Supplemental Tables

Host genetic determinants of the gut microbiota of wild mice

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Table S1. Metadata of wild-caught individuals.

ID	MVZ_IDs	Localities	Latitude	Longitude	Sex	Body length (mm)	Weight (g)	BMI (g/mm^2)	Repro status	Carbon ($\delta^{13}C$)	Nitrogen ($\delta^{15}N$)	ClimatePC1	ClimatePC2	BarcodeSequence
MPR.108	MVZ:Mamm:230591	FL	29.67445	-82.33093333	F	77	13.0	0.002192613	adult	-21.8	5.2	2.97062216	1.499308753	CGGACTCGTTAC
MPR.110	MVZ:Mamm:230601	FL	29.6233	-82.340333	F	90	23.5	0.002901235	pregnant	-21.8	7	3.096504907	1.513670142	TCTCGCACTGGA
MPR.112	MVZ:Mamm:230593	FL	29.778929	-82.416971	M	77	12.8	0.002150447	adult	-18.8	5.9	2.998892477	1.501471275	TTCTGGTCTTGT
MPR.113	MVZ:Mamm:230590	FL	29.78685	-82.495877	F	84	11.4	0.001612103	adult	-20	6.2	2.998892477	1.501471275	GTCCACTTGGAC
MPR.114	MVZ:Mamm:230603	FL	29.37283	-82.19892	F	84	15.5	0.002196712	pregnant	-22.2	8	3.100624164	1.464651522	GATTTAGAGGCT
MPR.115	MVZ:Mamm:230595	FL	29.45224	-82.3403	F	84	14.0	0.001984127	adult	-22.6	4.5	3.205937396	1.469365645	GTCAGCCGTTAA
MPR.116	MVZ:Mamm:230597	FL	29.39018	-82.1299	M	82	14.3	0.002119274	adult	-17.9	7.1	3.028607066	1.351687486	ACGGTTTCTGGA
MPR.118	MVZ:Mamm:230599	FL	29.10066	-82.14192	M	68	9.5	0.002054498	adult	-21.8	7.1	3.133622652	1.147339587	GCAGCCATATTG
MPR.120	MVZ:Mamm:230594	FL	29.7828	-82.3755	M	82.5	14.0	0.002056933	adult	-24.2	7.7	2.998892477	1.501471275	ATAGGTGTGCTA
MPR.121	MVZ:Mamm:230596	FL	29.65652	-82.5872	F	92	23.0	0.002717391	pregnant	-16.8	7.6	3.052686779	1.310811624	ACCTAGCTAGTG
MPR.123	MVZ:Mamm:230612	GA	34.0989	-83.3454	M	75.5	11.0	0.00192974	adult	-17.9	7.1	0.694382471	2.870810123	GTCCTGACACTG
MPR.124	MVZ:Mamm:230604	GA	34.10006	-83.59695	F	78	14.5	0.0023833	pregnant	-19.9	6.5	0.720716609	2.954123495	GGACTCAACTAA
MPR.125	MVZ:Mamm:230609	GA	34.09889	-83.34537	M	69	11.0	0.002310439	adult	-21.4	9.9	0.694382471	2.870810123	ATACGGGTTCGT
MPR.126	MVZ:Mamm:230608	GA	34.11877	-83.57092	M	80	18.5	0.002890625	adult	-14.8	7.3	0.720716609	2.954123495	CCTTTCACCTGT
MPR.128	MVZ:Mamm:230606	GA	33.87025	-83.28893	M	81	15.8	0.002400549	adult	-21.3	7.8	0.558088177	2.61167319	ATCAGCCAGCTC
MPR.129	MVZ:Mamm:230615	GA	33.83757	-83.35049	M	77	12.8	0.002150447	adult	-20.4	6.6	0.586814091	2.694032322	GCTCCACAACGT
MPR.130	MVZ:Mamm:230610	GA	33.94638	-83.38383	F	80	16.1	0.002519531	adult	-17.3	6.4	0.586814091	2.694032322	AAGGAGTGCGCA
MPR.131	MVZ:Mamm:230613	GA	33.88584	-83.48023	F	65	9.0	0.002130178	pregnant	-9.5	9.6	0.586814091	2.694032322	AGGGAAAGGATC
MPR.132	MVZ:Mamm:230614	GA	33.8437	-83.33744	F	75.5	11.0	0.00192974	adult	-18.1	7.8	0.586814091	2.694032322	ACGACGCATTTG
MPR.133	MVZ:Mamm:230607	GA	33.94639	-83.38384	F	89	21.4	0.002698523	pregnant	-15.1	7.8	0.586814091	2.694032322	CGTCACTCCAAG
MPR.134	MVZ:Mamm:230616	NH-VT	44.11202	-72.04543	F	83	19.1	0.002776165	adult	-18	8.3	-2.941483795	2.077455579	TTACACAAAGGC
MPR.135	MVZ:Mamm:230617	NH-VT	44.11212	-72.04551	F	93	21.4	0.002471384	adult	-15.5	7.5	-2.941483795	2.077455579	GTATAGTCCGTG
MPR.137	MVZ:Mamm:230619	NH-VT	43.99797	-72.10448	F	81	13.4	0.002038561	adult	-17.6	10.8	-2.873866295	2.449812	TCGTAAGCCGTC
MPR.138	MVZ:Mamm:230622	NH-VT	43.97192	-72.08463	M	86	14.8	0.001994321	adult	-23.4	5.7	-2.873866295	2.449812	TGACGCCTCCAA
MPR.140	MVZ:Mamm:230621	NH-VT	43.97281	-72.09393	M	74	14.0	0.002556611	adult	-17.8	6.3	-2.873866295	2.449812	TTCTCGGTTCTC
MPR.141	MVZ:Mamm:230648	NH-VT	43.95075	-72.11753	M	86	19.5	0.00263656	adult	-19.5	11.8	-2.873866295	2.449812	GCTACTGGTATG
MPR.142	MVZ:Mamm:230649	NH-VT	43.9609	-72.11585	F	94	23.8	0.002687868	pregnant	-19.9	7.6	-2.873866295	2.449812	GAATCCTCACCG
MPR.143	MVZ:Mamm:230647	NH-VT	43.927907	-72.12301	M	81.5	15.5	0.002333547	adult	-14.4	11.3	-2.873866295	2.449812	CCTGACACACAC
MPR.144	MVZ:Mamm:230651	NH-VT	44.12806	-72.04328	M	87.5	18.3	0.002383673	adult	-15.5	7.5	-2.941483795	2.077455579	CAGCGTTTAGCC
MPR.145	MVZ:Mamm:230650	NH-VT	43.95596	-72.11164	F	98	21.0	0.002186589	adult	-19.3	6.7	-2.873866295	2.449812	GGTATGGCTACT
MPR.146	MVZ:Mamm:230633	PA	40.618763	-75.36362	F	86	13.1	0.001774608	adult	-19.9	8	-1.213822773	3.005363487	ACAATGTCACAG
MPR.147	MVZ:Mamm:230627	PA	40.50319	-75.3174	M	87	16.0	0.002113886	adult	-20.5	6.7	-1.221697022	3.105731663	GCCATAGTGTGT
MPR.148	MVZ:Mamm:230628	PA	40.45099	-75.40128	M	75	13.3	0.002355556	adult	-21.6	6.1	-1.21210531	3.021371305	GGTCCCGAAATT
MPR.150	MVZ:Mamm:230631	PA	40.59571	-75.65891	F	75	11.9	0.002111111	adult	-23.8	5.9	-1.253146437	2.969723195	TCTGCGAGTCTG
MPR.151	MVZ:Mamm:230634	PA	40.55189	-75.32455	M	78.5	15.0	0.002434176	adult	-23.2	7.1	-1.221697022	3.105731663	ATGTAGGCTTAG
MPR.152	MVZ:Mamm:230629	PA	40.53107	-75.34738	M	81	15.0	0.002286237	adult	-15.4	6.7	-1.213822773	3.005363487	TGCTTCCAATTC
MPR.153	MVZ:Mamm:230624	PA	40.500421	-76.103425	F	81.5	21.3	0.003199217	pregnant	-10.7	8.4	-1.362674566	3.08747214	GCCGAGATAATT
MPR.154	MVZ:Mamm:230623	PA	40.461968	-76.08789	F	82	17.3	0.002565437	adult	-19.9	6.3	-1.277569614	2.900451084	TCGAGTATCGAA
MPR.155	MVZ:Mamm:230632	PA	40.70747	-75.66738	M	78	14.5	0.0023833	adult	-19.9	7.6	-1.375142871	3.180181879	GCCCTATCTTCT
MPR.156	MVZ:Mamm:230625	PA	40.526708	-76.097258	F	96	21.0	0.002278646	adult	-17	6.8	-1.362674566	3.08747214	AGGTACGCAATT
MPR.159	MVZ:Mamm:230641	VA	37.74117	-77.57546	F	77	14.8	0.002487772	adult	-23.5	7.4	-0.54705521	2.680888784	GTCCCTATTATC
MPR.161	MVZ:Mamm:230638	VA	37.65535	-77.72927	F	80	15.3	0.002382813	pregnant	-24.1	8	-0.52685297	2.654121765	TGGGACATATCC
MPR.162	MVZ:Mamm:230645	VA	37.48763	-77.40208	M	86	17.3	0.002332342	adult	-19.5	6.5	-0.145751223	2.590674625	GAACGATCATGT
MPR.163	MVZ:Mamm:230637	VA	37.65501	-77.73977	M	78	15.1	0.002486029	adult	-22.8	5.9	-0.52685297	2.654121765	TTCAGACCAGCC
MPR.164	MVZ:Mamm:230642	VA	37.67885	-77.5166	M	91	18.3	0.00220384	adult	-20.3	6.9	-0.54705521	2.680888784	ACGCATCGCACT
MPR.165	MVZ:Mamm:230644	VA	37.55811	-77.48073	M	66	10.8	0.00246786	adult	-19.3	8.2	-0.366753804	2.692423969	CAGTAGCGATAT
MPR.166	MVZ:Mamm:230639	VA	37.76063	-77.48351	M	80	15.0	0.00234375	adult	-19	5.9	-0.468067251	2.664179717	TCCCTTGTCTCC
MPR.167	MVZ:Mamm:230635	VA	37.52756	-77.6492	F	80	13.0	0.00203125	adult	-14.7	9.6	-0.488569853	2.718535468	ACGAGACTGATT
MPR.168	MVZ:Mamm:230646	VA	37.85448	-77.26262	F	82	13.5	0.002007733	pregnant	NA	NA	-0.475831808	2.715734487	GCTGTACGGATT
MPR.169	MVZ:Mamm:230636	VA	37.55537	-77.66149	F	69	11.0	0.002310439	adult	-14.1	7.5	-0.488569853	2.718535468	ATCACCAGGTGT

Table S2. Principal components of climatic variables.

	PC1 (69.2%)	PC2 (22.1%)	PC3 (4.6%)	Prin4 (3.6%)
bio1	0.27111	0.0579	0.11257	0.09989
bio2	0.1859	-0.00256	-0.44368	0.7295
bio3	0.27115	-0.06465	-0.04618	0.12554
bio4	-0.27493	0.02479	-0.03135	-0.02992
bio5	0.25218	0.159	0.19138	0.16051
bio6	0.27079	0.05962	0.14904	0.03134
bio7	-0.27357	-0.00493	-0.12247	0.03852
bio8	0.06238	-0.36347	0.63004	0.23546
bio9	0.25284	0.16393	-0.20573	-0.01738
bio10	0.25949	0.12593	0.18248	0.141
bio11	0.27311	0.03834	0.097	0.07757
bio12	0.25318	0.10785	-0.00326	-0.38185
bio13	0.25923	-0.12326	-0.14616	-0.20514
bio14	-0.01549	0.48149	0.12471	0.04536
bio15	0.21244	-0.2939	-0.18019	-0.14671
bio16	0.25764	-0.13577	-0.10009	-0.24175
bio17	-0.00357	0.46494	0.30991	-0.04143
bio18	0.22948	-0.25794	0.06483	-0.17746
bio19	0.16001	0.37484	-0.22778	-0.16795

Table S3. Metadata of lab reared individuals from the most northern and southern populations.

ID	Breeding ID	Locality	Sex	Weight (g)	Age at collection (days)	Carbon ($\delta^{13}C$)	Nitrogen ($\delta^{15}N$)	BarcodeSequence
FL01F1	F1(DL95x54)	Florida_Lab	F	16.6	146	-19.0	6.7	TTGGTCTCCTCT
FL01F2	F1(DL95x54)	Florida_Lab	F	19	146	-19.0	6.7	CTGCATACTGAG
FL01M1	F1(DL95x54)	Florida_Lab	M	23.6	146	-19.0	6.7	TACCTAGTGAGA
FL01M2	F1(DL95x54)	Florida_Lab	M	21	146	-19.0	6.7	CGTTCTGGTGGT
FL02F1	F1(DL105x71)3	Florida_Lab	F	15.7	194	-19.0	6.7	GTCAATTAGTGG
FL02F2	F1(DL105x71)1	Florida_Lab	F	16.2	264	-19.0	6.7	AGTACGCAGTCT
FL02M1	F1(DL105x71)2	Florida_Lab	M	20.2	242	-19.0	6.7	CAGGGCCTTTGT
FL02M2	F1(DL105x71)	Florida_Lab	M	23.5	194	-19.0	6.7	CGATGAATATCG
FL03F1	F1(DL107x83)	Florida_Lab	F	17.5	194	-19.0	6.7	TTCCCGAAACGA
FL03F2	F1(DL107x83)3	Florida_Lab	F	20.5	265	-19.0	6.7	GAACTTTAGCGC
FL03M1	F1(DL107x83)4	Florida_Lab	M	25	194	-19.0	6.7	AGCAGCTATTGC
FL03M2	F1(DL107x83)6	Florida_Lab	M	27.2	194	-19.0	6.7	CTCGGATAGATC
FL04F1	F1(DL58x59)5	Florida_Lab	F	12.9	169	-19.0	6.7	TACTGAGCCTCG
FL04F2	F1(DL58x59)7	Florida_Lab	F	15.5	169	-19.0	6.7	AGAAGGCCTTAT
FL04M1	F1(DL58x59)	Florida_Lab	M	20	148	-19.0	6.7	TCCTTAGAAGGC
FL04M2	F1(DL58x59)	Florida_Lab	M	20.9	148	-19.0	6.7	GATGGACTTCAA
FL05F1	F1(DL69x77)3	Florida_Lab	F	11.9	126	-19.0	6.7	CATCGCGTTGAC
FL05F2	F1(DL69x77)1	Florida_Lab	F	11.8	126	-19.0	6.7	GCACATAGTCGT
FL05M1	F1(DL69x77)	Florida_Lab	M	19.5	129	-19.0	6.7	GGAATTATCGGT
FL05M2	F1(DL69x77)	Florida_Lab	M	15.8	129	-19.0	6.7	CATCAAGCATAG
FL06F1	F1(DL52x49)	Florida_Lab	F	16.1	177	-19.0	6.7	CCTAGTAAGCTG
FL06F2	F1(DL52x49)	Florida_Lab	F	12.5	100	-19.0	6.7	TTACCGACGAGT
FL06M1	F1(DL52x49)	Florida_Lab	M	19.2	177	-19.0	6.7	GGCAAATACACT
FL06M2	F1(DL52x49)	Florida_Lab	M	14.2	128	-19.0	6.7	GTCATGCTCCAG
FL07F1	F1(DL80x85)5	Florida_Lab	F	13.5	232	-19.0	6.7	TTACCTTACACC
FL07F2	F1(DL80x85)3	Florida_Lab	F	15.6	232	-19.0	6.7	TGACTAATGGCC
FL07M1	F1(DL80x85)	Florida_Lab	M	15.4	148	-19.0	6.7	GCTTAGATGTAG
FL07M2	F1(DL80x85)	Florida_Lab	M	16.9	148	-19.0	6.7	AAGACGTAGCGG
FL08F1	F1(DL67x66)3	Florida_Lab	F	18.5	266	-19.0	6.7	CACGTGACATGT
FL08F2	F1(DL67x66)5	Florida_Lab	F	22	266	-19.0	6.7	CACAGTTGAAGT
FL08M1	F1(DL67x66)	Florida_Lab	M	21.1	205	-19.0	6.7	CTCTCTCACTTG
FL08M2	F1(DL67x66)6	Florida_Lab	M	21.5	205	-19.0	6.7	ATTGCAAGCAAC
FL09F1	F1(DL81x82)1	Florida_Lab	F	15	213	-19.0	6.7	ACCGGAGTAGGA
FL09F2	F1(DL81x82)5	Florida_Lab	F	13	146	-19.0	6.7	TGAGGACTACCT
FL09M1	F1(DL81x82)	Florida_Lab	M	17.5	147	-19.0	6.7	CTAGGATCACTG
FL09M2	F1(DL81x82)2	Florida_Lab	M	20.1	213	-19.0	6.7	GATGACCCAAAT
FL10F1	F1(DL97x73)5	Florida_Lab	F	15.5	200	-19.0	6.7	TGACCGGCTGTT
FL10F2	F1(DL97x73)1	Florida_Lab	F	15	200	-19.0	6.7	GGAGGAGCAATA

