

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. ** $p < 0.01$.

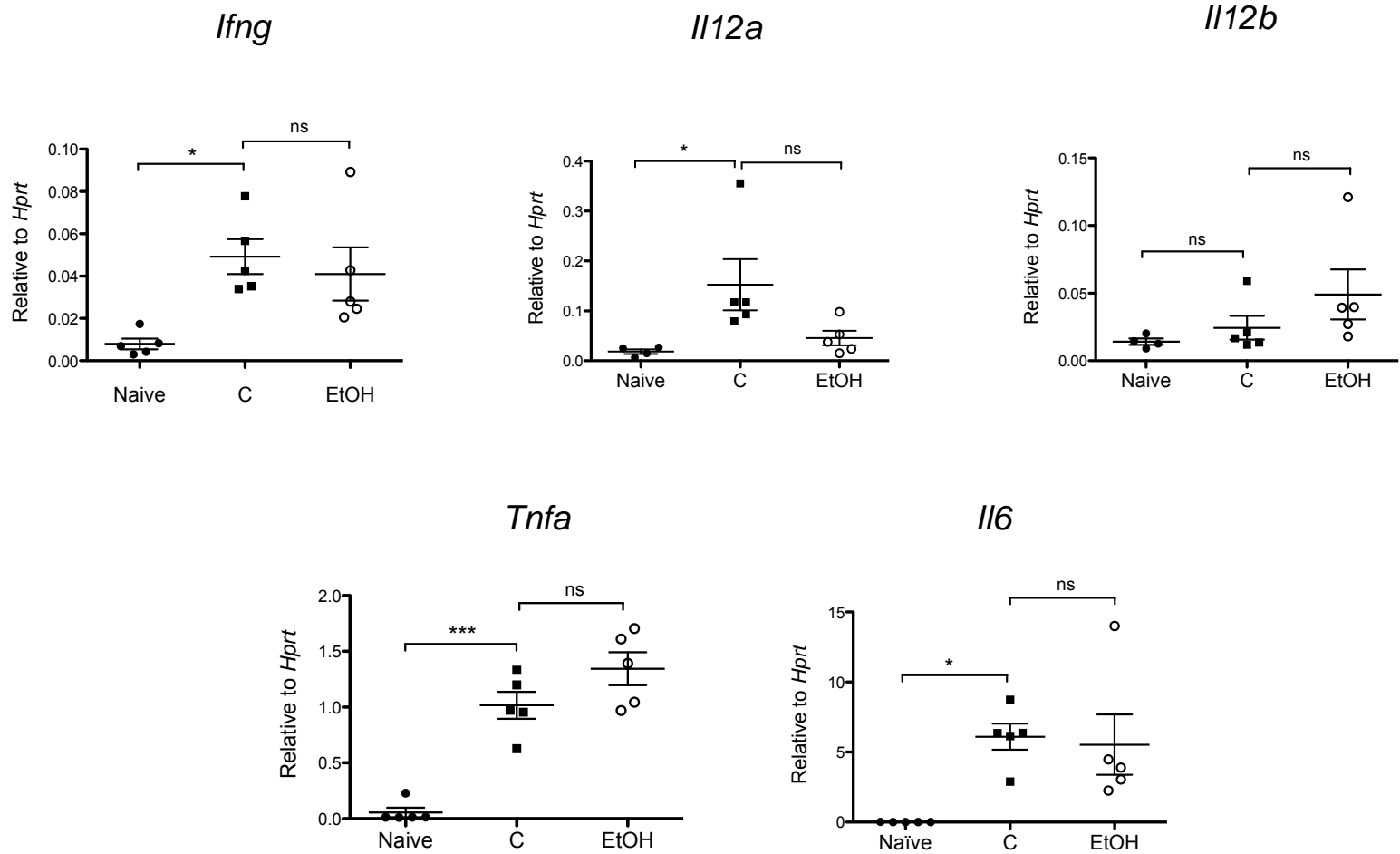


Figure S2: Expression of genes unrelated to IL-17 at 5 hours post infection. Each circle, square and empty circle represents one mouse. Naïve: uninfected mice, C: control group, EtOH: ethanol group. * P < 0.05, *** P < 0.001, ns: not significant . One-Way ANOVA).

