Supplementary tables

Supplementary table 1 Recruitment sites for study participants.

Study site	Dimethyl fumarate (n=27)	Injectable drug (n=9)
Akershus University Hospital	14	2
Haukeland University Hospital, Bergen	5	0
Innlandet Hospital, Lillehammer	1	2
Oslo University Hospital, Ullevål	0	1
Vestre Viken HF, Drammen	2	0
Helse Møre og Romsdal HF, Molde	3	1
Stavanger Universitetssykehus	2	3

Supplementary table 2

Please find attached excel-file.

Supplementary table 3. Previous cross-sectional studies of the gut microbiota profile in adults with RRMS compared with healthy controls.

Study	**Participants**	**Associated genera**
Cantarel BL et al(41)	7 RRMS, 8 healthy controls	Reduced: *Bacteroidaceae, Faecalibacterium* Increased: *Ruminococcus*
Miyake et al. 2015(3)	20 MS patients, 40 healthy controls	Reduced: *Faecalibacterium, Prevotella, Anaerostipes*
Jangi et al. 2016(1)	60 MS patient, 43 healthy controls	Reduced: *Butyricimonas, Paraprevotella, Haemophilus, Slackia, Collinsella, Veillonellaceae_unc, Prevotella, Sutterella, Sarcina, Mollicutes_unc, Prevotellaceae_unc, Barnesiella, Acidaminococcaceae_unc, Guggenheimella, Buttiauxella, Sporanaerobacter* Increased: *Methanobrevibacter, Akkermansia, Megasphaera, Cloacibacillus, Clostridia_unc, Holdemania, Desulfovibrio, Peptococcaceae_unc, Megamonas, Thermoplasmatales_unc,*
Chen et al. 2016(2)	31 MS patients, 36 controls	Reduced: *Adlercreutzia, Collinsella, Actinobacteria_unclassified, Parabacteroides, Coprobacillus, Lactobacillus, Haemophilus* Increased: *Flavobacterium, Pedobacter, Blautia, Dorea, Mycoplana, Pseudomonas*
Cekanaviciute E et al. 2017(6)	71 RRMS, 71 HC	Reduced: *Paraprevotellaceae_unc, Prevotella, Serratia, Bacillus, Acidaminococcus, Clostridium, Aquamonas, Parabacteroides, Phascolarctobacterium, Pseudomonadaceae_unc* Increased: *Acinetobacter, Varibaculum, Corynebacterium, Bifidobacterium, Megamonas, Mogibacteriaceae_unc, Megasphaera, Klebsiella, Peptostreptococcaceae_unc, ph2, actinomyces, Mogibacterium, Akkermansia, SMB53, Bulleidia*

Supplementary table 4. Differences in gut microbial taxa the subset of patients having increased GSRS score after 2 weeks of treatment with DMF (n=10).

	Baseline	**2 weeks**	**P-value**
Actinobacteria	0.021 (0.008-0.035)	0.011 (0.003-0.024)	0.20
Bacteroidetes	0.206 (0.171-0.372)	0.192 (0.145-0.368)	0.59
Firmicutes	0.708 (0.528-0.767)	0.686 (0.515-0.782)	0.80
Bacteroides	0.124 (0.078-0.21)	0.14 (0.052-0.26)	0.59
Bifidobacterium	0.012 (0.003-0.031)	0.005 (0-0.015)	0.37
Faecalibacterium	0.056 (0.031-0.088)	0.058 (0.024-0.139)	0.58

Supplementary table 5. Differences in gut microbial taxa at different phylogenetic levels at baseline and at two weeks in patients having increase or no increase in GSRS score after 2 weeks of treatment with DMF.

