Supplementary Data

Supplementary table 1. Comparison of relapse risk in previously naïve patients and switchers.

Supplementary table 2. Premature discontinuation is associated with occurrence of relapses.

Supplementary table 3. Cox regression analysis.

Supplementary figure 1. Flow chart of the study.

Supplementary figure 2. Effect size.

Supplementary figure 3. Propensity score matching.

Supplementary table 1. Comparison of relapse risk in previously naïve patients and switchers. Statistics done by Fisher's exact test.

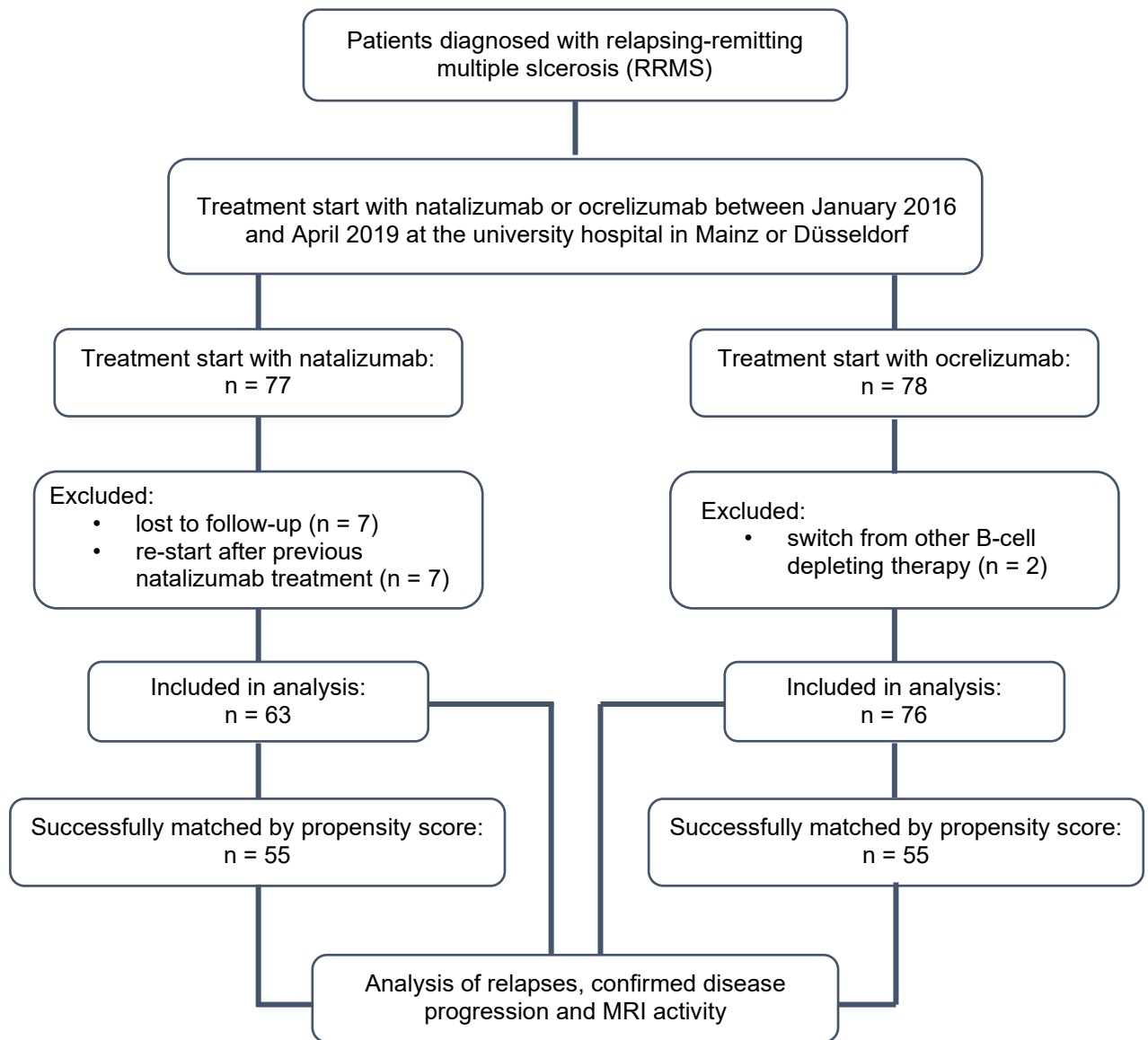| Treatment naïve	Yes n (%)	No n (%)	p-Value
Relapses in total patient cohort	5 (21.7)	24 (20.7)	1.000
Relapses in natalizumab group	2 (20.0)	16 (30.2)	0.710
Relapses in ocrelizumab group	3 (23.1)	8 (12.7)	0.388

Supplementary table 2. Premature discontinuation is associated with occurrence of relapses. Statistics done by Fisher's exact test. NEDA: no evidence of disease activity.

