

**Table S1.** Predominant constituents from HPLC analysis and the cytotoxicity (CC<sub>50</sub>) of lichen extracts

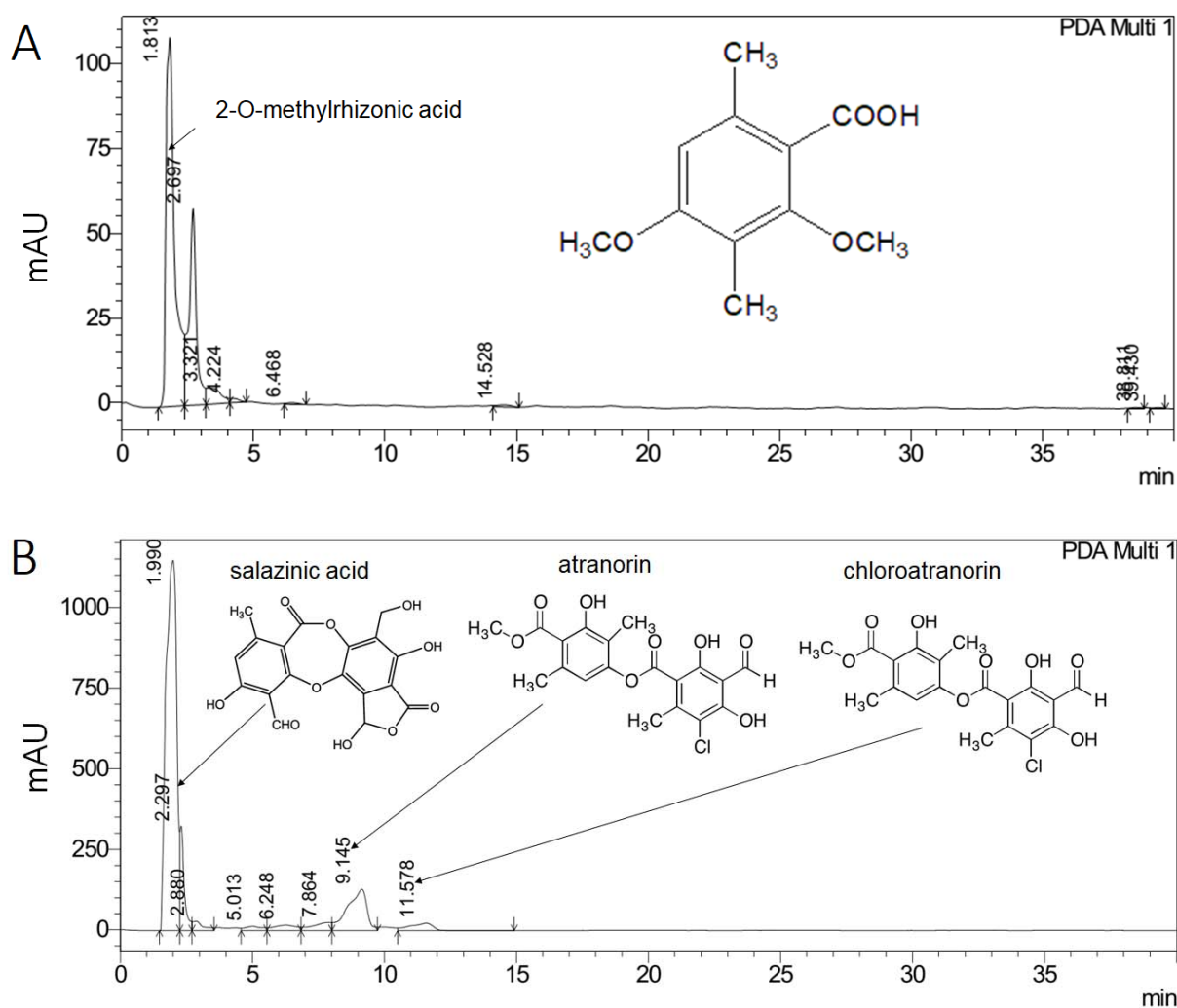
Lichen species	Sample code	Acetone extracts		Methanol extracts	
		Predominant compounds	CC <sub>50</sub> (µg/ml)	Predominant compounds	CC <sub>50</sub> (µg/ml)
<i>Cladonia macilentata</i>	LC1	Usnic; Homosekikaic; Didymic acid	>200	Anzop-1, Cldma-1, usnic acid	>200
<i>Cladonia pyxidata</i>	LC2	Merochlorophaeic; Usnic acid	>200	cryptochlorophaeic acid, merochlorophaeic acid, Cldma-1, usnic acid	>200
<i>Cladonia rangiferina</i>	LC3	Fumarprotocetraric; usnic; isousnic acid	>200	usnic acid	>200
<i>Parmotrema cristiferum</i>	LC4	Salazinic; 2-O-methylrhizonic; atranorin; chloroatranorin acid	262.4	salazinic acid, 2-O-methylrhizonic acid, thamnolic acid	>200
<i>Xanthoparmelia mexicana</i>	LC5	Salazinic; norstictic; usnic acid	>200	salazinic acid, usnic acid	>200
<i>Ramalina sp. 1</i>	LC6	Dirap- 2; evernic; obtusatic; colensoic acid	136.1	Anzop-1, usnic acid	>200
<i>Ramalina sp. 2</i>	LC7	Dirap- 2; usnic; thiophanic acid		usnic acid	>200
<i>Ramalina pollinaria</i>	LC8	lecanoric acid, evernic acid, obtusatic acid, usnic acid	237.6	obtusatic acid, usnic acid	>200
<i>Xanthoparmelia coreana</i>	LC9	salazinic acid, norstictic acid, usnic acid	>200	salazinic acid, usnic acid	>200
<i>Cladonia ramulosa</i>	LC10	salazinic acid, norstictic acid, usnic acid	175.7	cryptochlorophaeic acid, homosekikaic acid	>200
<i>Cladonia dehiscens</i>	LC11	Dirap-2, fumarprotocetraric acid, Anzop-1, sekikaic acid, homosekikaic acid	63.32	cryptochlorophaeic acid, sekikaic acid, homosekikaic acid	>200
<i>Ramalina litoralis</i>	LC12	salazinic acid, usnic acid, atranorin, thiophanic acid	167	usnic acid	>200
<i>Parmotrema austrosinense</i>	LC13	lecanoric acid, gyrophoric acid, methyl gyrophorate, atranorin, chloroatranorin	>200	2-O-methylrhizonic acid	>200
<i>Cladonia furcata</i>	LC14	norstictic acid, fumarprotocetraric acid, usnic acid	>200	protocetraric acid	>200
<i>Sticta nylanderiana</i>	LC15	lecanoric acid, gyrophoric acid, methyl gyrophorate, chloroatranorin	>200	lecanoric acid	>200
<i>Myelochroa entotheiochroa</i>	LC16	secalonic acid A, atranorin, chloroatranorin	71.64	2-O-methylrhizonic acid, Stcja-2	>200
<i>Lobaria spathulata</i>	LC17	lecanoric acid, gyrophoric acid, methyl gyrophorate	>200	Dirap-2, gyrophoric acid	>200
<i>Lobaria aff. adscripturiens</i>	LC18	lecanoric acid, gyrophoric acid, methyl gyrophorate, chloroatranorin	>200	Dirap-2, 2-O-methylrhizonic acid	>200
<i>Cetrelia</i>	LC19	2-O-methylrhizonic acid,	>200	2-O-methylrhizonic	>200

