

Supplementary Documents

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Table S1. STROBE-MR checklist of the present study.

No.	Section	Checklist item	Position
1	Title and abstract	Indicate MR as the study's design in the title and the abstract as a main purpose of the study	Title, Abstract
2	Background	Explain the scientific background and rationale for the reported study. Explain the exposure and a plausible potential causal relationship between exposure and outcome. Justify why MR is a helpful method to address the study question.	Introduction: paragraph 1-2
3	Objectives	State specific objectives clearly, including prespecified causal hypotheses. State that MR is a method that intends to estimate causal effects.	Introduction: paragraph 3
4a	Study design and data sources	Setting: Describe the study design (two-sample MR) and the underlying population. Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection.	Materials and methods: <i>Study design, Data sources, Figure 1</i>
4b		Participants: Report the eligibility criteria and the sources and methods of selection of participants. Report the sample size and whether any power or sample size calculations were carried out prior to the main analysis.	Materials and methods: <i>Study design, Data sources, Ethical approval</i>
4c		Describe measurement, quality control, and selection of genetic variants.	Materials and methods: <i>Selection of eligible instrumental variables</i>

4d		For each exposure, outcome, and other relevant variables, describe methods of assessment and diagnostic criteria for diseases.	Materials and methods: <i>Data sources</i>
4e		Provide details of ethics committee approval and participant informed consent, if relevant.	Materials and methods: <i>Ethical approval</i>
5	Assumptions	Explicitly state the 3 core instrumental variable (IV) assumptions for the main analysis (relevance, independence, and exclusion restriction), as well assumptions for any additional or sensitivity analysis.	Materials and methods: <i>Selection of eligible instrumental variables, Statistical methods and sensitivity analysis</i>
6a	Statistical methods:	Describe how quantitative variables were handled in the analyses.	Materials and methods: <i>Selection of eligible instrumental variable</i>
6b		Describe how genetic variants were handled in the analyses and, if applicable, how their weights were selected	
6c		Describe the MR estimator and related statistics. Detail the included covariates and, in case of 2-sample MR, whether the same covariate set was used for adjustment in the 2 samples.	Materials and methods: <i>Statistical methods and sensitivity analysis</i>
6d		Explain how missing data were addressed.	
6e		Indicate how multiple testing was addressed (Bonferroni correction)	
7	Assessment of assumptions	Describe any methods or prior knowledge used to assess the assumptions or justify their validity	

8	Sensitivity analyses and additional analyses	Describe any sensitivity analyses or additional analyses performed (eg, comparison of effect estimates from different approaches, independent replication, bias analytic techniques, validation of instruments, simulations).	
9a	Software and preregistration	Name statistical software and package(s), including version and settings used.	
9b		State whether the study protocol and details were preregistered (as well as when and where).	N/A
10a	Descriptive data	Report the numbers of individuals at each stage of included studies and reasons for exclusion. Use of a flow diagram.	Figure 1
10b		Report summary statistics for phenotypic exposure , outcomes, and other relevant variables (eg, means, SDs, proportions).	Materials and methods: <i>Study design, Data sources, Figure 1</i>
10c		If the data sources include meta-analyses of previous studies, provide the assessments of heterogeneity across these studies.	N/A
10d		For 2-sample MR: i. Provide justification of the similarity of the genetic variant–exposure associations between the exposure and outcome samples. ii. Provide information on the number of individuals who overlap between the exposure and outcome studies.	Materials and methods: <i>Selection of eligible instrumental variables</i>
			N/A

11a	Main results	Report the associations between genetic variant and exposure and between genetic variant and outcome, preferably on an interpretable scale.	Results, Table S3
11b		Report MR estimates of the relationship between exposure and outcome and the measures of uncertainty from the MR analysis, on an interpretable scale, such as odds ratio or relative risk per SD difference.	Results-Figure 2-3, Table S4, Table S6
11c		If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period.	N/A
11d		Consider plots to visualize results (eg, forest plot, scatterplot of associations between genetic variants and outcome vs between genetic variants and exposure).	Figure 2-3, Figure S1-2
12a	Assessment of assumptions	Report the assessment of the validity of the assumptions by removing confounders-related SNPs.	Results: <i>Sensitivity analysis</i>
12b		Report any additional statistics (eg, assessments of heterogeneity across genetic variants, such as I^2 , Q statistic).	Results: <i>Sensitivity analysis</i>
13a	Sensitivity analyses and additional analyses	Report any sensitivity analyses to assess the robustness of the main results to violations of the assumptions.	Results: <i>Sensitivity analysis</i>
13b		Report results from other sensitivity analyses or additional analyses	Results: <i>Sensitivity analysis</i>

13c		Report any assessment of the direction of the causal relationship.	Figure 2-3
13d		When relevant, report and compare with estimates from other RCTs and meta-analyses.	N/A
13e		Consider additional plots to visualize results.	All Figure and Table
14	Key results	Summarize key results with reference to study objectives.	Discussion: Paragraph 1
15	Limitations	Discuss limitations of the study, taking into account the validity of the IV assumptions, other sources of potential bias, and imprecision. Discuss both direction and magnitude of any potential bias and any efforts to address them.	Discussion: Paragraph 5
16a	Interpretation	Meaning: Give a cautious overall interpretation of results in the context of their limitations and in comparison with other studies.	Discussion: Paragraph 1-2
16b		Mechanism: Discuss underlying biological mechanisms that could drive a potential causal relationship between the investigated exposure and the outcome, and whether the gene-environment equivalence assumption is reasonable. Use causal language carefully, clarifying that IV estimates may provide causal effects only under certain assumptions.	Discussion
16c		Clinical relevance: Discuss whether the results have clinical or public policy relevance, and to what extent they inform effect sizes of possible interventions.	

17		Discuss the generalizability of the study results (a) to other populations, (b) across other exposure periods/timings, and (c) across other levels of exposure.	
18	Funding	Describe sources of funding and the role of funders in the present study.	Acknowledgment: <i>Funding</i>
19	Data and data sharing	Provide the data used to perform all analyses or report where and how the data can be accessed, and reference these sources in the article.	Materials and methods: <i>Data sources</i>
20	Conflicts of interest	All authors should declare all potential conflicts of interest.	Conflicts of Interest

Three fundamental assumptions

- a. The instrument variables (IVs) must be associated with exposures;
- b. The IVs must not be associated with any confounders, such as age, sex, lifestyle;
- c. The IVs must influence the outcomes only through exposures and not through any direct or alternative pathways.

Table S2. Detailed information of genome-wide association studies included in this study.

Year	Dataset	Trait	Abbreviation	Population	Sample size	Numbers of SNPs	PMID	Author	Consortium
2018	ukb-b-1712	Job involves shift work	JSW	European	263,315	9,851,867		Ben Elsworth	MRC-IEU
2015	ieu-a-7	Coronary heart disease	CHD	Mixed	184,305	9,455,779	26343387	Nikpay	CARDIoGRAMplusC4D
2021	finn-b-E4_DM2	Type 2 diabetes	T2DM	European	215,654	16,380,440			
2021	finn-b-E4_OBESITY	Obesity		European	218,735	16,380,465			
2021	finn-b-I9_HYPTENS	Hypertension		European	218,754	16,380,466			
2013	JFx8ih	Total cholesterol		Mixed	188,577		24097068	Willer	
2013	Z5Cb3y	Low-density lipoprotein cholesterol	LDL	Mixed	188,577		24097068	Willer	
2013	hherZu	Triglyceride		Mixed	188,577		24097068	Willer	
2013	z4b4uv	High-density lipoprotein cholesterol	HDL	Mixed	188,577		24097068	Willer	
2021	MiBioGen	Gut microbiota	GM	European, Hispanic, Middle Eastern, Asian and African	18,340		33462485	Kurilshikov	

Table S3. Information about the selected SNPs associated with JSW.

SNP	chr	pos	effect_allele	other_allele	eaf	samplesize.exposure	beta.exposure	se.exposure	pval.exposure	R2	F
rs666923	1	234812041	C	A	0.207135	263315	0.0141163	0.00283646	6.50E-07	9.40529E-05	24.76766889
rs12129219	1	247622621	C	T	0.207537	263315	0.0128194	0.00287978	8.50E-06	7.52503E-05	19.81588516
rs62172878	2	154602637	C	T	0.076895	263315	0.019206	0.00429974	7.90E-06	7.57672E-05	19.95198732
rs4664365	2	161600498	C	T	0.518708	263315	-0.0102738	0.00230906	8.60E-06	7.51767E-05	19.79650297
rs13009008	2	174043233	G	A	0.671752	263315	-0.0119654	0.00243581	9.00E-07	9.16331E-05	24.13038917
rs10932655	2	217209739	C	A	0.450518	263315	-0.0107063	0.00230369	3.40E-06	8.202E-05	21.59869164
rs10865397	2	73358292	G	A	0.523443	263315	-0.011909	0.00233352	3.30E-07	9.89029E-05	26.04499251
rs73092583	3	71837464	T	C	0.419498	263315	-0.0106678	0.00236436	6.40E-06	7.7306E-05	20.35725536
rs11922926	3	23656565	A	G	0.004871	263315	0.0868543	0.0189282	4.50E-06	7.99565E-05	21.0552653
rs75814777	3	171067183	C	G	0.028444	263315	-0.0323784	0.00688637	2.60E-06	8.39495E-05	22.10684482
rs2087035	3	131264657	C	T	0.169258	263315	-0.0159674	0.00306423	1.90E-07	0.000103111	27.15328581
rs1375563	3	85657946	T	C	0.885203	263315	-0.0172282	0.00362126	2.00E-06	8.59503E-05	22.63378029
rs34038856	3	52263967	A	G	0.049096	263315	-0.02352	0.00530601	9.30E-06	7.46157E-05	19.64876271
rs113510893	4	94636518	C	T	0.068784	263315	0.0207489	0.00462343	7.20E-06	7.64809E-05	20.13994514
rs41534644	5	121800881	C	T	0.146049	263315	-0.0153986	0.003246	2.10E-06	8.5458E-05	22.50412574
rs13159978	5	80547883	A	G	0.083399	263315	0.0187682	0.00414676	6.00E-06	7.7789E-05	20.48444235
rs152603	5	106774922	G	A	0.366346	263315	-0.0113181	0.0023761	1.90E-06	8.61598E-05	22.68894625
rs115496811	5	175952776	T	C	0.039503	263315	-0.0275965	0.00607468	5.50E-06	7.83703E-05	20.63753871
rs76713680	6	105878480	T	C	0.034675	263315	0.0320549	0.00635982	4.60E-07	9.64677E-05	25.40363744
rs1087294	6	24203724	G	T	0.702746	263315	-0.0114844	0.00251637	5.00E-06	7.90966E-05	20.82880358
rs9380970	6	40590738	A	C	0.156953	263315	0.0140895	0.00314703	7.60E-06	7.61168E-05	20.04407865
rs9375656	6	130010372	C	T	0.746128	263315	-0.0118034	0.00263883	7.70E-06	7.59771E-05	20.00728348
rs10282168	7	39437185	A	G	0.351957	263315	-0.0110603	0.00240291	4.20E-06	8.04541E-05	21.18631893
rs1860826	7	2112506	A	G	0.358721	263315	-0.0119023	0.00240053	7.10E-07	9.33537E-05	24.5835281

