

Supplementary Material

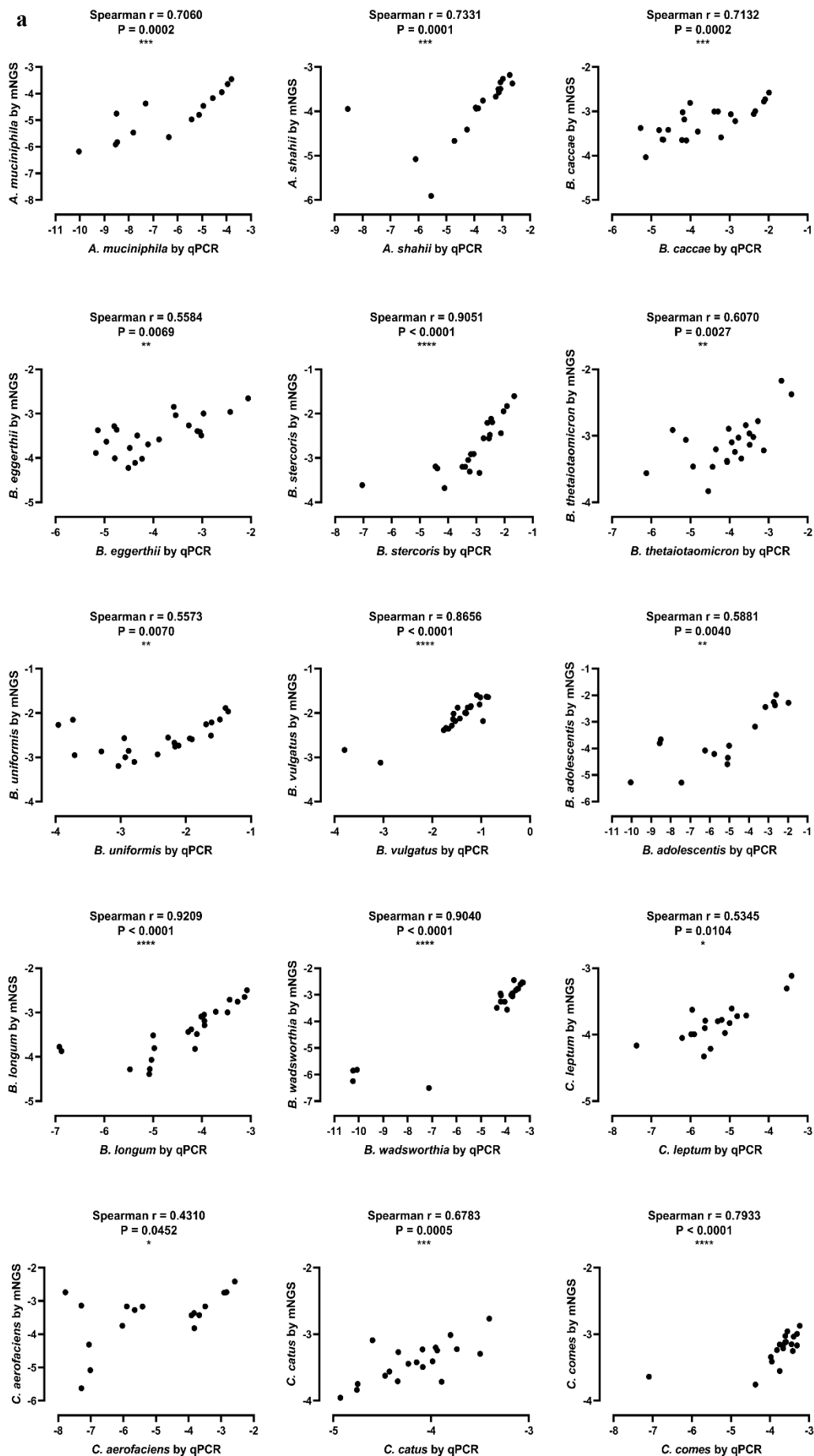
Quantitative and Dynamic Profiling of Human Gut Core Microbiota by Real-time PCR

