Supplemental Figure 1. *S. mansoni* co-infection leads to increased lung pathology during TB. *S. mansoni*-infected or control Yarg mice were either left untreated or aerosol infected with *Mtb*. (A) On day 30 post infection, pulmonary inflammation in *Mtb*-infected (*Mtb*) or co-infected (*Mtb*+*Sm*) mice was assessed on formalin-fixed, paraffin embedded (FFPE) lung sections stained with H&E. Upper panel, 200X magnification, lower panel, 400X magnification (B) Additional FFPE lung sections from uninfected (Un), *S. mansoni* (*Sm*)-infected, *Mtb*-infected or co-infected mice were stained with H&E. Total area occupied by inflammatory lesions per lobe was quantified. (C) Arginase-1 reporter expression in lung macrophages was determined by flow cytometry. (D) FFPE sections from co-infected mice underwent immunofluorescence staining using antibodies specific for arginase-1, CD3, B220, Epx and Gr1. (E) Arginase-1 reporter expression in different myeloid cell populations in lungs of *Mtb*-infected and co-infected mice was determined using flow cytometry. Macrophages were gated as $F4/80^{+}CD11c^{+}$; neutrophils as $CD11b^{+}Gr\text{-}1^{+}$; eosinophils were $SSC^{hi}Siglec\text{-}F^{+}CD11b^{+}$; B cells were $SSC^{lo}FSC^{lo}B220^{+}$; T cells were $SSC^{lo}FSC^{lo}CD3^{+}$. (F) Lung macrophages and neutrophils were sorted from lungs of co-infected mice and *Arg1* mRNA expression was assessed by RT-PCR and expression relative to *Gapdh* expression shown. n=4-5 mice. Lungs from all mice were included in the analysis, one representative image per group is shown. *p≤0.05, ***p≤0.001, ND- not detectable, one-way ANOVA with post-hoc Tukey (B,C, E), unpaired, two-tailed Student's *t*-test (F).

Supplemental Figure 2. Praziquantel treatment of *Mtb-S. mansoni* co-infected mice reduces *Schistosoma* egg burden and leads to decreased lung pathology upon *Mtb* infection. *S. mansoni*-infected (*Mtb*+*Sm*) or control C57BL/6 mice (*Mtb*) were infected with *Mtb* and treated with praziquantel (*Mtb*+*Sm*+PZQ) or PBS. (A) Liver *Schistosoma* egg burden was determined. (B) FFPE sections were processed for collagen deposition analysis using Gomori's Trichrome stain. 100X magnification. (C) FFPE sections were processed for immunofluorescence using antibodies for Muc5AC. 100X magnification. (D) Mucus and

glycogen accumulation were evaluated by the PAS stain. 100X magnification. Arrows indicate areas of positive staining. n=4-5 mice per group, one representative image per group is shown. *p≤0.05, one-way ANOVA with post-hoc Tukey (A), ND-not detectable.

Supplemental Figure 3. Depletion of Arginase-1 in macrophages using the *Tie2*^{cre} or *LysM*^{cre} deleter strains. Immunoblots from BMDMs stimulated with IL-4 and IL-10 from either individual *Arg1*$^{flox/flox}$ (WT) or *Tie2*^{Cre} *Arg1*$^{flox/flox}$ mice (A) or individual *Arg1*$^{flox/flox}$ (WT) or *LysM*^{Cre} *Arg1*$^{flox/flox}$ mice (B). Lysates were prepared from BMDMs and arginase-1 protein expression was measured in independent experiments. GRB2 was used as a loading control on each immunoblot.

