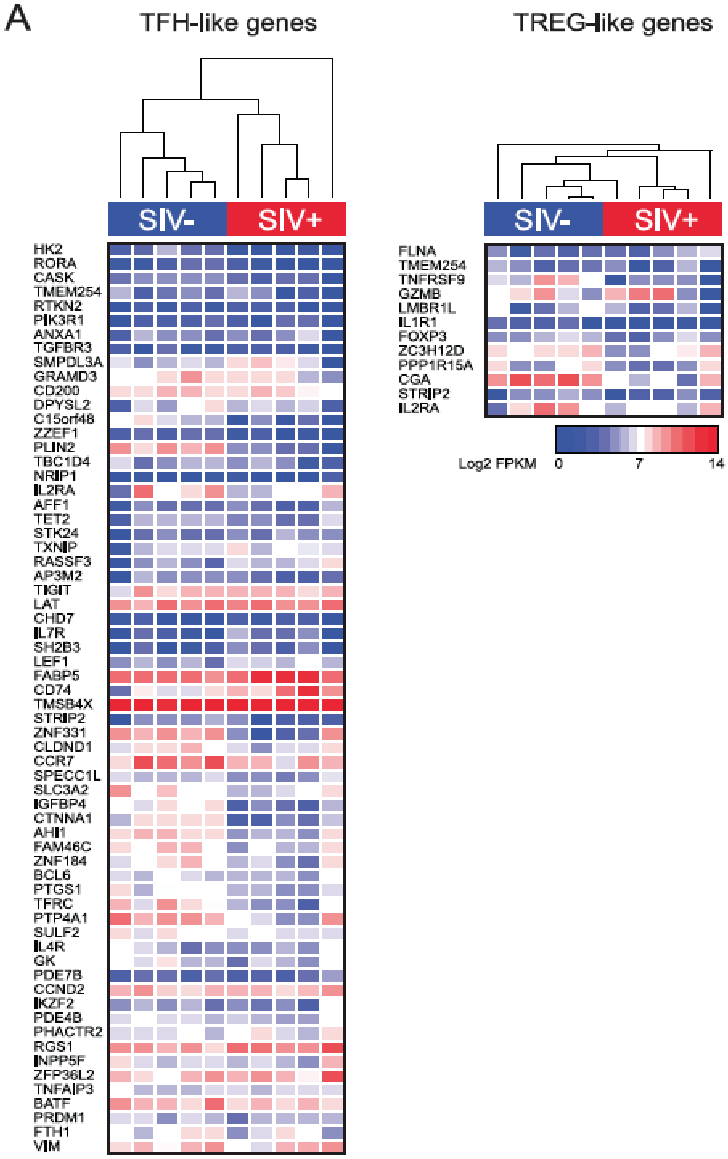
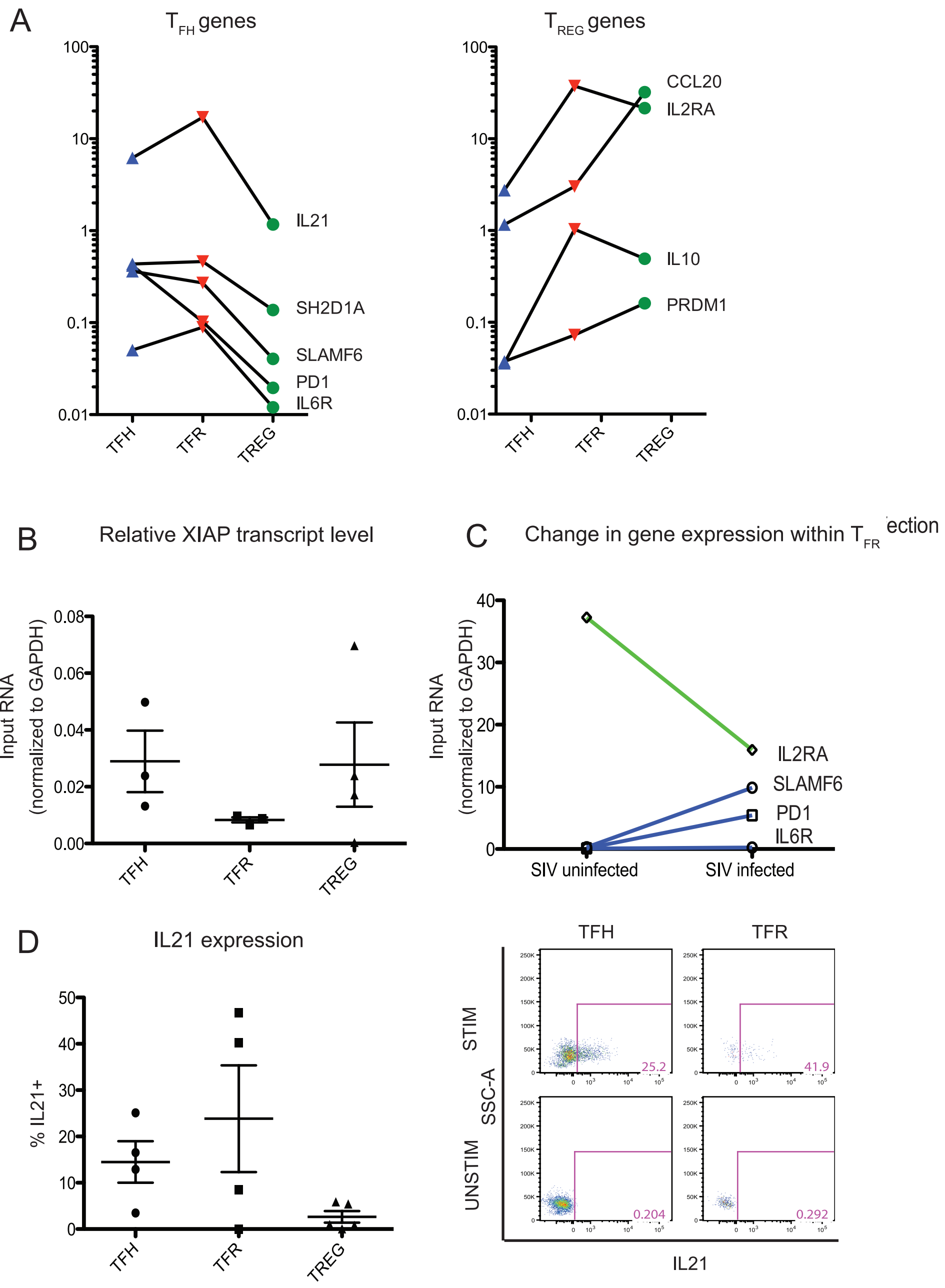
Supplementary Figure 1. RNA expression within T_{FR} in uninfected and SIV infected RM.