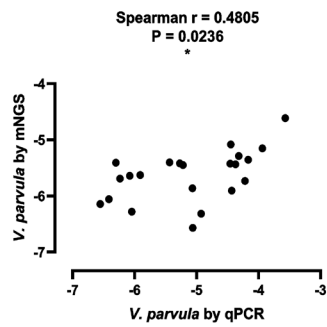
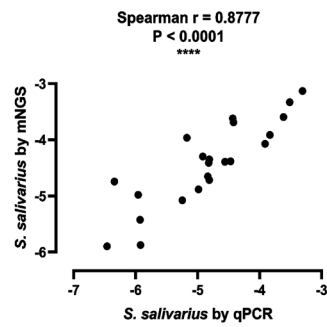
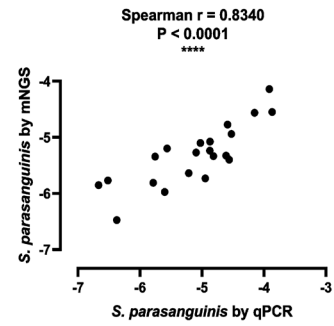
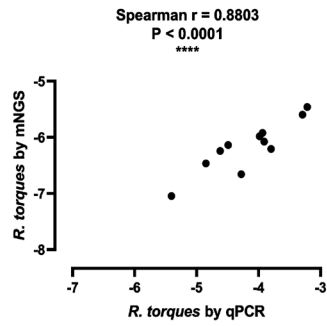
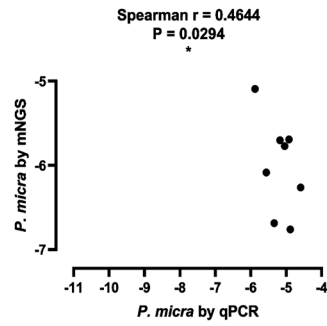
