SUPPLEMENTARY TABLE 1

Gene name and nucleotide composition for primers used in real-time PCR. Cycling parameters are described in references.

Gene	Primer Sequences
Hprt (1)	For: 5'-AGCCTAAGATGAGCGCAAGT-3'
	Rev: 5'-TTACTAGGCAGATGGCCACA-3'
*Stat1**	For: 5'-CCTGCAACTGAAGGAACAGA-3'
	Rev: 5'-TCACCACGACAGGAAGAGAG-3'
Stat6 (2)	For: 5'-GACTATGGTAGAGGACAGTTGCCTAA-3'
	Rev: 5'-GGTTCTCCAGGAGAAGCTTGGT-3'
Il4 (3)	For: 5'-CCACGGATGCGACAAAAATC-3'
	Rev: 5'-TGTTCTTCGTTGCTGTGAGGAC-3'
Il5 (4)	For: 5'-TGACAAGCAATGAGACGATGAGG-3'
	Rev: 5'-ACCCCCACGGACAGTTTGATTC-3'
Il13 (5)	For: 5'-GCAACATCACACAAGACCAGA-3'
	Rev: 5'-GTCAGGGAATCCAGGGCTAC-3'
Gata3 (6)	For: 5'-AGTTCGCGCAGGATGTCC-3'
	Rev: 5'-AGAACCGGCCCCTTATCAA-3'
Il1b (7)	For: 5'-CAACCAACAAGTGATATTCTCCATG-3'
	Rev: 5'-GATCCACACTCTCCAGCTGCA-3'
Il12p40 (3)	For: 5'-AAAGGCTGGGTATCGGTGG-3'
	Rev: 5'-ACTGGCTGTGCTGGAACTCC-3'
Tnfa (8)	For: 5'-AAGGGAGAGTGGTCAGTTGCC-3'

	Rev: 5’-CCTCAGGGAAGAGTCTGGAAAGG-3’
Tbet (6)	For: 5’-TTCTCTGTTTGGCTGGCTGTT-3’
	Rev: 5’-GGATTCTGGGGTTTACTTCTT-3’
Inos (9)	For: 5’-CACCAAGCTGAACTTGAGCGA-3’
	Rev: 5’-CCATAGGAAAAGACTGCACCGA-3’
Arg1 (9)	For: 5’-CAGAAGAATGGAAGAGTCAG-3’
	Rev: 5’-CAGATATGCAGGGAGTCACC-3’
Chi3l3 [Ym1] (10)	For: 5’-CATGAGCAAGACTTGCGTGAC-3’
	Rev: 5’-CATGAGCAAGACTTGCGTGAC-3’
Retnla [Fizz1] (10)	For: 5’-TCCCAGTGAATACTGATGAGA-3’
	Rev: 5’-CCACTCTGGATCTCCCAAGA-3’
Mmp12 (9)	For: 5’-TCAATTGGAATATGACCCCCTG-3’
	Rev: 5’-ACCAGCAAGCACCCTTCACTAC-3’
Il4ra (11)	For: 5’-GAGTGAGTGGAGTCCTAGCATC-3’
	Rev: 5’-GCTGAAGTAACAGAACAGGC-3’
Il13ra1 (11)	For: 5’-GCAGCCTGGAGAAAAGTCGTCAAT-3’
	Rev: 5’-ACAGCGTCGGCAAGAACACCA-3’
Il13ra2 (12)	For: 5’-TGCAGATGATGGAATTTGGA -3’
	Rev: 5’-GCTCAATGTGGGTTCAGGTT-3’
Ifng (13)	For: 5’ -AGCTCATCCGGTGGTCCAC-3 ‘
	Rev: 5’-AAAATTCAAATAGTGCTGGCAGAA-3’
Cxcl9	For: 5'-TCGAGGAACCCTAGTGATAA-3'
	Rev: 5'-ACTGTTTGAGGTCTTTGAGG-3'
Cxcl10	For: 5'-GTCTGAGTGGGACTCAAGG-3'

