

Table S1: Characteristics of patients having liver cirrhosis

Patient	Cohort	Child-Pugh score	Child Class	MELD score	INR	PT (s)	Creatinine (mg/dL)	Bilirubine (mg/dL)	Albumine (g/L)	Trombocytes (10*9/L)	Ascites	Hepatoencefalopaty	Dialyse
1	First	5	A	9,3	1,2	13,8	0,59	1,24	42	87	no	no	no
2	First	6	A	12,6	1,1	12,3	1,7	0,83	30,3	127	no	no	no
3	First	7	B	10,4	1,1	12,9	0,73	2,15	32,8	86	no	no	no
4	First	5	A	7,5	1,1	11,9	0,66	0,63	45,1	152	no	no	no
5	First	5	A	7,5	1,1	12,3	0,88	0,46	44	199	no	no	no
6	First	7	B	10,7	0,9	10,5	0,82	3,08	39,1	118	no	no	no
7	First	8	B	16,1	1,2	13,7	0,79	7,46	35,6	86	yes	no	no
8	First	5	A	7,2	1	10,9	1,08	1,02	45	183	no	no	no
9	First	5	A	8,7	1,1	12,4	1,13	0,76	42	178	no	no	no
10	Second	9	B	13,8	1,4	15,4	0,62	2,59	22,4	103	yes	no	no
11	Second	6	A	11,2	1,2	13,6	0,71	2,06	37,9	112	no	no	no
12	Second	6	A	7	0,9	10,7	0,83	1,17	44,7	236	yes	no	no
13	Second	5	A	7,5	1,1	11,6	0,99	0,34	44,7	374	no	no	no

Table S2: Difference in microbiota community composition between groups of patients (Adonis test on genus-level community Bray-Curtis dissimilarity, n=147).

Adonis	R2	p-value*
Control vs PSC only	0.0626	0.005
Control vs PSC-CD	0.1085	0.005
Control vs PSC-UC	0.1284	0.005
Control vs CD	0.2214	0.005
Control vs UC	0.0428	0.035
PSC only vs PSC-CD	0.0246	0.999
PSC only vs PSC-UC	0.0243	0.999
PSC-CD vs PSC-UC	0.0144	0.999
PSC-CD vs CD	0.0406	0.1618
PSC-UC vs UC	0.0808	0.012
CD vs UC	0.1363	0.003
Cirrhosis vs no cirrhosis	0.11753	0.001998
Cirrhosis vs HC	0.07188	0.001998
No cirrhosis vs HC	0.10085	0.001998
PSC+UDCA vs PSC-UDCA	0.02114	0.7232
PSC-UDCA vs Controls	0.12052	0.001998
PSC+Antibiotics vs PSC-Antibiotics	0.02698	0.2458
PSC-Antibiotics vs Controls	0.15184	0.000999

*p-value after multiple testing correction (FDR)

Table S3: Genera with significantly higher (red arrows) or lower (blue arrows) abundance in patients compared to healthy controls (n=147, Mann-Whitney U test, FDR correction).

Group	Genus	In patients
A	Alistipes	↓
	Aquabacterium	↑
	Barnesiella	↓
	Blautia	↓
	Dorea	↓
	Haemophilus	↑
	Odoribacter	↓
	Pelomonas	↑
	Scardovia	↑
	Victivallis	↓
	Weissella	↑
	B	Butyricoccus
C	Flavonifractor	↑
D	Acidaminococcus	↑
	Collinsella	↓
	Enterorhabdus	↓
	Slackia	↓
	Succinivibrio	↓
	Treponema	↑
E	Faecalibacterium	↓
F	Bacteroides	↑
	Ruminococcus	↓
G	Anaerostipes	↓
H	Morganella	↑
I	Butyricimonas	↓
	Veillonella	↑
J	Coprococcus	↓
	Oscillibacter	↓
	Sporobacter	↓
K	Gemmiger	↓
L	Enterococcus	↑
	Lactobacillus	↑
	Streptococcus	↑
M	Fusobacterium	↑

Table S4: Genus abundance comparisons between PSC patients without liver cirrhosis or liver transplantation and healthy controls (n=81). The Mann-Whitney U test p-values (FDR corrected) are reported in the table.