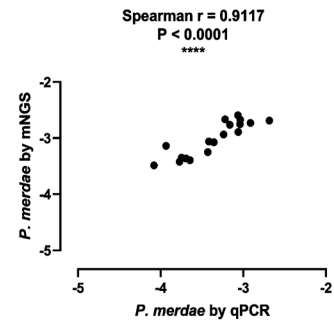
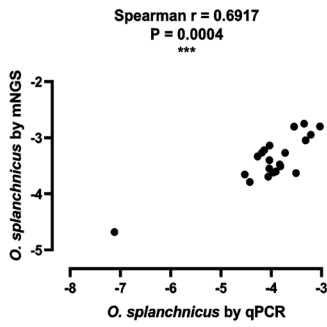
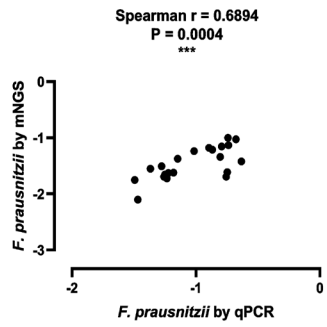
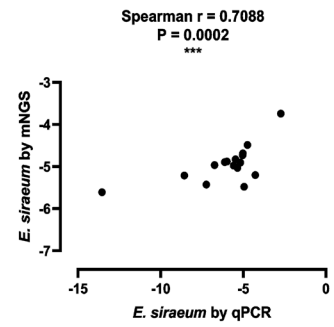
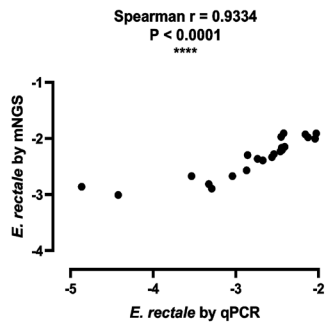
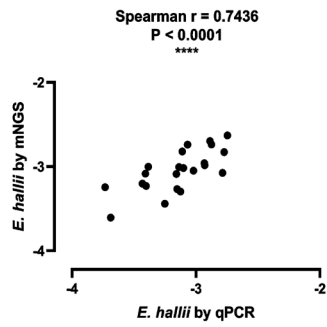
