

Identification of different proteins binding to Na, K-ATPase α 1 in lipopolysaccharide-induced acute respiratory distress syndrome cell model by proteomic analysis

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Supplemental Tables

Table S1. Top 20 up-regulated KEGG pathway analysis

Pathway ID	Definition	Counts	Q-value	P-value
hsa03013	RNA transport	28	3.63E-08	3.35E-10
hsa01200	Carbon metabolism	20	6.76E-06	9.35E-08
hsa03010	Ribosome	23	7.57E-06	1.40E-07
hsa01212	Fatty acid metabolism	13	1.01E-05	2.57E-07
hsa03050	Proteasome	12	1.01E-05	2.78E-07
hsa03008	Ribosome biogenesis in eukaryotes	18	1.41E-05	4.55E-07
hsa00010	Glycolysis / Gluconeogenesis	14	2.44E-05	8.99E-07
hsa00970	Aminoacyl-tRNA biosynthesis	13	8.99E-05	3.75E-06
hsa00620	Pyruvate metabolism	10	8.99E-05	4.14E-06
hsa00071	Fatty acid degradation	10	0.000262879	1.33E-05
hsa00020	Citrate cycle (TCA cycle)	8	0.000516237	2.86E-05
hsa04964	Proximal tubule bicarbonate reclamation	7	0.000596749	3.58E-05
hsa01230	Biosynthesis of amino acids	12	0.001215531	7.85E-05
hsa04141	Protein processing in endoplasmic reticulum	19	0.001237167	8.56E-05
hsa03030	DNA replication	8	0.001594835	0.000117677
hsa05230	Central carbon metabolism in cancer	10	0.005471872	0.000428984
hsa04961	"Endocrine and other factor-regulated calcium reabsorption"	8	0.009728765	0.000807582
hsa00280	Valine, leucine and isoleucine degradation	5	0.010651902	0.000933334
hsa00670	One carbon pool by folate	6	0.014429513	0.001330877
hsa00030			0.015175363	0.001539636

Table S2. Results of group Control-A549–IgG-A549. Significant proteins annotation (show 50 if available)

Symbol	#Unique	FC	Control-A549	IgG-A549	Annotation
PRKDC	159	6.43	200	0	protein kinase, DNA-activated, catalytic polypeptide
DYNC1H1	126	5.46	101	0	dynein, cytoplasmic 1, heavy chain 1; Cytoplasmic dynein 1 acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules. Dynein has ATPase activity; the force-producing power stroke is thought to occur on release of ADP
ATP1A1	40	5.39	96	0	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide; This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients
PRPF8	81	5.22	85	0	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae); Functions as a scaffold that mediates the ordered assembly of spliceosomal proteins and snRNAs. Required for the assembly of the U4/U6-U5 tri-snRNP complex. Functions as scaffold that positions spliceosomal U2, U5 and U6 snRNAs at splice sites on pre-mRNA substrates, so that splicing can occur. Interacts with both the 5' and the 3' splice site
FASN	77	5.06	76	0	fatty acid synthase
DDX21	35	4.64	56	0	DEAD (Asp-Glu-Ala-Asp) box helicase 21; Can unwind double-stranded RNA (helicase) and can fold or introduce a secondary structure to a single-stranded RNA (foldase). Functions as cofactor for JUN-activated transcription. Involved in rRNA processing
FLNA	61	4.61	55	0	ftlamin A, alpha; Promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. Interaction with FLNA may allow neuroblast migration from the ventricular zone into the cortical plate. Tethers cell surface- localized furin, modulates its rate of internalization and directs its intracellular trafficking (By similarity). Involved in ciliogenesis
MYOF	52	4.40	47	0	myoferlin
ILF3	32	4.37	46	0	interleukin enhancer binding factor 3, 90kDa
EEF2	39	4.37	46	0	eukaryotic translation elongation factor 2; Catalyzes the GTP-dependent ribosomal translocation step during translation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post- translocational (POST) state as the newly formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respectively. Catalyzes the coordinated movement of the two tRNA molecules, the mRNA and conformational changes in the ribosome
MYO1C	41	4.31	44	0	myosin IC; Myosins are actin-based motor molecules with ATPase activity. Unconventional myosins serve in intracellular movements. Their highly divergent tails are presumed to bind to membranous compartments, which would be moved relative to actin filaments. Involved in glucose transporter recycling in response to insulin by regulating movement of intracellular GLUT4-containing vesicles to the plasma membrane. Component of the hair cell's (the sensory cells of the inner ear) adaptation-motor complex. Acts as a mediator of adaptation of mechanoelectrical transduction in stereocilia of ve [...]

