

Supplementary Materials

Table S1: General data of study population for lncRNA microarray analysis

	CTD-ILD group (mixed specimens, n = 4)	CTD-NILD group (mixed specimens, n = 3)
Age (years)	38.56 ± 13.29	38.58 ± 13.84
M/F (case)	3/13	2/10
SSc, M/F (case)	1/3	1/2
RA, M/F (case)	1/3	1/2
SLE, M/F (case)	0/4	0/3
SS, M/F (case)	1/3	0/3

Values were expressed as numbers or the mean ± standard deviation. CTD-ILD, connective tissue disease-associated interstitial lung diseases; CTD-NILD, connective tissue disease-without interstitial lung diseases; SSc, systemic sclerosis; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus; SS, Sjogren's syndrome; M, male; F, female.

Table S2: Clinical and laboratory data of of SSc and RA

	(SSc+RA)- ILD (n = 60)	(SSc+RA)- NILD (n = 60)	SSc- (ILD+NILD) (n = 60)	RA- (ILD+NILD) (n = 60)	SSc-ILD (n = 30)	SSc-NILD (n = 30)	RA-ILD (n = 30)	RA-NILD (n = 30)
Age, mean ± SD years	55.18(10.21)	54.00(9.95)	53.98(9.32)	55.20(10.79)	54.57(9.04)	53.4(9.72)	55.8(11.39)	54.6(10.31)
Male/female	15/45	14/46	15/45	14/46	8/22	7/23	7/23	7/23
Disease duration median (IQR) years	6.10(1.90- 10.83) ^a	2.25(1.23- 6.95)	3.00(1.30- 6.15) ^b	6.65(1.58- 12.68)	4.50(1.00- 7.25)	2.10(1.30- 4.48)	7.90(3.30- 13.38)	2.50(1.18- 11.45)
ESR, mean ± SD (mm/h)	48.80(36.62)	39.27(35.24)	33.92(32.22) ^b	54.15(37.18)	39.73(37.81)	28.1(24.76)	57.87(33.6)	50.43(40.68)
CRP, mean ± SD (mg/L)	19.96(30.28)	14.48(29.22)	8.61(11.87) ^b	25.83(38.66)	11.89(14.07) ^c	5.34(8.14)	28.03(39.15)	23.62(38.7)
WBC, mean ± SD (× 10 ⁹ /L)	7.58(3.53)	7.23(2.86)	7.38(2.67)	7.44(3.68)	7.4(2.88)	7.36(2.50)	7.76(4.12)	7.11(3.22)
GR, mean ± SD (× 10 ⁹ /L)	5.26(2.89)	4.98(2.55)	5.02(2.06)	5.22(3.27)	5.07(2.30)	4.97(1.82)	5.46(3.42)	4.98(3.15)
LY, mean ± SD (× 10 ⁹ /L)	1.61(0.88)	1.66(0.76)	1.66(0.83)	1.60(0.80)	1.62(0.85)	1.71(0.83)	1.6(0.92)	1.6(0.69)
MO, mean ± SD (× 10 ⁹ /L)	0.55(0.26) ^a	0.45(0.18)	0.55(0.21) ^b	0.45(0.23)	0.58(0.21)	0.51(0.20)	0.52(0.3) ^d	0.39(0.13)
ALB, mean ± SD (g/L)	40.77(5.11) ^a	42.7(3.70)	41.1(4.18)	42.37(4.84)	40.37(4.49)	41.82(3.79)	41.16(5.72)	43.57(3.45)
GLOB, mean ± SD (g/L)	31.07(6.47)	32.48(5.86)	33.19(6.91) ^b	30.36(5.04)	32.85(7.47)	33.53(6.4)	29.28(4.77)	31.43(5.15)
Anticentromere antibody	-	-	19(31.67%)	-	10(33.33%)	9(30.00%)	-	-
Anti-topoisomerase I	-	-	8(13.33%)	-	4(13.33%)	4(13.33%)	-	-
Anti-Scl-70	-	-	21(35.00%)	-	11(36.67%)	10(33.33%)	-	-
RF-IgM, median (IQR) (IU/mL)	-	-	-	132.50(33.08- 337.25)	-	-	123.5(32.80- 285.50)	143.00(33.45- 443.00)
RF-IgG, median (IQR) (U/mL)	-	-	-	5.09(3.36-8.20)	-	-	5.02(3.16- 6.13)	5.41(3.85- 11.66)
RF-IgA, median (IQR) (U/mL)	-	-	-	45.95(22.33- 132.77)	-	-	51.73(30.16- 127.28)	42.60(10.07- 160.13)
CCP, median (IQR) (RU/mL)	-	-	-	313.19(34.19- 653.55)	-	-	260.79(49.54- 659.00)	105.02(25.50- 482.43)