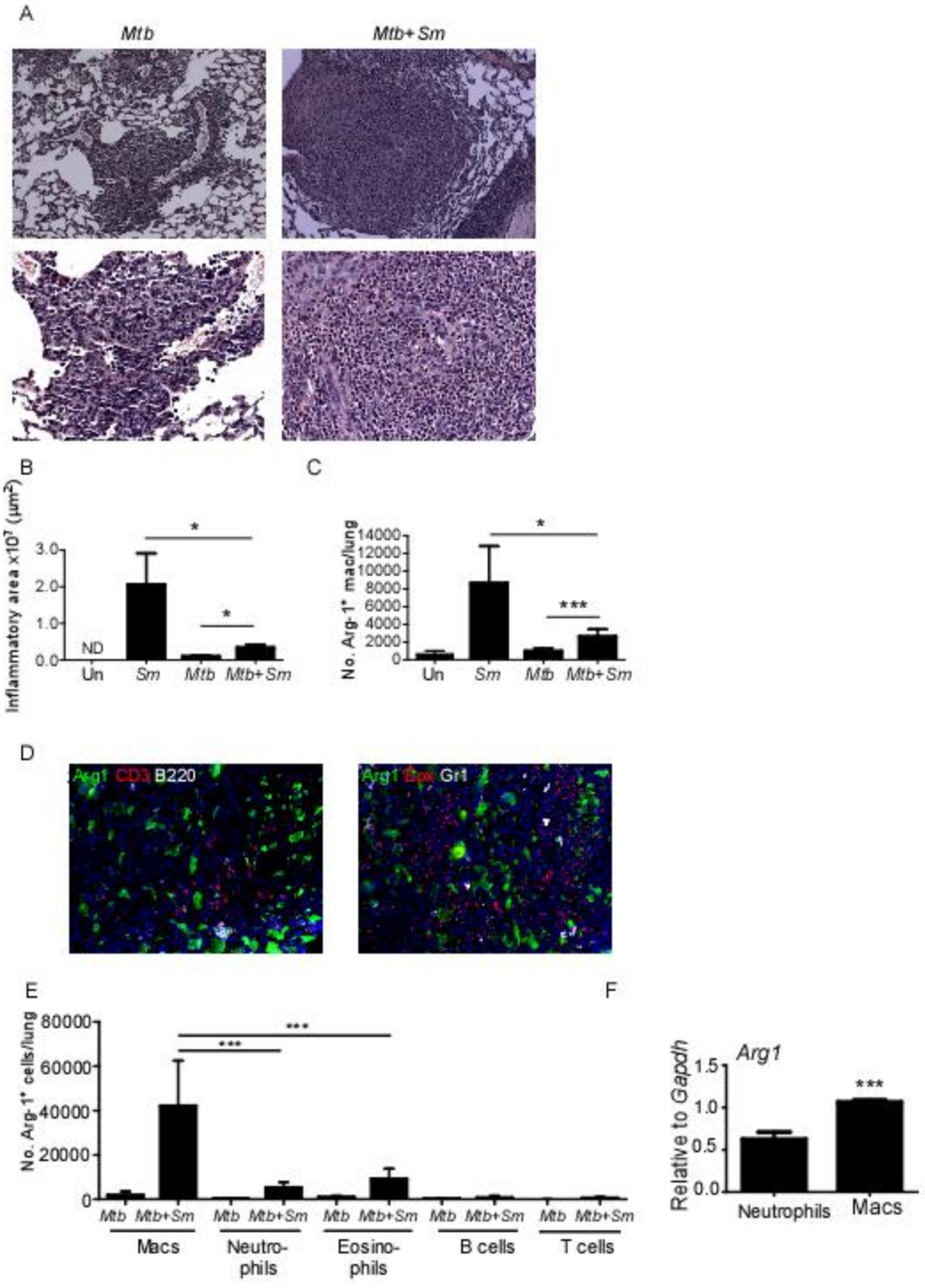
Supplemental Figure 4. *LysM*^{Cre} *Arg1*$^{flox/flox}$ BMC co-infected mice have reduced lung pathology upon co-infection. WT BMC or *LysM*^{Cre} *Arg1*$^{flox/flox}$ BMC mice were *S. mansoni-Mtb*-co-infected (*Mtb*+*Sm*) or infected with *Mtb* alone (*Mtb*). (A) On D25 post-infection, lung bacterial burden was determined by plating. (B) Pulmonary inflammation was assessed on FFPE lung sections stained with H&E. 100X magnification. (C) Total area occupied by inflammatory lesions per lobe was quantified. (D) FFPE sections were processed for immunofluorescence using antibodies for B220 and CD3. 200X magnification. The average size of B cell follicles within granulomas was determined. (E) The average area of perivascular T cell cuffing in B220 and CD3-stained sections was calculated. (F) FFPE sections were stained with antibodies specific for arginase-1, iNOS and F4/80. 200X magnification. The number of high arginase-1-expressing F4/80^{+} cells per 200X field was determined. n=5-10 mice per group. Lungs of all mice were included in the analysis, one representative image per group is shown. *p≤0.05, **p≤0.01, ***p≤0.001, ns-not significant. One-way ANOVA with post-hoc Tukey (A,C), unpaired, two-tailed Student's *t*-test (D-F).

