Table S1. Demographic and clinical characteristics of studied population

	SLE	**RA**	**SS**	**HD**
	n=34	*n*=29	*n*=25	*n*=28
Female *n* (%)	32 (94%)	27 (93%)	23 (92%)	26 (93%)
Age mean ± SD	33 ± 10.1	39 ± 8.8	51 ± 12.0	40 ± 11.8
Disease duration (m) mean ± SD	112 ± 73	101 ± 103	98 ± 73	
Prednisone *n* (%)	23 (67%)	4 (14%)	6 (24%)	
Antimalarial *n* (%)	23 (67%)	15 (52%)	7 (28%)	
Immunosuppressors *n* (%)	30 (88%)	28 (96%)	6 (24%)	
Disease activity mean ± SD	SLEDAI 4.2 ± 3.3	DAS28 3.2 ± 1.7	SSDAI 2 ± 3.8	

Abbreviations: SLE, systemic lupus erythematosus; RA, rheumatoid arthritis; SS, Sjögren's syndrome; HD, healthy donors; SD, standard deviation; m, months; SLEDAI, systemic lupus erythematosus disease activity index (20); DAS28, disease activity score in 28 joints (19); SSDAI, Sjögren's syndrome disease activity index (Vitali C, et al. Sjögren's Syndrome Disease Damage Index and disease activity index: scoring systems for the assessment of disease damage and disease activity in Sjögren's syndrome, derived from an analysis of a cohort of Italian patients. Arthritis Rheum. 2007;56(7):2223–2231).

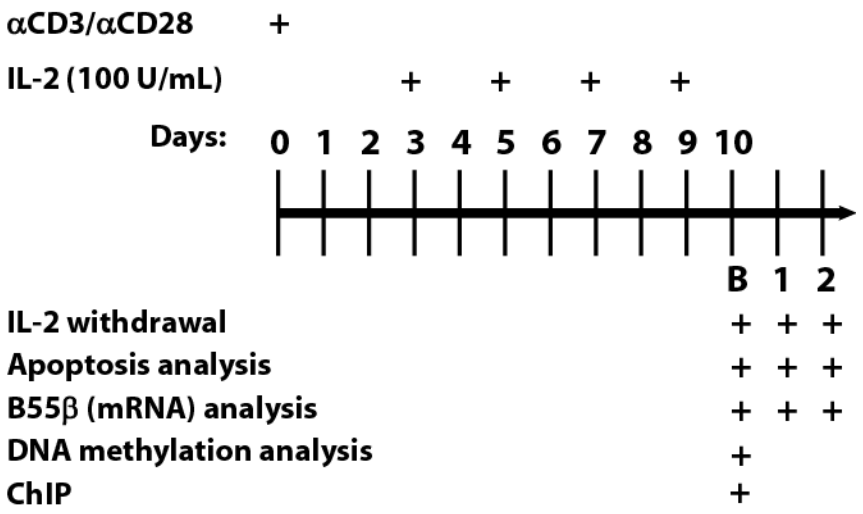

Figure S1. T cell activation and expansion protocol. T cells were isolated by negative selection and activated in vitro with plate-bound anti-CD3 (5 μg/mL) and anti-CD28 (5 μg/mL). IL-2 was added at the indicated time points. At Day 10, cells were washed, counted, and replated in fresh RPMI supplemented with 10% FCS. Apoptosis was quantified, RNA and DNA were isolated at the indicated time points.

Table S2. CAG repeat frequency in HD and patients with SLE and RA

	SLE	RA	HD
CAG(*n*)	*n*=20	*n*=20	*n*=21
Range	9 - 20	9 - 16	9 - 17
Mean (SEM)	12.35 (0.42)	12.45 (0.45)	13.31 (0.44)
Most common allele	10	10	10
Frequency of most common allele	47.5	45	47.6
P* value	>0.999	0.444	

*One way-ANOVA with post hoc Dunn' s test.