SSc, systemic sclerosis; RA, rheumatoid arthritis; ILD, interstitial lung disease; NILD, without interstitial lung disease; ESR, erythrocyte sedimentation rate; CRP, reactive protein; WBC, white blood cell counts; GR, neutrophil granulocyte counts; LY, lymphocyte counts; MO, monocyte counts; ALB, albumin; GLOB, globulin; RF, rheumatoid factor; CCP, anti-cyclic citrullinated peptide antibody. Data are presented as the mean with standard deviation (SD), median with interquartile range (IQR), and numbers with percentages. Differences were tested by independent-sample T-test, Mann-Whitney U-test, and Chi-square test. P < 0.05 was considered to denote statistical significance. ^a: in comparison with (SSc+RA)-NILD group, ^b: in comparison with RA-(ILD+NILD) group, ^c: in comparison with SSc-NILD group, ^d: in comparison with RA-NILD group.

Table S3: Primer sequences used in the validation of genes

Gene name	Forward primers sequence(5'-3')	Reverse primers sequence(5'-3')
β -actin	GAGCTACGAGCTGCCTGACG	GTAGTTTCGTGGATGCCACAG
ENST00000602277	CCTCCTATCAATCTCAGACTGCTGT	CCCCCTCTGAATGAAGACGTCT
ENST00000604692	TCATGCCATCACGGGAAACAT	ACCAACCAAAACCTAAGGAAAACAC
T311354	CCCTGCTCCAACCTGCCTTG	ATGCAGTCACTGTTCCCTCTTG
ENST00000453636	CTCGCCGAAGTGCTTGTGAAG	TTGCCTCTCTGGTTTGTGTGACTG
NR_038446	ATTCTACCATGCTACCAACAGACAAG	GTGACTGGCAATACAGGGACCTAAAG
ARG1(arginase-1)	GGACCTGCCCTTTGCTGACATC	AGGCTGATTCTCCGTTCTTCTTGAC

Table S4: Details of ten pairs of lincRNA-mRNA

lincRNA	mRNA	Chrom
ENST00000492960	ANKRD36	chr2
ENST00000493529	SERPINI1	chr3
ENST00000606452	TIGD5	chr8
NR_024627	SLC22A18AS	chr11
NR_037867	ACSL1	chr4
T140209	ZNF232	chr17
T200956	TNFAIP6	chr2
T260556	S100P	chr4
T311354	ARG1	chr6
TCONS_I2_00009699	RP11-812E19.9	chr16

Chrom, chromosome number from which the lincRNA or mRNA was transcribed.

Table S5: Details of two pairs of antisense lncRNA-mRNA (distance < 300 kb)

Antisense lncRNA	mRNA	Chrom
ENST00000464659	GK	chrX
NR_109857	WDR86	chr7

Chrom, chromosome number from which the lincRNA or mRNA was transcribed.

Table S6: Details of five lncRNAs and one mRNA

Transcript_type	Gene name	P-value	Fold change	Regulation	Chrom
long noncoding	ENST00000602277	0.008641533	4.7558537	up	chrX
long noncoding	ENST00000604692	0.033988100	2.6110634	up	chr2
long noncoding	T311354	0.01215425	2.4733744	up	chr6
long noncoding	ENST00000453636	0.002489511	3.7806322	down	chr2
long noncoding	NR_038446	0.046031098	2.6222282	down	chr8
protein_coding	ARG1(arginase-1)	0.019525748	6.9776168	up	chr6

P-value, P-value calculated from unpaired t-test; Fold change, the absolute ratio (no log scale) of normalized intensities between two groups (CTD-ILD vs CTD-NILD); Chrom, chromosome number from which the lncRNA or mRNA was transcribed.

