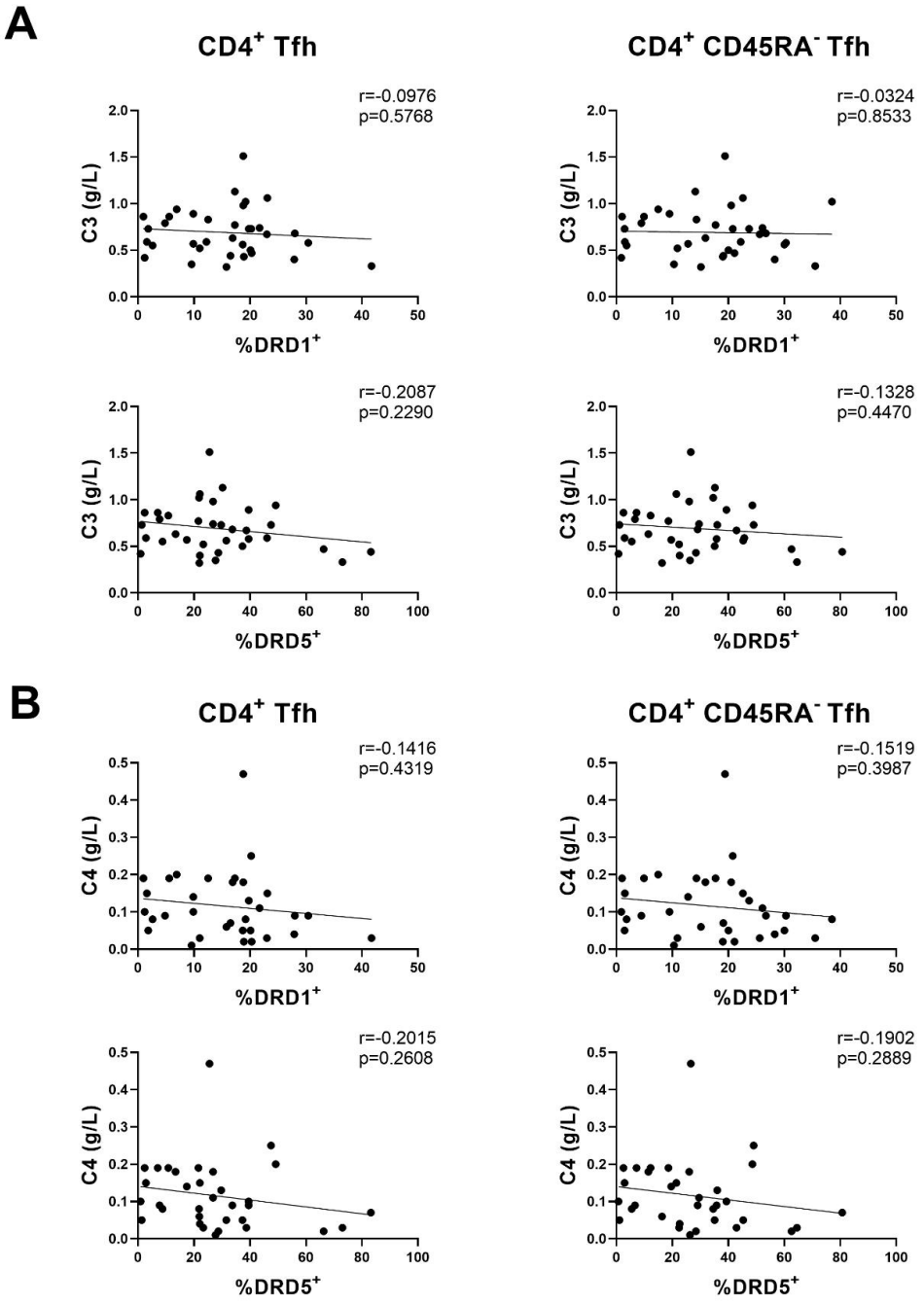

Fig. S4. Correlation analysis of D1-like receptors in CD4$^+$ Tfh and CD4$^+$ CD45RA$^-$ Tfh cells with the immune indexes of SLE patients.

The correlation analysis of D1-like receptors in CD4$^+$ Tfh cells with (A) C3 (n=35), (B) C4 (n=33).