	Rev: 5'-TGATTTCAAGCTTCCCTATG-3'
Irf1	For: 5'- AGAGAGAAAGTCCAAGTCCAGC -3'
	Rev: 5'- GTCCATCAGAGAAAGTGTCCG -3'
Ifnb	For: 5'- TACGTCTCCTGGATGAACTC -3'
	Rev: 5'- TCTTCAAGTGGAGAGCAGTT -3'
Socs1 (14)	For: 5'-ACCTTCTTGGTGCGCGAC -3'
	Rev: 5'- AAGCCATCTTCACGCTGAGC -3'
Rantes	For: 5'- GGAGTATTTCTACACCAGCAGC -3'
	Rev: 5'- TCTTGAACCCACTTCTTCTCTG -3'
Fasl	For: 5'- GGTGCTAATGGAGGAGAAGAGG -3'
	Rev: 5'- CACTGGTAAGATTGAATACTGCCC -3'
Fas	For: 5'- ACTTCTACTGCGATTCTCCTGG -3'
	Rev: 5'- TGTATTGCTGGTTGCTGTGC -3'
Tnfr1	For: 5'- CCCCAAATGGAAATGTGCTATG -3'
	Rev: 5'- GGATGCTACAGATGCGGTGG -3'
Ccl3	For: 5'-CCAATTCATCGTTGACTATTT-3'
	Rev: 5'-CTTGGACCCAGGTCTCTT-3'
Ccl4	For: 5'-CCTGCTGTTTCTCTTACACC-3'
	Rev: 5'-TTTGGTCAGGAATACCACAG-3'
Mcp1	For: 5'- TCTGCCCTAAGGTCTTCAGCAC -3'
	Rev: 5'- GCTTGAGGTGGTTGTGGAAAAG -3'
Il17a(6)	For: 5'- CAGACTACCTCAACCGTTCC -3'
	Rev: 5'- AGCATCTTCTCGACCCTGAA -3'

*Purchased from Real Time Primers, LLC (Elkins Park, PA)

SUPPLEMENTARY TABLE 2

Correlation coefficient matrix for 10 genes from Figure 9A and C in a cohort of 45 patients with biliary atresia.

		CCR4	*IL18*	*CD74*	*CD86*	*AREG/AREGB-1*	*IL4R*	*BCL3*	*BCL6*	*IL1RL1*	*IL6*
CCR4	Pearson's r	1.									
	R Std Error										
	t										
	p-value										
IL18	Pearson's r	-0.094	1.								
	R Std Error	0.023									
	t	-0.623									
	p-value	0.535									
CD74	Pearson's r	0.165	0.450	1.							
	R Std Error	0.022	0.018								
	t	1.100	3.311								
	p-value	0.277	0.001								
CD86	Pearson's r	0.264	0.341	0.634	1.						
	R Std Error	0.021	0.020	0.013							
	t	1.801	2.380	5.381							
	p-value	0.078	0.021	<0.001							
AREG/AREGB-1	Pearson's r	0.384	0.316	0.140	0.535	1.					
	R Std Error	0.019	0.020	0.029	0.016						
	t	2.727	2.186	0.928	4.153						
	p-value	0.009	0.034	0.358	<0.001						
IL4R	Pearson's r	0.124	0.117	-0.087	0.153	0.612	1.				
	R Std Error	0.022	0.022	0.023	0.022	0.014					
	t	0.824	0.778	-0.573	1.019	5.078					
	p-value	0.414	0.440	0.569	0.313	<0.001					
BCL3	Pearson's r	0.331	0.143	0.075	0.331	0.646	0.866	1.			

	R Std Error	0.021	0.022	0.0231	0.020	0.013	0.005				
	t	2.307	0.950	0.494	2.302	5.556	11.385				
	p-value	0.025	0.347	0.623	0.026	<0.001	<0.001				
BCL6	Pearson's r	0.127	0.113	-0.025	0.216	0.549	0.835	0.815	1.		
	R Std Error	0.022	0.022	0.023	0.022	0.016	0.007	0.007			
	t	0.844	0.752	-0.167	1.450	4.310	9.953	9.237			
	p-value	0.402	0.456	0.868	0.154	<0.001	<0.001	<0.001			
IL1RL1	Pearson's r	0.248	0.172	0.094	0.587	0.846	0.712	0.699	0.656	1.	
	R Std Error	0.021	0.022	0.0230	0.015	0.006	0.011	0.011	0.013		
	t	1.684	1.151	0.621	4.750	10.431	6.660	6.421	5.711		
	p-value	0.099	0.256	0.537	<0.001	<0.001	<0.001	<0.001	<0.001		
IL6	Pearson's r	0.318	0.131	-0.062	0.373	0.752	0.544	0.647	0.652	0.692	1.
	R Std Error	0.021	0.022	0.023	0.020	0.010	0.016	0.013	0.013	0.012	
	t	2.206	0.870	-0.407	2.640	7.493	4.256	5.564	5.639	6.293	
	p-value	0.032	0.388	0.685	0.011	<0.001	<0.001	<0.001	<0.001	<0.001	

SUPPLEMENTARY TABLE 3

Correlation coefficient matrix for 10 genes from Figure 9A and C in a cohort of 7 normal controls.

