Supplementary-material

1. PHES

The PHES consists of a battery of six tests including the number connection test NCT-A, the NCT-B, digit symbol test, serial dotting test, and the line tracing test for time (t) and error (e). Due to concerns about some patients who are not acquainted with English alphabets and not able to perform NCT-B, it was replaced by figure connection test (FCT-A). The FCT and the NCT are similar in principle, but the numbers are substituted by figures. FCT is used to assess the mental state and it surpasses the hurdles of the differences in language and the level of education and literacy of the person. Previous work in the Indian population has suggested a cut-off between normal and pathological results to be -5 points(1) and hence PHES ≤-5 were considered abnormal and diagnostic of MHE. The 6 tests: were applied to the individual patients in a random order. Test normal values were calculated using the equation corrected for age and education (Supplementary Table 10).

Each test was expressed as a Z score, indicating the difference (in standard deviation) between the observed and expected scores for given age and education based on control. A mean Z score will be calculated for each patient in order to avoid bias related to multiple comparisons. The Z scores are rounded off to the nearest integer, with a minimum of -3 and maximum of +1.

The sum-score of the PHES was calculated as follows: the results with *Z* score ± 1 will score 0 points, those with -1 and -2 will score -1, those between -2 and -3 will score -2 points and those with score less than -3 will score -3. Results better than +1 *Z* score will score +1 point. The individual test scores of PHES were summarized to a sum-score ranging from +6 to -18 points.

Supplementary Table 10. Multiple linear regression: Factors associated with Psychometric tests

sTest	r	Equation	Standard deviation
NCT-A	0.49	38.57 + 0.18 x Age – 1.117 x Education	8.97
FCT-A	0.57	53.77 + 0.38 x Age – 2.044 x Education	13.73
SDT	0.23	51.471+ 0.045 x Age – 0.606 x Education	10.03
DST	0.60	32.83 – 0.312 x Age + 1.532 x Education	9.73
LTT-E	0.50	53.04 + 0.188 x Age – 3.002 x Education	19.41
LTT	0.13	70.90	18.45

Abbreviations: NCT-A, Number Connection Test A; FCT-A, Figure Connection Test A; SDT, Serial Dotting Test; DST, Digit Symbol Test; LTT-E, Line Tracing Test for Error.

2. Animal Naming Test (2)

The Animal Naming Test (ANT) is an analysis of semantic fluency consisting of saying as many animal names as possible within one minute. It is a verbal questionnaire to obtain a rapid assessment of patients who have cirrhosis either in an office setting or at the bedside. It is an easily obtainable measure of cognition like the Glasgow Coma Scale (GCS) for patients with coma or questions regarding orientation in time, space and identity. In a well- lit room with quiet surroundings not having any obvious external disturbances, the patient is asked to speak out the names of as many animals as possible in 1 minute and responses are recorded. If the patient stops before 1 minute, he is asked about any more animals he would like to add. If the patient does not speak for 15 seconds, he is given a hint; e.g. a lion is an animal, can he/she name any more animals? After 1 minute, all the responses are counted excluding repetitions and non-animal words. inhibition of responses, when required. These cognitive skills require adequate memory as well as effective executive functions. The ANT is very sensitive to functions associated with anterior cortical and prefrontal cortex areas. These parts of the brain are particularly sensitive to the initial

stages of HE. Therefore, ANT can be used as a first-line test for a patient with cirrhosis for the evaluation of HE.

3. ***Inclusion and exclusion criteria***

Inclusion Criteria

1. Age: ≥18 years - 60 years
2. Cirrhosis (diagnosed based on biopsy, radiology, fibroscan or imaging evidence of portal hypertension)
3. Willing and able to comply with the FMT regimen and all other study requirements
4. The patient or guardian can provide written informed consent to participate in the study

Exclusion Criteria

1. Cirrhosis with Overt HE
2. Pregnant or breastfeeding. Women of childbearing potential will be screened with beta-human chorionic gonadotropin (hCG).
3. Those receiving immunosuppression therapy
4. People living with HIV (PLHIV)
5. History of spontaneous bacterial peritonitis
6. Model for End-stage Liver disease score >18
7. Low protein (<1.5g) ascites
8. Medical conditions that require prolonged or frequent use of systemic acyclovir or famciclovir (e.g., for recurrent herpes virus infections, etc). Prolonged use means episodic treatment with these agents for 10 days every 3 months or chronic suppressive therapy.
9. Acute variceal bleeding within last 4 weeks
10. Patients with acute on chronic liver failure (ACLF)
11. Patients with hepatocellular carcinoma (HCC)

12. Patients with a spontaneous portosystemic shunt (as diagnosed on CT scan)
13. Patients with alcohol consumption of more than 30 gm of ethanol or abusing illicit drugs within last 1 month.
14. Medical conditions, requiring potentially hepatotoxic drugs (e.g. dapsone, erythromycin, fluconazole, ketoconazole, rifampin, anti-tuberculosis regimens, others) or nephrotoxic drugs (e.g., frequent NSAIDs, aminoglycosides, amphotericin B, foscarnet).
15. Patients on warfarin or other anticoagulants for 30 days prior to screening or if expected during the present study.
16. Other concurrent medical conditions likely to preclude compliance with the schedule of evaluations in the protocol or likely to confound the efficacy or safety observations of the study (e.g., concurrent malignancies, history of unstable angina, repeated myocardial infarction or congestive heart failure, renal insufficiency, uncontrolled asthma or diabetes, unstable thyroid disease or other significant hormonal conditions, uncontrolled seizure disorders, severe psychiatric disorders, active tuberculosis under current treatment, etc)

17. Patient on antibiotics

18. Patient on Renal replacement therapy

19. Patients with a history of surgery within the last 3 months
20. Patients with an active autoimmune liver disease requiring treatment with steroids and immunomodulators
21. Post tranjugular intrahepatic portosystemic shunt

4. **FMT: Preparation and Mode of Administration**

Fresh faecal material, within 6 hours after defecation, was used. The storage and preparation was kept as brief as possible to protect the anaerobic bacteria. The stool sample was stored at ambient temperature (20°C–30°C) until further processing. A minimum amount of 30 g of faeces was used. The faecal material was suspended in 0.9% saline using a blender or manual effort and sieved to avoid clogging infusion syringes and tubes.

A total of 200 mL of fecal suspension was transferred to the patient's jejunum via Upper GI endoscopy on day 0. During the 2nd session at 1 month after 1st procedure. 200 ml of fecal suspension was transferred to patient's jejunum via Upper GI endoscopy.