rs80346402	8	2584778	A	G	0.018327	263315	-0.0394924	0.00890063	9.10E-06	7.47614E-05	19.68712325
rs10739536	9	122151550	T	A	0.698464	263315	-0.0111603	0.00251445	9.10E-06	7.48097E-05	19.69982786
rs2123202	9	28153553	C	A	0.26047	263315	-0.0118602	0.00262893	6.40E-06	7.72888E-05	20.3527305
rs2474711	10	33441017	C	G	0.679375	263315	0.0117616	0.0024578	1.70E-06	8.69614E-05	22.90005009
rs77215157	10	133599654	A	G	0.043115	263315	0.0268539	0.00583403	4.20E-06	8.04576E-05	21.18722701
rs61844343	10	54557687	G	T	0.271581	263315	0.0126239	0.00259585	1.20E-06	8.98076E-05	23.6496439
rs34057425	11	123341589	A	T	0.32332	263315	0.0115364	0.00251462	4.50E-06	7.99255E-05	21.0471154
rs1729200	11	79986182	G	A	0.204588	263315	0.0130309	0.00284574	4.70E-06	7.96248E-05	20.96790733
rs11063070	12	4377716	T	C	0.123618	263315	-0.0162818	0.00347529	2.80E-06	8.3351E-05	21.94923718
rs12811792	12	38054256	T	A	0.168576	263315	-0.0144489	0.0031307	3.90E-06	8.08865E-05	21.30018451
rs4415916	13	114261351	T	G	0.020808	263315	-0.0386079	0.00826928	3.00E-06	8.27762E-05	21.7978503
rs9575634	13	85238702	T	C	0.141606	263315	0.0153421	0.00329452	3.20E-06	8.2352E-05	21.6861283
rs150774726	14	88402313	G	T	0.008599	263315	0.0588643	0.0128172	4.40E-06	8.00953E-05	21.09183411
rs55665482	15	78066376	T	C	0.048328	263315	-0.0251651	0.00539579	3.10E-06	8.25992E-05	21.7512362
rs28613960	16	26213558	A	G	0.454628	263315	-0.0114863	0.00230665	6.40E-07	9.4163E-05	24.79668402
rs62090078	17	74006655	A	G	0.03446	263315	0.0282575	0.00630101	7.30E-06	7.63727E-05	20.11147096
rs950608	17	55329305	A	G	0.251751	263315	-0.0121723	0.00265425	4.50E-06	7.98641E-05	21.03092353
rs57885255	19	768333	C	T	0.018709	263315	0.0419422	0.0090367	3.50E-06	8.18034E-05	21.54167083
rs6039504	20	9547230	T	C	0.163981	263315	-0.0161786	0.00308805	1.60E-07	0.00010423	27.44795098

Table S4. MR-estimated effect of JSW on CHD and risk factors.

Exposure	Outcome	nSNP	Method	beta	SE	OR (95%CI)	p	p-FDR	Horizontal pleiotropy (MR-Egger)			Heterogeneity (Cochran's Q test)			MR-PRESSO			
									Egger intercept	SE	p	Q_MR_Egger	p	Q_IVW	p	p		
JSW	CHD	40	Inverse variance weighted	0.3078	0.1482	1.36 (95%CI 1.02-1.82)	0.04											
			Weighted median	0.2577	0.2031	1.29 (95%CI 0.87-1.93)	0.20											
			Simple mode	0.1613	0.4298	1.18 (95%CI 0.51-2.73)	0.71											
CHD	JSW	39	Inverse variance weighted	-0.0049	0.0054	0.99 (95%CI 0.98-1.01)	0.37											
			Weighted median	-0.0002	0.0072	0.99 (95%CI 0.98-1.01)	0.98											
			Simple mode	0.0058	0.0134	1.00 (95%CI 0.97-1.03)	0.67											
JSW	T2DM	42	Inverse variance weighted	0.4614	0.1701	1.59 (95%CI 1.14-2.21)	0.01	0.03	-0.0032	0.0070	0.65	53.7765	0.07	54.0610	0.08		0.10	
			Weighted median	0.3926	0.2239	1.48 (95%CI 0.95-2.30)	0.08	0.28										
			Simple mode	0.2228	0.4549	1.25 (95%CI 0.51-3.05)	0.63	0.66										
JSW	Obesity	41	Inverse variance weighted	0.3911	0.2731	1.48 (95%CI 0.87-2.53)	0.15	0.25	-0.0058	0.0111	0.60	51.2125	0.09	51.5741	0.10		0.10	
			Weighted median	0.4283	0.3539	1.53 (95%CI 0.77-3.07)	0.23	0.32										
			Simple mode	1.0097	0.7737	2.74 (95%CI 0.60-12.50)	0.20	0.56										
JSW	Hypertension	43	Inverse variance weighted	0.3604	0.1357	1.43 (95%CI 1.10-1.87)	0.01	0.03	-0.0079	0.0055	0.16	44.5664	0.32	46.8023	0.28		0.28	
			Weighted median	0.3449	0.1932	1.41 (95%CI 0.97-2.06)	0.07	0.28										
			Simple mode	1.0870	0.4483	2.97 (95%CI 1.23-7.14)	0.02	0.14										
JSW	TC	11	Inverse variance weighted	0.1943	0.1455	1.21 (95%CI 0.91-1.62)	0.18	0.25	0.0066	0.0076	0.41	4.9540	0.84	5.6929	0.84		0.84	
			Weighted median	0.2378	0.1897	1.27 (95%CI 0.87-1.84)	0.21	0.32										
			Simple mode	0.3720	0.2969	1.45 (95%CI 0.81-2.60)	0.24	0.56										
JSW	LDL	13	Inverse variance weighted	0.2501	0.1390	1.28 (95%CI 0.98-1.69)	0.07	0.17	0.0029	0.0071	0.69	9.0434	0.62	9.2154	0.68		0.71	
			Weighted median	0.2523	0.1860	1.29 (95%CI 0.89-1.85)	0.18	0.32										
			Simple mode	0.3095	0.3048	1.36 (95%CI 0.75-2.48)	0.33	0.58										

JSW	TG	12	Inverse variance weighted	0.1509	0.1589	1.16 (95%CI 0.85-1.59)	0.34	0.34	0.0094	0.0078	0.26	14.5298	0.15	16.6110	0.12	0.13	
			Weighted median	0.1137	0.1786	1.12 (95%CI 0.79-1.59)	0.52	0.52									
			Simple mode	0.1447	0.3195	1.16 (95%CI 0.62-2.16)	0.66	0.66									
JSW	HDL	13	Inverse variance weighted	-0.1360	0.1282	0.87 (95%CI 0.68-1.12)	0.29	0.34	0.0050	0.0067	0.47	10.6535	0.47	11.2197	0.51	0.50	
			Weighted median	-0.1294	0.1804	0.88 (95%CI 0.62-1.25)	0.47	0.52									
			Simple mode	0.1920	0.3483	1.21 (95%CI 0.61-2.40)	0.59	0.66									

CHD: coronary heart disease

JSW: jobs involving shift work

T2DM: type 2 diabetes

TC: total cholesterol

HDL: high-density lipoprotein cholesterol

LDL: low-density lipoprotein cholesterol

TG: triglyceride

Table S5. Multivariable and mediation MR analyses of the causal effect of JSW on CHD mediated by traditional risk factors and gut microbiota.

outcome	id.exposure	exposure	number of variants	IVW			Heterogeneity test		MR-Egger			Heterogeneity test		Mediation effect	Mediation effect	Proportion mediated
				b (95%CI)	se	p	statistic	p	b (95%CI)	se	p	statistic	p	$\beta_1 \times \beta_2$	95%CI	$\beta_1 \times \beta_2 / (\beta_1 \times \beta_2 + \beta_3)$
CHD	ukb-b-1712	JSW	71	0.301 [-0.001, 0.603]	0.154	0.05	73.9735	0.32	0.264 [-0.241, 0.769]	0.257	0.31	73.9371	0.29	0.0406	0.0090, 0.0830	0.118857134
	finn-b- E4_DM2	T2DM	71	0.088 [0.041, 0.135]	0.024	<0.001			0.086 [0.035, 0.138]	0.026	0.00					
		(intercept)							0.000 [-0.005, 0.006]	0.003	0.86					
CHD	ukb-b-1712	JSW	78	0.278 [-0.057, 0.612]	0.171	0.10	98.7714	0.04	0.344 [-0.154, 0.842]	0.254	0.18	98.6058	0.04	0.0483	0.0114, 0.0947	0.148006581
	finn-b- I9_HYPTENS	Hypertension	78	0.134 [0.076, 0.191]	0.029	<0.001			0.135 [0.077, 0.193]	0.030	<0.001					
		(intercept)							-0.001 [-0.006, 0.004]	0.002	0.72					
CHD	ukb-b-1712	JSW	104	0.312 [-0.048, 0.672]	0.184	0.09	#####	0.00	0.353 [-0.154, 0.861]	0.259	0.17	143.8480	0.00			
	finn-b- E4_DM2	T2DM	104	0.069 [0.010, 0.128]	0.030	0.02			0.071 [0.009, 0.132]	0.031	0.02					
	finn-b- I9_HYPTENS	Hypertension		0.123 [0.060, 0.185]	0.032	<0.001			0.123 [0.060, 0.186]	0.032	<0.001					
	(intercept)							0.000 [-0.005, 0.004]	0.002	0.82						
CHD	ukb-b-1712	JSW	45	0.324 [0.005, 0.643]	0.163	0.05	40.2734	0.59	0.228 [-0.398, 0.853]	0.319	0.48	40.1498	0.55	-0.0241	-0.0808, 0.0124	0.069336594
		phylum Actinobacteria	45	-0.063 [-0.158, 0.031]	0.048	0.19			-0.064 [-0.158, 0.030]	0.048	0.18					

		(intercept)							0.001 [-0.005, 0.008]	0.003	0.73					
CHD	ukb-b-1712	JSW	48	0.284 [-0.029, 0.597]	0.160	0.08	37.3520	0.81	0.610 [-0.115, 1.334]	0.370	0.10	36.3960	0.82	0.0116	-0.0252, 0.0581	0.039366282
		class														
		Coriobacteriia	48	0.029 [-0.057, 0.115]	0.044	0.51			0.023 [-0.064, 0.110]	0.044	0.61					
		(intercept)							-0.004 [-0.012, 0.004]	0.004	0.33					
CHD	ukb-b-1712	JSW	48	0.284 [-0.029, 0.597]	0.160	0.08	37.3520	0.81	0.610 [-0.115, 1.334]	0.370	0.10	36.3960	0.82	0.0116	-0.0252, 0.0581	0.039366282
		order														
		Coriobacteriales	48	0.029 [-0.057, 0.115]	0.044	0.51			0.023 [-0.064, 0.110]	0.044	0.61					
		(intercept)							-0.004 [-0.012, 0.004]	0.004	0.33					
CHD	ukb-b-1712	JSW	48	0.284 [-0.029, 0.597]	0.160	0.08	37.3520	0.81	0.610 [-0.115, 1.334]	0.370	0.10	36.3960	0.82	0.0116	-0.0252, 0.0581	0.039366282
		family														
		Coriobacteriaceae	48	0.029 [-0.057, 0.115]	0.044	0.51			0.023 [-0.064, 0.110]	0.044	0.61					
		(intercept)							-0.004 [-0.012, 0.004]	0.004	0.33					
CHD	ukb-b-1712	JSW	41	0.213 [-0.110, 0.537]	0.165	0.20	33.1470	0.73	0.837 [0.109, 1.564]	0.371	0.02	29.6340	0.83	0.0262	-0.0301, 0.0982	0.109612937
		genus														
		<i>Eubacterium</i>	41	0.025 [-0.029, 0.079]	0.027	0.36			0.027 [-0.026, 0.081]	0.027	0.32					
		<i>brachy</i> group														
		(intercept)							-0.008 [-0.016, 0.000]	0.004	0.06					
CHD	ukb-b-1712	JSW	44	0.234 [-0.082, 0.550]	0.161	0.15	29.0741	0.93	0.775 [0.092, 1.458]	0.348	0.03	26.0039	0.97	-0.0229	-0.0840, 0.0185	0.088991755