		CCR4	*IL18*	*CD74*	*CD86*	*AREG/AREGB-1*	*IL4R*	*BCL3*	*BCL6*	*IL1RL1*	*IL6*
CCR4	**Pearson's r**	*1.*									
	R Std Error										
	t										
	p-value										
IL18	**Pearson's r**	*-0.537*	*1.*								
	R Std Error	*0.142*									
	t	*-1.425*									
	p-value	*0.214*									
CD74	**Pearson's r**	*0.748*	*-0.310*	*1.*							
	R Std Error	*0.088*	*0.181*								
	t	*2.521*	*-0.729*								
	p-value	*0.053*	*0.499*								
CD86	**Pearson's r**	*0.503*	*0.271*	*0.275*	*1.*						
	R Std Error	*0.149*	*0.185*	*0.185*							
	t	*1.301*	*0.631*	*0.641*							
	p-value	*0.250*	*0.556*	*0.550*							
AREG/AREGB-1	**Pearson's r**	*0.032*	*0.050*	*0.258*	*-0.447*	*1.*					
	R Std Error	*0.200*	*0.199*	*0.187*	*0.160*						
	t	*0.072*	*0.113*	*0.596*	*-1.118*						
	p-value	*0.945*	*0.915*	*0.577*	*0.315*						
IL4R	**Pearson's r**	*0.431*	*-0.272*	*0.770*	*-0.059*	*0.421*	*1.*				
	R Std Error	*0.163*	*0.185*	*0.081*	*0.199*	*0.165*					

	t	*1.068*	*-0.631*	*2.701*	*-0.131*	*1.038*					
	p-value	*0.334*	*0.556*	*0.043*	*0.901*	*0.347*					
BCL3	**Pearson's r**	*0.001*	*0.114*	*0.585*	*-0.047*	*0.062*	*0.741*	*1.*			
	R Std Error	*0.200*	*0.197*	*0.132*	*0.200*	*0.199*	*0.090*				
	t	*0.003*	*0.256*	*1.612*	*-0.104*	*0.139*	*2.470*				
	p-value	*0.998*	*0.808*	*0.168*	*0.921*	*0.895*	*0.057*				
BCL6	**Pearson's r**	*-0.025*	*0.145*	*0.472*	*-0.337*	*0.456*	*0.323*	*0.554*	*1.*		
	R Std Error	*0.200*	*0.196*	*0.155*	*0.177*	*0.158*	*0.179*	*0.139*			
	t	*-0.056*	*0.327*	*1.198*	*-0.800*	*1.145*	*0.762*	*1.489*			
	p-value	*0.958*	*0.757*	*0.285*	*0.460*	*0.304*	*0.480*	*0.197*			
IL1RL1	**Pearson's r**	*-0.457*	*0.745*	*-0.468*	*0.260*	*-0.216*	*-0.171*	*0.096*	*-0.205*	*1.*	
	R Std Error	*0.158*	*0.089*	*0.156*	*0.186*	*0.191*	*0.194*	*0.198*	*0.192*		
	t	*-1.149*	*2.499*	*-1.183*	*0.603*	*-0.495*	*-0.388*	*0.215*	*-0.467*		
	p-value	*0.303*	*0.055*	*0.290*	*0.573*	*0.642*	*0.714*	*0.838*	*0.660*		
IL6	**Pearson's r**	*0.411*	*-0.164*	*0.316*	*0.439*	*-0.573*	*0.302*	*0.419*	*-0.044*	*0.300*	*1.*
	R Std Error	*0.166*	*0.195*	*0.180*	*0.161*	*0.134*	*0.182*	*0.165*	*0.200*	*0.182*	
	t	*1.007*	*-0.371*	*0.746*	*1.094*	*-1.564*	*0.709*	*1.032*	*-0.098*	*0.703*	
	p-value	*0.360*	*0.726*	*0.489*	*0.324*	*0.179*	*0.510*	*0.349*	*0.926*	*0.514*	

