

The role of the gut-joint axis in the care of psoriatic arthritis: a two-sample bidirectional Mendelian randomization study

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Supplementary Table 1 Instrumental variables used in MR analysis of the association between PSA and gut microbiota.

Bacterial taxa (outcome)	SNP	EAE	OAE	EAO	OAO	Exposure (psoriatic arthritis)			Outcome (Bacteria)			F
						Beta	Se	pval	Beta	Se	pval	
family Clostridiaceae1	rs11085727	C	T	C	T	-0.186	2.939E-02	2.627E-10	-0.001	1.331E-02	9.506E-01	40.052
family Clostridiaceae1	rs11758312	C	A	C	A	0.237	2.536E-02	8.815E-21	0.002	1.193E-02	8.459E-01	87.337
family Clostridiaceae1	rs11773159	A	C	A	C	0.153	3.224E-02	1.963E-06	0.010	1.476E-02	4.731E-01	22.521
family Clostridiaceae1	rs12203031	C	T	C	T	-0.164	3.296E-02	6.608E-07	-0.019	1.695E-02	2.672E-01	24.758
family Clostridiaceae1	rs12458499	A	C	A	C	-0.143	3.178E-02	7.209E-06	-0.012	1.458E-02	3.972E-01	20.247
family Clostridiaceae1	rs12485562	T	C	T	C	-0.136	3.001E-02	6.092E-06	-0.010	1.469E-02	4.841E-01	20.537
family Clostridiaceae1	rs1579218	A	G	A	G	-0.160	3.019E-02	1.098E-07	-0.003	1.696E-02	5.181E-01	28.088
family Clostridiaceae1	rs16839196	T	C	T	C	-0.173	3.271E-02	1.286E-07	-0.008	1.587E-02	6.403E-01	27.972
family Clostridiaceae1	rs16952374	A	G	A	G	0.172	3.866E-02	8.726E-06	-0.011	2.714E-02	6.693E-01	19.794
family Clostridiaceae1	rs17837468	A	G	A	G	0.201	4.456E-02	6.702E-06	-0.007	1.847E-02	6.551E-01	20.347
family	rs1812491	G	A	G	A	0.132	2.612E-02	4.298E-07	-0.001	1.260E-02	8.898E-01	25.539

Clostridiaceae1													
family	rs1832741	C	T	C	T	0.120	2.527E-02	2.215E-06	-0.003	1.192E-02	8.169E-01	22.550	
Clostridiaceae1													
family	rs2250140	T	C	T	C	0.128	2.523E-02	4.162E-07	0.002	1.190E-02	8.573E-01	25.739	
Clostridiaceae1													
family	rs2523589	G	T	G	T	-0.293	2.493E-02	6.369E-32	-0.002	1.208E-02	8.879E-01	138.131	
Clostridiaceae1													
family	rs2546890	A	G	A	G	-0.228	2.592E-02	1.235E-18	-0.002	1.190E-02	8.263E-01	77.375	
Clostridiaceae1													
family	rs28998802	G	A	G	A	0.210	3.123E-02	1.855E-11	0.008	1.780E-02	6.043E-01	45.216	
Clostridiaceae1													
family	rs33980500	C	T	C	T	0.241	4.546E-02	1.152E-07	-0.009	2.291E-02	6.384E-01	28.104	
Clostridiaceae1													
family	rs34473406	T	G	T	G	0.223	4.772E-02	3.112E-06	0.018	2.387E-02	5.266E-01	21.838	
Clostridiaceae1													
family	rs3954248	G	T	G	T	-0.130	2.534E-02	2.995E-07	-0.011	1.200E-02	3.607E-01	26.319	
Clostridiaceae1													
family	rs4713636	G	A	G	A	0.139	2.636E-02	1.233E-07	0.009	1.360E-02	5.514E-01	27.806	
Clostridiaceae1													
family	rs57922664	G	A	G	A	0.158	3.557E-02	9.482E-06	-0.003	2.105E-02	7.814E-01	19.731	
Clostridiaceae1													
family	rs62443225	G	A	G	A	0.234	4.502E-02	2.036E-07	-0.017	2.297E-02	5.430E-01	27.016	
Clostridiaceae1													
family	rs674451	T	C	T	C	0.170	2.607E-02	7.145E-11	0.010	1.268E-02	4.488E-01	42.522	
Clostridiaceae1													
family	rs6966660	C	T	C	T	-0.151	2.537E-02	2.704E-09	-0.005	1.219E-02	6.827E-01	35.425	