		genus														
		<i>Ruminococcus</i>	44	0.032 [-0.025, 0.089]	0.029	0.27			0.035 [-0.022, 0.092]	0.029	0.23					
		<i>gnavus</i> group														
		(intercept)							-0.007 [-0.014, 0.001]	0.004	0.08					
CHD	ukb-b-1712	JSW	41	0.289 [-0.031, 0.609]	0.163	0.08	30.3255	0.84	0.158 [-0.595, 0.912]	0.384	0.68	30.1835	0.81	-0.0293	-0.0941, 0.0118	0.091939953
		genus														
		<i>Lachnoclostridium</i>	41	0.078 [-0.029, 0.185]	0.055	0.15			0.073 [-0.038, 0.184]	0.057	0.20					
		(intercept)							0.002 [-0.007, 0.010]	0.004	0.71					
CHD	ukb-b-1712	JSW	44	0.257 [-0.060, 0.574]	0.162	0.11	32.7855	0.85	0.690 [-0.051, 1.431]	0.378	0.07	31.1786	0.87	-0.0148	-0.0875, 0.0520	0.054488765
		genus <i>Roseburia</i>	44	0.023 [-0.076, 0.122]	0.051	0.65			0.033 [-0.067, 0.134]	0.051	0.52					
		(intercept)							-0.005 [-0.014, 0.003]	0.004	0.21					
CHD	ukb-b-1712	JSW	45	0.286 [-0.029, 0.601]	0.161	0.08	35.1942	0.80	-0.116 [-0.829, 0.596]	0.363	0.75	33.6708	0.82	0.0299	-0.0076, 0.0895	0.094770633
		genus														
		<i>Ruminococcus2</i>	45	0.067 [-0.015, 0.150]	0.042	0.11			0.064 [-0.019, 0.146]	0.042	0.13					
		(intercept)							0.005 [-0.003, 0.013]	0.004	0.22					
T2DM	ukb-b-1712	JSW	47	0.312 [-0.119, 0.744]	0.220	0.16	74.6523	0.00	0.842 [0.002, 1.682]	0.429	0.05	71.3125	0.01	-0.0211	-0.0908, 0.0299	0.063269866
		phylum														
		Actinobacteria	47	-0.055 [-0.182, 0.072]	0.065	0.40			-0.048 [-0.174, 0.078]	0.064	0.46					
		(intercept)							-0.007 [-0.016, 0.002]	0.005	0.15					

T2DM	ukb-b-1712	JSW	48	0.311 [-0.101, 0.723]	0.210	0.14	71.8031	0.01	-0.091 [-1.097, 0.915]	0.513	0.86	70.6450	0.01	0.0221	-0.0256, 0.0878	0.066269082
		class	48	0.055 [-0.110, 0.120]	0.059	0.93			0.014 [-0.103, 0.131]	0.060	0.82					
		Coriobacteriia														
		(intercept)							0.005 [-0.006, 0.017]	0.006	0.39					
T2DM	ukb-b-1712	JSW	48	0.311 [-0.101, 0.723]	0.210	0.14	71.8031	0.01	-0.091 [-1.097, 0.915]	0.513	0.86	70.6450	0.01	0.0221	-0.0256, 0.0878	0.066269082
		order	48	0.055 [-0.110, 0.120]	0.059	0.93			0.014 [-0.103, 0.131]	0.060	0.82					
		Coriobacteriales														
		(intercept)							0.005 [-0.006, 0.017]	0.006	0.39					
T2DM	ukb-b-1712	JSW	48	0.311 [-0.101, 0.723]	0.210	0.14	71.8031	0.01	-0.091 [-1.097, 0.915]	0.513	0.86	70.6450	0.01	0.0221	-0.0256, 0.0878	0.066269082
		family	48	0.055 [-0.110, 0.120]	0.059	0.93			0.014 [-0.103, 0.131]	0.060	0.82					
		Coriobacteriaceae														
		(intercept)							0.005 [-0.006, 0.017]	0.006	0.39					
T2DM	ukb-b-1712	JSW	43	0.282 [-0.176, 0.740]	0.234	0.23	73.7647	0.00	0.857 [-0.166, 1.881]	0.522	0.10	71.0774	0.00	-0.0241	-0.1228, 0.0599	0.078804849
		genus	43													
		<i>Eubacterium</i>	43	-0.023 [-0.099, 0.053]	0.039	0.56			-0.024 [-0.100, 0.052]	0.039	0.53					
		<i>brachy</i> group														
		(intercept)							-0.007 [-0.019, 0.004]	0.006	0.22					
T2DM	ukb-b-1712	JSW	45	0.307 [-0.124, 0.738]	0.220	0.16	71.5728	0.00	0.311 [-0.653, 1.274]	0.492	0.53	71.5727	0.00	-0.0414	-0.1335, 0.0169	0.118906346
		genus	45													
		<i>Ruminococcus</i>	45	0.058 [-0.022, 0.138]	0.041	0.15			0.058 [-0.023, 0.140]	0.041	0.16					
		<i>gnavus</i> group														
		(intercept)							0.000 [-0.011, 0.011]	0.005	0.99					

T2DM	ukb-b-1712	JSW	42	0.331 [-0.087, 0.749]	0.213	0.12	60.9646	0.02	-0.064 [-1.085, 0.958]	0.521	0.90	59.9056	0.02	-0.0244	-0.1033, 0.3303	0.068613305
		genus	42	0.065 [-0.081, 0.211]	0.075	0.39			0.044 [-0.110, 0.199]	0.079	0.58					
		<i>Lachnospirillum</i>														
		(intercept)							0.005 [-0.007, 0.017]	0.006	0.41					
T2DM	ukb-b-1712	JSW	45	0.302 [-0.163, 0.767]	0.237	0.20	83.4119	0.00	0.372 [-0.754, 1.497]	0.574	0.52	83.3767	0.00	0.0129	-0.0882, 0.1191	0.04090083
		genus <i>Roseburia</i>	45	-0.020 [-0.170, 0.129]	0.076	0.79			-0.019 [-0.171, 0.134]	0.078	0.81					
		(intercept)							-0.001 [-0.014, 0.012]	0.007	0.89					
T2DM	ukb-b-1712	JSW	46	0.279 [-0.155, 0.713]	0.222	0.21	75.8055	0.00	0.593 [-0.385, 1.571]	0.499	0.24	74.9416	0.00	0.0487	-0.0046, 0.1337	0.148641811
		genus	46	0.109 [-0.001, 0.219]	0.056	0.05			0.116 [0.003, 0.228]	0.057	0.04					
		<i>Ruminococcus2</i>														
		(intercept)							-0.004 [-0.015, 0.007]	0.006	0.48					
Hypertension	ukb-b-1712	JSW	47	0.271 [-0.107, 0.649]	0.193	0.16	73.9889	0.00	0.007 [-0.739, 0.754]	0.381	0.98	72.9177	0.00	-0.0330	-0.1030, 0.0109	0.092300608
		phylum	47	-0.086 [-0.197, 0.026]	0.057	0.13			-0.089 [-0.201, -0.023]	0.057	0.12					
		<i>Actinobacteria</i>														
		(intercept)							0.003 [-0.005, 0.011]	0.004	0.42					
Hypertension	ukb-b-1712	JSW	48	0.262 [-0.168, 0.691]	0.219	0.23	#####	<0.001	-0.600 [-1.620, 0.419]	0.520	0.25	93.8299	<0.001	0.0245	-0.0446, 0.0696	0.10054325
		class	48	0.022 [-0.099, 0.142]	0.061	0.73			0.040 [-0.079, 0.159]	0.061	0.51					
		<i>Coriobacteriia</i>														
		(intercept)							0.011 [-0.001, 0.022]	0.006	0.07					

Hypertension	ukb-b-1712	JSW	48	0.262 [-0.168, 0.691]	0.219	0.23	#####	<0.001	-0.600 [-1.620, 0.419]	0.520	0.25	93.8299	<0.001	0.0245	-0.0446, 0.0696	0.10054325
		order	48	0.022 [-0.099, 0.142]	0.061	0.73			0.040 [-0.079, 0.159]	0.061	0.51					
		Coriobacteriales														
		(intercept)							0.011 [-0.001, 0.022]	0.006	0.07					
Hypertension	ukb-b-1712	JSW	48	0.262 [-0.168, 0.691]	0.219	0.23	#####	<0.001	-0.600 [-1.620, 0.419]	0.520	0.25	93.8299	<0.001	0.0245	-0.0446, 0.0696	0.10054325
		family	48	0.022 [-0.099, 0.142]	0.061	0.73			0.040 [-0.079, 0.159]	0.061	0.51					
		Coriobacteriaceae														
		(intercept)							0.011 [-0.001, 0.022]	0.006	0.07					
Hypertension	ukb-b-1712	JSW	43	0.268 [-0.033, 0.568]	0.153	0.08	54.3254	0.08	0.742 [-0.027, 1.511]	0.392	0.06	51.9542	0.10	-0.0535	-1.3334e-1, - 5.0082e-5	0.16638797
		genus														
		<i>Eubacterium</i>	43	-0.051 [-0.101,-0.001]	0.025	0.05			-0.052 [-0.109, 0.005]	0.029	0.08					
		<i>brachy</i> group														
		(intercept)							-0.006 [-.015, 0.003]	0.004	0.18					
Hypertension	ukb-b-1712	JSW	45	0.272 [-0.022, 0.565]	0.150	0.07	41.8241	0.52	0.027 [-0.622, 0.676]	0.331	0.94	41.1382	0.51	-0.0279	-0.0904, 0.0119	0.09290553
		genus														
		<i>Ruminococcus</i>	45	0.039 [-0.015, 0.094]	0.028	0.16			0.037 [-0.017, 0.092]	0.028	0.18					
		<i>gnavus</i> group														
		(intercept)							0.003 [-0.004, 0.010]	0.004	0.41					
Hypertension	ukb-b-1712	JSW	42	0.268 [-0.029, 0.566]	0.152	0.08	43.9392	0.31	0.288 [-0.483, 1.059]	0.393	0.46	43.9358	0.27	-0.0218	-0.0802, 0.0180	0.075090563

		genus	42	0.058 [-0.046, 0.163]	0.053	0.28			0.059 [-0.058, 0.176]	0.060	0.32					
		<i>Lachnospirillum</i>														
		(intercept)							0.000 [-0.009, 0.009]	0.005	0.96					
Hypertension	ukb-b-1712	JSW	45	0.257 [-0.037, 0.551]	0.150	0.09	54.5771	0.11	-0.299 [-1.078, 0.480]	0.397	0.45	51.6622	0.15	-0.0155	-0.0843, 0.0472	0.056723459
		genus <i>Roseburia</i>	45	0.024 [-0.071, 0.118]	0.048	0.62			0.011 [-0.095, 0.117]	0.054	0.84					
		(intercept)							0.007 [-0.002, 0.016]	0.005	0.12					
Hypertension	ukb-b-1712	JSW	46	0.254 [-0.037, 0.545]	0.148	0.09	53.1198	0.16	0.250 [-0.474, 0.975]	0.370	0.50	53.1197	0.14	0.0089	-0.0272, 0.0526	0.033992504
		genus <i>Ruminococcus2</i>	46	0.020 [-0.054, 0.094]	0.038	0.60			0.020 [-0.064, 0.103]	0.043	0.65					
		(intercept)							0.000 [-0.008, 0.008]	0.004	0.99					

CHD: coronary heart disease

JSW: jobs involving shift work

T2DM: type 2 diabetes

Table S6. MR-estimated effects of JSW on each gut microbiota taxon.

