

Table S1. [Clinical characteristics of animals used in the study], Related to Figures 1 and 2.

	Ctrl (Saline) n=12 (IA n=11; IM n=1)	IA LPS 16h n=15	IA/SC Adalimuma b + IA LPS 16h n=6	IA LPS 48h n=3[#]	IA LPS 5d n=3[#]
maternal age, year ± SD	10 ± 3	8 ± 3	10.3 ± 2	9.5 ± 2.5	8.7 ± 2.3
maternal weight (Kg)	8.9 ± 1.5	9.6 ± 1.9	10.6 ± 1	8.2 ± 1.4	7 ± 1
Median gestational age at delivery, day [range]	131 [128-136]	131 [129-136]	131 [127- 134]	127 [126- 137]	133 [131- 133]
mean birth weight, gram ± SD	339.4 ± 44.1	315.7 ± 47.2	338.3 ± 81.6	283.6 ± 26.5	318 ± 21.6
Fetal gender (F/M)	7/5	10/5	3/3	3/0	1/2
n for bulk RNA-seq	3	6	6	n/a	n/a
n for scRNA-seq	2*	3	3	n/a	n/a
shared with bulk RNA-seq	1/3	2/6	3/3	n/a	n/a
shared with qPCR	2/8	2/8	3/5	n/a	n/a
shared ELISA	0/2	1/3	2/3	n/a	n/a
shared with flow cytometry	0	0	n/a	n/a	n/a
shared with immunohistology	1/2	2/4	n/a	n/a	n/a
n for qPCR	8	8	5	n/a	n/a
shared with bulk RNA-seq	2/8	2/8	5/5	n/a	n/a
shared with ELISA	7/9	7/11	n/a	n/a	n/a
shared with flow cytometry	0	0	n/a	n/a	n/a
n for ELISA	9	11	n/a	n/a	n/a
shared with flow cytometry	0	0	n/a	n/a	n/a
n for flow cytometry	2	2	n/a	n/a	n/a
n for immunohistology	4	4	n/a	3	3

IA=intraamniotic; IM=intramuscular; SC=subcutaneous

*Analysis of scRNA-seq data did not show any amnion signature in one control and therefore such animal was excluded.

[#]IA LPS 4h and 5 days animals were only used for immunohistology

Note: It was not always possible to obtain all the tissues/fluids from each animal. The numbers of animals for each experiment are also shown in the corresponding figure.

Table S2. [Clinical characteristics of pregnant women who delivered preterm newborns and number of samples used/experiment], Related to Figure1.

	Preterm chorio negative (n=8)	Preterm chorio positive (n=7)	P value
Maternal age, year \pm SD	30.5 \pm 6.27	30.5 \pm 6.77	>0.99 [#]
Median GA at delivery, weeks [range]	32 [27-35]	31 [29-34]	0.61 [#]
Causes of preterm birth			
• PTL or preterm-PROM	3/6*	7/7	0.004 [‡]
• Other indications	3/6*	2/7	0.9 [‡]
Antenatal steroid use	6/6*	7/7	0.9 [‡]
Antenatal antibiotics use	1/6*	5/7	0.3 [‡]
Cesarean delivery	6/8	3/7	0.15 [‡]
The presence of labor	3/6*	6/7	0.26 [‡]
Spontaneous labor	3/6*	5/6*	0.54 [‡]
Neonatal male gender M/F	3/4*	4/3	>0.99 [‡]
Mean birth weight, gram \pm SD	1485 \pm 650*	1808 \pm 341	0.31 [#]
White Caucasian race	5	3	0.61 [‡]
African American race	3	4	0.61 [‡]
n for bulk RNA-seq	8	7	
n for qPCR	8	6-7	

PTL=preterm labor; PROM=premature rupture of membranes

Other indications: PIH=pregnancy induced hypertension; HTN=hypertension

[‡]Fisher's exact test

[#]Student t test in yellow

*Some values are missing

Table S3. [List of Rhesus and Human Taqman probes].

	Rhesus	Human
<i>SI00A9</i>	Rh02801277	m1
<i>CCL5</i>	Rh02621811	m1
<i>ADORA2A</i>	Rh02902837	m1
<i>ICAM1</i>	Rh02621706	m1
<i>NOD2</i>	Rh02879855	m1
<i>TNFAIP3</i>	Rh02860236	m1
<i>CXCL3</i>	Rh02788128	gH
<i>TNF</i>	Hs99999043	m1
<i>NFKB2</i>	Rh02621752	m1
<i>RELA</i>	Rh02802962	

Table S4. [List of the 104 genes upregulated and in common between amnion of LPS-exposed animals and human of preterm positive samples], Related to Figure 1.

