

**Table 1. qPCR probe sequences of miRNAs and mRNAs.**

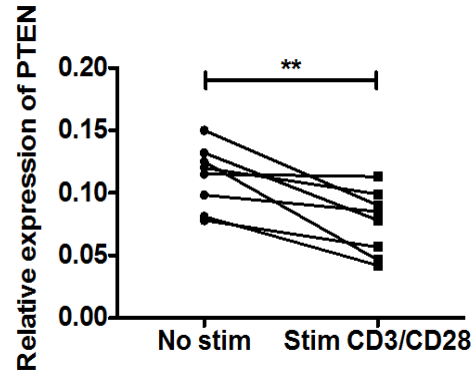
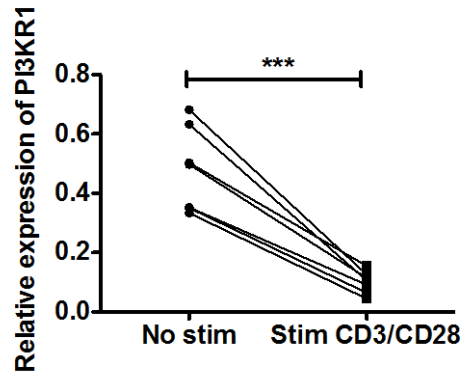
**Figure S1. PI3KR1 and PTEN expression analysis.** (A) CD4<sup>+</sup>T cells isolated from HV samples were stimulated with CD3/CD28 antibodies *in vitro* for 24 hours. Transcriptional expression of PI3KR1 (N=7) and PTEN (n=8) were analyzed with real time RT-PCR. (B) Western blot analysis of lysates from purified CD4<sup>+</sup>T cells (HV) after mitogenic stimulation with CD3/CD28 antibodies and probed for PI3KR1, PTEN, and phospho-PTEN. Actin levels were monitored as a control for loading. (C) Transcriptional expression of PI3KR1 was analyzed with real-time RT-PCR in and in CD4<sup>+</sup>T cells from untreated and natalizumab treated patients (untreated: n=8; Nat. treated: n=10). \*\*\* $p < 0.001$ ; \*\* $p < 0.01$ ; n.s: not significant.

**Figure S2. Correlation of age with relative expression of miR-17.** Non-parametric Spearman correlation, with two-tailed p-value, between miR-17 expression and age in HVs, untreated and natalizumab treated RRMS patients, was calculated. 95% confidence interval is depicted by dotted curves.

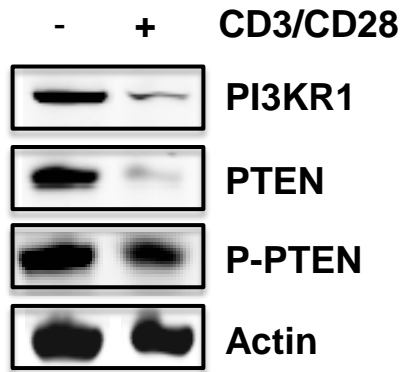
miR-17	CAAAGUGCUUACAGUGCAGGUAG
miR-106b	UAAAGUGCUGACAGUGCAGAU
RNU44	CCTGGATGATGATAGCAAATGCTGACTGAACATGAAGGTCTTAATTAGCTCTAACTGACT
PTEN	CCTCTTCCTCGGCTTCTCCTGAAAG
BIM	CAGTGCAATGGCTTCCATGAGGCAG
P21	CAGCATGACAGATTTCTACCACTCC
E2F1	TCCAGTGGCTGGGCAGCCACACCAC
TGFBR2	GCTCAACCACCAGGGCATCCAGATG
PI3KR1	GGGAGATATCTCGAGGGAAGAAGTG
PUM1	CTACCGCTCCGCCC GTGTTGGTGGA

Supplementary Table 1.

A.



B.



C.

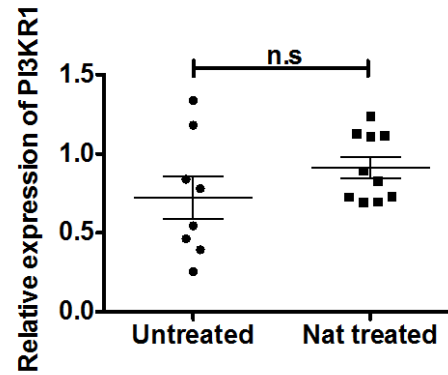
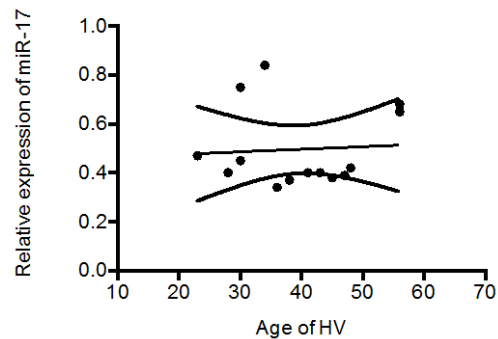
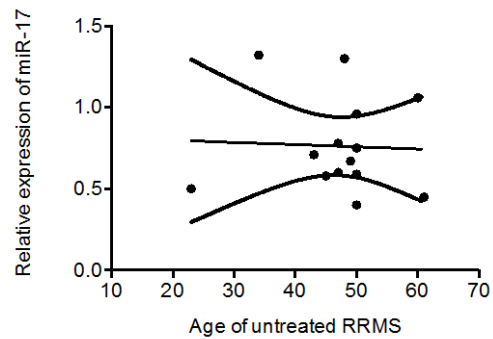


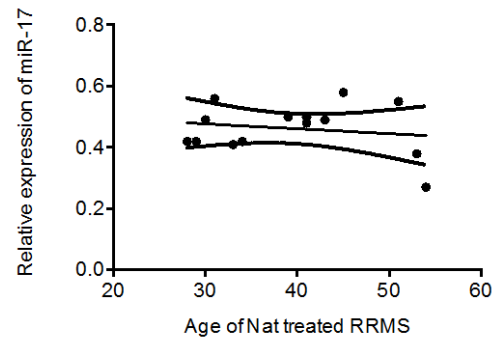
Figure S1.



Spearman r	-0.07080
95% confidence interval	-0.5912 to 0.4912
P value (two-tailed)	0.8099
P value summary	ns



Spearman r	-0.1090
95% confidence interval	-0.6157 to 0.4614
P value (two-tailed)	0.7106
P value summary	ns



Spearman r	-0.02104
95% confidence interval	-0.5578 to 0.5281
P value (two-tailed)	0.9431
P value summary	ns

Figure S2.