Supplementary Table 1. Two-sample Mendelian randomization of the effects of gut microbiota on endometriosis.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	ıtercept, S	ntercept, *P*	Global Test	stortion Test
nily *Peptostreptococcac*	Endometriosis	19	0.161	0.060	**0.008**	21.183	0.270	0.138	0.076	0.071	0.173	0.165	0.310	-0.001	0.012	0.938	0.288	NA
Family *Prevotellaceae*	Endometriosis	20	0.198	0.072	**0.006**	30.228	**0.049**	0.192	0.082	**0.020**	0.338	0.257	0.205	-0.010	0.018	0.576	**0.035**	0.304
Genus *Anaerotruncus*	Endometriosis	13	0.244	0.086	**0.005**	16.045	0.189	0.271	0.099	**0.006**	0.083	0.258	0.753	0.012	0.017	0.520	0.227	NA
Genus *Holdemania*	Endometriosis	14	-0.137	0.058	**0.017**	15.065	0.303	-0.121	0.072	0.092	-0.241	0.174	0.191	0.011	0.017	0.535	0.218	NA
nknown genus (id.1000	Endometriosis	15	-0.149	0.054	**0.005**	12.584	0.559	-0.172	0.078	**0.027**	-0.110	0.146	0.466	-0.004	0.013	0.780	0.561	NA
Propionic acid	Endometriosis	3	-0.091	0.034	**0.007**	1.088	0.580	-0.068	0.043	0.114	-0.107	0.048	0.271	0.009	0.020	0.732	NA	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 2. Two-sample Mendelian randomization of the effects of gut microbiota on adenomyosis.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
Lentisph	denomyos	13	-0.151	0.071	**0.033**	10.513	0.571	-0.141	0.098	0.152	-0.133	0.225	0.567	-0.003	0.029	0.933	0.652	NA
r Victival	denomyos	13	-0.151	0.071	**0.033**	10.513	0.571	-0.141	0.101	0.164	-0.133	0.225	0.567	-0.003	0.029	0.933	0.629	NA
Prevotel	denomyos	20	0.255	0.103	**0.013**	15.828	0.669	0.147	0.138	0.287	0.192	0.358	0.599	0.005	0.025	0.856	0.618	NA
s Anaero	denomyos	11	-0.189	0.082	**0.022**	9.272	0.507	-0.229	0.113	**0.042**	-0.089	0.453	0.849	-0.011	0.050	0.828	0.500	NA
s Anaeros	denomyos	13	-0.296	0.139	**0.033**	5.519	0.938	-0.324	0.180	0.072	-0.550	0.501	0.296	0.017	0.032	0.608	0.902	NA
n genus (	denomyos	15	-0.192	0.096	**0.045**	11.747	0.627	-0.253	0.133	0.057	-0.118	0.262	0.661	-0.007	0.024	0.766	0.741	NA
own gen	denomyos	13	-0.306	0.089	**0.001**	10.898	0.538	-0.324	0.124	**0.009**	-0.499	0.332	0.162	0.020	0.033	0.560	0.517	NA
opionic a	denomyos	3	-0.167	0.061	**0.007**	0.557	0.757	-0.149	0.076	**0.050**	-0.120	0.088	0.403	-0.026	0.035	0.598	NA	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 3. Two-sample Mendelian randomization of the effects of gut microbiota on inflammatory diseases of the cervix.

			Inverse variance weighted			Heterogeneity		Weighted median			MR Egger						MR-PRESSO	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
: *Pasteure*	diseases	17	-0.355	0.135	**0.009**	13.460	0.639	-0.399	0.189	**0.035**	-0.379	0.411	0.371	0.002	0.033	0.952	0.744	NA
Pasteure	diseases	17	-0.355	0.135	**0.009**	13.460	0.639	-0.399	0.193	**0.039**	-0.379	0.411	0.371	0.002	0.033	0.952	0.736	NA
enus *Blau*	diseases	12	0.512	0.240	**0.033**	13.845	0.242	0.352	0.303	0.245	1.127	0.602	0.091	-0.047	0.042	0.293	0.277	NA
s *Haemop*	diseases	9	-0.494	0.162	**0.002**	9.218	0.324	-0.560	0.219	**0.010**	-1.020	0.335	**0.019**	0.070	0.040	0.122	0.532	NA
piraceae (	diseases	12	-0.462	0.234	**0.048**	19.549	0.052	-0.304	0.248	0.220	-0.999	0.619	0.137	0.043	0.046	0.370	0.147	NA
piraceae (	diseases	3	0.986	0.412	**0.017**	1.772	0.412	1.118	0.527	**0.034**	1.939	9.183	0.868	-0.056	0.540	0.934	NA	NA
us *Prevote*	diseases	11	-0.2249	0.10603	**0.034**	10.783	0.375	-0.219	0.143	0.124	-0.424	0.648	0.529	0.028	0.090	0.762	0.495	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 4. Two-sample Mendelian randomization of the effects of gut microbiota on inflammatory diseases of the uterus.

