Table S5. Genetic predictors of CBD-related diarrhea adjusted for treatment arm, sex, race, baseline weight, and clobazam

Gene	SNP	CHR	Effect allele	Consequence	Model	OR	[95% CI]	p	EMP p
ABCB1	rs2214102	7	A	5' UTR	dominant	0.28	[0.08 - 0.98]	0.05	0.04
ABCB11	rs7563233	2	G	synonymous	dominant	0.09	[0.01 - 0.56]	0.01	0.003
ABCB11	rs3770603	2	A	intron	dominant	6.05	[1.59 - 23.02]	0.01	0.01
ABCB11	rs496550	2	G	3' UTR	recessive	0.31	[0.11 - 0.94]	0.04	0.04
ABCB11	rs473351	2	A	3' UTR	dominant	2.85	[1.06 - 7.68]	0.04	0.04
ABCB4	rs4148808	7	G	intron	dominant	6.05	[1.59 - 23.02]	0.01	0.01
ABCB4	rs4148805	7	A	splice region	dominant	4.60	[1.20 - 17.67]	0.03	0.02
ABCB4	rs2230028	7	G	missense	dominant	0.29	[0.09 - 0.91]	0.03	0.04
ABCC4	rs2274405	13	A	synonymous	recessive	0.10	[0.02 - 0.55]	0.007	0.002
ABCC4	rs2274406	13	A	missense	recessive	0.14	[0.03 - 0.63]	0.01	0.01
ABCC4	rs1678339	13	A	missense	dominant	0.18	[0.04 - 0.77]	0.02	0.01
ABCC4	rs1059751	13	C	3' UTR	recessive	5.16	[1.24 - 21.54]	0.02	0.02
ABCC4	rs4148553	13	A	3' UTR	recessive	5.16	[1.24 - 21.54]	0.02	0.02
ABCC4	rs4148551	13	G	3' UTR	dominant	0.32	[0.11 - 0.91]	0.03	0.03
ABCG1	rs3788010	21	G	intron	recessive	0.30	[0.09 – 1.00]	0.05	0.05
ABP1	rs12539	7	T	3' UTR	dominant	3.25	[1.2 - 8.85]	0.02	0.02
ADH5	rs7687322	4	T	intron	dominant	0.09	[0.02 - 0.49]	0.006	0.002
ALDH3A1	rs887241	17	T	missense	recessive	0.15	[0.03 - 0.77]	0.02	0.01
CA5P	rs11859842	16	G	regulatory region	dominant	3.13	[1.10 - 8.90]	0.03	0.03
CHST1	rs9787901	11	T	intergenic	dominant	4.80	[1.24 - 18.55]	0.02	0.02
CYP17A1	rs6163	10	T	synonymous	dominant	3.33	[1.24 - 8.96]	0.02	0.02
CYP17A1	rs743572	10	C	5' UTR	dominant	3.33	[1.24 - 8.96]	0.02	0.02
CYP2A6	rs28399433	19	G	intron	dominant	12.15	[2.64 - 55.93]	0.001	0.001
CYP2A7	rs3869579	19	C	missense	recessive	0.33	[0.11 - 0.93]	0.04	0.04
CYP2E1	rs2070673	10	A	intron	dominant	0.16	[0.05 - 0.51]	0.002	0.002
CYP2E1	rs2515641	10	T	missense	dominant	0.30	[0.1 - 0.86]	0.03	0.03
CYP39A1	rs7761731	6	A	missense	recessive	9.03	[1.34 - 60.65]	0.02	0.02
CYP4B1	rs2297810	1	A	stop gained	dominant	0.32	[0.12 - 0.88]	0.03	0.04
CYP4F3	rs4646904	19	A	synonymous	recessive	0.20	[0.06 - 0.72]	0.01	0.01
CYP4F8	rs4646523	19	G	noncoding exon	dominant	2.60	[1.05 - 6.44]	0.04	0.03
FMO3	rs2266780	1	G	missense	dominant	5.94	[1.80 - 19.56]	0.003	0.003
FMO3	rs1736557	1	A	missense	dominant	0.20	[0.05 - 0.83]	0.03	0.02
FMO3	rs2266782	1	A	missense	dominant	2.88	[1.12 - 7.43]	0.03	0.02
FMO4	rs2223477	1	G	intron	dominant	0.30	[0.11 - 0.85]	0.02	0.03
FMO6	rs2272797	1	A	missense	dominant	7.34	[2.25 - 23.91]	0.001	0.001
FMO6	rs7886938	1	A	synonymous	dominant	7.34	[2.25 - 23.91]	0.001	0.001
FMO6	rs7889839	1	G	missense	dominant	7.34	[2.25 - 23.91]	0.001	0.001
GSTA1	rs4715333	6	A	intergenic	dominant	3.13	[1.11 - 8.85]	0.03	0.04
GSTA3	rs512795	6	G	intron	dominant	0.19	[0.06 - 0.66]	0.01	0.01
NAT2	rs1799930	8	A	missense	dominant	2.73	[1.07 - 6.98]	0.04	0.04
PON3	rs2072200	7	G	TF binding	recessive	0.07	[0.01 - 0.53]	0.010	0.003
PPARD	rs2076167	6	C	missense	dominant	0.28	[0.10 - 0.74]	0.01	0.01
PPARD	rs2267667	6	G	intron	dominant	0.31	[0.12 - 0.82]	0.02	0.02
PPARD	rs6457816	6	C	intron	dominant	0.24	[0.08 - 0.77]	0.02	0.02
PPARD	rs1053046	6	A	3' UTR	dominant	0.23	[0.06 - 0.81]	0.02	0.02
PPARD	rs6901410	6	C	intron	dominant	0.25	[0.08 - 0.79]	0.02	0.02
PPARD	rs6922548	6	G	intron	dominant	0.25	[0.08 - 0.79]	0.02	0.02
PPARD	rs7739752	6	T	intron	dominant	0.25	[0.08 - 0.79]	0.02	0.02
PPARD	rs1883322	6	C	intron	dominant	0.31	[0.12 - 0.83]	0.02	0.02
PPARD	rs7751481	6	A	intron	dominant	0.31	[0.12 - 0.83]	0.02	0.02
PPARD	rs7746988	6	C	intron	dominant	0.22	[0.05 - 0.94]	0.04	0.03
PPARD	rs6457815	6	C	intron	dominant	0.24	[0.06 - 0.88]	0.03	0.03
PPARD	rs6906237	6	A	intron	dominant	0.27	[0.08 - 0.90]	0.03	0.04
SLC13A1	rs2204295	7	G	intron	dominant	0.34	[0.13 - 0.90]	0.03	0.03