Clostridiaceae1													
family	rs7177110	G	A	G	A	-0.134	2.869E-02	3.120E-06	0.002	1.440E-02	9.247E-01	21.815	
Clostridiaceae1													
family	rs7194171	C	T	C	T	-0.156	3.378E-02	3.634E-06	-0.013	1.499E-02	3.969E-01	21.327	
Clostridiaceae1													
family	rs75257908	C	T	C	T	0.309	4.314E-02	7.437E-13	0.009	2.058E-02	7.446E-01	51.305	
Clostridiaceae1													
family	rs76076434	G	A	G	A	-0.227	4.620E-02	8.708E-07	0.009	1.995E-02	6.674E-01	24.142	
Clostridiaceae1													
family	rs78376604	C	A	C	A	0.264	5.514E-02	1.656E-06	0.018	2.381E-02	4.059E-01	22.923	
Clostridiaceae1													
family	rs7989997	A	G	A	G	-0.136	2.969E-02	4.795E-06	0.001	1.389E-02	9.059E-01	20.983	
Clostridiaceae1													
family	rs847	T	C	T	C	0.186	2.671E-02	3.528E-12	0.008	1.423E-02	5.780E-01	48.493	
Clostridiaceae1													
family	rs8904	G	A	G	A	-0.170	2.616E-02	8.582E-11	-0.008	1.221E-02	4.985E-01	42.230	
Clostridiaceae1													
family	rs9461693	G	A	G	A	0.609	2.597E-02	1.219E-121	0.018	1.347E-02	1.954E-01	549.909	
Clostridiaceae1													
family	rs11085727	C	T	C	T	-0.186	2.939E-02	2.630E-10	-0.024	1.755E-02	1.738E-01	40.052	
Defluviitaleaceae													
family	rs11758312	C	A	C	A	0.237	2.536E-02	8.810E-21	0.006	1.567E-02	6.918E-01	87.337	
Defluviitaleaceae													
family	rs11773159	A	C	A	C	0.153	3.224E-02	1.960E-06	0.019	1.887E-02	3.080E-01	22.521	
Defluviitaleaceae													
family	rs12130556	G	A	G	A	0.130	2.772E-02	2.720E-06	-0.005	1.609E-02	7.375E-01	21.994	

Defluviitaleaceae													
family	rs12203031	C	T	C	T	-0.164	3.296E-02	6.610E-07	0.026	2.190E-02	2.764E-01	24.758	
Defluviitaleaceae													
family	rs12458499	A	C	A	C	-0.143	3.178E-02	7.210E-06	-0.015	1.930E-02	5.002E-01	20.247	
Defluviitaleaceae													
family	rs12485562	T	C	T	C	-0.136	3.001E-02	6.090E-06	0.009	1.908E-02	6.631E-01	20.537	
Defluviitaleaceae													
family	rs13181047	T	G	T	G	-0.115	2.540E-02	5.960E-06	-0.005	1.576E-02	7.616E-01	20.499	
Defluviitaleaceae													
family	rs16839196	T	C	T	C	-0.173	3.271E-02	1.290E-07	-0.015	2.099E-02	4.583E-01	27.972	
Defluviitaleaceae													
family	rs16870824	A	G	A	G	-0.137	3.006E-02	5.420E-06	-0.014	1.955E-02	4.825E-01	20.771	
Defluviitaleaceae													
family	rs16952374	A	G	A	G	0.172	3.866E-02	8.730E-06	-0.019	3.715E-02	5.811E-01	19.794	
Defluviitaleaceae													
family	rs1812491	G	A	G	A	0.132	2.612E-02	4.300E-07	0.018	1.666E-02	2.779E-01	25.539	
Defluviitaleaceae													
family	rs1832741	C	T	C	T	0.120	2.527E-02	2.210E-06	0.011	1.570E-02	5.066E-01	22.550	
Defluviitaleaceae													
family	rs2250140	T	C	T	C	0.128	2.523E-02	4.160E-07	-0.014	1.567E-02	3.682E-01	25.739	
Defluviitaleaceae													
family	rs2523589	G	T	G	T	-0.293	2.493E-02	6.370E-32	-0.011	1.584E-02	4.796E-01	138.131	
Defluviitaleaceae													
family	rs2546890	A	G	A	G	-0.228	2.592E-02	1.230E-18	-0.007	1.567E-02	6.481E-01	77.375	
Defluviitaleaceae													
family	rs28998802	G	A	G	A	0.210	3.123E-02	1.860E-11	0.029	2.308E-02	1.976E-01	45.216	