Supplemental Figure 5. PPD and BSA immunization of *Mtb*-infected mice does not exacerbate lung inflammation and *Mtb* control. C57BL/6 mice were aerosol infected with *Mtb* and immunized with saline (*Mtb*), PPD (*Mtb*+PPD) or BSA (*Mtb*+BSA). (A) Pulmonary inflammation was assessed on D30 post-infection on H&E stained FFPE lung sections. 50X magnification for H&E sections. (B) Total area occupied by inflammatory lesions per lobe was

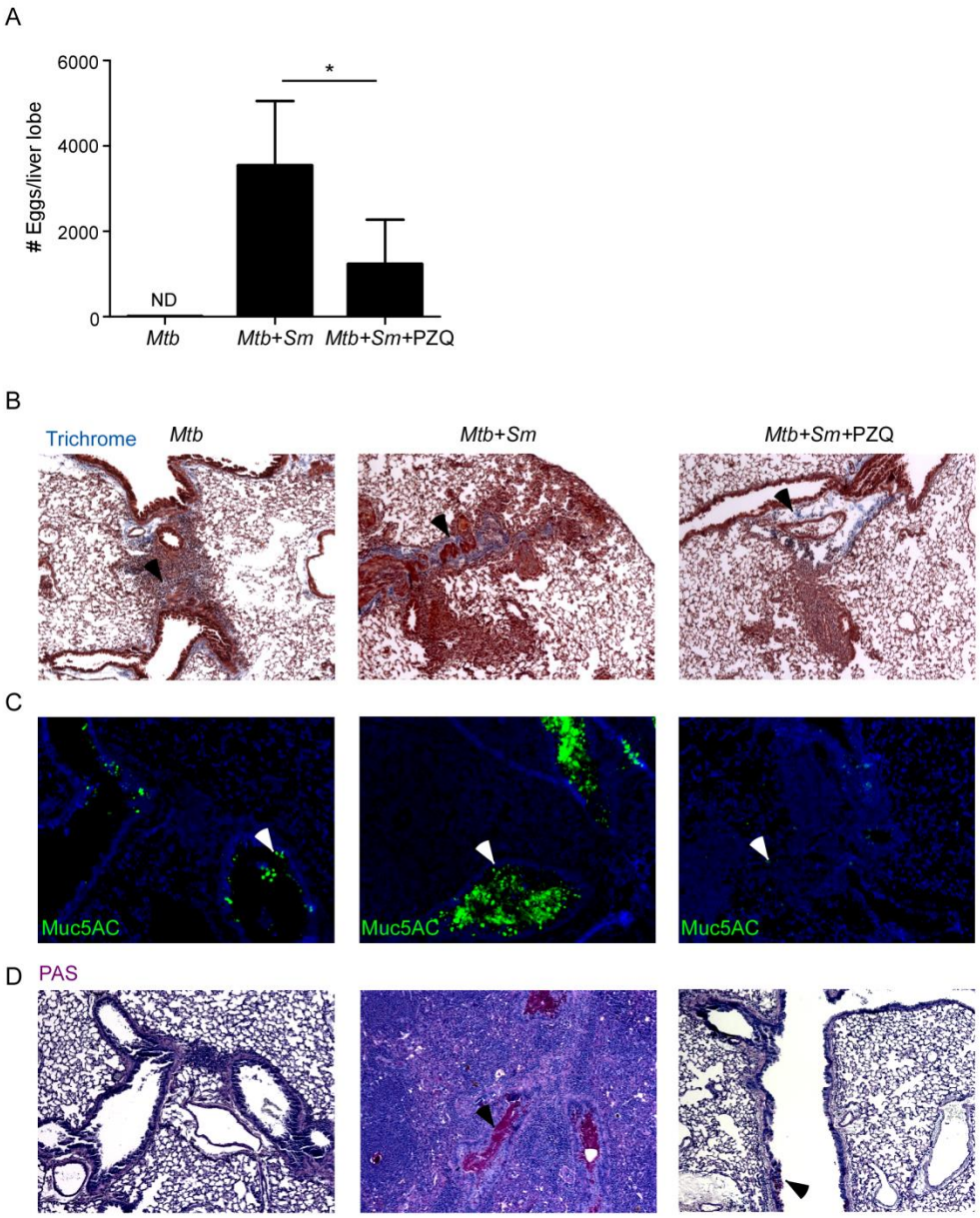
quantified. (C) Lung bacterial burden was determined on D30 post-infection. n=5 mice per group. Lungs from all mice were included in the analysis, one representative image per group is shown. *p≤0.05, **p≤0.01, ns-not significant, one-way ANOVA with post-hoc Tukey (B,C).