ACLY	39	4.28	43	0	ATP citrate lyase; ATP citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. Has a central role in de novo lipid synthesis. In nervous tissue it may be involved in the biosynthesis of acetylcholine
FLNB	53	4.21	41	0	ftlamin B, beta
SNRNP200	50	4.21	41	0	small nuclear ribonucleoprotein 200kDa (U5); RNA helicase that plays an essential role in pre-mRNA splicing as component of the U5 snRNP and U4/U6-U5 tri-snRNP complexes. Involved in spliceosome assembly, activation and disassembly. Mediates changes in the dynamic network of RNA-RNA interactions in the spliceosome. Catalyzes the ATP-dependent unwinding of U4/U6 RNA duplexes, an essential step in the assembly of a catalytically active spliceosome
CLTC	72	4.21	84	1	clathrin, heavy chain (Hc); Clathrin is the major protein of the polyhedral coat of coated pits and vesicles. Two different adapter protein complexes link the clathrin lattice either to the plasma membrane or to the trans-Golgi network
TJP1	36	4.07	37	0	tight junction protein 1; The N-terminal may be involved in transducing a signal required for tight junction assembly, while the C-terminal may have specific properties of tight junctions. The alpha domain might be involved in stabilizing junctions. Plays a role in the regulation of cell migration by targeting CDC42BPB to the leading edge of migrating cells
PGD	20	4.07	37	0	phosphogluconate dehydrogenase; Catalyzes the oxidative decarboxylation of 6- phosphogluconate to ribulose 5-phosphate and CO(2), with concomitant reduction of NADP to NADPH (By similarity)
NOP56	25	4.03	36	0	NOP56 ribonucleoprotein homolog (yeast); Involved in the early to middle stages of 60S ribosomal subunit biogenesis
MATR3	26	4.00	35	0	matrin 3; May play a role in transcription or may interact with other nuclear matrix proteins to form the internal fibrogranular network. In association with the SFPQ-NONO heteromer may play a role in nuclear retention of defective RNAs
RSL1D1	29	4.00	35	0	ribosomal L1 domain containing 1
H2AFY	16	3.96	34	0	H2A histone family, member Y; Variant histone H2A which replaces conventional H2A in a subset of nucleosomes where it represses transcription. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post- translational modifications of histones, also called histone code, and nucleosome remodeling. Involved in stable X chromosome inactiv [...]
HNRNPM	28	3.96	34	0	heterogeneous nuclear ribonucleoprotein M; Pre-mRNA binding protein in vivo, binds avidly to poly(G) and poly(U) RNA homopolymers in vitro. Involved in splicing. Acts as a receptor for carcinoembryonic antigen in Kupffer cells, may initiate a series of signaling events leading to tyrosine phosphorylation of proteins and induction of IL-1 alpha, IL-6, IL-10 and tumor necrosis factor alpha cytokines
MYH9	59	3.92	33	0	myosin, heavy chain 9, non-muscle; Cellular myosin that appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping
MYO1B	29	3.83	31	0	myosin IB; Motor protein that may participate in process critical to neuronal development and function such as cell migration, neurite outgrowth and vesicular transport (By similarity)

IQGAP1	36	3.79	30	0	IQ motif containing GTPase activating protein 1; Binds to activated CDC42 but does not stimulate its GTPase activity. It associates with calmodulin. Could serve as an assembly scaffold for the organization of a multimolecular complex that would interface incoming signals to the reorganization of the actin cytoskeleton at the plasma membrane. May promote neurite outgrowth
RRP12	28	3.79	30	0	ribosomal RNA processing 12 homolog (S. cerevisiae)
XRCC5	27	3.79	30	0	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining); Single stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation. The DNA helicase II complex binds preferentially to fork-like ends of double-stranded DNA in a cell cycle-dependent manner. It works in the 3'-5' direction. Binding to DNA may be mediated by XRCC6. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination. The XRCC5/6 dimer acts as regulatory subunit of the DNA-dependent protein kinase [...]
CAD	36	3.74	29	0	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; This protein is a "fusion" protein encoding four enzymatic activities of the pyrimidine pathway (GATase, CPSase, ATCase and DHOase)
DDX3X	25	3.70	28	0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked; Multifunctional ATP-dependent RNA helicase. The ATPase activity can be stimulated by various ribo- and deoxynucleic acids indicative for a relaxed substrate specificity. In vitro can unwind partially double stranded DNA with a preference for 5'- single stranded DNA overhangs. Is involved in several steps of gene expression, such as transcription, mRNA maturation, mRNA export and translation. However, the exact mechanisms are not known and some functions may be specific for a subset of mRNAs. Involved in transcriptional regulation. Can [...]
COPA	34	3.70	28	0	coatamer protein complex, subunit alpha; The coatamer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatamer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatamer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the [...]
EL52	19	3.65	27	0	heat shock protein 90kDa alpha (cytosolic), class A member 1; Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved for instance in cell cycle control and signal transduction. Undergoes a functional cycle that is linked to its ATPase activity. This cycle probably induces conformational changes in the client proteins, thereby causing their activation. Interacts dynamically with various co-chaperones that modulate its substrate recognition, ATPase cycle and chaperone function
ATP1A3	17	3.60	26	0	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide; This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients

ATP1B1	15	3.60	26	0	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide; This is the non-catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of Na ⁽⁺⁾ and K ⁽⁺⁾ ions across the plasma membrane. The beta subunit regulates, through assembly of alpha/beta heterodimers, the number of sodium pumps transported to the plasma membrane
NOP2	23	3.60	26	0	NOP2 nucleolar protein homolog (yeast); May play a role in the regulation of the cell cycle and the increased nucleolar activity that is associated with the cell proliferation. May act as ribosomal RNA methyltransferase
CPS1	30	3.55	25	0	carbamoyl-phosphate synthase 1, mitochondrial; Involved in the urea cycle of ureotelic animals where the enzyme plays an important role in removing excess ammonia from the cell
HADHA	24	3.55	25	0	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit; Bifunctional subunit
PDCD11	26	3.55	25	0	programmed cell death 11; Essential for the generation of mature 18S rRNA, specifically necessary for cleavages at sites A0, 1 and 2 of the 47S precursor. Directly interacts with U3 snoRNA
RPN1	21	3.49	24	0	ribophorin I; Essential subunit of the N-oligosaccharyl transferase (OST) complex which catalyzes the transfer of a high mannose oligosaccharide from a lipid-linked oligosaccharide donor to an asparagine residue within an Asn-X-Ser/Thr consensus motif in nascent polypeptide chains
HADHB	24	3.49	24	0	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit
SRRM2	24	3.44	23	0	serine/arginine repetitive matrix 2
DDX27	20	3.44	23	0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27
SMARCA5	24	3.44	23	0	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5; Helicase that possesses intrinsic ATP-dependent nucleosome-remodeling activity. Complexes containing SMARCA5 are capable of forming ordered nucleosome arrays on chromatin; this may require intact histone H4 tails. Also required for replication of pericentric heterochromatin in S-phase specifically in conjunction with BAZ1A. Probably plays a role in repression of polI dependent transcription of the rDNA locus, through the recruitment of the SIN3/HDAC1 corepressor complex to the rDNA promot [...]
DHX15	23	3.44	23	0	DEAH (Asp-Glu-Ala-His) box polypeptide 15; Pre-mRNA processing factor involved in disassembly of spliceosomes after the release of mature mRNA (By similarity)
BRX1	16	3.44	23	0	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae); Required for biogenesis of the 60S ribosomal subunit
DHX9	50	3.40	72	2	DEAH (Asp-Glu-Ala-His) box polypeptide 9; Unwinds double-stranded DNA and RNA in a 3' to 5' direction. Alteration of secondary structure may subsequently influence interactions with proteins or other nucleic acids. Functions as a transcriptional activator. Component of the CRD- mediated complex that promotes MYC mRNA stability. Involved with LARP6 in the stabilization of type I collagen mRNAs for CO1A1 and CO1A2. Positively regulates HIV-1 LTR-directed gene expression

HEL-S-123m	29	3.40	47	1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle; Mitochondrial membrane ATP synthase (F1)F(0) ATP synthase or Complex V) produces ATP from ADP in the presence of a proton gradient across the membrane which is generated by electron transport complexes of the respiratory chain. F-type ATPases consist of two structural domains, F(1) - containing the extramembraneous catalytic core, and F(0) - containing the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, ATP synthesis in the catalytic domain of [...]
UGDH	20	3.38	22	0	UDP-glucose 6-dehydrogenase; Involved in the biosynthesis of glycosaminoglycans; hyaluronan, chondroitin sulfate, and heparan sulfate
HEL-S-53e	18	3.38	22	0	aldehyde dehydrogenase 1 family, member A1; Binds free retinal and cellular retinol-binding protein- bound retinal. Can convert/oxidize retinaldehyde to retinoic acid (By similarity)
HNRNPUL2	20	3.38	22	0	heterogeneous nuclear ribonucleoprotein U-like 2
XRCC6	17	3.32	21	0	X-ray repair complementing defective repair in Chinese hamster cells 6; Single stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation. The DNA helicase II complex binds preferentially to fork-like ends of double-stranded DNA in a cell cycle-dependent manner. It works in the 3'-5' direction. Binding to DNA may be mediated by XRCC6. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination. The XRCC5/6 dimer acts as regulatory subunit of the DNA-dependent protein kinase complex DNA-PK by increasing the [...]

Table S3. Results of group LPS-A549–IgG-LPS. Significant proteins annotation (show 50 if available)

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PGD	20	3.55	35	0 phosphogluconate dehydrogenase; Catalyzes the oxidative decarboxylation of 6- phosphogluconate to ribulose 5-phosphate and CO(2), with concomitant reduction of NADP to NADPH (By similarity)
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ATP1A1	40	3.33	95	2 ATPase, Na+/K+ transporting, alpha 1 polypeptide; This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients
MATR3	26	3.31	29	0 matrin 3; May play a role in transcription or may interact with other nuclear matrix proteins to form the internal fibrogranular network. In association with the SFPQ-NONO heteromer may play a role in nuclear retention of defective RNAs
XRCC5	27	3.31	29	0 X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining); Single stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation. The DNA helicase II complex binds preferentially to fork-like ends of double-stranded DNA in a cell cycle-dependent manner. It works in the 3'-5' direction. Binding to DNA may be mediated by XRCC6. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination. The XRCC5/6 dimer acts as regulatory subunit of the DNA-dependent protein kinase [...]
LRPPRC	33	3.26	28	0 leucine-rich pentatricopeptide repeat containing; May play a role in RNA metabolism in both nuclei and mitochondria. In the nucleus binds to HNRPA1-associated poly(A) mRNAs and is part of nmRNP complexes at late stages of mRNA maturation which are possibly associated with nuclear mRNA export. May bind mature mRNA in the nucleus outer membrane. In mitochondria binds to poly(A) mRNA. Plays a role in translation or stability of mitochondrially encoded cytochrome c oxidase (COX) subunits. May be involved in transcription regulation. Cooperates with PPARGC1A to regulate certain mitochondria [...]
HEL-S-89n	21	3.21	27	0 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); Probably plays a role in facilitating the assembly of multimeric protein complexes inside the ER
eIF3a	27	3.17	26	0 eukaryotic translation initiation factor 3, subunit A; Component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is required for several steps in the initiation of protein synthesis. The eIF-3 complex associates with the 40S ribosome and facilitates the recruitment of eIF-1, eIF-1A, eIF-2:GTP:methionyl-tRNAi and eIF-5 to form the 43S preinitiation complex (43S PIC). The eIF-3 complex stimulates mRNA recruitment to the 43S PIC and scanning of the mRNA for AUG recognition. The eIF-3 complex is also required for disassembly and recycling of post-termination ribosome [...]