Exposure	Outcome	Nsnp	Inverse variance weighted							Weighted_median							Simple_mode						
			beta	SE	p	OR	CI_low	CI_high	p-FDR	beta	SE	p	OR	CI_low	CI_high	p-FDR	beta	SE	p	OR	CI_low	CI_high	p-FDR
JSW	phylum Actinobacteria id 400	28	0.38	0.19	0.05	1.47	1.01	2.14	0.32	0.23	0.26	0.39	1.26	0.75	2.10	0.70	0.14	0.60	0.82	1.15	0.35	3.74	0.92
JSW	phylum Bacteroidetes id 905	28	-0.11	0.19	0.56	0.90	0.62	1.29	0.61	-0.03	0.26	0.92	0.97	0.58	1.63	0.94	0.30	0.60	0.63	1.34	0.41	4.35	0.92
JSW	phylum Cyanobacteria id 1500	28	0.33	0.31	0.29	1.39	0.76	2.54	0.55	0.53	0.43	0.22	1.70	0.73	3.99	0.70	0.49	0.83	0.56	1.63	0.32	8.33	0.92
JSW	phylum Euryarchaeota id 55	26	0.42	0.47	0.37	1.52	0.61	3.81	0.55	0.05	0.60	0.94	1.05	0.32	3.40	0.94	0.99	1.28	0.45	2.69	0.22	33.01	0.92
JSW	phylum Firmicutes id 1672	28	-0.10	0.19	0.61	0.91	0.63	1.31	0.61	-0.03	0.26	0.91	0.97	0.59	1.61	0.94	0.05	0.55	0.92	1.06	0.36	3.08	0.92
JSW	phylum Lentisphaerae id 2238	27	-0.34	0.37	0.36	0.71	0.35	1.47	0.55	-0.72	0.50	0.15	0.49	0.18	1.29	0.70	-0.93	1.07	0.39	0.40	0.05	3.20	0.92
JSW	phylum Proteobacteria id 2375	28	-0.34	0.19	0.07	0.72	0.50	1.03	0.32	-0.08	0.24	0.75	0.93	0.57	1.49	0.94	0.07	0.52	0.89	1.07	0.39	2.94	0.92
JSW	phylum Tenericutes id 3919	28	0.18	0.26	0.48	1.20	0.72	2.00	0.61	0.34	0.35	0.32	1.41	0.71	2.78	0.70	0.51	0.70	0.48	1.66	0.42	6.58	0.92
JSW	phylum Verrucomicrobia id 3982	28	-0.28	0.22	0.22	0.76	0.49	1.18	0.55	-0.31	0.32	0.34	0.74	0.39	1.37	0.70	0.21	0.65	0.75	1.23	0.35	4.40	0.92
JSW	class Actinobacteria id 419	28	0.09	0.23	0.71	1.09	0.69	1.71	0.94	-0.16	0.28	0.57	0.85	0.49	1.48	0.83	-0.77	0.60	0.21	0.46	0.14	1.51	0.69
JSW	class Alphaproteobacteria id 2379	28	-0.02	0.28	0.94	0.98	0.57	1.68	0.99	-0.01	0.37	0.98	0.99	0.48	2.05	0.98	-0.20	0.71	0.79	0.82	0.20	3.33	0.84
JSW	class Bacilli id 1673	28	0.00	0.19	0.99	1.00	0.69	1.46	0.99	0.06	0.25	0.82	1.06	0.65	1.74	0.98	0.29	0.49	0.56	1.34	0.51	3.51	0.69
JSW	class Bacteroidia id 912	28	-0.11	0.19	0.57	0.90	0.63	1.29	0.83	0.02	0.26	0.93	1.02	0.61	1.72	0.98	0.34	0.56	0.55	1.40	0.47	4.21	0.69
JSW	class Betaproteobacteria id 2867	28	-0.22	0.19	0.25	0.80	0.55	1.17	0.69	-0.28	0.26	0.28	0.76	0.45	1.26	0.59	-0.54	0.51	0.30	0.58	0.22	1.58	0.69
JSW	class Clostridia id 1859	28	0.03	0.19	0.88	1.03	0.72	1.48	0.99	0.25	0.26	0.33	1.28	0.78	2.12	0.59	0.45	0.53	0.40	1.57	0.55	4.47	0.69
JSW	class Coriobacteriia id 809	28	0.40	0.19	0.03	1.49	1.03	2.17	0.55	0.36	0.27	0.18	1.44	0.84	2.45	0.59	0.40	0.59	0.50	1.49	0.47	4.72	0.69
JSW	class Deltaproteobacteria id 3087	28	-0.19	0.22	0.39	0.83	0.54	1.27	0.69	-0.37	0.29	0.21	0.69	0.39	1.22	0.59	-0.56	0.59	0.34	0.57	0.18	1.79	0.69
JSW	class Erysipelotrichia id 2147	28	-0.22	0.21	0.30	0.80	0.53	1.22	0.69	-0.29	0.26	0.27	0.75	0.45	1.25	0.59	-0.36	0.48	0.46	0.70	0.27	1.80	0.69
JSW	class Gammaproteobacteria id 3303	28	-0.33	0.20	0.10	0.72	0.49	1.06	0.69	-0.20	0.27	0.45	0.82	0.49	1.38	0.72	-0.41	0.55	0.46	0.66	0.23	1.93	0.69
JSW	class Lentisphaeria id 2250	27	-0.34	0.37	0.35	0.71	0.34	1.46	0.69	-0.70	0.50	0.16	0.49	0.18	1.33	0.59	-1.02	1.08	0.35	0.36	0.04	2.99	0.69
JSW	class Melainabacteria id 1589	28	0.46	0.38	0.22	1.59	0.76	3.33	0.69	1.03	0.49	0.03	2.80	1.08	7.24	0.55	1.33	0.97	0.18	3.77	0.57	25.01	0.69
JSW	class Methanobacteria id 119	26	0.38	0.44	0.39	1.46	0.62	3.45	0.69	0.19	0.60	0.75	1.21	0.38	3.90	0.98	0.61	1.21	0.62	1.83	0.17	19.73	0.71
JSW	class Mollicutes id 3920	28	0.18	0.26	0.48	1.20	0.72	2.00	0.77	0.34	0.35	0.33	1.41	0.70	2.82	0.59	0.51	0.74	0.50	1.66	0.39	7.10	0.69

JSW	class Negativicutes id 2164	28	0.00	0.19	0.99	1.00	0.70	1.44	0.99	-0.03	0.26	0.90	0.97	0.58	1.61	0.98	-0.10	0.54	0.86	0.91	0.31	2.63	0.86
JSW	class Verrucomicrobiae id 4029	28	-0.33	0.23	0.14	0.72	0.46	1.12	0.69	-0.32	0.31	0.30	0.72	0.39	1.34	0.59	-1.00	0.63	0.12	0.37	0.11	1.26	0.69
JSW	order Actinomycetales id 420	28	0.17	0.28	0.55	1.18	0.68	2.06	0.81	0.22	0.40	0.58	1.25	0.57	2.72	0.89	0.69	0.76	0.37	1.99	0.45	8.78	0.68
JSW	order Bacillales id 1674	26	0.20	0.45	0.66	1.22	0.50	2.97	0.88	0.02	0.64	0.98	1.02	0.29	3.59	0.98	-0.39	1.36	0.78	0.68	0.05	9.69	0.88
JSW	order Bacteroidales id 913	28	-0.11	0.19	0.57	0.90	0.63	1.29	0.81	0.02	0.27	0.93	1.02	0.61	1.72	0.98	0.34	0.60	0.58	1.40	0.43	4.54	0.77
JSW	order Bifidobacteriales id 432	28	0.20	0.24	0.41	1.22	0.76	1.94	0.71	0.20	0.30	0.51	1.22	0.68	2.20	0.85	-0.79	0.71	0.28	0.46	0.11	1.84	0.68
JSW	order Burkholderiales id 2874	28	-0.20	0.19	0.31	0.82	0.56	1.20	0.71	-0.27	0.25	0.28	0.76	0.47	1.24	0.60	-0.62	0.50	0.22	0.54	0.20	1.42	0.68
JSW	order Clostridiales id 1863	28	0.03	0.19	0.88	1.03	0.72	1.48	0.99	0.25	0.26	0.33	1.29	0.78	2.13	0.60	0.45	0.52	0.40	1.57	0.56	4.37	0.68
JSW	order Coriobacteriales id 810	28	0.40	0.19	0.03	1.49	1.03	2.17	0.61	0.36	0.27	0.18	1.44	0.85	2.45	0.60	0.40	0.52	0.45	1.49	0.54	4.15	0.68
JSW	order Desulfovibrionales id 3156	28	-0.19	0.22	0.37	0.82	0.54	1.26	0.71	-0.38	0.28	0.18	0.68	0.39	1.19	0.60	-0.58	0.65	0.38	0.56	0.16	2.00	0.68
JSW	order Enterobacteriales id 3468	28	-0.40	0.22	0.06	0.67	0.44	1.02	0.61	-0.62	0.31	0.04	0.54	0.29	0.99	0.45	-0.68	0.58	0.26	0.51	0.16	1.60	0.68
JSW	order Erysipelotrichales id 2148	28	-0.22	0.21	0.30	0.80	0.53	1.22	0.71	-0.29	0.26	0.27	0.75	0.45	1.25	0.60	-0.36	0.50	0.48	0.70	0.26	1.87	0.68
JSW	order Gastranaerophilales id 1591	28	0.45	0.37	0.22	1.58	0.77	3.24	0.71	1.00	0.47	0.03	2.71	1.07	6.84	0.45	1.31	0.96	0.18	3.71	0.57	24.26	0.68
JSW	order Lactobacillales id 1800	28	0.01	0.19	0.97	1.01	0.69	1.46	0.99	0.07	0.27	0.78	1.08	0.63	1.83	0.98	0.41	0.52	0.44	1.50	0.54	4.18	0.68
JSW	order Methanobacteriales id 120	26	0.38	0.44	0.39	1.46	0.62	3.45	0.71	0.19	0.63	0.76	1.21	0.36	4.13	0.98	0.61	1.28	0.64	1.83	0.15	22.52	0.80
JSW	order MollicutesRF9 id 11579	28	0.22	0.28	0.43	1.25	0.72	2.16	0.71	0.48	0.35	0.17	1.62	0.81	3.26	0.60	0.92	0.73	0.22	2.52	0.60	10.58	0.68
JSW	order NBIn id 3953	27	0.02	0.37	0.95	1.02	0.49	2.12	0.99	0.03	0.51	0.95	1.03	0.38	2.82	0.98	-0.18	1.06	0.87	0.84	0.11	6.62	0.88
JSW	order Pasteurellales id 3688	28	0.05	0.28	0.87	1.05	0.61	1.80	0.99	-0.14	0.39	0.72	0.87	0.40	1.88	0.98	-0.11	0.75	0.88	0.89	0.20	3.89	0.88
JSW	order Rhodospirillales id 2667	28	0.27	0.31	0.39	1.30	0.71	2.39	0.71	0.38	0.39	0.33	1.46	0.68	3.11	0.60	0.94	0.73	0.21	2.55	0.62	10.59	0.68
JSW	order Selenomonadales id 2165	28	0.00	0.19	0.99	1.00	0.70	1.44	0.99	-0.03	0.26	0.90	0.97	0.58	1.62	0.98	-0.10	0.51	0.85	0.91	0.33	2.49	0.88
JSW	order Verrucomicrobiales id 4030	28	-0.33	0.23	0.14	0.72	0.46	1.12	0.71	-0.32	0.31	0.30	0.72	0.39	1.34	0.60	-1.00	0.63	0.13	0.37	0.11	1.27	0.68
JSW	order Victivallales id 2254	27	-0.34	0.37	0.35	0.71	0.34	1.46	0.71	-0.70	0.51	0.17	0.49	0.18	1.35	0.60	-1.02	1.02	0.33	0.36	0.05	2.66	0.68
JSW	family Acidaminococcaceae id 2166	28	0.20	0.22	0.37	1.22	0.79	1.90	0.73	0.18	0.31	0.57	1.20	0.65	2.22	0.87	0.07	0.61	0.91	1.07	0.33	3.53	0.91
JSW	family Actinomycetaceae id 421	28	0.17	0.28	0.55	1.18	0.68	2.06	0.89	0.22	0.41	0.60	1.24	0.55	2.79	0.87	0.72	0.76	0.36	2.05	0.46	9.12	0.80
JSW	family Alcaligenaceae id 2875	28	-0.18	0.19	0.34	0.83	0.57	1.22	0.73	-0.25	0.25	0.31	0.78	0.48	1.26	0.85	-0.41	0.48	0.40	0.66	0.26	1.69	0.80
JSW	family Bacteroidaceae id 917	28	-0.25	0.19	0.18	0.78	0.54	1.12	0.73	-0.01	0.27	0.98	0.99	0.58	1.69	0.98	0.12	0.52	0.81	1.13	0.41	3.15	0.87