			Inverse variance weighted			Heterogeneity		Weighted median			MR Egger						MR-PRESSO	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
n *Proteob*	diseases	15	-0.338	0.137	**0.013**	7.023	0.934	-0.334	0.182	0.067	-0.227	0.541	0.682	-0.006	0.029	0.835	0.555	NA
rium (fiss	diseases	9	0.255	0.082	**0.002**	7.083	0.528	0.179	0.107	0.095	0.166	0.426	0.709	0.012	0.055	0.838	0.567	NA
terium (n	diseases	8	-0.382	0.170	**0.025**	3.617	0.823	-0.353	0.223	0.114	-0.745	0.621	0.275	0.024	0.039	0.565	0.343	NA
s *Desulfov*	diseases	10	0.238	0.117	**0.042**	4.642	0.864	0.274	0.154	0.076	0.030	0.345	0.933	0.022	0.034	0.540	0.736	NA
uminiclos	diseases	14	0.247	0.121	**0.041**	13.468	0.412	0.176	0.172	0.307	0.072	0.300	0.815	0.016	0.026	0.533	0.463	NA
nown gen	diseases	9	0.235	0.113	**0.037**	5.278	0.727	0.324	0.153	**0.034**	0.374	0.310	0.267	-0.015	0.032	0.645	0.713	NA
droxybuty	diseases	4	0.242	0.082	**0.003**	2.359	0.501	0.304	0.106	**0.004**	0.596	0.462	0.326	-0.084	0.108	0.519	0.167	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 5. Two-sample Mendelian randomization of the effects of gut microbiota on female infertility.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
Coproco	ale infert	8	0.182	0.088	**0.039**	5.030	0.656	0.143	0.115	0.213	0.089	0.695	0.903	0.007	0.050	0.897	0.095	NA
s *Desulfo*	ale infert	10	-0.161	0.071	**0.022**	7.251	0.611	-0.135	0.098	0.167	-0.280	0.209	0.217	0.012	0.020	0.563	0.670	NA
Faecaliba	ale infert	10	0.211	0.087	**0.015**	12.712	0.176	0.349	0.104	**0.001**	0.421	0.157	**0.028**	-0.026	0.016	0.157	0.133	NA
XIII (A L	ale infert	13	-0.198	0.075	**0.009**	11.482	0.488	-0.151	0.103	0.141	-0.612	0.359	0.117	0.034	0.029	0.264	0.525	NA
s *Holdem*	ale infert	14	-0.125	0.063	**0.046**	15.163	0.297	-0.064	0.081	0.425	-0.183	0.192	0.358	0.006	0.018	0.752	0.511	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 6. Two-sample Mendelian randomization of the effects of gut microbiota on dysplasia of female genital tract.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
etaproteo	of female	9	0.280	0.107	**0.009**	4.579	0.802	0.232	0.150	0.122	0.081	0.223	0.728	0.017	0.016	0.341	0.902	NA
Lactobac	of female	9	0.201	0.073	**0.006**	4.830	0.776	0.270	0.101	**0.007**	0.426	0.190	0.060	-0.027	0.021	0.241	0.427	NA
ium (rum	of female	18	-0.125	0.052	**0.016**	13.855	0.677	-0.072	0.071	0.313	-0.200	0.174	0.269	0.007	0.017	0.661	0.742	NA
erium ven	of female	15	0.182	0.092	**0.048**	16.910	0.261	0.158	0.122	0.195	0.586	0.410	0.176	-0.031	0.031	0.330	0.211	NA
'ethanobr	of female	6	-0.139	0.070	**0.048**	1.866	0.867	-0.141	0.090	0.118	-0.124	0.264	0.664	-0.002	0.038	0.955	0.895	NA