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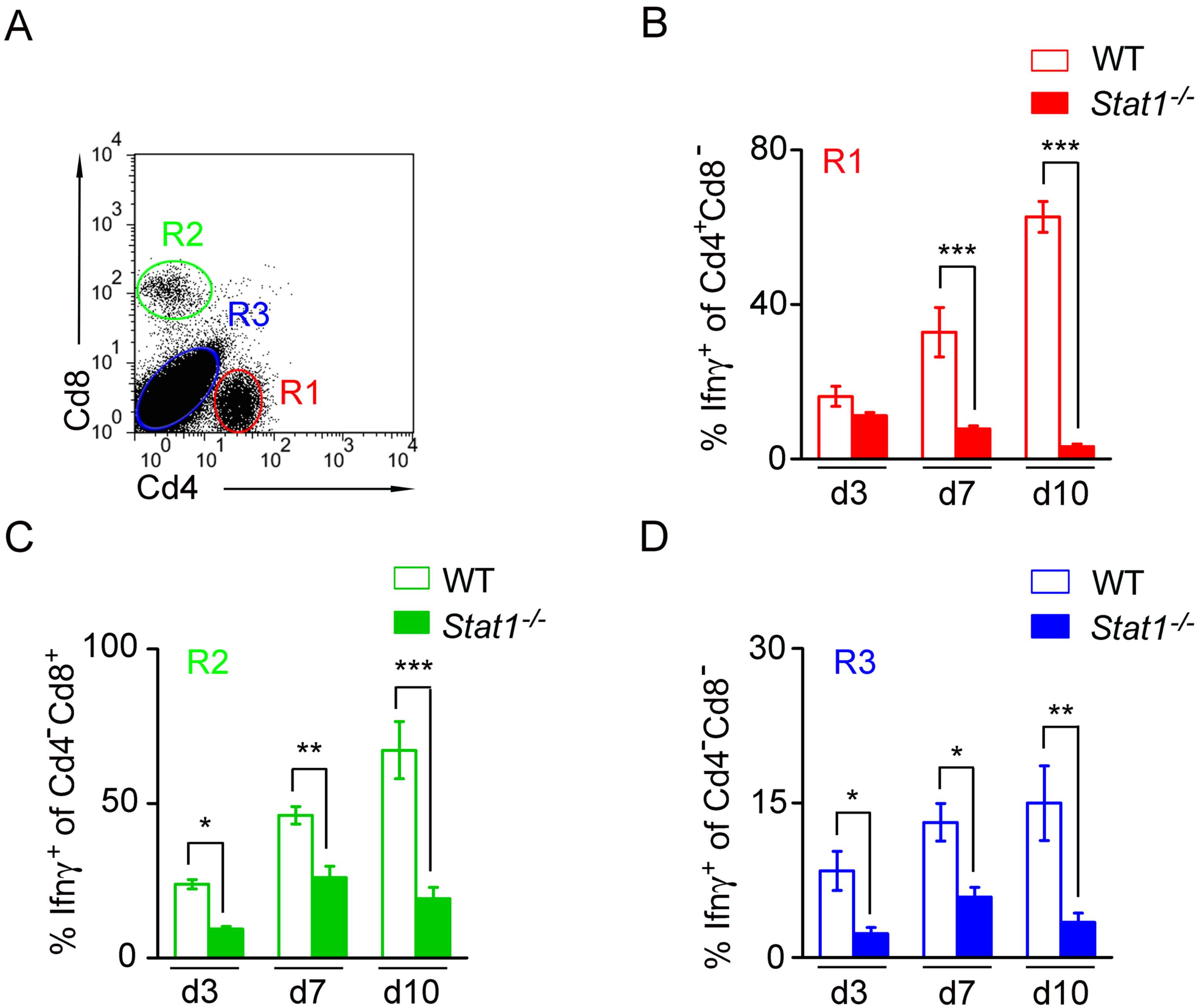
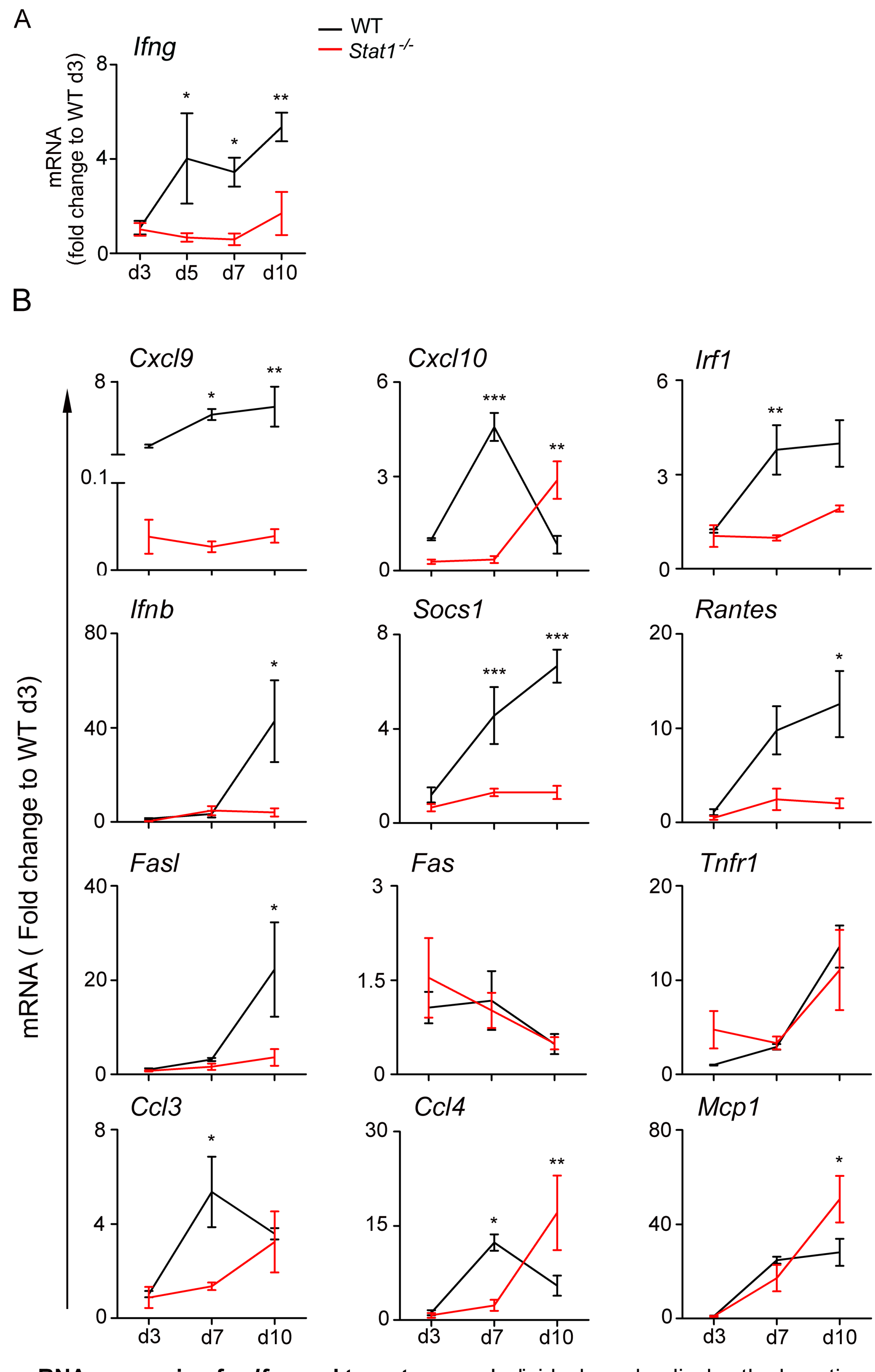
Supplementary Figure 1