Supplementary Figure 1. **RNA expression within T_{FR} in uninfected and SIV infected RM.** (A) Heat map of log 2 transformed gene expression of transcripts in FPKM between T_{FR} cells from SIV uninfected and infected RM.

Supplementary Figure 2. PCR and flow cytometry validation of RNA-sequencing data.



Supplementary Figure 2. PCR and flow cytometry validation of RNA-sequencing data. Relative RNA transcript levels of key T_{FH} and T_{REG} genes (A) and XIAP (B) in T_{FH}, T_{FR} and T_{REG} populations from five SIV uninfected RM measured by RT-PCR. (C) Change in expression of genes post SIV-infection in sorted T_{FR} cells from 5 infected and 5 uninfected RM. All genes were normalized to the housekeeping gene, GAPDH. (D) Levels of IL21 expression as measured by low cytometry following PMA/ionomycin stimulatoion in T_{FH}, T_{FR} and T_{REG} populations and represetative FACS plot derived from LN of SIV uninfected RM. For this analysis T_{FR} cells were defined as CXCR5^{+}PD1^{hi}CD127^{-}CD25^{+} cells.

Supplementary Table 1. Quantification of T_{FH} and T_{FR} cells by immunohistochemistry.

Animal	Timepoint	Number of TFH	Number of TFR	TFR/TFH Ratio
RM1	Uninfected	43	4	0.093
	Uninfected	72	6	0.083
RM2	Uninfected	57	6	0.105
	Uninfected	38	2	0.052
RM3	Acute Infection	67	6	0.089
	Acute Infection	47	5	0.106
RM4	Acute Infection	78	9	0.115
	Acute Infection	60	7	0.116
RM5	Chronic Infection	139	4	0.028
	Chronic Infection	95	4	0.042
RM6	Chronic Infection	66	3	0.045
	Chronic Infection	89	5	0.056

Supplementary Table 1. Quantification of T_{FH} and T_{FR} cells by immunohistochemistry.
Number of T_{FH} and T_{FR} cells counted per unit area within individual representative germinal centers of RM. T_{FH} cells were identified as $CD4^+PD1^+$ cell and T_{FR} cells were identified as $CD4^+PD1^+Foxp3^+$ cells.