FL10M1	F1(DL97x73)	Florida_Lab	M	18.8	179	-19.0	6.7	CAATCGGCTTGC
FL10M2	F1(DL97x73)	Florida_Lab	M	18.4	179	-19.0	6.7	AACACTCGATCG
NY01F1	F1(MJS19x13)5	New_York_Lab	F	17.8	235	-19.1	6.4	AGAGAGACAGGT
NY01F2	F1(MJS19x13)3	New_York_Lab	F	17.9	235	-19.1	6.4	TCGCCAGTGCAT
NY01M1	F1(MJS19x13)8	New_York_Lab	M	20.1	142	-19.1	6.4	TCAACCCGTGAA
NY01M2	F1(MJS19x13)10	New_York_Lab	M	21.5	142	-19.1	6.4	GTTTGAAACACG
NY02F1	F1(MJS66x67)3	New_York_Lab	F	13.5	166	-19.1	6.4	TCTAGCCTGGCA
NY02F2	F1(MJS66x67)1	New_York_Lab	F	16.8	166	-19.1	6.4	AATGCAATGCGT
NY02M1	F1(MJS66x67)	New_York_Lab	M	21	140	-19.1	6.4	GCTCAGGACTCT
NY02M2	F1(MJS66x67)	New_York_Lab	M	24.8	140	-19.1	6.4	CACTTTGGGTGC
NY03F1	F1(MJS34x38)3	New_York_Lab	F	17.9	236	-19.1	6.4	ATCAGAGCCCAT
NY03F2	F1(MJS34x38)1	New_York_Lab	F	22.1	236	-19.1	6.4	TCTGTAGAGCCA
NY03M1	F1(MJS34x38)	New_York_Lab	M	20.1	144	-19.1	6.4	CGAATGAGTCAT
NY03M2	F1(MJS34x38)2	New_York_Lab	M	22	210	-19.1	6.4	CAACGCTAGAAT
NY04F1	F1(MJS44x42)5	New_York_Lab	F	16.4	165	-19.1	6.4	GACAACGAATCT
NY04F2	F1(MJS44x42)9	New_York_Lab	F	17.8	233	-19.1	6.4	TGCGGTTGACTC
NY04M1	F1(MJS44x42)	New_York_Lab	M	22.6	142	-19.1	6.4	CCGACTCTAGGT
NY04M2	F1(MJS44x42)	New_York_Lab	M	23.9	142	-19.1	6.4	ATCCTACGAGCA
NY05F1	F1(MJS49x60)	New_York_Lab	F	17.5	139	-19.1	6.4	CACAGGATTACC
NY05M1	F1(MJS49x60)	New_York_Lab	M	23.4	139	-19.1	6.4	TGAGAAGAAAGG
NY05M2	F1(MJS49x60)	New_York_Lab	M	25.1	139	-19.1	6.4	TCGGATCTGTGA
NY05M3	F1(MJS49x60)	New_York_Lab	M	21.9	139	-19.1	6.4	GCCGGTACTCTA
NY06F1	F1(MJS105x104)3	New_York_Lab	F	15	165	-19.1	6.4	TGTGTTACTCCT
NY06F2	F1(MJS105x104)1	New_York_Lab	F	16.5	165	-19.1	6.4	GGTACCTGCAAT
NY06M1	F1(MJS105x104)	New_York_Lab	M	24.2	141	-19.1	6.4	CGATATCAGTAG
NY06M2	F1(MJS105x104)	New_York_Lab	M	25.2	141	-19.1	6.4	CATAAGGGAGGC
NY07F1	F1(MJS9x11)5	New_York_Lab	F	20.1	154	-19.1	6.4	TAACCCGATAGA
NY07F2	F1(MJS9x11)7	New_York_Lab	F	20	154	-19.1	6.4	GTGTGCTAACGT
NY07M1	F1(MJS9x11)	New_York_Lab	M	20.9	133	-19.1	6.4	TCGCCTATAAGG
NY07M2	F1(MJS9x11)	New_York_Lab	M	24.8	180	-19.1	6.4	AGTGGCACTATC
NY08F1	F1(MJS83x80)	New_York_Lab	F	13.8	203	-19.1	6.4	ATTGCTGGTCGA
NY08F2	F1(MJS83x80)1	New_York_Lab	F	15	226	-19.1	6.4	AAGAAGCCGGAC
NY08M1	F1(MJS83x80)	New_York_Lab	M	17	130	-19.1	6.4	CTTGCGGCAATC
NY08M2	F1(MJS83x80)4	New_York_Lab	M	16.2	203	-19.1	6.4	TGAGGTTTGATG
NY09F1	F1(MJS82x81)1	New_York_Lab	F	21.1	226	-19.1	6.4	TCCGTCATGGGT
NY09F2	F1(MJS82x81)7	New_York_Lab	F	23.2	169	-19.1	6.4	AGATCTATGCAG
NY09M1	F1(MJS82x81)4	New_York_Lab	M	24.5	204	-19.1	6.4	ACGGGATACAGG
NY09M2	F1(MJS82x81)	New_York_Lab	M	27	147	-19.1	6.4	AAGAGTCTCTAG
NY10F1	F1(MJS92x91)5	New_York_Lab	F	17	226	-19.1	6.4	GCGAGTTCCTGT
NY10F2	F1(MJS92x91)	New_York_Lab	F	20.9	168	-19.1	6.4	TTCCGAATCGGC
NY10M1	F1(MJS92x91)2	New_York_Lab	M	24.2	204	-19.1	6.4	GCACAAGGCAAG
NY10M2	F1(MJS92x91)	New_York_Lab	M	25.5	144	-19.1	6.4	CGGCAAACACTT

Table S4. Correlations with latitude and metadata.

Variable	All adult individuals			Adults without pregnant females		
	n	rho	p-value	n	rho	p-value
Body weight (g)	50	0.32	**0.02**	40	0.51	**0.0008**
BMI (g/mm^2)	50	0.21	0.14	40	0.35	**0.03**
Diet ($\delta^{13}C$)	49	0.19	0.19	40	0.25	0.12
Diet ($\delta^{15}N$)	49	0.14	0.35	40	0.24	0.14
Climate PC1	50	-0.97	**<0.0001**	40	-0.98	**<0.0001**
Climate PC2	50	0.32	**0.02**	40	0.23	0.15

Table S5. Human SNPs and genes associated with microbial measurements from previously published mGWAS.

References*	chr	ps	rs	Gene1	Gene2	Gene3	Gene4	Gene5	Gene6	Gene7	notes
Knights et al. 2014	5	130768383	rs10051722	rs10051722							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	56143024	rs10065637	IL31RA							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	62324337	rs10865331	rs10865331							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	16	30471173	rs11150589	LOC613037							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	593968	rs11739663	SLC9A3							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	40410482	rs11742570	PTGER4							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	7	2830351	rs1182188	LFNG							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	198006693	rs1440088	SF3B1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	7	50264865	rs1456896	VWC2							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	191066738	rs1517352	GLS							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	13	26957130	rs17085007	GPR12							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	198658398	rs17229285	rs17229285							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	16	68557327	rs1728785	ZFP90							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	15	67150258	rs17293632	SMAD3							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	11	61785208	rs174537	SYT7							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	17	72646784	rs17780256	LOC100499467							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	6	90263440	rs1847472	rs1847472							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	18	12809341	rs1893217	PTPN2							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	6	159069404	rs212388	EZR							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	22	39263768	rs2413583	TAB1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	1	197662011	rs2488389	CRB1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	135107916	rs254560	C5orf24							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	1	200132792	rs2816958	NR5A2							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	21	15445619	rs2823286	rs2823286							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	15	41271752	rs28374715	INO80							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	10695414	rs2930047	DAP							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	3	49684099	rs3197999	MST1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	13	99255087	rs3742130	DOCK9							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	13	43883789	rs3764147	ENOX1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	7	117255109	rs38911	ST7							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	9	114790969	rs4246905	TNFSF15							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	1	151829204	rs4845604	RORC							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	16	11279463	rs529866	CLEC16A							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	11	114516108	rs561722	NNMT							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	16	50722863	rs5743289	ADCY7							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	20	35211477	rs6088765	MYH7B							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	1	155908941	rs670523	rs670523							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	102446909	rs6708413	IL18RAP							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	65440138	rs6740462	SPRED2							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	5	159399784	rs6871626	IL12B							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	6	137685367	rs6920220	OLIG3							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	8	89863690	rs7015630	RIPK2							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	18	69863203	rs727088	CD226							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	4	48361228	rs7438704	TXK							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	1	172884320	rs7517810	FASLG							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	2	60977721	rs7608910	PAPOLG							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	8	125522429	rs921720	TRIB1							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	3	53028645	rs9847710	PRKCD							Associated with bacterial taxa from intestinal biopsies
Knights et al. 2014	NA	NA	NA	NOD2							NOD2 gene associated with bacterial taxa from intestinal biopsies
Davenport et al. 2015	2	26320519	rs10048683	RAB10	RP11-214J9.1						Associated with bacterial taxa from stool
Davenport et al. 2015	14	83577467	rs10132493								Associated with bacterial taxa from stool
Davenport et al. 2015	2	18924471	rs10173922								Associated with bacterial taxa from stool
Davenport et al. 2015	2	84428819	rs10180739								Associated with bacterial taxa from stool
Davenport et al. 2015	1	209512373	rs1021993								Associated with bacterial taxa from stool
Davenport et al. 2015	2	84519663	rs1031532	FUNDC2P2							Associated with bacterial taxa from stool
Davenport et al. 2015	1	165399577	rs10489747	RXRG							Associated with bacterial taxa from stool
Davenport et al. 2015	2	56772337	rs10490411								Associated with bacterial taxa from stool
Davenport et al. 2015	1	209527706	rs10494924								Associated with bacterial taxa from stool
Davenport et al. 2015	1	216722622	rs10495027	ESRRG							Associated with bacterial taxa from stool

Davenport et al. 2015	2	115697773	rs10496481	DPP10			Associated with bacterial taxa from stool
Davenport et al. 2015	14	81124336	rs10498546	CEP128			Associated with bacterial taxa from stool
Davenport et al. 2015	8	17535058	rs10503602	MTUS1	MIR548V		Associated with bacterial taxa from stool
Davenport et al. 2015	12	71408076	rs10506621	CTD-2021H9.1			Associated with bacterial taxa from stool
Davenport et al. 2015	9	14141071	rs10511591	NFIB			Associated with bacterial taxa from stool
Davenport et al. 2015	4	91740550	rs10516879	CCSER1			Associated with bacterial taxa from stool
Davenport et al. 2015	11	30874751	rs10767880	DCDC1			Associated with bacterial taxa from stool
Davenport et al. 2015	11	32300458	rs10767929	RP1-65P5.1			Associated with bacterial taxa from stool
Davenport et al. 2015	12	23493161	rs10770976				Associated with bacterial taxa from stool
Davenport et al. 2015	11	19142375	rs10833064	ZDHHC13			Associated with bacterial taxa from stool
Davenport et al. 2015	12	23258003	rs10842120	RP11-153K16.1	RP11-686N4.1	RP11-114G22.1	Associated with bacterial taxa from stool
Davenport et al. 2015	12	24864421	rs10842398	RN7SL38P	RP11-625L16.1		Associated with bacterial taxa from stool
Davenport et al. 2015	2	84433641	rs10865473				Associated with bacterial taxa from stool
Davenport et al. 2015	6	124236735	rs10872275	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	9	27688778	rs10968061				Associated with bacterial taxa from stool
Davenport et al. 2015	11	19853179	rs11025278	NAV2			Associated with bacterial taxa from stool
Davenport et al. 2015	12	24875122	rs11047591	RP11-625L16.1			Associated with bacterial taxa from stool
Davenport et al. 2015	1	216722328	rs11117612	ESRRG			Associated with bacterial taxa from stool
Davenport et al. 2015	2	115683104	rs11123259	DPP10			Associated with bacterial taxa from stool
Davenport et al. 2015	2	84433756	rs11126953				Associated with bacterial taxa from stool
Davenport et al. 2015	2	84433896	rs11126954				Associated with bacterial taxa from stool
Davenport et al. 2015	8	17535257	rs11203893	MTUS1	MIR548V		Associated with bacterial taxa from stool
Davenport et al. 2015	10	1702581	rs11250714	ADARB2			Associated with bacterial taxa from stool
Davenport et al. 2015	10	71503932	rs11596374				Associated with bacterial taxa from stool
Davenport et al. 2015	10	124037599	rs11596483	BTBD16			Associated with bacterial taxa from stool
Davenport et al. 2015	8	59305290	rs1160133				Associated with bacterial taxa from stool
Davenport et al. 2015	17	10458111	rs11651216	MYH2	CTC-297N7.11		Associated with bacterial taxa from stool
Davenport et al. 2015	2	84528756	rs11686691				Associated with bacterial taxa from stool
Davenport et al. 2015	20	17264604	rs11696277	PCSK2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	87236328	rs11751618				Associated with bacterial taxa from stool
Davenport et al. 2015	12	71412932	rs11837284	CTD-2021H9.1			Associated with bacterial taxa from stool
Davenport et al. 2015	4	100477462	rs11935423	TRMT10A			Associated with bacterial taxa from stool
Davenport et al. 2015	1	216716320	rs12145418	ESRRG			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124218474	rs12208734	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	10	86548569	rs12240997				Associated with bacterial taxa from stool
Davenport et al. 2015	9	21656749	rs12338476				Associated with bacterial taxa from stool
Davenport et al. 2015	12	45290466	rs12367572	NELL2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124235916	rs12530210	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124236284	rs12530266	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	8	117918897	rs12541437				Associated with bacterial taxa from stool
Davenport et al. 2015	2	84437352	rs12714120				Associated with bacterial taxa from stool
Davenport et al. 2015	1	216716537	rs12757165	ESRRG			Associated with bacterial taxa from stool
Davenport et al. 2015	4	109301049	rs13132148				Associated with bacterial taxa from stool
Davenport et al. 2015	8	17523779	rs13262658	MTUS1			Associated with bacterial taxa from stool
Davenport et al. 2015	2	38745624	rs13423976	AC016995.3			Associated with bacterial taxa from stool
Davenport et al. 2015	12	24856642	rs1386638	RN7SL38P	RP11-625L16.1		Associated with bacterial taxa from stool
Davenport et al. 2015	1	209488564	rs1395747				Associated with bacterial taxa from stool
Davenport et al. 2015	11	30892824	rs1448938	DCDC1			Associated with bacterial taxa from stool
Davenport et al. 2015	11	15726208	rs1466553	RP11-396O20.2	RP11-396O20.1		Associated with bacterial taxa from stool
Davenport et al. 2015	11	15729415	rs1471759	RP11-396O20.2	RP11-396O20.1		Associated with bacterial taxa from stool
Davenport et al. 2015	6	124248788	rs1490350	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124236221	rs1490359	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124236318	rs1490360	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	18	26248508	rs1496486				Associated with bacterial taxa from stool
Davenport et al. 2015	2	25714916	rs1507705	DTNB			Associated with bacterial taxa from stool
Davenport et al. 2015	6	87248029	rs1508348				Associated with bacterial taxa from stool
Davenport et al. 2015	1	103040474	rs1517426				Associated with bacterial taxa from stool
Davenport et al. 2015	2	16186454	rs1529404	AC010145.4	AC130710.1		Associated with bacterial taxa from stool
Davenport et al. 2015	12	24858390	rs1565122	RN7SL38P	RP11-625L16.1		Associated with bacterial taxa from stool
Davenport et al. 2015	18	26245677	rs1615700				Associated with bacterial taxa from stool
Davenport et al. 2015	18	26246051	rs1618992				Associated with bacterial taxa from stool
Davenport et al. 2015	2	170151746	rs16856759	LRP2			Associated with bacterial taxa from stool
Davenport et al. 2015	2	7171364	rs16865853	RNF144A			Associated with bacterial taxa from stool

Davenport et al. 2015	2	7186608	rs16865867	RNF144A			Associated with bacterial taxa from stool
Davenport et al. 2015	8	97327679	rs16894459	PTDSS1			Associated with bacterial taxa from stool
Davenport et al. 2015	9	21673153	rs16938524				Associated with bacterial taxa from stool
Davenport et al. 2015	4	109385403	rs17039065				Associated with bacterial taxa from stool
Davenport et al. 2015	2	56771307	rs17039629				Associated with bacterial taxa from stool
Davenport et al. 2015	2	56798398	rs17048179				Associated with bacterial taxa from stool
Davenport et al. 2015	2	129752049	rs17048958				Associated with bacterial taxa from stool
Davenport et al. 2015	6	124237244	rs17086323	NKAIN2			Associated with bacterial taxa from stool
Davenport et al. 2015	10	124041701	rs17103336	BTBD16			Associated with bacterial taxa from stool
Davenport et al. 2015	10	86427347	rs17103802				Associated with bacterial taxa from stool
Davenport et al. 2015	10	86547930	rs17104132				Associated with bacterial taxa from stool
Davenport et al. 2015	10	86426712	rs17259859				Associated with bacterial taxa from stool
Davenport et al. 2015	2	56750209	rs17268931				Associated with bacterial taxa from stool
Davenport et al. 2015	3	120106820	rs1733329	FSTL1	RP11-174O3.4		Associated with bacterial taxa from stool
Davenport et al. 2015	12	23259999	rs17459026	RP11-153K16.1	RP11-686N4.1	RP11-114G22.1	Associated with bacterial taxa from stool
Davenport et al. 2015	3	189498828	rs17505775	TP63			Associated with bacterial taxa from stool
Davenport et al. 2015	10	83289794	rs17551124				Associated with bacterial taxa from stool
Davenport et al. 2015	2	6863415	rs17649894	LINC00487			Associated with bacterial taxa from stool
Davenport et al. 2015	4	177610424	rs17697515	VEGFC	RP11-313E19.2		Associated with bacterial taxa from stool
Davenport et al. 2015	4	92368346	rs1922233	CCSER1			Associated with bacterial taxa from stool
Davenport et al. 2015	2	25729721	rs1965239	DTNB			Associated with bacterial taxa from stool
Davenport et al. 2015	2	56743667	rs1978531				Associated with bacterial taxa from stool
Davenport et al. 2015	5	125020797	rs2029549				Associated with bacterial taxa from stool
Davenport et al. 2015	5	125020984	rs2029550				Associated with bacterial taxa from stool
Davenport et al. 2015	12	45239348	rs2055676	NELL2			Associated with bacterial taxa from stool
Davenport et al. 2015	12	45238904	rs2055677	NELL2			Associated with bacterial taxa from stool
Davenport et al. 2015	2	84534978	rs2061080				Associated with bacterial taxa from stool
Davenport et al. 2015	4	126408144	rs2068148	FAT4			Associated with bacterial taxa from stool
Davenport et al. 2015	10	124045854	rs2104176	BTBD16			Associated with bacterial taxa from stool
Davenport et al. 2015	7	42374402	rs2108370				Associated with bacterial taxa from stool
Davenport et al. 2015	4	91720598	rs2123959	CCSER1			Associated with bacterial taxa from stool
Davenport et al. 2015	2	84524937	rs2124177				Associated with bacterial taxa from stool
Davenport et al. 2015	11	15738775	rs2141673	RP11-396O20.2			Associated with bacterial taxa from stool
Davenport et al. 2015	9	27688029	rs2150022				Associated with bacterial taxa from stool
Davenport et al. 2015	6	84695892	rs215974	RP4-676J13.2			Associated with bacterial taxa from stool
Davenport et al. 2015	2	56746396	rs2162025				Associated with bacterial taxa from stool
Davenport et al. 2015	3	171419179	rs2168205	PLD1			Associated with bacterial taxa from stool
Davenport et al. 2015	14	83583841	rs2225378				Associated with bacterial taxa from stool
Davenport et al. 2015	2	26357748	rs2243834	RAB10			Associated with bacterial taxa from stool
Davenport et al. 2015	11	19167850	rs2271001	ZDHHC13			Associated with bacterial taxa from stool
Davenport et al. 2015	7	42023400	rs2299148	GLI3			Associated with bacterial taxa from stool
Davenport et al. 2015	17	10466474	rs2320952	CTC-297N7.11			Associated with bacterial taxa from stool
Davenport et al. 2015	2	84464227	rs2364267				Associated with bacterial taxa from stool
Davenport et al. 2015	16	10750548	rs2541522	TEKT5			Associated with bacterial taxa from stool
Davenport et al. 2015	8	6303025	rs2584	MCPH1			Associated with bacterial taxa from stool
Davenport et al. 2015	3	21875126	rs2630788	ZNF385D	AC023798.1		Associated with bacterial taxa from stool
Davenport et al. 2015	3	120108004	rs2702158	FSTL1	RP11-174O3.4		Associated with bacterial taxa from stool
Davenport et al. 2015	3	120101527	rs2702164				Associated with bacterial taxa from stool
Davenport et al. 2015	17	5582334	rs2716882				Associated with bacterial taxa from stool
Davenport et al. 2015	1	209512897	rs2843167				Associated with bacterial taxa from stool
Davenport et al. 2015	2	84431500	rs2886029				Associated with bacterial taxa from stool
Davenport et al. 2015	8	117929674	rs2921738				Associated with bacterial taxa from stool
Davenport et al. 2015	8	117929458	rs2921739				Associated with bacterial taxa from stool
Davenport et al. 2015	6	167765251	rs3010562	TTLL2			Associated with bacterial taxa from stool
Davenport et al. 2015	6	167765251	rs3010562	RP3-366N23.4			Associated with bacterial taxa from stool
Davenport et al. 2015	2	135483381	rs3739034				Associated with bacterial taxa from stool
Davenport et al. 2015	2	135483534	rs3739036				Associated with bacterial taxa from stool
Davenport et al. 2015	22	24717518	rs3747113	SPECC1L	SPECC1L-ADORA2A		Associated with bacterial taxa from stool
Davenport et al. 2015	4	177438265	rs374816				Associated with bacterial taxa from stool
Davenport et al. 2015	3	171380174	rs3774039	PLD1			Associated with bacterial taxa from stool
Davenport et al. 2015	6	87237249	rs3846772				Associated with bacterial taxa from stool
Davenport et al. 2015	5	158544501	rs41406347	RP11-175K6.1			Associated with bacterial taxa from stool
Davenport et al. 2015	1	165394087	rs41419946	RXRG			Associated with bacterial taxa from stool