Genera	All PSC (n=29)	PSC-only (n=7)	PSC-UC (n=9)	PSC-CD (n=13)
Acidaminococcus	0.041189399	ns	0.00197916	ns
Anaerostipes	0.01878444	ns	ns	ns
Aquabacterium	0.033255202	ns	ns	ns
Bacteroides	0.000632405	ns	0.014597243	ns
Barnesiella	ns	ns	0.034747644	ns
Bifidobacterium	ns	ns	ns	0.044341633
Coprococcus	0.002030428	ns	ns	0.003258311
Dorea	0.041189399	ns	ns	ns
Enterococcus	1.92804E-08	0.016277985	0.00068809	1.63082E-05
Enterorhabdus	0.00571491	ns	ns	ns
Faecalibacterium	0.006229379	ns	ns	0.009604592
Fusobacterium	1.91737E-08	0.016277985	0.000858219	1.63082E-05
Haemophilus	ns	ns	0.029095261	ns
Lactobacillus	1.98535E-08	0.028123052	0.006014667	0.000134073
Megamonas	0.004134015	ns	ns	ns
Morganella	0.033255202	ns	ns	0.022508496
Oscillibacter	0.026014282	ns	ns	ns
Ruminococcus	0.042899981	ns	0.014597243	ns
Scardovia	ns	ns	0.00197916	ns
Sporobacter	0.003118588	ns	ns	0.029308616
Streptococcus	0.000119109	ns	0.040464562	0.009604592
Succiniclasticum	0.01878444	ns	ns	ns
Veillonella	5.03455E-06	ns	0.00197916	0.003258311
Victivallis	0.003599138	ns	ns	ns

Table S5: Multivariate analysis in the first cohort with MaAsLin taking into account sex, age, BMI, smoking status, antibiotic use, UDCA and PSC disease severity (stable disease, liver cirrhosis or liver transplantation). (n=104)

Variable	Genus	Coefficient	p-value	Q-value
Age	Eggerthella	0,000	0,001	0,058
Age	Methanobrevibacter	0,000	0,002	0,074
Age	Slackia	0,000	0,005	0,194
Healthy Control	Fusobacterium	-0,021	<0,001	<0,001
Healthy Control	Enterococcus	-0,015	<0,001	<0,001
Healthy Control	Lactobacillus	-0,034	<0,001	0,003
Healthy Control	Oscillibacter	0,033	<0,001	0,034
Healthy Control	Coprococcus	0,074	<0,001	0,058
Healthy Control	Anaerostipes	0,047	<0,001	0,058
Healthy Control	Blautia	0,075	<0,001	0,058
Healthy Control	Desulfovibrio	-0,014	0,002	0,227

Table S6: Spearman correlation between the relative abundance of the most significant genera and gamma-glutamyl transpeptidase (GGT) and alkaline phosphatase (ALP).

Adjusted p value

	GGT	ALP
Enterococcus	0.002	0.014
Lactobacillus	0.003	0.171
Fusobacterium	0.216	0.213

Spearman rho

	GGT	ALP
Enterococcus	0.323	0.292
Lactobacillus	0.288	0.169
Fusobacterium	0.115	-0.152

Table S7: BLAST hits for the centroid sequences of the OTU clusters assigned to the genus *Enterococcus*.