<i>pseudolivetorum</i>		Canap-1, atranorin, chloroatranorin		acid	
<i>Parmotrema cetratum</i>	LC20	secalonic acid A, atranorin, chloroatranorin	>200	2-0-methylrhizonic acid, Cldma-1, Cldma-4	>200
<i>Myelochroa aurulenta</i>	LC21	2-0-methylrhizonic acid, atranorin, chloroatranorin	>200	2-0-methylrhizonic acid, Stcja-2	>200
<i>Heterodermia hypoleuca</i>	LC22	2-0-methylrhizonic acid, atranorin, chloroatranorin	>200	2-0-methylrhizonic acid, echinocarpic acid	>200
<i>Peltigera rufescens</i>	LC23	2-0-methylrhizonic acid, gyrophoric acid, methyl gyrophorate, tenuiorin	>200	Pyxso-2	>200
<i>Nipponoparmelia laevior</i>	LC24	salazinic acid, atranorin, chloroatranorin	>200	2-0-methylrhizonic acid	>200
<i>Lobaria meridionalis</i>	LC25	stictic acid	>200	stictic acid	>200
<i>Physcia aff. orientalis</i>	LC26	lecanoric acid, gyrophoric acid, atranorin	>200	Pyxso-2	>200
<i>Parmotrema tinctorum</i>	LC27	lecanoric acid, gyrophoric acid, atranorin	>200	lecanoric acid	>200
<i>Parmotrema reticulatum</i>	LC28	salazinic acid, lecanoric acid, atranorin, chloroatranorin	>200	2-0-methylrhizonic acid, Stcja-2	>200
<i>Physconia hokkaidensis</i>	LC29	secalonic acid A, atranorin	142.2	secalonic acid A	>200
<i>Stereocaulon japonicum</i>	LC30	stictic acid, Stcex-2, atranorin, isosphaeric acid	>200	b-orcinolcarboxylic acid	>200
<i>Cladonia gracilis subsp. turbinata</i>	LC31	Anzop-1, Cldrm-3, sekikaic acid, homosekikaic acid	194.4	echinocarpic acid, cryptochlorophaeic acid, sekikaic acid, homosekikaic acid	>200
<i>Cladonia squamosa</i>	LC32	Anzop-1, Cldrm-3, sekikaic acid, homosekikaic acid	139.9	echinocarpic acid, cryptochlorophaeic acid, sekikaic acid, homosekikaic acid	>200

