

Supplementary Table S3. Spearman correlation analysis between MMSE and gut microbiota.

Genus	N	Missing	Spearman_r	p_value	FDR_q
g__Bifidobacterium	578	0	0.141	0.001	0.017
f__Enterobacteriaceae__	578	0	-0.128	0.002	0.038
g__Subdoligranulum	578	0	0.115	0.006	0.077
f__Lachnospiraceae;__	578	0	0.109	0.009	0.096
observed_features	578	0	-0.106	0.010	0.094
g__Lachnospira	578	0	0.099	0.017	0.129
shannon_entropy	578	0	-0.099	0.017	0.115
g__Clostridium_sensu_stricto_1	578	0	-0.097	0.019	0.115
g__Blautia	578	0	0.096	0.021	0.113
g__Clostridia_UCG-014	578	0	0.094	0.024	0.109
g__Lactobacillus	578	0	-0.092	0.026	0.109
g__Prevotella	578	0	0.087	0.037	0.143
g__Lachnoclostridium	578	0	0.079	0.059	0.211
g__Dialister	578	0	0.078	0.059	0.200
g__Anaerostipes	578	0	0.076	0.066	0.211
g__Bacteroides	578	0	0.074	0.076	0.228
g__Faecalibacterium	578	0	0.074	0.076	0.217
g__Megamonas	578	0	0.073	0.079	0.214
g__UCG-005	578	0	-0.068	0.105	0.270
g__[Eubacterium]_ruminantium_group	578	0	0.064	0.125	0.306
g__[Ruminococcus]_gnavus_group	578	0	0.063	0.128	0.299
f__Ruminococcaceae;__	578	0	-0.054	0.198	0.446
g__Parabacteroides	578	0	0.054	0.198	0.429
g__Streptococcus	578	0	-0.051	0.220	0.441
g__Agathobacter	578	0	0.050	0.230	0.428
g__Phascolarctobacterium	578	0	-0.047	0.260	0.467
g__Coprococcus	578	0	0.046	0.273	0.475
g__Megasphaera	578	0	0.042	0.310	0.523
g__Lachnospiraceae_NK4A136_group	578	0	0.042	0.311	0.509
g__Fusicatenibacter	578	0	0.042	0.315	0.501
g__Roseburia	578	0	0.040	0.338	0.521
g__Ruminococcus	578	0	0.038	0.365	0.548
g__Christensenellaceae_R-7_group	578	0	-0.037	0.379	0.553
g__Dorea	578	0	0.035	0.404	0.575
g__Romboutsia	578	0	-0.034	0.408	0.565
g__CAG-352	578	0	0.033	0.425	0.574
g__[Eubacterium]_hallii_group	578	0	0.031	0.463	0.610
g__Holdemanella	578	0	0.029	0.485	0.623
g__Akkermansia	578	0	-0.026	0.527	0.662
g__Escherichia-Shigella	578	0	-0.021	0.607	0.728
g__[Eubacterium]_eligans_group	578	0	-0.021	0.618	0.726
g__[Ruminococcus]_torques_group	578	0	0.020	0.630	0.723
g__UCG-002	578	0	-0.016	0.704	0.792
g__Sutterella	578	0	-0.015	0.713	0.786
g__Klebsiella	578	0	-0.015	0.719	0.776
g__[Eubacterium]_coprostanoligenes_group	578	0	-0.012	0.770	0.816
g__Veillonella	578	0	0.012	0.771	0.801
g__Alistipes	578	0	-0.002	0.959	0.977
g__Collinsella	578	0	-0.001	0.974	0.974