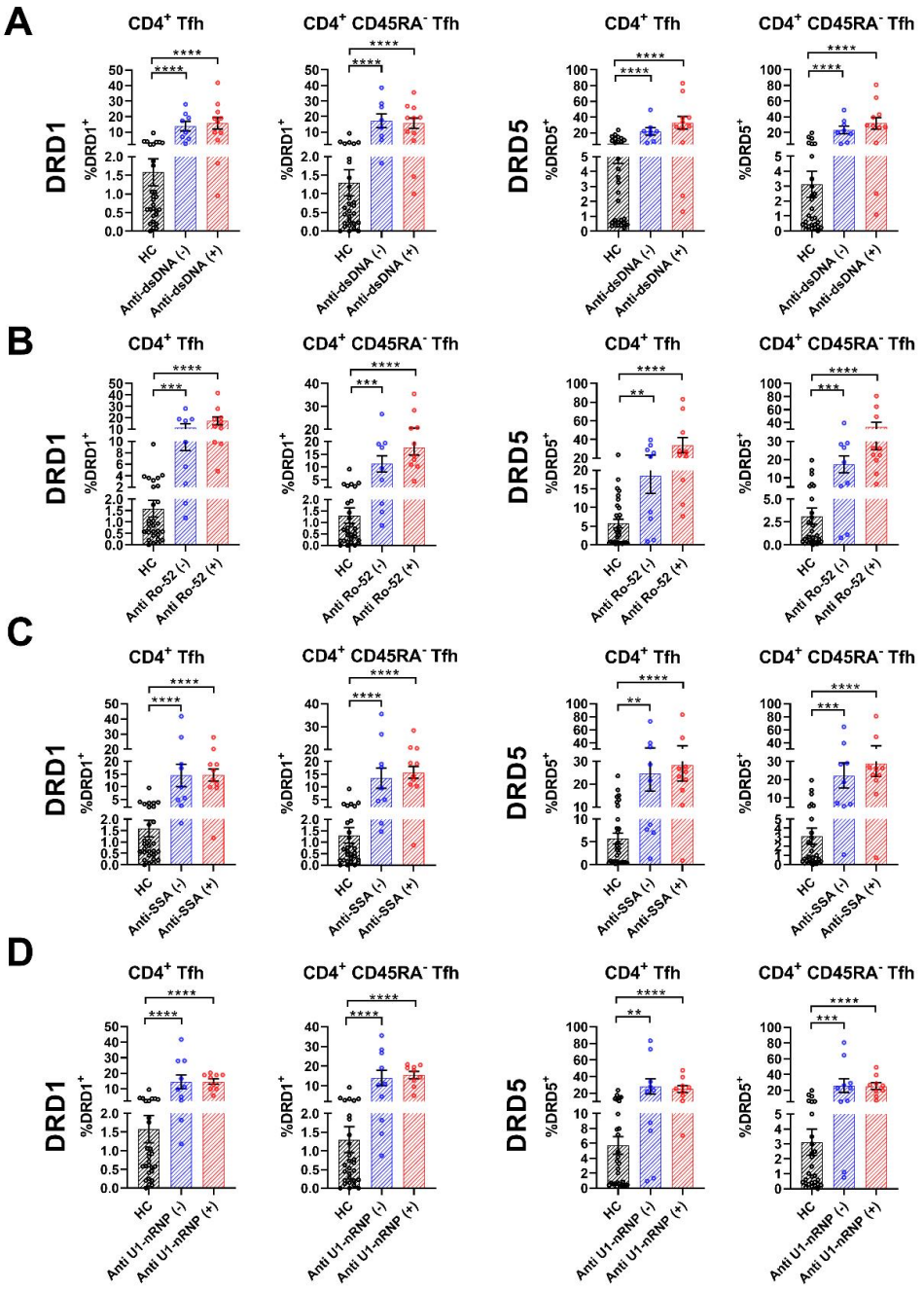

Fig. S5. The expression of D1-like receptors in Tfh cells from SLE patients in different autoantibody groups.

The statistical analysis of the expression of (A) $CD4^+$ Tfh DRD1, (B) $CD4^+$ $CD45RA^-$ Tfh DRD1, (C) $CD4^+$ Tfh DRD5, (D) $CD4^+$ $CD45RA^-$ Tfh DRD5, in different autoantibody groups (** p<0.01, *** p<0.005, **** p<0.0001).