5. **Demographic details of the 2 healthy donors**

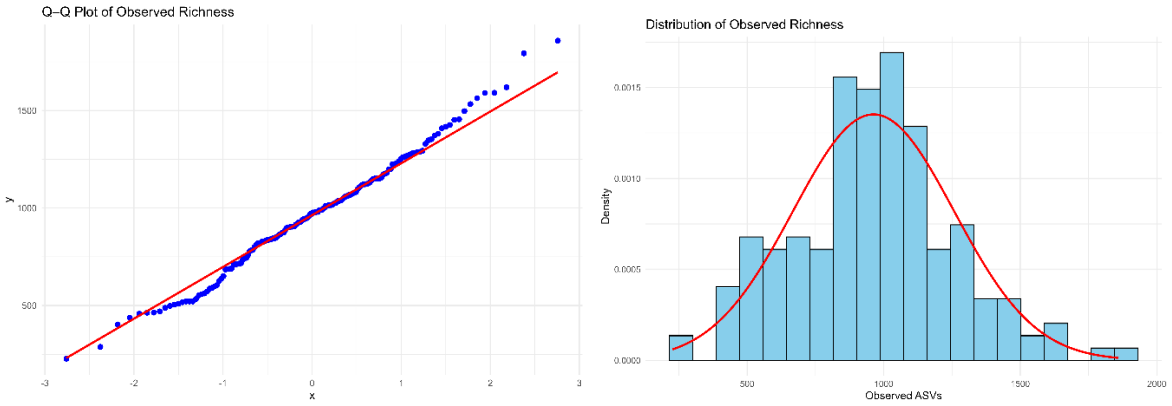
Donor 1: 40-year lady

Donor 2: 39-year-old male

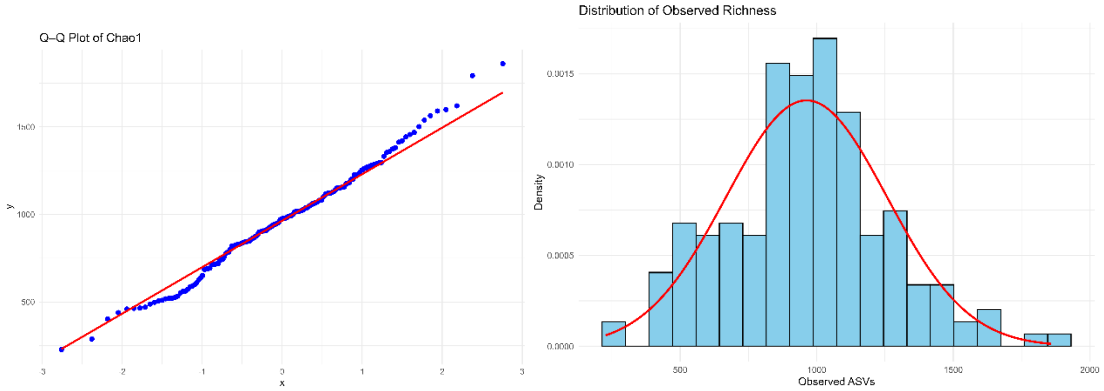
6. **Results of normality testing**

Normality of alpha diversity indices was assessed using the Shapiro- Wilk test. The results for the same are shown below:

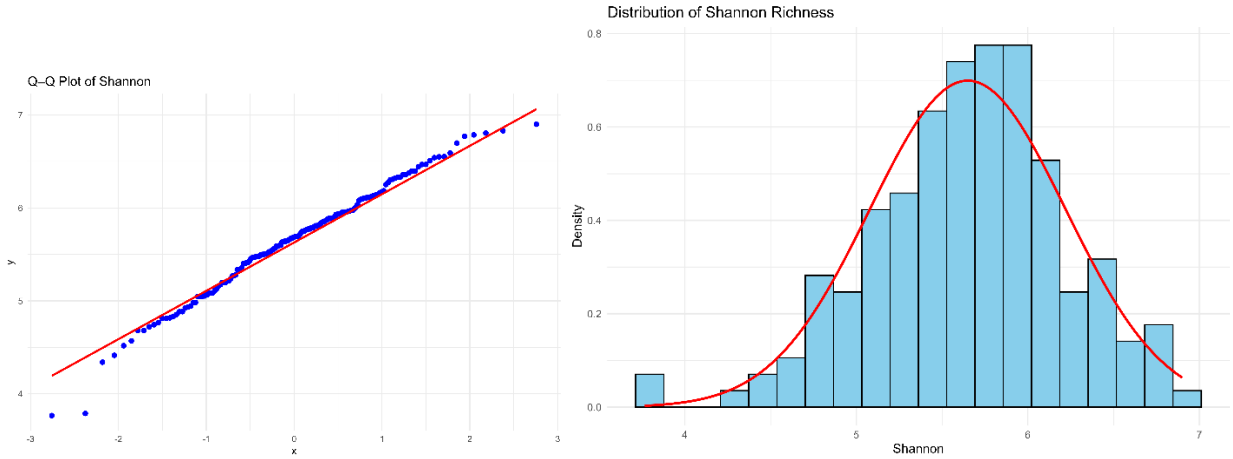
Observed OTUs (W = 0.992, p = 0.458)



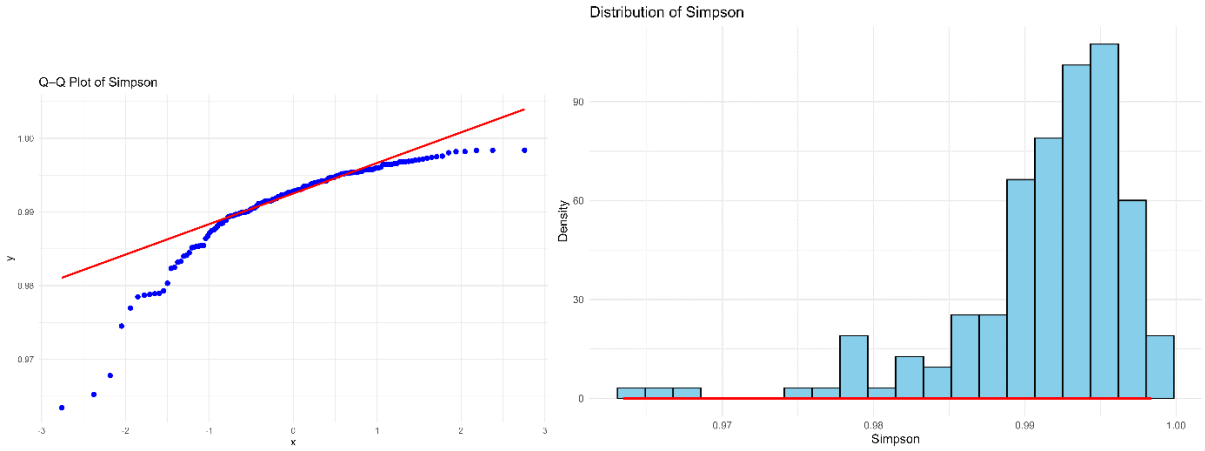
Chao1 (W = 0.992, p = 0.451)



