Cell Reports, Volume *39*

Supplemental information

Mycobacterium tuberculosis infection drives a type I IFN signature in lung lymphocytes

Sadia Akter, Kuldeep S. Chauhan, Micah D. Dunlap, José Alberto Choreño-Parra, Lan Lu, Ekaterina Esaulova, Joaquin Zúñiga, Maxim N. Artyomov, Deepak Kaushal, and Shabaana A. Khader

Supplementary Information

Mycobacterium tuberculosis infection drives a Type I IFN signature in lung lymphocytes

Sadia Akter[1,5], Kuldeep S. Chauhan[1,5], Micah D. Dunlap[1], José Alberto Choreño-Parra[1,2], Lan Lu[1], Ekaterina Esaulova[3], Joaquin Zúñiga[2], Maxim Artyomov[3], Deepak Kaushal[4,*], Shabaana A. Khader[1,6,*]

[1]Department of Molecular Microbiology, Washington University School of Medicine in St. Louis, St. Louis, MO 63110, USA.

[2]Laboratory of Immunobiology and Genetics, Instituto Nacional de Enfermedades Respiratorias "Ismael Cosío Villegas," Mexico City 14080, Mexico; Laboratorio de Inmunoquímica I, Posgrado en Ciencias Quimicobiológicas, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City 07320, Mexico.

[3]Department of Pathology and Immunology, Washington University School of Medicine, St. Louis, MO 63110, USA.

[4]Southwest National Primate Research Center, Texas Biomedical Research Institute, San Antonio, TX 78227, USA.

[5]Equal authorship

[6]Lead Contact

[*]Correspondence: khader@wustl.edu (S.A.K.), dkaushal@txbiomed.org (D. K.)