JSW	family BacteroidalesS24 7group id 11173	28	0.14	0.28	0.62	1.15	0.66	2.00	0.89	0.33	0.42	0.43	1.39	0.62	3.14	0.85	0.95	0.90	0.30	2.57	0.44	15.05	0.80
JSW	family Bifidobacteriaceae id 433	28	0.20	0.24	0.41	1.22	0.76	1.94	0.73	0.20	0.30	0.50	1.22	0.68	2.18	0.85	-0.79	0.70	0.27	0.46	0.12	1.80	0.80
JSW	family Christensenellaceae id 1866	28	-0.11	0.21	0.61	0.90	0.59	1.36	0.89	-0.21	0.28	0.45	0.81	0.47	1.39	0.85	-0.28	0.54	0.60	0.75	0.26	2.15	0.80
JSW	family Clostridiaceae1 id 1869 family	28	-0.24	0.22	0.27	0.79	0.51	1.21	0.73	-0.08	0.30	0.80	0.93	0.51	1.67	0.88	0.26	0.58	0.65	1.30	0.42	4.04	0.80
JSW	ClostridialesvadinBB60group id 11286	28	-0.01	0.27	0.98	0.99	0.58	1.69	0.98	0.04	0.36	0.91	1.04	0.52	2.10	0.94	-0.27	0.69	0.70	0.77	0.20	2.95	0.83
JSW	family Coriobacteriaceae id 811	28	0.40	0.19	0.03	1.49	1.03	2.17	0.71	0.36	0.27	0.18	1.44	0.84	2.46	0.85	0.40	0.56	0.48	1.49	0.50	4.49	0.80
JSW	family Defluviitaleaceae id 1924	28	0.13	0.28	0.64	1.14	0.66	1.96	0.89	0.34	0.38	0.37	1.40	0.67	2.95	0.85	1.05	0.76	0.17	2.87	0.65	12.61	0.80
JSW	family Desulfovibrionaceae id 3169	28	-0.20	0.22	0.37	0.82	0.53	1.26	0.73	-0.40	0.30	0.19	0.67	0.37	1.21	0.85	-0.55	0.58	0.35	0.58	0.19	1.79	0.80
JSW	family Enterobacteriaceae id 3469	28	-0.40	0.22	0.06	0.67	0.44	1.02	0.71	-0.62	0.31	0.04	0.54	0.29	0.98	0.85	-0.68	0.67	0.32	0.51	0.14	1.88	0.80
JSW	family Erysipelotrichaceae id 2149	28	-0.22	0.21	0.30	0.80	0.53	1.22	0.73	-0.29	0.27	0.28	0.75	0.44	1.27	0.85	-0.36	0.48	0.46	0.70	0.27	1.80	0.80
JSW	family FamilyXI id 1936	22	-0.05	0.59	0.94	0.95	0.30	3.02	0.98	-0.20	0.71	0.78	0.82	0.20	3.31	0.88	1.18	1.72	0.50	3.26	0.11	94.56	0.80
JSW	family FamilyXIII id 1957	28	0.10	0.23	0.67	1.10	0.70	1.73	0.89	0.41	0.30	0.17	1.51	0.84	2.71	0.85	0.99	0.68	0.16	2.69	0.71	10.21	0.80
JSW	family Lachnospiraceae id 1987	28	-0.31	0.19	0.09	0.73	0.51	1.05	0.73	-0.45	0.26	0.08	0.64	0.38	1.06	0.85	-0.46	0.55	0.41	0.63	0.22	1.85	0.80
JSW	family Lactobacillaceae id 1836	27	0.09	0.32	0.79	1.09	0.58	2.03	0.93	0.41	0.41	0.31	1.51	0.68	3.35	0.85	0.38	0.79	0.64	1.46	0.31	6.86	0.80
JSW	family Methanobacteriaceae id 121	26	0.38	0.44	0.39	1.46	0.62	3.45	0.73	0.19	0.61	0.75	1.21	0.37	4.02	0.88	0.61	1.23	0.63	1.83	0.17	20.30	0.80
JSW	family Oxalobacteraceae id 2966	27	0.05	0.38	0.90	1.05	0.50	2.22	0.98	-0.12	0.49	0.80	0.88	0.34	2.32	0.88	-0.93	1.14	0.42	0.39	0.04	3.65	0.80
JSW	family Pasteurellaceae id 3689	28	0.05	0.28	0.87	1.05	0.61	1.80	0.98	-0.14	0.37	0.71	0.87	0.42	1.80	0.88	-0.11	0.76	0.88	0.89	0.20	3.98	0.91
JSW	family Peptococcaceae id 2024 family Peptostreptococcaceae id 2042	28	0.26	0.26	0.32	1.29	0.78	2.14	0.73	0.28	0.34	0.41	1.32	0.68	2.54	0.85	0.16	0.64	0.80	1.17	0.34	4.09	0.87
JSW	family Porphyromonadaceae id 943	28	0.00	0.19	0.98	1.00	0.70	1.45	0.98	0.06	0.26	0.82	1.06	0.64	1.75	0.88	0.25	0.50	0.61	1.29	0.49	3.42	0.80
JSW	family Prevotellaceae id 960	28	-0.09	0.28	0.75	0.91	0.53	1.58	0.92	-0.19	0.32	0.55	0.83	0.44	1.55	0.87	-0.66	0.70	0.36	0.52	0.13	2.05	0.80
JSW	family Rhodospirillaceae id 2717	28	0.25	0.30	0.41	1.28	0.71	2.32	0.73	0.28	0.40	0.48	1.33	0.60	2.91	0.85	0.95	0.80	0.24	2.58	0.54	12.26	0.80

JSW	family Rikenellaceae id 967	28	0.22	0.19	0.24	1.25	0.86	1.81	0.73	-0.06	0.27	0.83	0.94	0.55	1.61	0.88	-0.33	0.56	0.56	0.72	0.24	2.16	0.80
JSW	family Ruminococcaceae id 2050	28	0.39	0.21	0.07	1.47	0.97	2.22	0.71	0.26	0.27	0.34	1.30	0.76	2.20	0.85	0.25	0.51	0.63	1.29	0.47	3.49	0.80
JSW	family Streptococcaceae id 1850	28	-0.08	0.19	0.69	0.93	0.63	1.36	0.89	-0.13	0.27	0.63	0.88	0.51	1.50	0.88	-0.33	0.56	0.56	0.72	0.24	2.15	0.80
JSW	family Veillonellaceae id 2172	28	-0.10	0.20	0.62	0.91	0.61	1.34	0.89	-0.19	0.27	0.49	0.83	0.49	1.41	0.85	-0.20	0.56	0.72	0.82	0.27	2.44	0.83
JSW	family Verrucomicrobiaceae id 4036	28	-0.34	0.23	0.14	0.71	0.46	1.12	0.73	-0.32	0.30	0.29	0.72	0.40	1.31	0.85	-1.00	0.63	0.12	0.37	0.11	1.27	0.80
JSW	family Victivallaceae id 2255	27	0.38	0.41	0.35	1.46	0.66	3.22	0.73	0.55	0.56	0.32	1.74	0.58	5.23	0.85	0.56	1.22	0.65	1.76	0.16	19.31	0.80
JSW	genus Clostridiuminnocuumgroup id 14397	27	0.67	0.39	0.09	1.95	0.90	4.20	0.88	0.22	0.54	0.68	1.25	0.43	3.57	0.94	-0.37	1.03	0.72	0.69	0.09	5.23	0.96
JSW	genus Eubacteriumbrachygroup id 11296	27	1.05	0.40	0.01	2.85	1.30	6.25	0.51	0.70	0.55	0.20	2.02	0.69	5.93	0.94	0.00	1.14	1.00	1.00	0.11	9.35	1.00
JSW	genus Eubacteriumcoprostanoligenesgroup id 11375	28	0.16	0.24	0.52	1.17	0.73	1.88	0.88	-0.06	0.30	0.83	0.94	0.53	1.67	0.95	0.76	0.64	0.24	2.14	0.61	7.51	0.96
JSW	genus Eubacteriumeligensgroup id 14372	28	0.16	0.21	0.43	1.18	0.79	1.77	0.88	-0.01	0.28	0.98	0.99	0.57	1.73	0.99	-0.46	0.60	0.45	0.63	0.20	2.04	0.96
JSW	genus Eubacteriumfissicatena group id 14373	27	-0.45	0.44	0.31	0.64	0.27	1.53	0.88	-0.77	0.60	0.20	0.47	0.14	1.51	0.94	-1.41	1.28	0.28	0.24	0.02	3.02	0.96
JSW	genus Eubacteriumhalli group id 11338	28	0.35	0.19	0.07	1.42	0.97	2.08	0.88	0.35	0.28	0.21	1.42	0.82	2.45	0.94	0.29	0.52	0.58	1.34	0.48	3.69	0.96
JSW	genus Eubacteriumnodatum group id 11297	26	-0.51	0.48	0.29	0.60	0.23	1.53	0.88	-0.03	0.64	0.96	0.97	0.28	3.35	0.99	0.21	1.28	0.87	1.23	0.10	15.05	0.97
JSW	genus Eubacteriumoxidoreducens group id 11339	27	-0.27	0.35	0.44	0.77	0.39	1.51	0.88	-0.50	0.48	0.30	0.61	0.24	1.55	0.94	-0.49	0.92	0.59	0.61	0.10	3.68	0.96

