

Figure S1: A) Relative expression of *cpsA* pneumococcal gene in sucrose control group (C) versus ethanol (EtOH) group in monkey BAL cell pellets at Day 1 post pneumococcal infection. Relative abundance of *cpsA* bacterial gene is compared to relative abundance in macaques bronchial cells by GAPDH. ** p< 0.01.



Figure S2: Expression of genes unrelated to IL-17 at 5 hours post infection. Each circle, square and empty circle represents one mouse. Naïve: uninfected mice, C: control group, EtOH: ethanol group. * P< 0.05, *** P< 0.001, ns: not significant . One-Way ANOVA).

Ethanol group at day1 post pneumococcal infection

Pre Post

46

47

48

Stabilin 1

hypothetical LOC100507341

Asp (abnormal spindle) homolog, microcephaly associated (Drosophila)

1		Small proline-rich protein 1B (cornifin)		Pre	Post
2		Small proline-rich protein 1A			
3		Selectin L	49		Keratin 6C
4		Tumor necrosis factor, alpha-induced protein 6	50		Kinesin family member 4A
5		S100 calcium binding protein A8	51		Kinesin family member 20A
6		Collagen, type X, alpha 1	52		Budding uninhibited by benzimidazoles 1 homolog beta (yeast)
7		Interleukin 8 receptor, alpha	53		Myeloid-associated differentiation marker-like
8		Interleukin 8 receptor, beta	54		Kinesin family member 2C
9		Purinergic receptor P2Y, G-protein coupled, 8	55		SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
10		Dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	56		NDC80 homolog, kinetochore complex component (S. cerevisiae)
11		Nuclear factor (erythroid-derived 2), 45kDa	57		Keratin 6B
12		chemokine (C-X-C motif) receptor 2 pseudogene 1	58		UDP-GlcNAc:betaGal beta-1.3-N-acetylolucosaminyltransferase 6 (core 3 synthase)
13		Interleukin 1 receptor, type II	59		Calcvon neuron-specific vesicular protein
14		G-2 and S-phase expressed 1	60		Chromosome 1 open reading frame 106
15		Formvl peptide receptor 2	61		Chromosome 6 open reading frame 15
16		Transmembrane protein 190	62		5'-nucleotidase domain containing 2
17		Myosin binding protein C, cardiac	63		Cvclin-dependent kinase inhibitor 3
18		Serpin peptidase inhibitor, clade B (ovalbumin), member 10	64		UDP-GlcNAc:betaGal beta-1.3-N-acetylolucosaminyltransferase 8
19		uroplakin 3B–like	65		Interferon-induced protein with tetratricopeptide repeats 1-like
20		Indoleamine 2.3-dioxygenase 1	66		GTPase activating Bap/BanGAP domain-like 4
21		Solute carrier family 2 (facilitated glucose transporter), member 14	67		Kinase suppressor of ras 2
22		Family with sequence similarity 83, member D	68		Keratin 79
23		Keratin 4	69		Lipase, endothelial
24		Peptidyl arginine deiminase, type IV	70		Glycosyltransferase 1 domain containing 1
25		Potassium voltage-gated channel, shaker-related subfamily, member 6	71		Thrombomodulin
26		Chemokine (C-X3-C motif) receptor 1	72		RAD51 homolog (RecA homolog, E, coli) (S, cerevisiae)
27		Centrosomal protein 55kDa	73		Exonuclease 1
28		Baculoviral IAP repeat-containing 5	74		Apolipoprotein B mBNA editing enzyme, catalytic polypeptide-like 3D
29		Peptidase inhibitor 16	75		Svnaptotagmin V
30		Chromosome 9 open reading frame 110	76		Histone cluster 1, H1d
31		Chromosome 15 open reading frame 42	77		Egf-like module containing, mucin-like, hormone receptor-like 3
32		Patched domain containing 2	78		Annexin A8–like 1
33		Ubiguitin-conjugating enzyme E2C	79		Cholineraic receptor, nicotinic, epsilon
34		Chromosome 12 open reading frame 48	80		Chromosome 13 open reading frame 3
35		Ring finger protein, transmembrane 2	81		Pituitary tumor-transforming 1
36		Keratin 13	82		Chromatin licensing and DNA replication factor 1
37		Cell division cycle associated 5	83		PDZ binding kinase
38		G protein-coupled receptor, family C, group 5, member A	84		Hypothetical LOC100130933
39		Forkhead box M1	85		Translocation associated membrane protein 1-like 1
40		Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	86		Hypothetical protein LOC100133039
41		RAS guanyl releasing protein 2 (calcium and DAG-regulated)	87		Solute carrier family 4, sodium bicarbonate cotransporter, member 5
42		Hemoglobin, theta 1	88		potassium inwardly-rectifying channel, subfamily J, member 12
43		Lectin, galactoside-binding, soluble, 7B	89		hypothetical LOC100507167
44		Antigen identified by monoclonal antibody Ki-67			
45		Surfactant protein B	Figure	S3:	: Differentially expressed genes in ethanol g