COPA	34	3.17	26	0	coatomer protein complex, subunit alpha; The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the [...]
CPS1	30	3.12	25	0	carbamoyl-phosphate synthase 1, mitochondrial; Involved in the urea cycle of ureotelic animals where the enzyme plays an important role in removing excess ammonia from the cell
PABPC1	15	3.12	25	0	poly(A) binding protein, cytoplasmic 1; Binds the poly(A) tail of mRNA. May be involved in cytoplasmic regulatory processes of mRNA metabolism such as pre-mRNA splicing. Its function in translational initiation regulation can either be enhanced by PAIP1 or repressed by PAIP2. Can probably bind to cytoplasmic RNA sequences other than poly(A) in vivo. Involved in translationally coupled mRNA turnover. Implicated with other RNA-binding proteins in the cytoplasmic deadenylation/translational and decay interplay of the FOS mRNA mediated by the major coding-region determinant of instability [...]
MYO1B	29	3.12	25	0	myosin IB; Motor protein that may participate in process critical to neuronal development and function such as cell migration, neurite outgrowth and vesicular transport (By similarity)
SLC3A2	21	3.06	24	0	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2; Required for the function of light chain amino-acid transporters. Involved in sodium-independent, high-affinity transport of large neutral amino acids such as phenylalanine, tyrosine, leucine, arginine and tryptophan. Involved in guiding and targeting of LAT1 and LAT2 to the plasma membrane. When associated with SLC7A6 or SLC7A7 acts as an arginine/glutamine exchanger, following an antiport mechanism for amino acid transport, influencing arginine release in exchange for extracellular amino acids [...]
HEL107	20	3.06	24	0	transketolase; Catalyzes the transfer of a two-carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate
ILF3	32	3.06	51	1	interleukin enhancer binding factor 3, 90kDa
DDX21	35	3.03	50	1	DEAD (Asp-Glu-Ala-Asp) box helicase 21; Can unwind double-stranded RNA (helicase) and can fold or introduce a secondary structure to a single-stranded RNA (foldase). Functions as cofactor for JUN-activated transcription. Involved in rRNA processing
ATP2A2	23	3.01	23	0	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2; This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the translocation of calcium from the cytosol to the sarcoplasmic reticulum lumen. Isoform 2 is involved in the regulation of the contraction/relaxation cycle
EL52	19	3.01	23	0	heat shock protein 90kDa alpha (cytosolic), class A member 1; Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved for instance in cell cycle control and signal transduction. Undergoes a functional cycle that is linked to its ATPase activity. This cycle probably induces conformational changes in the client proteins, thereby causing their activation. Interacts dynamically with various co-chaperones that modulate its substrate recognition, ATPase cycle and chaperone function