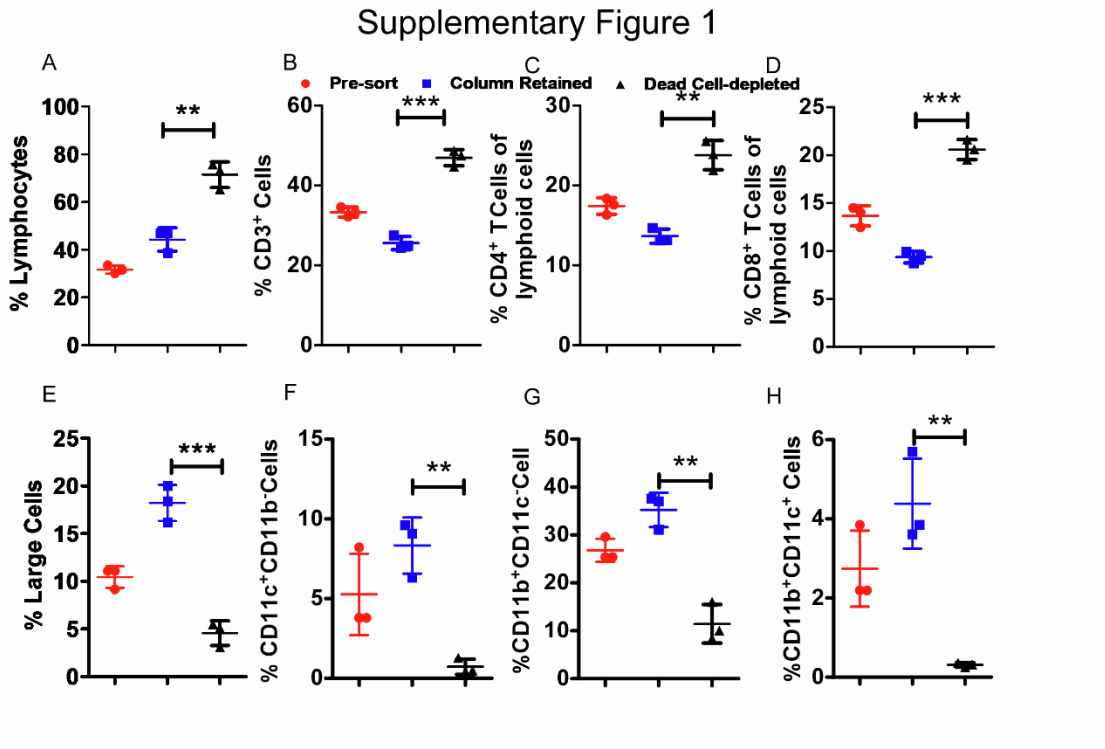


Fig. S1, related to Fig. 1. Enrichment of lymphoid populations post live cells sorting. Dead cells were eliminated from the cells derived from mouse lungs using dead cell removal kit. Frequency of lymphoid cells (A-D) and innate immune cell types (E-H) were determined by flow cytometry. Student's t-test was performed to calculate significance (n=3). Data points represent the mean ± SD of values. *p < 0.05, **p < 0.01, ***p < 0.001, NS = not significant.

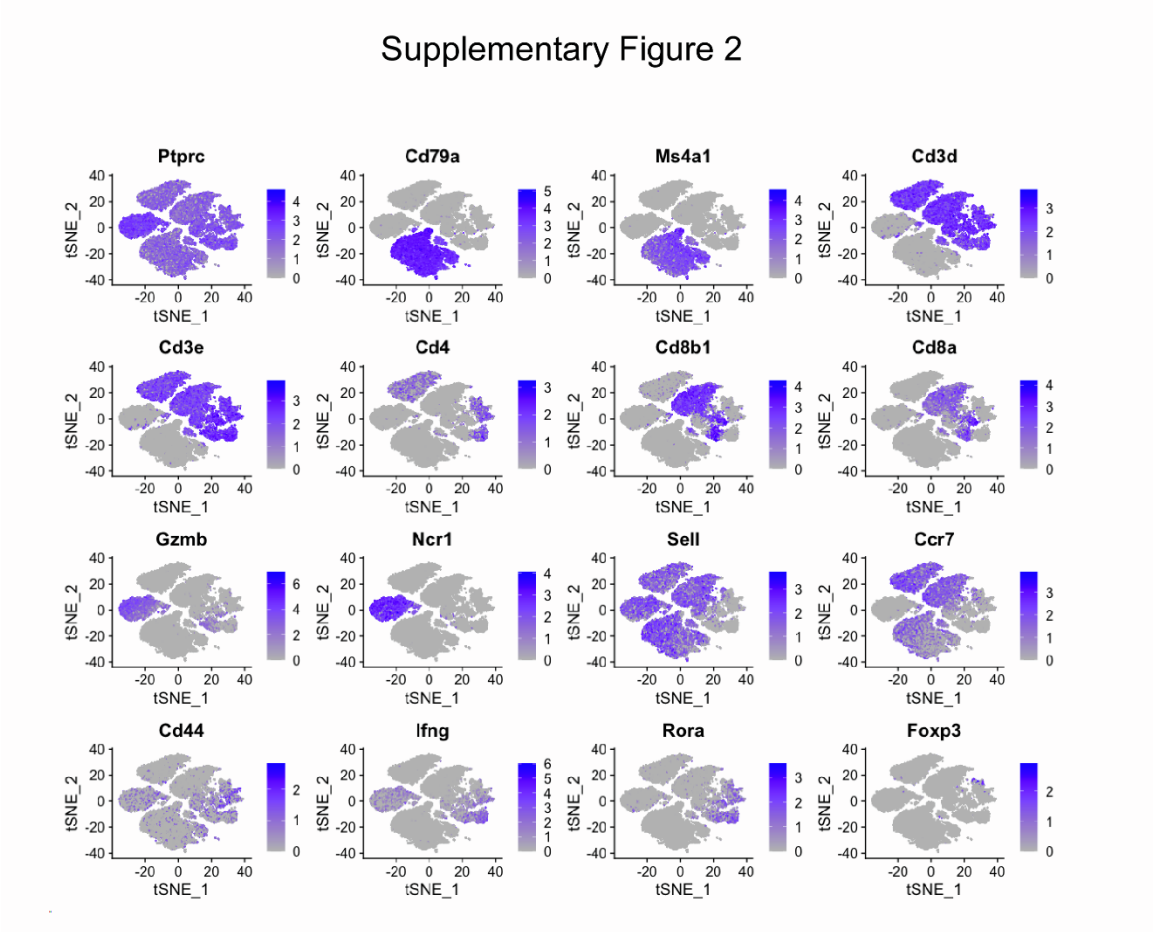
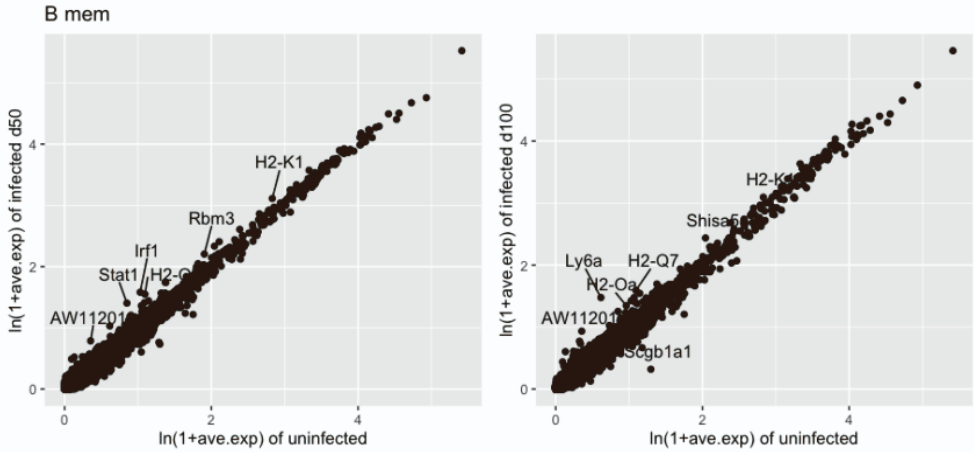


