

## SUPPLEMENTARY MATERIALS

### Supplementary Table S1. Microbiota composition at different taxonomic levels.

Supplementary Tables S1a, S1b and S1c show median and quartiles 25% (p25) and 75% (p75) values for all RRMS patients for each phylum, family and genus members identified in the microbiota analysis, respectively.

**Supplementary Table S1a. Phylum**

<b>Stats</b>	<b>median</b>	<b>p25</b>	<b>p75</b>
<i>Firmicutes</i>	58.70	54.94	65.62
<i>Bacteroidetes</i>	30.81	23.81	37.91
<i>Actinobacteria</i>	2.82	1.17	5.15
<i>Proteobacteria</i>	2.48	1.73	3.13
<i>Verrucomicrobia</i>	0.44	0.01	3.25
<i>Synergistetes</i>	0.02	0.00	0.07
<i>Lentisphaerae</i>	0.01	0.00	0.02
<i>Euryarchaeota</i>	0.01	0.00	0.18

**Supplementary Table S1b. Family**

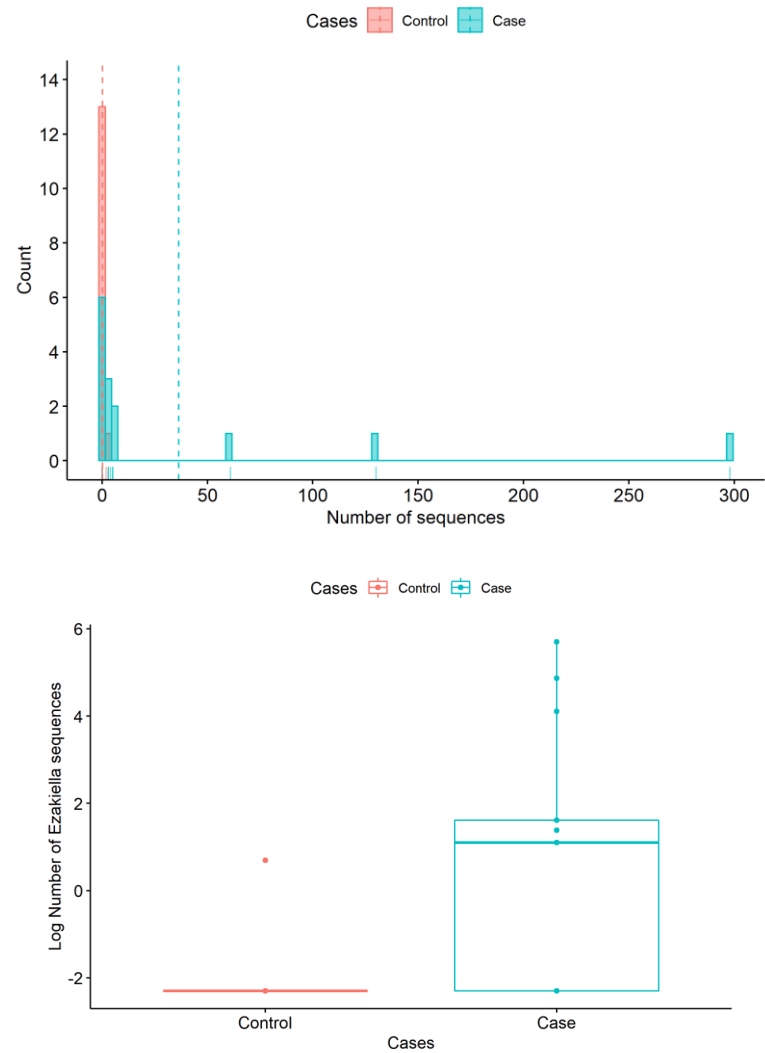
<b>Stats</b>	<b>median</b>	<b>p25</b>	<b>p75</b>
<i>Ruminococcaceae*</i>	24.31	18.29	32.38
<i>Bacteroidaceae</i>	15.89	12.24	21.18
<i>Lachnospiraceae*</i>	15.87	13.31	17.40
<i>Porphyromonadaceae</i>	5.08	3.29	7.19
<i>Prevotellaceae</i>	3.29	0.01	8.53
<i>Rikenellaceae</i>	2.79	1.97	3.24
<i>Eubacteriaceae</i>	2.56	1.63	3.81
<i>Oscillospiraceae</i>	2.43	1.59	4.04
<i>Veillonellaceae</i>	1.84	0.02	4.33
<i>Erysipelotrichaceae</i>	1.75	1.32	3.32
<i>Acidaminococcaceae</i>	1.19	0.00	1.99
<i>Bifidobacteriaceae</i>	1.04	0.61	3.09
<i>Sutterellaceae</i>	1.00	0.40	1.34
<i>Coriobacteriaceae</i>	0.64	0.35	1.77
<i>Desulfovibrionaceae</i>	0.55	0.40	1.06
<i>Akkermansiaceae</i>	0.44	0.01	3.25
<i>Clostridiaceae</i>	0.38	0.20	0.82
<i>Streptococcaceae</i>	0.19	0.09	0.44
<i>Christensenellaceae</i>	0.15	0.05	0.56
<i>Defluviitaleaceae</i>	0.12	0.02	1.30
<i>Lactobacillaceae</i>	0.10	0.00	0.49
<i>Eggerthellaceae</i>	0.09	0.05	0.17
<i>Gracilibacteraceae</i>	0.05	0.00	0.46
<i>Enterobacteriaceae</i>	0.02	0.00	0.13