Supplemental Figure 6. Impairment of Th1 responses in SEA treated Th cells is reversible. C57BL/6 mice were aerosol infected with *Mtb* and pulmonary $CD4^+$ T cells were purified on D30 post-infection. Cells were then incubated for 6 days, alone (*Mtb*) or in the presence of SEA (*Mtb*+SEA) along with APCs. Cells were washed multiple times and restimulated for 48h with irradiated splenocytes and ESAT-6_{1-20} peptide and then layered over *Mtb*-infected alveolar macrophages (MOI 1:1) for 6 days. Alveolar macrophages that did not contain T cells (-) and alveolar macrophages incubated with T cells isolated from uninfected mice were included as controls (Un). (A) Culture supernatants were assessed to determine IFN-γ levels and (B) nitrite production by macrophages was determined using the Griess reaction. (C) At the end of the culture period, macrophages were washed, lysed and intracellular *Mtb* burden determined by plating. n=4-6 samples. *p≤0.05, ***p≤0.001, ****p≤0.0001, ns-not significant, one-way ANOVA with post-hoc Tukey (A-C).

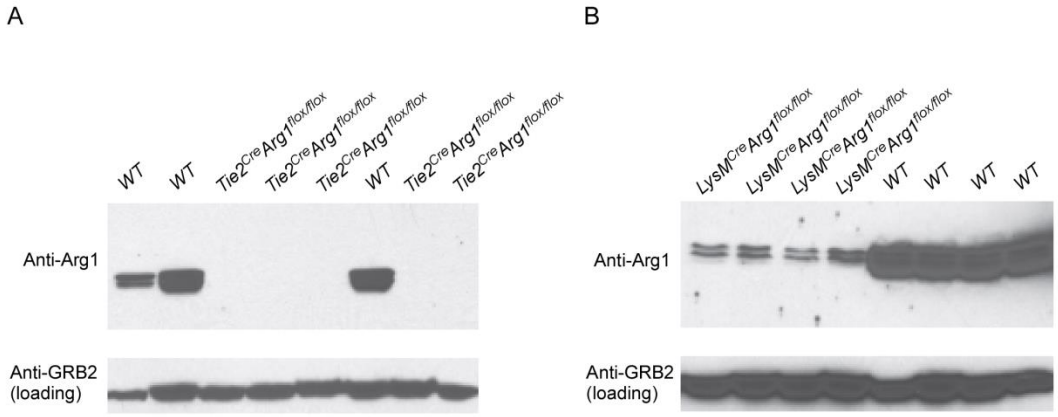
Supplemental Figure 7. SEA treatment increases TB reactivation in mice. C57BL/6 mice were aerosol infected with *Mtb* for 30 days, and were subsequently treated with rifampicin and isoniazid in the drinking water for 6 weeks. 2 and 4 weeks after antibiotic treatment cessation, mice were immunized with SEA (*Mtb*+SEA) or saline (*Mtb*) and lungs and spleen were harvested 2 weeks later. Lung and spleen bacterial burden were determined by plating on 7H11 agar plates. n=7 mice per group. *p≤0.05, **p≤0.01, unpaired, two-tailed Student's *t*-test.