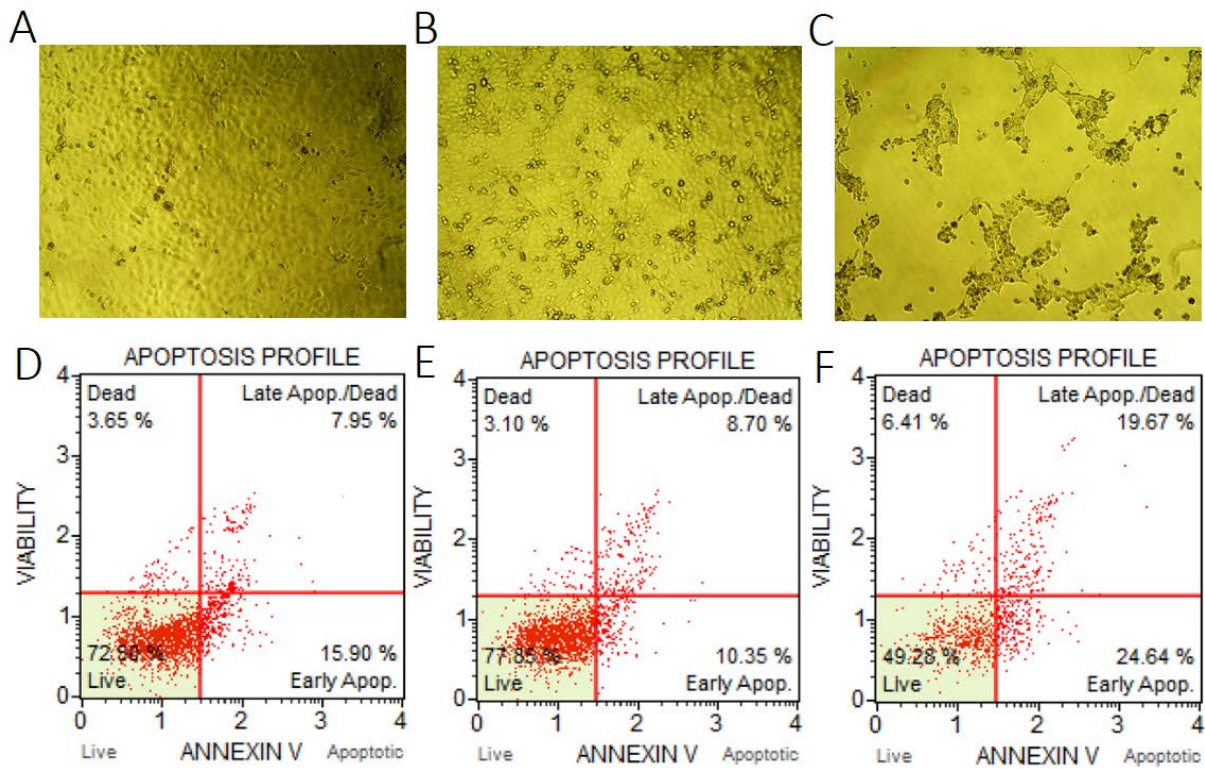
**Table S2.** Primer sequences of targeted genes used for qRT-PCR

<b>Gene</b>	<b>Primer sequence ('5-3')</b>	<b>Functions</b>
<i>IAV- PA</i>	F: CGGTCCAAATTCCTGCTGA R: CATTGGGTTTCCTTCCATCCA	For relative quantification of IAV PA-gene mRNA expression in infected MDCK cells
<i>18S</i>	F: TGTGCCGCTAGAGGTGAAATT R: TGGCAAATGCTTTCGCTTT	Housekeeping gene was used as internal control
<i>HSPA4</i>	F: TGAGGAAAACGAGGAACCGA R: TGATGCAGCTTGAGAGGTCT	Heat shock protein
<i>HSPA5</i>	F: GCCAAGAACCAGCTCACTTC R: CTTTGTTTGCCACCTCCAA	Heat shock protein
<i>HPSA8</i>	F: GCCTACCTTGGGAAGACTGT R: CGTTCCTTTCAGCTCCAACC	Heat shock protein
<i>ANXA1</i>	F: ATGCACAGCGTCAACAGATC R: TCAGTTCCAAGGCCCTTCAT	Annexin proteins
<i>ANXA2</i>	F: CTGGGGACTGATGAGGACTC R: CATCAGCTTGCGGAAGTCAC	Annexin proteins
<i>AKT1</i>	F: GGCACATCAAGATCACGGAC R: TCCTGGTTGTAGAAGGGCAG	The serine-threonine protein kinase
<i>HIF-1a</i>	F: AAGCCCTGGATGGTTTTTGT R: TCACAAGGCCATTTCTGTGTG	Hypoxia inducible factor 1 alpha

## Supplementary



**Fig. S1.** HPLC spectrum acquired at 254 nm together with the chemical structures of their predominant constituents of extracts from *Nipponoparmelia laevior* lichen (LC24). (A) Methanol and (B) acetone extracts of LC24.



**Fig. S2.** Effect of LC24 extract on IAV infection-induced cytopathic effect (CPE) and the apoptotic effect (APE) in MDCK cells. **(A)** CPE of mock without virus infection; **(B)** CPE of LC24 treatment and IAV infection; **(C)** CPE of IAV infection without lichen treatment; **(D)** APE of mock without virus infection; **(E)** APE of LC24 treatment and IAV infection; **(F)** APE of IAV infection without lichen treatment.

**Table S3.** Proteomic result summary of 214 proteins identified in MDCK cells by Progenesis QIP and their relative expression ratios according to IAV infection and LC24 treatment.