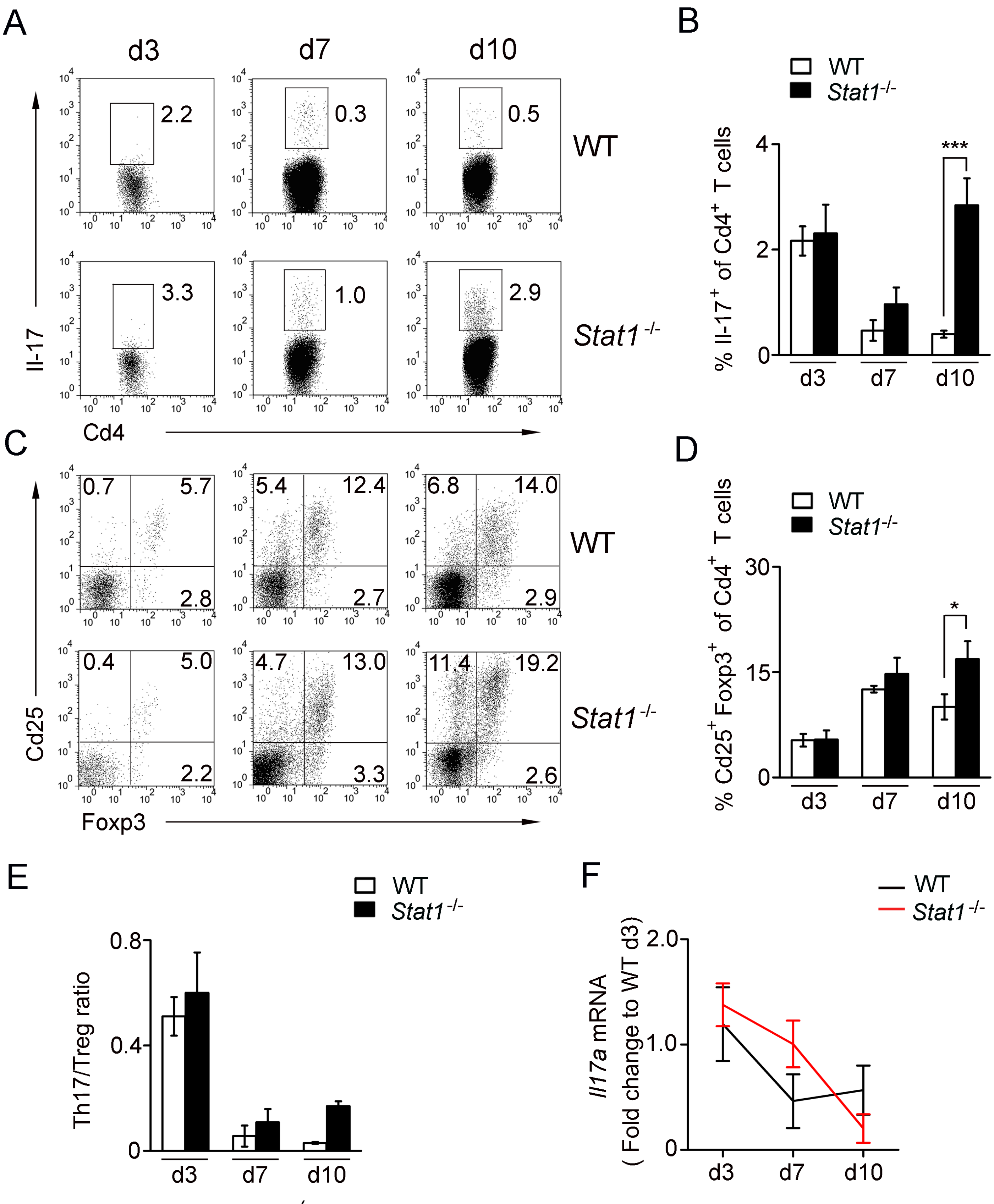
Decrease in Ifnγ production in *$Stat1^{-/-}$* mice after RRV. Gating strategy for $Cd4^+$ (R1), $Cd8^+$ (R2) and $Cd4^-Cd8^-$ (R3) hepatic mononuclear cells (A). The quantification of the percent of these cells expressing Ifnγ at days 3, 7 and 10 after RRV infection is higher in WT than *$Stat1^{-/-}$* mice. $^*P<0.05$, $^{**}P<0.01$, $^{***}P<0.001$. Note that panel B is also in Figure 3B, but it is shown here to demonstrate the gating strategy to quantify these cells.