SF3B1	28	3.01	23	0 splicing factor 3b, subunit 1, 155kDa; Subunit of the splicing factor SF3B required for 'A' complex assembly formed by the stable binding of U2 snRNP to the branchpoint sequence (BPS) in pre-mRNA. Sequence independent binding of SF3A/SF3B complex upstream of the branch site is essential, it may anchor U2 snRNP to the pre-mRNA. May also be involved in the assembly of the 'E' complex. Belongs also to the minor U12-dependent spliceosome, which is involved in the splicing of rare class of nuclear pre-mRNA intron
RPN1	21	3.01	23	0 ribophorin I; Essential subunit of the N-oligosaccharyl transferase (OST) complex which catalyzes the transfer of a high mannose oligosaccharide from a lipid-linked oligosaccharide donor to an asparagine residue within an Asn-X-Ser/Thr consensus motif in nascent polypeptide chains
PBEF1	19	2.95	22	0 nicotinamide phosphoribosyltransferase; Catalyzes the condensation of nicotinamide with 5-phosphoribosyl-1-pyrophosphate to yield nicotinamide mononucleotide, an intermediate in the biosynthesis of NAD. It is the rate limiting component in the mammalian NAD biosynthesis pathway (By similarity)
TRA1	19	2.95	22	0 heat shock protein 90kDa beta (Grp94), member 1; Molecular chaperone that functions in the processing and transport of secreted proteins. When associated with CNPY3, required for proper folding of Toll-like receptors (By similarity). Functions in endoplasmic reticulum associated degradation (ERAD). Has ATPase activity
FBL	14	2.95	22	0 ftbrrillarin; Involved in pre-rRNA processing. Utilizes the methyl donor S-adenosyl-L-methionine to catalyze the site-specific 2'-hydroxyl methylation of ribose moieties in pre-ribosomal RNA. Site specificity is provided by a guide RNA that base pairs with the substrate. Methylation occurs at a characteristic distance from the sequence involved in base pairing with the guide RNA
UQCRC2	14	2.95	22	0 ubiquinol-cytochrome c reductase core protein II; This is a component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is part of the mitochondrial respiratory chain. The core protein 2 is required for the assembly of the complex
PFKP	22	2.95	22	0 phosphofructokinase, platelet; Catalyzes the third step of glycolysis, the phosphorylation of fructose-6-phosphate (F6P) by ATP to generate fructose-1,6-bisphosphate (FBP) and ADP
ASPH	23	2.95	22	0 aspartate beta-hydroxylase
NOP58	20	2.90	21	0 NOP58 ribonucleoprotein homolog (yeast); Required for 60S ribosomal subunit biogenesis (By similarity)
XRCC6	17	2.84	20	0 X-ray repair complementing defective repair in Chinese hamster cells 6; Single stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation. The DNA helicase II complex binds preferentially to fork-like ends of double-stranded DNA in a cell cycle-dependent manner. It works in the 3'-5' direction. Binding to DNA may be mediated by XRCC6. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination. The XRCC5/6 dimer acts as regulatory subunit of the DNA-dependent protein kinase complex DNA-PK by increasing the [...]
ATP1A3	17	2.84	20	0 ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide; This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients
RRP12	28	2.84	20	0 ribosomal RNA processing 12 homolog (S. cerevisiae)

CCT3	18	2.77	19	0	chaperonin containing TCP1, subunit 3 (gamma); Molecular chaperone; assists the folding of proteins upon ATP hydrolysis. As part of the BBS/CCT complex may play a role in the assembly of BBSome, a complex involved in ciliogenesis regulating transports vesicles to the cilia. Known to play a role, in vitro, in the folding of actin and tubulin
CAD	36	2.77	19	0	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; This protein is a "fusion" protein encoding four enzymatic activities of the pyrimidine pathway (GATase, CPSase, ATCase and DHOase)
EPRS	26	2.77	19	0	glutamyl-prolyl-tRNA synthetase
ACLY	39	2.76	41	1	ATP citrate lyase; ATP citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. Has a central role in de novo lipid synthesis. In nervous tissue it may be involved in the biosynthesis of acetylcholine
BRX1	16	2.71	18	0	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae); Required for biogenesis of the 60S ribosomal subunit
DHX15	23	2.64	17	0	DEAH (Asp-Glu-Ala-His) box polypeptide 15; Pre-mRNA processing factor involved in disassembly of spliceosomes after the release of mature mRNA (By similarity)
G6PD	29	2.63	37	1	glucose-6-phosphate dehydrogenase; Produces pentose sugars for nucleic acid synthesis and main producer of NADPH reducing power
PTBP1	12	2.56	16	0	polypyrimidine tract binding protein 1; Plays a role in pre-mRNA splicing and in the regulation of alternative splicing events. Activates exon skipping of its own pre-mRNA during muscle cell differentiation. Binds to the polypyrimidine tract of introns. May promote RNA looping when bound to two separate polypyrimidine tracts in the same pre-mRNA. May promote the binding of U2 snRNP to pre-mRNA. Cooperates with RAVER1 to modulate switching between mutually exclusive exons during maturation of the TPM1 pre-mRNA. Represses the splicing of MAPT/Tau exon 10
SND1	22	2.56	16	0	staphylococcal nuclease and tudor domain containing 1; Functions as a bridging factor between STAT6 and the basal transcription factor. Plays a role in PIM1 regulation of MYB activity. Functions as a transcriptional coactivator for the Epstein-Barr virus nuclear antigen 2 (EBNA2)

Table S4. Abbreviations used in this study

Abbreviation	Full name
ARDS	Acute respiratory distress syndrome;
ALI	Acute lung injury;
ICU	Intensive care unit;
LC-MS/MS:	Liquid chromatography-tandem mass spectrometry;
AP-MS/MS	Affinity purification mass spectrometry;
Co-IP-MS	co-immunoprecipitation mass spectrometry;
AT II	Alveolar type II epithelial cells;
LPS	Lipopolysaccharide;
ENaC	Apically-located epithelial Na ⁺ channel;
A549	Human non-small cell lung cancer cell line/Human AT II cell line;
AFC	Alveolar fluid clearance;
GO:	Gene Ontology;
KEGG:	Kyoto Encyclopedia of Genes and Genomes;