Ethanol group at day1 post pneumococcal infection

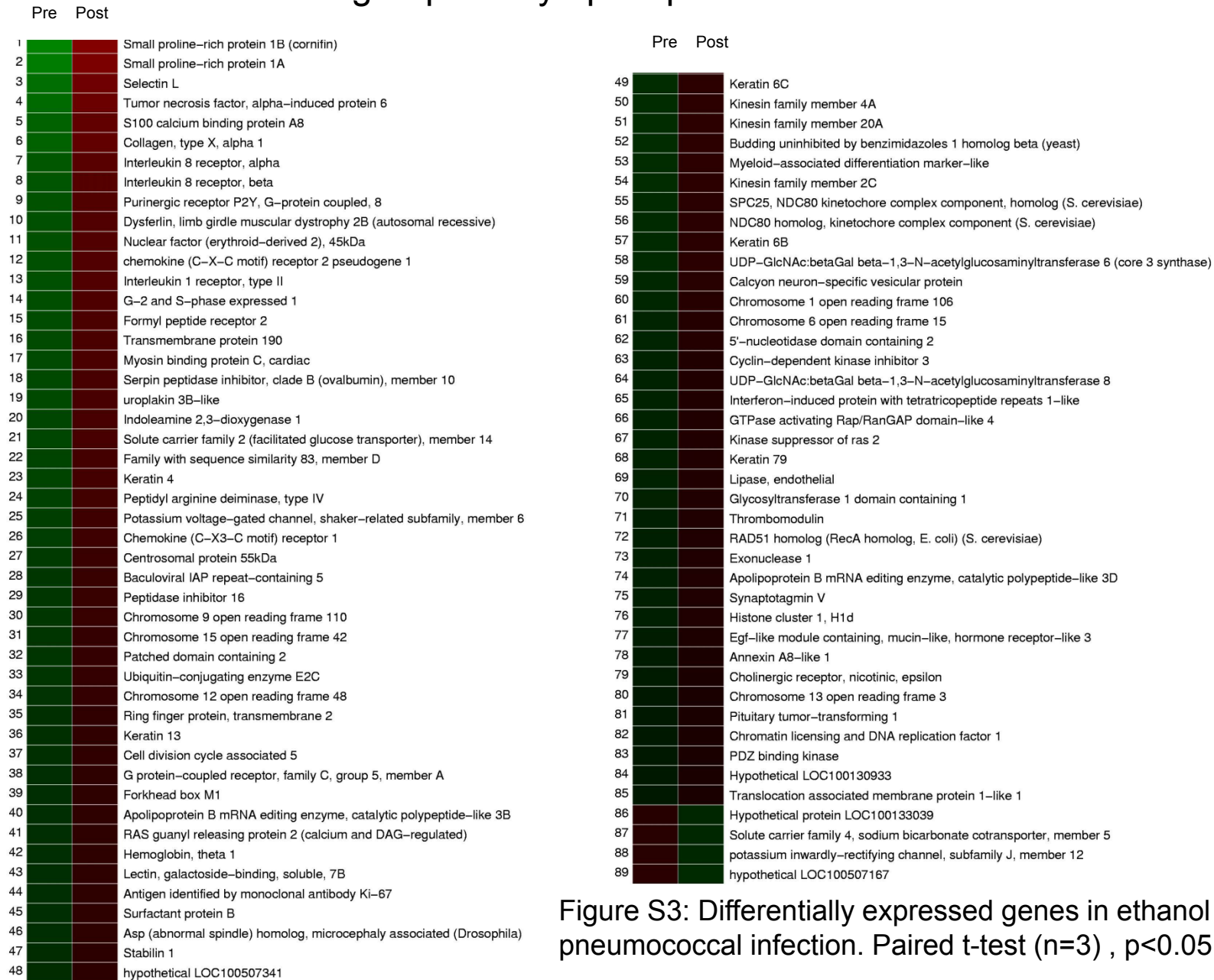


Figure S3: Differentially expressed genes in ethanol group post pneumococcal infection. Paired t-test (n=3) , p<0.05