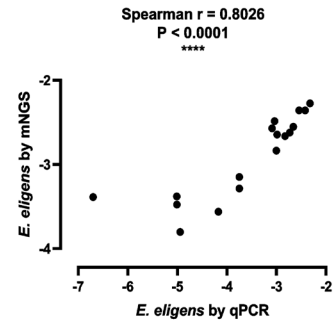
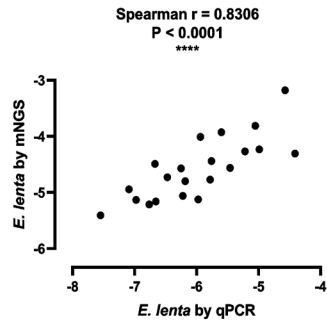
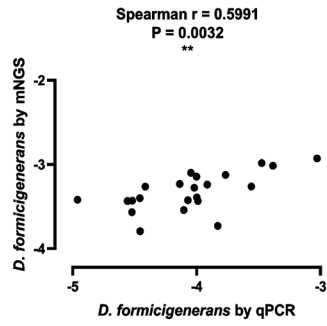
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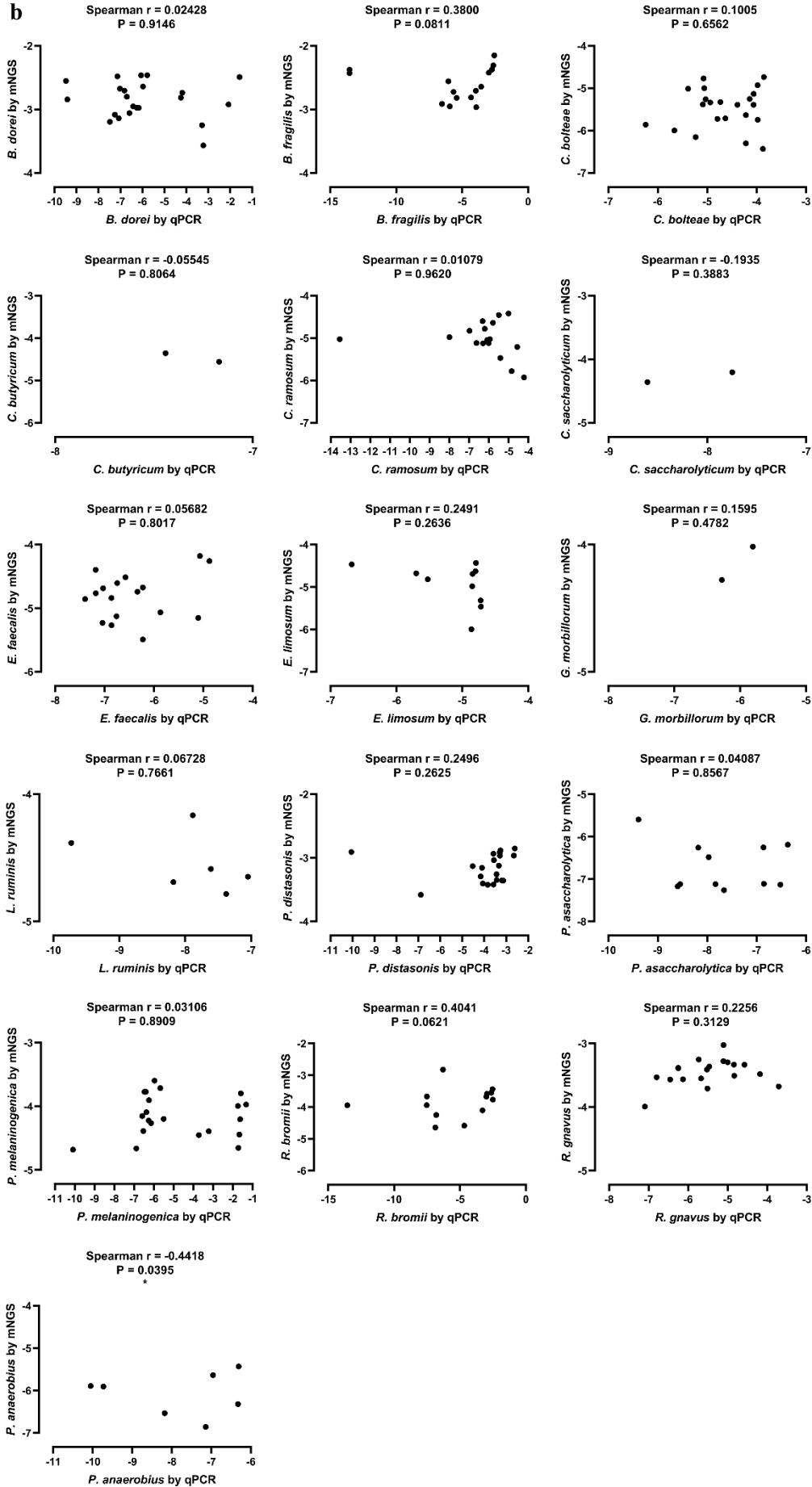