Supplemental Figures

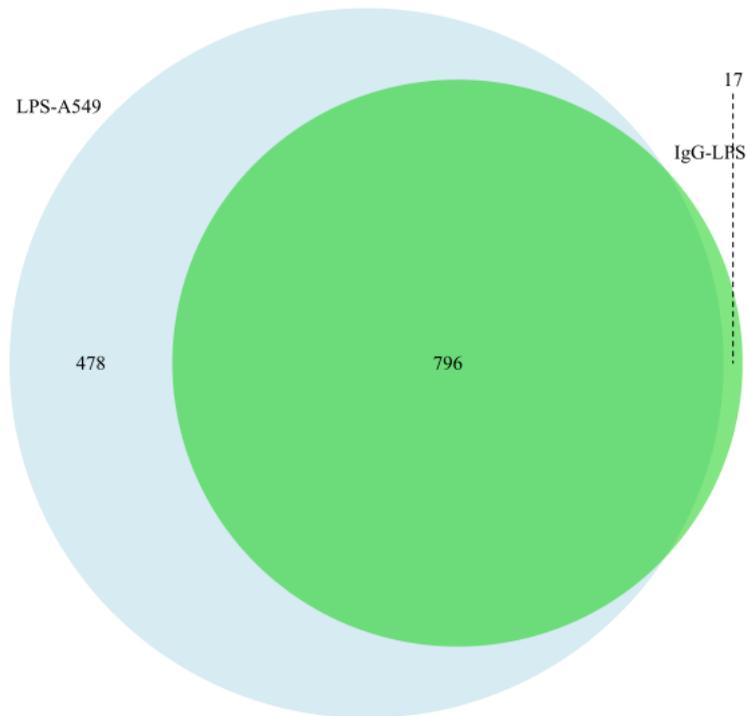


Figure S1. Venn diagram of the different proteins in LPS-A549 vs. IgG-LPS. Venn diagram of the different proteins in LPS-A549 vs. IgG-LPS. The green part represents proteins enriched in IgG-LPS; The light blue represents proteins enriched in LPS-A549; The middle part is the protein identified by both of them.

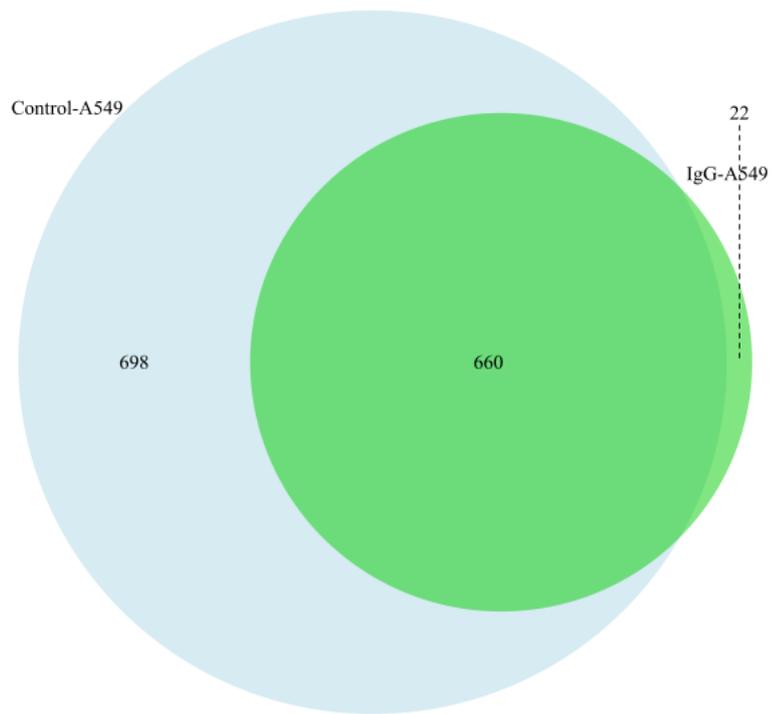


Figure S2. Venn diagram of the different proteins in control-A549 vs. IgG-A549. The green part represents proteins enriched in IgG-A549; The light blue represents proteins enriched in Control-A549; The middle part is the protein identified by both of them.