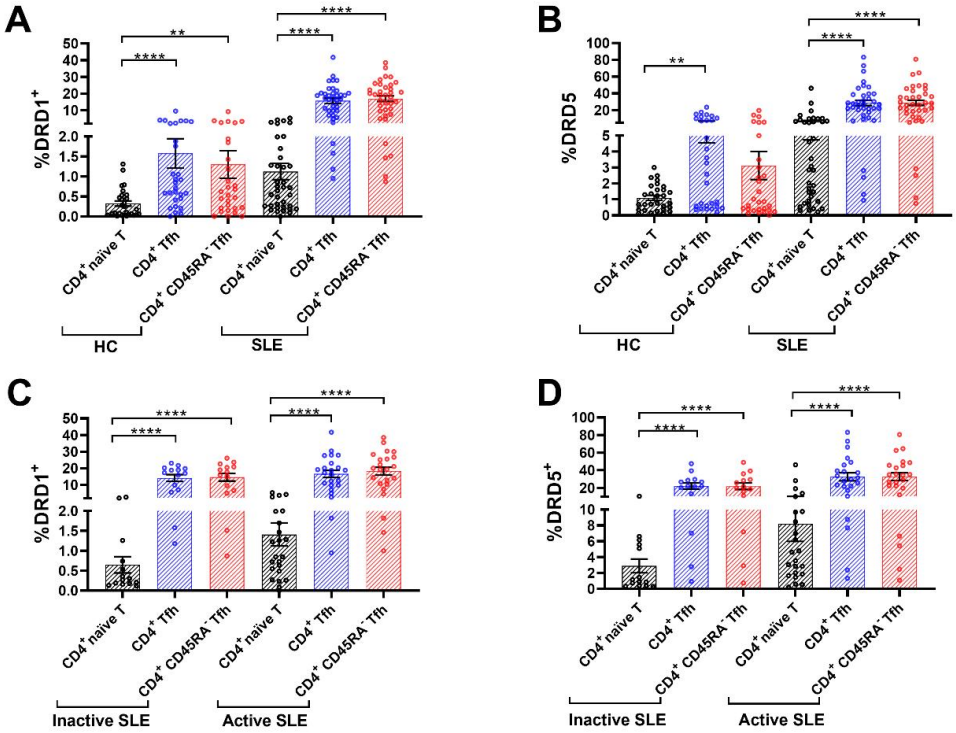

Fig. S6. Upregulated expression level of D1-like receptors in differentiated Tfh than that in naïve CD4$^+$ T cells.

Comparison of DRD1 (A) and DRD5 (B) expression during the differentiation of naïve cells in SLE patients (n=37) and HCs (n=29).

Comparison of DRD1 (C) and DRD5 (D) expression during the differentiation of naïve cells in Active SLE patients (n=23) and Inactive SLE patients (n=14). (** p<0.01, **** p<0.0001)

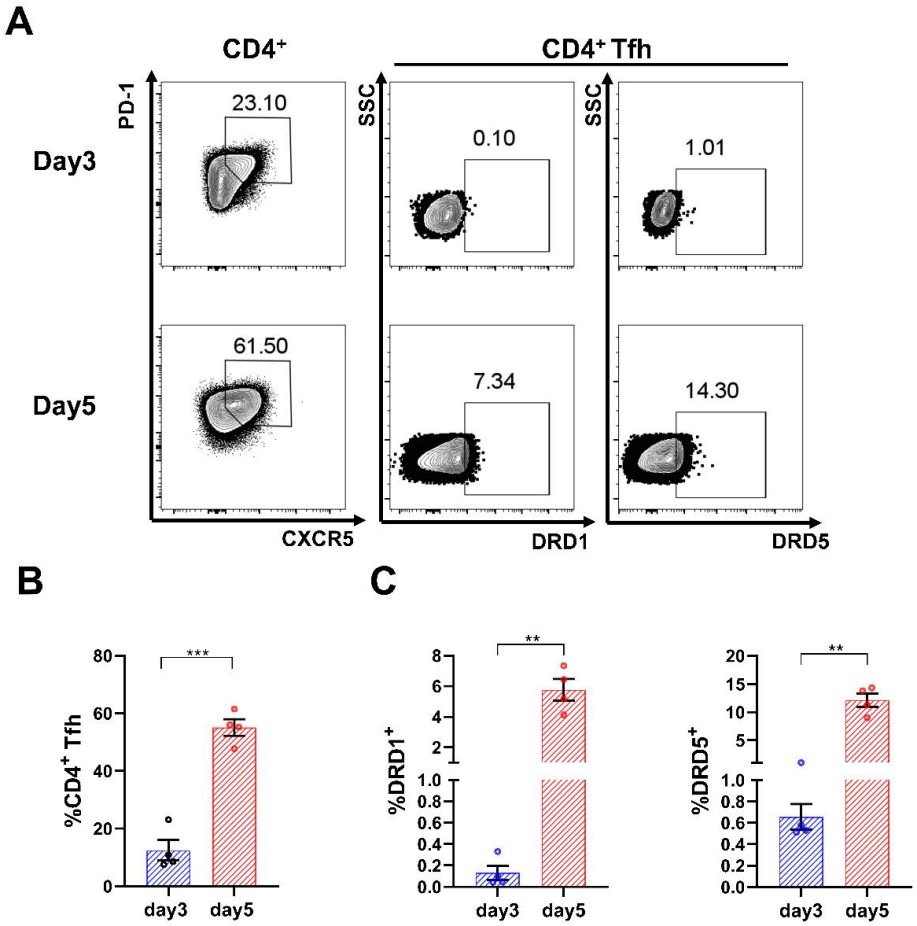

Fig. S7. Changes in the frequency of Tfh cells and the expression of D1-like receptors during the differentiation of naïve CD4$^+$ T cells toward Tfh cells.