GenPept / UniProt / Accession	Symbol	Gene Name	Location	LCV/V Fold Change	V/M Fold Change
J9NST7	ACLY	ATP citrate lyase	Cytoplasm	-1.027	1.084
F1PVC1	ACTA1	actin, alpha 1, skeletal muscle	Cytoplasm	-1.199	1.691
O18840	ACTB	actin beta	Cytoplasm	1	1.058
F2Z4N8	ACTG2	actin, gamma 2, smooth muscle, enteric	Cytoplasm	1.135	-1.254
E2QY08	ACTN1	actinin alpha 1	Cytoplasm	-1.083	1.221
E2R5T9	ACTN4	actinin alpha 4	Cytoplasm	-1.168	1.236
J9PAK3	ACTR3	ARP3 actin related protein 3 homolog	Plasma Membrane	-1.006	-1.067
F1PS82	ALDOC	aldolase, fructose-bisphosphate C	Cytoplasm	-1.002	-1.003
F1P6B7	ANXA1	annexin A1	Plasma Membrane	-1.187	1.232
Q6TEQ7	ANXA2	annexin A2	Plasma Membrane	-1.09	1.142
F1PL93	ARHGDI1A	Rho GDP dissociation inhibitor alpha	Cytoplasm	-1.096	1.075
J9NZA9	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	Plasma Membrane	1.025	-1.056
P50997	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	Plasma Membrane	1.027	-1.045
F1PJF0	ATP1A2	ATPase Na+/K+ transporting subunit alpha 2	Plasma Membrane	1.395	-1.531
F1PL53	ATP1A2	ATPase Na+/K+ transporting subunit alpha 2	Plasma Membrane	-1.069	1.171
E2RNG2	ATP5F1A	ATP synthase F1 subunit alpha	Cytoplasm	-1.128	1.078
F1PDB4	ATP5F1B	ATP synthase F1 subunit beta	Cytoplasm	-1.035	-1.024
F1P8B4	CANX	calnexin	Cytoplasm	-1.092	1.141
P24643	CANX	calnexin	Cytoplasm	-1.092	1.141
E2QZ50	CAP1	cyclase associated actin cytoskeleton regulatory protein 1	Plasma Membrane	-1.149	1.228
E2R413	CAPG	capping actin protein, gelsolin like	Nucleus	-1.201	1.31
F1PCU8	CCDC137	coiled-coil domain containing 137	Nucleus	-1.152	1.198
E2RP08	CCDC83	coiled-coil domain containing 83	Other	1.042	1.07
F6V0D8	CCT2	chaperonin containing TCP1 subunit 2	Cytoplasm	-1.078	1.235
E2RB79	CCT3	chaperonin containing TCP1 subunit 3	Cytoplasm	-1.104	1.189
F1PDX9	CCT3	chaperonin containing TCP1 subunit 3	Cytoplasm	1.119	-1.094
F1Q331	CCT4	chaperonin containing TCP1 subunit 4	Cytoplasm	-1.099	1.189
E2RB81	CCT5	chaperonin containing TCP1 subunit 5	Cytoplasm	-1.105	1.238
E2RLL6	CCT6A	chaperonin containing TCP1 subunit 6A	Cytoplasm	1.216	-1.052

J9NRN0	CCT8	chaperonin containing TCP1 subunit 8	Cytoplasm	-1.126	1.19
F1PBY2	CDK18	cyclin dependent kinase 18	Cytoplasm	-1	-1.195
F1PQN5	CFL1	cofilin 1	Nucleus	-1.016	1.119
F1PHQ0	CLTC	clathrin heavy chain	Plasma Membrane	-1.096	1.103
F1PID8	DDX17	DEAD-box helicase 17	Nucleus	-1.019	1.017
J9P0V9	DDX3X	DEAD-box helicase 3, X-linked	Cytoplasm	1.257	-1.061
F1PEA6	DDX5	DEAD-box helicase 5	Nucleus	-1.112	1.19
Q5XFN2	DES	desmin	Cytoplasm	-1.08	1.116
J9P8P4	DNAJA3	DnaJ heat shock protein family (Hsp40) member A3	Cytoplasm	1.04	-1.157
E2R574	EEF1G	eukaryotic translation elongation factor 1 gamma	Cytoplasm	-1.071	1.172
F6XRY2	EEF2	eukaryotic translation elongation factor 2	Cytoplasm	-1.13	1.133
E2R3J1	EIF4A2	eukaryotic translation initiation factor 4A2	Cytoplasm	1.038	-1.168
E2RDZ4	EIF4A3	eukaryotic translation initiation factor 4A3	Nucleus	-1.104	1.32
E2RAS8	ENO2	enolase 2	Cytoplasm	-1.108	1.157
E2R5B2	ENO3	enolase 3	Cytoplasm	-1.136	1.3
E2RSI6	EZR	ezrin	Plasma Membrane	1.043	-1.135
F1P926	FDPS	farnesyl diphosphate synthase	Cytoplasm	-1.432	1.101
E2QWF5	FKBP4	FK506 binding protein 4	Nucleus	-1.118	1.118
E2RLB3	FKBP5	FK506 binding protein 5	Nucleus	1.29	-1.572
F1PTZ9	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	Cytoplasm	-1.076	1.118
E2RC89	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	Cytoplasm	1.166	-1.191
F1P8L7	GDI2	GDP dissociation inhibitor 2	Cytoplasm	1.002	1.095
E2RT94	GOPC	golgi associated PDZ and coiled-coil motif containing	Cytoplasm	-1.129	1.184
E2R2C3	GPI	glucose-6-phosphate isomerase	Extracellular Space	1.066	-1.041
F6Y3P9	GSN	gelsolin	Extracellular Space	-1.026	1.052
E2RPG1	GTF2B	general transcription factor IIB	Nucleus	1.352	-1.193
J9P6M9	HIST1H2A G	histone cluster 1 H2A family member g	Nucleus	-1.23	1.315
J9P7X1	HIST2H3A	histone cluster 2 H3 family member a	Nucleus	-1.123	1.314
E2RJI3	HNRNPA1 L2	heterogeneous nuclear ribonucleoprotein A1-like 2	Other	1.075	1.702
F1Q1K6	HNRNPA2 B1	heterogeneous nuclear ribonucleoprotein A2/B1	Nucleus	-1.127	1.176
F1PA19	Hnrnpab	heterogeneous nuclear ribonucleoprotein A/B	Nucleus	-1.016	-1.006
E2RIX2	HNRNPD	heterogeneous nuclear ribonucleoprotein D	Nucleus	-1.087	1.022
E2QRT0	HNRNPDL	heterogeneous nuclear ribonucleoprotein D like	Nucleus	-1.33	1.417
E2RB90	HNRNPF	heterogeneous nuclear ribonucleoprotein F	Nucleus	-1.032	-1.059
E2R8D6	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1	Nucleus	-1.101	1.141
E2RJH5	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2	Nucleus	1.137	-1.166
F1Q3W0	HNRNPU	heterogeneous nuclear ribonucleoprotein U	Nucleus	-1.127	1.216