Figure S3: Differentially expressed genes in ethanol group post pneumococcal infection. Paired t-test (n=3) , p<0.05

Table S1: KEGG pathway in Ethanol group at day1 post pneumococcal infection

		Totals	z-score
Pathway	List	Gene Se	t
Chemokine signaling pathway	4	189	3.71
Chemokine (C-X3-C motif) receptor 1			
Interleukin 8 receptor, alpha			
Interleukin 8 receptor, beta			
RAS guanyl releasing protein 2 (calcium and DAG-reg	gulated)		
Cytokine-cytokine receptor interaction	4	275	2.75
Amoebiasis	2	105	2.40
Cell cycle	2	125	2.09
Epithelial cell signaling in Helicobacter pylori infection	2	68	3.27
African trypanosomiasis	1	35	2.26
Homologous recombination	1	28	2.61
Mismatch repair	1	23	2.94
Mucin type O-Glycan biosynthesis	1	30	2.50



Figure S4: Decreased neutrophil numbers with 1A8 antibody impairs *S. pneumoniae* 19F clearance at 24 hours post infection. C: control group, 1A8: group that received 1A8 antibody 8 hours before infection. Each circle and square represents a mouse. *** P< 0.001 (unpaired t- test)



Figure S5: IL-17 A is highly expressed in cytokine rescue group at 5 hours post infection IL-17 A protein expression was measured in lung homogenates by ELISA at 5 hour post pneumococcal infection. Ethanol group that was rescued with IL23+IL1b and IL17 had higher IL-17A protein levels than control group. *** p<0.001 (One-Way ANOVA)



Figure S6: Alcohol decreases CXCL1 protein expression upon cytokine stimulation in HBE-1 cell line. NS: not stimulated, No EtOH: no ethanol, 100mM: 100mM of ethanol *P< 0.05, **P< 0.01, ns: not significant (One-Way ANOVA)

Table S2: IPA generated canonical pathways enriched in bronchial epithelial samples obtained from rhesus macaques on sucrose-and alcohol-fed diet.

Ingenuity Canonical Pathways Sucrose-fed R. macaques	-log(p-value)	Ratio	z-score	Genes
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	10.6	1.42x10 ⁻¹	2.111	CXCL8 ,OAS1,C5AR1,NLRP3,C3,IL10,TLR8,TLR2,TLR4,CLEC7A,TGFB1, PIK3CG,DDX58,MAPK10,CASP1,PIK3R6,OSM,C3AR1
TREM1 Signaling	8.96	1.73x10 ⁻¹	2.496	CXCL8,TREM1,NLRP3,IL10,TYROBP,TLR8,CD83,FCGR2B,TLR2,TLR4, CXCL3,CASP1,ITGAX
IL-8 Signaling	5.77	8.2x10 ⁻²	2.324	CXCL8 ,HBEGF, CXCR1 ,RHOH,EIF4EBP1,ITGB2,ITGAM, CXCR2 ,PIK3CG, PIK3R6,MAPK10,CYBB,PTGS2,ITGAX,IRAK2
Production of Nitric Oxide an Reactive Oxygen Species in Macrophages	5.16	7.78x10 ⁻²	2.138	SAA4,SPI1,RHOH,APOL1,TLR2,TLR4,PIK3CG,PPP2R2B,PIK3R6, MAPK10,CYBB,S100A8,TNFRSF1B,SIRPA
Ingenuity Canonical Pathways Alcohol-fed R. macaques	-log(p-value)	Ratio	z-score	Genes
EIF2 Signaling	3.57	9.88x10 ⁻²	3.162	RPLP1,RPL3,RPLP2,RPS8,RPLP0,RPS12,PIK3R3,EIF3G,RPL8,RPL28, EIF4A1,RPS9,RPS5,RPL41,RPL13,ATM,RPSA
Gαq Signaling	2.94	9.66x10 ⁻²	1.732	RGS2,RGS18,ADRBK1,CSK,CHP1,GNG2,GNG3,PIK3R3,CALM1 (includes others),RND3,GNB2,PLCB3,PRKCB,ATM
ATM Signaling	2.81	1.36x10 ⁻¹	0.707	RAD51,FANCD2,H2AFX,CREB5,CDK1,CHEK1,CCNB1,ATM