CLEC4E	TNFRSF10C	NFKBIA
IL1A	STEAP4	CD44
CCL5	SPATC1	KCNK5
IL1B	MFSD2A	IFNGR2
NKX3-1	TRAF1	NFKBIE
CSF3R	SAMSN1	PSME2
S100A9	DGAT2	MYO10
APOBEC3A	MUC22	TIPARP
CCL20	PTGIR	CFLAR
CXCR1	MEDAG	MXD1
ANGPTL4	ADAMTS4	FAS
CLEC4D	PNP	NFKB1
MMP3	IER3	DRAM1
LTF	OLR1	ARHGEF3
TNIP3	GCH1	TNIP1
EBI3	TNFAIP2	APOL6
PLEK	SLC41A2	PANX1
TNF	FOSL1	SLC43A3
CXCL3	HAMP	OSMR
IL18RAP	TNFAIP3	PLK3
SELL	HILPDA	SLC43A2
CSF3	CCL3	NFKB2
SLAMF7	ICAM1	ZDHHC9
S100A8	RNF207	SERPINB8
ADORA2A	RIPK2	TRAF3IP2
MMP10	IRF1	SLC25A37
FDCSP	PTGS2	SOCS3
OSM	CHI3L2	STAT5A
SLAMF1	IL2RG	REL
ANKRD33B	SLC7A2	NOD2
RHOH	ACSL4	TNFAIP8L3
SGPP2	CSF1	BCL6
G0S2	IFIH1	ETS2
GK	CSTA	ETHE1
CXCL1	BATF	

Table S5. [Rhesus top 30 GO terms based on 257 LPS-induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
cytokine-mediated signaling pathway (GO:0019221)	51	25.56	1.42E-22
inflammatory response (GO:0006954)	30	19.72	4.84E-17
cellular response to cytokine stimulus (GO:0071345)	34	15.91	2.11E-13
positive regulation of cytokine production (GO:0001819)	19	10.14	9.14E-08
positive regulation of response to external stimulus (GO:0032103)	13	9.88	1.34E-07
positive regulation of intracellular signal transduction (GO:1902533)	27	9.87	1.16E-07
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	18	9.79	1.18E-07
regulation of inflammatory response (GO:0050727)	16	9.33	2.99E-07
cellular response to interleukin-1 (GO:0071347)	15	9.00	5.62E-07
negative regulation of cytokine production (GO:0001818)	13	8.77	8.60E-07
positive regulation of inflammatory response (GO:0050729)	11	8.65	1.04E-06
neutrophil degranulation (GO:0043312)	25	8.48	1.40E-06
neutrophil activation involved in immune response (GO:0002283)	25	8.41	1.53E-06
negative regulation of type I interferon production (GO:0032480)	9	8.40	1.45E-06
neutrophil mediated immunity (GO:0002446)	25	8.34	1.56E-06
positive regulation of NF-kB transcription factor activity (GO:0051092)	13	7.96	3.50E-06
regulation of type I interferon production (GO:0032479)	11	7.93	3.53E-06
negative regulation of viral genome replication (GO:0045071)	9	7.88	3.72E-06
response to interferon-gamma (GO:0034341)	10	7.81	4.18E-06
cellular response to lipopolysaccharide (GO:0071222)	11	7.61	6.21E-06
response to cytokine (GO:0034097)	13	7.56	6.63E-06
cellular response to interferon-gamma (GO:0071346)	12	7.48	7.67E-06
positive regulation of defense response (GO:0031349)	10	7.44	7.98E-06
regulation of defense response (GO:0031347)	10	7.39	8.72E-06
regulation of interleukin-6 production (GO:0032675)	8	7.27	1.10E-05
negative regulation of viral life cycle (GO:1903901)	9	7.09	1.58E-05
positive regulation of type I interferon production (GO:0032481)	9	7.03	1.76E-05
regulation of viral genome replication (GO:0045069)	9	6.97	1.96E-05
response to lipopolysaccharide (GO:0032496)	13	6.96	1.91E-05
positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)	15	6.88	2.22E-05