(A) Representative flow cytometry diagrams of Tfh cells and the expression of D1-like receptors. (B) The frequency of CD4$^+$ Tfh cells in day3 (n=4) and day5 (n=4) after inducing naïve CD4$^+$ T cells differentiate toward Tfh cells. The PBMCs were first isolated from peripheral blood of volunteers. Subsequently, CD4$^+$ naïve T cells were sorted by immunomagnetic beads and cultured for day3 and day5. (C) The expression of D1-like receptors in CD4$^+$ Tfh cells in day3 and day5 after inducing naïve CD4$^+$ T cells differentiate toward Tfh cells. (** p<0.01, *** p<0.005)

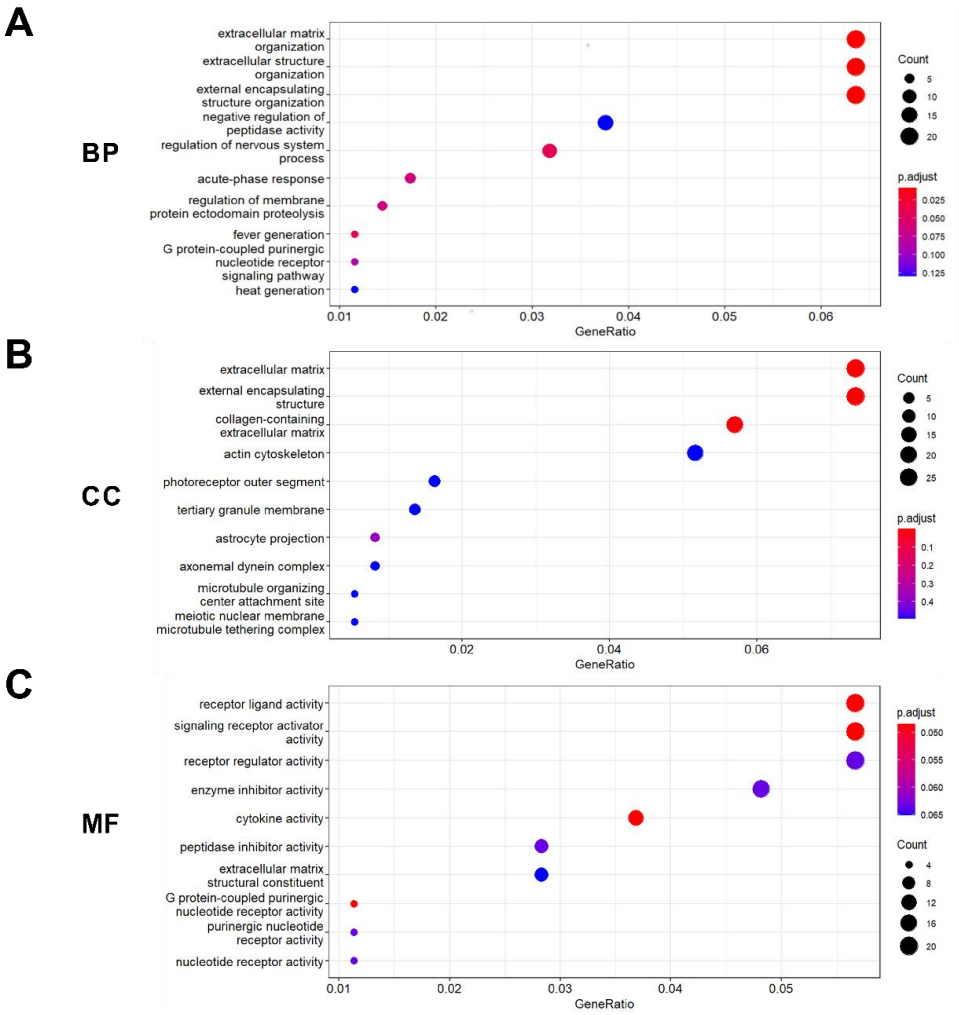

Fig. S8. Go analysis of differentially expressed genes between SKF38393 group and DMSO group.

(A) Analysis of biological processes (BP) of differential genes. (B) Analysis of cell components (CC) of differentially expressed genes. (C) Analysis of molecular functions (MF) of differentially expressed genes.