OTU	hit	description		alignment		
		species	strain	%identity	length	evalue
OTU1	NR_042386.1	<i>Enterococcus canintestini</i>	strain LMG 13590	99.21	253	1.32E-128
OTU1	NR_113931.1	<i>Enterococcus canis</i>	strain NBRC 100695	99.21	253	1.32E-128
OTU1	NR_113927.1	<i>Enterococcus dispar</i>	strain NBRC 100678	99.21	253	1.32E-128
OTU1	NR_119293.1	<i>Enterococcus dispar</i>	strain NCIMB 13000	99.21	253	1.32E-128
OTU1	NR_024904.1	<i>Enterococcus dispar</i>	strain ATCC 51266	99.21	253	1.32E-128
OTU1	NR_113257.1	<i>Enterococcus durans</i>	strain JCM 8725	99.21	253	1.32E-128
OTU1	NR_113900.1	<i>Enterococcus durans</i>	strain NBRC 100479	99.21	253	1.32E-128
OTU1	NR_036922.1	<i>Enterococcus durans</i>	strain 98D	99.21	253	1.32E-128
OTU1	NR_074637.1	<i>Enterococcus faecalis</i>	strain V583	99.21	253	1.32E-128
OTU1	NR_113901.1	<i>Enterococcus faecalis</i>	strain NBRC 100480	99.21	253	1.32E-128
OTU1	NR_115765.1	<i>Enterococcus faecalis</i>	strain ATCC 19433	99.21	253	1.32E-128
OTU1	NR_040789.1	<i>Enterococcus faecalis</i>	strain JCM 5803	99.21	253	1.32E-128
OTU1	NR_102790.1	<i>Enterococcus faecium</i>	strain Aus0004	99.21	253	1.32E-128
OTU1	NR_113904.1	<i>Enterococcus faecium</i>	strain NBRC 100486	99.21	253	1.32E-128
OTU1	NR_113903.1	<i>Enterococcus faecium</i>	strain NBRC 100485	99.21	253	1.32E-128
OTU1	NR_115764.1	<i>Enterococcus faecium</i>	strain ATCC 19434	99.21	253	1.32E-128
OTU1	NR_114742.1	<i>Enterococcus faecium</i>	strain DSM 20477	99.21	253	1.32E-128
OTU1	NR_114783.2	<i>Enterococcus hirae</i>	strain LMG 6399	99.21	253	1.32E-128
OTU1	NR_075022.1	<i>Enterococcus hirae</i>	strain ATCC 9790	99.21	253	1.32E-128
OTU1	NR_113574.1	<i>Enterococcus hirae</i>	strain NBRC 3181	99.21	253	1.32E-128
OTU1	NR_113256.1	<i>Enterococcus hirae</i>	strain JCM 8729	99.21	253	1.32E-128
OTU1	NR_037082.1	<i>Enterococcus hirae</i>	strain R	99.21	253	1.32E-128
OTU1	NR_114452.1	<i>Enterococcus hirae</i>	strain ATCC 8043	99.21	253	1.32E-128
OTU1	NR_117562.1	<i>Enterococcus lactis</i>	strain BT159 16S	99.21	253	1.32E-128
OTU1	NR_121694.1	<i>Enterococcus mundtii</i>	strain QU 25	99.21	253	1.32E-128
OTU1	NR_113906.1	<i>Enterococcus mundtii</i>	strain NBRC 100490	99.21	253	1.32E-128
OTU1	NR_024906.1	<i>Enterococcus mundtii</i>	strain ATCC 43186	99.21	253	1.32E-128
OTU1	NR_125610.1	<i>Enterococcus olivae</i>	strain IGG16.11 16S	99.21	253	1.32E-128
OTU1	NR_113934.1	<i>Enterococcus ratti</i>	strain NBRC 100698	99.21	253	1.32E-128
OTU1	NR_041933.1	<i>Enterococcus ratti</i>	strain DS 2705-87	99.21	253	1.32E-128
OTU1	NR_117043.1	<i>Enterococcus rivorum</i>	strain S299	99.21	253	1.32E-128
OTU1	NR_113935.1	<i>Enterococcus villorum</i>	strain NBRC 100699	99.21	253	1.32E-128
OTU1	NR_036921.1	<i>Enterococcus villorum</i>	strain 88-5474	99.21	253	1.32E-128
OTU2	NR_102793.1	<i>Enterococcus casseliflavus</i>	strain EC20	98.42	253	1.03E-124
OTU2	NR_104560.1	<i>Enterococcus casseliflavus</i>	strain NBRC 100478	98.42	253	1.03E-124
OTU2	NR_119280.1	<i>Enterococcus casseliflavus</i>	strain NCIMB 11449	98.42	253	1.03E-124
OTU2	NR_041704.1	<i>Enterococcus casseliflavus</i>		98.42	253	1.03E-124
OTU2	NR_104559.2	<i>Enterococcus gallinarum</i>	strain LMG 13129	98.42	253	1.03E-124
OTU2	NR_113924.1	<i>Enterococcus gallinarum</i>	strain NBRC 100675	98.42	253	1.03E-124
OTU2	NR_041703.1	<i>Enterococcus gallinarum</i>		98.42	253	1.03E-124
OTU2	NR_114786.2	<i>Enterococcus saccharolyticus</i>	strain LMG 11427	98.42	253	1.03E-124
OTU2	NR_113909.1	<i>Enterococcus saccharolyticus</i>	strain NBRC 100493	98.42	253	1.03E-124
OTU2	NR_115767.1	<i>Enterococcus saccharolyticus</i>	strain ATCC 43076	98.42	253	1.03E-124
OTU2	NR_119292.1	<i>Enterococcus saccharolyticus</i>	strain NCDO 2594	98.42	253	1.03E-124
OTU2	NR_041707.1	<i>Enterococcus saccharolyticus</i>	strain ATCC 43076	98.42	253	1.03E-124
OTU3	NR_113923.1	<i>Enterococcus cecorum</i>	strain NBRC 100674	100	253	6.11E-132
OTU3	NR_119291.1	<i>Enterococcus cecorum</i>	strain NCDO 2674	100	253	6.11E-132
OTU3	NR_024905.1	<i>Enterococcus cecorum</i>	strain A60	100	253	6.11E-132