	Baseline				**2 weeks**			
	No increase in GSRS	**Increased GSRS**	**P**	Q_{FDR}	**No increase in GSRS**	**Increased GSRS**	**P**	Q_{FDR}
Uncultered Christensenellaceae	0(0-0.001)	0(0-0)	0.014	0.96	0(0-0)	0(0-0)	0.48	1
Lachnospiraceae NK4A136 group	0.01(0.004-0.022)	0.034(0.013-0.058)	0.014	0.96	0.02(0.009-0.027)	0.025(0.01-0.09)	0.38	1
Peptoclostridium	0(0-0)	0.001(0-0.001)	0.017	0.96	0(0-0)	0(0-0)	0.31	1
Peptostreptococcaceae	0(0-0.001)	0.001(0-0.003)	0.024	1	0(0-0.001)	0.001(0-0.002)	0.28	1
Bacteroidaceae	0.308(0.125-0.408)	0.124(0.078-0.21)	0.033	1	0.133(0.088-0.361)	0.14(0.052-0.26)	0.41	1
Bacteroides	0.308(0.125-0.408)	0.124(0.078-0.21)	0.033	1	0.133(0.088-0.361)	0.14(0.052-0.26)	0.41	1
Prevotellaceae	0(0-0)	0(0-0.004)	0.037	1	0(0-0)	0(0-0.003)	0.48	1
Odoribacter	0.004(0.002-0.005)	0.001(0-0.002)	0.046	1	0.004(0.003-0.005)	0.003(0-0.004)	0.19	1
Dialister	0.018(0-0.028)	0.006(0-0.018)	0.50	1	0.018(0.008-0.032)	0.005(0-0.015)	0.023	1
Intestinimonas	0(0-0.001)	0(0-0)	0.51	1	0(0-0)	0(0-0)	0.029	1
Coprobacter	0(0-0)	0(0-0.001)	0.22	1	0(0-0)	0(0-0)	0.046	1
Actinobacteria	0.015(0.012-0.031)	0.021(0.008-0.035)	0.93	1	0.011(0.006-0.022)	0.011(0.003-0.024)	0.74	1
Bifidobacterium	0.011(0.005-0.02)	0.012(0.003-0.031)	0.76	1	0.008(0.002-0.015)	0.005(0-0.015)	0.45	1

Supplementary table 6 Dietary differences in patients experiencing GI symptoms in DMF-group compared to those without worsening of symptoms

	No increase in GSRS score	**Increased GSRS score**	**P-value**	**Q_{FDR}**
Energy (kJ/day, IQR)	9875(8776-12822)	10328(7758-12290)	0.742	0.80
Proteins, E% (IQR)	14(13.4-15.88)	16.9(14.8-17.7)	0.078	0.34
Fat, E% (IQR)	35.9(33.6-38.2)	37.5(33.8-40.88)	0.409	0.70
Saturated, E% (IQR)	13.5(11.18-15)	13.8(12.2-15.6)	0.551	0.72
Trans saturated, E% (IQR)	0.4(0.2-0.4)	0.4(0.3-0.4)	0.679	0.80
Monounsaturated, E% (IQR)	13(12.2-13.9)	13.7(10.9-15.58)	0.424	0.70
Polyunsaturated, E% (IQR)	6.5(5.3-7.6)	5.9(5.1-7.3)	0.454	0.70
Carbohydrates, E% (IQR)	47(42-51)	40.1(37.9-44.6)	**0.011**	**0.07**
Starch, E% (IQR)	23.1(19.1-24.8)	20.1(17.3-22.8)	0.291	0.70
Fiber, E% (IQR)	2.1(1.9-3.1)	2.1(1.9-2.38)	0.467	0.70
Mono- and di-saccharides, E% (IQR)	20.3(16.5-23.28)	19(13.3-24)	0.486	0.70
Sugar, E% (IQR)	5.6(3.4-14.2)	6(4.1-9.7)	0.86	0.86
Alcohol, E% (IQR)	0.3(0-0.8)	1.9(0.4-6.1)	**0.011**	**0.07**

GSRS: Gastrointestinal symptom rating scale