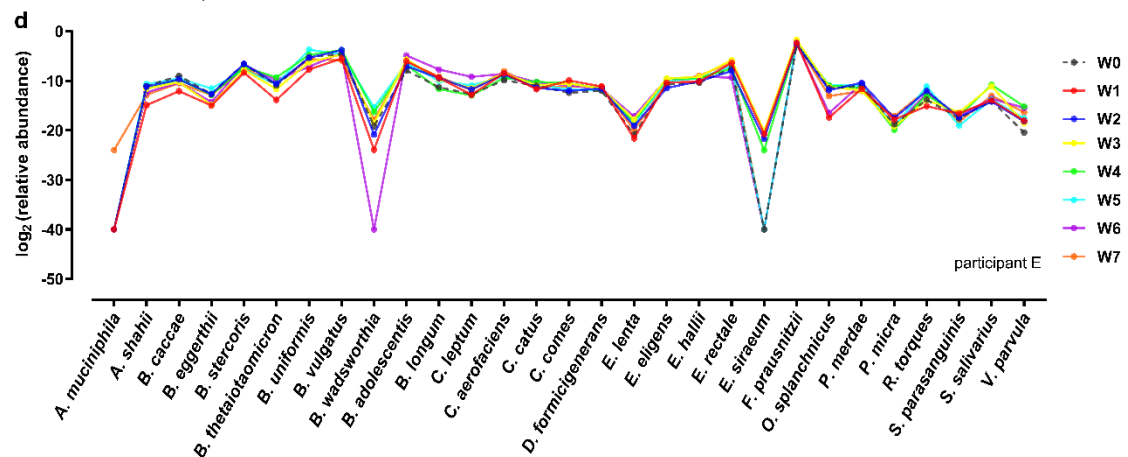
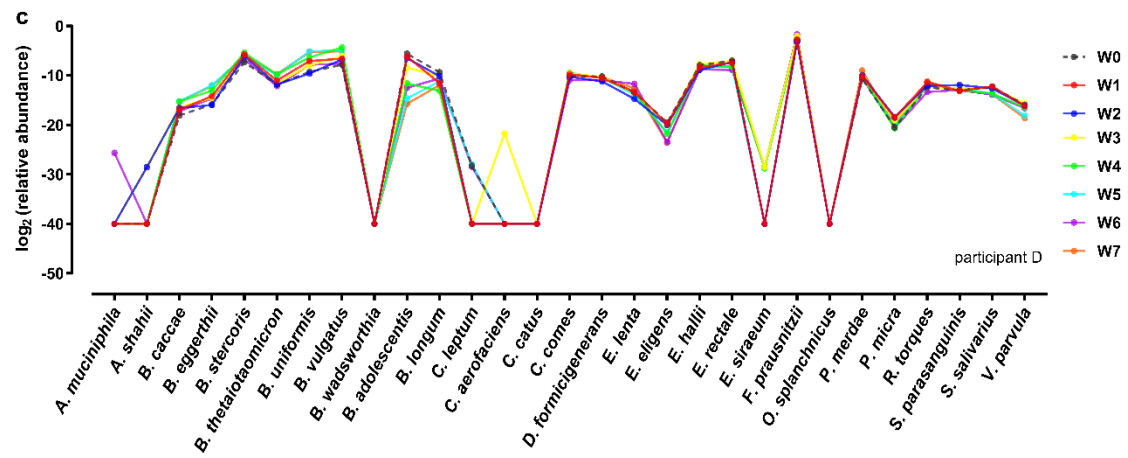
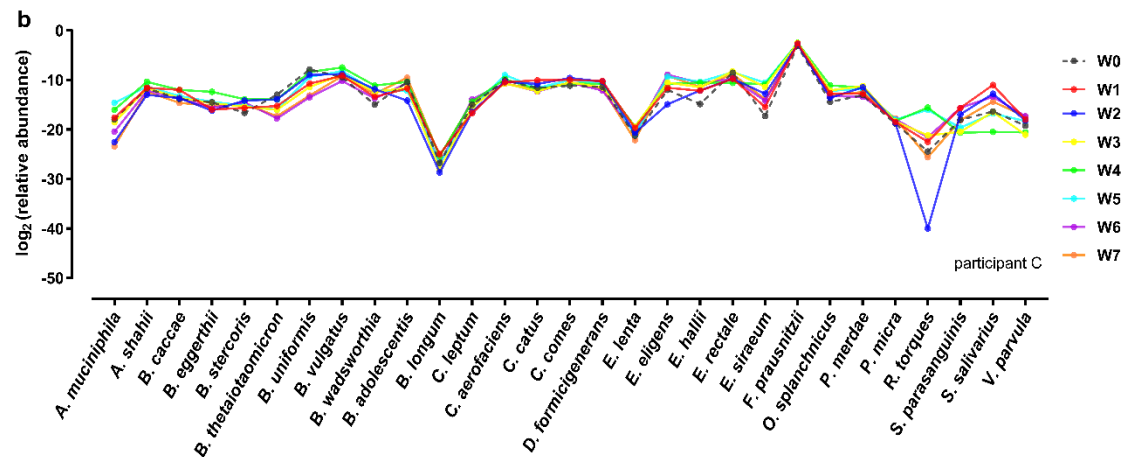
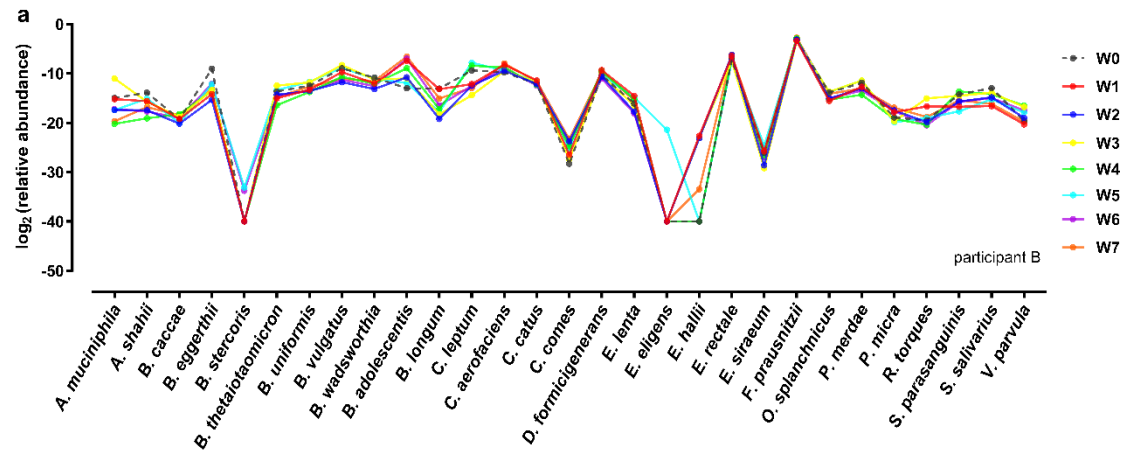
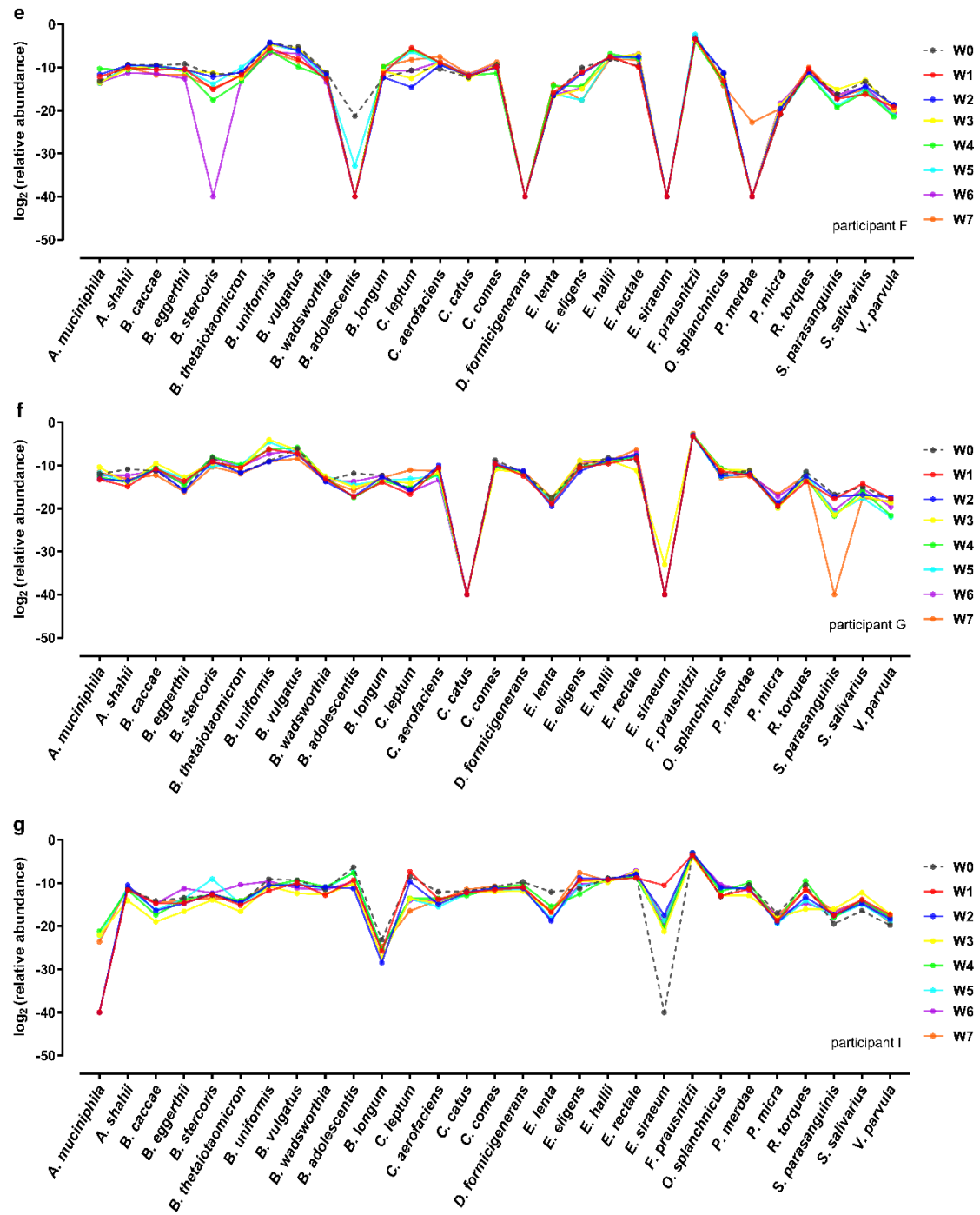