JSW	genus Eubacteriumrectalegroup id 14374	28	-0.21	0.21	0.32	0.81	0.54	1.22	0.88	-0.32	0.27	0.23	0.72	0.42	1.23	0.94	-0.46	0.49	0.35	0.63	0.24	1.64	0.96
JSW	genus Eubacteriumruminantiumgroup id 11340	28	-0.14	0.33	0.67	0.87	0.45	1.66	0.88	-0.22	0.43	0.61	0.80	0.35	1.85	0.94	-1.75	1.03	0.10	0.17	0.02	1.30	0.96
JSW	genus Eubacteriumventriosumgroup id 11341	28	-0.04	0.20	0.85	0.96	0.65	1.43	0.93	-0.21	0.29	0.47	0.81	0.46	1.43	0.94	-0.63	0.55	0.26	0.53	0.18	1.56	0.96
JSW	genus Eubacteriumxylanophilumgroup id 14375	28	-0.34	0.22	0.11	0.71	0.46	1.08	0.88	-0.52	0.30	0.08	0.60	0.33	1.07	0.94	-0.79	0.64	0.22	0.45	0.13	1.58	0.96
JSW	genus Ruminococcusgavreuiiigroup id 11342	28	-0.13	0.22	0.57	0.88	0.57	1.36	0.88	-0.10	0.31	0.74	0.90	0.49	1.65	0.94	-0.73	0.68	0.29	0.48	0.13	1.82	0.96
JSW	genus Ruminococcusgnavusgroup id 14376	27	-0.71	0.36	0.05	0.49	0.24	0.99	0.88	-1.20	0.46	0.01	0.30	0.12	0.75	0.58	-1.50	0.87	0.10	0.22	0.04	1.24	0.96
JSW	genus Ruminococcustorquesgroup id 14377	28	0.11	0.19	0.57	1.12	0.76	1.64	0.88	0.11	0.26	0.68	1.12	0.67	1.87	0.94	-0.05	0.56	0.93	0.95	0.32	2.86	0.98
JSW	genus Actinomyces id 423	28	0.17	0.29	0.56	1.18	0.67	2.08	0.88	0.28	0.40	0.49	1.32	0.60	2.91	0.94	0.41	0.82	0.62	1.51	0.30	7.54	0.96
JSW	genus Adlercreutzia id 812	28	0.55	0.36	0.12	1.74	0.86	3.49	0.88	0.52	0.42	0.22	1.69	0.74	3.87	0.94	0.92	0.91	0.32	2.52	0.42	15.04	0.96
JSW	genus Akkermansia id 4037	28	-0.34	0.23	0.14	0.71	0.45	1.12	0.88	-0.35	0.30	0.25	0.70	0.39	1.28	0.94	-1.01	0.66	0.14	0.37	0.10	1.33	0.96
JSW	genus Alistipes id 968	28	0.13	0.19	0.51	1.13	0.78	1.66	0.88	-0.14	0.27	0.61	0.87	0.51	1.48	0.94	-0.42	0.57	0.47	0.66	0.21	2.01	0.96
JSW	genus Allisonella id 2174	23	-0.76	0.48	0.11	0.47	0.18	1.19	0.88	-0.52	0.63	0.41	0.59	0.17	2.06	0.94	-0.33	1.24	0.79	0.72	0.06	8.10	0.96
JSW	genus Alloprevotella id 961	14	0.16	0.74	0.83	1.17	0.28	4.95	0.93	0.75	0.89	0.40	2.12	0.37	12.05	0.94	1.20	1.45	0.42	3.32	0.19	57.01	0.96
JSW	genus Anaerofilum id 2053	27	-0.17	0.40	0.67	0.84	0.38	1.85	0.88	-0.01	0.55	0.98	0.99	0.33	2.91	0.99	0.57	1.12	0.61	1.77	0.20	15.75	0.96
JSW	genus Anaerostipes id 1991	28	-0.10	0.22	0.66	0.91	0.59	1.40	0.88	-0.08	0.29	0.77	0.92	0.52	1.62	0.94	0.08	0.56	0.89	1.08	0.36	3.24	0.97

JSW	genus Anaerotruncus id 2054	28	-0.23	0.23	0.33	0.80	0.51	1.25	0.88	-0.22	0.31	0.47	0.80	0.44	1.46	0.94	0.54	0.70	0.45	1.71	0.43	6.75	0.96
JSW	genus Bacteroides id 918	28	-0.25	0.19	0.18	0.78	0.54	1.12	0.88	-0.01	0.26	0.98	0.99	0.60	1.65	0.99	0.12	0.55	0.82	1.13	0.38	3.33	0.96
JSW	genus Barnesiella id 944	28	0.35	0.23	0.12	1.42	0.92	2.22	0.88	0.53	0.30	0.07	1.70	0.95	3.04	0.94	0.20	0.60	0.74	1.22	0.38	3.95	0.96
JSW	genus Bifidobacterium id 436	28	0.20	0.23	0.39	1.22	0.78	1.90	0.88	0.19	0.30	0.53	1.21	0.67	2.20	0.94	-0.66	0.63	0.30	0.51	0.15	1.78	0.96
JSW	genus Bilophila id 3170	28	-0.22	0.22	0.31	0.80	0.52	1.23	0.88	-0.21	0.31	0.50	0.81	0.44	1.49	0.94	0.58	0.68	0.40	1.78	0.47	6.78	0.96
JSW	genus Blautia id 1992	28	-0.14	0.19	0.46	0.87	0.60	1.25	0.88	0.10	0.25	0.70	1.10	0.67	1.80	0.94	0.24	0.49	0.63	1.27	0.48	3.36	0.96
JSW	genus Butyricoccus id 2055	28	0.06	0.19	0.75	1.06	0.73	1.55	0.92	0.03	0.26	0.92	1.03	0.62	1.70	0.97	0.11	0.52	0.83	1.12	0.40	3.10	0.96
JSW	genus Butyricimonas id 945	28	0.04	0.24	0.87	1.04	0.65	1.67	0.93	-0.15	0.32	0.64	0.86	0.46	1.60	0.94	-0.20	0.62	0.75	0.82	0.24	2.78	0.96
JSW	genus Butyrivibrio id 1993	26	0.37	0.51	0.46	1.45	0.54	3.92	0.88	0.68	0.67	0.31	1.98	0.54	7.28	0.94	1.00	1.43	0.49	2.72	0.17	44.49	0.96
JSW	genus CandidatusSoleaferrea id 11350	27	-0.06	0.39	0.88	0.94	0.44	2.03	0.93	-0.27	0.46	0.56	0.77	0.31	1.89	0.94	-0.61	0.91	0.51	0.55	0.09	3.26	0.96
JSW	genus Catenibacterium id 2153	23	-0.47	0.48	0.32	0.62	0.24	1.59	0.88	-0.45	0.61	0.46	0.64	0.19	2.10	0.94	-0.59	1.18	0.62	0.56	0.06	5.57	0.96
JSW	genus ChristensenellaceaeR 7group id 11283	28	-0.02	0.22	0.91	0.98	0.64	1.49	0.94	-0.24	0.28	0.39	0.79	0.46	1.36	0.94	-0.26	0.50	0.61	0.77	0.29	2.06	0.96
JSW	genus Clostridiumsensustricto1 id 1873	28	-0.24	0.21	0.26	0.79	0.52	1.19	0.88	-0.09	0.30	0.76	0.91	0.50	1.64	0.94	0.25	0.60	0.68	1.28	0.40	4.14	0.96
JSW	genus Collinsella id 815	28	0.33	0.21	0.12	1.39	0.92	2.09	0.88	0.50	0.29	0.08	1.65	0.94	2.91	0.94	0.70	0.61	0.26	2.01	0.61	6.60	0.96
JSW	genus Coprobacter id 949	27	-0.13	0.31	0.67	0.88	0.48	1.60	0.88	-0.58	0.43	0.18	0.56	0.24	1.32	0.94	-0.81	0.92	0.39	0.45	0.07	2.69	0.96
JSW	genus Coprococcus1 id 11301	28	0.23	0.21	0.28	1.26	0.83	1.92	0.88	-0.08	0.28	0.79	0.93	0.53	1.62	0.94	-0.10	0.53	0.85	0.91	0.32	2.55	0.96
JSW	genus Coprococcus2 id 11302	28	-0.10	0.27	0.72	0.91	0.54	1.53	0.91	0.40	0.34	0.25	1.49	0.76	2.92	0.94	0.37	0.69	0.60	1.45	0.37	5.61	0.96
JSW	genus Coprococcus3 id 11303	28	0.14	0.20	0.49	1.15	0.78	1.70	0.88	0.21	0.30	0.48	1.24	0.69	2.22	0.94	0.35	0.58	0.55	1.42	0.46	4.41	0.96
JSW	genus DefluviitaleaceaeUCG011 id 11287	28	0.15	0.28	0.58	1.16	0.68	2.00	0.88	0.35	0.39	0.37	1.42	0.66	3.02	0.94	1.12	0.78	0.16	3.06	0.67	14.01	0.96
JSW	genus Desulfovibrio id 3173	28	-0.04	0.29	0.88	0.96	0.55	1.67	0.93	-0.39	0.39	0.32	0.67	0.31	1.46	0.94	-0.98	0.88	0.27	0.38	0.07	2.09	0.96
JSW	genus Dialister id 2183	28	-0.22	0.27	0.42	0.80	0.47	1.37	0.88	-0.23	0.34	0.50	0.79	0.40	1.55	0.94	-0.26	0.67	0.70	0.77	0.21	2.85	0.96
JSW	genus Dorea id 1997	28	0.05	0.19	0.79	1.05	0.73	1.53	0.92	0.07	0.26	0.77	1.08	0.65	1.80	0.94	-0.58	0.60	0.34	0.56	0.17	1.80	0.96