Senegalin	of female	5	-0.334	0.166	**0.044**	9.525	**0.049**	-0.264	0.164	0.108	-0.978	0.645	0.227	0.060	0.058	0.378	**0.042**	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 7. Two-sample Mendelian randomization of the effects of gut microbiota on cervical dysplasia.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
etaproteo	ical dysp	9	0.265	0.115	**0.022**	6.275	0.616	0.281	0.150	0.062	0.004	0.239	0.988	0.022	0.018	0.253	0.823	NA
Lactobac	ical dysp	9	0.166	0.079	**0.035**	4.055	0.852	0.258	0.105	**0.014**	0.453	0.204	0.062	-0.035	0.023	0.171	0.494	NA
rium ven	ical dysp	15	0.232	0.097	**0.017**	16.349	0.293	0.140	0.123	0.257	0.635	0.434	0.167	-0.031	0.032	0.358	0.229	NA
Senegalin	ical dysp	5	-0.380	0.157	**0.016**	7.441	0.114	-0.338	0.172	**0.049**	-0.999	0.611	0.200	0.058	0.055	0.372	**0.047**	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 8. Two-sample Mendelian randomization of the effects of gut microbiota on prolapse and hernia of ovary and fallopian tube.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
s *Holdem*	a of ovary	14	-0.403	0.177	**0.023**	12.175	0.513	-0.351	0.233	0.132	-0.056	0.521	0.916	-0.036	0.050	0.492	0.535	NA
s *Parasutt*	a of ovary	14	0.405	0.206	**0.049**	16.731	0.212	0.626	0.267	**0.019**	0.810	0.578	0.187	-0.035	0.047	0.466	0.251	NA
own gen	a of ovary	10	-0.507	0.227	**0.025**	9.381	0.403	-0.306	0.293	0.296	-1.373	0.780	0.116	0.080	0.069	0.280	0.519	NA
own gen	a of ovary	15	-0.461	0.203	**0.023**	10.669	0.712	-0.281	0.286	0.327	-0.722	1.024	0.493	0.021	0.081	0.799	0.254	NA
Tyrosine	a of ovary	8	-0.059	0.028	**0.037**	9.740	0.204	-0.066	0.030	**0.026**	-0.080	0.035	0.063	0.030	0.029	0.354		NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 9. Two-sample Mendelian randomization of the effects of gut microbiota on polyp of the female genital tract.

			Inverse variance weighted			Heterogeneity		Weighted median			MR Egger						MR-PRESSO	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
eltaproteo	e female	9	0.204	0.103	**0.049**	5.767	0.673	0.180	0.139	0.195	0.434	0.492	0.407	-0.014	0.029	0.647	0.829	NA
Enterobac	e female	13	-0.245	0.088	**0.005**	16.005	0.191	-0.205	0.107	0.054	-0.290	0.536	0.599	0.003	0.035	0.934	0.236	NA
Enterobac	e female	13	-0.245	0.088	**0.005**	16.005	0.191	-0.205	0.104	**0.047**	-0.290	0.536	0.599	0.003	0.035	0.934	0.231	NA
Streptoco	e female	11	-0.194	0.091	**0.032**	5.597	0.848	-0.196	0.114	0.086	-0.319	0.297	0.311	0.009	0.020	0.669	0.931	NA
ococcus (t	e female	7	-0.330	0.116	**0.005**	1.894	0.929	-0.321	0.151	**0.033**	-0.008	0.351	0.982	-0.023	0.024	0.376	0.754	NA
us *Roseb*	p of the u	14	0.349	0.166	**0.036**	6.221	0.938	0.415	0.227	0.068	0.270	0.505	0.603	0.006	0.036	0.871	0.885	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 10. Two-sample Mendelian randomization of the effects of gut microbiota on uterine fibroids.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