Davenport et al. 2015	1	216717338	rs4147271	ESRRG		Associated with bacterial taxa from stool
Davenport et al. 2015	4	177439156	rs443233			Associated with bacterial taxa from stool
Davenport et al. 2015	6	129971544	rs4479964	ARHGAP18		Associated with bacterial taxa from stool
Davenport et al. 2015	4	177438117	rs448261			Associated with bacterial taxa from stool
Davenport et al. 2015	2	18868188	rs4614937			Associated with bacterial taxa from stool
Davenport et al. 2015	2	129669656	rs4662863			Associated with bacterial taxa from stool
Davenport et al. 2015	2	26251361	rs4665809	AC013449.1		Associated with bacterial taxa from stool
Davenport et al. 2015	2	26367503	rs4665826	SMARCE1P6	AC011742.3	Associated with bacterial taxa from stool
Davenport et al. 2015	3	10441147	rs4684687	ATP2B2	MIR885	Associated with bacterial taxa from stool
Davenport et al. 2015	8	17500223	rs4705	PDGFRL	MTUS1	Associated with bacterial taxa from stool
Davenport et al. 2015	7	42270322	rs4724101	GLI3		Associated with bacterial taxa from stool
Davenport et al. 2015	8	106400667	rs4734860	ZFPM2	RP11-127H5.1	Associated with bacterial taxa from stool
Davenport et al. 2015	8	59132711	rs4737490			Associated with bacterial taxa from stool
Davenport et al. 2015	18	40418431	rs473976	RIT2		Associated with bacterial taxa from stool
Davenport et al. 2015	9	5881364	rs4740829	KIAA2026		Associated with bacterial taxa from stool
Davenport et al. 2015	15	92814603	rs4777900	RP11-152L20.3		Associated with bacterial taxa from stool
Davenport et al. 2015	9	27664432	rs4879677			Associated with bacterial taxa from stool
Davenport et al. 2015	10	1705508	rs4880904	ADARB2		Associated with bacterial taxa from stool
Davenport et al. 2015	3	171369776	rs4894707	PLD1		Associated with bacterial taxa from stool
Davenport et al. 2015	14	78028378	rs4903604	SPTLC2		Associated with bacterial taxa from stool
Davenport et al. 2015	5	158545464	rs4921164	RP11-175K6.1		Associated with bacterial taxa from stool
Davenport et al. 2015	5	2015330	rs4975794			Associated with bacterial taxa from stool
Davenport et al. 2015	2	25730439	rs517403	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	20	17297511	rs6080636	PCSK2		Associated with bacterial taxa from stool
Davenport et al. 2015	20	11393882	rs6108958			Associated with bacterial taxa from stool
Davenport et al. 2015	20	17304195	rs6111497	PCSK2		Associated with bacterial taxa from stool
Davenport et al. 2015	2	25754670	rs636586	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	1	246853200	rs6413860	RP11-439E19.7	RP11-439E19.9	Associated with bacterial taxa from stool
Davenport et al. 2015	7	42281481	rs6463094	GLI3		Associated with bacterial taxa from stool
Davenport et al. 2015	7	42287633	rs6463097			Associated with bacterial taxa from stool
Davenport et al. 2015	8	106401296	rs6469000	ZFPM2	RP11-127H5.1	Associated with bacterial taxa from stool
Davenport et al. 2015	2	20338020	rs6531212			Associated with bacterial taxa from stool
Davenport et al. 2015	1	218965463	rs6541219			Associated with bacterial taxa from stool
Davenport et al. 2015	2	25845467	rs6546314	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	2	84477813	rs6547544			Associated with bacterial taxa from stool
Davenport et al. 2015	2	84486725	rs6547547			Associated with bacterial taxa from stool
Davenport et al. 2015	1	216722850	rs6604635	ESRRG		Associated with bacterial taxa from stool
Davenport et al. 2015	1	218958105	rs6683441			Associated with bacterial taxa from stool
Davenport et al. 2015	2	230210521	rs6717477			Associated with bacterial taxa from stool
Davenport et al. 2015	2	26342537	rs6742226	RAB10		Associated with bacterial taxa from stool
Davenport et al. 2015	2	25659244	rs6746082	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	2	135469769	rs6747870	TMEM163		Associated with bacterial taxa from stool
Davenport et al. 2015	2	17834452	rs6751113	VSNL1		Associated with bacterial taxa from stool
Davenport et al. 2015	2	84477956	rs6761743			Associated with bacterial taxa from stool
Davenport et al. 2015	3	171321314	rs6781853	PLD1		Associated with bacterial taxa from stool
Davenport et al. 2015	5	2015103	rs6867032			Associated with bacterial taxa from stool
Davenport et al. 2015	6	87248703	rs6903888			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124246347	rs6907236	NKAIN2		Associated with bacterial taxa from stool
Davenport et al. 2015	6	87248657	rs6926527			Associated with bacterial taxa from stool
Davenport et al. 2015	8	106397116	rs6999452	ZFPM2	RP11-127H5.1	Associated with bacterial taxa from stool
Davenport et al. 2015	12	23494704	rs7134941			Associated with bacterial taxa from stool
Davenport et al. 2015	14	104912876	rs7150255	CEND1P1		Associated with bacterial taxa from stool
Davenport et al. 2015	12	46085330	rs7299538			Associated with bacterial taxa from stool
Davenport et al. 2015	13	20637140	rs7324021	ZMYM2		Associated with bacterial taxa from stool
Davenport et al. 2015	8	17522582	rs7464566	MTUS1		Associated with bacterial taxa from stool
Davenport et al. 2015	5	152516889	rs753768	AC091969.1		Associated with bacterial taxa from stool
Davenport et al. 2015	2	230209037	rs7563766			Associated with bacterial taxa from stool
Davenport et al. 2015	2	56759264	rs7580218			Associated with bacterial taxa from stool
Davenport et al. 2015	17	10504591	rs758139	CTC-297N7.7		Associated with bacterial taxa from stool
Davenport et al. 2015	17	10504591	rs758139	CTC-297N7.11		Associated with bacterial taxa from stool
Davenport et al. 2015	2	26279810	rs7599132	RAB10		Associated with bacterial taxa from stool
Davenport et al. 2015	2	84486944	rs7604649			Associated with bacterial taxa from stool
Davenport et al. 2015	2	56741751	rs7605943			Associated with bacterial taxa from stool
Davenport et al. 2015	2	25843252	rs764956	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	4	92431609	rs7677760	CCSER1		Associated with bacterial taxa from stool

Davenport et al. 2015	4	81378966	rs7683819	C4orf22		Associated with bacterial taxa from stool
Davenport et al. 2015	6	124245836	rs7744763	NKAIN2		Associated with bacterial taxa from stool
Davenport et al. 2015	9	21667762	rs7868228			Associated with bacterial taxa from stool
Davenport et al. 2015	10	95072536	rs787665	MYOF		Associated with bacterial taxa from stool
Davenport et al. 2015	11	15685570	rs7943358	RP11-396O20.1		Associated with bacterial taxa from stool
Davenport et al. 2015	12	23485126	rs7955257			Associated with bacterial taxa from stool
Davenport et al. 2015	14	104838403	rs8020729	RP11-260M19.1		Associated with bacterial taxa from stool
Davenport et al. 2015	15	33464534	rs8037033	FMN1		Associated with bacterial taxa from stool
Davenport et al. 2015	16	82787053	rs8056064	CDH13		Associated with bacterial taxa from stool
Davenport et al. 2015	16	82627952	rs8063330			Associated with bacterial taxa from stool
Davenport et al. 2015	2	170156880	rs830964	LRP2		Associated with bacterial taxa from stool
Davenport et al. 2015	11	126310082	rs878830	ST3GAL4	KIRREL3	Associated with bacterial taxa from stool
Davenport et al. 2015	2	56734035	rs890100			Associated with bacterial taxa from stool
Davenport et al. 2015	16	82628494	rs892244			Associated with bacterial taxa from stool
Davenport et al. 2015	12	118146742	rs895470	KSR2		Associated with bacterial taxa from stool
Davenport et al. 2015	1	209527925	rs906351			Associated with bacterial taxa from stool
Davenport et al. 2015	1	101749974	rs910633			Associated with bacterial taxa from stool
Davenport et al. 2015	4	177433597	rs921312			Associated with bacterial taxa from stool
Davenport et al. 2015	2	230214951	rs9288646			Associated with bacterial taxa from stool
Davenport et al. 2015	2	25755848	rs936012	DTNB		Associated with bacterial taxa from stool
Davenport et al. 2015	6	68029041	rs9363741			Associated with bacterial taxa from stool
Davenport et al. 2015	6	124250159	rs9401713	NKAIN2		Associated with bacterial taxa from stool
Davenport et al. 2015	1	218969908	rs9431487			Associated with bacterial taxa from stool
Davenport et al. 2015	1	101745077	rs9434166			Associated with bacterial taxa from stool
Davenport et al. 2015	1	101750747	rs9434172			Associated with bacterial taxa from stool
Davenport et al. 2015	5	125018357	rs963445			Associated with bacterial taxa from stool
Davenport et al. 2015	3	171320227	rs9822322	PLD1		Associated with bacterial taxa from stool
Davenport et al. 2015	3	116356010	rs9847048	LSAMP		Associated with bacterial taxa from stool
Davenport et al. 2015	7	42217027	rs9886211	GLI3		Associated with bacterial taxa from stool
Davenport et al. 2015	6	124245340	rs991795	NKAIN2		Associated with bacterial taxa from stool
Davenport et al. 2015	8	59110041	rs992900	FAM110B		Associated with bacterial taxa from stool
Blekhman et al. 2015	2	24290671	rs61742149	SF3B14		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	10	129921195	rs1063536	MKI67		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	14	93276654	rs1040835	GOLGA5		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	16	84522897	rs436278	KIAA1609		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	13	78216873	rs1053985	SCEL		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	2	186625770-186671912	NA	FSIP2		Associated with bacterial taxa from Anterior nares
Blekhman et al. 2015	6	80741243	rs1801465	TTK		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	17	67125840	rs4968839	ABCA6		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	17	67212031	rs11077414	ABCA10		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	3	174814920	rs9836841	NAALADL2		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	10	125528048	rs1219725	CPXM2		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	9	104309445	rs2273976	RNF20		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	16	81398635	rs2608555	GAN		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	2	228230945	NA	TM4SF20		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	7	47840387	rs13231277	PKD1L1		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	1	159824967	rs2501340	C1orf204		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	3	128344786	rs1126828	RPN1		Associated with bacterial taxa from Attached Keratinized gingiva
Blekhman et al. 2015	22	30689998	rs11089442	TBC1D10A		Associated with bacterial taxa from Buccal mucosa
Blekhman et al. 2015	11	87013438	rs2276102	TMEM135		Associated with bacterial taxa from Buccal mucosa
Blekhman et al. 2015	17	76157266	rs4071641	C17orf99		Associated with bacterial taxa from Buccal mucosa
Blekhman et al. 2015	3	183211906	rs1520101	KLHL6		Associated with bacterial taxa from Buccal mucosa
Blekhman et al. 2015	4	40337523	rs56241474	CHRNA9		Associated with bacterial taxa from Buccal mucosa
Blekhman et al. 2015	16	842450	rs2277897	CHTF18		Associated with bacterial taxa from Hard palate
Blekhman et al. 2015	19	10794630	rs2229383	ILF3		Associated with bacterial taxa from Hard palate
Blekhman et al. 2015	4	41673604	rs11734372	LIMCH1		Associated with bacterial taxa from Hard palate
Blekhman et al. 2015	1	92457843	rs10747493	BRDT		Associated with bacterial taxa from Left Antecubital fossa
Blekhman et al. 2015	9	38615698	rs1832313	ANKRD18A		Associated with bacterial taxa from Left Antecubital fossa
Blekhman et al. 2015	15	100514614	rs2573652	ADAMTS17		Associated with bacterial taxa from Left Antecubital fossa
Blekhman et al. 2015	14	88693725	rs2277524	KCNK10		Associated with bacterial taxa from Left Antecubital fossa
Blekhman et al. 2015	2	163208893	rs17783344	GCA		Associated with bacterial taxa from Left Antecubital fossa
Blekhman et al. 2015	9	33442952	rs2228332	AQP3		Associated with bacterial taxa from Left Retroauricular crease
Blekhman et al. 2015	1	111862074	rs2820092	CHIA		Associated with bacterial taxa from Left Retroauricular crease

Blekhman et al. 2015	12	10782115-10783729	rs3759259-rs2290717	STYK1		Associated with bacterial taxa from Left Retroauricular crease
Blekhman et al. 2015	10	134017295	rs12313	DPYSL4		Associated with bacterial taxa from Left Retroauricular crease
Blekhman et al. 2015	17	78073355	rs56407805	CCDC40		Associated with bacterial taxa from Palatine Tonsils
Blekhman et al. 2015	1	169512027	rs6021	F5		Associated with bacterial taxa from Palatine Tonsils
Blekhman et al. 2015	4	155241572	rs11935573	DCHS2		Associated with bacterial taxa from Palatine Tonsils
Blekhman et al. 2015	6	34831866	rs3734264	UHRF1BP1		Associated with bacterial taxa from Right Retroauricular crease
Blekhman et al. 2015	1	223116240	rs61746477	DISP1		Associated with bacterial taxa from Right Retroauricular crease
Blekhman et al. 2015	17	40714804	rs615942	COASY		Associated with bacterial taxa from Saliva
Blekhman et al. 2015	10	64927823	rs1935	JMJD1C		Associated with bacterial taxa from Saliva
Blekhman et al. 2015	15	43632549	rs2278857	ADAL		Associated with bacterial taxa from Saliva
Blekhman et al. 2015	15	43661802	rs3809482	ZSCAN29		Associated with bacterial taxa from Saliva
Blekhman et al. 2015	15	43748304	rs690367	TP53BP1		Associated with bacterial taxa from Saliva
Blekhman et al. 2015	2	136511817	rs1050115	UBXN4		Associated with bacterial taxa from Stool
Blekhman et al. 2015	2	136561557	rs2304371	LCT		Associated with bacterial taxa from Stool
Blekhman et al. 2015	2	136590746	rs3754689	LCT		Associated with bacterial taxa from Stool
Blekhman et al. 2015	3	129297223	rs1110168	PLXND1		Associated with bacterial taxa from Stool
Blekhman et al. 2015	11	57982620	rs1966834	OR1S1		Associated with bacterial taxa from Stool
Blekhman et al. 2015	14	55907172	rs8019270	TBPL2		Associated with bacterial taxa from Stool
Blekhman et al. 2015	20	2816821	rs2274669	FAM113A		Associated with bacterial taxa from Stool
Blekhman et al. 2015	7	37961001	rs10248138	EPDR1		Associated with bacterial taxa from Stool
Blekhman et al. 2015	10	73111408	rs780668	SLC29A3		Associated with bacterial taxa from Subgingival plaque
Blekhman et al. 2015	2	216300482	rs1250259	FN1		Associated with bacterial taxa from Subgingival plaque
Blekhman et al. 2015	5	41049389	rs325863	HEATR7B2		Associated with bacterial taxa from Subgingival plaque
Blekhman et al. 2015	5	41049397	rs325864	HEATR7B2		Associated with bacterial taxa from Subgingival plaque
Blekhman et al. 2015	15	100821576	rs7496668	ADAMTS17		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	5	150696447	rs369907	SLC36A2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	10	96954360	rs11188225	C10orf129		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	11	124096247	rs2466613	OR8G2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52556890	rs4434138	STAB1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52558133	rs13621	STAB1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52584787	rs2251219	PBRM1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52820981	rs678	ITIH1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52821011	rs1042779	ITIH1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	1	231906589	rs2492367	DISC1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	5	6600150	rs3822434	NSUN2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	5	150696447	rs369907	SLC36A2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	8	21956108	rs35497596	FAM160B2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	11	124096247	rs2466613	OR8G2		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52556890	rs4434138	STAB1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	3	52558133	rs13621	STAB1		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	11	64081445	rs2276014	ESRRA		Associated with bacterial taxa from Supragingival plaque
Blekhman et al. 2015	4	121957559	rs34766411	NDNF		Associated with bacterial taxa from Throat
Blekhman et al. 2015	6	32410987	rs3135391	HLA-DRA		Associated with bacterial taxa from Throat
Blekhman et al. 2015	10	11805354	rs12258196	ECHDC3		Associated with bacterial taxa from Throat
Blekhman et al. 2015	10	11805357	rs10906011	ECHDC3		Associated with bacterial taxa from Throat
Blekhman et al. 2015	7	149474393	rs709061	SSPO		Associated with bacterial taxa from Tongue dorsum
Blekhman et al. 2015	12	1893170	rs9805042	ADIPOR2		Associated with bacterial taxa from Tongue dorsum
Blekhman et al. 2015	4	38799710	rs4833095	TLR1		Associated with bacterial taxa from Tongue dorsum
Blekhman et al. 2015	12	661656	rs7298766	B4GALNT3		Associated with bacterial taxa from Tongue dorsum
Blekhman et al. 2015	6	168709385	rs6925614	DACT2		Associated with bacterial taxa from Tongue dorsum
Goodrich et al.. 2016	7	113115671	rs10233359			Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	37336088	rs12607607	KC6		Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	106479033	rs1376236			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	60471107	rs159373	NDUFAF2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	168362905	rs10055309	SLIT3	LOC728095	Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	65939087	rs7524581			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	31242627	rs11733214			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	196967488	rs7587067	HECW2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	61981226	rs730589	DAPK2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	21071787	rs2293702	SALL2	SALL2	Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	184585954	rs2136233	MCF2L2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	90550513	rs7486170			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	56212663	rs4901725			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927			Associated with bacterial taxa from stool

Goodrich et al.. 2016	3	123411977	rs12489943	CASR		Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	36791724	rs1346183			Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	43256559	rs7134690	NELL2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	68549551	rs7749517			Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	90574334	rs11831423			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	23026012	rs10148020	NGDN		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	155305663	rs9397756			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	106478896	rs1376235			Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	113159007	rs493456	PHLDB2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78519816	rs2166343			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78519816	rs2166343			Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	17903945	rs11880147	CCDC124	CCDC124	Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	186725611	rs6656158			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	121593671	rs2475321	MCMBP		Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	63241282	rs7732898			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	94664580	rs498018			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78519816	rs2166343			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	36791724	rs1346183			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	30964718	rs347941	FMN1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	64200381	rs17079032			Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	14427476	rs508259			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78519816	rs2166343			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	30760851	rs2269706	PPP1R18	NRM	Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	155704640	rs4717021			Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	10368339	rs7499858			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	136123949	rs1446585	R3HDM1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	156712530	rs9397927			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	20900570	rs16907036	NELL1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	95319407	rs2278067	PROM2	KCNIP3	Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	29846491	rs9889895			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	136123949	rs1446585	R3HDM1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	136123949	rs1446585	R3HDM1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	73956482	rs4883972			Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	73956482	rs4883972			Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	73956482	rs4883972			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	136123949	rs1446585	R3HDM1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	67055507	rs9599240			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	188889256	rs687746	LOC440704		Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	101319681	rs2866194	DDIT4L		Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	55254428	rs12577205			Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	54023045	rs1420227			Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	93722673	rs10242192			Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	65258156	rs10507725			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	36791724	rs1346183			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	130041583	rs2704557			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	116396380	rs12776647	ABLIM1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	109108739	rs6542797	SH3RF3-AS1	SH3RF3	Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	41570268	rs692899	SLC14A1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	37353216	rs12606140	KC6		Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	82335279	rs4628206	PCLO		Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	42132203	rs17242235	ZNF568		Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	90574334	rs11831423			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927			Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	147292289	rs10229688	MIR548T	CNTNAP2	Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	89658740	rs17862118	STEAP2-AS1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	96326159	rs502656			Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	18166933	rs13067391	LOC339862		Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	90432029	rs4342835			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	131352801	rs7761311	EPB41L2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	68541538	rs13214269			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	12508420	rs7644	PARVA		Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	151467432	rs737301	PRR9		Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	114270048	rs10114968	HSDL2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	41663873	rs495078	SIGLEC15		Associated with bacterial taxa from stool