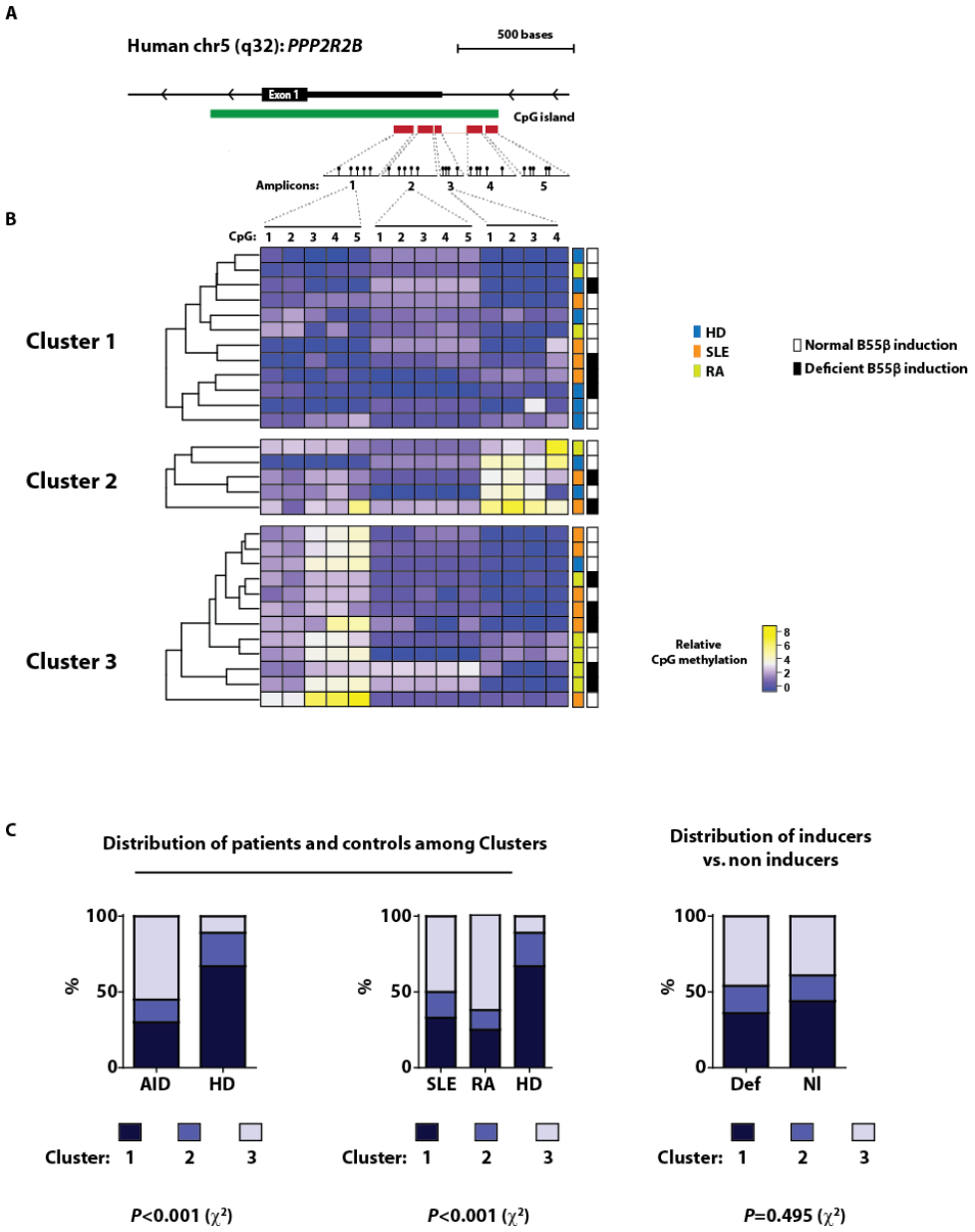

Figure S2. Methylation of *PPP2R2B* discriminates between HD and patients with AID. (**A**) Schematic representation of *PPP2R2B*, indicating the location of the CpG dinucleotides examined by pyrosequencing. (**B**) Heatmap showing relative methylation (fold change over the mean of HD) of the CpG dinucleotides from Amplicons 1 to 3. Samples were ordered by unsupervised clustering. The colored boxes on the right side of the heatmap indicate whether the sample corresponds to a HD or a patient; the black and white boxes indicate B55β induction after cytokine withdrawal. (**C**) Segregation of HD and patients, of HD and patients with SLE and RA, and of individuals with normal or defective B55β induction. *P* values were calculated using chi square.