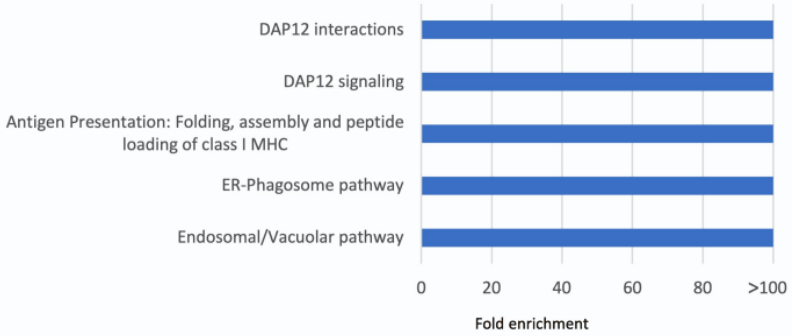
Fig. S2, related to Fig. 1. tSNE plot with the expression of known cell markers. Un, n=2; D50 Inf, n=3; D100 Inf, n=3. The expression of marker genes was used to characterize distinct clusters according to cell identity.

Supplementary Figure 3

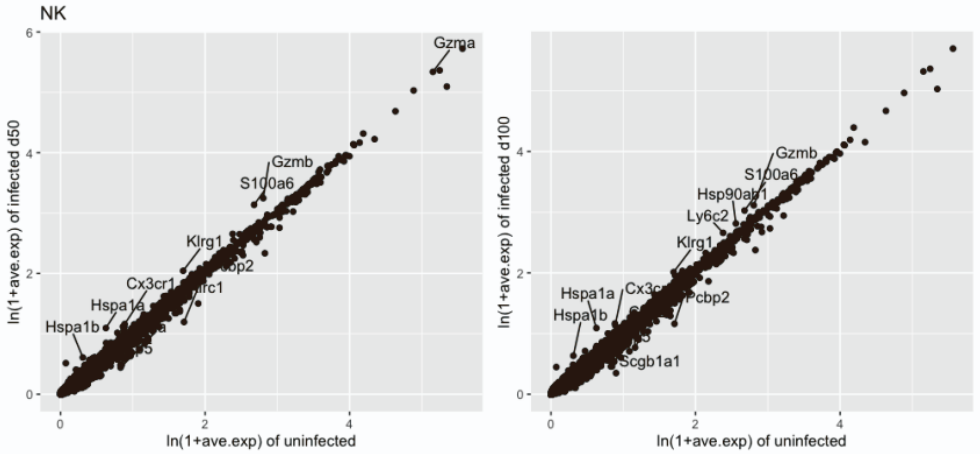
A



B



C



D

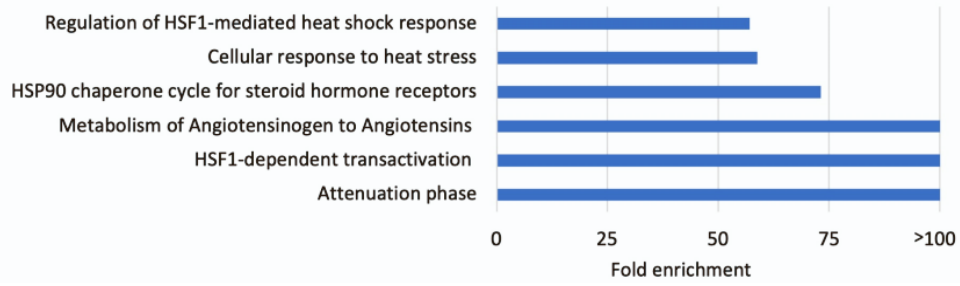


Fig. S3, related to Fig. 3-4: Transcriptional analysis of B mem and NK cell clusters.

(A) Scatterplots depicting the comparison of average expression of genes in infected (50/100 dpi) versus uninfected samples in ***B mem*** cluster, where each dot represents a gene. Top DEGs are highlighted. Adjusted p-value $\leq$ 0.05. (B) Statistical over-representation test was performed with reactome pathways as annotation set. Top over-represented pathways in *Mtb-infected* mice lungs at 50 dpi with respective fold enrichment in ***B mem*** cluster. FDR <0.05. (C) Scatterplots depicting the comparison of average expression of genes in infected (50/100 dpi) versus uninfected samples in ***NK*** cluster. Each dot represents a gene, highlighting the top DEGs. Adjusted p-value $\leq$ 0.05. Each dot represents a gene. (D) Top over-represented reactome pathways in *Mtb-infected* mice lungs at 100 dpi with respective fold enrichment in ***NK*** cluster. FDR <0.05.

Table S1, related to Fig. 3-4: Common DEGs across three *CD4⁺ T* clusters (*CD4⁺ T naïve, CD4⁺ T IFN⁺* and *CD4⁺ T act1*) in *Mtb*-infected (50/100 dpi) versus uninfected samples.