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

Pathway	List	Totals Gene Set	Z-SCORE
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-regulated)			
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

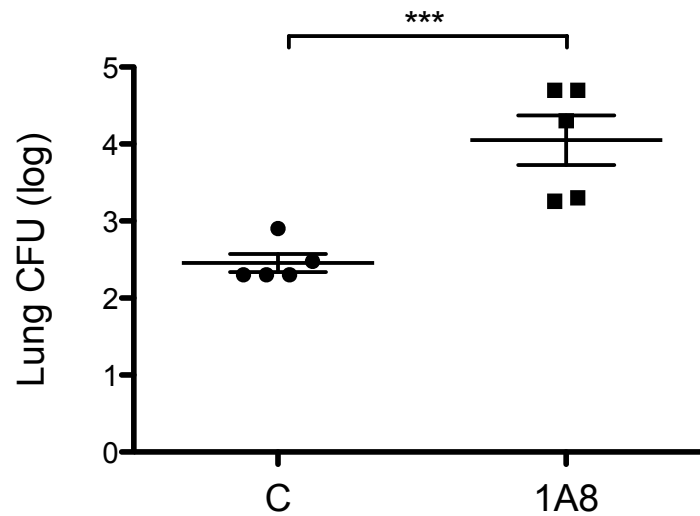


Figure S4: Decreased neutrophil numbers with 1A8 antibody impairs *S. pneumoniae* 19F clearance at 24 hours post infection. C: control group, 1A8: group that received 1A8 antibody 8 hours before infection. Each circle and square represents a mouse. *** $P < 0.001$ (unpaired t- test)

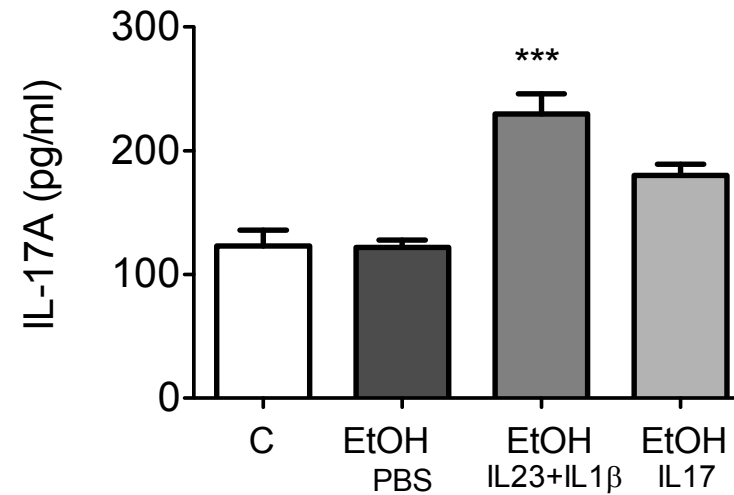


Figure S5: IL-17 A is highly expressed in cytokine rescue group at 5 hours post infection
IL-17 A protein expression was measured in lung homogenates by ELISA at 5 hour post pneumococcal infection. Ethanol group that was rescued with IL23+IL1b and IL17 had higher IL-17A protein levels than control group.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