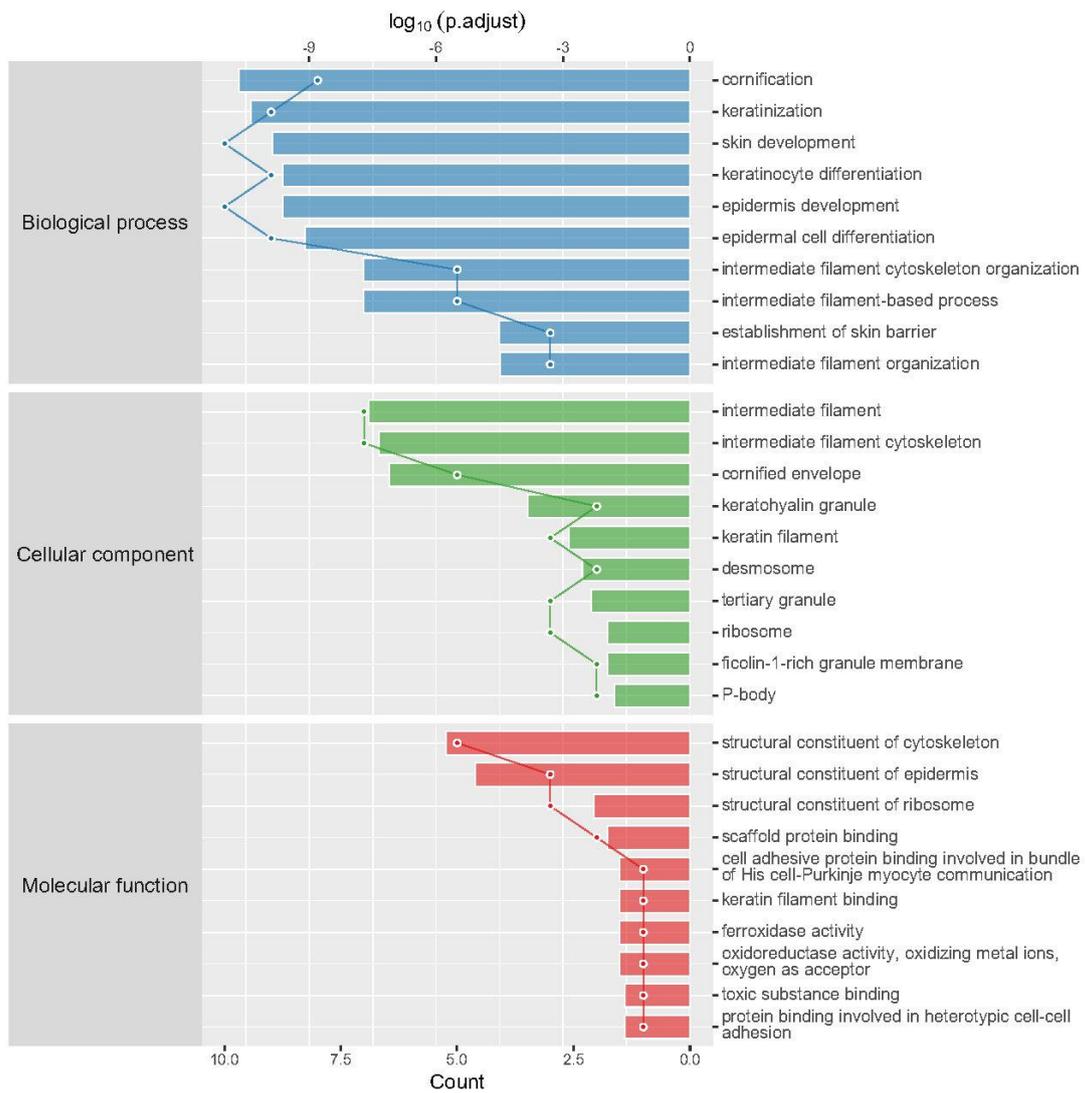


Figure S3. Enriched GO items of < C > in Control-A549 vs. IgG-A549. top axis is $\log_{10}(\text{adjust p-value})$, bottom axis is gene count.