Table S7: Gene Ontology (GO) analysis enriches the top 10 items in the molecular function, cell composition, and biological process of upregulated mRNAs

GO.ID	Term	Gene.Ontology	Count	P value	Enrichment. Score(-log10(P value))	Genes
GO:0030593	neutrophil chemotaxis	Biological process	13	6.07217×10^{-14}	13.21665624	CXCL8//THBS4//CXCL1//CXCL2//CXCL3//IL1B//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24
GO:0070098	chemokine-mediated signaling pathway	Biological process	12	2.26516×10^{-13}	12.64490043	CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//CCRL2
GO:1990266	neutrophil migration	Biological process	13	5.65549×10^{-13}	12.24752981	CXCL1//CXCL2//CXCL3//IL1B//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4
GO:1990868	response to chemokine	Biological process	12	7.50896×10^{-13}	12.12442021	CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//CCRL2
GO:1990869	cellular response to chemokine	Biological process	12	7.50896×10^{-13}	12.12442021	CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//CCRL2
GO:0071621	granulocyte chemotaxis	Biological process	13	9.54757×10^{-13}	12.02010724	CXCL1//CXCL2//CXCL3//IL1B//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4
GO:0097530	granulocyte migration	Biological process	13	8.17045×10^{-12}	11.08775416	CXCL1//CXCL2//CXCL3//IL1B//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4
GO:0030595	leukocyte chemotaxis	Biological process	15	1.29557×10^{-11}	10.88753902	GPR183//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//DEFA1//CXCL1//CXCL2//CXCL3//IL1B//CXCL8//THBS4
GO:0006950	response to stress	Biological process	58	3.23412×10^{-11}	10.49024433	CDC45//IL1A//IL1B//NAMPT1//DEFA1//LTF//HAVCR2//UCHL1//GADD45A//CDK1//CCNH//WDR33//CRISP3//INHBA//CD83//GBP5//CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//NFE2L2//PTGS2//CCL3//CCL3L1//CCL18//CCL20//CCL24//NFKBIZ//TNFAIP6//NFKBID//CCRL2//FOSL1//E2F7//RGCC//E2F8//THBS4//PLAUR//BCL2A1//MELK//METRNL//ATP2B1//ARG1//RNF103//ATF3//FANCI//BIRC3//SERPINB2//ANXA3//AP1G1//CD55//CCNA2//SLC12A6//NUP98//SKIL//PPP1R10//IER3
GO:0060326	cell chemotaxis	Biological process	16	7.96729×10^{-11}	10.09868951	GPR183//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//DEFA1//CXCL1//CXCL2//CXCL3//IL1B//CXCL8//THBS4//CCRL2
GO:0042581	specific granule	Cellular component	8	5.05935×10^{-6}	5.295904849	PLAUR//SLC2A3//CRISP3//CXCL1//ARG1//LTF//TCN1//ANXA3
GO:1904724	tertiary granule lumen	Cellular component	5	1.84733×10^{-5}	4.733455402	CRISP3//CXCL1//LTF//TCN1//TNFAIP6
GO:0035580	specific granule lumen	Cellular component	5	3.32468×10^{-5}	4.478249933	CRISP3//CXCL1//ARG1//LTF//TCN1
GO:0030141	secretory granule	Cellular component	16	4.54057×10^{-5}	4.342889919	SKIL//ABCA13//CD55//SLC2A3//GPII//S100P//DEFA1//ARG1//PLAUR//CRISP3//CXCL1//LTF//TCN1//ANXA3//TNFAIP6//IL1B
GO:0070820	tertiary granule	Cellular component	7	5.55607×10^{-5}	4.255232081	SLC2A3//CD55//CRISP3//CXCL1//LTF//TCN1//TNFAIP6
GO:0099503	secretory vesicle	Cellular component	16	0.000333796	3.476519221	SKIL//IL1B//LTF//ABCA13//CD55//SLC2A3//GPII//S100P//DEFA1//ARG1//PLAUR//CRISP3//CXCL1//TCN1//ANXA3//TNFAIP6
GO:0034774	secretory granule lumen	Cellular component	8	0.000674105	3.171272193	DEFA1//ARG1//CRISP3//CXCL1//LTF//TCN1//GPII//S100P
GO:0060205	cytoplasmic vesicle lumen	Cellular component	8	0.000730487	3.136387666	GPII//S100P//DEFA1//ARG1//CRISP3//CXCL1//LTF//TCN1
GO:0031983	vesicle lumen	Cellular component	8	0.00076007	3.119146212	GPII//S100P//DEFA1//ARG1//CRISP3//CXCL1//LTF//TCN1