Shaded rows represent 50% GO terms shared between Rhesus and human

Tbale S6. [Human top 30 GO terms based on 1619 chorioamnionitis-induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
cytokine-mediated signaling pathway (GO:0019221)	121	18.77	8.60E-16
inflammatory response (GO:0006954)	66	17.43	9.55E-15
cellular response to cytokine stimulus (GO:0071345)	90	14.93	1.98E-12
response to lipopolysaccharide (GO:0032496)	44	13.17	8.54E-11
response to molecule of bacterial origin (GO:0002237)	32	11.57	2.77E-09
response to lipid (GO:0033993)	36	9.57	2.31E-07
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	43	8.36	3.21E-06
positive regulation of inflammatory response (GO:0050729)	23	8.16	4.37E-06
neutrophil mediated immunity (GO:0002446)	76	7.73	1.07E-05
positive regulation of intracellular signal transduction (GO:1902533)	75	7.69	1.03E-05
cellular response to tumor necrosis factor (GO:0071356)	40	7.54	1.34E-05
regulation of cell proliferation (GO:0042127)	103	7.52	1.30E-05
cellular response to lipopolysaccharide (GO:0071222)	25	7.47	1.34E-05
regulation of leukocyte chemotaxis (GO:0002688)	13	6.72	6.99E-05
neutrophil degranulation (GO:0043312)	72	6.69	6.88E-05
positive regulation of defense response (GO:0031349)	21	6.64	7.34E-05
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	34	6.64	6.95E-05
neutrophil activation involved in immune response (GO:0002283)	72	6.55	7.95E-05
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	18	6.55	7.64E-05
positive regulation of acute inflammatory response (GO:0002675)	9	6.34	1.17E-04
cellular response to molecule of bacterial origin (GO:0071219)	22	6.26	1.35E-04
positive regulation of leukocyte chemotaxis (GO:0002690)	18	6.06	2.04E-04
cellular response to interleukin-1 (GO:0071347)	31	6.02	2.13E-04
positive regulation of leukocyte migration (GO:0002687)	13	5.96	2.32E-04
negative regulation of apoptotic process (GO:0043066)	70	5.86	2.80E-04
response to cytokine (GO:0034097)	29	5.83	2.92E-04
MyD88-independent toll-like receptor signaling pathway (GO:0002756)	12	5.79	3.05E-04
regulation of intrinsic apoptotic signaling pathway (GO:2001242)	15	5.62	4.35E-04
cellular zinc ion homeostasis (GO:0006882)	12	5.61	4.29E-04
regulation of inflammatory response (GO:0050727)	32	5.50	5.39E-04

Shaded rows represent 50% GO terms shared between Rhesus and human

Table S7. [Rhesus top 30 Wiki pathways based on 257 LPS-induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
Photodynamic therapy-induced NF-kB survival signaling WP3617	11	12.39	1.91E-10
Type II interferon signaling (IFNG) WP619	10	10.58	6.24E-09
miRNAs involvement in the immune response in sepsis WP4329	9	9.12	1.19E-07
EBV LMP1 signaling WP262	7	7.96	1.29E-06
The human immune response to tuberculosis WP4197	7	7.96	1.04E-06
TNF alpha Signaling Pathway WP231	10	6.53	2.32E-05
Non-genomic actions of 1,25 dihydroxyvitamin D3 WP4341	9	6.51	2.08E-05
Vitamin D Receptor Pathway WP2877	13	6.16	4.12E-05
Cytokines and Inflammatory Response WP530	6	6.10	4.13E-05
Toll-like Receptor Signaling Pathway WP75	10	6.07	4.02E-05
Selenium Micronutrient Network WP15	9	5.79	6.92E-05
Regulation of toll-like receptor signaling pathway WP1449	11	5.73	7.35E-05
Thymic Stromal LymphoPoietin (TSLP) Signaling Pathway WP2203	7	5.67	7.85E-05
T-Cell antigen Receptor (TCR) Signaling Pathway WP69	9	5.63	7.99E-05
Vitamin B12 Metabolism WP1533	7	5.48	1.05E-04
Apoptosis-related network due to altered Notch3 in ovarian cancer WP2864	7	5.30	1.46E-04
RIG-I-like Receptor Signaling WP3865	7	4.94	3.20E-04
IL1 and megakaryocytes in obesity WP2865	5	4.93	3.08E-04
Apoptosis WP254	8	4.90	3.11E-04
Nucleotide-binding Oligomerization Domain (NOD) pathway WP1433	6	4.88	3.09E-04
IL-7 Signaling Pathway WP205	5	4.84	3.26E-04
TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway WP2036	6	4.82	3.24E-04
Oncostatin M Signaling Pathway WP2374	7	4.71	4.04E-04
Folate Metabolism WP176	7	4.66	4.28E-04
Prolactin Signaling Pathway WP2037	7	4.26	0.001034078
Platelet-mediated interactions with vascular and circulating cells WP4462	4	4.26	0.001008738
Signal transduction through IL1R WP4496	5	4.22	0.001041671
IL-4 Signaling Pathway WP395	6	4.18	0.001102918
Nuclear Receptors Meta-Pathway WP2882	14	4.15	0.001147749
Hematopoietic Stem Cell Differentiation WP2849	6	4.14	0.001143122