Defluviitaleaceae													
family	rs33980500	C	T	C	T	0.241	4.546E-02	1.150E-07	0.035	3.011E-02	2.193E-01	28.104	
Defluviitaleaceae													
family	rs34473406	T	G	T	G	0.223	4.772E-02	3.110E-06	0.024	3.028E-02	4.626E-01	21.838	
Defluviitaleaceae													
family	rs3954248	G	T	G	T	-0.130	2.534E-02	2.990E-07	-0.012	1.576E-02	4.519E-01	26.319	
Defluviitaleaceae													
family	rs4713636	G	A	G	A	0.139	2.636E-02	1.230E-07	0.007	1.802E-02	6.901E-01	27.806	
Defluviitaleaceae													
family	rs493090	G	A	G	A	-0.113	2.538E-02	8.550E-06	-0.005	1.583E-02	7.834E-01	19.823	
Defluviitaleaceae													
family	rs62443225	G	A	G	A	0.234	4.502E-02	2.040E-07	0.004	2.971E-02	9.050E-01	27.016	
Defluviitaleaceae													
family	rs674451	T	C	T	C	0.170	2.607E-02	7.140E-11	0.020	1.665E-02	2.463E-01	42.522	
Defluviitaleaceae													
family	rs6966660	C	T	C	T	-0.151	2.537E-02	2.700E-09	-0.013	1.598E-02	4.310E-01	35.425	
Defluviitaleaceae													
family	rs7177110	G	A	G	A	-0.134	2.869E-02	3.120E-06	0.003	1.863E-02	8.649E-01	21.815	
Defluviitaleaceae													
family	rs7194171	C	T	C	T	-0.156	3.378E-02	3.630E-06	0.011	1.987E-02	6.047E-01	21.327	
Defluviitaleaceae													
family	rs75257908	C	T	C	T	0.309	4.314E-02	7.440E-13	0.009	2.681E-02	6.932E-01	51.305	
Defluviitaleaceae													
family	rs76076434	G	A	G	A	-0.227	4.620E-02	8.710E-07	-0.012	2.585E-02	5.967E-01	24.142	
Defluviitaleaceae													
family	rs7627880	A	G	A	G	0.127	2.560E-02	6.700E-07	0.001	1.564E-02	9.606E-01	24.611	