GO:0005615	extracellular space	Cellular component	35	0.001528587	2.815709936	<i>INHBA//NAMPT//CD55//DEFA1//GK//GPI//METRNL//ATAD2//ANXA3//LTF//ATP2B1//ERMN//S100P//SLC2A3//THBS4//CDK1//CRISP3//SCGB3A2//CXCL1//CXCL2//CXCL3//IL1A//IL1B//CXCL8//ARG1//CCL4L1//CCL3L3//SERPINB2//CCL3//CCL3L1//CCL18//CCL20//CCL24//TCN1//TNFAIP6</i>
GO:0008009	chemokine activity	Molecular function	11	9.43998×10^{-15}	14.0250288	<i>CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24</i>
GO:0042379	chemokine receptor binding	Molecular function	12	1.77742×10^{-14}	13.75020881	<i>CXCL8//CXCL1//CXCL2//CXCL3//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//CCRL2</i>
GO:0005125	cytokine activity	Molecular function	16	1.74962×10^{-12}	11.75705636	<i>CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//NAMPT//GPI//IL1A//IL1B//INHBA</i>
GO:0048020	CCR chemokine receptor binding	Molecular function	8	5.10992×10^{-10}	9.2915855	<i>CCL3//CCL24//CCL20//CCL4L1//CCL3L3//CCL3L1//CCL18//CCRL2</i>
GO:0048018	receptor ligand activity	Molecular function	18	1.59097×10^{-9}	8.798337049	<i>NAMPT//GPI//IL1A//IL1B//INHBA//METRNL//CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4</i>
GO:0005126	cytokine receptor binding	Molecular function	14	1.77089×10^{-9}	8.75180935	<i>IL1A//IL1B//CXCL8//CXCL1//CXCL2//CXCL3//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//CCRL2</i>
GO:0030546	signaling receptor activator activity	Molecular function	18	1.86949×10^{-9}	8.728277929	<i>NAMPT//GPI//IL1A//IL1B//INHBA//METRNL//CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4</i>
GO:0030545	receptor regulator activity	Molecular function	18	6.74076×10^{-9}	8.171291332	<i>NAMPT//GPI//IL1A//IL1B//INHBA//METRNL//CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4</i>
GO:0001664	G protein-coupled receptor binding	Molecular function	13	4.25292×10^{-8}	7.371312408	<i>CXCL8//CXCL1//CXCL2//CXCL3//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//UCHL1//CCRL2</i>
GO:0098772	molecular function regulator	Molecular function	46	2.27062×10^{-6}	5.643855999	<i>E2F7//ATF3//NFE2L2//SKIL//TBX15//E2F8//FOSL1//KLF7//ZNF267//ZNF644//MYSM1//NUP98//GMNN//PHACTR1//PPP1R10//SERPINB2//LTF//FGD6//RASGEF1B//DEPDC1B//NAMPT//GPI//IL1A//IL1B//INHBA//METRNL//CXCL1//CXCL2//CXCL3//CXCL8//CCL4L1//CCL3L3//CCL3//CCL3L1//CCL18//CCL20//CCL24//THBS4//ST20//CCNH//CCNA2//DENND3//ANXA3//RGCC//BIRC3//SOCS4</i>

Table S7: Gene Ontology (GO) analysis enriches the top 10 items in the molecular function, cell composition, and biological process of downregulated mRNAs

GO.ID	Term	Gene.Ontology	Count	P value	Enrichment. Score (-log ₁₀ (P value))	Genes
GO:0050854	regulation of antigen receptor-mediated signaling pathway	Biological process	3	0.001663014	2.779104055	<i>CD19//PAWR//STAP1</i>
GO:1901880	negative regulation of protein depolymerization	Biological process	3	0.001805414	2.743423243	<i>CAMSAP2//AVIL//ADD1</i>
GO:0046058	cAMP metabolic process	Biological process	2	0.002504874	2.60121414	<i>ADCY9//PDE7A</i>
GO:0043242	negative regulation of protein-containing complex disassembly	Biological process	3	0.002631008	2.579877824	<i>CAMSAP2//AVIL//ADD1</i>
GO:0046339	diacylglycerol metabolic process	Biological process	2	0.003231852	2.490548567	<i>GPAM//AVIL</i>