Goodrich et al.. 2016	15	92699262	rs16948999	MCTP2	MCTP2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	83679509	rs7106602	DLG2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	87053016	rs11073804				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	11988388	rs7979513				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78457715	rs3733890	BHMT			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	65142782	rs1193851	MAP3K11	PCNXL3		Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	49066516	rs3105827				Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	54029584	rs17299191				Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	57679532	rs11125721				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	67253530	rs6914260				Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	26748979	rs11792081				Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	28056798	rs898031	BRE			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	132608771	rs9321334				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	97277190	rs3909540				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78457715	rs3733890	BHMT			Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	172792314	rs360402	PLD1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	122454421	rs2198863				Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	59834998	rs2273623	PPM1A	PPM1A		Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	11605759	rs12936861	DNAH9			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	91945539	rs11845652	SLC24A4			Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	101693527	rs12311520				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	101693527	rs12311520				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	101693527	rs12311520				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	101693527	rs12311520				Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	123633020	rs6466898				Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	73956482	rs4883972				Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	103720795	rs938421				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	71052221	rs10252758	CALN1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	132269034	rs9373001				Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	238754423	rs7604350	ILKAP			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	72431928	rs3808393	EYA1	EYA1	EYA1	Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	115503981	rs2170226				Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	79487728	rs1489848	ROBO1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	20896231	rs3740874	NELL1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	118764835	rs1948223	LINC01378			Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	270822	rs4897946	MIER2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	21	42429801	rs11701867	UMODL1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	99186507	rs4699323	STPG2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	79366702	rs641527				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	104285792	rs7302174	C12orf75			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	88146339	rs2007084	ANPEP			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	21071787	rs2293702	SALL2	SALL2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	63950783	rs9350764				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	171158984	rs12407389				Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	19878006	rs10811270				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	89975001	rs12704545				Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	66436021	rs1922100				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	60463551	rs12128018				Associated with bacterial taxa from stool
Goodrich et al.. 2016	21	30474885	rs2832648				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	89697913	rs194522	STEAP2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	157235820	rs9397979	ARID1B			Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	76494978	rs12951596	RPTOR			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	30619064	rs6999713	GTF2E2	SMIM18		Associated with bacterial taxa from stool
Goodrich et al.. 2016	22	29586733	rs5997791	OSBP2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	46140968	rs7236263				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	48782572	rs10484857				Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	61017518	rs9938742				Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	111255851	rs1125819	ELOVL6			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	76481162	rs3758054				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	192653939	rs10801316				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	1451116	rs2997983	ADARB2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	141437110	rs10928081	LRP1B			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	97555873	rs922408				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	7580947	rs4747490				Associated with bacterial taxa from stool

Goodrich et al.. 2016	7	20328398	rs206196	ITGB8	LOC101927811			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927					Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	109081945	rs1443930	RSPO2				Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	92899613	rs2248020	SMCO4				Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	29486823	rs1231637					Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	31474478	rs1278911					Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	61527138	rs7156837	SYT16				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	57734534	rs4620568	DAB1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	60374195	rs3859542	DNAAF3	SYT5	SYT5		Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	163737438	rs185902	LOC400794				Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	22706199	rs9552886	SGCG				Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	95433599	rs10501839	MAML2				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	8976653	rs380915					Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	88602610	rs11018543	TYR				Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	34014997	rs11710273					Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	145796966	rs1405597					Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	14214435	rs6461075	DGKB				Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	44882581	rs11082729	DYM				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	168362905	rs10055309	SLIT3	LOC728095			Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	155278861	rs1636874	SHH	SHH			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	32709243	rs2505338	LOC102031319	EPC1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	55936079	rs17369648					Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	107585336	rs7318523					Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	3829058	rs17763551					Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	72431928	rs3808393	EYA1	EYA1	EYA1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	103720795	rs938421					Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	73373291	rs12552904					Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	55467869	rs10493180	MIR4422				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	141900444	rs10081087					Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	44564645	rs786402	CAMKMT				Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	17242000	rs722075	XYLT1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	51114995	rs4548008					Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	58877088	rs232905					Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	104256711	rs1128880	ADSSL1	INF2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	88146339	rs2007084	ANPEP				Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	21071787	rs2293702	SALL2	SALL2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	57707459	rs4360824	LINC00374				Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	64921131	rs1523451	ADAMTS9-AS2				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	21809051	rs7804316	DNAH11				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	40611185	rs1234013					Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	3681041	rs7258176	TJP3				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	149477421	rs2228440	PDGFRB	CSF1R			Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	4045775	rs350916	MAP2K2				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	35551900	rs1148245					Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	238748040	rs4663855	ILKAP	FAM132B			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	13985102	rs1204250					Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	17385766	rs1918707					Associated with bacterial taxa from stool
Goodrich et al.. 2016	21	26791471	rs2830259	CYYR1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	73206697	rs7231241					Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	2637391	rs151216	KCNQ1OT1	KCNQ1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	21819339	rs1479056	DOK2				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	127407050	rs10847601	TMEM132C				Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	123035055	rs7646523	IQCB1	EAF2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	200877238	rs4673912	SPATS2L	SPATS2L	SPATS2L	SPATS2L	Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	81739635	rs11969591					Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	73278536	rs10898950	PAAF1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	55965983	rs1945216					Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	19909284	rs7095285	MALRD1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	27907215	rs2763309					Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	77224488	rs10160195	C10orf11				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	110648935	rs12245886					Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	46034867	rs9567705	LRCH1				Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	76626535	rs1955390	CLEC3A				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	81800564	rs6674509	LOC101927434				Associated with bacterial taxa from stool

Goodrich et al.. 2016	2	4941253	rs7602355				Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	65020965	rs11126024	LOC400958			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	123084639	rs4848184				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78457715	rs3733890	BHMT			Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	3231254	rs13223655				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	19876055	rs10264784				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	130867974	rs9402233				Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	51083490	rs17585587	FRMD6	FRMD6-AS2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	47400335	rs10517198	CORIN			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	72431928	rs3808393	EYA1	EYA1	EYA1	Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	72431928	rs3808393	EYA1	EYA1	EYA1	Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	56925640	rs4968435	TBX4			Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	36894026	rs17170765	ELMO1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	19954140	rs1760889	TEP1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	68666312	rs6933411				Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	124110549	rs984668				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	33299398	rs7296338				Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	41663873	rs495078	SIGLEC15			Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	96323544	rs9790095				Associated with bacterial taxa from stool
Goodrich et al.. 2016	20	23045880	rs1320561	LINC00656			Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	24987831	rs3950612	BCAT1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	22	32803652	rs5754822				Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	50880734	rs16880682				Associated with bacterial taxa from stool
Goodrich et al.. 2016	22	44263738	rs6007059				Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	57547006	rs6591450	OR6Q1	OR9Q1		Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	37854826	rs6929224				Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	28927722	rs1986785	MTUS2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	81849078	rs1221172				Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	155004615	rs7566589	LOC100144595	GALNT13		Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	20328398	rs206196	ITGB8	LOC101927811		Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	124898204	rs820335	MYLK	MYLK-AS2		Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	50744067	rs6561627	FAM124A			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	109081945	rs1443930	RSPO2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	76559855	rs17098734	ST6GALNAC3			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	60478048	rs295569	NDUFAF2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	73278536	rs10898950	PAAF1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	109081945	rs1443930	RSPO2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	73278536	rs10898950	PAAF1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	109081945	rs1443930	RSPO2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	16	12580363	rs10852352	SNX29			Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	123104151	rs2282644	ZNF202			Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	1797101	rs7634041				Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	118310410	rs17506987				Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	74950676	rs3117600	CXCL1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	218030535	rs4565719				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	46635612	rs10488566				Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	173936757	rs7527642	TNR			Associated with bacterial taxa from stool
Goodrich et al.. 2016	2	35801306	rs10221827				Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	165194141	rs6536782	MARCH1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	68700500	rs7139612	LINC00383			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	25904387	rs12359026	GPR158			Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	29536701	rs586749				Associated with bacterial taxa from stool
Goodrich et al.. 2016	22	45247677	rs3788704	CELSR1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	169387892	rs7886938	FMO6P			Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	92508459	rs1881456	CCSER1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	61182485	rs470497				Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	58103214	rs1514537				Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	52213813	rs2447859	ITGA1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	27907215	rs2763309				Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	62812338	rs718362	RHOJ			Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	126805344	rs2209683	CTBP2			Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	91943634	rs4777927				Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	142832579	rs10226151	EPHA1-AS1			Associated with bacterial taxa from stool
Goodrich et al.. 2016	19	7156240	rs10426094	INSR			Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	179596220	rs6601104	MAPK9			Associated with bacterial taxa from stool

Goodrich et al.. 2016	17	50918261	rs11868220								Associated with bacterial taxa from stool
Goodrich et al.. 2016	8	76481162	rs3758054								Associated with bacterial taxa from stool
Goodrich et al.. 2016	12	71632224	rs10879524								Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	7933909	rs7744601	PIP5K1P1	BLOC1S5-TXNDC5						Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	72272815	rs12915891	STRA6							Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	110733308	rs2282637	POU2AF1	MIR4491						Associated with bacterial taxa from stool
Goodrich et al.. 2016	10	106511862	rs10786820	SORCS3							Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	78457715	rs3733890	BHMT							Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	36791724	rs1346183								Associated with bacterial taxa from stool
Goodrich et al.. 2016	9	86161066	rs4877854	SLC28A3							Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	114838051	rs987694	CAMK2D							Associated with bacterial taxa from stool
Goodrich et al.. 2016	20	25429117	rs404775	NINL							Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	26091594	rs6772506								Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	73293142	rs1684851								Associated with bacterial taxa from stool
Goodrich et al.. 2016	5	118673219	rs17145135	TNFAIP8							Associated with bacterial taxa from stool
Goodrich et al.. 2016	4	7047030	rs3892490	TBC1D14							Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	69720601	rs1889879	ADGRB3							Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	148069900	rs6901947								Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	25717895	rs1874835	OCA2							Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	37343774	rs16968570	C15orf54							Associated with bacterial taxa from stool
Goodrich et al.. 2016	14	67238753	rs11621258	RDH12	RDH11						Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	83894200	rs1367534	DLG2							Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	83894200	rs1367534	DLG2							Associated with bacterial taxa from stool
Goodrich et al.. 2016	18	41610180	rs12455458								Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	83738314	rs16977800	AKAP13							Associated with bacterial taxa from stool
Goodrich et al.. 2016	17	34200870	rs228307	PIP4K2B	CWC25						Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	103751762	rs16845116								Associated with bacterial taxa from stool
Goodrich et al.. 2016	13	31117386	rs9548456								Associated with bacterial taxa from stool
Goodrich et al.. 2016	15	88122043	rs12900413	MESP2	ANPEP						Associated with bacterial taxa from stool
Goodrich et al.. 2016	1	224575268	rs10915971								Associated with bacterial taxa from stool
Goodrich et al.. 2016	3	28147601	rs13100072								Associated with bacterial taxa from stool
Goodrich et al.. 2016	7	14927739	rs10276618								Associated with bacterial taxa from stool
Goodrich et al.. 2016	6	158491694	rs6933878	SERAC1							Associated with bacterial taxa from stool
Goodrich et al.. 2016	11	83894200	rs1367534	DLG2							Associated with bacterial taxa from stool
Wang et al. 2016	1	172700868	rs1102737	FASLG							Associated with beta-diversity from stool
Wang et al. 2016	8	10576753	rs11986935	SOX7	SOX7	-	PINX1				Associated with beta-diversity from stool
Wang et al. 2016	17	782416	rs12601692	-	NXN						Associated with beta-diversity from stool
Wang et al. 2016	7	104219681	rs12705241	-	LHFPL3						Associated with beta-diversity from stool
Wang et al. 2016	1	53885577	rs1288616	DMRTB1	DMRTB1						Associated with beta-diversity from stool
Wang et al. 2016	15	26603288	rs12910631	-							Associated with beta-diversity from stool
Wang et al. 2016	6	87217958	rs1292672	HTR1E							Associated with beta-diversity from stool
Wang et al. 2016	16	11031741	rs12931878	CLEC16A	DEXI	CLEC16A					Associated with beta-diversity from stool
Wang et al. 2016	3	146250561	rs13099587	PLSCR1	PLSCR1						Associated with beta-diversity from stool
Wang et al. 2016	3	49898318	rs13100903	SEMA3F	RBM5	MST1R	CAMKV	MON1A	RBM6	SEMA3F	Associated with beta-diversity from stool
Wang et al. 2016	9	37626956	rs1325919	FRMPD1							Associated with beta-diversity from stool
Wang et al. 2016	8	3705807	rs13260600	CSMD1	CSMD1						Associated with beta-diversity from stool
Wang et al. 2016	8	19815256	rs138022915	LPL	LPL						Associated with beta-diversity from stool
Wang et al. 2016	17	32248813	rs16969051	ACCN1	ACCN1						Associated with beta-diversity from stool
Wang et al. 2016	2	135172338	rs2010917	MGAT5	MGAT5						Associated with beta-diversity from stool
Wang et al. 2016	11	8852239	rs2251536	-	ST5						Associated with beta-diversity from stool
Wang et al. 2016	19	18217350	rs2267922	IFI30	MAST3	IFI30	PIK3R2				Associated with beta-diversity from stool
Wang et al. 2016	19	51739767	rs273647	C19orf75	CD33	C19orf75					Associated with beta-diversity from stool
Wang et al. 2016	19	51739767	rs273647	C19orf75	CD33	C19orf75					Associated with beta-diversity from stool
Wang et al. 2016	21	38657572	rs2835692	DSCR3							Associated with beta-diversity from stool
Wang et al. 2016	15	89623490	rs293377	ABHD2	ABHD2						Associated with beta-diversity from stool
Wang et al. 2016	7	151515842	rs35148810	-	PRKAG2						Associated with beta-diversity from stool
Wang et al. 2016	11	120798714	rs4472950	-	GRIK4						Associated with beta-diversity from stool
Wang et al. 2016	2	33808725	rs4670302 - rs6711771	FAM98A	FAM98A						Associated with beta-diversity from stool
Wang et al. 2016	12	93011759	rs4760399	C12orf74							Associated with beta-diversity from stool
Wang et al. 2016	20	48428863	rs4809760	SLC9A8	RNF114	SLC9A8	SPATA2				Associated with beta-diversity from stool
Wang et al. 2016	16	3065924	rs59986499	CLDN6	MMP25	TNFRSF12A	CLDN6	CCDC64B	HCFC1R1	THOC6	Associated with beta-diversity from stool
Wang et al. 2016	4	102769693	rs60500975	-	BANK1						Associated with beta-diversity from stool
Wang et al. 2016	17	66166300	rs62085746	AMZ2							Associated with beta-diversity from stool
Wang et al. 2016	5	74171398	rs62367773	FAM169A							Associated with beta-diversity from stool

Wang et al. 2016	14	65119676	rs6573564	PLEKHG3						Associated with beta-diversity from stool
Wang et al. 2016	10	87865009	rs7082134	GRID1	GRID1					Associated with beta-diversity from stool
Wang et al. 2016	2	102309520	rs71415332	-	IL1R2	MAP4K4				Associated with beta-diversity from stool
Wang et al. 2016	2	25323083	rs72853661	POMC	POMC	EFR3B				Associated with beta-diversity from stool
Wang et al. 2016	2	61384324	rs7567349	XPO1	AHSA2	USP34	XPO1	KIAA1841		Associated with beta-diversity from stool
Wang et al. 2016	8	135273640	rs7818750	ZFAT						Associated with beta-diversity from stool
Wang et al. 2016	12	48256280	rs7974353	-	VDR					Associated with beta-diversity from stool
Wang et al. 2016	15	101414167	rs8040493	-						Associated with beta-diversity from stool
Wang et al. 2016	1	33538964	rs804427	AK2	ADC	TRIM62	AK2			Associated with beta-diversity from stool
Wang et al. 2016	16	84566729	rs8055365	KIAA1609	KIAA1609					Associated with beta-diversity from stool
Wang et al. 2016	3	171759410	rs9647379	FNDC3B	FNDC3B					Associated with beta-diversity from stool
Wang et al. 2016	22	31520338	rs9917541	PLA2G3	PLA2G3	INPP5J				Associated with beta-diversity from stool
Wang et al. 2016	12	4779313	rs1009634	AKAP3	NDUFA9	GALNT8	RP11-234B24.2			Associated with bacterial taxa from stool
Wang et al. 2016	2	129426740	rs10928827	HS6ST1						Associated with bacterial taxa from stool
Wang et al. 2016	14	90681816	rs11626933	C14orf102	C14orf102					Associated with bacterial taxa from stool
Wang et al. 2016	4	77441448	rs11724031	SHROOM3	SHROOM3					Associated with bacterial taxa from stool
Wang et al. 2016	18	10566345	rs11877825	NAPG						Associated with bacterial taxa from stool
Wang et al. 2016	3	1452602	rs11915634	CNTN6						Associated with bacterial taxa from stool
Wang et al. 2016	16	27205994	rs12149695	FLJ21408	NSMCE1	FLJ21408	KDM8			Associated with bacterial taxa from stool
Wang et al. 2016	15	37968393	rs12442649	TMCO5A						Associated with bacterial taxa from stool
Wang et al. 2016	3	58014818	rs13096731	FLNB	FLNB					Associated with bacterial taxa from stool
Wang et al. 2016	8	56589428	rs13276516	TGS1						Associated with bacterial taxa from stool
Wang et al. 2016	16	51955443	rs1362404	TOX3						Associated with bacterial taxa from stool
Wang et al. 2016	19	38497288	rs148330122	SIPA1L3	SIPA1L3					Associated with bacterial taxa from stool
Wang et al. 2016	9	71165704	rs17085775	C9orf71						Associated with bacterial taxa from stool
Wang et al. 2016	4	131293675	rs17421787	RP11-422J15.1						Associated with bacterial taxa from stool
Wang et al. 2016	7	48381902	rs17661843	ABCA13	ABCA13					Associated with bacterial taxa from stool
Wang et al. 2016	20	43030809	rs2071199	HNF4A-AS1	HNF4A					Associated with bacterial taxa from stool
Wang et al. 2016	8	139889972	rs2318350	COL22A1	COL22A1					Associated with bacterial taxa from stool
Wang et al. 2016	5	141877862	rs249733	SPRY4						Associated with bacterial taxa from stool
Wang et al. 2016	21	32184901	rs34613612	KRTAP8-1	KRTAP8-1					Associated with bacterial taxa from stool
Wang et al. 2016	15	60027987	rs35275482	BNIP2						Associated with bacterial taxa from stool
Wang et al. 2016	3	38161078	rs3925158	SLC22A13	SLC22A13	MYD88	DLEC1	ACAA1	OXSR1	Associated with bacterial taxa from stool
Wang et al. 2016	2	217857450	rs4621152	AC007557.1						Associated with bacterial taxa from stool
Wang et al. 2016	2	9801744	rs4669413	RP11-521D12.1						Associated with bacterial taxa from stool
Wang et al. 2016	12	3357596	rs479105	PRMT8						Associated with bacterial taxa from stool
Wang et al. 2016	2	228486044	rs56006724	C2orf83	C2orf83					Associated with bacterial taxa from stool
Wang et al. 2016	3	95359287	rs59042687	LINC00879						Associated with bacterial taxa from stool
Wang et al. 2016	1	112379026	rs597205	C1orf183	C1orf183					Associated with bacterial taxa from stool
Wang et al. 2016	3	162444724	rs62295801	LINC01192	LINC01192					Associated with bacterial taxa from stool
Wang et al. 2016	10	7020329	rs7083345	RP11-554I8.2						Associated with bacterial taxa from stool
Wang et al. 2016	11	122091502	rs7113056	RP11-166D19.1						Associated with bacterial taxa from stool
Wang et al. 2016	1	37717219	rs75036654	LINC01137						Associated with bacterial taxa from stool
Wang et al. 2016	3	185729634	rs7646786	LOC344887						Associated with bacterial taxa from stool
Wang et al. 2016	4	9721358	rs7656342	DRD5	SLC2A9	DRD5				Associated with bacterial taxa from stool
Wang et al. 2016	2	103099953	rs79387448	SLC9A2	SLC9A2					Associated with bacterial taxa from stool
Wang et al. 2016	5	66515817	rs9291879	CD180						Associated with bacterial taxa from stool
Wang et al. 2016	13	98269478	rs9300430	RAP2A						Associated with bacterial taxa from stool
Wang et al. 2016	14	58476448	rs9323326	SLC35F4	C14orf37					Associated with bacterial taxa from stool
Wang et al. 2016	1	16087164	rs938295	FBLIM1	FBLIM1					Associated with bacterial taxa from stool
Wang et al. 2016	3	98879786	rs9831278	LINC00973						Associated with bacterial taxa from stool
Wang et al. 2016	14	60787269	rs986417	SIX6	SIX6	C14orf39	SIX1			Associated with bacterial taxa from stool
Turpin et al. 2016	1	18103049	rs6666120	ACTL8						Associated with bacterial taxa from stool
Turpin et al. 2016	1	87721008	rs6692744	LOC101927844	LOC105378832	LMO4				Associated with bacterial taxa from stool
Turpin et al. 2016	2	130199082	rs10202734	LOC105373613						Associated with bacterial taxa from stool
Turpin et al. 2016	13	19674718	rs36082470	GTF2IP3	RNA5SP24	PHF2P1	CENPIP1	RNU6-52		Associated with bacterial taxa from stool
Turpin et al. 2016	5	11089822	rs16901246	CTNND2						Associated with bacterial taxa from stool
Turpin et al. 2016	7	96414393	chr7:96414393:D	LOC100506136	LOC105375413	SHFM1	LOC105375414			Associated with bacterial taxa from stool
Turpin et al. 2016	19	28117024	rs115795847	LOC105376906	LOC105372345					Associated with bacterial taxa from stool
Turpin et al. 2016	1	119944761	rs147600757	HAO2	HSD3B2					Associated with bacterial taxa from stool
Turpin et al. 2016	2	170657022	rs62171178	SSB	METTL5	UBR3				Associated with bacterial taxa from stool
Turpin et al. 2016	10	82453481	rs9421681	RPS7P9	SH2D4B	LOC105378387	LOC105378386			Associated with bacterial taxa from stool
Turpin et al. 2016	1	60346014	chr1:60346014:D	HOOK1	CYP2J2					Associated with bacterial taxa from stool
Turpin et al. 2016	6	80338468	chr6:80338468:I	LCA5	LOC105377866	SH3BGRL2				Associated with bacterial taxa from stool