Defluviitaleaceae													
family	rs78376604	C	A	C	A	0.264	5.514E-02	1.660E-06	-0.004	3.014E-02	8.730E-01	22.923	
Defluviitaleaceae													
family	rs7989997	A	G	A	G	-0.136	2.969E-02	4.800E-06	0.005	1.808E-02	7.319E-01	20.983	
Defluviitaleaceae													
family	rs847	T	C	T	C	0.186	2.671E-02	3.530E-12	0.007	1.897E-02	7.199E-01	48.493	
Defluviitaleaceae													
family	rs8904	G	A	G	A	-0.170	2.616E-02	8.580E-11	-0.003	1.606E-02	8.469E-01	42.230	
Defluviitaleaceae													
family	rs9461693	G	A	G	A	0.609	2.597E-02	1.220E-121	0.018	1.767E-02	2.937E-01	549.909	
Defluviitaleaceae													
genus Butyrivibrio	rs11085727	C	T	C	T	-0.186	2.939E-02	2.63E-10	0.037	2.702E-02	1.773E-01	39.934	
genus Butyrivibrio	rs11758312	C	A	C	A	0.237	2.536E-02	8.81E-21	-0.012	2.394E-02	6.028E-01	87.411	
genus Butyrivibrio	rs11773159	A	C	A	C	0.153	3.224E-02	1.96E-06	-0.007	2.957E-02	8.305E-01	22.631	
genus Butyrivibrio	rs12130556	G	A	G	A	0.130	2.772E-02	2.72E-06	-0.028	2.470E-02	2.614E-01	22.006	
genus Butyrivibrio	rs12203031	C	T	C	T	-0.164	3.296E-02	6.61E-07	0.030	3.341E-02	3.815E-01	24.726	
genus Butyrivibrio	rs12458499	A	C	A	C	-0.143	3.178E-02	7.21E-06	0.015	2.976E-02	6.088E-01	20.137	
genus Butyrivibrio	rs13181047	T	G	T	G	-0.115	2.540E-02	5.96E-06	0.003	2.410E-02	8.746E-01	20.501	
genus Butyrivibrio	rs16839196	T	C	T	C	-0.173	3.271E-02	1.29E-07	-0.001	3.228E-02	9.709E-01	27.887	
genus Butyrivibrio	rs16870824	A	G	A	G	-0.137	3.006E-02	5.42E-06	-0.012	3.011E-02	7.385E-01	20.682	
genus Butyrivibrio	rs17837468	A	G	A	G	0.201	4.456E-02	6.70E-06	0.008	3.720E-02	8.740E-01	20.276	
genus Butyrivibrio	rs1812491	G	A	G	A	0.132	2.612E-02	4.30E-07	-0.026	2.543E-02	3.076E-01	25.556	
genus Butyrivibrio	rs2250140	T	C	T	C	0.128	2.523E-02	4.16E-07	-0.003	2.403E-02	8.936E-01	25.618	
genus Butyrivibrio	rs2523589	G	T	G	T	-0.293	2.493E-02	6.37E-32	-0.014	2.476E-02	5.705E-01	138.268	
genus Butyrivibrio	rs2546890	A	G	A	G	-0.228	2.592E-02	1.23E-18	0.006	2.403E-02	8.306E-01	77.643	
genus Butyrivibrio	rs28998802	G	A	G	A	0.210	3.123E-02	1.86E-11	0.038	3.555E-02	2.838E-01	45.117	

genus Butyrivibrio	rs3954248	G	T	G	T	-0.130	2.534E-02	2.99E-07	0.016	2.424E-02	4.922E-01	26.253
genus Butyrivibrio	rs4713636	G	A	G	A	0.139	2.636E-02	1.23E-07	-0.009	2.755E-02	7.536E-01	27.969
genus Butyrivibrio	rs57922664	G	A	G	A	0.158	3.557E-02	9.48E-06	0.006	4.518E-02	8.364E-01	19.613
genus Butyrivibrio	rs62443225	G	A	G	A	0.234	4.502E-02	2.04E-07	-0.032	4.630E-02	4.623E-01	26.999
genus Butyrivibrio	rs674451	T	C	T	C	0.170	2.607E-02	7.14E-11	-0.025	2.537E-02	3.337E-01	42.479
genus Butyrivibrio	rs6966660	C	T	C	T	-0.151	2.537E-02	2.70E-09	0.023	2.500E-02	3.532E-01	35.386
genus Butyrivibrio	rs7177110	G	A	G	A	-0.134	2.869E-02	3.12E-06	0.028	2.835E-02	3.202E-01	21.742
genus Butyrivibrio	rs7194171	C	T	C	T	-0.156	3.378E-02	3.63E-06	0.031	3.086E-02	3.735E-01	21.449
genus Butyrivibrio	rs75257908	C	T	C	T	0.309	4.314E-02	7.44E-13	-0.011	4.114E-02	8.200E-01	51.425
genus Butyrivibrio	rs76076434	G	A	G	A	-0.227	4.620E-02	8.71E-07	-0.013	3.946E-02	7.573E-01	24.194
genus Butyrivibrio	rs7627880	A	G	A	G	0.127	2.560E-02	6.70E-07	-0.020	2.397E-02	4.127E-01	24.700
genus Butyrivibrio	rs7989997	A	G	A	G	-0.136	2.969E-02	4.80E-06	-0.015	2.798E-02	6.497E-01	20.917
genus Butyrivibrio	rs847	T	C	T	C	0.186	2.671E-02	3.53E-12	-0.038	2.889E-02	1.767E-01	48.371
genus Butyrivibrio	rs8904	G	A	G	A	-0.170	2.616E-02	8.58E-11	-0.026	2.457E-02	3.021E-01	42.121
genus Butyrivibrio	rs9461693	G	A	G	A	0.609	2.597E-02	1.22E-121	-0.066	2.683E-02	1.239E-02	550.064
genus	rs11085727	C	T	C	T	-0.186	2.939E-02	2.63E-10	-0.022	1.757E-02	2.083E-01	39.934
Defluviitaleaceae												
genus	rs11191088	G	A	G	A	0.180	3.671E-02	8.91E-07	0.047	4.318E-02	2.677E-01	24.151
Defluviitaleaceae	8											
genus	rs11758312	C	A	C	A	0.237	2.536E-02	8.81E-21	0.007	1.568E-02	6.476E-01	87.411
Defluviitaleaceae												
genus	rs11773159	A	C	A	C	0.153	3.224E-02	1.96E-06	0.018	1.889E-02	3.434E-01	22.631
Defluviitaleaceae												
genus	rs12130556	G	A	G	A	0.130	2.772E-02	2.72E-06	-0.006	1.611E-02	7.292E-01	22.006
Defluviitaleaceae												
genus	rs12203031	C	T	C	T	-0.164	3.296E-02	6.61E-07	0.024	2.193E-02	3.059E-01	24.726