GO:1901879	regulation of protein depolymerization	Biological process	3	0.003327459	2.477887293	CAMSAP2//AVIL//ADD1
GO:0120032	regulation of plasma membrane bound cell projection assembly	Biological process	4	0.003459571	2.460977741	AVIL//C15ORF62//STAP1//EPS8L1
GO:0051016	barbed-end actin filament capping	Biological process	2	0.003493543	2.456733907	AVIL//ADD1
GO:0060491	regulation of cell projection assembly	Biological process	4	0.003596459	2.444124875	AVIL//C15ORF62//STAP1//EPS8L1
GO:0050855	regulation of B cell receptor signaling pathway	Biological process	2	0.004335786	2.362932206	STAP1//CD19
GO:0015629	actin cytoskeleton	Cellular component	7	0.002010957	2.696597316	SIPA1L3//ACTL7B//AVIL//PAWR//ADD1//GYS2//DDX58
GO:0031256	leading edge membrane	Cellular component	4	0.00340537	2.46783565	CNTNAP2//DDX58//EPS8L1//SGCE
GO:0005911	cell-cell junction	Cellular component	6	0.007811412	2.107270449	ADD1//TNKS1BP1//DDX58//MAGI2//CNTNAP2//SIPA1L3
GO:0070160	tight junction	Cellular component	3	0.010700046	1.970614347	DDX58//MAGI2//SIPA1L3
GO:0005887	integral component of plasma membrane	Cellular component	12	0.012156394	1.915195247	CNTNAP2//KCNG1//ADCY9//FCRL1//DCBLD2//ADORA3//OPN3//SLC10A1//TLR5//FCRLA//SGCE//CD19
GO:0031252	cell leading edge	Cellular component	5	0.016451279	1.783800323	AVIL//CNTNAP2//DDX58//EPS8L1//SGCE
GO:0031226	intrinsic component of plasma membrane	Cellular component	12	0.017172376	1.765169621	ADCY9//FCRL1//DCBLD2//ADORA3//OPN3//SLC10A1//TLR5//FCRLA//SGCE//CD19//CNTNAP2//KCNG1
GO:0000790	nuclear chromatin	Cellular component	10	0.018177597	1.74046353	PPARGC1A//TNKS1BP1//E2F5//ZNF718//SMAD9//ARGFX//PAWR//NEUROG2//ZNF232//ZNF697
GO:0032589	neuron projection membrane	Cellular component	2	0.019632547	1.707023363	CNTNAP2//SGCE
GO:0043005	neuron projection	Cellular component	10	0.021080223	1.676124805	OPN3//PDC//AVIL//ADCY9//CNTNAP2//PIAS3//MAGI2//CDK5R2//SGCE//PPARGC1A
GO:0030159	signaling receptor complex adaptor activity	Molecular function	3	0.000510617	3.291904622	STAP1//BLNK//MAGI2
GO:0005068	transmembrane receptor protein tyrosine kinase adaptor activity	Molecular function	2	0.001088674	2.96310215	STAP1//BLNK
GO:0035591	signaling adaptor activity	Molecular function	3	0.002230455	2.651606456	STAP1//BLNK//MAGI2
GO:0030507	spectrin binding	Molecular function	2	0.005084637	2.293740017	ADD1//CAMSAP2
GO:0016779	nucleotidyltransferase activity	Molecular function	3	0.014310479	1.844345816	NMNAT1//POLR1A//CTU1
GO:0005089	Rho guanyl-nucleotide exchange factor activity	Molecular function	2	0.022016884	1.657244146	EPS8L1//PLEKHG1
GO:0017048	Rho GTPase binding	Molecular function	3	0.024023052	1.619371813	EPS8L1//PLEKHG1//C15ORF62
GO:0003779	actin binding	Molecular function	5	0.025597474	1.591802885	AVIL//ADD1//PAWR//EPS8L1//CDK5R2
GO:0030971	receptor tyrosine kinase binding	Molecular function	2	0.030880058	1.510321888	STAP1//BLNK
GO:0001618	virus receptor activity	Molecular function	2	0.032473957	1.488464789	CR2//SLC10A1

Table S8: Kyoto encyclopedia of genes and genomes (KEGG) analysis enriched the top 10 items of upregulated mRNAs