Shannon (W = 0.987, p = 0.113)

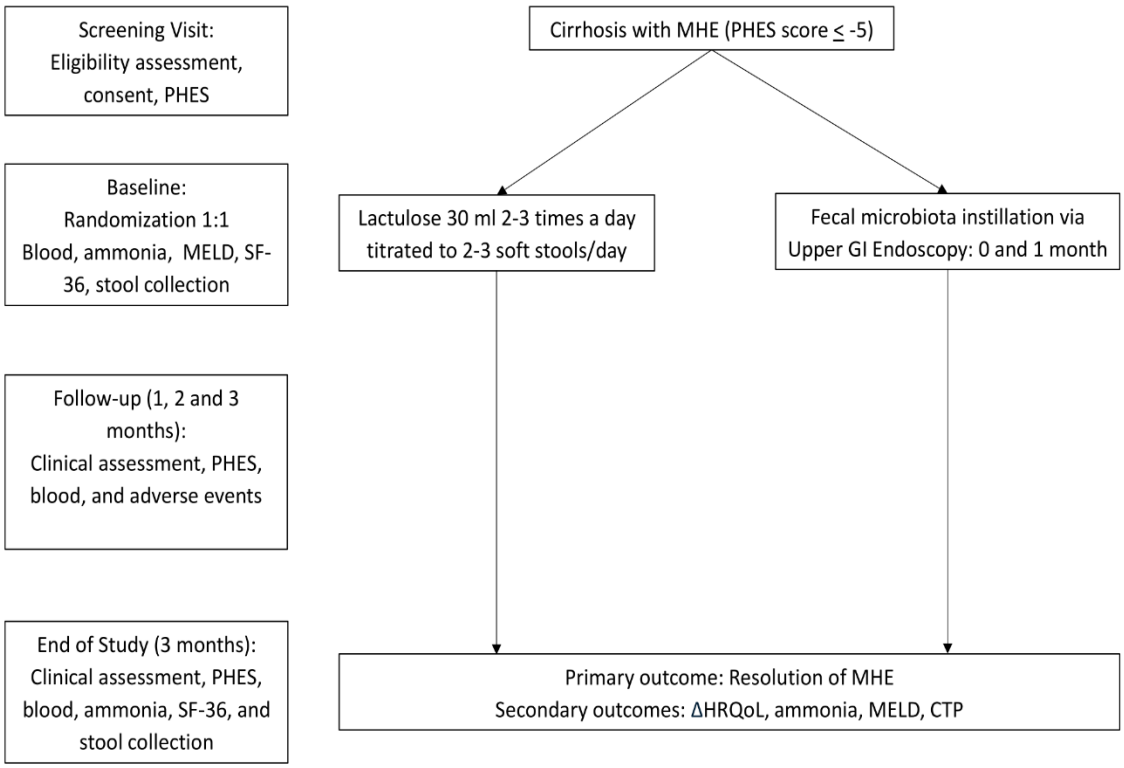


Simpson (W=0.820, p= 2.83e-13)