Gene	SNP	CHR	Effect allele	Consequence	Model	OR	[95% CI]	p	EMP p
SLC22A1	rs1867351	6	C	synonymous	dominant	0.29	[0.11 - 0.76]	0.01	0.01
SLC22A1	rs628031	6	A	missense	recessive	5.71	[1.12 - 29.20]	0.04	0.04
SLC22A11	rs2078267	11	T	noncoding exon	dominant	3.65	[1.25 - 10.69]	0.02	0.02
SLC22A14	rs2298419	3	T	regulatory region	dominant	0.24	[0.08 - 0.70]	0.01	0.01
SLC22A2	rs624249	6	T	synonymous	dominant	0.37	[0.14 - 0.99]	0.05	0.04
SLC22A3	rs2292334	6	A	synonymous	recessive	7.13	[1.49 - 34.05]	0.01	0.01
SLC22A4	rs1050152	5	T	missense	dominant	3.01	[1.12 - 8.12]	0.03	0.03
SLC22A5	rs274548	5	T	3’ UTR	recessive	0.13	[0.02 - 0.96]	0.05	0.03
SLC22A7	rs2270860	6	T	splice region	recessive	0.15	[0.03 - 0.67]	0.01	0.01
SLC22A7	rs2242416	6	A	missense	recessive	0.28	[0.09 - 0.90]	0.03	0.03
SLC25A27	rs953062	6	C	intron	recessive	5.93	[1.1 - 32.12]	0.04	0.03
SLC28A1	rs2242046	15	A	missense	recessive	8.00	[1.84 - 34.72]	0.01	0.01
SLC28A1	rs2305367	15	A	missense	dominant	0.36	[0.13 - 0.95]	0.04	0.04
SLCO1B1	rs4149057	12	T	synonymous	dominant	0.28	[0.09 - 0.82]	0.02	0.02
SLCO1B1	rs11045819	12	A	missense	dominant	3.54	[1.13 - 11.13]	0.03	0.03
SLCO1B3	rs3764006	12	G	synonymous	dominant	0.21	[0.07 - 0.61]	0.005	0.004
SLCO1B3	rs2053098	12	A	synonymous	dominant	0.32	[0.12 - 0.85]	0.02	0.02
SLCO1B3	rs4149117	12	T	missense	dominant	0.32	[0.12 - 0.85]	0.02	0.02
SLCO1B3	rs7311358	12	G	missense	dominant	0.32	[0.12 - 0.85]	0.02	0.02
SLCO3A1	rs2190748	15	A	intron	dominant	0.15	[0.04 - 0.51]	0.002	0.002
SLCO5A1	rs1138541	8	A	3’ UTR	recessive	0.08	[0.01 - 0.90]	0.04	0.01
SLCO5A1	rs2380563	8	A	intron	dominant	0.19	[0.05 - 0.74]	0.02	0.01
SLCO5A1	rs16936279	8	C	3’ UTR	dominant	0.35	[0.13 - 0.98]	0.05	0.05
UGT2A1	rs11249454	4	G	intron	dominant	0.35	[0.12 - 0.98]	0.05	0.03
VKORC1	rs2359612	16	T	intron	recessive	0.18	[0.04 - 0.85]	0.03	0.02
VKORC1	rs9923231	16	A	regulatory region	recessive	0.19	[0.04 - 0.89]	0.03	0.02

CHR: chromosome; OR: odds ratio; EMP p: empirical p-value obtained after 1,000 permutations
Variants in grey were removed due to LD
Consequences indicate the most severe consequence reported for the variant in Ensembl (GRCh37 Release 104)