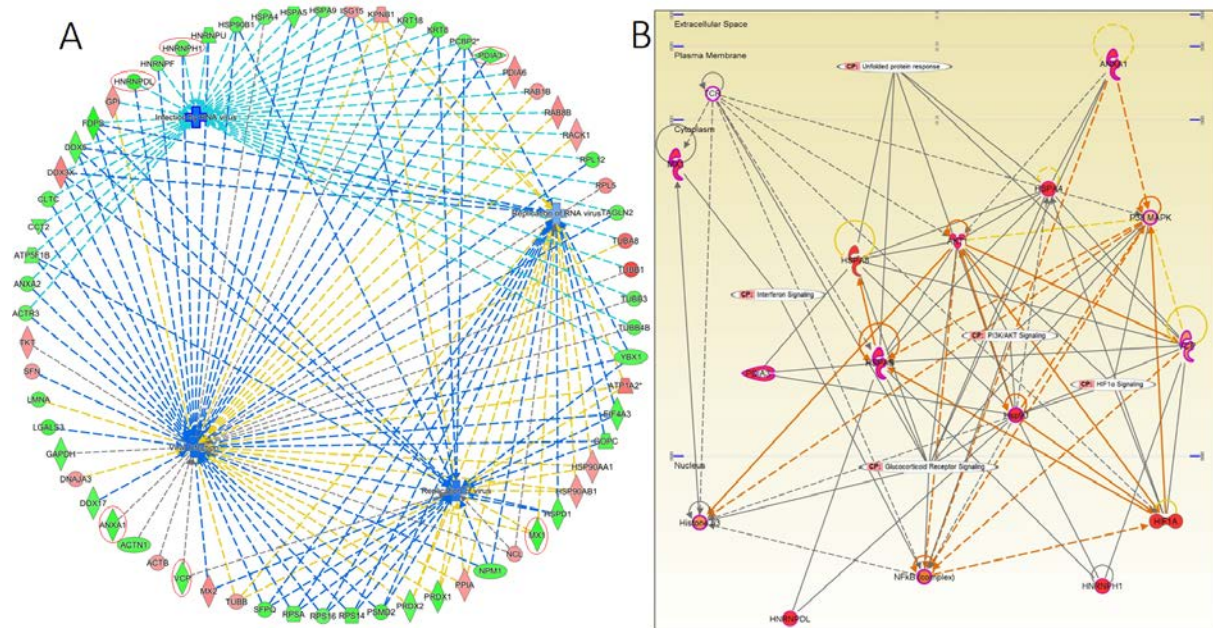
F1PGY1	HSP90AA1	heat shock protein 90 alpha family class A member 1	Cytoplasm	1.002	1.014
E2RLS3	HSP90AB1	heat shock protein 90 alpha family class B member 1	Cytoplasm	1.049	1.025
P41148	HSP90B1	heat shock protein 90 beta family member 1	Cytoplasm	-1.118	1.297
G1K268	Hspa1b	heat shock protein 1B	Cytoplasm	-1.102	1.282
E2QX84	HSPA2	heat shock protein family A (Hsp70) member 2	Cytoplasm	1.018	1.002
Q2TFN9	HSPA4	heat shock protein family A (Hsp70) member 4	Cytoplasm	-1.059	1.107
F1PIC7	HSPA5	heat shock protein family A (Hsp70) member 5	Cytoplasm	-1.098	1.229
E2R0T6	HSPA8	heat shock protein family A (Hsp70) member 8	Cytoplasm	-1.005	-1.002
E2RAU5	HSPA9	heat shock protein family A (Hsp70) member 9	Cytoplasm	-1.034	1.084
E2QUU5	HSPD1	heat shock protein family D (Hsp60) member 1	Cytoplasm	-1.153	1.175
E2RB31	HYOU1	hypoxia up-regulated 1	Cytoplasm	2.042	2.036
E2RE99	INA	internexin neuronal intermediate filament protein alpha	Cytoplasm	-1.021	1.497
E2R7R1	ISG15	ISG15 ubiquitin-like modifier	Extracellular Space	1.067	-1.351
F1PD49	KIF7	kinesin family member 7	Extracellular Space	-1.099	1.17
F6X637	KPNB1	karyopherin subunit beta 1	Nucleus	1.053	1.193
Q6EIY9	KRT1	keratin 1	Cytoplasm	-1.088	1.252
J9P4H9	KRT13	keratin 13	Cytoplasm	-1.01	1.02
F1Q0R0	KRT14	keratin 14	Cytoplasm	-1.108	1.239
E2R8Q7	KRT15	keratin 15	Cytoplasm	-1.113	1.208
E2REU6	KRT18	keratin 18	Cytoplasm	-1.134	1.333
F1Q0N9	KRT19	keratin 19	Cytoplasm	-1.228	1.266
E2R150	KRT24	keratin 24	Cytoplasm	-1.12	1.356
E2R7T3	KRT35	keratin 35	Cytoplasm	-1.251	1.663
E2R7W6	Krt42	keratin 42	Other	-1.144	1.238
E2R8Z5	KRT5	keratin 5	Cytoplasm	-1.125	1.223
L7N095	KRT5	keratin 5	Cytoplasm	-1.339	1.436
E2R917	KRT75	keratin 75	Cytoplasm	-1.148	1.2
F1PVL5	KRT79	keratin 79	Extracellular Space	-1.157	1.492
F1PW98	KRT8	keratin 8	Cytoplasm	-1.212	1.283
F1PVW0	LDHA	lactate dehydrogenase A	Cytoplasm	-1.151	1.091
E2R761	LDHB	lactate dehydrogenase B	Cytoplasm	1.342	-1.464
F6PME1	LGALS3	galectin 3	Extracellular Space	-1.238	1.237
J9NSW5	LMNA	lamin A/C	Nucleus	-1.102	1.134
F1Q1R1	MDH1	malate dehydrogenase 1	Cytoplasm	-1.035	1.057
F1PYG8	MDH2	malate dehydrogenase 2	Cytoplasm	-1.054	1.068
E2RSJ4	MIA2	melanoma inhibitory activity 2	Cytoplasm	-1.042	1.141
E2R7F1	MSN	moesin	Plasma Membrane	1.242	-1.276
F6XNH4	MTHFD1	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1	Cytoplasm	1.093	-1.149
Q9N0Y3	MX1	MX dynamin like GTPase 1	Cytoplasm	-1.254	1.29
Q9N0Y2	MX2	MX dynamin like GTPase 2	Nucleus	1.184	-1.37
F1Q0B0	NCL	nucleolin	Nucleus	1.051	-1.137
J9NTL0	NCOA5	nuclear receptor coactivator 5	Nucleus	-1.1	1.311
F1PZZ3	NEFH	neurofilament heavy	Cytoplasm	-1.083	1.23



