Supplementary Information

Cholesterol metabolism drives regulatory B cell IL-10 through provision of geranylgeranyl pyrophosphate

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Supplementary Figure 1. Outline of cholesterol metabolism showing key metabolites and enzymes of the pathway. An outline of key metabolites and enzymes in the multi-step conversion of acetyl-CoA to cholesterol and its derivatives, generally termed cholesterol metabolism. Mevalonate kinase deficient patients suffer a mutation in mevalonate kinase (MVK) enzyme, and progress to a severe autoinflammatory syndrome.



Supplementary Figure 2. IL-10 production by B cells, and the effect of IL-10 on T cell effector function. a. Gating strategy for analysis of human B cells. b. IL-10 production by human B cells after stimulation with the indicated ligand for 40 hours. c. Representative plots and quantification of IFN_Y, TNF α expression, and proliferation in CD4⁺ T cells after stimulation with anti-CD3/anti-CD28, titration of recombinant human IL-10, and culture for 4 days (n=6 for cytokine measurement, pvals = 0.01, 0.001, 0.001, 0.02, 0.04, 0.02; n=3 for proliferation). Each data point represents individual donors. All data presented are mean ± SD. Statistical testing in all figures was done by a Friedman's test with Dunns's multiple comparisons test. **P*<0.05, ***P*<0.01 and all significant values are shown.



Supplementary Figure 3. Cholesterol metabolism specifically regulates IL-10 expression. a. IL-10 secretion from human B cells after TLR9 stimulation at 40 hours, \pm atorvastatin (AT) \pm mevalonate (MA) (n=4, pval = 0.005). b. IC50 of IL-10 expression in human B cells stimulated through TLR9 in the presence of titrated levels of AT (n=4). c-d. Expression of TNF α (ELISA) and IFN γ (flow cytometry) in human B cells stimulated with TLR9 \pm AT \pm MA (n=3 for TNF α and 7 for IFN γ). Each data point represents individual donors. All data presented are mean \pm SD. Statistical testing in all figures was done by a Friedman's test with Dunns's multiple comparisons test. ***P*<0.01 and all significant values are shown.







Supplementary Figure 4. IL-10 expression within B cell populations, and the contribution of cholesterol metabolism to B cell phenotype. a. Gating of naïve versus memory B cells after CpG stimulation. CpG stimulation results in the downregulation of CD27, in comparison to unstimulated cells, or phorbol 12-myristate 13-acetate and ionomycin stimulated cells. Memory cells were defined from the upper left quadrant, whereas naïve cells were defined in the lower right. b. Percentage of IL-10⁺ human B cells within each population (bulk (CD19⁺), B10, CD24^{hi}CD38^{hi}, naïve, and memory) (n=6, pvals = 0.02, 0.05). c. IL-10 expression analysed with respect to proliferation, as measured by CellTrace Violet staining prior to stimulation (n=3). d-e. Proportional analysis of B cell populations upon stimulation with TLR9 ± atorvastatin (AT) ± mevalonate (MA), and viability measured by live/dead stain (d, n=6) or annexin positivity (e, n=3). f. Representative expression of HLA-DR, CD86, and CD40 on B cells after TLR9 stimulation ± AT ± MA. G. IL-10 expression within human B cell populations after stimulation through TLR9 ± AT. g. IL-10 expression in B cell populations following CpG stimulation in the presence or absence of AT. Each data point represents individual donors. All data presented are mean ± SD. Statistical testing in all figures was done by a Friedman's test with Dunns's multiple comparisons test. **P*<0.05 and all significant values are shown.



Supplementary Figure 5. Cholesterol metabolism regulates IL-10 via GGTase and GGPP. a. IL-10 secretion in TLR9 stimulated human B cells in the presence of geranylgeranyl transferase inhibition (GGTi), measured by ELISA (n=6, pval = 0.001). b. IL-10 expression in human B cells after stimulation through TLR9 \pm GGTi-2133 (n=3). c. Proliferation, differentiation, viability (all at day 5), and IgM production (at day 7) by human B cells after stimulation through TLR9 \pm AT \pm GGTi-2133 (n=3). d-f. IL-10 production in TLR9 stimulated human B cells \pm psoromic acid (d, n=3), \pm atorvastatin (AT) \pm geranylgeranyl pyrophosphate (GGPP) (e, n=4, pva = 0.03), or \pm AT \pm Squalene (f, n=3). Each data point represents individual donors. All data presented are mean \pm SD. Statistical testing in (a) was done by a paired t test, or in (e) by a Friedman's test with Dunns's multiple comparisons test. **P*<0.05, ****P*<0.001 and all significant values are shown.