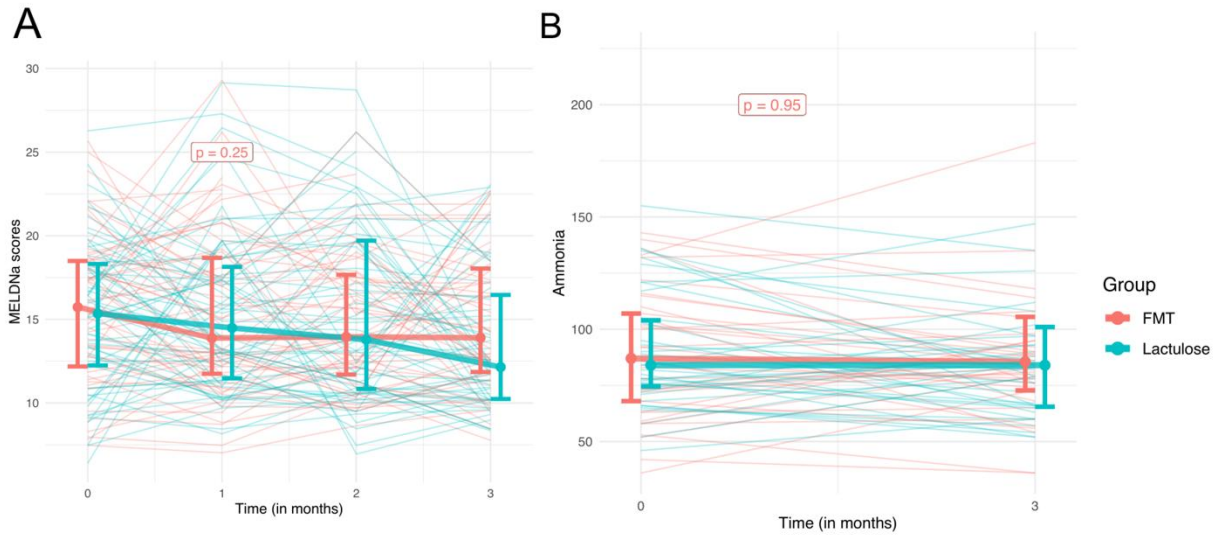


1. Supplementary figures

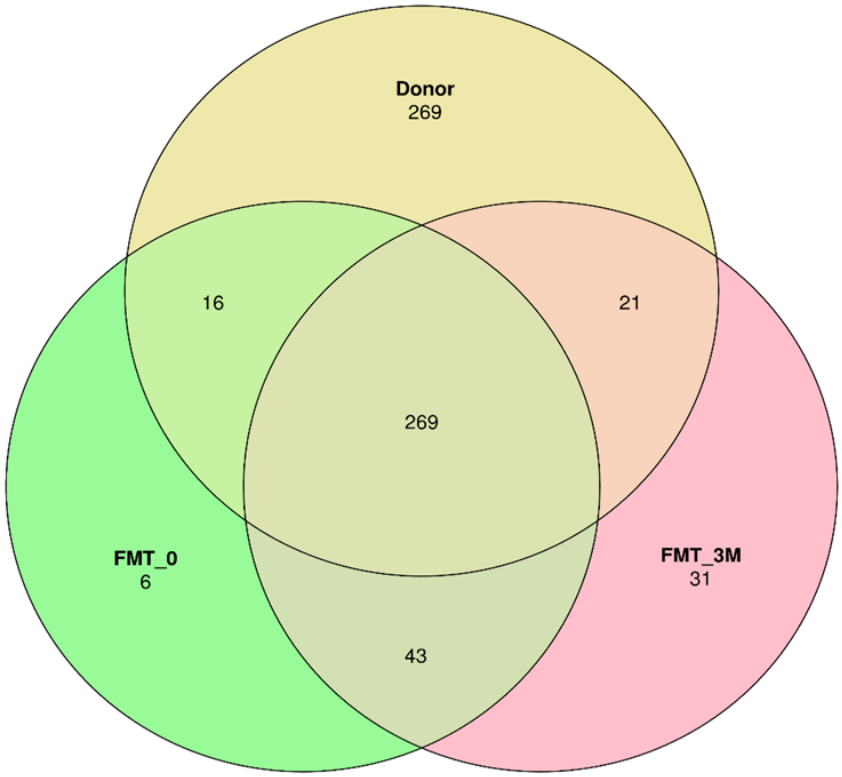
Supplementary Figure 1. Study protocol overview.



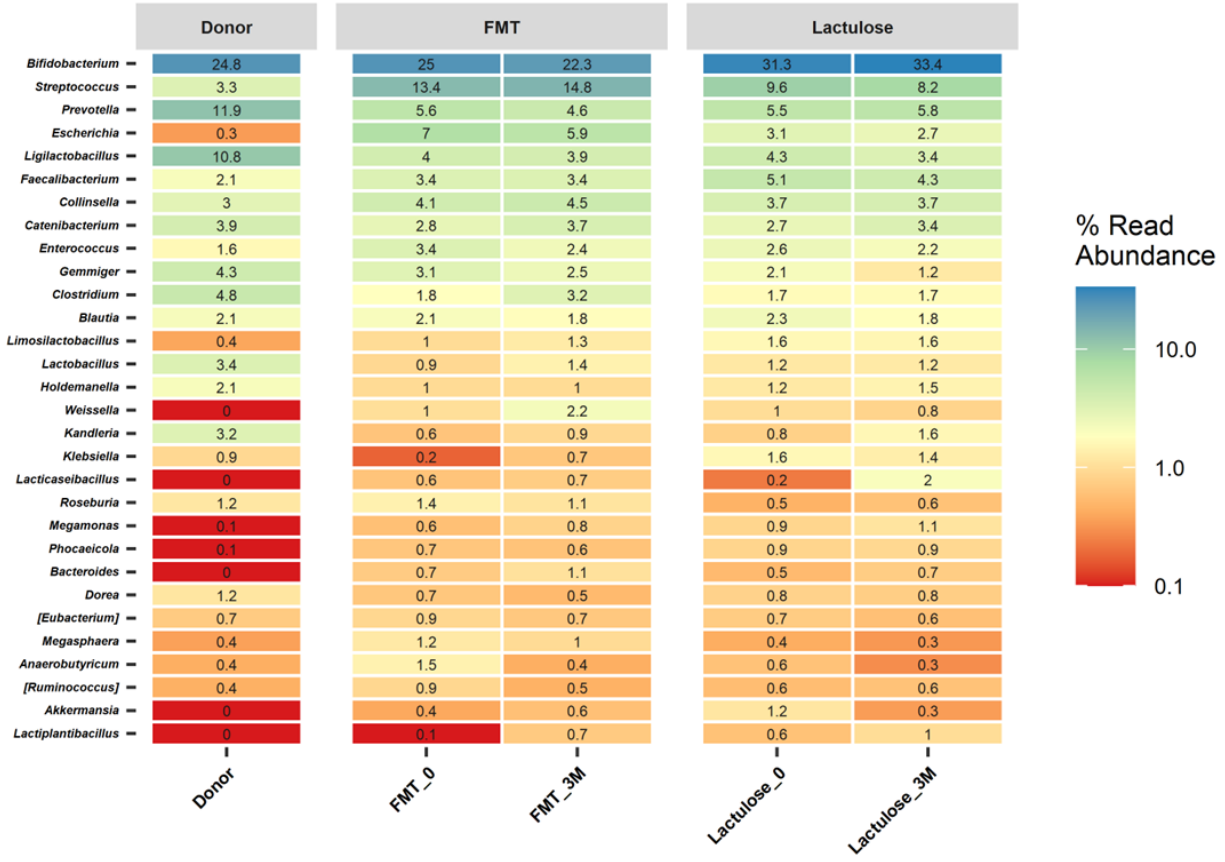
Supplementary Figure 2: Changes in MELD-Na and ammonia over 3 months



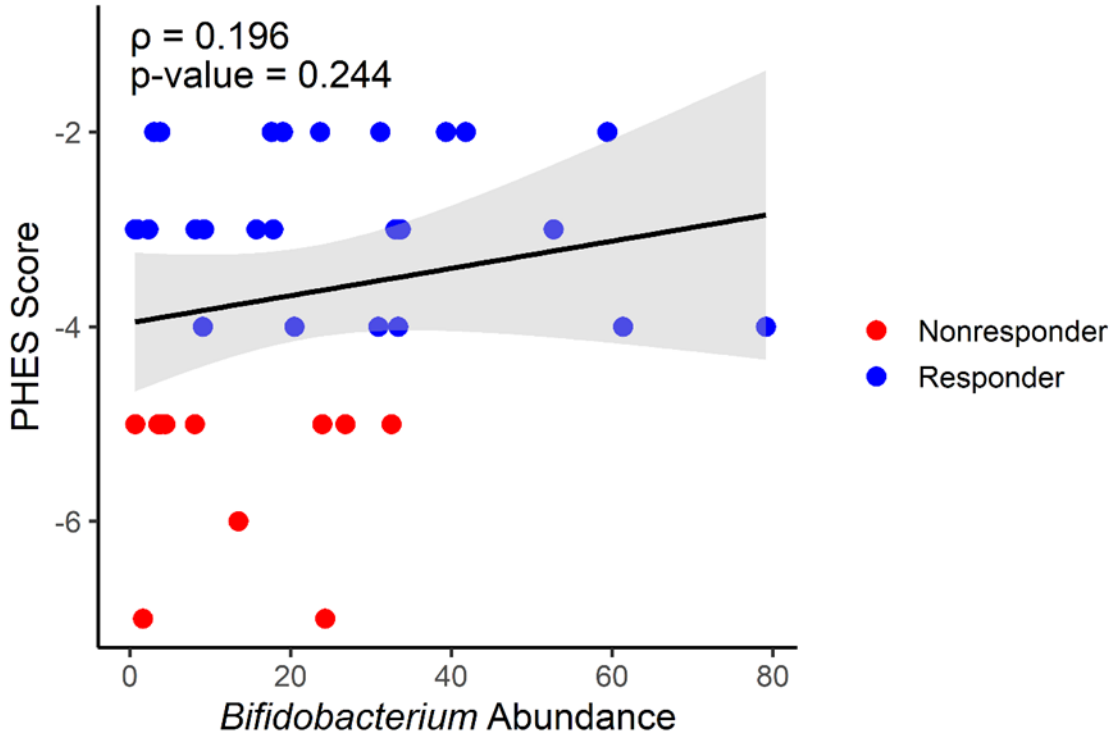
Supplementary Figure 3. Venn diagram illustrating shared and unique amplicon sequence variants (ASV) between Donor, FMT baseline (FMT_0), and FMT 3 months (FMT_3M), highlighting the core microbiota retained over time.