F6UNP7	NEFM	neurofilament medium	Plasma Membrane	-1.147	1.155
Q50KA8	NME2	NME/NM23 nucleoside diphosphate kinase 2	Nucleus	-1.057	1.21
E2RTB1	NPM1	nucleophosmin 1	Nucleus	-1.113	1.116
F1PBZ4	NQO1	NAD(P)H quinone dehydrogenase 1	Cytoplasm	-1.033	1.21
J9P7Y9	PCBP1	poly(rC) binding protein 1	Nucleus	-1.046	1.189
E2RCF9	PCBP2	poly(rC) binding protein 2	Nucleus	1.01	1.005
J9P8W8	PCBP2	poly(rC) binding protein 2	Nucleus	-1.025	1.124
E2RD86	PDIA3	protein disulfide isomerase family A member 3	Cytoplasm	-1.177	1.245
E2RB37	PDIA6	protein disulfide isomerase family A member 6	Cytoplasm	1.181	-1.124
Q3YIX4	PEBP1	phosphatidylethanolamine binding protein 1	Cytoplasm	-1.044	1.009
E2RT65	PGAM1	phosphoglycerate mutase 1	Cytoplasm	1.024	-1.073
F1PE09	PGD	phosphogluconate dehydrogenase	Cytoplasm	-1.149	1.285
F1PAR8	PHB	prohibitin	Nucleus	-1.148	1.033
E2RGN6	PHB2	prohibitin 2	Cytoplasm	-1.124	1.203
L7N0I9	PHGDH	phosphoglycerate dehydrogenase	Cytoplasm	-1.108	-1.002
E2RN04	PISD	phosphatidylserine decarboxylase	Cytoplasm	2.044	-2.761
H9KUV7	PKLR	pyruvate kinase L/R	Cytoplasm	-1.068	-1.093
F1PHR2	PKM	pyruvate kinase M1/2	Cytoplasm	-1.13	1.099
E2RHY0	PKP2	plakophilin 2	Plasma Membrane	-1.016	1.095
J9NZV2	PLEC	plectin	Cytoplasm	-1.125	1.255
J9P1V4	PLXNA3	plexin A3	Plasma Membrane	-1.011	1.124
F1PQM1	PNP	purine nucleoside phosphorylase	Nucleus	1.17	-1.382
J9NV93	PPIA	peptidylprolyl isomerase A	Cytoplasm	1.03	-1.133
E2RHG2	PRDX1	peroxiredoxin 1	Cytoplasm	-1.193	1.141
F1PCG4	PRDX2	peroxiredoxin 2	Cytoplasm	-1.033	-1.053
E2RNL3	PRDX4	peroxiredoxin 4	Cytoplasm	1.28	-1.611
E2RCP9	PSMD2	proteasome 26S subunit, non-ATPase 2	Cytoplasm	-1.227	1.522
J9P5T5	PTBP1	polypyrimidine tract binding protein 1	Nucleus	1.485	-1.132
E2R002	PTGR1	prostaglandin reductase 1	Cytoplasm	-1.083	1.685
P24409	RAB10	RAB10, member RAS oncogene family	Cytoplasm	-1.224	1.758
P51152	RAB12	RAB12, member RAS oncogene family	Cytoplasm	1.128	-1.206
E2R0K4	RAB14	RAB14, member RAS oncogene family	Cytoplasm	-1.23	1.332
F1PVP9	RAB1B	RAB1B, member RAS oncogene family	Cytoplasm	1.048	1.003
E2R2R0	RAB26	RAB26, member RAS oncogene family	Plasma Membrane	-1.169	1.159
E2RG98	RAB30	RAB30, member RAS oncogene family	Cytoplasm	-1.15	1.275
J9NTY1	RAB39B	RAB39B, member RAS oncogene family	Plasma Membrane	-1.071	1.101
E2QSW2	RAB3C	RAB3C, member RAS oncogene family	Cytoplasm	-1.126	1.385
E2RP90	RAB43	RAB43, member RAS oncogene family	Cytoplasm	1.089	-2.404
E2QTP7	RAB4A	RAB4A, member RAS oncogene family	Cytoplasm	-1.376	1.478
J9PAQ4	RAB4B	RAB4B, member RAS oncogene family	Plasma Membrane	-1.174	1.288