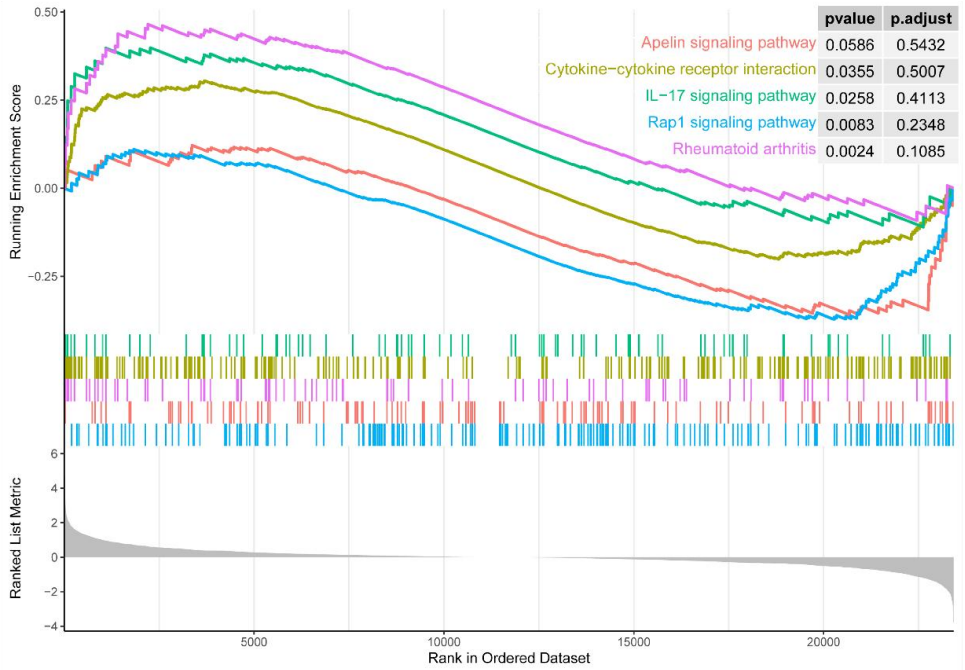

Fig. S9. GSEA analysis of differentially expressed genes between SKF38393 group and DMSO group.

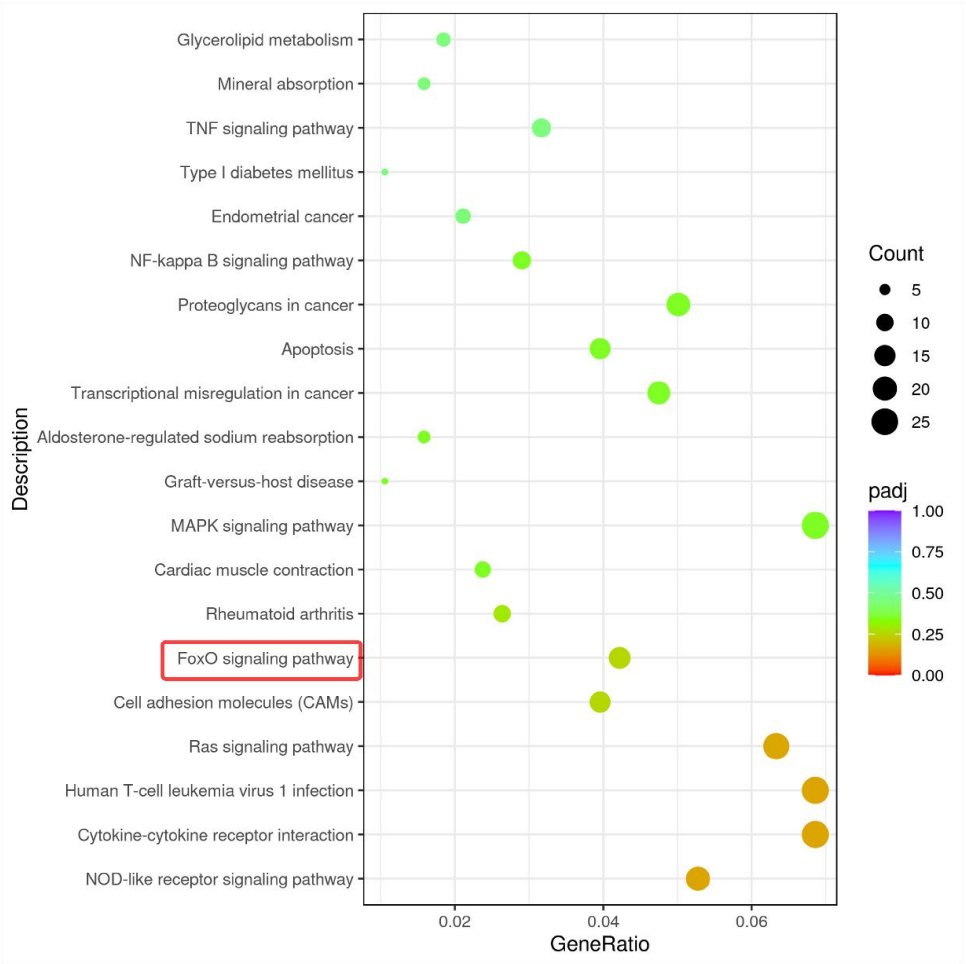

Fig. S10. The KEGG reanalysis of differentially expressed genes between SKF38393 group and DMSO group.