Premature discontinuation	Yes (n = 26)	No (n = 113)	*p*-Value
	n (%)	*n* (%)	
Relapse	11 (42.3)	18 (15.9)	**0.006**
Confirmed disability progression	5 (19.2)	17 (15.0)	0.562
Total MRI activity	8 (30.8)	30 (26.5)	0.635
Proportion of patients with NEDA-3	10 (38.5)	63 (55.8)	0.131

Supplementary table 3. Cox regression analysis. Analysis was performed in both the matched cohort and the total cohort. HRs < 1.0 would mean more disease activity in the natalizumab group. HR: hazard ratio; CI: confidence interval.
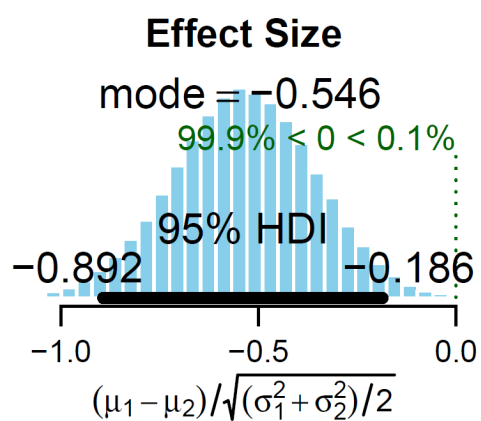
Combined disease activity	HR	95% CI	*p*-Value
Matched patient cohort	0.78	0.44-1.39	0.393
Total patient cohort	0.83	0.51-1.36	0.465

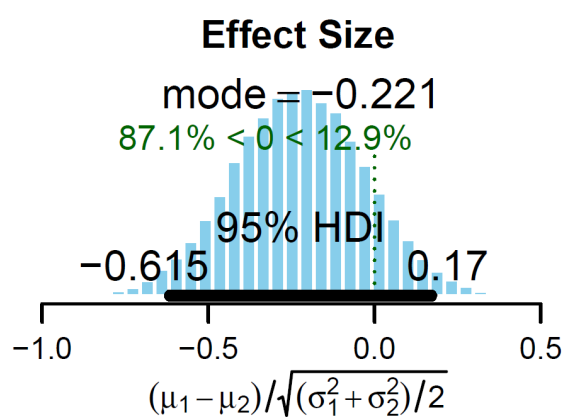**Supplementary figure 1. Flow chart of the study.**

Supplementary figure 2. Effect size. The effect size is shown before (A) and after (B) propensity score matching. Based on the Bayesian posterior distribution analyses the effect size for the groups are within the high density interval (HDI) dark bold line which indicates a sufficient sample size for the conclusion achieved in this study.

A

Effect Size

mode = −0.546

99.9% < 0 < 0.1%

95% HDI

−0.892   −0.186

$-1.0 \qquad -0.5 \qquad 0.0$

$$(\mu_1 - \mu_2)/\sqrt{(\sigma_1^2 + \sigma_2^2)/2}$$

B

Effect Size

mode = −0.221

87.1% < 0 < 12.9%

95% HDI

−0.615   0.17

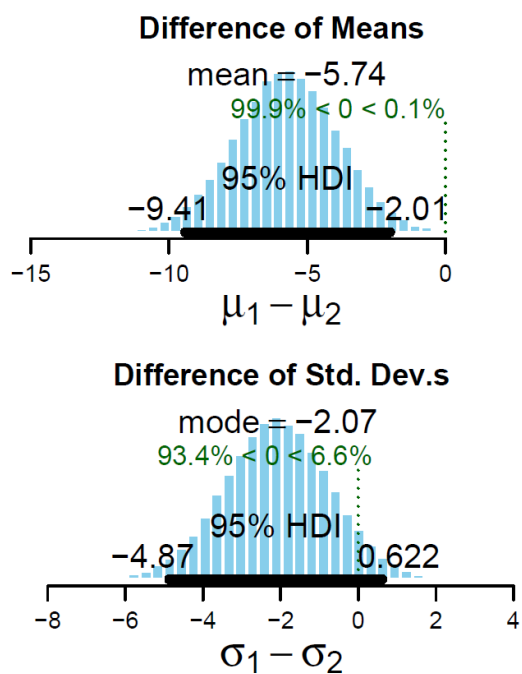$-1.0 \qquad -0.5 \qquad 0.0 \qquad 0.5$

$$(\mu_1 - \mu_2)/\sqrt{(\sigma_1^2 + \sigma_2^2)/2}$$

Supplementary figure 3. Propensity score matching.

A

Difference of Means
mean = −5.74

99.9% < 0 < 0.1%

95% HDI

−9.41   −2.01

$\mu_1 - \mu_2$

(−15 −10 −5 0)

Difference of Std. Dev.s
mode = −2.07

93.4% < 0 < 6.6%

95% HDI

−4.87   0.622

$\sigma_1 - \sigma_2$

(−8 −6 −4 −2 0 2 4)

B

Difference of Means
mean = −2.22

87.1% < 0 < 12.9%

95% HDI

−6.02   1.7

$\mu_1 - \mu_2$

(−10 −5 0 5)

Difference of Std. Dev.s
mode = 0.154

44.3% < 0 < 55.7%

95% HDI

−2.62   3.17

$\sigma_1 - \sigma_2$

(−6 −4 −2 0 2 4 6)