Turpin et al. 2016	17	15099895	rs76906435	LOC105371547	PMP22	CDRT8					Associated with bacterial taxa from stool
Turpin et al. 2016	11	76322252	rs11236806	C11orf30	LOC101928813	LRRC32					Associated with bacterial taxa from stool
Turpin et al. 2016	14	92611999	rs10148302	CPSF2							Associated with bacterial taxa from stool
Turpin et al. 2016	3	111964548	rs13100905	SLC9C1							Associated with bacterial taxa from stool
Turpin et al. 2016	5	18599038	rs1826812	RPL36AP21	LOC100421308						Associated with bacterial taxa from stool
Turpin et al. 2016	21	24749215	rs35197943	D21S2088E							Associated with bacterial taxa from stool
Turpin et al. 2016	1	246909388	rs143179968	SCCPDH							Associated with bacterial taxa from stool
Turpin et al. 2016	12	67276489	rs10748061	GRIP1							Associated with bacterial taxa from stool
Turpin et al. 2016	3	1261480	rs1394174	CNTN6							Associated with bacterial taxa from stool
Turpin et al. 2016	1	58670059	rs6683259	DAB1							Associated with bacterial taxa from stool
Turpin et al. 2016	3	294484	rs73005672	CHL1							Associated with bacterial taxa from stool
Turpin et al. 2016	7	12127071	rs7782745	TMEM106B							Associated with bacterial taxa from stool
Turpin et al. 2016	8	55244463	rs10112815	CHCHD2P10	RNU105C	LOC100419615					Associated with bacterial taxa from stool
Turpin et al. 2016	12	104558085	rs17806643	HCFC2	NFYB	LOC105369947	LOC105369948	TXNRD1			Associated with bacterial taxa from stool
Turpin et al. 2016	12	84247859	rs11608507	LOC105369874							Associated with bacterial taxa from stool
Turpin et al. 2016	5	42220431	rs34869836		FBXO4	LOC101926960	LOC102723768	GHR			Associated with bacterial taxa from stool
Turpin et al. 2016	9	120467576	rs10818073	TLR4							Associated with bacterial taxa from stool
Turpin et al. 2016	8	39933549	chr8:39933549:I	IDO1	IDO2	LOC105379385	LOC105379386	C8orf4			Associated with bacterial taxa from stool
Turpin et al. 2016	8	64277954	rs13249293	YTHDF3	LOC105375873	LOC105375875					Associated with bacterial taxa from stool
Turpin et al. 2016	18	25848516	rs12457158	CDH2							Associated with bacterial taxa from stool
Turpin et al. 2016	2	138532756	rs2925216	THSD7B	LOC101928273						Associated with bacterial taxa from stool
Turpin et al. 2016	5	160455937	rs113045860	LOC285629	LOC105377693						Associated with bacterial taxa from stool
Turpin et al. 2016	13	107282972	rs9558805	LINC00551							Associated with bacterial taxa from stool
Turpin et al. 2016	10	97301978	rs11188353	SORBS1							Associated with bacterial taxa from stool
Turpin et al. 2016	4	90832608	rs3775467	MMRN1							Associated with bacterial taxa from stool
Turpin et al. 2016	12	13622839	chr12:13622839:D	LINC01559	RNA5SP353	GRIN2B					Associated with bacterial taxa from stool
Turpin et al. 2016	1	198157740	rs55987656	NEK7							Associated with bacterial taxa from stool
Turpin et al. 2016	1	53946829	rs59846192	DMRTB1	GLIS1						Associated with bacterial taxa from stool
Turpin et al. 2016	5	107323372	rs10058249	FBXL17							Associated with bacterial taxa from stool
Turpin et al. 2016	2	4666664	rs7581129	NPM1P48	LINC01249						Associated with bacterial taxa from stool
Turpin et al. 2016	1	16265904	rs41269155	ZBTB17	SPEN						Associated with bacterial taxa from stool
Turpin et al. 2016	3	139347358	rs62273067	NMNAT3							Associated with bacterial taxa from stool
Turpin et al. 2016	5	90301196	chr5:90301196:I	ADGRV1							Associated with bacterial taxa from stool
Turpin et al. 2016	7	21281203	rs17739409	ASS1P11	RNU1-15P						Associated with bacterial taxa from stool
Turpin et al. 2016	8	111058713	rs1450758	KCNV1	RPSAP48						Associated with bacterial taxa from stool
Turpin et al. 2016	10	71870981	rs7899016	H2AFY2							Associated with bacterial taxa from stool
Turpin et al. 2016	18	76714322	rs28473221	LOC105372224	LOC645321	SALL3					Associated with bacterial taxa from stool
Turpin et al. 2016	9	116185117	rs112294212	C9orf43	RGS3						Associated with bacterial taxa from stool
Turpin et al. 2016	2	128648546	rs111870934	POLR2D	AMMECR1L	SAP130					Associated with bacterial taxa from stool
Turpin et al. 2016	7	38465243	rs74997447	LOC100506776	AMPH						Associated with bacterial taxa from stool
Turpin et al. 2016	13	67967187	rs9541094	LINC00364							Associated with bacterial taxa from stool
Turpin et al. 2016	22	38219943	rs1800694	GALR3	ANKRD54	MIR658	MIR659	EIF3L			Associated with bacterial taxa from stool
Turpin et al. 2016	3	29561962	rs13081014	RBMS3							Associated with bacterial taxa from stool
Turpin et al. 2016	6	23943584	chr6:23943584:I	LOC100129616	SPTLC1P2	LOC100128365	HNRNPA1P58				Associated with bacterial taxa from stool
Turpin et al. 2016	4	122695318	rs6534322	TMEM155	PP12613	EXOSC9	CCNA	BBS7			Associated with bacterial taxa from stool
Turpin et al. 2016	6	30092231	rs9357092	HLA	ZNRD1-AS1	PPP1R11	RNF39	HCG8	HLA-J	HCG9	Associated with bacterial taxa from stool
Bonder et al. 2016	4	7584767	rs10012347	SORCS2							Associated with bacterial pathway from stool
Bonder et al. 2016	10	130938725	rs1041530								Associated with bacterial pathway from stool
Bonder et al. 2016	12	19469078	rs10743315	PLEKHA5							Associated with bacterial taxa from stool
Bonder et al. 2016	9	29398625	rs10813066								Associated with bacterial taxa from stool
Bonder et al. 2016	3	143214462	rs10935496	SLC9A9							Associated with bacterial pathway from stool
Bonder et al. 2016	18	13329915	rs113062739	LDLRAD4							Associated with bacterial pathway from stool
Bonder et al. 2016	11	131213874	rs11606643	AP002856.5							Associated with bacterial pathway from stool
Bonder et al. 2016	1	151244986	rs12048670								Associated with bacterial pathway from stool
Bonder et al. 2016	1	116209762	rs12137699	VANGL1							Associated with bacterial taxa from stool
Bonder et al. 2016	1	42273653	rs12563071	HIVEP3							Associated with bacterial pathway from stool
Bonder et al. 2016	4	36068571	rs12645801	ARAP2	RP11-640B6.1						Associated with bacterial pathway from stool
Bonder et al. 2016	3	139283462	rs1497266	NMNAT3	RP11-319G6.1						Associated with bacterial pathway from stool
Bonder et al. 2016	5	8536853	rs1666789								Associated with bacterial pathway from stool
Bonder et al. 2016	11	87905990	rs16913594	RAB38	MIR3166						Associated with bacterial taxa from stool
Bonder et al. 2016	11	113157283	rs17115310	RP11-839D17.3							Associated with bacterial taxa from stool
Bonder et al. 2016	14	95670887	rs74773701	CLMN							Associated with bacterial pathway from stool
Bonder et al. 2016	2	108943203	rs17770672	SULT1C2P1							Associated with bacterial pathway from stool
Bonder et al. 2016	20	48892374	rs17789629	RP11-290F20.3							Associated with bacterial pathway from stool

Bonder et al. 2016	10	29388639	rs1889714				Associated with bacterial taxa from stool
Bonder et al. 2016	1	4396539	rs199545687				Associated with bacterial pathway from stool
Bonder et al. 2016	2	84017088	rs2084597				Associated with bacterial pathway from stool
Bonder et al. 2016	5	168211254	rs2163761	SLIT3			Associated with bacterial pathway from stool
Bonder et al. 2016	3	27024452	rs2166811				Associated with bacterial pathway from stool
Bonder et al. 2016	22	26283714	rs2285198	MYO18B	CTA-125H2.2	Z98949.1	Associated with bacterial pathway from stool
Bonder et al. 2016	21	35264397	rs2834288	ITSN1	AP000304.12		Associated with bacterial taxa from stool
Bonder et al. 2016	3	186092559	rs35598536				Associated with bacterial pathway from stool
Bonder et al. 2016	14	99194007	rs4144435				Associated with bacterial pathway from stool
Bonder et al. 2016	6	98399521	rs4548017	RP11-436D23.1			Associated with bacterial taxa from stool
Bonder et al. 2016	2	1855567	rs4553849	MYT1L			Associated with bacterial pathway from stool
Bonder et al. 2016	3	41570365	rs4973961	ULK4			Associated with bacterial pathway from stool
Bonder et al. 2016	5	171998938	rs56879175				Associated with bacterial pathway from stool
Bonder et al. 2016	2	71101426	rs6546647				Associated with bacterial pathway from stool
Bonder et al. 2016	6	88902490	rs6933130				Associated with bacterial pathway from stool
Bonder et al. 2016	8	42472274	rs7016086				Associated with bacterial pathway from stool
Bonder et al. 2016	12	27957533	rs7133214	RN7SKP15	RP11-860B13.3		Associated with bacterial pathway from stool
Bonder et al. 2016	2	241123546	rs7605872				Associated with bacterial taxa from stool
Bonder et al. 2016	5	104668046	rs78533343	RP11-6N13.1			Associated with bacterial pathway from stool
Bonder et al. 2016	13	60824702	rs7992913				Associated with bacterial pathway from stool
Bonder et al. 2016	3	63644694	rs924067	SNTN			Associated with bacterial pathway from stool
Bonder et al. 2016	6	56209251	rs9475677	COL21A1			Associated with bacterial pathway from stool
Bonder et al. 2016	1	110770223	rs958798	KCNC4			Associated with bacterial pathway from stool
Bonder et al. 2016	12	8397529	rs9669179	FAM86FP	RP11-266K4.9		Associated with bacterial pathway from stool

* See main text for full references.

Table S6. Correlations between microbial beta-diversity measurements and predictor variables using Mantel test.

	n	Bray Curtis		unweighted UniFrac		weighted UniFrac	
		Mantel r	p-value*	Mantel r	p-value*	Mantel r	p-value*
Genetic distance	50	**0.14**	**0.004**	0.12	*0.012*	0.10	*0.037*
Geographic distance (km)	50	0.07	0.078	0.10	*0.035*	0.06	0.148
Body weight (g)	50	0.08	0.232	0.12	0.121	0.07	0.337
BMI (g/mm^2)	50	**0.25**	**<0.001**	0.12	0.165	**0.23**	**0.005**
Diet (δ^{13}C)	50	0.14	0.044	0.06	0.482	-0.01	0.898
Diet (δ^{15}N)	50	0.04	0.67	-0.01	0.924	0.00	0.993
ClimatePC1	50	0.10	0.066	0.09	0.156	0.10	0.072
ClimatePC2	50	0.01	0.913	0.04	0.488	-0.05	0.403

*Raw P-values that are lower than Bonferroni corrected p-value = 0.05/8 = 0.0063 are bolded

Table S7. Correlations between host genetic distance and Bray-Curtis dissimilarity using Partial Mantel test controlling for seven variables.

Variables controlled	n	Partial Mantel r	p-value
Geographic distance (km)	50	0.12	0.008
Body weight (g)	50	0.13	0.002
BMI (g/mm^2)	50	0.13	0.004
Diet ($\delta^{13}C$)	50	0.14	0.002
Diet ($\delta^{15}N$)	50	0.14	0.003
ClimatePC1	50	0.10	0.028
ClimatePC2	50	0.09	0.008

Table S8. Differences in microbial measurements among wild and lab populations.

	Wild				Lab				Significance (Wilcoxon test)				
Microbial measurements[1]	North (n=10)		South (n=10)		North (n=40)		South (n=38)		Wild vs Lab[2]	Wild		Lab	
										North	South	North	South
	Mean	*(SD)*	Mean	*(SD)*	Mean	*(SD)*	Mean	*(SD)*	Raw p-values	Pairwise comparisons[3]			
Alpha-diversity													
OTU counts	408.5	*(46.8)*	351.2	*(41.4)*	365.7	*(43.5)*	345.9	*(44.7)*	NS	a	ab	ab	b
Phylogenetic diversity	38.7	*(3.4)*	34.6	*(2.5)*	33.7	*(3.2)*	32.6	*(3.4)*	0.0005	a	b	b	b
Shannon index	6.57	*(0.41)*	6.15	*(0.63)*	5.87	*(0.45)*	5.89	*(0.41)*	0.0002	a	ab	b	b
Phylum Firmicutes	0.477	*(0.100)*	0.426	*(0.162)*	0.284	*(0.090)*	0.366	*(0.150)*	0.0004	a	ab	b	ab
Genus *Clostridiales_unc*	0.251	*(0.081)*	0.213	*(0.120)*	0.181	*(0.054)*	0.234	*(0.101)*	NS	a	a	a	a
Genus *Lachnospiracea_unc*	0.063	*(0.040)*	0.057	*(0.030)*	0.025	*(0.017)*	0.044	*(0.028)*	0.0003	a	a	b	a
Genus *Lactobacillus*	0.016	*(0.023)*	0.007	*(0.006)*	0.014	*(0.016)*	0.022	*(0.018)*	0.01	a	a	a	a
Genus *Oscillospira*	0.062	*(0.023)*	0.064	*(0.014)*	0.028	*(0.016)*	0.031	*(0.020)*	<0.0001	a	a	b	b
Genus *Ruminococcaceae_unc*	0.049	*(0.014)*	0.050	*(0.023)*	0.018	*(0.013)*	0.021	*(0.019)*	<0.0001	a	a	b	b
Genus *Ruminococcus*	0.013	*(0.006)*	0.017	*(0.008)*	0.004	*(0.002)*	0.006	*(0.004)*	<0.0001	ac	a	b	bc
Phylum Bacteroidetes	0.325	*(0.109)*	0.420	*(0.201)*	0.618	*(0.100)*	0.535	*(0.158)*	<0.0001	a	ab	b	b
Genus *Bacteroides*	0.084	*(0.051)*	0.112	*(0.089)*	0.090	*(0.057)*	0.093	*(0.071)*	NS	a	a	a	a
Genus *Bacteroidales_unc*	0.036	*(0.022)*	0.016	*(0.020)*	0.073	*(0.035)*	0.064	*(0.043)*	<0.0001	ab	a	b	b
Genus *Odoribacter*	0.013	*(0.013)*	0.013	*(0.020)*	0.044	*(0.038)*	0.058	*(0.038)*	<0.0001	a	a	b	b
Genus *Parabacteroides*	0.016	*(0.015)*	0.012	*(0.007)*	0.003	*(0.006)*	0.004	*(0.004)*	<0.0001	a	a	b	b
Genus *Prevotella*	0.020	*(0.024)*	0.022	*(0.033)*	0.011	*(0.035)*	0.004	*(0.015)*	<0.0001	a	a	b	b
Genus *Rikenellaceae_unc*	0.046	*(0.029)*	0.033	*(0.026)*	0.181	*(0.092)*	0.148	*(0.083)*	<0.0001	a	a	b	b
Genus *S24_7_unc*	0.103	*(0.053)*	0.199	*(0.129)*	0.202	*(0.128)*	0.149	*(0.102)*	NS	a	a	a	a
Phylum Proteobacteria	0.161	*(0.054)*	0.117	*(0.103)*	0.072	*(0.037)*	0.063	*(0.036)*	<0.0001	a	ab	b	b
Genus *Desulfovibrionaceae_unc*	0.044	*(0.042)*	0.027	*(0.038)*	0.001	*(0.002)*	0.004	*(0.006)*	<0.0001	a	ab	b	b
Genus *Helicobacteraceae_unc*	0.039	*(0.025)*	0.047	*(0.102)*	0.050	*(0.034)*	0.029	*(0.024)*	NS	a	a	a	a
Genus *Helicobacter*	0.064	*(0.064)*	0.001	*(0.003)*	0.165	*(0.019)*	0.008	*(0.013)*	NS	ab	a	b	a
Phylum Deferribacteres	0.021	*(0.016)*	0.028	*(0.052)*	0.004	*(0.005)*	0.012	*(0.014)*	0.03	a	ab	b	ab
Genus *Mucispirillum*	0.021	*(0.016)*	0.028	*(0.052)*	0.004	*(0.005)*	0.012	*(0.014)*	0.03	a	ab	b	ab

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[1] Microbial measurements include three alpha-diversity measurements and relative abundance of bacterial phyla and genera.