Defluviitaleaceae													
genus	rs12458499	A	C	A	C	-0.143	3.178E-02	7.21E-06	-0.015	1.932E-02	4.962E-01	20.137	
Defluviitaleaceae													
genus	rs12485562	T	C	T	C	-0.136	3.001E-02	6.09E-06	0.007	1.911E-02	7.469E-01	20.459	
Defluviitaleaceae													
genus	rs13181047	T	G	T	G	-0.115	2.540E-02	5.96E-06	-0.006	1.578E-02	7.052E-01	20.501	
Defluviitaleaceae													
genus	rs16839196	T	C	T	C	-0.173	3.271E-02	1.29E-07	-0.017	2.101E-02	4.087E-01	27.887	
Defluviitaleaceae													
genus	rs16870824	A	G	A	G	-0.137	3.006E-02	5.42E-06	-0.014	1.957E-02	4.700E-01	20.682	
Defluviitaleaceae													
genus	rs16952374	A	G	A	G	0.172	3.866E-02	8.73E-06	-0.018	3.717E-02	6.109E-01	19.772	
Defluviitaleaceae													
genus	rs1812491	G	A	G	A	0.132	2.612E-02	4.30E-07	0.020	1.667E-02	2.433E-01	25.556	
Defluviitaleaceae													
genus	rs1832741	C	T	C	T	0.120	2.527E-02	2.21E-06	0.010	1.572E-02	5.128E-01	22.399	
Defluviitaleaceae													
genus	rs2250140	T	C	T	C	0.128	2.523E-02	4.16E-07	-0.016	1.569E-02	3.230E-01	25.618	
Defluviitaleaceae													
genus	rs2523589	G	T	G	T	-0.293	2.493E-02	6.37E-32	-0.012	1.586E-02	4.431E-01	138.268	
Defluviitaleaceae													
genus	rs2546890	A	G	A	G	-0.228	2.592E-02	1.23E-18	-0.009	1.569E-02	5.727E-01	77.643	
Defluviitaleaceae													
genus	rs28998802	G	A	G	A	0.210	3.123E-02	1.86E-11	0.031	2.311E-02	1.692E-01	45.117	
Defluviitaleaceae													
genus	rs33980500	C	T	C	T	0.241	4.546E-02	1.15E-07	0.035	3.015E-02	2.130E-01	28.099	