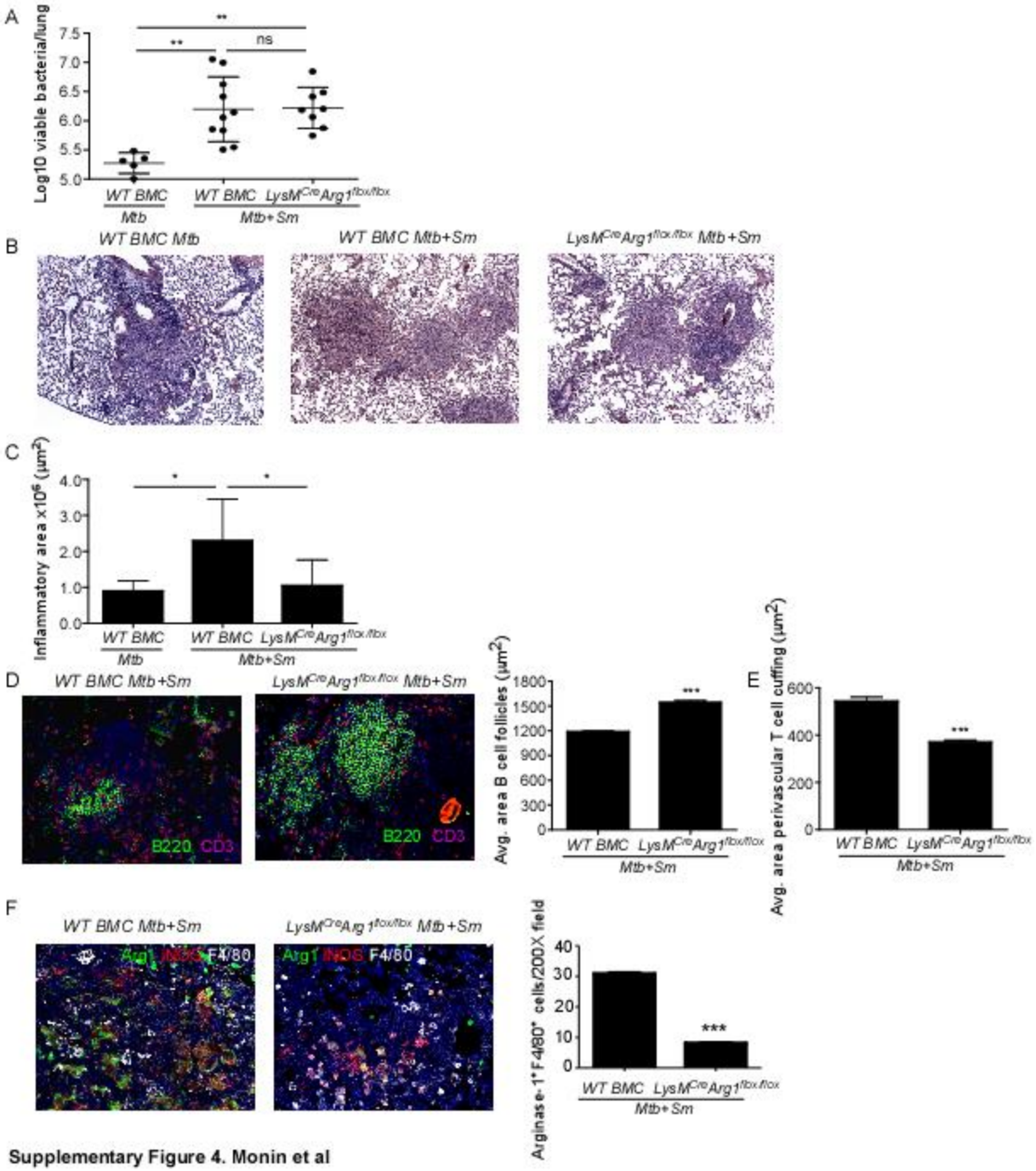
Supplementary Figure 1. Monin et al



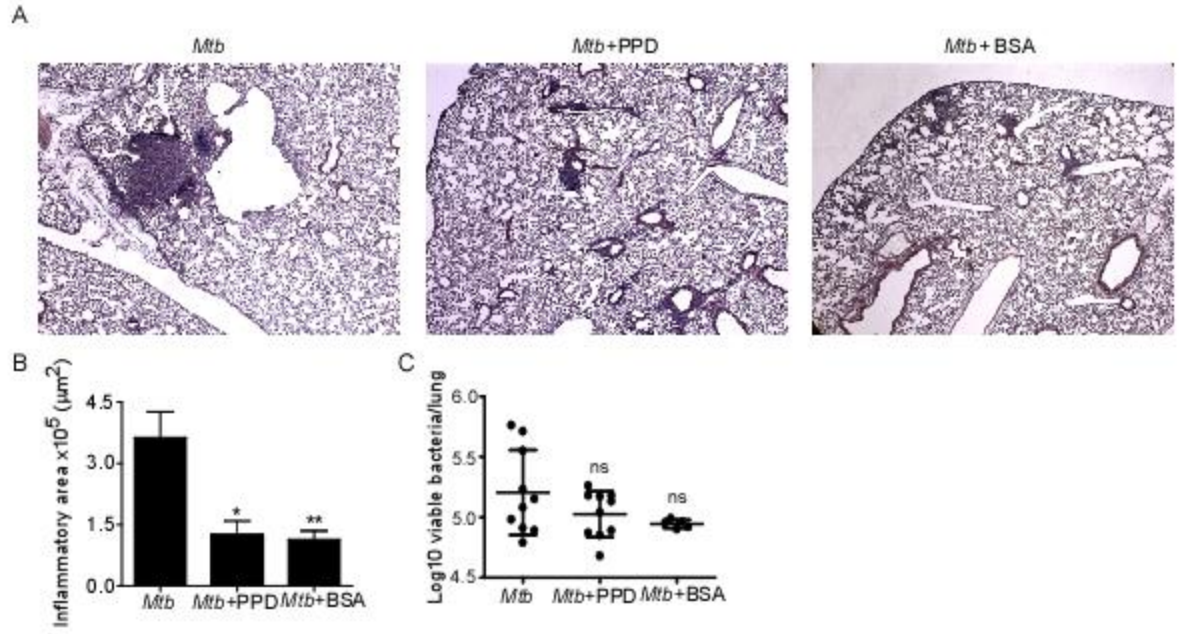
Supplementary Figure 2. Monin et al



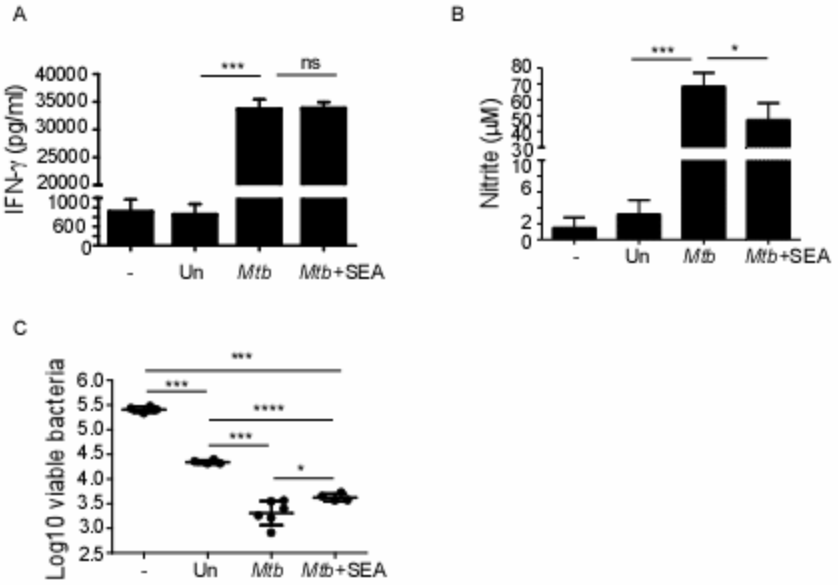
Supplementary Figure 3. Monin et al



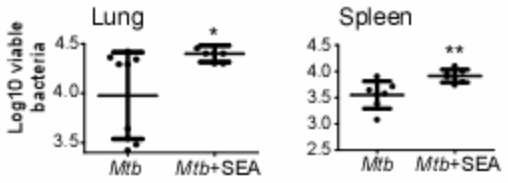
Supplementary Figure 4. Monin et al



Supplementary Figure 5. Monin et al



Supplementary Figure 6. Monin et al



Supplementary Figure 7. Monin et al

Gene	Uninfected 1	Uninfected 2	Uninfected 3	Infected 1	Infected 2	Infected 3	Fold Change	edgeR	DESeq	baySeq
IFNG	95.9	261	281	3700	2810	2620	14.3	3.18E-34	6.14E-25	0.000025
IL12RB1	86.5	139	106	501	568	517	4.79	1.26E-34	8.01E-24	2.18E-06
IL12RB2	71.5	56.5	60.1	395	320	301	5.4	6.74E-32	1.42E-19	1.78E-06
STAT1	32.9	21.9	27.3	102	94	96.9	3.57	8.17E-12	2.9E-06	2.56E-05
TNF	4.7	1.82	12	73.2	86.4	82.5	13	1.73E-22	3.36E-13	8.97E-06
IL1A	57.4	149	102	1110	870	897	9.32	2.36E-39	2.52E-35	5.6E-06