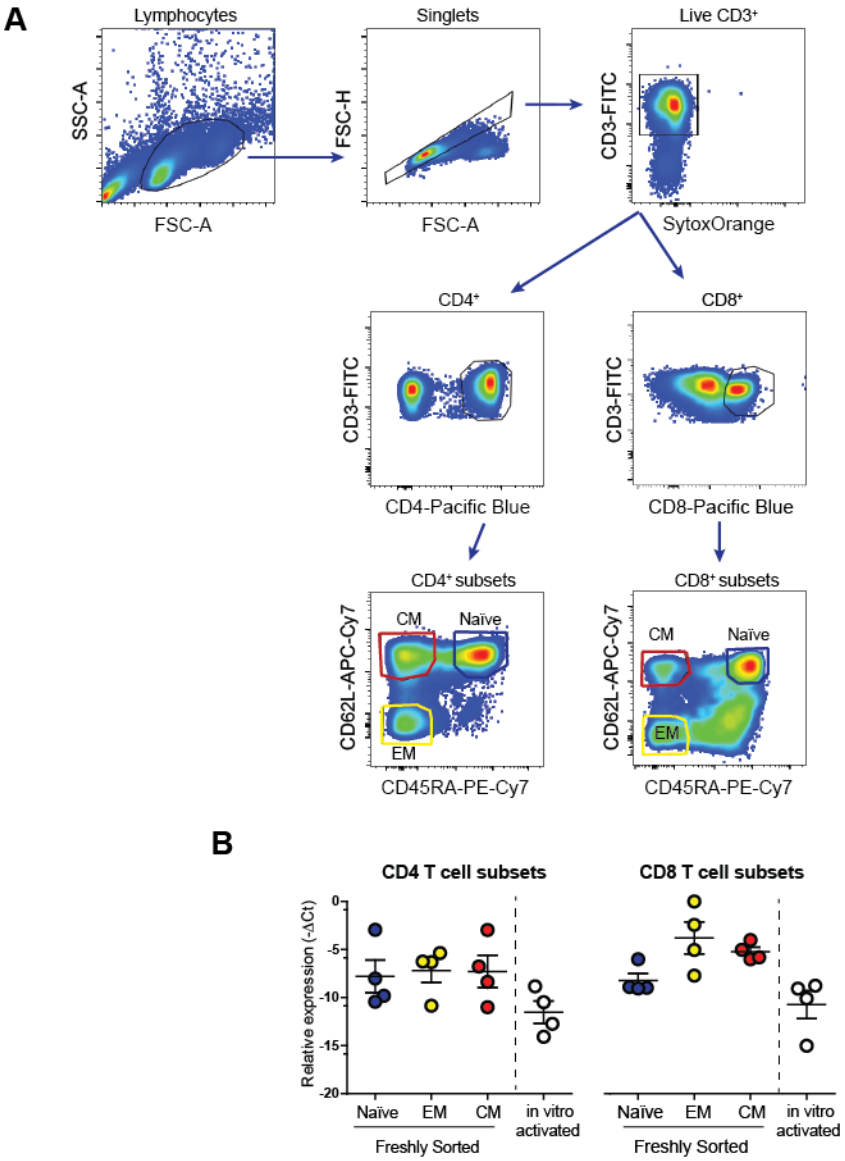

Figure S3. Levels of *PPP2R2B* in freshly isolated T cell subsets. The following CD4 and CD8 T cell subsets were sorted from peripheral blood of 4 healthy donors: CD4 naïve ($CD3^+CD4^+CD45RA^+CD62L^+$), CD4 effector memory (EM, $CD3^+CD4^+CD45RA^-CD62L^-$), CD4 central memory (CM, $CD3^+CD4^+CD45RA^-CD62L^+$), CD8 naïve ($CD3^+CD8^+CD45RA^+CD62L^+$), CD8 EM ($CD3^+CD8^+CD45RA^-CD62L^-$), CD8 CM ($CD3^+CD8^+CD45RA^-CD62L^+$), following the gating strategy depicted in (**A**). (**B**) Total RNA was isolated from the sorted T cell subsets and *PPP2R2B* mRNA levels were quantified by qPCR. Shown is -ΔCt (normalized with *ACTB*). A fraction of the naïve CD4 and CD8 cells was activated and expanded in vitro (Figure S1) and *PPP2R2B* levels were determined.

Table S3. Primers used in the study

Procedure	Target	Sequence
qPCR	*PPP2R2B*	F: 5' -ATCCTGCCACCATCACAAC-3' R: 5' -GCGTTGGCAAATACTCTTCG-3'
	ACTB	F: 5' - ATGATGATATCGCCGCGCTC-3' R: 5' - CCACCATCACGCCCTGG-3'