JSW	genus Eggerthella id 819	27	0.21	0.35	0.55	1.23	0.62	2.45	0.88	-0.03	0.48	0.95	0.97	0.38	2.47	0.99	-0.09	0.94	0.92	0.91	0.14	5.80	0.98
JSW	genus Eisenbergiella id 11304	27	-0.19	0.42	0.66	0.83	0.37	1.89	0.88	-0.52	0.49	0.29	0.60	0.23	1.57	0.94	-0.80	0.94	0.40	0.45	0.07	2.81	0.96
JSW	genus Enterothabdis id 820	28	0.27	0.30	0.37	1.31	0.73	2.36	0.88	-0.18	0.42	0.67	0.84	0.37	1.92	0.94	-0.65	0.86	0.46	0.52	0.10	2.85	0.96
JSW	genus Erysipelatoclostridium id 11381	28	-0.18	0.25	0.47	0.83	0.51	1.37	0.88	-0.12	0.35	0.73	0.89	0.44	1.77	0.94	-0.35	0.82	0.67	0.70	0.14	3.54	0.96
JSW	genus ErysipelotrichaceaeUCG003 id 11384	28	-0.24	0.22	0.27	0.79	0.52	1.21	0.88	-0.19	0.29	0.51	0.83	0.47	1.45	0.94	-0.24	0.57	0.67	0.78	0.25	2.42	0.96
JSW	genus Escherichia Shigella id 3504	28	-0.26	0.24	0.29	0.77	0.48	1.24	0.88	-0.28	0.34	0.41	0.76	0.39	1.47	0.94	-0.42	0.72	0.56	0.66	0.16	2.69	0.96
JSW	genus Faecalibacterium id 2057	28	0.05	0.19	0.79	1.05	0.73	1.52	0.92	0.04	0.26	0.88	1.04	0.62	1.73	0.96	0.10	0.50	0.84	1.11	0.42	2.96	0.96
JSW	genus FamilyXIIIAD3011group id 11293	28	0.16	0.22	0.47	1.17	0.77	1.78	0.88	0.20	0.30	0.51	1.22	0.68	2.20	0.94	0.35	0.62	0.58	1.42	0.42	4.78	0.96
JSW	genus FamilyXIIIUCG001 id 11294	28	-0.17	0.24	0.48	0.84	0.53	1.35	0.88	0.16	0.33	0.63	1.17	0.61	2.24	0.94	0.43	0.73	0.57	1.53	0.36	6.44	0.96
JSW	genus Flavonifactor id 2059	28	0.10	0.26	0.70	1.11	0.66	1.86	0.90	0.16	0.34	0.64	1.18	0.60	2.30	0.94	0.24	0.61	0.69	1.28	0.39	4.21	0.96
JSW	genus Fusicatenibacter id 11305	28	-0.13	0.21	0.52	0.88	0.59	1.31	0.88	-0.03	0.29	0.91	0.97	0.55	1.70	0.97	0.03	0.56	0.96	1.03	0.34	3.11	0.98
JSW	genus Gordonibacter id 821	27	0.39	0.41	0.35	1.47	0.66	3.30	0.88	0.44	0.58	0.45	1.55	0.50	4.84	0.94	0.75	1.17	0.52	2.12	0.22	20.86	0.96
JSW	genus Haemophilus id 3698	28	0.11	0.26	0.68	1.12	0.67	1.87	0.89	0.15	0.37	0.69	1.16	0.57	2.37	0.94	0.67	0.74	0.37	1.96	0.46	8.41	0.96
JSW	genus Holdemanella id 11393	28	-0.08	0.29	0.77	0.92	0.52	1.63	0.92	0.00	0.41	1.00	1.00	0.45	2.22	1.00	0.05	0.85	0.96	1.05	0.20	5.50	0.98
JSW	genus Holdemanella id 2157	27	-0.15	0.26	0.57	0.86	0.51	1.45	0.88	-0.17	0.38	0.66	0.84	0.40	1.78	0.94	0.02	0.74	0.98	1.02	0.24	4.38	0.98
JSW	genus Howardella id 2000	27	0.30	0.41	0.47	1.35	0.60	3.01	0.88	0.60	0.60	0.31	1.83	0.56	5.92	0.94	1.34	1.16	0.26	3.83	0.40	37.10	0.96
JSW	genus Hungatella id 11306	27	0.36	0.39	0.36	1.44	0.67	3.09	0.88	0.87	0.54	0.11	2.39	0.83	6.90	0.94	1.14	1.02	0.27	3.11	0.42	22.87	0.96
JSW	genus Intestinibacter id 11345	28	0.07	0.23	0.76	1.07	0.69	1.67	0.92	-0.21	0.31	0.50	0.81	0.44	1.50	0.94	-0.38	0.65	0.56	0.68	0.19	2.44	0.96
JSW	genus Intestinimonas id 2062	28	0.41	0.23	0.08	1.50	0.96	2.35	0.88	0.08	0.30	0.80	1.08	0.60	1.96	0.94	-0.30	0.60	0.63	0.74	0.23	2.41	0.96
JSW	genus Lachnoclostridium id 11308	28	-0.38	0.19	0.05	0.69	0.48	0.99	0.88	-0.42	0.27	0.11	0.66	0.39	1.11	0.94	-0.82	0.55	0.15	0.44	0.15	1.29	0.96
JSW	genus Lachnospira id 2004	28	-0.36	0.20	0.07	0.70	0.48	1.03	0.88	-0.09	0.27	0.74	0.92	0.54	1.54	0.94	0.14	0.50	0.79	1.15	0.43	3.03	0.96

	genus																						
JSW	LachnospiraceaeFCS020group id 11314	28	-0.30	0.23	0.20	0.74	0.47	1.17	0.88	-0.33	0.30	0.28	0.72	0.40	1.30	0.94	-0.38	0.64	0.56	0.68	0.20	2.40	0.96
	genus																						
JSW	LachnospiraceaeNC2004group id 11316	27	0.22	0.32	0.49	1.24	0.67	2.33	0.88	0.29	0.42	0.49	1.34	0.59	3.08	0.94	0.30	0.82	0.72	1.35	0.27	6.67	0.96
	genus																						
JSW	LachnospiraceaeND3007group id 11317	28	-0.18	0.20	0.37	0.83	0.56	1.24	0.88	-0.24	0.26	0.37	0.79	0.47	1.33	0.94	-0.43	0.54	0.43	0.65	0.23	1.87	0.96
	genus																						
JSW	LachnospiraceaeNK4A136group id 11319	28	-0.12	0.19	0.52	0.88	0.61	1.29	0.88	-0.24	0.27	0.37	0.78	0.46	1.33	0.94	-0.55	0.52	0.30	0.58	0.21	1.59	0.96
	genus LachnospiraceaeUCG001 id 11321	28	-0.24	0.25	0.34	0.79	0.49	1.28	0.88	0.06	0.34	0.87	1.06	0.54	2.07	0.96	0.15	0.62	0.81	1.17	0.35	3.91	0.96
	genus LachnospiraceaeUCG004 id 11324	28	-0.30	0.23	0.19	0.74	0.47	1.16	0.88	-0.35	0.31	0.26	0.71	0.39	1.29	0.94	-0.19	0.56	0.73	0.83	0.28	2.46	0.96
	genus LachnospiraceaeUCG008 id 11328	27	0.47	0.30	0.12	1.60	0.88	2.88	0.88	0.91	0.43	0.03	2.48	1.07	5.76	0.94	1.02	0.80	0.21	2.78	0.58	13.41	0.96
	genus LachnospiraceaeUCG010 id 11330	28	-0.09	0.22	0.66	0.91	0.59	1.40	0.88	-0.08	0.30	0.79	0.92	0.52	1.65	0.94	-0.13	0.59	0.83	0.88	0.27	2.82	0.96
JSW	genus Lactobacillus id 1837	27	0.06	0.32	0.86	1.06	0.56	1.99	0.93	0.38	0.43	0.38	1.46	0.63	3.40	0.94	0.10	0.76	0.90	1.10	0.25	4.89	0.97
JSW	genus Lactococcus id 1851	27	-0.22	0.40	0.59	0.81	0.37	1.76	0.88	-0.60	0.57	0.29	0.55	0.18	1.68	0.94	-1.33	1.15	0.26	0.27	0.03	2.54	0.96
JSW	genus Marvinbryantia id 2005	28	-0.05	0.23	0.82	0.95	0.61	1.48	0.93	-0.15	0.34	0.66	0.86	0.44	1.68	0.94	-0.41	0.71	0.57	0.66	0.16	2.68	0.96
JSW	genus Methanobrevibacter id 123	26	0.35	0.45	0.43	1.42	0.59	3.44	0.88	-0.14	0.63	0.83	0.87	0.26	2.97	0.95	-0.54	1.39	0.70	0.59	0.04	8.86	0.96
JSW	genus Odoribacter id 952	28	-0.04	0.22	0.85	0.96	0.62	1.48	0.93	0.29	0.30	0.32	1.34	0.75	2.40	0.94	0.60	0.48	0.22	1.82	0.71	4.62	0.96
JSW	genus Olsenella id 822	27	0.44	0.46	0.33	1.56	0.63	3.81	0.88	-0.32	0.59	0.59	0.73	0.23	2.33	0.94	-1.37	1.20	0.26	0.25	0.02	2.67	0.96

JSW	genus Oscillibacter id 2063	28	0.03	0.28	0.92	1.03	0.59	1.79	0.94	-0.07	0.36	0.84	0.93	0.46	1.90	0.95	-0.39	0.73	0.59	0.67	0.16	2.83	0.96
JSW	genus Oscillospira id 2064	28	0.03	0.25	0.90	1.03	0.63	1.68	0.94	0.08	0.34	0.81	1.09	0.56	2.12	0.94	0.84	0.70	0.24	2.31	0.58	9.09	0.96
JSW	genus Oxalobacter id 2978	27	0.11	0.38	0.78	1.11	0.52	2.36	0.92	0.26	0.52	0.61	1.30	0.47	3.58	0.94	1.13	1.14	0.33	3.08	0.33	28.77	0.96
JSW	genus Parabacteroides id 954	28	0.09	0.19	0.65	1.09	0.75	1.59	0.88	0.12	0.28	0.67	1.13	0.66	1.93	0.94	0.86	0.57	0.14	2.37	0.77	7.24	0.96
JSW	genus Paraprevotella id 962	28	-0.09	0.31	0.78	0.92	0.50	1.67	0.92	0.22	0.41	0.60	1.24	0.55	2.79	0.94	0.57	0.80	0.48	1.77	0.37	8.42	0.96
JSW	genus Parasutterella id 2892	28	-0.23	0.24	0.32	0.79	0.50	1.26	0.88	-0.24	0.32	0.46	0.79	0.42	1.48	0.94	-0.20	0.66	0.77	0.82	0.22	3.00	0.96
JSW	genus Peptococcus id 2037	27	0.51	0.39	0.19	1.67	0.77	3.61	0.88	0.39	0.49	0.43	1.47	0.57	3.81	0.94	0.26	1.05	0.81	1.30	0.16	10.19	0.96
JSW	genus Phascolarctobacterium id 2168	28	0.15	0.24	0.53	1.16	0.73	1.86	0.88	0.36	0.33	0.27	1.44	0.76	2.73	0.94	0.70	0.59	0.25	2.02	0.63	6.43	0.96
JSW	genus Prevotella7 id 11182	26	0.25	0.43	0.56	1.29	0.55	3.01	0.88	0.46	0.61	0.45	1.58	0.48	5.21	0.94	1.32	1.27	0.31	3.76	0.31	45.55	0.96
JSW	genus Prevotella9 id 11183	28	0.03	0.33	0.93	1.03	0.54	1.98	0.94	-0.28	0.38	0.46	0.75	0.36	1.59	0.94	-0.71	0.79	0.37	0.49	0.10	2.30	0.96
JSW	genus RikenellaceaeRC9gutgroup id 11191	26	0.46	0.44	0.31	1.58	0.66	3.77	0.88	0.09	0.60	0.89	1.09	0.34	3.53	0.96	-0.27	1.18	0.82	0.77	0.08	7.81	0.96
JSW	genus Romboutsia id 11347	28	0.20	0.21	0.33	1.23	0.81	1.85	0.88	0.28	0.30	0.34	1.33	0.74	2.38	0.94	0.42	0.61	0.49	1.53	0.46	5.03	0.96
JSW	genus Roseburia id 2012	28	-0.64	0.19	0.00	0.53	0.36	0.76	0.07	-0.81	0.25	0.00	0.44	0.27	0.73	0.17	-0.92	0.48	0.07	0.40	0.15	1.03	0.96
JSW	genus Ruminiclostridium5 id 11355	28	0.05	0.19	0.80	1.05	0.72	1.52	0.93	0.19	0.26	0.47	1.21	0.72	2.03	0.94	0.31	0.57	0.59	1.36	0.45	4.13	0.96
JSW	genus Ruminiclostridium6 id 11356	28	0.29	0.26	0.28	1.33	0.80	2.24	0.88	0.14	0.33	0.66	1.15	0.61	2.18	0.94	-0.12	0.64	0.86	0.89	0.25	3.14	0.96
JSW	genus Ruminiclostridium9 id 11357	28	-0.11	0.19	0.58	0.90	0.61	1.31	0.88	-0.28	0.26	0.29	0.76	0.45	1.27	0.94	-0.50	0.49	0.32	0.61	0.23	1.60	0.96
JSW	genus RuminococcaceaeNK4A214group id 11358	28	0.18	0.20	0.37	1.20	0.81	1.79	0.88	0.06	0.28	0.84	1.06	0.61	1.85	0.95	-0.29	0.55	0.61	0.75	0.26	2.20	0.96
JSW	genus RuminococcaceaeUCG002 id 11360	28	-0.07	0.19	0.73	0.93	0.64	1.37	0.91	-0.07	0.27	0.79	0.93	0.55	1.57	0.94	-0.06	0.63	0.92	0.94	0.27	3.25	0.98
JSW	genus RuminococcaceaeUCG003 id 11361	28	0.01	0.21	0.97	1.01	0.67	1.52	0.97	-0.24	0.30	0.43	0.79	0.44	1.42	0.94	-0.25	0.66	0.71	0.78	0.22	2.83	0.96