GATA3	638	458	447	79	71.7	75.3	-6.83	2.69E-40	8.3E-14	1.1E-06
IL4RA	3320	3550	2980	1940	2280	2080	-1.56	3E-05	0.00488	0.00542
IL13RA1	532	645	529	1430	1240	1370	2.36	3.7E-16	3.7E-10	2.1E-05
IL17A	4.7	9.11	4.01	13.5	4.9	3.2	1.21	0.837	0.957	0.23
RORC	70.5	72.9	79.4	30.8	14.7	17.6	-3.53	4.97E-10	1.37E-06	0.000117
IL17RA	3630	2210	2110	842	906	907	-2.99	1.75E-13	0.00157	7.57E-05
IL-6RA	2140	1180	1130	272	387	411	-4.17	1.58E-15	0.00241	0.000816
IL21	0	0	3.21	19.3	9.36	14.4	13.4	3.09E-06	0.00607	0.00356
IL10	4.7	10.9	8.02	63.6	61.5	61.6	7.89	4.5E-17	2.14E-09	5.38E-06
TGFB1	1600	1450	1100	1240	1660	1480	1.06	0.732	0.501	0.305
CCL4	56.4	164	192	3830	3840	3490	27.1	7.07E-47	8.6E-110	6.05E-07
CCL7	30.1	31	42.5	1410	767	821	29	3.52E-69	9.38E-10	9.08E-07
CXCL3	5.64	1.82	9.62	214	148	138	29.2	2.28E-39	1.8E-16	3.14E-06
CXCL9	16.9	23.7	24.1	1780	1540	1510	74.8	7.97E-179	6.30E-127	2.31E-09
CXCL10	23.5	56.5	48.9	1810	1400	1150	33.8	2.83E-87	1.53E-25	1.14E-06