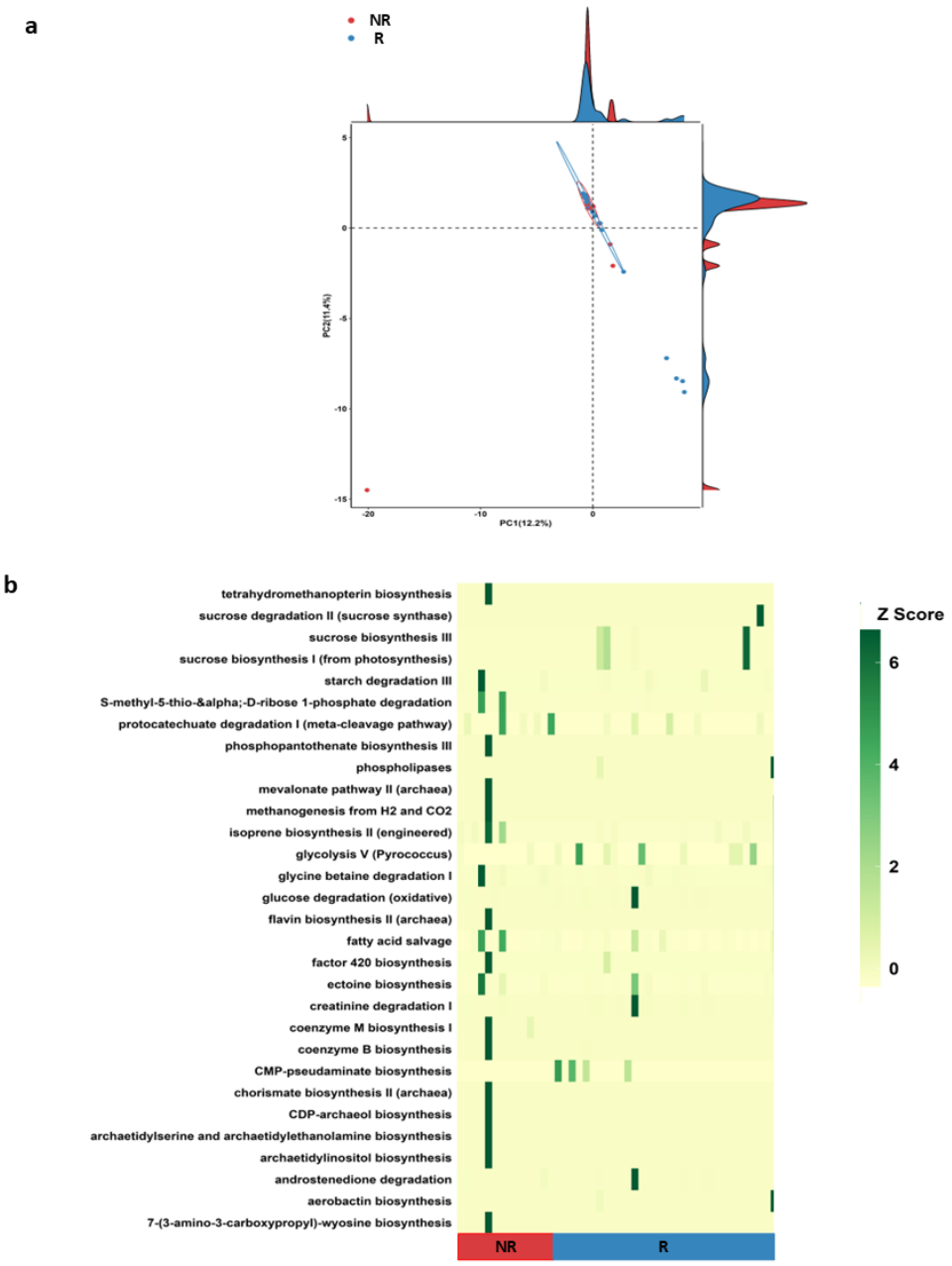
Supplementary Figure 4. Heatmap displaying the relative bacterial abundance across Donor, FMT, and Lactulose groups.



Supplementary Figure 5: Spearman correlation analysis using Liner regression between *Bifidobacterium* and PHES score post 3 months. The analysis revealed a weak positive correlation (Spearman, rho=0.196, p-value= 0.244). The x-axis is showing the relative abundance of Bifidobacterium whereas the y-axis is showing the PHES scores.



Supplementary Figure 6. Functional Analysis of MHE Resolution (R) and Non-Resolution (NR) in the Lactulose Group.



2. Supplementary Tables

Supplementary Table 1. Effect of FMT and lactulose on monthly PHES score.

Group	Baseline	1 month	2 months	3 months
PHES FMT (n = 60)	-6 (-7 to -5)	-4.5 (-5 to -3)	-3 (-5 to -2)	-3 (-4 to -2)
PHES Lactulose (n = 62)	-5.5 (-7 to -5)	-5 (-5 to -3)	-3 (-5 to -2)	-3 (-5 to -2)

Supplementary Table 2. Effect of donor on MHE resolution.

	FMT group donor 1 (n=30)	FMT group donor 2 (n=30)	P- value
1 month	11 (36.7%)	16 (53.3%)	0.508
2 months	16 (53.3%)	17 (56.7%)	0.743
3 months	20 (66.7%)	21 (70%)	0.525

Supplementary Table 3. Effect of FMT and Lactulose on quality of life and components of SF-36 scores.