ophyrom	erine fibro	18	0.112	0.056	**0.044**	21.713	0.196	0.151	0.071	**0.032**	0.088	0.189	0.648	0.002	0.011	0.895	0.227	NA
us *Bacter*	erine fibro	7	0.168	0.074	**0.023**	6.416	0.378	0.230	0.098	**0.019**	0.931	0.356	**0.048**	-0.050	0.023	0.081	0.625	NA
Enterorh	erine fibro	6	-0.159	0.054	**0.003**	2.375	0.795	-0.160	0.074	**0.030**	-0.250	0.144	0.157	0.013	0.019	0.532	0.317	NA
Gordoni	erine fibro	10	0.070	0.034	**0.041**	12.291	0.197	0.044	0.040	0.273	0.174	0.141	0.254	-0.016	0.021	0.470	0.107	NA
us *Howar*	erine fibro	9	-0.060	0.029	**0.036**	6.745	0.564	-0.069	0.038	0.073	-0.204	0.115	0.118	0.023	0.018	0.235	0.533	NA
nospirace	erine fibro	10	0.086	0.041	**0.036**	10.597	0.304	0.057	0.051	0.265	0.114	0.220	0.618	-0.003	0.023	0.898	0.415	NA
us *Turicib*	erine fibro	9	0.118	0.050	**0.018**	9.169	0.328	0.163	0.062	**0.009**	0.299	0.204	0.187	-0.019	0.021	0.391	0.251	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 11. Two-sample Mendelian randomization of the effects of gut microbiota on cervical erosion and ectropion.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
piraceae (	osion and	12	0.948	0.262	**0.000**	3.527	0.982	0.901	0.342	**0.009**	1.110	0.690	0.138	-0.013	0.051	0.805	0.952	NA
nospiracea	osion and	10	-0.514	0.207	**0.013**	8.196	0.515	-0.706	0.295	**0.017**	-2.352	1.056	0.057	0.194	0.110	0.114	0.484	NA
Betaine	osion and	11	0.160	0.071	**0.024**	9.072	0.525	0.136	0.102	0.184	0.137	0.131	0.322	0.008	0.037	0.839	0.504	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 12. Two-sample Mendelian randomization of the effects of gut microbiota on excessive, freguent, and irrelgular menstruation.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
n *Lentispi*	t, and irre	15	-0.060	0.029	**0.037**	17.199	0.246	-0.058	0.037	0.112	-0.016	0.103	0.879	-0.005	0.012	0.660	0.246	NA
ily *Family*	t, and irre	20	0.087	0.042	**0.038**	17.208	0.576	0.077	0.059	0.190	0.174	0.110	0.129	-0.007	0.008	0.400	0.666	NA
ıs *Coprob*	t, and irre	10	0.106	0.038	**0.006**	5.664	0.773	0.091	0.052	0.082	0.002	0.143	0.987	0.011	0.015	0.474	0.201	NA
enus *Dor*	t, and irre	10	0.128	0.063	**0.041**	8.190	0.515	0.154	0.085	0.072	0.142	0.177	0.444	-0.001	0.012	0.934	0.472	NA
Fusicaten	t, and irre	18	-0.120	0.046	**0.010**	13.893	0.675	-0.129	0.066	0.052	-0.259	0.174	0.155	0.010	0.012	0.415	0.659	NA
uminiclos	t, and irre	11	0.179	0.058	**0.002**	5.391	0.864	0.242	0.077	**0.002**	0.095	0.243	0.706	0.005	0.015	0.728	0.075	NA
ıococcace	t, and irre	11	-0.131	0.065	**0.043**	14.426	0.154	-0.121	0.076	0.110	-0.095	0.197	0.641	-0.003	0.015	0.848	0.316	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 13. Two-sample Mendelian randomization of the effects of gut microbiota on oligomenorrhea.

