## **Supplemental Figures**



Supplemental Figure 1. Example of Gating Strategy for Th1, Th17, Th1-Th17, Th2 and Treg. (A) Th1, Th17, Th1-Th17 and Th2 Gating. PBMCs isolated using a Ficoll-hypaque density gradient centrifugation were stained with fluorochrome-conjugated anti-CD3, CD4, CXCR3, CD161, CCR6 and CRTH2. The stained cells were then analyzed using the BD FACSCanto<sup>™</sup> II system followed by data analysis using Flowjo 7.6.5. T helper subsets are marked and defined as follows: Th1: CD3<sup>+</sup>CD4<sup>+</sup>CXCR3<sup>+</sup>CCR6<sup>-</sup>CD161<sup>-</sup>; Th17: CD3<sup>+</sup>CD4<sup>+</sup>CXCR3<sup>-</sup>CCR6<sup>+</sup>CD161<sup>+</sup>; Th2: CD3<sup>+</sup>CD4<sup>+</sup>CXCR3<sup>-</sup>CCR6<sup>+</sup>CD161<sup>-</sup>; Th1-Th17: CD3<sup>+</sup>CD4<sup>+</sup>CXCR3<sup>+</sup>CCR6<sup>+</sup>CD161<sup>+</sup>; Th2: CD3<sup>+</sup>CD4<sup>+</sup>CXCR3<sup>-</sup>CCR6<sup>-</sup>CD161<sup>-</sup>CRTH2 (CD294<sup>+</sup>). SSC-A/W: Side Scatter Area/Width, FSC-A/H: Forward Scatter Area/Height. (B) Treg Gating. PBMCs were stained with fluorochrome-conjugated anti-CD3, CD4, CD25, followed by fixation and permeabilization using eBioscience<sup>™</sup> Foxp3 / Transcription Factor Staining Buffer Set, and stained with fluorochrome-conjugated anti-human Fox P3. The stained cells were then

analyzed using the BD FACSCanto<sup>TM</sup> II system followed by data analysis using Flowjo 7.6.5. Treg are marked and defined as CD3<sup>+</sup>CD4<sup>+</sup>CD25<sup>+</sup>FoxP3<sup>+</sup>



Supplemental Figure 2. Example of Gating Strategy for B cell subsets. PBMCs isolated using a Ficoll-hypaque density gradient centrifugation were stained with fluorochrome-conjugated anti-CD19, CD20, CD27, IgD, CD38, CD24 and CD43. The stained cells were then analyzed using the BD FACSCanto<sup>™</sup> II system followed by data analysis using Flowjo 7.6.5. B subsets are marked and defined as the following: Memory T cells: CD20<sup>+</sup>19<sup>+</sup>CD27<sup>+</sup>; Naive: CD20<sup>+</sup>19<sup>+</sup>CD27<sup>-</sup> IgD<sup>+</sup>; Unswitched Memory B cells: CD20<sup>+</sup>19<sup>+</sup>CD27<sup>+</sup> IgD<sup>+</sup>; Switched Memory B cells: CD20<sup>+</sup>19<sup>+</sup>CD27<sup>+</sup> IgD<sup>+</sup>; B1 cells: CD20<sup>+</sup>CD19<sup>+</sup>CD27<sup>+</sup> CD43<sup>+</sup>.



Supplemental Figure 3 Increased frequency of proliferative CD4<sup>+</sup> T cells after siponimod treatment. (A) Cross-section comparison of Ki67<sup>+</sup>% of CD4 T at baseline, 6 month and 9-12 month after treatment with placebo or siponimod. (B) Cross-section comparison of Ki67<sup>+</sup>% of FoxP3<sup>-</sup> CD4<sup>+</sup> T cells at baseline, 6 month and 9-12 month after treatment with placebo or siponimod. *P* values represent statistically significant different P value between placebo and siponimod at the same time point using Mann-Whitney U test for (A-B) 6 months and 9-12 months; unpaired t test for (B) 0 month; unpaired t test with Welch's correction for (A) 0 month. Placebo (0 month: N=8; 6 months: N=8; 9-12 months: N=12) or Siponimod (0 month: N=13; 6 months: N=13; 9-12 months: N=16).