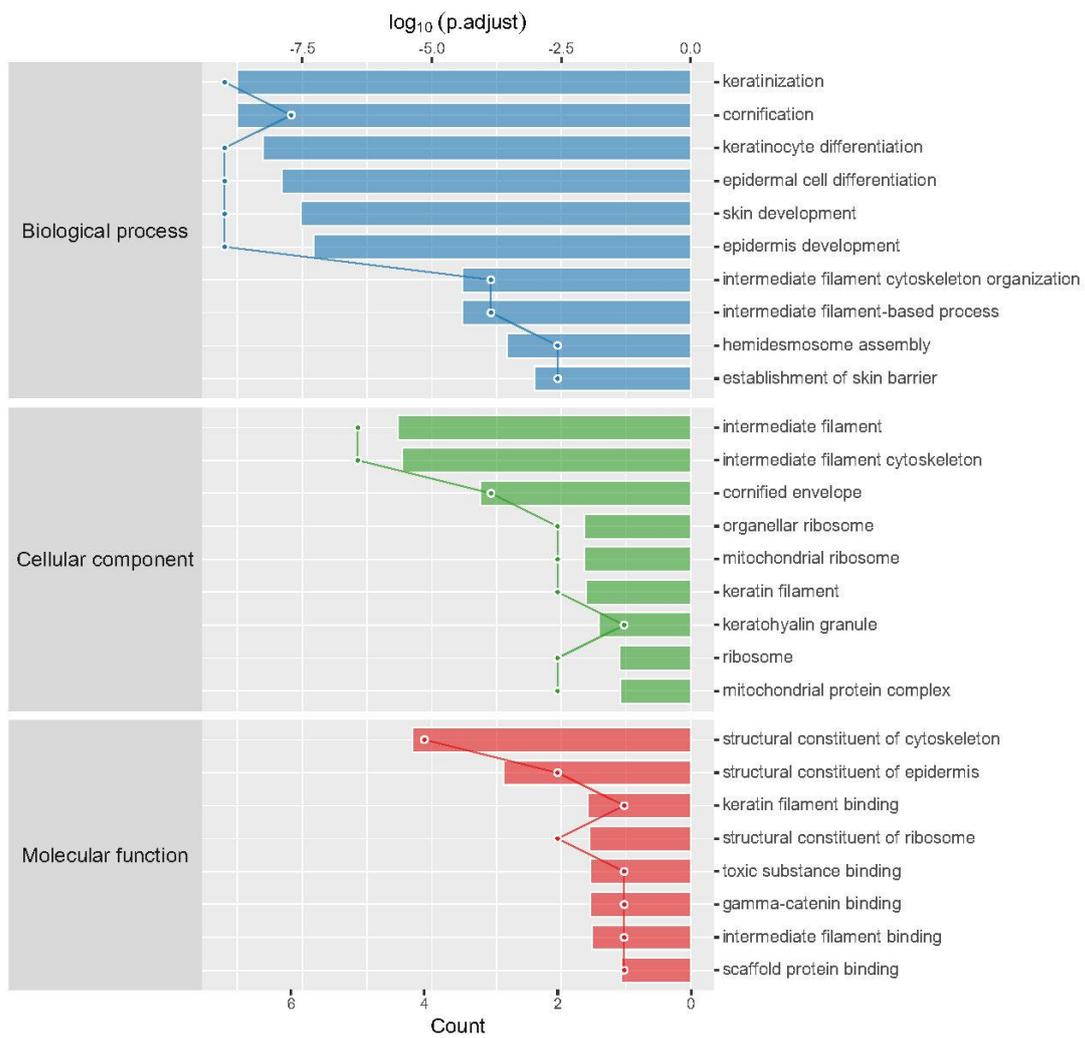


Figure S4. Enriched GO items of < C > in LPS-A549 vs. IgG-LPS. top axis is $\log_{10}(\text{adjust p-value})$, bottom axis is gene count.

proteins: 345
interactions: 12373
expected interactions: 6258 (p-value: 0)

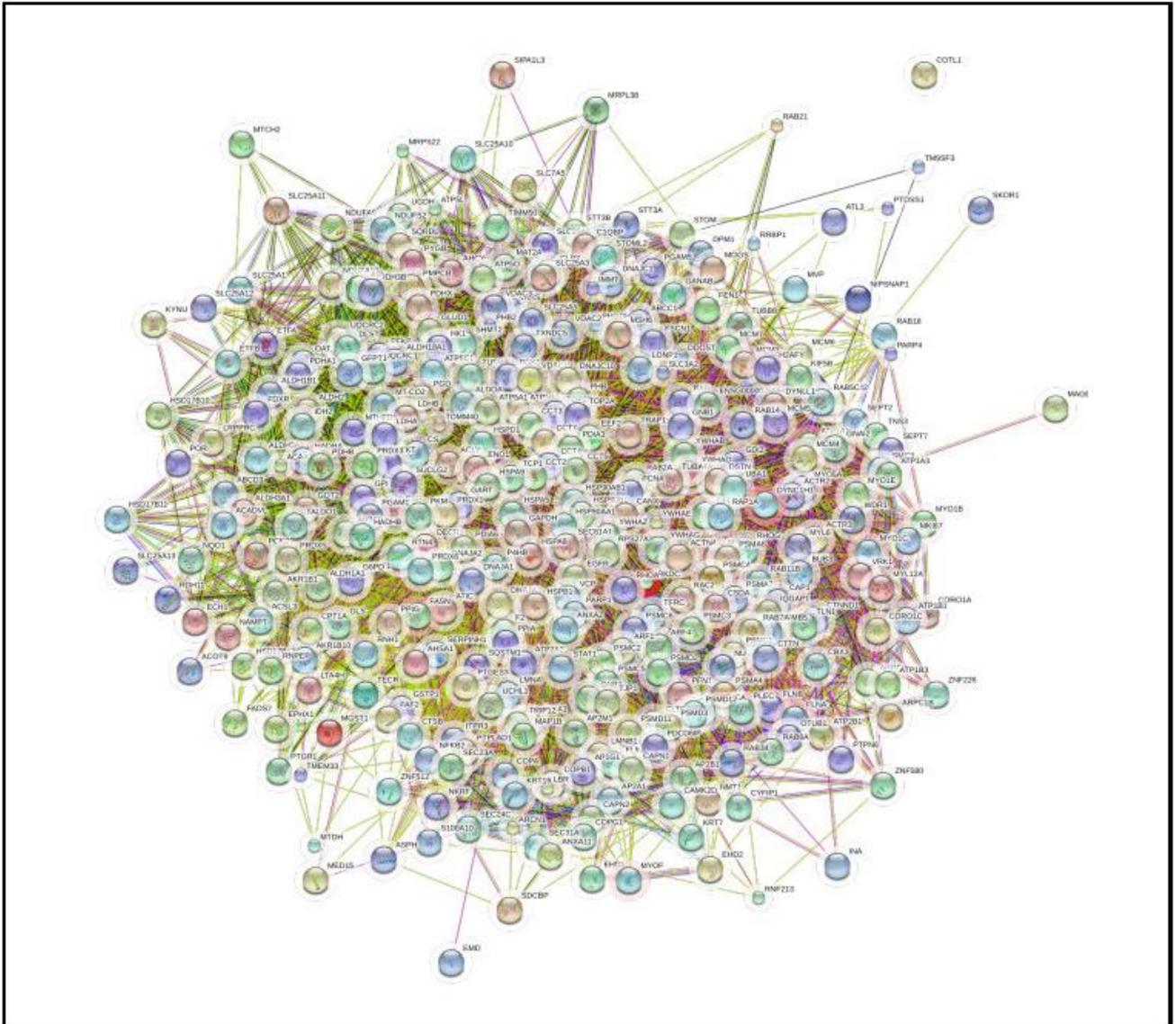


Figure S5. Control-A549--IgG-A549-STRINGdb-T-1.