**Supplementary Table S1c. Genus**

<b>Stats</b>	<b>median</b>	<b>p25</b>	<b>p75</b>
<i>Bacteroides</i>	15.89	12.24	21.18
<i>Faecalibacterium</i>	9.74	8.32	12.17
<i>Ruminococcus</i> *	4.34	2.76	7.68
<i>Gemmiger</i> *	3.33	2.55	5.67
<i>Roseburia</i>	3.17	1.48	4.99
<i>Alistipes</i>	2.79	1.97	3.24
<i>Eubacterium</i>	2.56	1.62	3.80
<i>Oscillibacter</i>	2.43	1.59	4.04
<i>Lachnoclostridium</i> *	2.00	1.43	2.81
<i>Barnesiella</i>	1.97	0.70	2.40
<i>Parabacteroides</i>	1.96	1.56	3.29
<i>Ruminiclostridium</i>	1.82	1.13	3.58
<i>Blautia</i>	1.73	1.37	2.35
<i>Phascolarctobacterium</i>	1.12	0.00	1.99
<i>Erysipelatoclostridium</i>	1.10	0.36	1.75
<i>Bifidobacterium</i>	1.04	0.61	3.09
<i>Fusicatenibacter</i>	0.98	0.50	1.67
<i>Intestinimonas</i>	0.70	0.30	1.15
<i>Dorea</i>	0.58	0.38	0.71
<i>Desulfovibrio</i>	0.55	0.40	1.06
<i>Collinsella</i>	0.54	0.25	1.77
<i>Sporobacter</i>	0.52	0.26	1.05
<i>Coprococcus</i>	0.49	0.36	0.89
<i>Akkermansia</i>	0.44	0.01	3.25
<i>Tyzzerella</i>	0.33	0.22	0.67
<i>Pseudoflavonifractor</i>	0.31	0.13	0.45
<i>Acetanaerobacterium</i>	0.30	0.04	0.64
<i>Odoribacter</i>	0.27	0.11	0.66
<i>Anaerobacterium</i>	0.19	0.01	0.90
<i>Streptococcus</i> *	0.19	0.09	0.42
<i>Sutterella</i>	0.18	0.00	0.48
<i>Christensenella</i>	0.15	0.05	0.56
<i>Vallitalea</i>	0.10	0.02	1.23
<i>Lactobacillus</i>	0.10	0.00	0.49
<i>Lachnospira</i>	0.10	0.01	0.52
<i>Prevotella</i> *	0.09	0.01	8.53
<i>Parasutterella</i>	0.08	0.01	1.16
<i>Anaerostipes</i>	0.08	0.05	0.38
<i>Dialister</i>	0.07	0.00	3.16
<i>Eisenbergiella</i>	0.06	0.01	0.11
<i>Gracilibacter</i>	0.05	0.00	0.46
<i>Hungatella</i>	0.05	0.03	0.15
<i>Clostridium</i>	0.03	0.01	0.13
<i>Lachnobacterium</i>	0.02	0.00	0.02
<i>Escherichia</i>	0.01	0.00	0.06
<i>Paraprevotella</i>	0.00	0.00	0.27

**Supplementary Figure S1. Analysis of cases and controls. Genera Ezakiella and Bilophila.**  
Number of cases and controls with detection of genera sequences and mean log value of sequences for both genera are included.

**Ezakiella**



**Bilophila**