Supplemental Figure 4. Siponimod did not alter the relative frequencies of Th1, Th1-17 and Th17. Frequencies of effector T cell subsets shown as a fraction of total CD3<sup>+</sup>CD4<sup>+</sup> T cells. (A) T helper (Th1) (CD4<sup>+</sup> CXCR3<sup>+</sup>CCR6<sup>-</sup>CD161<sup>-</sup>. (B) Th1-Th17 (CD4<sup>+</sup>CXCR3<sup>+</sup>CCR6<sup>+</sup>CD161<sup>+</sup>). (C) Th17 (CD4<sup>+</sup>CXCR3<sup>-</sup>CCR6<sup>+</sup>CD161<sup>+</sup>). Comparisons were done with multiple t tests with Holm-Sidak adjusted P value. None showed significance. Points represent individual participants, lines show means for placebo (black) and siponimod (red). Placebo N: 0 month=10, 6 months=9, 9-12 months=12; Siponimod N: 0 month=17, 6 months=16, 9-12 months=18.



Supplemental Figure 5. Siponimod alters immune cell gene expression profile leading to downregulation of mTOR pathway. mRNA content from peripheral blood measured using the Affymetrix Human Gene ST 2.1 microarray from same cohort of patients as in Figures 2 and 3: SPMS patients at baseline (n=21) and after siponimod treatment (n=12) or placebo (n=7). Genes involved in the mTOR signaling pathway decreased following siponimod treatment relative to baseline. The box and whisker plot on the lower left summarizes the distribution of all the differentially expressed genes that are annotated to this GO term. The box represents the  $1^{st}$  guartile, the median, and the  $3^{rd}$  guartile, while the outliers are represented by circles.

## Table 1 Antibodies used in this study

Vender	Catalog #	Conjugated Antibodies	Clone
Tonbo Biosciences	60-0038-T100	CD3 PE-Cy7	UCHT1
(San Diego, CA.	50-0048-T100	CD4 PE	OKT4
USA)	20-0086-T100	CD8 APC	ОКТ8
	60-0199-T100	CD19 PE-Cy7	HIB19
Biolegend	304128	CD45RA APC-Cy7	H100
(San Diego, CA	304216	CD45RO Pacific Blue	UCHL1
USA)	353214	CCR7 APC	G043H7
	353716	CXCR3 Brilliant Violet 421™	G025H7
	339936	CD161-FITC	HP-3G10
	353406	CCR6 Per CP-Cy5.5	G034E3
	302616	CD25 Alexa Fluor <sup>®</sup> 488	BC96
	318328	CD56 Brilliant Violet 421™	HCD56
	310936	CD69 Brilliant Violet 510™	FN50
	317444	CD4 Brilliant Violet 510™	OKT4
	317429	CD4 Pacific Blue	ОКТ4
	303504	CD38 FITC	HIT2
	302326	CD20 PerCP-Cy5.5	2H7
	311118	CD24 APC	ML5
	350109	CD294 (CRTH2) APC	BM16
	348224	IgD Pacific Blue	IA6-2
<b>BD Biosciences</b>	557831	CD14 APC-Cy7	ΜφΡ9
(San Diego, CA.	555547	$TCR_{\alpha\beta}FITC$	T10B9.1A-31
USA)	563071	CCR3 Horizon <sup>™</sup> BV510	5E8
	560199	CD43 PE	1G10
	561159	CD5 Alexa Fluor <sup>®</sup> 700	UCHT2
	560609	CD27 Pe-Cy7	M-T271
	551773	CCR6 PE	11A9 (RUO)
eBiosciences	12-4776-42	Fox P3 PE	PCH101
(San Diego, CA.	48-5699-42	Ki67 eFluor <sup>®</sup> 450	20Raj1
USA)			

## **Supplemental Acknowledgments**

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