E2RRT3	RAB8B	RAB8B, member RAS oncogene family	Cytoplasm	1.196	-1.349
F1PLR0	RACK1	receptor for activated C kinase 1	Cytoplasm	1.025	-1.03
E2RRC6	RDX	radixin	Cytoplasm	1.001	1.069
J9P540	RGD1562758	similar to glyceraldehyde-3-phosphate dehydrogenase	Other	-1.218	1.109
E2RR58	RPL12	ribosomal protein L12	Nucleus	-1.18	1.325
E2R4F5	RPL13	ribosomal protein L13	Nucleus	-1.085	1.308
F1PF85	RPL14	ribosomal protein L14	Cytoplasm	-1.117	1.219
E2QXF3	RPL15	ribosomal protein L15	Cytoplasm	-1.064	1.083
J9NVM6	RPL18A	ribosomal protein L18a	Cytoplasm	-1.15	1.22
F1P7B0	RPL5	ribosomal protein L5	Cytoplasm	1.204	-1.131
F1Q424	RPL6	ribosomal protein L6	Nucleus	-1.095	1.112
F1Q0Z2	RPL7	ribosomal protein L7	Nucleus	-1.062	1.125
F1PUX4	RPLP0	ribosomal protein lateral stalk subunit P0	Cytoplasm	1.273	-1.773
E2RQ08	RPN1	ribophorin 1	Cytoplasm	-1.154	1.204
F2Z4N1	RPS14	ribosomal protein S14	Cytoplasm	-1.161	1.34
J9P798	RPS15A	ribosomal protein S15a	Cytoplasm	1.159	-1.447
F1PKR6	RPS16	ribosomal protein S16	Cytoplasm	-1.008	-1.026
E2QWY6	RPS2	ribosomal protein S2	Cytoplasm	1.004	1.154
E2RLE2	RPS27	ribosomal protein S27	Cytoplasm	1.134	-1.056
E2RH47	RPS3	ribosomal protein S3	Cytoplasm	-1.215	1.113
F2Z4Q1	RPS4Y2	ribosomal protein S4, Y-linked 2	Other	1.429	-2.173
E2RFR0	RPS8	ribosomal protein S8	Cytoplasm	1.117	-1.377
E2RJ06	RPSA	ribosomal protein SA	Cytoplasm	-1.062	1.111
E2R925	RTN4	reticulon 4	Cytoplasm	-1.252	1.227
F1PQ93	SFN	stratifin	Cytoplasm	1.024	1.001
F1P7J0	SFPQ	splicing factor proline and glutamine rich	Nucleus	-1.166	1.116
F1PXY4	SLC25A3	solute carrier family 25 member 3	Cytoplasm	-1.066	1.264
J9NZZ1	SLC25A3	solute carrier family 25 member 3	Cytoplasm	-1.088	1.288
E2RRG4	SLC25A31	solute carrier family 25 member 31	Cytoplasm	-1.049	1.091
F1PRL5	SLC25A5	solute carrier family 25 member 5	Cytoplasm	-1.149	1.106
F1Q1J6	SLC25A6	solute carrier family 25 member 6	Cytoplasm	1.092	-1.131
J9NW72	SPAG8	sperm associated antigen 8	Cytoplasm	-1.042	1.128
J9P0H2	SREK1	splicing regulatory glutamic acid and lysine rich protein 1	Nucleus	-1.201	1.341
F1PZB5	SSUH2	ssu-2 homolog (C. elegans)	Cytoplasm	-1.122	-1.075
F1PFN9	SURF1	SURF1, cytochrome c oxidase assembly factor	Cytoplasm	-1.176	1.13
J9P675	SYCE3	synaptonemal complex central element protein 3	Nucleus	-1.091	1.206
F6XIK8	SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein	Nucleus	1.053	-1.12
F1P6P2	TAGLN2	transgelin 2	Cytoplasm	-1.061	1.081
E2R0L9	TCP1	t-complex 1	Cytoplasm	-1.058	1.108
F1PE28	TKT	transketolase	Cytoplasm	1.054	-1.01
A0A0A0M	TPI1	triosephosphate isomerase 1	Cytoplasm	-1.032	1.197
PDO					
F1P916	Tpm1	tropomyosin 1, alpha	Plasma Membrane	-1.165	1.167
J9NSW0	TRAP1	TNF receptor associated protein 1	Cytoplasm	1.508	-1.558
F6X9E9	TUBA8	tubulin alpha 8	Cytoplasm	1.56	-1.785
E2QSF4	TUBB	tubulin beta class I	Cytoplasm	1.01	1.039
J9P716	TUBB1	tubulin beta 1 class VI	Cytoplasm	1.897	3.267