Supplementary Table 1. Induction of genes associated with Th1 cell function in CD4+ T cells during *M. tuberculosis* infection.

Gene	Infected 1	Infected 2	Infected 3	Infected+SEA 1	Infected+SEA 2	Infected+SEA 3	Fold Change	edgeR	DESeq	baySeq
Top 20 downregulated genes										
KLRC1	36.7	33.6	47.1	1.01	0	0	-116	2.13E-24	3.72E-15	0.000353
CCL1	316	263	367	4.05	1.4	3.49	-106	5.46E-114	6.33E-53	4.53E-07
IFNG	4400	3370	3150	38.5	43.5	36.1	-92.5	0	2.38E-54	3.84E-13
THEMIS	273	249	265	2.03	2.1	4.66	-89.5	9.08E-133	4.88E-94	2.57E-08
RGS16	1160	1310	1120	22.3	14.7	5.82	-83.8	0	1.39E-191	3.07E-08
CXCR6	2320	2110	2210	37.5	23.8	31.4	-71.6	0	0	7.12E-12
KLRC2	11.5	15.5	22.1	0	0.701	0	-70	5.99E-11	6.92E-06	0.00735
GZMC	22.9	34.7	10.6	1.01	0	0	-67.3	1.27E-09	1.34E-04	0.0518
TRAT1	57.3	39	43.3	1.01	0	1.16	-64.1	4.51E-25	1.23E-16	1.58E-04
LCK	22.9	26.7	29.8	0	1.4	0	-56.6	2.61E-17	3.02E-09	6.63E-04
APOL7E	91.6	66.7	70.2	3.04	1.4	0	-51.5	1.57E-39	6.47E-26	2.08E-05
CD40LG	156	106	105	2.03	2.81	2.33	-51.2	1.82E-51	7.97E-21	1.18E-06
CCR8	36.7	28.3	35.6	2.03	0	0	-49.6	3.93E-19	1.2E-11	0.000532
B4GALNT4	199	245	226	5.06	3.51	5.82	-46.6	6.82E-101	5.18E-77	2.19E-08
MMP3	1050	4.27	377	21.3	4.91	4.66	-46.5	1.13E-07	2.18E-01	1.04E-06
FASL	128	115	114	6.08	3.51	0	-37.2	1.01E-59	1.45E-38	5.51E-07
CD5	559	629	631	18.2	12.6	19.8	-35.9	5.47E-213	1.92E-169	2.88E-09
MS4A4B	1630	1460	1480	48.6	37.9	43.1	-35.2	0	2.58E-308	1.28E-10
ICOS	887	734	797	26.3	21.7	21	-35	3.58E-231	4.64E-126	8.72E-09
IL18RAP	314	288	270	12.2	6.31	6.99	-34.3	1.87E-119	1.52E-88	1.78E-08
Top 20 upregulated genes										
NOTCH3	4.58	5.87	4.81	39.5	21.7	24.5	5.61	4.23E-07	4.33E-04	2.30E-03
MOSPD4	0	4.27	2.89	11.1	11.9	15.1	5.34	3.99E-04	1.16E-01	2.89E-02
SLC32A1	4.58	9.61	3.85	23.3	40	28	5.06	1.41E-06	5.86E-04	5.18E-03
RPPH1	0	11.7	4.81	25.3	28.8	25.6	4.81	1.55E-05	1.29E-02	6.24E-03
BFSP2	2.29	3.2	3.85	9.11	21	11.6	4.47	2.39E-03	4.03E-02	6.41E-02
VPREB3	11.5	16	9.62	47.6	49.1	43.1	3.77	3.24E-09	1.39E-04	5.08E-04
TECTA	6.87	8.54	0.962	17.2	27.4	16.3	3.72	1.54E-03	2.43E-02	5.35E-02
MYH14	6.87	2.67	2.89	21.3	11.2	11.6	3.55	4.44E-03	4.37E-02	5.40E-02
DUSP13	4.58	10.1	11.5	29.4	34.4	28	3.49	6.12E-06	7.75E-03	2.56E-03
CGN	2.29	9.08	5.77	23.3	17.5	16.3	3.33	1.80E-03	1.30E-01	2.79E-02
LINGO4	4.58	5.87	7.7	19.2	23.1	17.5	3.3	4.64E-04	4.22E-02	8.67E-03