Fig. S1 Correlation analysis of the relative abundance of 45 bacteria determined by qPCR and mNGS.

a The species abundances of 29 bacteria obtained by the two methods were significantly correlated ($P < 0.05$); **b** the other 16 bacteria were not correlated ($P > 0.05$). The data were analyzed by Spearman's correlation ($n=22$). Since the scale of the x/y axis was converted to $\log_{10}$, the results of undetected targets are not included in the graphs





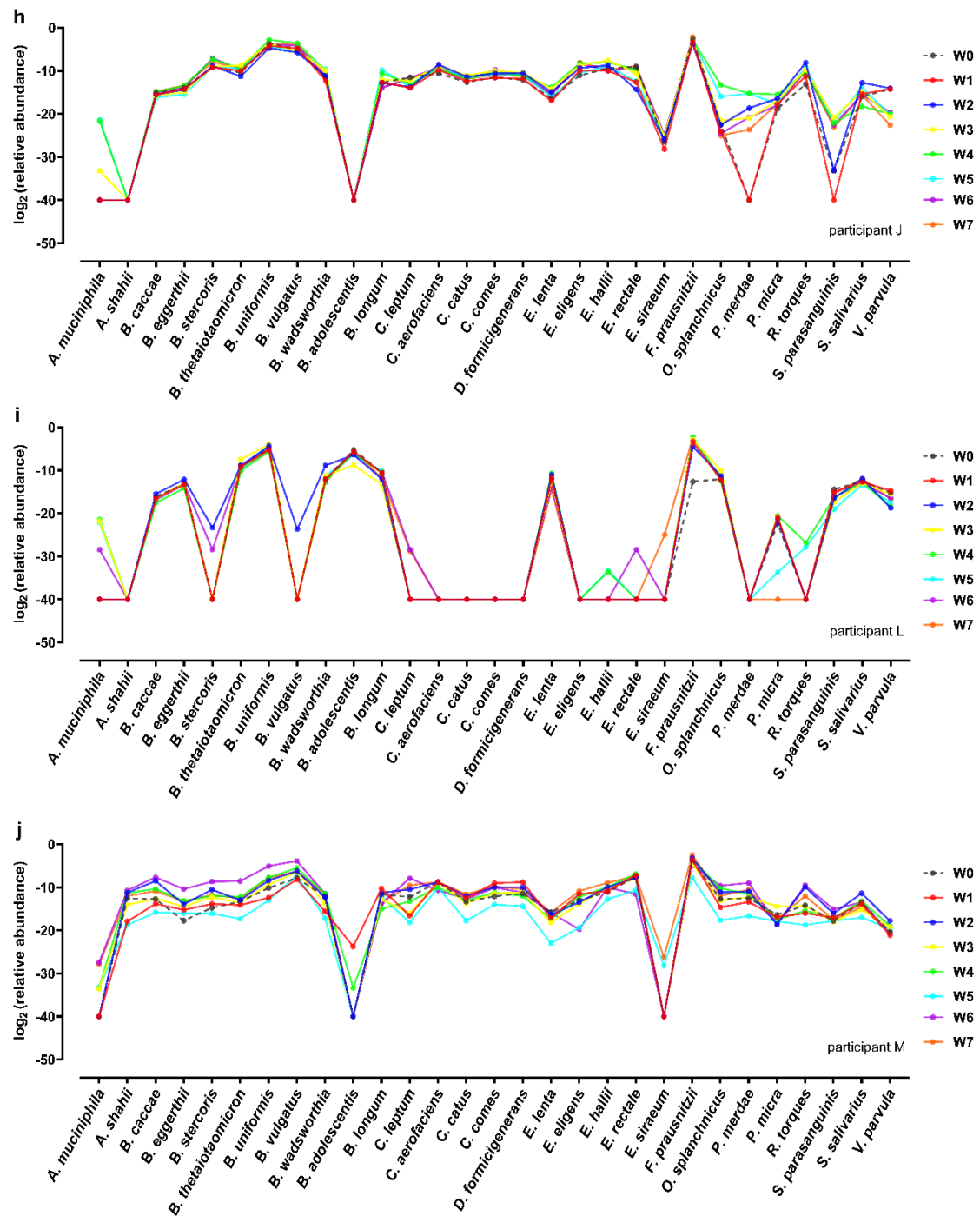


Fig. S2 Dynamic changes in the species abundance of each target bacteria for the 14 participants. The x-axis represents the 29 selected core microbes. The y-axis [$\log_2$ (relative abundance)] represents the relative abundance of these 29 bacteria. The samples were collected from 14 participants once a week for 8 weeks

Table S1 Selection criteria for the 45 gut core microbes

No.	Species	Experiment Strains	Selection Criteria
1	<i>Akkermansia muciniphila</i>	^a ATCC BAA-835	[1] [2] [6] [7]
2	<i>Alistipes shahii</i>	^b BIME 1191250	[1] [3] [5] [6]
3	<i>Bacteroides caccae</i>	BIME 1190883	[1] [3] [4] [6] [7]
4	<i>Bacteroides dorei</i>	BIME 1100298	[1] [4] [6] [7]
5	<i>Bacteroides eggerthii</i>	BIME 1191590	[1] [3] [4] [6] [7]
6	<i>Bacteroides fragilis</i>	BIME 1190664	[1] [3] [4] [6] [7]
7	<i>Bacteroides stercoris</i>	BIME 1100005	[1] [3] [4] [6] [7]
8	<i>Bacteroides thetaiotaomicron</i>	BIME 1100297	[1] [4] [6] [7]
9	<i>Bacteroides uniformis</i>	BIME 1100008	[1] [3] [4] [5] [6] [7]
10	<i>Bacteroides vulgatus</i>	BIME 1100007	[1] [4] [5] [6] [7]
11	<i>Bifidobacterium adolescentis</i>	BIME 1191119	[1] [3] [7]
12	<i>Bifidobacterium longum</i>	BIME 1100004	[1] [3] [7]
13	<i>Bilophila wadsworthia</i>	BIME 1503827	[1] [2] [6]
14	<i>Clostridium bolteae</i>	BIME 1191010	[1] [3] [7]
15	<i>Clostridium butyricum</i>	BIME 1191138	[2] [6]
16	<i>Clostridium leptum</i>	ATCC 29065	[1] [3] [4] [6] [7]
17	<i>Clostridium ramosum</i>	BIME 1192289	[1] [6]
18	<i>Clostridium saccharolyticum</i>	ATCC 35040	[3] [7]
19	<i>Collinsella aerofaciens</i>	BIME 1191121	[1] [3] [4] [7]
20	<i>Coprococcus catus</i>	ATCC 27761	[3] [6]
21	<i>Coprococcus comes</i>	ATCC 27758	[1] [3] [4] [6] [7]
22	<i>Dorea formicigenerans</i>	ATCC 27755	[1] [3] [4] [7]
23	<i>Eggerthella lenta</i>	BIME 1100065	[3] [6] [7]
24	<i>Enterococcus faecalis</i>	BIME 1100003	[3] [4]
25	<i>Eubacterium eligens</i>	ATCC 27750	[1] [3] [7]
26	<i>Eubacterium hallii</i>	ATCC 27751	[3] [4] [6] [7]
27	<i>Eubacterium limosum</i>	BIME 1100036	[1] [3]
28	<i>Eubacterium rectale</i>	ATCC 33656	[1] [3] [4] [5] [6] [7]
29	<i>Eubacterium siraeum</i>	ATCC 29066	[1] [3] [4] [6] [7]
30	<i>Faecalibacterium prausnitzii</i>	ATCC 27768	[3] [4] [5] [6] [7]
31	<i>Gemella morbillorum</i>	BIME 1502088	[3]
32	<i>Lactobacillus ruminis</i>	^c DSM 20403	[3] [7]