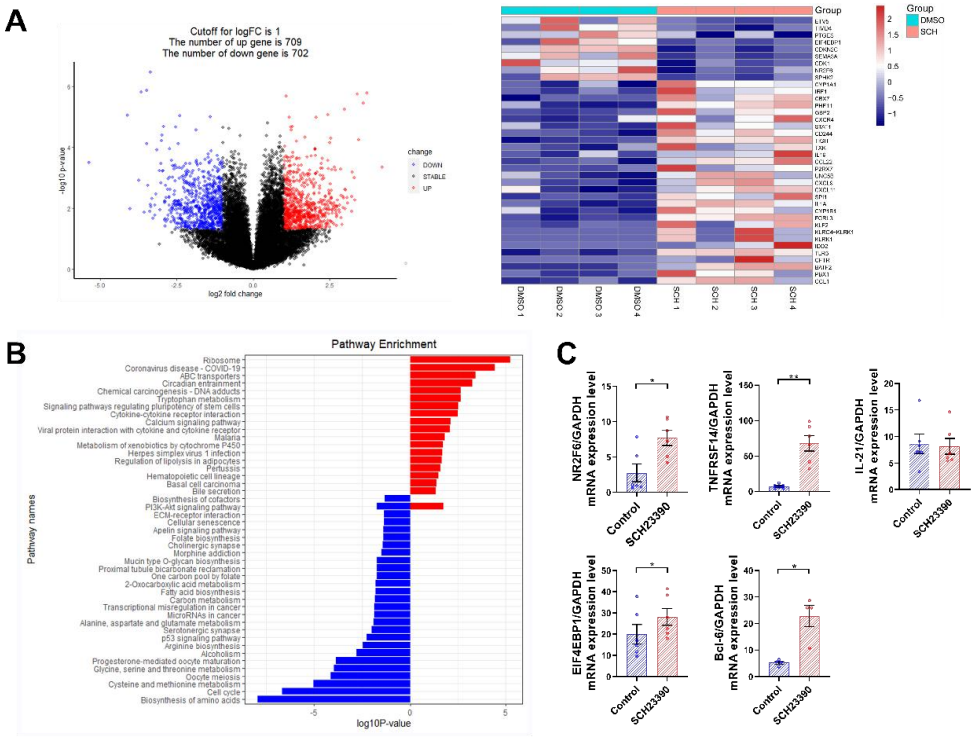

Fig. S11. Biological information analysis and genetic authentication of SCH23390 group and DMSO group.

(A) Volcano plot and heat map of datasets of $CD4^+$ T cells in DMSO and SCH23390 groups from RNA-seq. Blue plots represent expressions of genes with $p < 0.05$ and $\log_2FC < -1$. Red plots represent expressions of genes mRNA with $P < 0.05$ and $log2FC > 1$. Grey plots represent genes expressed in mRNA normally. (B) KEGG pathway analysis of the DEGs. Red represents pathways with increased DEGs in the SCH23390 group, and blue represents pathways with decreased DEGs in the SCH23390 group. (C) The mRNA expression levels of DEGs associated with the Tfh cells. (* $p<0.05$, ** $p<0.01$)