Outcomes	FMT_ baseline	FMT_3mths	P-value	Lactulose_ baseline	Lactulose_3 months	P-value	Adjusted mean difference (± standard error)*	P-value
Physical functioning	657 ± 183	783 ± 145	0.001	637 ± 193	798 ± 136	<0.001	15.07 ± 27.69	0.59
Role limitation Physical health	193 ± 140	290 ± 134	0.005	161 ± 130	302 ± 124	<0.001	7.36 ± 25.69	0.78
Role limitation mental health	237 ± 84	280 ± 46	0.007	242 ± 82	260 ± 78	0.250	-19.64 ± 12.85	0.13
Energy/fatigue	188 ± 40	217 ± 42	0.002	185 ± 39	206 ± 42	0.005	-11.23 ± 8.27	0.18
Emotional well being	345 ± 33	363 ± 25	0.003	338 ± 38	359 ± 31	0.004	-4.76 ± 5.62	0.40

Social functioning	164 ± 33	186 ± 23	0.001	166 ± 33	179 ± 25	0.018	-7.58 ± 4.76	0.12
Pain	150 ± 29	183 ± 22	<0.001	148 ± 24	175 ± 25	<0.001	-8.86 ± 4.64	0.059
General health	241 ± 47	276 ± 41	0.001	229 ± 39	284 ± 36	<0.001	7.84 ± 7.72	0.312

*Final observation at 3 months is compared between two treatment groups adjusted for respective baseline parameters. Positive values indicate higher value in lactulose group and vice versa

Supplementary Table 4. Table showing the read in formation of each sample (From DADA2 16S pipeline)

Illumina nextseq2000 ID	input	filtered	denoisedF	denoisedR	merged	nonchim
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20250103NXQR12016S4296	308831	308498	302032	302962	283670	114377
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20250103NXQR12016S4298	258876	255601	250429	250391	231181	130560
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20250117NXQR12116S4500	257950	256730	249358	252849	217524	114299
20250117NXQR12116S4501	326141	322022	311553	315772	261573	136208

20250117NXQR12116S4502	329927	326152	313298	318486	268552	143088
20250117NXQR12116S4503	291187	289426	281665	285110	225715	122693
20250117NXQR12116S4504	276408	276230	269222	271761	235759	118287
20250117NXQR12116S4505	273652	272965	265128	268856	221863	109967
20250117NXQR12116S4506	300600	299607	292534	296060	241515	117195
20250117NXQR12116S4507	239626	238770	233305	236187	198633	112510
20250117NXQR12116S4508	286908	286663	279190	282256	244030	116858
20250117NXQR12116S4509	209653	208109	203496	205479	167510	106951
20250117NXQR12116S4510	265166	264217	257366	260273	230091	136589
20250117NXQR12116S4511	254365	253229	245215	248525	207548	111465
20250117NXQR12116S4512	258474	256522	249734	252945	217666	93372
20250117NXQR12116S4513	249198	248380	241504	245071	209979	96331
20250117NXQR12116S4514	295799	292924	286790	289105	248766	132308
20250117NXQR12116S4515	280455	275367	267841	271661	232355	116015
20250117NXQR12116S4516	301772	301557	292634	296893	251029	132088
20250117NXQR12116S4517	254688	241233	233818	237162	203654	119994
20250117NXQR12116S4518	317781	317342	304443	310800	247703	123933
20250117NXQR12116S4519	225300	225114	213837	219879	172885	64299
20250117NXQR12116S4520	305263	304636	294347	300194	236911	117681
20250117NXQR12116S4521	252889	251189	243746	248472	197044	102113
20250117NXQR12116S4522	276522	276413	268845	273083	224548	76141
20250117NXQR12116S4523	183585	183513	179489	181658	148276	68348
20250117NXQR12116S4524	302135	302001	293141	297399	249866	99373
20250117NXQR12116S4525	280410	280270	271115	276070	226549	77487
20250117NXQR12116S4526	317739	317608	307567	313013	248537	104730
20250117NXQR12116S4527	240357	240269	230776	235327	185101	61296
20250117NXQR12116S4528	275225	275130	263334	268774	202585	77275
20250117NXQR12116S4529	226117	226031	219320	222044	184407	72611
20250117NXQR12116S4530	298032	297583	287725	292232	232512	114862
20250117NXQR12116S4531	256759	256431	249320	252768	199828	87017
20250117NXQR12116S4532	307676	307502	295859	303899	236163	76170
20250117NXQR12116S4533	293039	292904	283070	288478	226526	87820
20250117NXQR12116S4534	227742	220753	215297	216823	183660	74766
20250117NXQR12116S4535	206206	200331	194609	196106	167825	64645
20250117NXQR12116S4536	276587	276219	269252	272831	222745	86529
20250117NXQR12116S4537	332672	331551	323642	327391	249693	145250
20250117NXQR12116S4538	228583	223892	218946	219651	189250	65001
20250117NXQR12116S4539	280280	280144	273279	276914	221596	100738
20250117NXQR12116S4540	324320	323869	314655	318291	267360	131927
20250117NXQR12116S4541	326301	325903	314305	320460	258860	92762

20250117NXQR12116S4542	297945	297602	288236	293405	234629	110152
20250117NXQR12116S4543	301757	301641	290382	295911	233297	91519
20250117NXQR12116S4544	331250	331114	316619	323502	239023	88672
20250117NXQR12116S4545	255201	255090	249670	252506	211657	101196
20250117NXQR12116S4546	313479	313116	302208	307566	241278	102011
20250117NXQR12116S4547	299033	297711	289835	293976	234106	116257
20250117NXQR12116S4548	341275	341079	327989	334782	262568	82589
20250117NXQR12116S4549	311432	311315	298304	305316	230492	77586
20250117NXQR12116S4550	290784	290495	280742	284639	229743	91093
20250117NXQR12116S4551	301140	300598	292933	296991	240766	115871
20250117NXQR12116S4552	297158	296214	288968	293022	225837	126546
20250117NXQR12116S4553	306488	306193	296495	301519	221611	101528
20250117NXQR12116S4554	322812	322648	312797	318466	260963	106335
20250117NXQR12116S4555	288647	285233	279324	281451	239820	128834
20250117NXQR12116S4556	310925	310387	302968	306351	255780	130716
20250117NXQR12116S4557	268583	268243	262694	265277	227410	106102
20250117NXQR12116S4558	263775	263661	257736	260826	219121	112099
20250117NXQR12116S4559	246003	245855	239853	242484	210719	97877