[2] Comparisons between Wild (North and South combined, n=20) and Lab (North and South combined, n = 78).

[3] Non-overlapping letters indicate significance based on Wilcoxon test using Bonferroni corrected p-value (alpha = 0.05/24 = 0.002)

Table S9. Genotype-bacteria associations using all populations and within populations.

				All populations		Within Populations					
Chr	Bp	Genes[1]	Bacterial measurements[2]	Genotype directions[3]	ANOVA P-values	Consistent genotype directions[4]	ANOVA P-values[5]				
							FL	GA	VA	PA	NH_VT
3	68695548	*Il12a*	*Odoribacter*	AA > GA > GG	0.0014	3 out of 5	0.020	0.001	(0.259)	0.428	(0.045)
3	86138574	*Snord73a, Rnu73b, Rps3a1*	*Bacteroides*	AC > AA	0.0021	2 out of 3	0.013	-	-	0.001	(0.830)
4	103170679	*Mier1, Slc35d1*	Phylogenetic diversity	TT > TC	0.1107	2 out of 2	-	-	-	0.130	0.220
4	89692441	*Dmrta1*	*Bacteroides*	GG > GA > AA	0.0005	2 out of 3	0.017	-	(0.367)	<0.0001	-
5	90490831	*Afp*	*Bacteroides*	AA > GA > GG	0.0006	3 out of 4	0.030	-	(0.336)	0.001	0.978
6	121222841	*Tuba8, Gm15856*	*Bacteroides*	TC > TT	0.0004	3 out of 4	0.010	-	0.209	0.001	(0.813)
6	128374454	*Foxm1, Tex52*	Phylogenetic diversity	GG > GT	< 0.0001	5 out of 5	0.046	0.018	0.128	0.025	0.250
8	120092803	*Zdhhc7, Gm20388, Gm15898*	*Bacteroides*	CT > CC	< 0.0001	3 out of 3	0.010	0.059	-	0.001	-
8	13142468	*Cul4a*	*Bacteroides*	CT > CC	0.0006	4 out of 4	0.334	0.076	-	0.001	0.720
8	16358320	*Csmd1*	Phylogenetic diversity	CC > CT > TT	0.0125	4 out of 4	0.681	0.352	-	0.014	0.541
11	3132802	*Sfi1, Pisd-ps1*	Phylogenetic diversity	CC > CA	0.0159	4 out of 4	0.262	0.560	-	0.041	0.220
13	33671503	*Serpinb6d*	*Bacteroides*	CT > CC	< 0.0001	2 out of 2	0.0014	-	-	0.0007	-
					Total:	37 out of 43					

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[1] The SNP with lowest p-value was selected when more than one SNP was included in the gene.

[2] Residuals after covariate regression (i.e. Genetic PC1-4 and Latitude) on box-cox transformed relative abundances of bacterial taxa and alpha-diversity were used.

[3] The directions of the genotype-bacteria associations were based on the average values of bacterial measurements for each genotype.

[4] The proportions of individual populations that genotype-bacteria associations are in the same direction as the all-population result.

[5] P-values in parentheses indicate that genotype-bacteria associations are in the opposite direction compared to the all-population result.

Table S10. Loci significantly associated with microbial measurements (q-value < 0.1) in wild mouse mGWAS using human candidate genes.

Chr	Bp	Annotated gene(s)	Associated microbial measurements	P-values[1]	Q-values
2	21367906	*Gpr158*	*Clostridiales_unc*	9.03E-06	0.053
5	148315352	*Mtus2*	*Phylogenetic diversity*	5.44E-05	0.084
6	113765833	*Atp2b2*	*Ruminococcus*	7.55E-06	0.074
6	113817432		*Phylogenetic diversity*	4.01E-05	0.074
6	113817441		*Phylogenetic diversity*	1.31E-05	0.030
6	144993723	*Bcat1*	*Clostridiales_unc*	1.12E-05	0.053
6	48445226	*Sspo*	*Bacteroides*	4.38E-05	0.088
8	16358320	*Csmd1*	*Phylogenetic diversity*	1.09E-06	0.010
8	16358359			3.89E-06	0.018
12	104780917	*Clmn*	*Bacteroides*	3.07E-05	0.088
12	75308870	*Bcat1*	*Bacteroides*	1.90E-05	0.088
12	75308871			5.83E-05	0.093
12	75308874			1.53E-05	0.088
12	75394205	*Rhoj*	*Phylogenetic diversity*	5.70E-06	0.018
13	69612885	*Nsun2*	*Bacteroides*	4.40E-05	0.088
15	5217545	*Ptger4*	*Bacteroides*	6.50E-05	0.093

[1] Likelihood ratio p-values.

[2] ANOVA R^2 values. Residuals after covariate regression (i.e. Genetic PC1-4 and Latitude) on box-cox transformed relative abundances of bacterial taxa and alpha-diversity were used.

Table 11. Significant loci associated with microbial measurements in wild mouse mGWAS (Q<0.2)

Taxa	chr	rs	ps	n_miss	allele1	allele0	af	beta	se	l_remle	l_mle	p_wald	p_lrt	qvalues	p_score	EnsembleID	VariantType	Codon Change
Phylogenetic diversity	6	6_128374454	128374454	0	T	G	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000001517	downstream_gene_variant	-
Phylogenetic diversity	6	6_128374454	128374454	0	T	G	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000001517	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128374454	128374454	0	T	G	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000079304	upstream_gene_variant	-
Phylogenetic diversity	6	6_128374521	128374521	0	C	T	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000001517	downstream_gene_variant	-
Phylogenetic diversity	6	6_128374521	128374521	0	C	T	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000001517	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128374521	128374521	0	C	T	0.11	-5.10E-01	1.03E-01	1.00E-05	1.00E+05	9.33E-06	4.09E-07	0.051478	4.62E-05	ENSMUSG00000079304	upstream_gene_variant	-
Phylogenetic diversity	11	11_3132802	3132802	2	A	C	0.073	-6.05E-01	1.24E-01	1.00E-05	1.00E+05	1.23E-05	8.39E-07	0.054876	6.32E-05	ENSMUSG00000023764	non_coding_exon_variant,nc_transcript_variant	-
Phylogenetic diversity	11	11_3132802	3132802	2	A	C	0.073	-6.05E-01	1.24E-01	1.00E-05	1.00E+05	1.23E-05	8.39E-07	0.054876	6.32E-05	ENSMUSG00000023764	intron_variant	-
Phylogenetic diversity	11	11_3132802	3132802	2	A	C	0.073	-6.05E-01	1.24E-01	1.00E-05	1.00E+05	1.23E-05	8.39E-07	0.054876	6.32E-05	ENSMUSG00000082286	downstream_gene_variant	-
Phylogenetic diversity	11	11_3132802	3132802	2	A	C	0.073	-6.05E-01	1.24E-01	1.00E-05	1.00E+05	1.23E-05	8.39E-07	0.054876	6.32E-05	ENSMUSG00000023764	downstream_gene_variant	-
Phylogenetic diversity	6	6_128374742	128374742	0	A	T	0.12	-4.48E-01	9.05E-02	1.00E-05	1.00E+05	9.44E-06	9.63E-07	0.054876	6.71E-05	ENSMUSG00000001517	downstream_gene_variant	-
Phylogenetic diversity	6	6_128374742	128374742	0	A	T	0.12	-4.48E-01	9.05E-02	1.00E-05	1.00E+05	9.44E-06	9.63E-07	0.054876	6.71E-05	ENSMUSG00000001517	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128374742	128374742	0	A	T	0.12	-4.48E-01	9.05E-02	1.00E-05	1.00E+05	9.44E-06	9.63E-07	0.054876	6.71E-05	ENSMUSG00000079304	upstream_gene_variant	-
Phylogenetic diversity	8	8_16358320	16358320	0	T	C	0.18	-3.84E-01	7.60E-02	2.80E+00	1.00E+05	6.58E-06	1.09E-06	0.054876	7.10E-05	ENSMUSG00000060924	intron_variant	-
Phylogenetic diversity	4	4_103170679	103170679	2	C	T	0.042	-8.05E-01	1.72E-01	1.94E+00	1.00E+05	2.41E-05	2.19E-06	0.09188	9.78E-05	ENSMUSG00000028522	downstream_gene_variant	-
Phylogenetic diversity	4	4_103170679	103170679	2	C	T	0.042	-8.05E-01	1.72E-01	1.94E+00	1.00E+05	2.41E-05	2.19E-06	0.09188	9.78E-05	ENSMUSG00000028521	3_prime_UTR_variant	-
Phylogenetic diversity	8	8_13142468	13142468	1	T	C	0.041	-7.20E-01	1.63E-01	1.00E-05	1.00E+05	5.81E-05	3.48E-06	0.122402	1.22E-04	ENSMUSG00000031446	upstream_gene_variant	-
Phylogenetic diversity	8	8_13142468	13142468	1	T	C	0.041	-7.20E-01	1.63E-01	1.00E-05	1.00E+05	5.81E-05	3.48E-06	0.122402	1.22E-04	ENSMUSG00000031446	intron_variant	-
Phylogenetic diversity	8	8_16358359	16358359	2	C	A	0.146	-3.38E-01	7.91E-02	1.00E-05	1.00E+05	8.93E-05	3.89E-06	0.122402	1.28E-04	ENSMUSG00000060924	non_coding_exon_variant,nc_transcript_variant	-
Phylogenetic diversity	8	8_16358359	16358359	2	C	A	0.146	-3.38E-01	7.91E-02	1.00E-05	1.00E+05	8.93E-05	3.89E-06	0.122402	1.28E-04	ENSMUSG00000060924	synonymous_variant	gcT/gcG
Phylogenetic diversity	12	12_75394205	75394205	0	T	C	0.18	-3.47E-01	7.51E-02	2.23E+00	1.00E+05	2.94E-05	5.70E-06	0.159427	1.55E-04	ENSMUSG00000046768	intron_variant	-
Phylogenetic diversity	12	12_75394205	75394205	0	T	C	0.18	-3.47E-01	7.51E-02	2.23E+00	1.00E+05	2.94E-05	5.70E-06	0.159427	1.55E-04	ENSMUSG00000046768	3_prime_UTR_variant	-
Phylogenetic diversity	1	1_88236753	88236753	0	T	C	0.48	9.53E-01	2.30E-01	1.00E-05	1.00E+05	1.34E-04	7.16E-06	0.161824	1.73E-04	ENSMUSG00000079429	intron_variant	-
Phylogenetic diversity	1	1_88236753	88236753	0	T	C	0.48	9.53E-01	2.30E-01	1.00E-05	1.00E+05	1.34E-04	7.16E-06	0.161824	1.73E-04	ENSMUSG00000079429	upstream_gene_variant	-
Phylogenetic diversity	1	1_88236753	88236753	0	T	C	0.48	9.53E-01	2.30E-01	1.00E-05	1.00E+05	1.34E-04	7.16E-06	0.161824	1.73E-04	ENSMUSG00000079429	downstream_gene_variant	-
Phylogenetic diversity	5	5_90526381	90526381	1	A	G	0.041	-5.35E-01	1.35E-01	1.00E-05	1.00E+05	2.50E-04	8.32E-06	0.161824	1.87E-04	ENSMUSG00000029369	missense_variant	Gga/Aga
Phylogenetic diversity	11	11_57787336	57787336	0	A	G	0.16	-4.12E-01	9.59E-02	5.23E-02	1.00E+05	8.53E-05	6.91E-06	0.161824	1.70E-04	ENSMUSG00000020520	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128375274	128375274	0	T	C	0.13	-4.00E-01	9.22E-02	1.00E-05	1.00E+05	7.21E-05	8.79E-06	0.161824	1.92E-04	ENSMUSG00000001517	downstream_gene_variant	-

Phylogenetic diversity	6	6_128375274	128375274	0	T	C	0.13	-4.00E-01	9.22E-02	1.00E-05	1.00E+05	7.21E-05	8.79E-06	0.161824	1.92E-04	ENSMUSG00000001517	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128375274	128375274	0	T	C	0.13	-4.00E-01	9.22E-02	1.00E-05	1.00E+05	7.21E-05	8.79E-06	0.161824	1.92E-04	ENSMUSG00000079304	upstream_gene_variant	-
Phylogenetic diversity	2	2_94301405	94301405	0	T	A	0.04	-6.95E-01	1.72E-01	5.01E-01	1.00E+05	1.95E-04	1.16E-05	0.161824	2.21E-04	ENSMUSG00000027194	3_prime_UTR_variant	-
Phylogenetic diversity	7	7_141426886	141426886	0	T	A	0.29	-2.41E-01	6.36E-02	1.00E-05	1.00E+05	4.26E-04	1.20E-05	0.161824	2.25E-04	ENSMUSG00000019082	downstream_gene_variant	-
Phylogenetic diversity	7	7_141426886	141426886	0	T	A	0.29	-2.41E-01	6.36E-02	1.00E-05	1.00E+05	4.26E-04	1.20E-05	0.161824	2.25E-04	ENSMUSG00000060240	intron_variant	-
Phylogenetic diversity	7	7_141426886	141426886	0	T	A	0.29	-2.41E-01	6.36E-02	1.00E-05	1.00E+05	4.26E-04	1.20E-05	0.161824	2.25E-04	ENSMUSG00000060240	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128374511	128374511	0	T	A	0.1	-4.60E-01	1.13E-01	1.00E-05	1.00E+05	1.74E-04	1.22E-05	0.161824	2.27E-04	ENSMUSG00000001517	downstream_gene_variant	-
Phylogenetic diversity	6	6_128374511	128374511	0	T	A	0.1	-4.60E-01	1.13E-01	1.00E-05	1.00E+05	1.74E-04	1.22E-05	0.161824	2.27E-04	ENSMUSG00000001517	3_prime_UTR_variant	-
Phylogenetic diversity	6	6_128374511	128374511	0	T	A	0.1	-4.60E-01	1.13E-01	1.00E-05	1.00E+05	1.74E-04	1.22E-05	0.161824	2.27E-04	ENSMUSG00000079304	upstream_gene_variant	-
Phylogenetic diversity	7	7_24925094	24925094	0	A	G	0.09	-4.83E-01	1.17E-01	1.00E-05	1.00E+05	1.53E-04	1.25E-05	0.161824	2.30E-04	ENSMUSG00000040940	downstream_gene_variant	-
Phylogenetic diversity	7	7_24925094	24925094	0	A	G	0.09	-4.83E-01	1.17E-01	1.00E-05	1.00E+05	1.53E-04	1.25E-05	0.161824	2.30E-04	ENSMUSG00000040940	intron_variant	-
Phylogenetic diversity	12	12_32205995	32205995	0	T	C	0.11	-3.84E-01	9.17E-02	3.48E-01	1.00E+05	1.18E-04	1.27E-05	0.161824	2.32E-04	ENSMUSG00000020573	upstream_gene_variant	-
Phylogenetic diversity	12	12_32205995	32205995	0	T	C	0.11	-3.84E-01	9.17E-02	3.48E-01	1.00E+05	1.18E-04	1.27E-05	0.161824	2.32E-04	ENSMUSG00000020573	5_prime_UTR_variant	-
Phylogenetic diversity	6	6_113817441	113817441	0	T	C	0.41	-2.72E-01	6.22E-02	1.00E-05	1.00E+05	6.51E-05	1.31E-05	0.161824	2.35E-04	ENSMUSG00000030302	intron_variant	-
Phylogenetic diversity	3	3_10314899	10314899	1	G	A	0.082	-5.19E-01	1.22E-01	1.00E-05	1.00E+05	1.00E-04	1.32E-05	0.161824	2.36E-04	ENSMUSG00000027531	3_prime_UTR_variant	-
Phylogenetic diversity	2	2_91674525	91674525	1	T	G	0.061	-4.49E-01	1.21E-01	1.00E-05	1.00E+05	5.65E-04	1.35E-05	0.161824	2.39E-04	ENSMUSG00000027247	downstream_gene_variant	-
Phylogenetic diversity	2	2_91674525	91674525	1	T	G	0.061	-4.49E-01	1.21E-01	1.00E-05	1.00E+05	5.65E-04	1.35E-05	0.161824	2.39E-04	ENSMUSG00000027244	downstream_gene_variant	-
Phylogenetic diversity	7	7_134270142	134270142	0	T	C	0.08	-4.34E-01	1.04E-01	2.10E+00	1.00E+05	1.30E-04	1.65E-05	0.188795	2.65E-04	ENSMUSG00000030994	intron_variant	-
Clostridiales_unc	9	9_106071836	106071836	0	T	C	0.18	1.60E-01	3.12E-02	1.00E-05	1.00E+05	5.12E-06	5.05E-07	0.12347	5.06E-05	ENSMUSG00000032572	intron_variant	-
Clostridiales_unc	2	2_21367906	21367906	0	T	C	0.23	1.21E-01	2.70E-02	9.74E-01	1.00E+05	4.62E-05	9.03E-06	0.1577	1.95E-04	ENSMUSG00000085680	intron_variant	-
Clostridiales_unc	2	2_21367906	21367906	0	T	C	0.23	1.21E-01	2.70E-02	9.74E-01	1.00E+05	4.62E-05	9.03E-06	0.1577	1.95E-04	ENSMUSG00000045967	5_prime_UTR_variant	-
Clostridiales_unc	2	2_21367906	21367906	0	T	C	0.23	1.21E-01	2.70E-02	9.74E-01	1.00E+05	4.62E-05	9.03E-06	0.1577	1.95E-04	ENSMUSG00000045967	non_coding_exon_variant,nc_transcript_variant	-
Clostridiales_unc	3	3_87440123	87440123	0	G	T	0.32	9.05E-02	2.15E-02	1.00E-05	1.00E+05	1.12E-04	7.48E-06	0.1577	1.77E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87440335	87440335	0	C	G	0.26	1.16E-01	2.62E-02	2.38E-01	1.00E+05	5.29E-05	5.25E-06	0.1577	1.48E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87440340	87440340	0	T	C	0.25	1.19E-01	2.77E-02	6.29E-02	1.00E+05	8.75E-05	9.02E-06	0.1577	1.95E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87440341	87440341	0	G	A	0.25	1.19E-01	2.77E-02	6.29E-02	1.00E+05	8.75E-05	9.02E-06	0.1577	1.95E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87442103	87442103	0	A	G	0.3	1.20E-01	2.33E-02	1.00E+05	1.00E+05	5.01E-06	2.84E-06	0.1577	1.10E-04	ENSMUSG00000048031	missense_variant	Gta/Ata
Clostridiales_unc	3	3_87442103	87442103	0	A	G	0.3	1.20E-01	2.33E-02	1.00E+05	1.00E+05	5.01E-06	2.84E-06	0.1577	1.10E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87442187	87442187	0	G	A	0.3	1.20E-01	2.33E-02	1.00E+05	1.00E+05	5.01E-06	2.84E-06	0.1577	1.10E-04	ENSMUSG00000048031	missense_variant	Aag/Gag
Clostridiales_unc	3	3_87442187	87442187	0	G	A	0.3	1.20E-01	2.33E-02	1.00E+05	1.00E+05	5.01E-06	2.84E-06	0.1577	1.10E-04	ENSMUSG00000048031	intron_variant	-
Clostridiales_unc	3	3_87443684	87443684	0	A	C	0.32	1.10E-01	2.24E-02	1.00E+05	1.00E+05	1.04E-05	6.14E-06	0.1577	1.61E-04	ENSMUSG00000048031	missense_variant	tAt/tCt
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000066043	downstream_gene_variant	-
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000085241	upstream_gene_variant	-
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000066043	3_prime_UTR_variant	-
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000091021	downstream_gene_variant	-
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000064387	upstream_gene_variant	-

Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000065353	upstream_gene_variant	-
Clostridiales_unc	4	4_132356533	132356533	0	A	G	0.15	1.63E-01	3.32E-02	1.00E-05	1.00E+05	1.10E-05	5.04E-06	0.1577	1.46E-04	ENSMUSG00000028896	upstream_gene_variant	-
Clostridiales_unc	10	10_13553200	13553200	0	G	T	0.08	2.17E-01	4.54E-02	2.01E+00	1.00E+05	1.69E-05	4.97E-06	0.1577	1.45E-04	ENSMUSG00000019809	upstream_gene_variant	-
Clostridiales_unc	10	10_13553200	13553200	0	G	T	0.08	2.17E-01	4.54E-02	2.01E+00	1.00E+05	1.69E-05	4.97E-06	0.1577	1.45E-04	ENSMUSG00000019808	5_prime_UTR_variant	-
Clostridiales_unc	10	10_70448825	70448825	1	A	T	0.173	1.29E-01	2.84E-02	1.00E-05	1.00E+05	3.56E-05	6.61E-06	0.1577	1.67E-04	ENSMUSG00000043259	intron_variant	-
Clostridiales_unc	12	12_112775647	112775647	0	T	A	0.39	1.13E-01	2.41E-02	1.83E+00	1.00E+05	2.44E-05	5.24E-06	0.1577	1.48E-04	ENSMUSG00000072812	missense_variant	Att/Ttt
Clostridiales_unc	12	12_112775647	112775647	0	T	A	0.39	1.13E-01	2.41E-02	1.83E+00	1.00E+05	2.44E-05	5.24E-06	0.1577	1.48E-04	ENSMUSG00000072812	upstream_gene_variant	-
Clostridiales_unc	12	12_112775647	112775647	0	T	A	0.39	1.13E-01	2.41E-02	1.83E+00	1.00E+05	2.44E-05	5.24E-06	0.1577	1.48E-04	ENSMUSG00000072812	downstream_gene_variant	-
Clostridiales_unc	15	15_73783540	73783540	0	A	G	0.23	1.21E-01	2.34E-02	1.00E-05	1.00E+05	5.01E-06	1.59E-06	0.1577	8.42E-05	ENSMUSG00000072487	downstream_gene_variant	-
Clostridiales_unc	15	15_73783540	73783540	0	A	G	0.23	1.21E-01	2.34E-02	1.00E-05	1.00E+05	5.01E-06	1.59E-06	0.1577	8.42E-05	ENSMUSG00000072487	non_coding_exon_variant,nc_transcript_variant	-
Clostridiales_unc	15	15_73783540	73783540	0	A	G	0.23	1.21E-01	2.34E-02	1.00E-05	1.00E+05	5.01E-06	1.59E-06	0.1577	8.42E-05	ENSMUSG00000072487	missense_variant	aCg/aTg
Clostridiales_unc	2	2_181601302	181601302	0	T	C	0.14	1.40E-01	3.22E-02	1.00E-05	1.00E+05	7.25E-05	1.20E-05	0.162139	2.25E-04	ENSMUSG00000038605	upstream_gene_variant	-
Clostridiales_unc	2	2_181601302	181601302	0	T	C	0.14	1.40E-01	3.22E-02	1.00E-05	1.00E+05	7.25E-05	1.20E-05	0.162139	2.25E-04	ENSMUSG00000002455	upstream_gene_variant	-
Clostridiales_unc	2	2_181601302	181601302	0	T	C	0.14	1.40E-01	3.22E-02	1.00E-05	1.00E+05	7.25E-05	1.20E-05	0.162139	2.25E-04	ENSMUSG00000002455	intron_variant	-
Clostridiales_unc	3	3_87443666	87443666	0	C	A	0.33	1.09E-01	2.30E-02	1.00E+05	1.00E+05	2.07E-05	1.26E-05	0.162139	2.31E-04	ENSMUSG00000048031	missense_variant	cCt/cAt
Clostridiales_unc	6	6_144993723	144993723	1	A	G	0.071	2.05E-01	4.50E-02	1.00E-05	1.00E+05	3.77E-05	1.12E-05	0.162139	2.17E-04	ENSMUSG00000030268	downstream_gene_variant	-
Clostridiales_unc	8	8_110971625	110971625	0	T	C	0.09	1.64E-01	3.60E-02	1.00E-05	1.00E+05	3.80E-05	1.26E-05	0.162139	2.30E-04	ENSMUSG00000015023	downstream_gene_variant	-
Clostridiales_unc	8	8_110971625	110971625	0	T	C	0.09	1.64E-01	3.60E-02	1.00E-05	1.00E+05	3.80E-05	1.26E-05	0.162139	2.30E-04	ENSMUSG00000031749	downstream_gene_variant	-
Clostridiales_unc	8	8_110971625	110971625	0	T	C	0.09	1.64E-01	3.60E-02	1.00E-05	1.00E+05	3.80E-05	1.26E-05	0.162139	2.30E-04	ENSMUSG00000031749	3_prime_UTR_variant	-
Clostridiales_unc	19	19_10218949	10218949	1	C	A	0.133	-1.62E-01	3.57E-02	1.00E-05	1.00E+05	3.97E-05	1.17E-05	0.162139	2.22E-04	ENSMUSG00000036098	intron_variant	-
Clostridiales_unc	17	17_34216100	34216100	0	T	C	0.42	-9.11E-02	2.19E-02	1.00E-05	1.00E+05	1.28E-04	1.37E-05	0.16748	2.41E-04	ENSMUSG00000024339	non_coding_exon_variant,nc_transcript_variant	-
Clostridiales_unc	17	17_34216100	34216100	0	T	C	0.42	-9.11E-02	2.19E-02	1.00E-05	1.00E+05	1.28E-04	1.37E-05	0.16748	2.41E-04	ENSMUSG00000024339	3_prime_UTR_variant	-
Clostridiales_unc	17	17_34216100	34216100	0	T	C	0.42	-9.11E-02	2.19E-02	1.00E-05	1.00E+05	1.28E-04	1.37E-05	0.16748	2.41E-04	ENSMUSG00000081512	upstream_gene_variant	-
Bacteroides	5	5_90490831	90490831	0	A	G	0.09	3.65E-01	5.81E-02	7.23E-01	1.00E+05	9.13E-08	1.27E-08	0.001556	1.20E-05	ENSMUSG00000054932	synonymous_variant	gcG/gcA
Bacteroides	5	5_90490846	90490846	0	T	C	0.09	3.65E-01	5.81E-02	7.23E-01	1.00E+05	9.13E-08	1.27E-08	0.001556	1.20E-05	ENSMUSG00000054932	synonymous_variant	caC/caT
Bacteroides	5	5_90491657	90491657	0	A	C	0.12	2.96E-01	5.07E-02	8.02E-01	1.00E+05	4.43E-07	8.67E-08	0.007083	2.46E-05	ENSMUSG00000054932	intron_variant	-
Bacteroides	8	8_120092803	120092803	0	T	C	0.04	5.25E-01	9.65E-02	1.00E-05	1.00E+05	1.74E-06	3.38E-07	0.02071	4.27E-05	ENSMUSG00000089742	upstream_gene_variant	-
Bacteroides	8	8_120092803	120092803	0	T	C	0.04	5.25E-01	9.65E-02	1.00E-05	1.00E+05	1.74E-06	3.38E-07	0.02071	4.27E-05	ENSMUSG00000031823	intron_variant	-
Bacteroides	8	8_120092803	120092803	0	T	C	0.04	5.25E-01	9.65E-02	1.00E-05	1.00E+05	1.74E-06	3.38E-07	0.02071	4.27E-05	ENSMUSG00000031823	upstream_gene_variant	-
Bacteroides	8	8_120092803	120092803	0	T	C	0.04	5.25E-01	9.65E-02	1.00E-05	1.00E+05	1.74E-06	3.38E-07	0.02071	4.27E-05	ENSMUSG00000031823	downstream_gene_variant	-
Bacteroides	8	8_120092803	120092803	0	T	C	0.04	5.25E-01	9.65E-02	1.00E-05	1.00E+05	1.74E-06	3.38E-07	0.02071	4.27E-05	ENSMUSG00000092329	intron_variant	-
Bacteroides	4	4_89692441	89692441	0	G	A	0.09	3.47E-01	6.45E-02	2.66E+00	1.00E+05	2.21E-06	4.73E-07	0.023186	4.92E-05	ENSMUSG00000043753	downstream_gene_variant	-
Bacteroides	4	4_89692441	89692441	0	G	A	0.09	3.47E-01	6.45E-02	2.66E+00	1.00E+05	2.21E-06	4.73E-07	0.023186	4.92E-05	ENSMUSG00000043753	3_prime_UTR_variant	-
Bacteroides	3	3_86138574	86138574	0	C	A	0.07	3.92E-01	7.75E-02	1.00E-05	1.00E+05	6.66E-06	6.90E-07	0.028185	5.79E-05	ENSMUSG00000064984	downstream_gene_variant	-
Bacteroides	3	3_86138574	86138574	0	C	A	0.07	3.92E-01	7.75E-02	1.00E-05	1.00E+05	6.66E-06	6.90E-07	0.028185	5.79E-05	ENSMUSG00000064390	downstream_gene_variant	-
Bacteroides	3	3_86138574	86138574	0	C	A	0.07	3.92E-01	7.75E-02	1.00E-05	1.00E+05	6.66E-06	6.90E-07	0.028185	5.79E-05	ENSMUSG00000028081	synonymous_variant	ggG/ggT
Bacteroides	13	13_33671503	33671503	0	T	C	0.04	4.79E-01	1.01E-01	1.00E-05	1.00E+05	2.07E-05	1.38E-06	0.048318	7.89E-05	ENSMUSG00000047889	3_prime_UTR_variant	-
Bacteroides	3	3_86138475	86138475	0	C	T	0.08	3.62E-01	7.43E-02	1.00E-05	1.00E+05	1.23E-05	1.77E-06	0.054226	8.84E-05	ENSMUSG00000064984	downstream_gene_variant	-
Bacteroides	3	3_86138475	86138475	0	C	T	0.08	3.62E-01	7.43E-02	1.00E-05	1.00E+05	1.23E-05	1.77E-06	0.054226	8.84E-05	ENSMUSG00000064390	downstream_gene_variant	-
Bacteroides	3	3_86138475	86138475	0	C	T	0.08	3.62E-01	7.43E-02	1.00E-05	1.00E+05	1.23E-05	1.77E-06	0.054226	8.84E-05	ENSMUSG00000028081	intron_variant	-
Bacteroides	3	3_86138625	86138625	1	C	T	0.071	3.38E-01	6.75E-02	1.00E-05	1.00E+05	7.78E-06	2.00E-06	0.054464	9.36E-05	ENSMUSG00000064984	downstream_gene_variant	-
Bacteroides	3	3_86138625	86138625	1	C	T	0.071	3.38E-01	6.75E-02	1.00E-05	1.00E+05	7.78E-06	2.00E-06	0.054464	9.36E-05	ENSMUSG00000064390	downstream_gene_variant	-
Bacteroides	3	3_86138625	86138625	1	C	T	0.071	3.38E-01	6.75E-02	1.00E-05	1.00E+05	7.78E-06	2.00E-06	0.054464	9.36E-05	ENSMUSG00000028081	intron_variant	-

Bacteroides	6	6_121222841	121222841	0	C	T	0.06	4.24E-01	8.22E-02	1.00E-05	1.00E+05	4.83E-06	3.03E-06	0.074262	1.14E-04	ENSMUSG00000030137	synonymous_variant	taT/taC
Bacteroides	6	6_121222841	121222841	0	C	T	0.06	4.24E-01	8.22E-02	1.00E-05	1.00E+05	4.83E-06	3.03E-06	0.074262	1.14E-04	ENSMUSG00000086527	downstream_gene_variant	-
Bacteroides	8	8_13142468	13142468	1	T	C	0.041	4.78E-01	1.02E-01	1.00E-05	1.00E+05	2.17E-05	3.56E-06	0.07932	1.23E-04	ENSMUSG00000031446	upstream_gene_variant	-
Bacteroides	8	8_13142468	13142468	1	T	C	0.041	4.78E-01	1.02E-01	1.00E-05	1.00E+05	2.17E-05	3.56E-06	0.07932	1.23E-04	ENSMUSG00000031446	intron_variant	-
Bacteroides	6	6_121221243	121221243	1	A	G	0.061	4.19E-01	8.28E-02	1.00E-05	1.00E+05	6.48E-06	4.19E-06	0.085577	1.33E-04	ENSMUSG00000030137	intron_variant	-
Bacteroides	6	6_121221243	121221243	1	A	G	0.061	4.19E-01	8.28E-02	1.00E-05	1.00E+05	6.48E-06	4.19E-06	0.085577	1.33E-04	ENSMUSG00000086527	downstream_gene_variant	-
Bacteroides	5	5_90491714	90491714	0	T	C	0.11	2.83E-01	6.10E-02	3.34E-01	1.00E+05	2.78E-05	5.90E-06	0.111233	1.57E-04	ENSMUSG00000054932	synonymous_variant	tcC/tcT
Bacteroides	5	5_141952954	141952954	0	T	C	0.09	3.36E-01	7.18E-02	1.00E-05	1.00E+05	2.40E-05	8.80E-06	0.154057	1.92E-04	ENSMUSG00000039683	intron_variant	-
Bacteroides	2	2_91674525	91674525	1	T	G	0.061	3.14E-01	7.47E-02	1.00E-05	1.00E+05	1.14E-04	9.96E-06	0.159309	2.05E-04	ENSMUSG00000027247	downstream_gene_variant	-
Bacteroides	2	2_91674525	91674525	1	T	G	0.061	3.14E-01	7.47E-02	1.00E-05	1.00E+05	1.14E-04	9.96E-06	0.159309	2.05E-04	ENSMUSG00000027244	downstream_gene_variant	-
Bacteroides	4	4_148006547	148006547	0	T	C	0.04	4.95E-01	9.98E-02	1.00E-05	1.00E+05	9.39E-06	1.04E-05	0.159309	2.09E-04	ENSMUSG00000029016	downstream_gene_variant	-
Bacteroides	4	4_148006547	148006547	0	T	C	0.04	4.95E-01	9.98E-02	1.00E-05	1.00E+05	9.39E-06	1.04E-05	0.159309	2.09E-04	ENSMUSG00000029016	3_prime_UTR_variant	-
Bacteroides	4	4_148006547	148006547	0	T	C	0.04	4.95E-01	9.98E-02	1.00E-05	1.00E+05	9.39E-06	1.04E-05	0.159309	2.09E-04	ENSMUSG00000086806	upstream_gene_variant	-
Bacteroides	4	4_148006547	148006547	0	T	C	0.04	4.95E-01	9.98E-02	1.00E-05	1.00E+05	9.39E-06	1.04E-05	0.159309	2.09E-04	ENSMUSG00000041616	downstream_gene_variant	-
Bacteroides	3	3_86139069	86139069	1	A	G	0.041	4.65E-01	1.03E-01	1.00E-05	1.00E+05	4.06E-05	1.90E-05	0.16785	2.86E-04	ENSMUSG00000064984	upstream_gene_variant	-
Bacteroides	3	3_86139069	86139069	1	A	G	0.041	4.65E-01	1.03E-01	1.00E-05	1.00E+05	4.06E-05	1.90E-05	0.16785	2.86E-04	ENSMUSG00000064390	downstream_gene_variant	-
Bacteroides	3	3_86139069	86139069	1	A	G	0.041	4.65E-01	1.03E-01	1.00E-05	1.00E+05	4.06E-05	1.90E-05	0.16785	2.86E-04	ENSMUSG00000028081	synonymous_variant	acT/acC
Bacteroides	4	4_89688171	89688171	0	T	C	0.1	3.00E-01	6.77E-02	2.16E+00	1.00E+05	5.40E-05	1.18E-05	0.16785	2.23E-04	ENSMUSG00000043753	intron_variant	-
Bacteroides	4	4_89688171	89688171	0	T	C	0.1	3.00E-01	6.77E-02	2.16E+00	1.00E+05	5.40E-05	1.18E-05	0.16785	2.23E-04	ENSMUSG00000043753	upstream_gene_variant	-
Bacteroides	5	5_90519074	90519074	0	C	A	0.07	3.56E-01	8.10E-02	1.00E-05	1.00E+05	6.01E-05	2.01E-05	0.16785	2.95E-04	ENSMUSG00000029369	missense_variant	gAc/gCc
Bacteroides	5	5_90526381	90526381	1	A	G	0.041	3.53E-01	8.47E-02	1.00E-05	1.00E+05	1.25E-04	1.81E-05	0.16785	2.79E-04	ENSMUSG00000029369	missense_variant	Gga/Aga
Bacteroides	5	5_118265460	118265460	0	G	A	0.21	1.87E-01	4.49E-02	1.00E-05	1.00E+05	1.32E-04	2.09E-05	0.16785	3.01E-04	ENSMUSG00000032840	3_prime_UTR_variant	-
Bacteroides	5	5_118265460	118265460	0	G	A	0.21	1.87E-01	4.49E-02	1.00E-05	1.00E+05	1.32E-04	2.09E-05	0.16785	3.01E-04	ENSMUSG00000095477	upstream_gene_variant	-
Bacteroides	6	6_41313290	41313290	2	T	G	0.042	3.65E-01	8.37E-02	1.00E-05	1.00E+05	6.65E-05	2.26E-05	0.16785	3.14E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_41313298	41313298	2	C	T	0.042	3.65E-01	8.37E-02	1.00E-05	1.00E+05	6.65E-05	2.26E-05	0.16785	3.14E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_41313339	41313339	2	C	T	0.042	3.65E-01	8.37E-02	1.00E-05	1.00E+05	6.65E-05	2.26E-05	0.16785	3.14E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_128374511	128374511	0	T	A	0.1	2.93E-01	7.17E-02	1.00E-05	1.00E+05	1.65E-04	1.85E-05	0.16785	2.83E-04	ENSMUSG00000001517	downstream_gene_variant	-
Bacteroides	6	6_128374511	128374511	0	T	A	0.1	2.93E-01	7.17E-02	1.00E-05	1.00E+05	1.65E-04	1.85E-05	0.16785	2.83E-04	ENSMUSG00000001517	3_prime_UTR_variant	-
Bacteroides	6	6_128374511	128374511	0	T	A	0.1	2.93E-01	7.17E-02	1.00E-05	1.00E+05	1.65E-04	1.85E-05	0.16785	2.83E-04	ENSMUSG00000079304	upstream_gene_variant	-
Bacteroides	7	7_46072425	46072425	0	T	C	0.06	3.83E-01	8.62E-02	1.00E-05	1.00E+05	5.15E-05	2.11E-05	0.16785	3.03E-04	ENSMUSG00000030835	intron_variant	-
Bacteroides	7	7_46081380	46081380	0	T	C	0.06	3.83E-01	8.62E-02	1.00E-05	1.00E+05	5.15E-05	2.11E-05	0.16785	3.03E-04	ENSMUSG00000030835	intron_variant	-
Bacteroides	7	7_46081380	46081380	0	T	C	0.06	3.83E-01	8.62E-02	1.00E-05	1.00E+05	5.15E-05	2.11E-05	0.16785	3.03E-04	ENSMUSG00000030835	upstream_gene_variant	-
Bacteroides	8	8_111715660	111715660	0	G	A	0.23	-2.37E-01	5.37E-02	4.58E+00	1.00E+05	5.84E-05	1.85E-05	0.16785	2.82E-04	ENSMUSG00000031955	synonymous_variant	gaT/gaC
Bacteroides	12	12_75308870	75308870	1	G	A	0.316	2.10E-01	5.03E-02	9.07E-01	1.00E+05	1.23E-04	1.90E-05	0.16785	2.86E-04	ENSMUSG00000046768	non_coding_exon_variant,nc_transcript_variant	-
Bacteroides	12	12_75308870	75308870	1	G	A	0.316	2.10E-01	5.03E-02	9.07E-01	1.00E+05	1.23E-04	1.90E-05	0.16785	2.86E-04	ENSMUSG00000046768	missense_variant	cAt/cGt
Bacteroides	12	12_75308870	75308870	1	G	A	0.316	2.10E-01	5.03E-02	9.07E-01	1.00E+05	1.23E-04	1.90E-05	0.16785	2.86E-04	ENSMUSG00000046768	upstream_gene_variant	-
Bacteroides	12	12_75308874	75308874	1	C	G	0.327	2.07E-01	4.71E-02	6.25E-01	1.00E+05	6.15E-05	1.53E-05	0.16785	2.56E-04	ENSMUSG00000046768	non_coding_exon_variant,nc_transcript_variant	-
Bacteroides	12	12_75308874	75308874	1	C	G	0.327	2.07E-01	4.71E-02	6.25E-01	1.00E+05	6.15E-05	1.53E-05	0.16785	2.56E-04	ENSMUSG00000046768	missense_variant	gaG/gaC
Bacteroides	12	12_75308874	75308874	1	C	G	0.327	2.07E-01	4.71E-02	6.25E-01	1.00E+05	6.15E-05	1.53E-05	0.16785	2.56E-04	ENSMUSG00000046768	upstream_gene_variant	-
Bacteroides	13	13_55403064	55403064	0	A	G	0.08	2.90E-01	6.79E-02	1.00E-05	1.00E+05	9.19E-05	1.46E-05	0.16785	2.49E-04	ENSMUSG00000021490	synonymous_variant	aaA/aaG
Bacteroides	14	14_32598040	32598040	0	C	T	0.04	4.44E-01	1.05E-01	1.00E-05	1.00E+05	1.03E-04	1.58E-05	0.16785	2.60E-04	ENSMUSG00000041730	upstream_gene_variant	-
Bacteroides	14	14_70604927	70604927	1	A	G	0.184	1.99E-01	4.86E-02	1.00E-05	1.00E+05	1.64E-04	1.47E-05	0.16785	2.50E-04	ENSMUSG00000022099	intron_variant	-
Bacteroides	4	4_129472127	129472127	2	T	C	0.052	3.98E-01	9.53E-02	1.00E-05	1.00E+05	1.26E-04	2.91E-05	0.17212	3.60E-04	ENSMUSG00000040859	intron_variant	-
Bacteroides	4	4_129472127	129472127	2	T	C	0.052	3.98E-01	9.53E-02	1.00E-05	1.00E+05	1.26E-04	2.91E-05	0.17212	3.60E-04	ENSMUSG00000040859	downstream_gene_variant	-
Bacteroides	5	5_139771573	139771573	1	G	A	0.041	4.39E-01	1.05E-01	1.00E-05	1.00E+05	1.26E-04	2.81E-05	0.17212	3.53E-04	ENSMUSG00000029547	synonymous_variant	gcT/gcC