Supplementary Figure 2



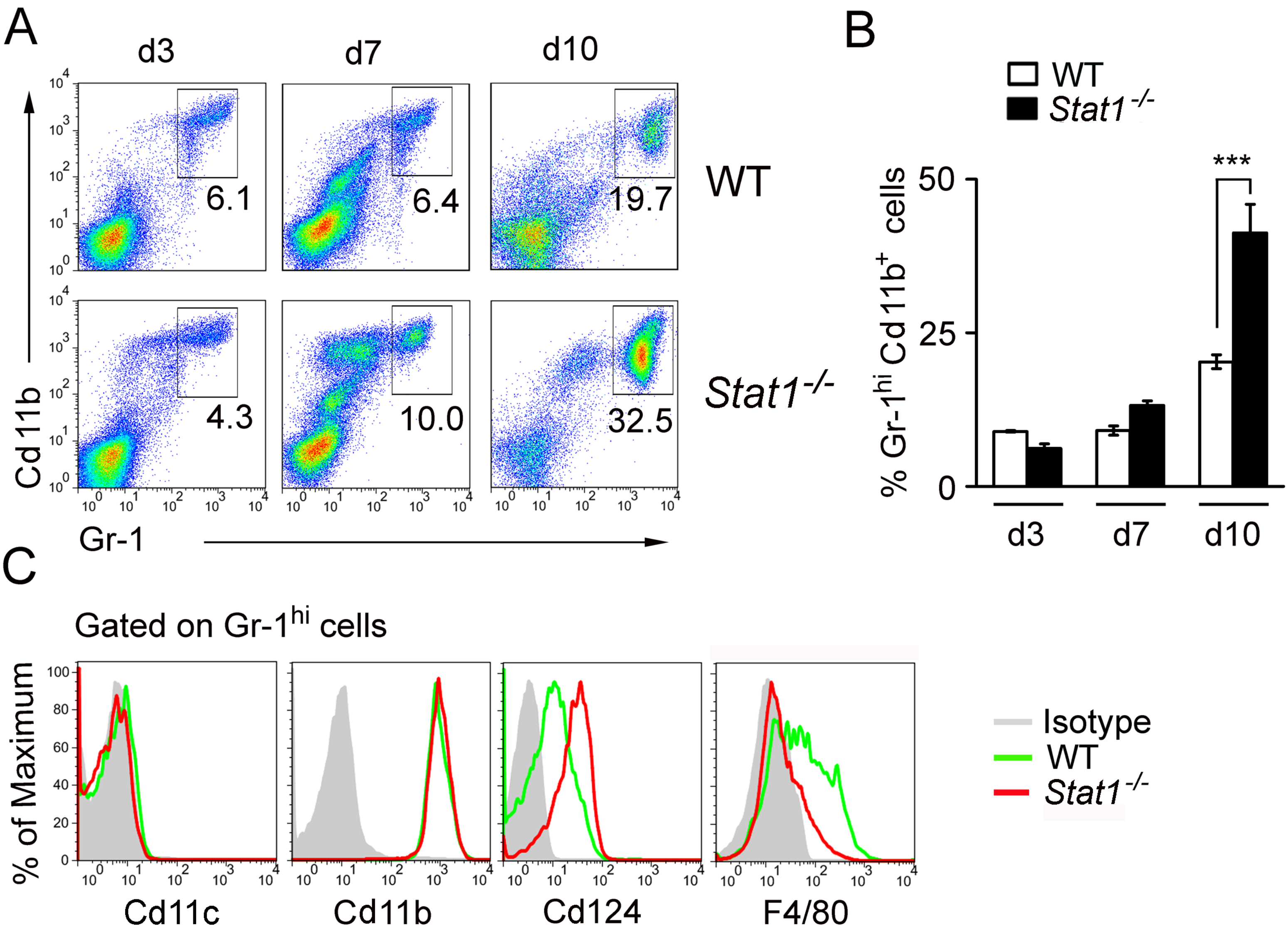
mRNA expression for *Ifng* and target genes. Individual graphs display the hepatic mRNA expression for *Ifng* (A) and *Ifng*-target genes (B) in WT and *Stat1*$^{-/-}$ mice at different time points after RRV challenge. mRNA expression for most genes is decreased in *Stat1*$^{-/-}$ livers when compared to WT. mRNA expression was first normalized to internal *Hprt* control and then normalized to the value from WT mice at day 3. N=3-4 livers per group and time point; *P<0.05, **P<0.01, ***P<0.001.