33	<i>Odoribacter splanchnicus</i>	BIME 1192728	[1] [3] [6]
34	<i>Parabacteroides distasonis</i>	BIME 1100006	[1] [4] [6] [7]
35	<i>Parabacteroides merdae</i>	BIME 1100038	[1] [3] [4] [6] [7]
36	<i>Parvimonas micra</i>	BIME 1502111	[2]
37	<i>Peptostreptococcus anaerobius</i>	ATCC 27337	[3]
38	<i>Porphyromonas asaccharolytica</i>	ATCC 25260	[3]
39	<i>Prevotella melaninogenica</i>	BIME 1502684	[2] [6]
40	<i>Ruminococcus bromii</i>	ATCC 27255	[1] [3] [4] [6]
41	<i>Ruminococcus gnavus</i>	ATCC 29149	[1] [3] [4] [6] [7]
42	<i>Ruminococcus torques</i>	ATCC 27756	[1] [3] [4] [7]
43	<i>Streptococcus parasanguinis</i>	BIME 1502022	[1] [3]
44	<i>Streptococcus salivarius</i>	BIME 1503401	[1] [3]
45	<i>Veillonella parvula</i>	BIME 1502010	[1]

^a ATCC (American Type Culture Collection, USA). ^b BIME (Beijing Institute of Microbiology and Epidemiology, China). ^c DSM (Deutsche Sammlung von Mikroorganismen und Zellkulturen, Germany).

[1] Species of relative abundance (in at least one sample) $\geq 1\%$ and prevalence $\geq 10\%$ (Tramontano et al. 2018)

[2] One of 316 core species present in at least one sample (4 samples) from 75 individuals (Olsson et al. 2022)

[3] One of 184 core species that were present in all 300 samples from 75 individuals (Olsson et al. 2022)

[4] One of the most common 57 species present in $\geq 90\%$ of individuals (n=124) with genome coverage $>1\%$ (Qin et al. 2010)

[5] Present in more than 95% of 8,208 individuals (Gacesa et al. 2022)

[6] The core species shared by dominant and/or common species (Liu et al. 2021)

[7] The most prevalent organisms from metagenomic sequence data of the NIH Human Microbiome Project (HMP) (Cheng et al. 2022)

Table S2 Bacterial strains used for the specificity test

No.	Species	Experiment Strains
1	<i>Actinomyces odontolyticus</i>	BIME 1502011
2	<i>Bacteroides fragilis enterotoxigenic</i>	ATCC 43860
3	<i>Bacteroides ovatus</i>	BIME 1100009
4	<i>Blautia hansenii</i>	ATCC 27752
5	<i>Clostridium difficile</i>	ATCC BAA-1382
6	<i>Escherichia coli</i>	DSM 682
7	<i>Fusobacterium nucleatum</i>	BIME 1502062
8	<i>Lactobacillus delbrueckii</i>	ATCC 9649
9	<i>Lactobacillus plantarum</i>	BIME 1700312
10	<i>Lactobacillus acidophilus</i>	ATCC 4356
11	<i>Lactobacillus fermentum</i>	ATCC 14931
12	<i>Lactobacillus gasseri</i>	ATCC 33323
13	<i>Lactobacillus paracasei</i>	DSM 5622
14	<i>Lactobacillus sakei</i>	ATCC 33323
15	<i>Lactobacillus salivarius</i>	DSM 20555
16	<i>Lactobacillus vaginalis</i>	DSM 5837
17	<i>Parabacteroides goldsteinii</i>	BIME 1190197
18	<i>Solobacterium moorei</i>	BIME 1507072
19	<i>Streptococcus gallolyticus</i>	BIME 1400439