CAG repeats	*PPP2R2B*	F: 5'-6-FAM-TGCTGGGAAAGAGTCGTG-3' R: 5'-GCCAGCGCACTCACCCTC-3'
MS-PCR	*PPP2R2B*-methylated	F: 5' -AGTAGTAGTTGCGAGTGCGC-3' R: 5' -GAACAACCGCGACAAAATAAT-3'
	PPP2R2B-unmethylated	F: 5' - AGTAGTAGTAGTTGTGAGTGTGT-3' R: 5' -AAACAAACAACCACAACAAAATAATACC-3'
Pyrosequencing	*PPP2R2B* Amp 1	F: 5' -AGATGGTAGGGATAGGATTTA-3' R: 5' -[Biotin]-CTCCCCTTTAATACACCA-3' Seq F: 5' -GGTAGGGATAGGATTTAG-3'
	PPP2R2B Amp 2	F: 5' -GATGGTAGGGATAGGATTTA-3' R: 5' -[Biotin]-CCTCCCCTTTAATACACC-3' Seq F: 5' -AGGAGGGGGTAGGGAA-3'
	PPP2R2B Amp 3	F: 5' -ATGAGGGTGTTGGTTTTA-3' R: 5' -[Biotin]-AACCTCCCCTTTAATACA-3' Seq F: 5' -TAGAGTATTTATTTTTATATTTA-3'
	PPP2R2B Amp 4	F: 5' -AGGAGGTTGGTGTATTAAAG-3' R: 5' -[Biotin]-TTCCACCTAAACCTACAAAC-3' Seq F: 5' -TTTTGTTGTAGTGGG-3
	PPP2R2B Amp 5	F: 5' -GAATAGGTATTTGGGTAGTAAG-3' R: 5' -[Biotin]-AAAACCTACTTCTCTTTACTATTC-3' Seq F: 5' - TGTAGGTTTAGGTGGA-3'
ChIP	*CTCF* positive control	F: 5' -TGTGGATAATGCCCGACCTGAAGATCTG-3' R: 5' -ACGGAATTGGTTGTAGTTGTGGAATCGGAAGT-3'
	PPP2R2B Amp 1	F: 5' -GTGTGGGTGTGAGGGTGAGT-3' R: 5' - AAAATGGTGCCTTTCTGGAC-3'