Infected lungs at 50 dpi vs uninfected		**Infected lungs at 100 dpi vs uninfected**	
Common in *CD4⁺T act1* and *CD4⁺T naive*	Common in *CD4⁺T act1* and *CD4⁺T IFN*	Common in *CD4⁺T act1* and *CD4⁺T naive*	Common in *CD4⁺T act1* and *CD4⁺T IFN*
Klf3	Klf2	Ppp1r15a	Klf2
Foxp1	H2-K1	Hbb-bs	Rps29
H2-Q7	B2m	Foxp1	H2-D1
Sesn1	H2-D1	Sesn1	Tagap
Srsf6	Rasgrp2	Lgals1	Pnrc1
Ly6a	Pnrc1	Actg1	AW112010
AW112010	Limd2	1110008F13Rik	Ly6a
Stat1	Tapbp	Tsc22d3	H2-K1
Psmb8	Crlf3	Nr4a1	Rpl35a
Igtp	Psmb10	Fam101b	Klf3
Ppp1r15a	Ly6a	Foxo1	Psmb8
Pcbp2	AW112010	Pdcd4	B2m
Ifi47	Stat1	AW112010	Stat1
Psmb9	Psmb8	Ly6a	Scgb1a1
Gbp2	Igtp	H2-K1	Pcbp2
Tgtp2	Ppp1r15a	Rpl35a	Limd2
Psme1	Pcbp2	Klf3	Igtp
Psme2	Ifi47	Psmb8	H2-Q7
Socs3	Psmb9	B2m	Ifi47
Zbp1	Gbp2	Stat1	Psmb9
Tgtp1	Tgtp2	Scgb1a1	Psme2
Irgm1	Psme1	Pcbp2	Gbp2
1110008F13Rik	Psme2	Limd2	Foxn3
	Socs3	Igtp	Zfp36l2
	Zbp1	H2-Q7	Tgtp2
	Tgtp1	Ifi47	Socs3
	Irgm1	Psmb9	Tgtp1
	1110008F13Rik	Psme2	Psmb10
		Gbp2	
		Foxn3	
		Zfp36l2	
		Tgtp2	
		Socs3	
		Tgtp1	
		Psmb10	

Table S2, related to Fig. 3-4: Common DEGs across three *CD8⁺ T* clusters (*CD8⁺ T naïve, CD8⁺ T eff* and *CD8⁺ T act2*) in *Mtb*-infected (50/100 dpi) versus uninfected samples.

Infected lungs at 50 dpi vs uninfected mice			**Infected lungs at 100 dpi vs uninfected mice**	
CD8⁺T naïve and *CD8⁺T eff*		*CD8⁺T naïve* and *CD8⁺T act2*	*CD8⁺T naïve* and *CD8⁺T eff*	*CD8⁺T naïve* and *CD8⁺T act2*
Ly6a	Tmed2	Ly6a	Ly6a	Ly6a
Stat1	Plac8	Stat1	Rpl35a	Rpl35a
Rpl35a	Tprgl	Rpl35a	Stat1	Stat1
Pcbp2	Ly6e	Pcbp2	Pcbp2	Pcbp2
AW112010	Mrpl52	AW112010	Scgb1a1	Scgb1a1
Klf3	Macf1	Klf3	AW112010	AW112010
H2-K1	Ucp2	H2-K1	Psmb8	Psmb8
Cd52	Tagap	Cd52	H2-K1	H2-K1
Klf2	Crlf3	Klf2	Klf3	Klf3
H2-Q7	Ets1	H2-Q7	Hbb-bs	Hbb-bs
Atp1b1	Gadd45g	Atp1b1	H2-Q7	H2-Q7
Actn1	Rac1	Actn1	Atp1b1	Atp1b1
Sesn1	Cd7	Sesn1	Tmem108	Tmem108
Itga4	Txnip	Itga4	Tprgl	Tprgl
Vim		Vim	Ppp1r15a	Ppp1r15a
Igtp		Psmb8	Igtp	Sesn1
Irf1		Ccr9	Psme2	Smc4
Tgtp1		Smc4	B2m	Ccr9
B2m		Fam101b	Pla2g16	Tagap
Psme1		Foxp1	Pdcd4	Fam101b
Psme2			1110008F13Rik	
Pdcd4			Zfp36l2	
Il7r			Txnip	
Zbp1			Anp32b	
Tapbp			Ucp2	
Anp32b			Tapbp	
Actg1			Rac1	
1110008F13Rik			Itga4	
Socs3			Crlf3	