F2Z4P1	TUBB3	tubulin beta 3 class III	Cytoplasm	-1.058	1.129
L7N0I7	TUBB4B	tubulin beta 4B class IVb	Cytoplasm	-1.093	1.349
E2QYC2	TUBB6	tubulin beta 6 class V	Cytoplasm	1.034	1.007
P63050	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	Cytoplasm	-1.1	1.129
Q9N2I9	UCP3	uncoupling protein 3	Cytoplasm	1.356	-1.472
E2R635	UTP14A	UTP14A, small subunit processome component	Nucleus	1.264	-1.331
F1PPZ6	UXT	ubiquitously expressed prefoldin like chaperone	Cytoplasm	-1.001	-1.427
P50551	VASP	vasodilator stimulated phosphoprotein	Plasma Membrane	-1.195	1.248
E2RLQ9	VCP	valosin containing protein	Cytoplasm	-1.136	1.303
F1PRZ1	VDAC1	voltage dependent anion channel 1	Cytoplasm	-1.121	1.07
E2R948	VDAC2	voltage dependent anion channel 2	Cytoplasm	1.057	-1.184
F1PLS4	VIM	vimentin	Cytoplasm	-1.051	1.18
E2R1A0	YBX1	Y-box binding protein 1	Nucleus	-1.081	1.173
J9NV99	YBX3	Y-box binding protein 3	Nucleus	-1.108	1.167
F1PKW7	YWHAB	tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein beta	Cytoplasm	-1.165	1.337
J9NRH5	YWHAG	tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein gamma	Cytoplasm	-1.162	1.279
J9P6N4	YWHAH	tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein eta	Cytoplasm	1.037	1.089
E2REA4	YWHAQ	tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein theta	Cytoplasm	1.045	1.01
F1PBL1	YWHAZ	tyrosine 3- monooxygenase/tryptophan 5-monooxygenase activation protein zeta	Cytoplasm	-1.073	1.129



**Fig. S3.** The interaction network of genes and protein involved in viral infection based on IPA analysis. **(A)** Total of 65 proteins are involved in viral replication, replication of virus, infection by RNA virus, and replication of RNA virus; Six proteins (ANXA1, HNRNPDL, HNRNPH1, PDIA3, MX1, and VCP) were significantly regulated by LC24 treatment in MDCK-IAV infected cells (in the red circle); **(B)** The most important canonical pathways groupings of genes and proteins differentially regulated between IAV infection and lichen treatment in MDCK cells. TCR, T Cell Receptor; HNRNPDL, Heterogeneous Nuclear Ribonucleoprotein D-like; HNRNPH1, Heterogeneous Nuclear Ribonucleoprotein H1; VCP, Valosin containing protein; PDIA3, Protein disulfide-isomerase A3.

**Table S4.** Protein profiling of diseases or functions related to Survival, Infectious disease and immune systems of MDCK cells regulated by IAV and lichen treatment

Categories	Diseases or Functions Annotation	-log(p-value)	Molecules
<b>Survival</b>	Necrosis	0,000121	RPL5, HNRNPH1, MSN, NEFM, MX1, PDIA3, ALDOA, PSMD2, VCP, KRT14, YWHAB, ANXA1
	Paracellular permeability of endothelial cell lines	0,00000567	VASP, ANXA1
	Cell death of gonadal cell lines	0,00299	PDIA3, YWHAB
	Cell viability of monocyte-derived dendritic cells	0,0148	MX1
	Cytolysis	0,0224	KRT19, ANXA1
	Apoptosis	0,0041	VASP, HNRNPH1, MSN, PDIA3, ALDOA, VCP, KRT14, YWHAB, ANXA1
<b>Infectious Diseases</b>	Infection of cells	0,00389	RPL5, HNRNPH1, MX1, PDIA3, HNRNPDL
	Replication of Crimean-Congo hemorrhagic fever virus	0,000996	MX1
	Inhibition of Influenza virus	0,00497	MX1
	Infection by Herpesviridae	0,00513	MX1, ANXA1
	Viral Infection	0,00537	RPL5, HNRNPH1, MX1, PDIA3, PSMD2, HNRNPDL, ANXA1
	Tuberculosis	0,00746	MX1, ANXA1
	Infection by Marburg virus	0,00893	RPL5
Inhibition of Thogoto virus	0,000996	MX1	
<b>Immune systems</b>	Immunological Disease	9,96E-06	MX1, MSN, PDIA3, ALDOA, VCP, ANXA1
	Inflammation of organ	0,000277	MSN, MX1, PDIA3, ALDOA, VCP, PSMD2, KRT14, ANXA1
	Candidiasis	0,0119	ANXA1
	Anterior segment inflammation	0,00497	ANXA1
	Systemic autoimmune syndrome	0,022	MX1, PDIA3, ALDOA, LDHB, ANXA1
	Chronic inflammatory disorder	0,00923	PDIA3, ALDOA, PSMD2, LDHB, ANXA1
	Inflammation of iris	0,0109	ANXA1
	Anti-inflammatory response	0,0197	ANXA1