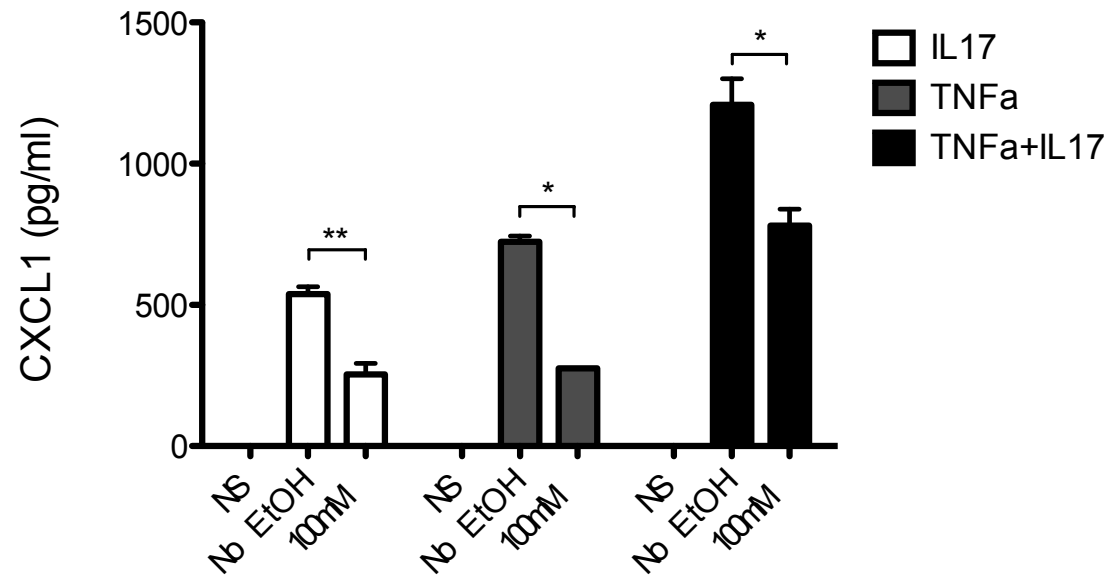



































Figure S6: Alcohol decreases CXCL1 protein expression upon cytokine stimulation in HBE-1 cell line. NS: not stimulated, No EtOH: no ethanol, 100mM: 100mM of ethanol *P< 0.05, **P< 0.01, ns: not significant (One-Way ANOVA)

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
Estrogen-mediated S-phase Entry	2.76	2.08x10 ⁻¹	2.000	CCNA2,CCNE1,TFDP1,CDK4,CDK1

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
Cluster 3	Enrichment Score: 9.92	Number of Genes	P_Value	Benjamini
INTERPRO	Immunoglobulin subtype	 36	1.30E-15	7.90E-13
SMART	IG	 36	1.20E-13	1.70E-11
SP_PIR_KEYWORDS	Immunoglobulin domain	 39	1.60E-13	1.00E-11
INTERPRO	Immunoglobulin	 26	5.50E-13	1.60E-10
INTERPRO	Immunoglobulin-like fold	 42	9.00E-13	1.80E-10
INTERPRO	Immunoglobulin-like	 38	1.40E-11	2.10E-09
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	 22	2.00E-10	3.60E-08
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	 22	2.20E-10	3.40E-08
UP_SEQ_FEATURE	domain:Ig-like V-type	 17	3.10E-09	3.70E-07
INTERPRO	Immunoglobulin V-set	 19	3.90E-06	4.70E-04
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	 13	5.50E-06	5.40E-04
UP_SEQ_FEATURE	domain:Ig-like C2-type 4	 10	1.90E-05	1.40E-03
Cluster 4	Enrichment Score: 9.62	Number of Genes	P_Value	Benjamini
GOTERM_BP_FAT	regulation of cytokine production	 23	3.00E-11	1.00E-08
GOTERM_BP_FAT	positive regulation of cytokine production	 17	5.00E-11	1.40E-08
GOTERM_BP_FAT	positive regulation of multicellular organismal process	 23	9.30E-09	1.70E-06