Table S3 LOD, linearity, and primer coverage rate of the 45 qPCR assays

No.	Species	LOD	Linearity Equation	R ²	^a Coverage
1	<i>Akkermansia muciniphila</i>	0.1 pg/μL	$y = -4.47x + 17.60$	0.9898	85.96%
2	<i>Alistipes shahii</i>	0.1 pg/μL	$y = -3.69x + 16.35$	0.9979	91.67%
3	<i>Bacteroides caccae</i>	0.1 pg/μL	$y = -4.77x + 15.74$	0.9929	70.00%
4	<i>Bacteroides dorei</i>	0.1 pg/μL	$y = -4.61x + 14.42$	0.9887	80.00%
5	<i>Bacteroides eggerthii</i>	0.1 pg/μL	$y = -4.85x + 15.15$	0.9955	100.00%
6	<i>Bacteroides fragilis</i>	1 pg/μL	$y = -5.10x + 19.02$	0.9703	89.24%
7	<i>Bacteroides stercoris</i>	1 pg/μL	$y = -4.60x + 17.95$	0.9942	94.03%
8	<i>Bacteroides thetaiotaomicron</i>	1 pg/μL	$y = -4.55x + 19.56$	0.9932	100.00%
9	<i>Bacteroides uniformis</i>	1 pg/μL	$y = -5.53x + 16.34$	0.9885	100.00%
10	<i>Bacteroides vulgatus</i>	0.1 pg/μL	$y = -4.55x + 15.06$	0.9988	73.33%
11	<i>Bifidobacterium adolescentis</i>	1 pg/μL	$y = -4.75x + 17.51$	0.9858	100.00%
12	<i>Bifidobacterium longum</i>	0.1 pg/μL	$y = -4.32x + 17.52$	0.9982	99.54%
13	<i>Bilophila wadsworthia</i>	1 pg/μL	$y = -5.16x + 18.88$	0.9971	^b -
14	<i>Clostridium bolteae</i>	0.1 pg/μL	$y = -4.84x + 14.86$	0.9962	100.00%
15	<i>Clostridium butyricum</i>	0.1 pg/μL	$y = -4.66x + 17.37$	0.9911	96.43%
16	<i>Clostridium leptum</i>	0.1 pg/μL	$y = -4.59x + 16.74$	0.9993	100.00%
17	<i>Clostridium ramosum</i>	1 pg/μL	$y = -5.29x + 17.42$	0.9932	94.74%
18	<i>Clostridium saccharolyticum</i>	1 pg/μL	$y = -4.82x + 18.10$	0.9952	25.00%
19	<i>Collinsella aerofaciens</i>	1 pg/μL	$y = -5.16x + 16.89$	0.9817	73.64%
20	<i>Coprococcus catus</i>	1 pg/μL	$y = -5.28x + 16.67$	0.9857	100.00%
21	<i>Coprococcus comes</i>	1 pg/μL	$y = -5.02x + 17.18$	0.9927	96.23%
22	<i>Dorea formicigenerans</i>	1 pg/μL	$y = -6.03x + 16.26$	0.981	100.00%
23	<i>Eggerthella lenta</i>	1 pg/μL	$y = -5.34x + 18.68$	0.9968	100.00%
24	<i>Enterococcus faecalis</i>	0.1 pg/μL	$y = -4.39x + 17.32$	0.9994	99.79%
25	<i>Eubacterium eligens</i>	1 pg/μL	$y = -4.70x + 17.74$	0.9975	91.67%
26	<i>Eubacterium hallii</i>	1 pg/μL	$y = -4.94x + 17.67$	0.9836	100.00%
27	<i>Eubacterium limosum</i>	1 pg/μL	$y = -4.41x + 17.23$	0.999	60.00%
28	<i>Eubacterium rectale</i>	0.1 pg/μL	$y = -3.73x + 20.52$	0.9903	95.00%
29	<i>Eubacterium siraeum</i>	1 pg/μL	$y = -5.57x + 16.00$	0.9966	100.00%
30	<i>Faecalibacterium prausnitzii</i>	0.1 pg/μL	$y = -4.78x + 14.34$	0.9974	81.25%

31	<i>Gemella morbillorum</i>	1 pg/μL	$y = -6.09x + 15.61$	0.9669	100.00%
32	<i>Lactobacillus ruminis</i>	1 pg/μL	$y = -5.11x + 16.59$	0.997	89.29%
33	<i>Odoribacter splanchnicus</i>	0.1 pg/μL	$y = -3.68x + 17.17$	0.999	97.50%
34	<i>Parabacteroides distasonis</i>	0.1 pg/μL	$y = -4.09x + 18.01$	0.9965	99.27%
35	<i>Parabacteroides merdae</i>	0.1 pg/μL	$y = -3.93x + 16.96$	0.9937	100.00%
36	<i>Parvimonas micra</i>	0.1 pg/μL	$y = -4.75x + 16.94$	0.992	100.00%
37	<i>Peptostreptococcus anaerobius</i>	1 pg/μL	$y = -4.86x + 16.25$	0.9943	88.89%
38	<i>Porphyromonas asaccharolytica</i>	1 pg/μL	$y = -5.36x + 16.13$	0.9959	100.00%
39	<i>Prevotella melaninogenica</i>	1 pg/μL	$y = -5.64x + 17.14$	0.992	85.71%
40	<i>Ruminococcus bromii</i>	0.1 pg/μL	$y = -4.91x + 14.94$	0.9948	96.23%
41	<i>Ruminococcus gnavus</i>	1 pg/μL	$y = -4.38x + 16.74$	0.9958	100.00%
42	<i>Ruminococcus torques</i>	0.1 pg/μL	$y = -4.68x + 15.97$	0.9971	75.00%
43	<i>Streptococcus parasanguinis</i>	1 pg/μL	$y = -4.80x + 17.85$	0.9985	100.00%
44	<i>Streptococcus salivarius</i>	1 pg/μL	$y = -5.73x + 17.49$	0.9947	100.00%
45	<i>Veillonella parvula</i>	0.1 pg/μL	$y = -4.08x + 16.01$	0.9976	90.63%

^a For primers designed in this study, the coverage rate was calculated based on the number of NCBI genomic sequences of corresponding target bacteria, including genomes at various assembly levels (the data was acquired in July 2021); for primers obtained from literature, the coverage rate was calculated based on the number of complete genomes.

^b The coverage rate was not calculated due to the unavailability of complete genomes of the target bacterium in the NCBI database.

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