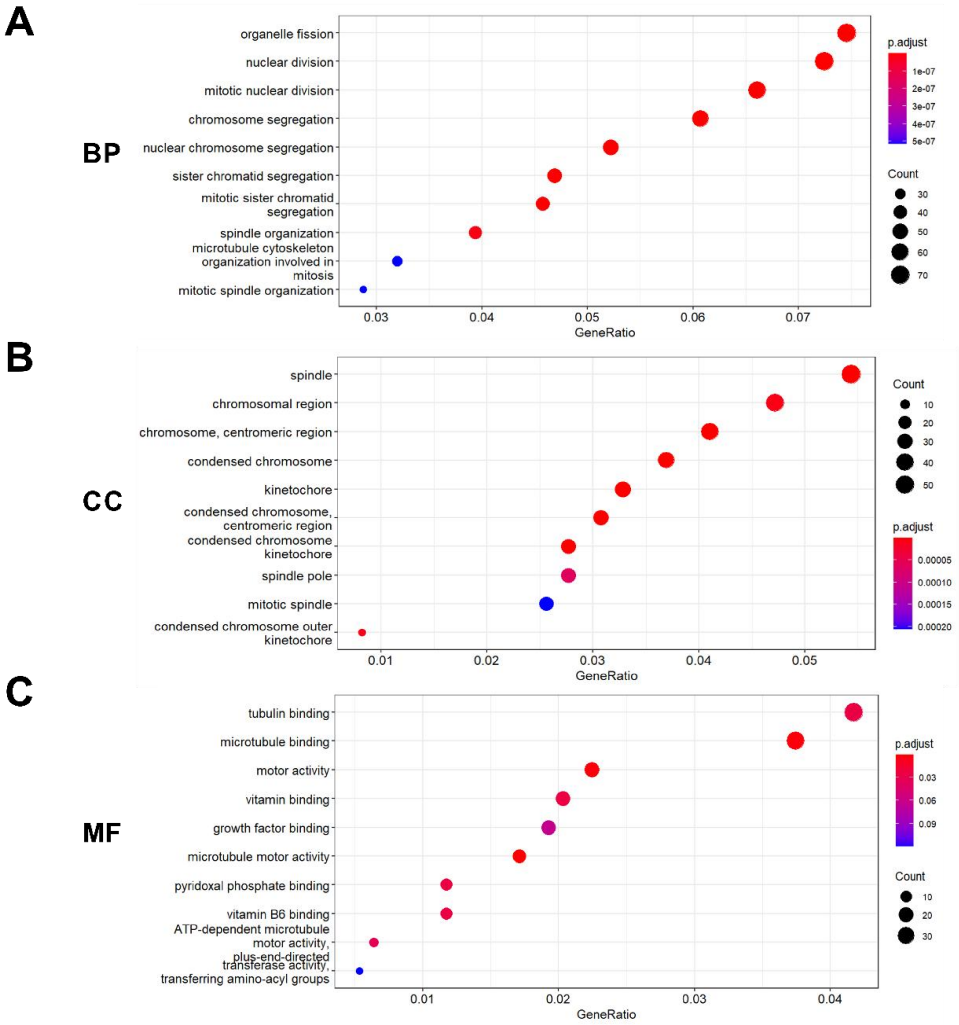

Fig. S12. Go analysis of differentially expressed genes between SCH23390 group and DMSO group.

(A) Analysis of biological processes (BP) of differential genes. (B) Analysis of cell components (CC) of differentially expressed genes. (C) Analysis of molecular functions (MF) of differentially expressed genes.

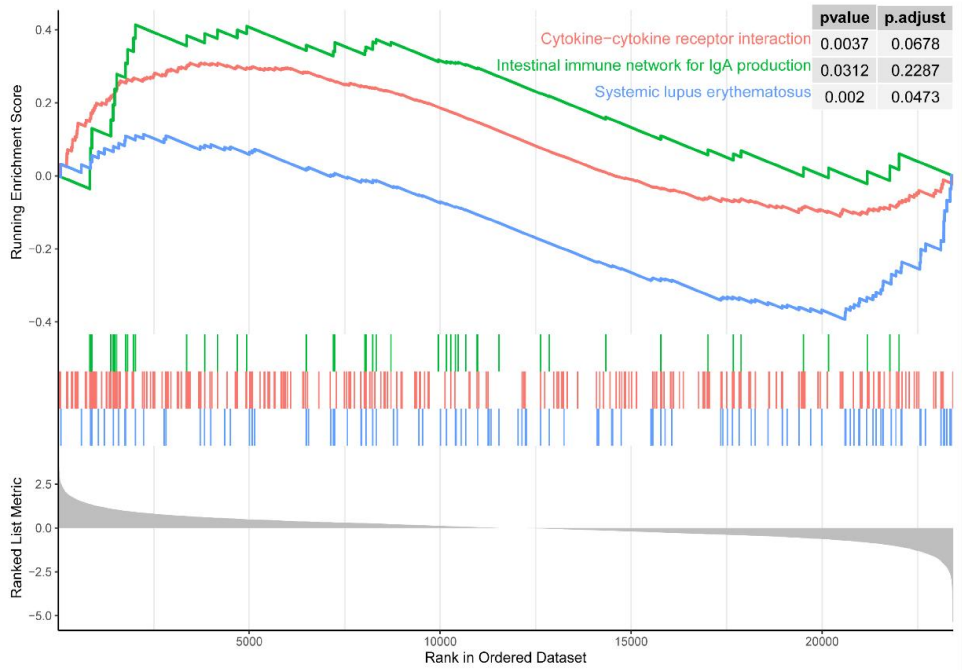

Fig. S13. GSEA analysis of differentially expressed genes between SCH23390 group and DMSO group.