HSPA5	9.16	39.5	20.2	59.8	91.9	67.5	3.18	2.04E-05	1.42E-02	5.97E-02
RTN4R	6.87	8.54	5.77	16.2	28.1	22.1	3.13	7.61E-04	3.75E-02	1.90E-02
DNAH2	59.6	71	58.7	209	198	165	3.02	2.29E-19	5.51E-13	9.18E-05
NA	10900	12200	10800	32100	32900	35200	2.95	2.63E-86	2.95E-84	3.74E-07
GM11166	6.87	8.01	16.4	25.3	30.2	36.1	2.93	2.62E-04	1.53E-02	1.54E-02
CYP4F18	667	838	785	1870	2590	2160	2.89	3.03E-35	4.24E-09	1.37E-04
HSPA5	16	46.4	31.8	73.9	121	72.2	2.84	2.05E-05	4.79E-02	1.39E-01
KCTD19	22.9	16.6	17.3	49.6	65.9	45.4	2.84	5.60E-07	9.42E-05	2.59E-03
AXDND1	6.87	9.08	13.5	26.3	22.4	32.6	2.77	1.04E-03	5.27E-02	1.93E-02

Supplementary Table 2. Top down- and upregulated genes in CD4+ T cells from *Mtb* -infected mice following ex vivo treatment with SEA.

Gene Annotation			FPKM (Provided by Cufflinks)							Fold Change, EC vs CI
Ensemble_id	Locus	Short Name	SI1	SI2	SI3	EC1	EC2	EC3	EC4	
ENSMUSG00000033508	6:86628173-86629702	Asprv1	3.3	39.9	86.3	1.3	0.6	0.9	1.8	-5.23
ENSMUSG00000029368	5:90460888-90476603	Alb	14.5	0.4	0.2	0.6	0.1	0.0	0.1	-4.77
ENSMUSG00000059657	16:36156810-36161948	Stfa2l1	19.0	85.6	392.4	5.7	10.5	7.4	2.7	-4.66
ENSMUSG00000000204	11:83175185-83190221	Slfn4	8.1	50.7	13.2	0.2	0.9	1.1	1.6	-4.62
ENSMUSG00000058427	5:90903898-90905909	Cxcl2	10.4	64.7	129.6	3.3	2.8	2.3	3.3	-4.56
ENSMUSG00000022598	15:74714838-74717063	Psca	1.0	36.5	0.1	0.5	0.0	0.0	1.6	-4.54
ENSMUSG00000019987	10:24915207-24927470	Arg1	11.1	26.8	149.8	10.1	1.7	1.6	0.3	-4.19
ENSMUSG00000045502	5:123863569-123865516	Niacr1	32.5	173.2	96.3	6.0	10.0	9.7	10.9	-3.46
ENSMUSG00000056071	3:90692631-90695721	S100a9	153.8	720.9	1968.9	26.5	50.0	223.8	76.2	-3.33
ENSMUSG00000056054	3:90669070-90670034	S100a8	322.6	643.5	1746.0	86.3	32.8	199.0	47.2	-3.31
ENSMUSG00000025461	7:140218266-140231145	Cd163l1	0.1	3.0	2.2	0.0	0.1	0.7	0.1	-3.06
ENSMUSG00000027398	2:129364569-129371139	Il1b	99.9	232.2	436.0	18.3	17.5	47.8	40.5	-3.04
ENSMUSG00000000982	11:83647843-83649355	Ccl3	167.4	692.0	436.1	40.3	96.7	32.3	56.8	-2.93
ENSMUSG00000027399	2:129299609-129309972	Il1a	28.2	54.4	45.7	3.1	9.1	4.6	6.4	-2.89
ENSMUSG00000015437	14:56258855-56262260	Gzmb	54.1	93.7	62.1	15.6	11.8	13.7	6.6	-2.55

Supplementary Table 3: The top 15 genes upregulated in lungs of DO mice with severe inflammation (SI) compared to mice with enhanced mycobacterial control (EC).