Defluviitaleaceae													
genus	rs34473406	T	G	T	G	0.223	4.772E-02	3.11E-06	0.023	3.032E-02	4.764E-01	21.746	
Defluviitaleaceae													
genus	rs3954248	G	T	G	T	-0.130	2.534E-02	2.99E-07	-0.011	1.578E-02	4.942E-01	26.253	
Defluviitaleaceae													
genus	rs4713636	G	A	G	A	0.139	2.636E-02	1.23E-07	0.011	1.804E-02	5.496E-01	27.969	
Defluviitaleaceae													
genus	rs493090	G	A	G	A	-0.113	2.538E-02	8.55E-06	-0.006	1.585E-02	7.469E-01	19.810	
Defluviitaleaceae													
genus	rs62443225	G	A	G	A	0.234	4.502E-02	2.04E-07	0.002	2.974E-02	9.673E-01	26.999	
Defluviitaleaceae													
genus	rs674451	T	C	T	C	0.170	2.607E-02	7.14E-11	0.022	1.667E-02	2.000E-01	42.479	
Defluviitaleaceae													
genus	rs6966660	C	T	C	T	-0.151	2.537E-02	2.70E-09	-0.011	1.600E-02	5.033E-01	35.386	
Defluviitaleaceae													
genus	rs7177110	G	A	G	A	-0.134	2.869E-02	3.12E-06	0.004	1.865E-02	8.237E-01	21.742	
Defluviitaleaceae													
genus	rs7194171	C	T	C	T	-0.156	3.378E-02	3.63E-06	0.011	1.989E-02	6.168E-01	21.449	
Defluviitaleaceae													
genus	rs75257908	C	T	C	T	0.309	4.314E-02	7.44E-13	0.007	2.684E-02	7.393E-01	51.425	
Defluviitaleaceae													
genus	rs76076434	G	A	G	A	-0.227	4.620E-02	8.71E-07	-0.014	2.588E-02	5.541E-01	24.194	
Defluviitaleaceae													
genus	rs7627880	A	G	A	G	0.127	2.560E-02	6.70E-07	0.004	1.566E-02	7.998E-01	24.700	
Defluviitaleaceae													
genus	rs78376604	C	A	C	A	0.264	5.514E-02	1.66E-06	-0.006	3.018E-02	8.214E-01	22.958	

Defluviitaleaceae													
genus	rs7989997	A	G	A	G	-0.136	2.969E-02	4.80E-06	0.006	1.810E-02	7.119E-01	20.917	
Defluviitaleaceae													
genus	rs847	T	C	T	C	0.186	2.671E-02	3.53E-12	0.008	1.899E-02	6.832E-01	48.371	
Defluviitaleaceae													
genus	rs8904	G	A	G	A	-0.170	2.616E-02	8.58E-11	-0.003	1.608E-02	8.415E-01	42.121	
Defluviitaleaceae													
genus	rs9461693	G	A	G	A	0.609	2.597E-02	1.22E-121	0.018	1.769E-02	2.974E-01	550.064	
Defluviitaleaceae													
genus Clostridium sensustricto1	rs11085727	C	T	C	T	-0.186	2.939E-02	2.627E-10	-0.001	1.337E-02	9.484E-01	39.934	
genus Clostridium sensustricto1	rs11758312	C	A	C	A	0.237	2.536E-02	8.815E-21	0.005	1.199E-02	6.335E-01	87.411	
genus Clostridium sensustricto1	rs11773159	A	C	A	C	0.153	3.224E-02	1.963E-06	0.010	1.483E-02	4.419E-01	22.631	
genus Clostridium sensustricto1	rs12203031	C	T	C	T	-0.164	3.296E-02	6.608E-07	-0.019	1.703E-02	2.607E-01	24.726	
genus Clostridium sensustricto1	rs12458499	A	C	A	C	-0.143	3.178E-02	7.209E-06	-0.012	1.465E-02	3.894E-01	20.137	
genus Clostridium sensustricto1	rs12485562	T	C	T	C	-0.136	3.001E-02	6.092E-06	-0.008	1.475E-02	5.873E-01	20.459	
genus Clostridium sensustricto1	rs1579218	A	G	A	G	-0.160	3.019E-02	1.098E-07	-0.001	1.705E-02	5.601E-01	28.193	
genus Clostridium sensustricto1	rs16839196	T	C	T	C	-0.173	3.271E-02	1.286E-07	-0.004	1.595E-02	8.293E-01	27.887	
genus Clostridium	rs16952374	A	G	A	G	0.172	3.866E-02	8.726E-06	-0.008	2.728E-02	7.220E-01	19.772	