Supplementary Figure 3



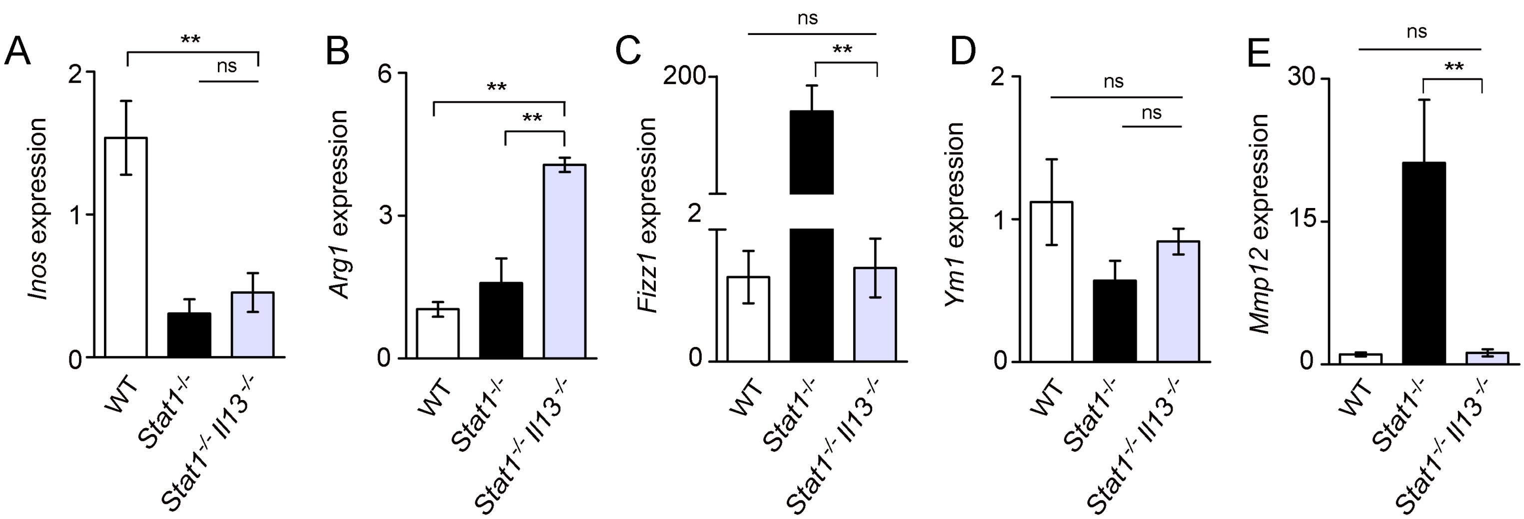
Th17 expression in *Stat1*$^{-/-}$ mice after RRV. Flow cytometric analysis showing the expression of Il-17 (A,B) or Cd25^{+}Foxp3^{+} (C,D) by hepatic Cd4^{+} cells in WT and *Stat1*$^{-/-}$ mice at different time points after RRV. Panel E shows a Th17:Treg ratio below 1, and panel F shows a similar pattern of hepatic *Il17a* mRNA expression in both groups after RRV. Data are shown as representative dot plots (A,C) and mean±SEM (B,D); N=3 livers per group per time point; *P<0.05, ***P<0.001.