Bacteroides	5	5_139771573	139771573	1	G	A	0.041	4.39E-01	1.05E-01	1.00E-05	1.00E+05	1.26E-04	2.81E-05	0.17212	3.53E-04	ENSMUSG00000098574	upstream_gene_variant	-
Bacteroides	6	6_41216082	41216082	1	T	C	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000076478	missense_variant	Cgg/Tgg
Bacteroides	6	6_41216085	41216085	1	T	C	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000076478	missense_variant	Ctc/Ttc
Bacteroides	6	6_41303204	41303204	1	G	A	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000054106	intron_variant	-
Bacteroides	6	6_41312455	41312455	1	G	A	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_41312456	41312456	1	T	C	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_41312497	41312497	1	T	A	0.041	3.61E-01	8.40E-02	1.00E-05	1.00E+05	8.38E-05	3.09E-05	0.17212	3.72E-04	ENSMUSG00000036938	intron_variant	-
Bacteroides	6	6_53816073	53816073	1	A	T	0.061	3.81E-01	9.24E-02	6.72E-01	1.00E+05	1.46E-04	3.02E-05	0.17212	3.67E-04	ENSMUSG00000078169	upstream_gene_variant	-
Bacteroides	6	6_53816073	53816073	1	A	T	0.061	3.81E-01	9.24E-02	6.72E-01	1.00E+05	1.46E-04	3.02E-05	0.17212	3.67E-04	ENSMUSG00000043496	3_prime_UTR_variant	-
Bacteroides	12	12_104780917	104780917	0	T	C	0.08	3.24E-01	7.63E-02	3.90E+00	1.00E+05	9.81E-05	3.07E-05	0.17212	3.70E-04	ENSMUSG00000021097	synonymous_variant	gaG/gaA
Bacteroides	19	19_4712684	4712684	0	A	G	0.06	3.52E-01	8.90E-02	1.00E-05	1.00E+05	2.54E-04	2.93E-05	0.17212	3.61E-04	ENSMUSG00000067889	intron_variant	-
Bacteroides	1	1_171237117	171237117	2	T	C	0.042	4.32E-01	1.06E-01	1.00E-05	1.00E+05	1.70E-04	3.89E-05	0.198746	4.22E-04	ENSMUSG00000058715	upstream_gene_variant	-
Bacteroides	1	1_171237117	171237117	2	T	C	0.042	4.32E-01	1.06E-01	1.00E-05	1.00E+05	1.70E-04	3.89E-05	0.198746	4.22E-04	ENSMUSG00000013593	intron_variant	-
Bacteroides	1	1_171237117	171237117	2	T	C	0.042	4.32E-01	1.06E-01	1.00E-05	1.00E+05	1.70E-04	3.89E-05	0.198746	4.22E-04	ENSMUSG00000013593	downstream_gene_variant	-
Bacteroides	1	1_171237117	171237117	2	T	C	0.042	4.32E-01	1.06E-01	1.00E-05	1.00E+05	1.70E-04	3.89E-05	0.198746	4.22E-04	ENSMUSG00000013593	upstream_gene_variant	-
Bacteroides	6	6_116692848	116692848	1	C	G	0.051	4.01E-01	9.48E-02	1.00E-05	1.00E+05	1.05E-04	3.92E-05	0.198746	4.24E-04	ENSMUSG00000048108	3_prime_UTR_variant	-
Bacteroides	6	6_116692848	116692848	1	C	G	0.051	4.01E-01	9.48E-02	1.00E-05	1.00E+05	1.05E-04	3.92E-05	0.198746	4.24E-04	ENSMUSG00000048108	downstream_gene_variant	-
Bacteroides	7	7_127375830	127375830	0	A	G	0.24	2.30E-01	5.78E-02	1.00E-05	1.00E+05	2.30E-04	4.06E-05	0.198746	4.32E-04	ENSMUSG00000054381	5_prime_UTR_variant	-
Bacteroides	9	9_72856998	72856998	0	A	G	0.35	1.58E-01	3.97E-02	1.00E-05	1.00E+05	2.33E-04	4.09E-05	0.198746	4.34E-04	ENSMUSG00000036030	synonymous_variant	cgG/cgA
Bacteroides	2	2_71209672	71209672	0	T	C	0.11	2.50E-01	6.27E-02	1.00E-05	1.00E+05	2.24E-04	4.27E-05	0.198746	4.44E-04	ENSMUSG00000027012	upstream_gene_variant	-
Bacteroides	6	6_48445226	48445226	0	A	C	0.03	4.74E-01	1.22E-01	1.00E-05	1.00E+05	3.27E-04	4.38E-05	0.198746	4.51E-04	ENSMUSG00000068551	intron_variant	-
Bacteroides	6	6_48445226	48445226	0	A	C	0.03	4.74E-01	1.22E-01	1.00E-05	1.00E+05	3.27E-04	4.38E-05	0.198746	4.51E-04	ENSMUSG00000029797	upstream_gene_variant	-
Bacteroides	6	6_48445226	48445226	0	A	C	0.03	4.74E-01	1.22E-01	1.00E-05	1.00E+05	3.27E-04	4.38E-05	0.198746	4.51E-04	ENSMUSG00000068551	upstream_gene_variant	-
Bacteroides	2	2_13010347	13010347	0	G	T	0.38	1.80E-01	4.41E-02	1.00E-05	1.00E+05	1.66E-04	4.40E-05	0.198746	4.51E-04	ENSMUSG00000049630	synonymous_variant	atA/atC
Bacteroides	13	13_69612885	69612885	2	T	C	0.042	4.35E-01	1.06E-01	1.00E-05	1.00E+05	1.54E-04	4.40E-05	0.198746	4.52E-04	ENSMUSG00000021594	upstream_gene_variant	-
Bacteroides	13	13_69612885	69612885	2	T	C	0.042	4.35E-01	1.06E-01	1.00E-05	1.00E+05	1.54E-04	4.40E-05	0.198746	4.52E-04	ENSMUSG00000091133	non_coding_exon_variant,nc_transcript_variant	-
Bacteroides	13	13_69612885	69612885	2	T	C	0.042	4.35E-01	1.06E-01	1.00E-05	1.00E+05	1.54E-04	4.40E-05	0.198746	4.52E-04	ENSMUSG00000021595	intron_variant	-
Bacteroides	10	10_40349413	40349413	1	C	A	0.082	3.36E-01	7.70E-02	1.00E-05	1.00E+05	6.65E-05	4.46E-05	0.198746	4.55E-04	ENSMUSG00000038491	non_coding_exon_variant,nc_transcript_variant	-
Bacteroides	10	10_40349413	40349413	1	C	A	0.082	3.36E-01	7.70E-02	1.00E-05	1.00E+05	6.65E-05	4.46E-05	0.198746	4.55E-04	ENSMUSG00000038481	5_prime_UTR_variant	-
Bacteroides	10	10_40349416	40349416	1	A	C	0.082	3.36E-01	7.70E-02	1.00E-05	1.00E+05	6.65E-05	4.46E-05	0.198746	4.55E-04	ENSMUSG00000038491	non_coding_exon_variant,nc_transcript_variant	-
Bacteroides	10	10_40349416	40349416	1	A	C	0.082	3.36E-01	7.70E-02	1.00E-05	1.00E+05	6.65E-05	4.46E-05	0.198746	4.55E-04	ENSMUSG00000038481	5_prime_UTR_variant	-
Bacteroides	14	14_79182968	79182968	0	T	C	0.07	3.65E-01	8.75E-02	9.11E-01	1.00E+05	1.28E-04	4.46E-05	0.198746	4.55E-04	ENSMUSG00000058997	intron_variant	-
Desulfovibrionaceae_unc	6	6_41617399	41617399	0	G	A	0.17	5.07E-01	9.67E-02	6.60E-01	1.00E+05	3.50E-06	8.04E-07	0.137653	6.20E-05	ENSMUSG00000029868	downstream_gene_variant	-
Desulfovibrionaceae_unc	6	6_41617399	41617399	0	G	A	0.17	5.07E-01	9.67E-02	6.60E-01	1.00E+05	3.50E-06	8.04E-07	0.137653	6.20E-05	ENSMUSG00000029869	downstream_gene_variant	-
Desulfovibrionaceae_unc	6	6_41617399	41617399	0	G	A	0.17	5.07E-01	9.67E-02	6.60E-01	1.00E+05	3.50E-06	8.04E-07	0.137653	6.20E-05	ENSMUSG00000029869	intron_variant	-
Desulfovibrionaceae_unc	6	6_41617399	41617399	0	G	A	0.17	5.07E-01	9.67E-02	6.60E-01	1.00E+05	3.50E-06	8.04E-07	0.137653	6.20E-05	ENSMUSG00000029869	upstream_gene_variant	-
Desulfovibrionaceae_unc	4	4_116557950	116557950	0	A	G	0.1	-6.96E-01	1.31E-01	1.00E+05	1.00E+05	2.88E-06	1.59E-06	0.137653	8.42E-05	ENSMUSG00000034042	upstream_gene_variant	-
Desulfovibrionaceae_unc	4	4_116557950	116557950	0	A	G	0.1	-6.96E-01	1.31E-01	1.00E+05	1.00E+05	2.88E-06	1.59E-06	0.137653	8.42E-05	ENSMUSG00000055900	upstream_gene_variant	-
Desulfovibrionaceae_unc	4	4_116557950	116557950	0	A	G	0.1	-6.96E-01	1.31E-01	1.00E+05	1.00E+05	2.88E-06	1.59E-06	0.137653	8.42E-05	ENSMUSG00000034042	intron_variant	-
Desulfovibrionaceae_unc	4	4_88807526	88807526	1	T	C	0.439	4.48E-01	8.51E-02	8.68E+01	1.00E+05	3.20E-06	1.69E-06	0.137653	8.66E-05	ENSMUSG00000094648	downstream_gene_variant	-
Desulfovibrionaceae_unc	4	4_88807526	88807526	1	T	C	0.439	4.48E-01	8.51E-02	8.68E+01	1.00E+05	3.20E-06	1.69E-06	0.137653	8.66E-05	ENSMUSG00000070908	3_prime_UTR_variant	-
Desulfovibrionaceae_unc	4	4_88807202	88807202	1	G	T	0.449	4.57E-01	9.02E-02	1.51E+02	1.00E+05	6.45E-06	3.60E-06	0.192063	1.24E-04	ENSMUSG00000094648	downstream_gene_variant	-
Desulfovibrionaceae_unc	4	4_88807202	88807202	1	G	T	0.449	4.57E-01	9.02E-02	1.51E+02	1.00E+05	6.45E-06	3.60E-06	0.192063	1.24E-04	ENSMUSG00000070908	3_prime_UTR_variant	-

Desulfovibrionaceae_unc	16	16_17209775	17209775	0	G	C	0.47	-3.68E-01	7.64E-02	1.04E+00	1.00E+05	1.46E-05	3.93E-06	0.192063	1.29E-04	ENSMUSG00000096434	upstream_gene_variant	-
Desulfovibrionaceae_unc	16	16_17209775	17209775	0	G	C	0.47	-3.68E-01	7.64E-02	1.04E+00	1.00E+05	1.46E-05	3.93E-06	0.192063	1.29E-04	ENSMUSG00000071636	missense_variant	caG/caC
Odoribacter	3	3_68695548	68695548	0	A	G	0.42	4.38E-01	6.76E-02	1.00E-05	1.00E+05	4.71E-08	7.79E-09	0.001924	1.02E-05	ENSMUSG00000027776	missense_variant	Ggc/Agc
Odoribacter	3	3_68695502	68695502	0	T	C	0.43	3.85E-01	7.15E-02	1.00E-05	1.00E+05	2.20E-06	4.13E-07	0.033164	4.64E-05	ENSMUSG00000027776	synonymous_variant	aaC/aaT
Odoribacter	3	3_68695379	68695379	0	A	G	0.43	3.78E-01	6.85E-02	1.00E-05	1.00E+05	1.35E-06	5.37E-07	0.033164	5.19E-05	ENSMUSG00000027776	intron_variant	-
Odoribacter	3	3_68695382	68695382	0	T	C	0.43	3.78E-01	6.85E-02	1.00E-05	1.00E+05	1.35E-06	5.37E-07	0.033164	5.19E-05	ENSMUSG00000027776	intron_variant	-
Odoribacter	3	3_68695209	68695209	1	G	C	0.214	5.18E-01	9.89E-02	1.00E-05	1.00E+05	3.51E-06	8.41E-07	0.041551	6.32E-05	ENSMUSG00000027776	missense_variant	aCt/aGt
Odoribacter	3	3_68695333	68695333	0	T	C	0.42	3.67E-01	6.87E-02	1.00E-05	1.00E+05	2.51E-06	1.10E-06	0.045289	7.11E-05	ENSMUSG00000027776	missense_variant	aCg/aTg

Table S12. Loci associated with microbial measurements in mouse and human mGWAS.

Chr	Bp	Annotated gene	Associated microbial measurements	P-values[1]	Q-values[2]	Effect size (%)[3]	Missense?	Tissue expressed[4]			
								Brain		Gut	
								mouse	human	mouse	human
2	21367906	*Gpr158*	*Clostridiales_unc*	9.03E-06	0.158	27.2	-	yes	yes	yes	-
6	48445226	*Sspo*	*Bacteroides*	4.38E-05	0.199	23.8	-	yes	NA	-	NA
6	113817441	*Atp2b2*	Phylogenetic diversity	1.31E-05	0.162	21.1	-	yes	yes	yes	-
6	144993723	*Bcat1*	*Clostridiales_unc*	1.12E-05	0.162	26.1	-	yes	yes	yes	yes
8	16358320	*Csmd1*	Phylogenetic diversity	1.09E-06	0.055	17.0	-	yes	yes	-	-
8	16358359			3.89E-06	0.122	13.8	-	yes	yes	-	-
12	75308870	*Rhoj*	*Bacteroides*	1.90E-05	0.168	28.7	yes	yes	yes	-	yes
12	75308874			1.53E-05	0.168	24.2	yes	yes	yes	-	yes
12	75394205	*Rhoj*	Phylogenetic diversity	5.70E-06	0.159	5.6	-	yes	yes	-	yes
12	104780917	*Clmn*	*Bacteroides*	3.07E-05	0.172	28.5	-	yes	yes	yes	yes
13	69612885	*Nsun2*	*Bacteroides*	4.40E-05	0.199	27.5	-	yes	yes	-	yes

[1] Likelihood ratio test p-values.

[2] SNPs with q-value < 0.2 were used to compare with human mGWAS gene set.

[3] ANOVA R^2 values. Residuals after covariate regression (i.e. Genetic PC1-4 and Latitude) on box-cox transformed relative abundances of bacterial taxa were used.

[4] Tissue expression data came from the Human Protein Atlas Database for humans and MGI Gene Expression Database for mice. All expression detected in brain tissue and gut (i.e. small and large intestines) as evidence of gene expression. "-" indicates no evidence of expression. "NA" indicates expression not tested.