Shaded rows represent 50% Wiki pathways shared between Rhesus and human

Table S8. [Human top 30 Wiki pathways based on 1619 chorioamnionitis induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
Photodynamic therapy-induced NF-kB survival signaling WP3617	20	12.91	5.84E-11
Apoptosis WP254	29	11.23	1.39E-09
miRNAs involvement in the immune response in sepsis WP4329	16	8.12	1.20E-06
TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway WP2036	17	8.06	1.04E-06
Regulation of toll-like receptor signaling pathway WP1449	33	7.89	1.22E-06
Oncostatin M Signaling Pathway WP2374	21	7.73	1.47E-06
TNF alpha Signaling Pathway WP231	25	7.36	2.92E-06
Thymic Stromal Lymphopoietin (TSLP) Signaling Pathway WP2203	17	7.19	3.77E-06
Toll-like Receptor Signaling Pathway WP75	26	6.92	6.26E-06
Senescence and Autophagy in Cancer WP615	26	6.74	8.52E-06
Lung fibrosis WP3624	19	6.52	1.29E-05
TLR4 Signaling and Tolerance WP3851	12	6.18	2.60E-05
Photodynamic therapy-induced AP-1 survival signaling. WP3611	16	5.97	3.85E-05
Mammary gland development pathway - Involution (Stage 4 of 4) WP2815	7	5.67	7.19E-05
Apoptosis Modulation and Signaling WP1772	22	5.62	7.56E-05
RIG-I-like Receptor Signaling WP3865	17	5.48	9.69E-05
IL-4 Signaling Pathway WP395	16	5.48	9.26E-05
EBV LMP1 signaling WP262	10	5.31	1.29E-04
Signal transduction through IL1R WP4496	12	5.28	1.31E-04
Adipogenesis WP236	26	4.88	3.08E-04
Folate Metabolism WP176	17	4.87	3.01E-04
TGF-beta Receptor Signaling WP560	15	4.80	3.44E-04
Toll-like Receptor Signaling WP3858	11	4.77	3.51E-04
Role Altered Glycolysation of MUC1 in Tumour Microenvironment WP4480	6	4.73	3.67E-04
IL-1 signaling pathway WP195	15	4.69	3.85E-04
RAC1/PAK1/p38/MMP2 Pathway WP3303	17	4.69	3.72E-04
Hepatitis C and Hepatocellular Carcinoma WP3646	14	4.67	3.76E-04
Structural Pathway of Interleukin 1 (IL-1) WP2637	14	4.67	3.63E-04
IL-9 Signaling Pathway WP22	8	4.65	3.62E-04
Vitamin D Receptor Pathway WP2877	32	4.64	3.60E-04

Shaded rows represent 50% Wiki pathways shared between Rhesus and human

Table S9. [Rhesus top 30 KEGG pathways based on 257 LPS-induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
TNF signaling pathway	19	15.69	6.31E-14
Cytokine-cytokine receptor interaction	26	13.96	1.68E-12
IL-17 signaling pathway	15	12.04	9.38E-11
NOD-like receptor signaling pathway	19	11.77	1.31E-10
Measles	17	11.60	1.55E-10
Osteoclast differentiation	15	10.03	4.75E-09
Leishmaniasis	12	9.77	7.47E-09
NF-kappa B signaling pathway	13	9.58	1.01E-08
Influenza A	16	9.14	2.49E-08
C-type lectin receptor signaling pathway	13	9.08	2.57E-08
Rheumatoid arthritis	12	8.70	5.64E-08
Chagas disease (American trypanosomiasis)	12	8.07	2.19E-07
Inflammatory bowel disease (IBD)	10	8.00	2.35E-07
JAK-STAT signaling pathway	14	7.62	5.26E-07
Epstein-Barr virus infection	15	7.27	1.11E-06
Tuberculosis	14	7.07	1.62E-06
Legionellosis	8	6.32	8.73E-06
Hematopoietic cell lineage	10	6.31	8.32E-06
Hepatitis C	12	6.10	1.30E-05
Toll-like receptor signaling pathway	10	6.03	1.44E-05
Salmonella infection	9	5.79	2.37E-05
Th17 cell differentiation	9	5.00	1.39E-04
Th1 and Th2 cell differentiation	8	4.61	3.28E-04
Human T-cell leukemia virus 1 infection	12	4.55	3.59E-04
Adipocytokine signaling pathway	7	4.54	3.59E-04
RIG-I-like receptor signaling pathway	7	4.49	3.80E-04
Chemokine signaling pathway	11	4.44	4.17E-04
Malaria	6	4.43	4.11E-04
Necroptosis	10	4.32	5.12E-04
Pathways in cancer	19	4.22	6.15E-04