Table S3: Functional Annotation Clustering (DAVID Bioinformatics) in bronchial epithelium of sucrose- fed Rhesus macaques before and after infection with *S. pneumoniae* 19F

Cluster 1	Enrichment Score: 26.42	Number of Genes	P_Value	Benjamini
GOTERM_BP_FAT	defense response	69	6.80E-31	6.80E-28
GOTERM_BP_FAT	inflammatory response	47	2.20E-25	1.50E-22
GOTERM_BP_FAT	response to wounding	58	3.60E-25	1.80E-22
Cluster 2	Enrichment Score: 13.35	Number of Genes	P_Value	Benjamini
SP_PIR_KEYWORDS	disulfide bond	135	5.60E-23	1.90E-20
UP_SEQ_FEATURE	disulfide bond	130	1.10E-21	1.20E-18
UP_SEQ_FEATURE	topological domain:Extracellular	120	2.90E-18	1.60E-15
UP_SEQ_FEATURE	glycosylation site:N-linked	155	1.20E-17	4.20E-15
SP_PIR_KEYWORDS	glycoprotein	158	2.80E-17	3.10E-15
SP_PIR_KEYWORDS	signal	130	2.20E-16	1.80E-14
UP_SEQ_FEATURE	signal peptide	130	2.90E-16	9.00E-14
UP_SEQ_FEATURE	topological domain:Cytoplasmic	126	2.00E-13	4.40E-11
SP_PIR_KEYWORDS	receptor	75	1.60E-12	8.80E-11
SP_PIR_KEYWORDS	membrane	187	8.50E-12	4.00E-10
GOTERM_CC_FAT	plasma membrane	140	3.90E-11	8.60E-09
UP_SEQ_FEATURE	transmembrane region	151	1.30E-09	1.70E-07
SP_PIR_KEYWORDS	transmembrane	151	2.00E-09	7.40E-08
GOTERM_CC_FAT	intrinsic to membrane	168	4.90E-07	5.40E-05
GOTERM_CC_FAT	integral to membrane	158	1.20E-05	5.20E-04
GOTERM_CC_FAT Cluster 3	integral to membrane Enrichment Score: 9.92	158 Number of Genes	1.20E-05 P_Value	5.20E-04 Benjamini
GOTERM_CC_FAT Cluster 3 INTERPRO	integral to membrane Enrichment Score: 9.92 Immunoglobulin subtype	158 Number of Genes 36	1.20E-05 P_Value 1.30E-15	5.20E-04 Benjamini 7.90E-13
GOTERM_CC_FAT Cluster 3 INTERPRO SMART	integral to membrane Enrichment Score: 9.92 Immunoglobulin subtype IG	158Number of Genes3636	1.20E-05 P_Value 1.30E-15 1.20E-13	5.20E-04 Benjamini 7.90E-13 1.70E-11
GOTERM_CC_FAT Cluster 3 INTERPRO SMART SP_PIR_KEYWORDS	integral to membrane Enrichment Score: 9.92 Immunoglobulin subtype IG Immunoglobulin domain	Number of Genes 36 36 39	1.20E-05 P_Value 1.30E-15 1.20E-13 1.60E-13	5.20E-04 Benjamini 7.90E-13 1.70E-11 1.00E-11
GOTERM_CC_FAT Cluster 3 INTERPRO SMART SP_PIR_KEYWORDS INTERPRO	integral to membrane Enrichment Score: 9.92 Immunoglobulin subtype IG Immunoglobulin domain Immunoglobulin	158 Number of Genes 36 36 39 26	1.20E-05 P_Value 1.30E-15 1.20E-13 1.60E-13 5.50E-13	5.20E-04 Benjamini 7.90E-13 1.70E-11 1.00E-11 1.60E-10
GOTERM_CC_FAT Cluster 3 INTERPRO SMART SP_PIR_KEYWORDS INTERPRO INTERPRO	integral to membrane Enrichment Score: 9.92 Immunoglobulin subtype IG Immunoglobulin domain Immunoglobulin Immunoglobulin-like fold	158 Number of Genes 36 36 39 26 42	1.20E-05 P_Value 1.30E-15 1.20E-13 1.60E-13 5.50E-13 9.00E-13	5.20E-04 Benjamini 7.90E-13 1.70E-11 1.00E-11 1.60E-10 1.80E-10
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