PathwayID	Definition	OriginalWebSite	Fisher-P value	Selection-Counts	Enrichment_Score	Genes
hsa04061	Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04061+6362+6364+6369+6348+6349+414062+388372+9560+2919+2920+2921+3576	7.04606×10^{-12}	12	11.152053	CCL18//CCL20//CCL24//CCL3//CCL3L1//CCL3L3//CCL4L1//CCL4L2//CXCL1//CXCL2//CXCL3//CXCL8
hsa04064	NF-kappa B signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04064+597+330+388372+9560+2919+2920+2921+3576+1647+3553+5743	2.32827×10^{-10}	11	9.632967	BCL2A1//BIRC3//CCL4L1//CCL4L2//CXCL1//CXCL2//CXCL3//CXCL8//GADD45A//IL1B//PTGS2
hsa05323	Rheumatoid arthritis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05323+6364+6348+6349+414062+2919+2920+2921+3576+3552+3553	1.4042×10^{-9}	10	8.852571	CCL20//CCL3//CCL3L1//CCL3L3//CXCL1//CXCL2//CXCL3//CXCL8//IL1A//IL1B
hsa04060	Cytokine-cytokine receptor interaction - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04060+6362+6364+6369+6348+6349+414062+388372+9560+2919+2920+2921+3576+3552+3553+3624	3.01729×10^{-9}	15	8.520384	CCL18//CCL20//CCL24//CCL3//CCL3L1//CCL3L3//CCL4L1//CCL4L2//CXCL1//CXCL2//CXCL3//CXCL8//IL1A//IL1B//INHBA
hsa04062	Chemokine signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04062+6362+6364+6369+6348+6349+414062+388372+9560+2919+2920+2921+3576	1.46616×10^{-8}	12	7.83382	CCL18//CCL20//CCL24//CCL3//CCL3L1//CCL3L3//CCL4L1//CCL4L2//CXCL1//CXCL2//CXCL3//CXCL8
hsa04657	IL-17 signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04657+6364+2919+2920+2921+3576+8061+3553+5743	4.45069×10^{-7}	8	6.351573	CCL20//CXCL1//CXCL2//CXCL3//CXCL8//FOSL1//IL1B//PTGS2
hsa04621	NOD-like receptor signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04621+330+2919+2920+2921+3576+1667+115362+3553+10135	7.47666×10^{-6}	9	5.126292	BIRC3//CXCL1//CXCL2//CXCL3//CXCL8//DEFA1//GBP5//IL1B//NAMPT
hsa05146	Amoebiasis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05146+383+2919+2920+2921+3576+3553+3914	1.04464×10^{-5}	7	4.981033	ARG1//CXCL1//CXCL2//CXCL3//CXCL8//IL1B//LAMB3
hsa04620	Toll-like receptor signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04620+6348+6349+414062+388372+9560+3576+3553	1.18764×10^{-5}	7	4.925315	CCL3//CCL3L1//CCL3L3//CCL4L1//CCL4L2//CXCL8//IL1B
hsa04668	TNF signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04668+330+6364+2919+2920+2921+3553+5743	1.93226×10^{-5}	7	4.713935	BIRC3//CCL20//CXCL1//CXCL2//CXCL3//IL1B//PTGS2

Table S8: Kyoto encyclopedia of genes and genomes (KEGG) analysis enriched the top 9 items (only 9 items in total) of downregulated mRNAs

PathwayID	Definition	OriginalWebSite	Fisher-P value	Selection-Counts	Enrichment_Score	Genes
hsa04662	B cell receptor signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04662+29760+930+1380	0.00275818	3	2.559377	BLNK//CD19//CR2

hsa05169	Epstein-Barr virus infection - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05169+29760+930+1380+23586	0.004870649	4	2.312413	<i>BLNK//CD19//CR2//DDX58</i>
hsa05340	Primary immunodeficiency - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05340+29760+930	0.007555506	2	2.121736	<i>BLNK//CD19</i>
hsa04015	Rap1 signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04015+115+9863+23094	0.03528105	3	1.452458	<i>ADCY9//MAGI2//SIPA1L3</i>
hsa04211	Longevity regulating pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04211+115+10891	0.03776135	2	1.422952	<i>ADCY9//PPARGC1A</i>
hsa04976	Bile secretion - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04976+115+6554	0.03853793	2	1.414112	<i>ADCY9//SLC10A1</i>
hsa05032	Morphine addiction - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05032+115+5150	0.03932068	2	1.405379	<i>ADCY9//PDE7A</i>
hsa04350	TGF-beta signaling pathway - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04350+1875+4093	0.04170544	2	1.379807	<i>E2F5//SMAD9</i>
hsa04640	Hematopoietic cell lineage - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04640+930+1380	0.04579888	2	1.339145	<i>CD19//CR2</i>