Shaded rows represent 70% KEGG pathways shared between Rhesus and human

Table S10. [Human top 30 KEGG pathways based on 1619 chorioamnionitis-induced genes], Related to Figure 1.

Term	# of genes	Fold enrichment	adj p-value
TNF signaling pathway	45	20.48	1.02E-18
IL-17 signaling pathway	37	16.48	5.14E-15
Cytokine-cytokine receptor interaction	60	10.78	1.72E-09
NOD-like receptor signaling pathway	43	10.33	3.60E-09
Influenza A	40	9.21	3.81E-08
Epstein-Barr virus infection	45	9.08	4.31E-08
Hepatitis C	37	8.83	6.51E-08
C-type lectin receptor signaling pathway	29	8.72	7.37E-08
Kaposi sarcoma-associated herpesvirus infection	41	8.60	8.63E-08
NF-kappa B signaling pathway	25	7.06	2.66E-06
Measles	31	6.86	3.83E-06
Toll-like receptor signaling pathway	26	6.83	3.77E-06
JAK-STAT signaling pathway	34	6.70	4.70E-06
Hepatitis B	34	6.64	5.09E-06
Human cytomegalovirus infection	41	6.18	1.36E-05
Th17 cell differentiation	25	6.00	1.93E-05
Cellular senescence	32	5.86	2.50E-05
Chagas disease (American trypanosomiasis)	24	5.76	2.96E-05
Necroptosis	32	5.74	2.97E-05
Prostate cancer	23	5.69	3.15E-05
Osteoclast differentiation	27	5.57	3.93E-05
Apoptosis	29	5.50	4.44E-05
Chemokine signaling pathway	35	5.48	4.42E-05
Rheumatoid arthritis	21	5.05	1.14E-04
MAPK signaling pathway	46	4.92	1.47E-04
Small cell lung cancer	21	4.90	1.50E-04
Pathways in cancer	71	4.79	1.85E-04
FoxO signaling pathway	27	4.76	1.90E-04
RIG-I-like receptor signaling pathway	17	4.51	3.27E-04
Human T-cell leukemia virus 1 infection	36	4.48	3.39E-04

Shaded rows represent 70% KEGG pathways shared between Rhesus and human

Table S11. [List of the 73 “TNF-dependent genes”], Related to Figure 2.

CLEC4E	PNP
CCL5	ENSMMUG00000017109
IL1B	ALAS1
CCL4L1	GCH1
NKX3-1	SLCO5A1
CSF3R	CLEC4A
ENSMMUG00000047942	TNFAIP3
S100A9	ICAM1
APOBEC3A	ENSMMUG00000018474
CLEC4D	CCN4
MMP3	RNF207
LTF	AZIN2
TNIP3	MGARP
PLEK	ENSMMUG00000010981
TNF	MGAM
IL18RAP	ARPP21
CAMP	ENSMMUG00000046980
NEURL3	NFKBIA
SLAMF7	ACER1
FAM163B	DHX58
MNP1A	TNNT2
BCL2A1	NFKBIE
GPR84	MYO10
ADORA2A	MEFV
OSM	MXD1
ANKRD33B	SPAG1
RHOH	ARHGEF3
ENSMMUG00000010370	TNIP1
G0S2	NFKB2
ENSMMUG00000019939	ZDHHC9
GK	SLC25A37
MPO	IPCEF1
TNFRSF10C	NOD2
TRAF1	RAB2B
MUC22	LIMK2
MYH11	MTMR7
ADAMTS4	