Supplementary Figure 4



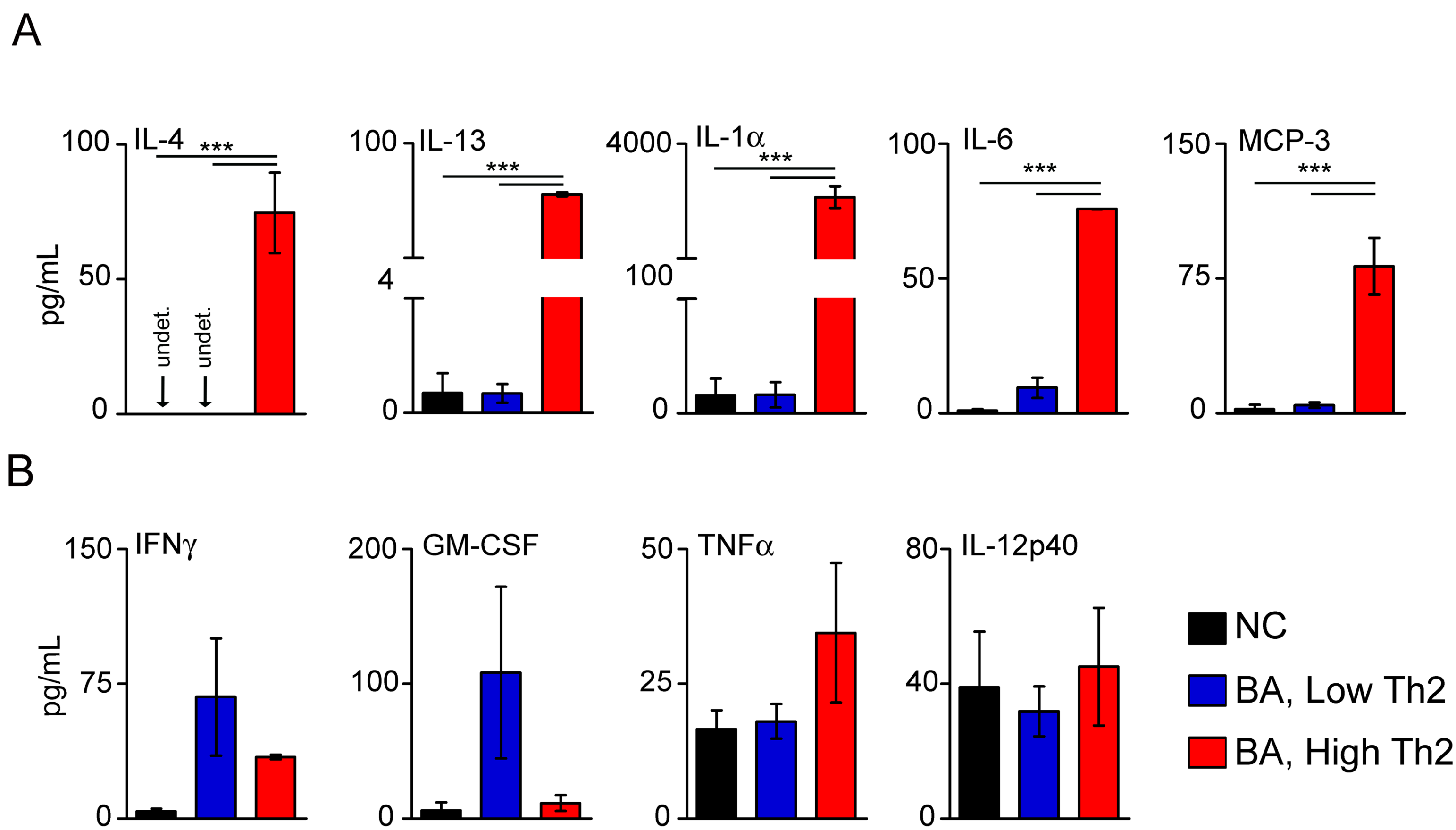
Expression of Il4Rα and F4/80 in Gr-1^hi cells in *Stat1*^-/- livers after RRV. Flow cytometry analyses show similar levels of Gr-1^hi cells in WT and *Stat1*^-/- livers 3 and 7 days after RRV, which increase in *Stat1*^-/- at day 10 (A,B). Expression of markers linked to the myeloid-derived suppressor cell (MDSC) phenotype shows an increased number of Gr-1^hi cells co-expressing Cd124 (Il4Rα) in *Stat1*^-/- livers but only few express F4/80^+ 10 days after RRV (C). N=6-10 livers per group and time point; experiments repeated twice; ***P<0.001.

Supplementary Figure 5



Decreased M2 activation after depletion of Il-13 in *Stat1$^{-/-}$* mice. Hepatic mRNA expression for M1 and M2 genes in WT, *Stat1$^{-/-}$* and *Stat1$^{-/-}$Il13$^{-/-}$* mice 7 days after RRV. Values are expressed as a ratio to *Hprt* and then normalized to WT; N=3-5 livers per genotype; **P<0.01; ns=no significant difference.

Supplementary Figure 6



Serum levels of Th1 and Th2 cytokines/chemokines at diagnosis of biliary atresia. Mean (±S.E.) serum concentration of Th1 and Th2 cytokines/chemokines for infants at the time of diagnosis of biliary atresia (BA; age < 4 months) and age-matched normal infants (normal controls=NC). Data in panel A are shown in three groups: NC (N=3), BA Low Th2 group (N=9) and BA High Th2 group (N=2). ***P<0.001 (one-way ANOVA).