JSW	genus RuminococcaceaeUCG004 id 11362	28	-0.05	0.26	0.84	0.95	0.57	1.59	0.93	0.10	0.34	0.78	1.10	0.56	2.16	0.94	0.09	0.68	0.90	1.09	0.29	4.17	0.97
JSW	genus RuminococcaceaeUCG005 id 11363	28	0.18	0.20	0.35	1.20	0.82	1.77	0.88	0.23	0.27	0.40	1.25	0.74	2.11	0.94	0.51	0.53	0.34	1.66	0.59	4.66	0.96
JSW	genus RuminococcaceaeUCG009 id 11366	27	0.20	0.31	0.52	1.22	0.67	2.23	0.88	-0.07	0.43	0.88	0.94	0.40	2.17	0.96	-0.33	0.88	0.71	0.72	0.13	4.02	0.96
JSW	genus RuminococcaceaeUCG010 id 11367	28	-0.01	0.23	0.96	0.99	0.63	1.56	0.96	-0.10	0.31	0.74	0.90	0.49	1.65	0.94	-0.04	0.65	0.95	0.96	0.27	3.43	0.98
JSW	genus RuminococcaceaeUCG011 id 11368	27	0.23	0.48	0.63	1.26	0.49	3.22	0.88	-0.60	0.61	0.32	0.55	0.17	1.80	0.94	-1.10	1.36	0.42	0.33	0.02	4.78	0.96
JSW	genus RuminococcaceaeUCG013 id 11370	28	0.12	0.21	0.56	1.13	0.75	1.70	0.88	0.13	0.28	0.65	1.13	0.65	1.97	0.94	0.10	0.51	0.85	1.10	0.40	3.03	0.96
JSW	genus RuminococcaceaeUCG014 id 11371	21	0.13	0.29	0.65	1.14	0.65	2.00	0.88	-0.25	0.35	0.46	0.78	0.39	1.53	0.94	-0.23	0.75	0.77	0.80	0.19	3.44	0.96
JSW	genus Ruminococcus1 id 11373	28	-0.24	0.19	0.21	0.78	0.54	1.15	0.88	-0.36	0.27	0.17	0.70	0.41	1.17	0.94	-0.97	0.63	0.14	0.38	0.11	1.31	0.96
JSW	genus Ruminococcus2 id 11374	28	0.45	0.21	0.04	1.56	1.03	2.38	0.88	0.36	0.29	0.21	1.44	0.82	2.52	0.94	0.63	0.57	0.27	1.88	0.62	5.73	0.96
JSW	genus Sellimonas id 14369	26	-0.53	0.45	0.25	0.59	0.24	1.44	0.88	0.17	0.63	0.79	1.19	0.34	4.09	0.94	0.89	1.40	0.53	2.44	0.16	37.65	0.96
JSW	genus Senegalimassilia id 11160	28	0.14	0.32	0.66	1.15	0.61	2.15	0.88	0.28	0.43	0.52	1.32	0.57	3.07	0.94	0.85	0.93	0.37	2.33	0.38	14.35	0.96
JSW	genus Slackia id 825	27	-0.08	0.32	0.81	0.93	0.49	1.74	0.93	0.56	0.45	0.21	1.76	0.72	4.27	0.94	0.74	0.95	0.44	2.09	0.33	13.43	0.96
JSW	genus Streptococcus id 1853	28	-0.09	0.20	0.66	0.92	0.62	1.35	0.88	-0.08	0.28	0.76	0.92	0.54	1.58	0.94	-0.05	0.58	0.94	0.96	0.30	3.00	0.98
JSW	genus Subdoligranulum id 2070	28	0.24	0.25	0.33	1.28	0.78	2.08	0.88	0.03	0.30	0.91	1.03	0.58	1.84	0.97	1.23	0.72	0.10	3.41	0.83	14.05	0.96
JSW	genus Sutterella id 2896	28	-0.18	0.22	0.42	0.84	0.55	1.29	0.88	-0.19	0.30	0.54	0.83	0.46	1.50	0.94	-0.14	0.60	0.81	0.87	0.27	2.79	0.96
JSW	genus Terrisporobacter id 11348	28	0.13	0.35	0.71	1.14	0.57	2.27	0.91	-0.40	0.45	0.37	0.67	0.28	1.62	0.94	-0.99	0.78	0.22	0.37	0.08	1.72	0.96
JSW	genus Turicibacter id 2162	28	0.17	0.28	0.55	1.19	0.68	2.07	0.88	0.29	0.39	0.46	1.33	0.63	2.83	0.94	0.48	0.73	0.51	1.62	0.39	6.77	0.96
JSW	genus Tyzzerella3 id 11335	27	0.24	0.35	0.48	1.28	0.65	2.52	0.88	0.48	0.48	0.32	1.61	0.63	4.10	0.94	1.33	1.03	0.21	3.77	0.50	28.65	0.96
JSW	genus Veillonella id 2198	27	-0.48	0.31	0.12	0.62	0.34	1.13	0.88	-0.51	0.38	0.18	0.60	0.28	1.27	0.94	-0.91	0.71	0.21	0.40	0.10	1.63	0.96

JSW	genus Victivallis id 2256	22	0.23	0.48	0.63	1.26	0.49	3.24	0.88	-0.32	0.69	0.64	0.72	0.19	2.81	0.94	-1.23	1.35	0.37	0.29	0.02	4.16	0.96
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JSW: jobs involving shift work

Table S7. Sensitivity analysis of the MR analysis of the causal effect of JSW on gut microbiota.

Exposure	Outcome	nSNP	Horizontal pleiotropy (MR-Egger)			Heterogeneity (Cochran's Q test)				MR-PRESSO
			Egger intercept	SE	p	Q_MR_Egger	p	Q_IVW	p	p
JSW	phylum Actinobacteria	28	-0.002796196	0.013912626	0.84	28.51573226	0.33	28.56003	0.38	0.38
JSW	class Coriobacteriia	28	-0.019893025	0.013384701	0.15	25.15848073	0.51	27.36742	0.44	0.44
JSW	order Coriobacteriales	28	-0.019893025	0.013384701	0.15	25.15848073	0.51	27.36742	0.44	0.46
JSW	family Coriobacteriaceae	28	-0.019893025	0.013384701	0.15	25.15848073	0.51	27.36742	0.44	0.46
JSW	genus <i>Eubacteriumbrachy</i> group	27	-0.019296882	0.029801414	0.52	18.99217137	0.80	19.41145	0.82	0.81
JSW	genus <i>Ruminococcusgnavus</i> group	27	0.005017939	0.02721106	0.86	33.25543714	0.12	33.30067	0.15	0.16
JSW	genus <i>Lachnoclostridium</i>	28	0.008625679	0.013310645	0.52	21.64226319	0.71	22.0622	0.73	0.76
JSW	genus <i>Roseburia</i>	28	-0.02289201	0.013327094	0.10	12.57190291	0.99	15.52241	0.96	0.97
JSW	genus <i>Ruminococcus2</i>	28	0.04630657	0.014354722	0.00	19.59460449	0.81	30.00089	0.31	0.34

JSW: jobs involving shift work

Figure S1. Scatter plots and leave-one-out stability test results of the causal estimates of exposure (JSW) on outcomes (coronary heart disease, diabetes, and hypertension). **Panel A.** Scatter plot of the causal estimates of exposure (JSW) on coronary heart disease; **Panel B.** scatter plot of the causal estimates of exposure (JSW) on type 2 diabetes; **Panel C.** scatter plot of the causal estimates of exposure (JSW) on hypertension); **Panel D.** leave-one-out stability test results for the causal estimates of exposure (JSW) on coronary heart disease; **Panel E.** Leave-one-out stability test results for the causal estimates of exposure (JSW) on type 2 diabetes; **Panel F.** Leave-one-out stability test results for the causal estimates of exposure (JSW) on hypertension. JSW: jobs involving shift work.

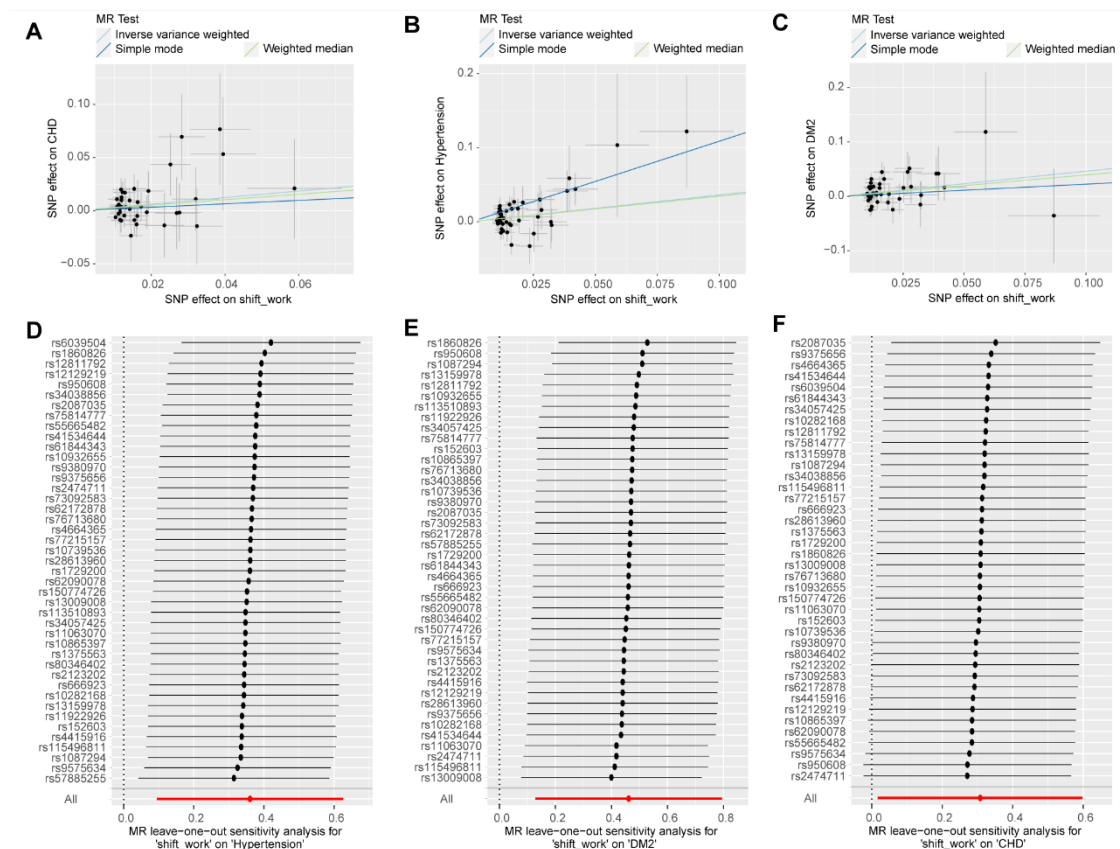


Figure S2. Scatter plots and leave-one-out stability test results for the causal estimates of exposure (JSW) on gut microbiota. **Panel A-I.** Scatter plots of the causal estimates of exposure (JSW) on nine significant gut microbiota taxa; **Panel J-R.** leave-one-out stability test results for the causal estimates of exposure (JSW) on the nine significant gut microbiota taxa. JSW: jobs involving shift work.