Supplementary Figure 6. GGTase and GGPP regulate IL-10 induction downstream of TLR9 via PI3K, AKT, and ERK. ab. Quantification of AKT (a) and ERK (b) phosphorylation over time in human B cells after stimulation through TLR9 ± geranylgeranyl transferase inhibitor (GGTi) (both n=3, pvals = 0.004, 0.001, 0.01). c. IL-10 secretion from human B cells after stimulation through TLR9 ± GGTi ± GSK3i (n=2). All data presented are mean ± SD. Statistical testing in all figures was done by a two-way ANOVA with Sidak's multiple comparisons test. **P*<0.05, ***P*<0.01 and all significant values are shown.



Supplementary Figure 7. A transcriptional event mediated by GGTase after TLR9 stimulation is required for the expression of a transcription factor necessary for IL-10. a. qRT-PCR analysis of IL-10 expression in B cells following TLR9 stimulation ± actinomysin D (ActD) added at the indicated time post-stimulation, with all cells acquired at 40 hours (n=2). **b.** A heatmap representing the global profile of differentially expressed genes (FDR<0.05, Fold change >1.5) in human B cells following stimulation through TLR9 ± geranylgeranyl transferase inhibition (GGTi). **c.** All previously experimentally validated IL-10 transcription factors, and their FDR and fold change in our data set. Red dashed lines represent FDR=0.05 and fold change=1.5. **d.** ChIP-seq (y-axis) vs RNA-seq (x-axis) data from GSE71698, showing enriched targets of BLIMP1, and the correlative change in gene expression. **e.** BLIMP1 protein levels after B cells were stimulated with CpG in the presence or absence of GGTi (n=2). **(f-g)** Expression of BLIMP1 in human B cells at 40 hours after stimulation through TLR9, either in bulk B cells (**f**, n=3), or in different B cell phenotypes (**g**, n=3). Each data point represents individual donors. All data presented are mean ± SD. FDR values were calculated in EdgeR using the default Benjamini-Hochberg correction

а	Patient	Status	Mutation	Sex	Age
	MKD1	MKD	V377I/I268T	Μ	26
	HD1	Healthy	NA	Μ	27
	MKD2	MKD	V377I/H380R	М	29
	HD2	Healthy	NA	Μ	32
	MKD3	MKD	V377I/G/G202R	Μ	26
	HD3	Healthy	NA	М	22
	MKD4	MKD	V377I//H380R	Μ	27
	HD4	Healthy	NA	М	27
	MKD5	MKD	V377I/R215X	М	26
	HD5	Healthy	NA	Μ	27
	MKD6	MKD	V377I/I268T	F	7
	HD6	Healthy	NA	М	40















Supplementary Figure 8. MKD patients show poor regulatory B cell responses, but normal T cell responses. a. Clinical information for healthy donors (HD) and mevalonate kinase deficient (MKD) patients used in this study. b. Naive versus memory B cell populations in MKD patients relative to healthy donors, as a percentage of total CD19⁺ B cells. c. Proliferation, differentiation, viability (at day 5), and IgM production (at day 7) by HD or MKD patient B cells after stimulation through TLR9. Technical repeats shown for MKD 5 as suffixed with -1 and -2. d. TNF α expression in human B cells from HD or MKD patients attimulated through TLR9 ± geranylgeranyl pyrophosphate (GGPP). e. IL-10 expression in B cells from MKD patients and HD after stimulation through TLR9 ± squalene (sq). Technical repeats shown for MKD 5 as suffixed with -1 and -2. f. IFN γ suppression in human CD4⁺ T cells of healthy controls and MKD patients after co-culture with autologous TLR9 activated B cells ± GGPP treated B cells prior to co-culture. g. Cytokine production in CD4⁺ T cells from MKD patients and healthy controls (n=4). Each data point represents individual donors. All data presented are mean ± SD. All significant values are shown.

Figure 3d



Figure 5f and g



Sup Fig 7e