			Inverse variance weighted			Heterogeneity		Weighted median			MR Egger						MR-PRESSO	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
n *Bactero*	gomenorr	17	0.791	0.246	**0.001**	14.379	0.571	0.813	0.332	**0.014**	1.490	0.614	**0.028**	-0.048	0.039	0.233	0.460	NA
Verrucon	gomenorr	11	0.641	0.280	**0.022**	10.735	0.379	0.538	0.392	0.170	0.236	0.989	0.817	0.033	0.076	0.678	0.481	NA
s *Bactero*	gomenorr	17	0.609	0.250	**0.015**	11.090	0.804	0.780	0.348	**0.025**	1.026	0.646	0.133	-0.028	0.040	0.494	0.459	NA
etaproteoi	gomenorr	9	0.604	0.293	**0.039**	4.613	0.798	0.476	0.406	0.241	1.209	0.587	0.079	-0.053	0.045	0.274	0.242	NA
: *Bacteroi*	gomenorr	17	0.609	0.250	**0.015**	11.090	0.804	0.780	0.352	**0.027**	1.026	0.646	0.133	-0.028	0.040	0.494	0.450	NA
Fusicaten	gomenorr	18	0.587	0.234	**0.012**	12.738	0.754	0.176	0.330	0.594	0.385	0.872	0.665	0.014	0.059	0.813	0.813	NA
Intestinii	gomenorr	16	0.531	0.241	**0.028**	22.171	0.103	0.087	0.305	0.776	1.360	0.651	0.055	-0.076	0.056	0.193	0.075	NA
iococcace	gomenorr	11	-0.467	0.219	**0.033**	6.112	0.806	-0.589	0.291	**0.043**	-0.772	1.222	0.543	0.026	0.102	0.805	0.865	NA
nown gen	gomenorr	13	-0.527	0.220	**0.017**	8.715	0.727	-0.730	0.300	**0.015**	-0.549	0.628	0.401	0.002	0.058	0.971	0.794	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 14. Two-sample Mendelian randomization of the effects of gut microbiota on polycystic ovary syndrome.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
etaproteo	ic ovary s	9	0.616	0.277	**0.026**	4.478	0.812	0.586	0.404	0.147	0.471	0.574	0.439	0.012	0.042	0.780	0.724	NA
ss *Clostri*	ic ovary s	15	-0.493	0.245	**0.044**	4.600	0.991	-0.728	0.314	**0.020**	-0.055	1.285	0.966	-0.027	0.078	0.734	0.996	NA
ius *Biloph*	ic ovary s	13	-0.737	0.291	**0.011**	19.967	0.068	-0.723	0.345	**0.036**	-0.054	1.473	0.971	-0.051	0.107	0.645	**0.046**	NA
ridium se	ic ovary s	7	0.546	0.265	**0.039**	6.243	0.397	0.356	0.345	0.301	0.417	0.743	0.599	0.014	0.074	0.858	0.453	NA
ıs *Holdem*	ic ovary s	14	-0.438	0.174	**0.012**	10.546	0.649	-0.320	0.233	0.169	-0.487	0.512	0.361	0.005	0.049	0.922	0.646	NA
Tryptopha	ic ovary s	3	-0.396	0.159	**0.013**	0.774	0.679	-0.480	0.205	0.019	-1.997	2.655	0.589	0.284	0.469	0.654	NA	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 15. Two-sample Mendelian randomization of the effects of gut microbiota on precocious puberty.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
roidales (	ocious pu	12	-1.075	0.518	**0.038**	9.587	0.568	-1.204	0.708	0.089	-1.155	1.390	0.425	0.009	0.144	0.952	0.612	NA
ıs Eggertl	ocious pu	10	1.057	0.497	**0.033**	3.804	0.924	1.400	0.659	**0.034**	1.636	2.298	0.497	-0.065	0.252	0.803	0.929	NA
scherichia	ocious pu	10	2.198	0.777	**0.005**	5.716	0.768	1.642	1.075	0.127	2.661	2.402	0.300	-0.037	0.180	0.844	0.704	NA
ıospiracec	ocious pu	12	1.665	0.761	**0.029**	7.610	0.748	1.521	0.990	0.124	4.317	3.174	0.204	-0.175	0.204	0.409	0.748	NA
ıococcace	ocious pu	11	-1.868	0.775	**0.016**	5.846	0.828	-2.212	1.044	**0.034**	-3.880	2.225	0.115	0.165	0.171	0.360	0.664	NA
ıown gen	ocious pu	12	1.201	0.532	**0.024**	8.732	0.647	0.858	0.736	0.244	0.896	1.727	0.615	0.030	0.162	0.857	0.645	NA
Betaine	ocious pu	11	0.357	0.181	**0.048**	10.473	0.400	0.415	0.240	0.083	0.641	0.326	0.081	-0.098	0.093	0.323	0.501	NA