Supplementary Table 5. Engraftment % of bacterial taxa derived from donor

	MHE resolution		**MHE-non resolution**
P1/3	0.4608049	P13/3	0.4846191
P15/3	0.6485127	P24/3	0.4258532
P17/3	0.2172457	P25/3	0.3520868
P35/3	0.5645474	P46/3	0.4932358
P45/3	0.3093487	P47/3	0.4603701
P63/3	0.6455456	P52/3	0.6365686
P65/3	0.1066769	P63/3	0.645597
P54/3	0.4001688	P40/3	0.7364083
P67/3	0.5459083	P34/3	0.4036392
P41/3	0.0798326	P43/3	0.7030739
P42/3	0.547224	P50/3	0.4556237
P75/3	0.4762286		
P76/3	0.509031		
P73/3	0.3450582		
P74/3	0.7040457		
P2/3	0.9094743		
P6/3	0.6949438		
P9/3	0.4473323		
P18/3	0.8024976		
P28/3	0.8780356		
P37/3	0.5098555		
P44/3	0.7469464		
P48/3	0.185118		
P59/3	0.900924		
P60/3	0.7102853		
P70/3	0.4534609		

Supplementary Table 6. Functional analysis between MHE resolution and non-resolution in the FMT group (EdgeR differential analysis).

Feature	p- values	p- adjusted	Description
LIPASYN-PWY	1.68E-31	6.88E-29	phospholipases
AEROBACTINSYN-PWY	4.07E-16	8.32E-14	aerobactin biosynthesis
P101-PWY	1.15E-12	1.57E-10	ectoine biosynthesis
PWY-6107	8.91E-12	9.11E-10	chlorosalicylate degradation
P341-PWY	3.14E-09	2.57E-07	glycolysis V (Pyrococcus)
PWY-6165	4.96E-09	3.38E-07	chorismate biosynthesis II (archaea)
PWY-6143	1.67E-07	9.73E-06	CMP-pseudaminate biosynthesis
PWY-4361	3.28E-06	1.68E-04	S-methyl-5-thio-α-D-ribose 1-phosphate degradation
PWY-5198	2.48E-05	0.001126188	factor 420 biosynthesis
HCAMHPDEG-PWY	7.76E-05	0.002645384	3-phenylpropanoate and 3-(3-hydroxyphenyl) propanoate degradation to 2-oxopent-4-enoate
P621-PWY	6.92E-05	0.002645384	nylon-6 oligomer degradation
PWY-6690	7.76E-05	0.002645384	cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate
PWY-5655	8.64E-05	0.002717611	L-tryptophan degradation IX
PWY-6876	0.000178553	0.005216304	isopropanol biosynthesis
PWY-722	0.000295519	0.008057814	nicotinate degradation I
PWY-6944	0.0003964	0.010132979	androstenedione degradation
METHGLYUT-PWY	0.00042388	0.010198061	superpathway of methylglyoxal degradation
PWY0-1277	0.000547972	0.012451146	3-phenylpropanoate and 3-(3-hydroxyphenyl) propanoate degradation
PWY-6572	0.000760639	0.016373761	chondroitin sulfate degradation I (bacterial)
PWY-5529	0.000980998	0.020061406	superpathway of bacteriochlorophyll a biosynthesis

PWY-7371	0.001340664	0.024924171	1,4-dihydroxy-6-naphthoate biosynthesis II
PWY-7446	0.001283784	0.024924171	sulfoglycolysis
PWY-6713	0.001454169	0.025858917	L-rhamnose degradation II
PWY-5647	0.001722276	0.029350457	2-nitrobenzoate degradation I
GALACTARDEG-PWY	0.002090993	0.032310792	D-galactarate degradation I
GLUCARGALACTSUPER-PWY	0.002090993	0.032310792	superpathway of D-glucarate and D-galactarate degradation
PWY-7527	0.002132986	0.032310792	L-methionine salvage cycle III
P125-PWY	0.002478177	0.034545502	superpathway of (R,R)-butanediol biosynthesis
PWY-6731	0.002434496	0.034545502	starch degradation III
PWY0-41	0.0025339	0.034545502	allantoin degradation IV (anaerobic)
GLUCARDEG-PWY	0.003787645	0.044826384	D-glucarate degradation I
GLYCOL-GLYOXDEG-PWY	0.003835999	0.044826384	superpathway of glycol metabolism and degradation
PWY-5654	0.003558399	0.044826384	2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate
PWY-5747	0.003768911	0.044826384	2-methylcitrate cycle II
PWY0-42	0.003436523	0.044826384	2-methylcitrate cycle I
3-HYDROXYPHENYLACETATE-DEGRADATION-PWY	0.004146044	0.047103668	4-hydroxyphenylacetate degradation

Supplementary Table 7. Functional analysis between MHE resolution and non-resolution in the Lactulose group (EdgeR differential analysis).

Feature	p_values	p_adjusted	Description
PWY-6167	1.36E-35	5.56E-33	flavin biosynthesis II (archaea)
PWY-6165	2.65E-33	5.42E-31	chorismate biosynthesis II (archaea)
PWY-6148	1.41E-31	1.44E-29	tetrahydromethanopterin biosynthesis
PWY-6174	1.25E-31	1.44E-29	mevalonate pathway II (archaea)
PWY-6654	2.93E-30	2.40E-28	phosphopantothenate biosynthesis III
PWY-4361	1.28E-29	8.74E-28	S-methyl-5-thio-α-D-ribose 1-phosphate degradation
P261-PWY	6.37E-29	3.72E-27	coenzyme M biosynthesis I
METHANOGENESIS-PWY	2.71E-28	1.38E-26	methanogenesis from H2 and CO2
P241-PWY	1.85E-26	8.41E-25	coenzyme B biosynthesis
PWY-7286	2.30E-26	9.41E-25	7-(3-amino-3-carboxypropyl)-wyosine biosynthesis
PWY-6349	2.81E-26	1.04E-24	CDP-archaeol biosynthesis
PWY-6350	1.07E-25	3.66E-24	archaetidylinositol biosynthesis
PWY-6141	4.43E-25	1.39E-23	archaetidylserine and archaetidylethanolamine biosynthesis
PWY-3661	1.30E-19	3.80E-18	glycine betaine degradation I
PWY-6731	1.38E-18	3.77E-17	starch degradation III
PWY-7391	3.39E-16	8.68E-15	isoprene biosynthesis II (engineered)
SUCSYN-PWY	2.85E-15	6.85E-14	sucrose biosynthesis I (from photosynthesis)
DHGLUCONATE-PYR-CAT-PWY	5.95E-13	1.35E-11	glucose degradation (oxidative)
LIPASYN-PWY	2.25E-12	4.84E-11	phospholipases
CRNFORCAT-PWY	5.35E-12	1.09E-10	creatinine degradation I
PWY-7347	4.10E-10	7.99E-09	sucrose biosynthesis III
PWY-5198	9.81E-10	1.82E-08	factor 420 biosynthesis
PWY-6944	2.87E-09	5.10E-08	androstenedione degradation
PWY-6143	5.25E-09	8.95E-08	CMP-pseudaminate biosynthesis
P341-PWY	1.51E-08	2.47E-07	glycolysis V (Pyrococcus)
AEROBACTINSYN-PWY	3.98E-08	6.25E-07	aerobactin biosynthesis