Table S1. The clinical information of SLE patients for qRT-PCR

	SLE patients (n=58)	HCs (n=50)
Demographics		
Age (year), Mean ± SD	33.83 ± 12.67	31.04 ± 5.38
Sex (female), n (%)	54 (93.10)	42 (84)
Inflammatory index		
ESR (mm/h)	26.04 ± 26.44	/
CRP (mg/L)	4.16 ± 5.58	/
Immunological index		
C3 (g/L)	0.85 ± 0.31	/
C4 (g/L)	0.18 ± 0.23	/
Autoantibody (positive)		
Anti-dsDNA, n (%)	12 (52.17)	/
Anti-Sm, n (%)	6 (26.09)	/
Anti-U1-nRNP, n (%)	11 (47.83)	/
Anti-SSA, n (%)	12(52.17)	/
Anti-SSB, n (%)	4 (17.39)	/
Anti-Ro-52, n (%)	11(47.83)	/
Anti-nucleosome, n (%)	3 (13.04)	/

Abbreviation: ESR: erythrocyte sedimentation rate; CRP:C-reactive protein; C3:Complement 3; C4: Complement 4; “/”: Indicates that this item has not been detected.

Table S2. The clinical information of SLE patients for flow cytometry

Characteristic	SLE (n=37)		HCs (n=29)
	Inactive SLE (SLEDAI≤4) (n=14)	Active SLE (SLEDAI>4) (n=23)	
Demographics			
Age (year), Mean ± SD	36.32 ± 11.32	35.54 (13.76)	30.68 (4.36)
Sex (female), n (%)	14 (85.71)	26 (84.62)	25 (86.21)
Inflammatory index			
ESR (mm/h)	24.55 (29.20)	32.71 (28.49)	/
CRP (mg/L)	3.11 (3.31)	7.44 (16.43)	/
Immunological index			
C3 (g/L)	0.70 (0.22)	0.70 (0.29)	
C4 (g/L)	0.14 (0.06)	0.11 (0.10)	
Autoantibody (positive)			
Anti-dsDNA, n (%)	2 (14.29)	10 (38.46)	/
Anti-Sm, n (%)	5 (35.71)	1 (3.85)	/
Anti-U1-nRNP, n (%)	6 (42.86)	3 (11.54)	/
Anti-SSA, n (%)	3 (21.43)	7 (26.92)	/
Anti-SSB, n (%)	0 (0)	2 (7.69)	/
Anti-Ro-52, n (%)	2 (14.29)	8 (30.77)	/
Anti-nucleosome, n (%)	2 (14.29)	4 (15.38)	/

Abbreviation: ESR: erythrocyte sedimentation rate; CRP:C-reactive protein; C3:Complement 3; C4: Complement 4; “/”: Indicates that this item has not been detected.

Table.3 Primer sequences

Gene (Human)	Primer sequences (5'→3')
DRD1	F: GACCTTGTCTGTACTCATCTCCT
	R: GTCACAGTTGTCTATGGTCTCAG
DRD2	F: CCCCGCCAAACCAGAGAAG
	R: TTTTGCCATTGGGCATGGTCT
DRD3	F: AGAAGGCAACCCAAATGGTGG
	R: TGTCGTGGCACTGTAAAGCTC
DRD4	F: CTGCCGCTCTTCGTCTACTC
	R: ATGGCGCACAGGTTGAAGAT
DRD5	F: CGACGTGAATGCAGAGAACTG
	R: TAGAAGCTGATGAGCGAGGAA
PI3K	F: GAAGCCATTGAGAAGAAAGGAC
	R: GAGGTGTTCAGTATTATCAGAGC
AKT	F: GTCATCGAACGCACCTTCCAT
	R: AGCTTCAGGTACTCAAACTCGT
FOXO1	F: TCGTCATAATCTGTCCCTACACA
	R: CGGCTTCGGCTCTTAGCAAA
KLF2	F: GCACGCACACAGGTGAGA
	R: CACAGATGGCACTGGAATGG
CXCR5	F: GCACCTCCCATCCTAATCATC
	R: CTAAGCTGATGGAGTGTGTTCT
PD-1	F: CCCTGGTGGTTGGTGTCGT
	R: GCCTGGCTCCTATTGTCCCTC
NR2F6	F: GAGCGGCAAGCATTACGGT
	R: GGCAGGTGTAGCTGAGGTT
EIF4EBP1	F: CTATGACCGGAAATTCCTGATGG
	R: CCCGCTTATCTTCTGGGCTA
TNFRSF14(*HVEM*)	F: GTGCAGTCCAGGTTATCGTGT
	R: CACTTGCTTAGGCCATTGAGG
IL-21	F: TAGAGACAAACTGTGAGTGGTCA
	R: GGGCATGTTAGTCTGTGTTTCTG
BCL-6	F: CCCAAGGAAACAATCCCAGAAGAG
	R: CTCATCTTCCGAGGAGGGTCTC
IL-1β	F: AGCTACGAATCTCCGACCAC
	R: CGTTATCCCATGTGTCGAAGAA
IL-12α	F: CCTTGCACTTCTGAAGAGATTGA
	R: ACAGGGCCATCATAAAAGAGGT
GAPDH	F: ACAACTTTGGTATCGTGGAAGG
	R: GCCATCACGCCACAGTTTC

Abbreviation: F, Forward; R, Reverse.