ıenylalani	ocious pu	7	-0.522	0.207	**0.012**	3.449	0.751	-0.401	0.262	0.125	-0.211	0.315	0.532	-0.133	0.102	0.247	0.826	NA
opionic a	ocious pu	3	1.003	0.335	**0.003**	1.357	0.507	0.830	0.451	0.066	0.611	0.477	0.422	0.227	0.196	0.455	NA	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 16. Two-sample Mendelian randomization of the effects of gut microbiota on primary ovary failure.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	tercept, S	ntercept, *P*	Global Test	ortion Te
cterium (	ry ovary	15	-0.766	0.349	**0.028**	13.539	0.485	-1.030	0.492	**0.036**	-0.901	0.744	0.247	0.012	0.058	0.840	0.495	NA
rium (ven	ry ovary	15	-0.831	0.371	**0.025**	10.510	0.724	-0.538	0.494	0.276	-0.014	1.653	0.993	-0.063	0.124	0.620	0.753	NA
scherichia	ry ovary	10	-0.883	0.432	**0.041**	7.303	0.606	-0.516	0.567	0.363	-0.522	1.342	0.708	-0.028	0.100	0.784	0.485	NA
us *Prevote*	ry ovary	11	-0.496	0.219	**0.023**	5.572	0.850	-0.602	0.281	**0.032**	-0.937	1.269	0.479	0.062	0.177	0.733	0.886	NA
n genus (	ry ovary	15	0.827	0.301	**0.006**	11.842	0.619	0.731	0.444	0.100	0.401	0.824	0.635	0.042	0.075	0.588	0.142	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 17. Two-sample Mendelian randomization of the effects of gut microbiota on amenorrhea.

			Inverse variance weighted			**Heterogeneity**		**Weighted median**			**MR Egger**						**MR-PRESSO**	
Exposure	Outcomes	nSNP	β	SE	*P*	Q	*P*	β	SE	*P*	β	SE	*P*	Intercept	itercept, S	ntercept, *P*	Global Test	ortion Te
Enterobac	menorrhe	13	-0.428	0.187	**0.022**	12.824	0.382	-0.488	0.241	**0.043**	-0.834	1.133	0.477	0.027	0.073	0.723	0.403	NA
Enterobac	menorrhe	13	-0.428	0.187	**0.022**	12.824	0.382	-0.488	0.250	0.051	-0.834	1.133	0.477	0.027	0.073	0.723	0.403	NA
Streptoco	menorrhe	11	-0.573	0.216	**0.008**	2.327	0.993	-0.576	0.274	**0.036**	-0.923	0.708	0.225	0.024	0.047	0.617	0.867	NA
cterium (	menorrhe	15	0.348	0.155	**0.024**	10.978	0.688	0.526	0.221	**0.017**	0.615	0.324	0.080	-0.024	0.025	0.365	0.704	NA
ococcus (	menorrhe	11	-0.255	0.125	**0.041**	6.011	0.814	-0.295	0.169	0.081	-0.428	0.599	0.492	0.019	0.066	0.774	0.810	NA
Anaerotr	menorrhe	13	0.595	0.225	**0.008**	17.580	0.129	0.479	0.271	0.078	1.214	0.656	0.091	-0.045	0.045	0.337	0.285	NA
Butyrici	menorrhe	13	0.377	0.174	**0.030**	14.205	0.288	0.351	0.230	0.127	0.009	0.634	0.989	0.033	0.054	0.557	0.340	NA
us *Roseb*	menorrhe	14	-0.440	0.186	**0.018**	10.842	0.624	-0.428	0.256	0.094	-0.766	0.573	0.206	0.025	0.041	0.559	0.513	NA
uminiclos	menorrhe	7	-0.541	0.262	**0.039**	2.236	0.897	-0.468	0.336	0.164	-0.342	1.192	0.786	-0.013	0.078	0.871	0.801	NA

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.

Supplementary Table 18. Two-sample Mendelian randomization after removing outliers identified in MR-PRESSO outlier test.

				Inverse variance weighted				**Heterogeneity**			**Weighted median**				**MR Egger**					
Exposure	Outcomes	nSNP		β	SE	*P*		Q	*P*		β	SE	*P*		β	SE	*P*	Intercept	itercept, S	ntercept, *P*
Prevotel	idometrio	19		0.155	0.059	**0.009**		17.625	0.481		0.179	0.080	**0.026**		0.199	0.207	0.350	-0.003	0.014	0.826

Abbreviations: nSNP, number of single-nucleotide polymorphisms; SE, standard error; MR, Mendelian randomization; MR-PRESSO, Mendelian randomization pleiotropy residual sum and outlier.