PWY-3801	4.44E-07	6.72E-06	sucrose degradation II (sucrose synthase)
P184-PWY	6.73E-07	9.83E-06	protocatechuate degradation I (meta-cleavage pathway)
PWY-7094	1.93E-06	2.72E-05	fatty acid salvage
P101-PWY	2.94E-06	4.01E-05	ectoine biosynthesis
PWY-6505	1.24E-05	1.63E-04	L-tryptophan degradation XII (Geobacillus)
CATECHOL-ORTHO-CLEAVAGE-PWY	1.93E-05	2.34E-04	catechol degradation to β-ketoadipate
PWY-5417	1.94E-05	2.34E-04	catechol degradation III (ortho-cleavage pathway)
PWY-5431	1.94E-05	2.34E-04	aromatic compounds degradation via β-ketoadipate
GALLATE-DEGRADATION-II-PWY	2.50E-05	2.93E-04	gallate degradation I
GALLATE-DEGRADATION-I-PWY	3.79E-05	4.31E-04	gallate degradation II
METHYLGALLATE-DEGRADATION-PWY	4.09E-05	4.52E-04	methylgallate degradation
PWY-5741	5.78E-05	6.08E-04	ethylmalonyl-CoA pathway
PWY-6185	5.80E-05	6.08E-04	4-methylcatechol degradation (ortho cleavage)
PWY-6182	8.47E-05	8.66E-04	superpathway of salicylate degradation
PWY-6071	0.000110687	0.001104174	superpathway of phenylethylamine degradation
PWY-6992	0.000120971	0.001178026	1,5-anhydrofructose degradation
PWY0-321	0.000131757	0.001253228	phenylacetate degradation I (aerobic)
PWY-5181	0.000156101	0.001451026	toluene degradation III (aerobic) (via p-cresol)
PWY-6338	0.000177236	0.00157586	superpathway of vanillin and vanillate degradation
PWY-7097	0.000177236	0.00157586	vanillin and vanillate degradation I
PWY-7098	0.000226506	0.001971087	vanillin and vanillate degradation II
PWY-1622	0.00032627	0.002780094	formaldehyde assimilation I (serine pathway)
PWY-7527	0.000385841	0.00322059	L-methionine salvage cycle III
PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY	0.00043277	0.003403902	protocatechuate degradation II (ortho-cleavage pathway)

PWY-1541	0.000429653	0.003403902	superpathway of taurine degradation
PWY-3781	0.000425155	0.003403902	aerobic respiration I (cytochrome c)
PWY-6210	0.000598541	0.004618933	2-aminophenol degradation
PWY-7007	0.00067542	0.005115683	methyl ketone biosynthesis
PWY-7376	0.000778163	0.005786705	cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation)
TYRFUMCAT-PWY	0.001159143	0.008465886	L-tyrosine degradation I
PWY-4722	0.001226415	0.008800068	creatinine degradation II
PWY-7255	0.001422684	0.010032375	ergothioneine biosynthesis I (bacteria)
PWY-5028	0.001509562	0.010464589	L-histidine degradation II
GLYOXYLATE-BYPASS	0.001573666	0.010656987	glyoxylate cycle
LEU-DEG2-PWY	0.001589428	0.010656987	L-leucine degradation I
PWY-5178	0.001669232	0.011011545	toluene degradation IV (aerobic) (via catechol)
PWY-6906	0.001832298	0.011895398	chitin derivatives degradation
PWY-5430	0.003084219	0.019710089	meta cleavage pathway of aromatic compounds
PWY-1882	0.003199197	0.020130333	superpathway of C1 compounds oxidation to CO2
PWY-6562	0.005408426	0.03351585	norspermidine biosynthesis
TCA-GLYOX-BYPASS	0.006013463	0.036709053	superpathway of glyoxylate bypass and TCA
FAO-PWY	0.007351193	0.044215264	fatty acid β-oxidation I

Supplementary Table 8: Table presenting the statistical comparison of AMR gene prevalence between FMT responders and non-responders. Differences in gene prevalence were analyzed using Fisher's Exact Test to compare responders and non-responders in the FMT arm.

Gene	**p_value**	**odds_ratio**	**FDR_adjusted**
NDM	0.622732	0.596148	1
CTX.M	0.443395	0.452685	1
KPC	0.297297	0	1
TEM	0.69464	0.611019	1
Cat	0.297297	0	1
AAC	0.205277	0.190143	1
Sul2	0.539897	Inf	1
oqxA	0.297297	0	1
OXA	1	Inf	1
Tet	0.512012	0.411374	1
aadA	1	1.295469	1
Sul1	1	0.804977	1
ermB	0.719475	1.614398	1
dfrA	1	0.822775	1
qnrS	0.566962	0.386474	1
mphA	1	1.069458	1

Supplementary 9: Table presenting the statistical comparison of AMR gene prevalence between FMT responders and non-responders. Differences in gene prevalence were analyzed using Fisher's Exact Test to compare responders and non-responders in the Lactulose arm.

Gene	p_value	odds_ratio	FDR_adjusted
NDM	0.304348	0	0.642942
CTX.M	0.321471	0.462836	0.642942
KPC	0.060166	0.174686	0.333183
TEM	0.083296	0	0.333183
Cat	0.21581	0.201723	0.642942
AAC	0.657631	0.531845	0.956554
Sul2	0.303449	Inf	0.642942
oqxA	1	Inf	1
OXA	1	Inf	1
Tet	0.060166	0.174686	0.333183
aadA	1	0.860095	1
Sul1	0.071737	7.526768	0.333183
ermB	1	1.216807	1
dfrA	0.632728	0.62761	0.956554
qnrS	1	1.108621	1
mphA	0.46046	2.308529	0.818596