sensustricto1												
genus Clostridium	rs17837468	A	G	A	G	0.201	4.456E-02	6.702E-06	-0.008	1.855E-02	6.568E-01	20.276
sensustricto1												
genus Clostridium	rs1812491	G	A	G	A	0.132	2.612E-02	4.298E-07	-0.001	1.266E-02	9.021E-01	25.556
sensustricto1												
genus Clostridium	rs1832741	C	T	C	T	0.120	2.527E-02	2.215E-06	-0.007	1.198E-02	5.515E-01	22.399
sensustricto1												
genus Clostridium	rs2250140	T	C	T	C	0.128	2.523E-02	4.162E-07	0.005	1.196E-02	6.999E-01	25.618
sensustricto1												
genus Clostridium	rs2523589	G	T	G	T	-0.293	2.493E-02	6.369E-32	-0.002	1.214E-02	9.003E-01	138.268
sensustricto1												
genus Clostridium	rs2546890	A	G	A	G	-0.228	2.592E-02	1.235E-18	-0.003	1.196E-02	8.013E-01	77.643
sensustricto1												
genus Clostridium	rs28998802	G	A	G	A	0.210	3.123E-02	1.855E-11	0.008	1.788E-02	6.390E-01	45.117
sensustricto1												
genus Clostridium	rs33980500	C	T	C	T	0.241	4.546E-02	1.152E-07	-0.009	2.302E-02	6.541E-01	28.099
sensustricto1												
genus Clostridium	rs34473406	T	G	T	G	0.223	4.772E-02	3.112E-06	0.022	2.397E-02	4.467E-01	21.746
sensustricto1												
genus Clostridium	rs3954248	G	T	G	T	-0.130	2.534E-02	2.995E-07	-0.014	1.206E-02	2.356E-01	26.253
sensustricto1												
genus Clostridium	rs4713636	G	A	G	A	0.139	2.636E-02	1.233E-07	0.008	1.367E-02	5.813E-01	27.969
sensustricto1												
genus Clostridium	rs493090	G	A	G	A	-0.113	2.538E-02	8.552E-06	-0.011	1.207E-02	3.469E-01	19.810
sensustricto1												
genus Clostridium	rs57922664	G	A	G	A	0.158	3.557E-02	9.482E-06	-0.012	2.117E-02	4.778E-01	19.613

sensustricto1												
genus Clostridium	rs62443225	G	A	G	A	0.234	4.502E-02	2.036E-07	-0.009	2.306E-02	8.070E-01	26.999
sensustricto1												
genus Clostridium	rs674451	T	C	T	C	0.170	2.607E-02	7.145E-11	0.010	1.274E-02	4.690E-01	42.479
sensustricto1												
genus Clostridium	rs6966660	C	T	C	T	-0.151	2.537E-02	2.704E-09	-0.007	1.225E-02	5.703E-01	35.386
sensustricto1												
genus Clostridium	rs7177110	G	A	G	A	-0.134	2.869E-02	3.120E-06	0.004	1.446E-02	7.741E-01	21.742
sensustricto1												
genus Clostridium	rs7194171	C	T	C	T	-0.156	3.378E-02	3.634E-06	-0.010	1.507E-02	4.849E-01	21.449
sensustricto1												
genus Clostridium	rs75257908	C	T	C	T	0.309	4.314E-02	7.437E-13	0.009	2.067E-02	7.535E-01	51.425
sensustricto1												
genus Clostridium	rs76076434	G	A	G	A	-0.227	4.620E-02	8.708E-07	0.013	2.004E-02	5.535E-01	24.194
sensustricto1												
genus Clostridium	rs78376604	C	A	C	A	0.264	5.514E-02	1.656E-06	0.021	2.390E-02	3.508E-01	22.958
sensustricto1												
genus Clostridium	rs7989997	A	G	A	G	-0.136	2.969E-02	4.795E-06	0.000	1.396E-02	9.797E-01	20.917
sensustricto1												
genus Clostridium	rs847	T	C	T	C	0.186	2.671E-02	3.528E-12	0.004	1.430E-02	7.461E-01	48.371
sensustricto1												
genus Clostridium	rs8904	G	A	G	A	-0.170	2.616E-02	8.582E-11	-0.007	1.227E-02	5.342E-01	42.121
sensustricto1												
genus Clostridium	rs9461693	G	A	G	A	0.609	2.597E-02	1.219E-121	0.015	1.353E-02	2.507E-01	550.064
sensustricto1												
genus	rs11085727	C	T	C	T	-0.186	2.939E-02	2.627E-10	-0.022	2.653E-02	3.730E-01	39.934

Ruminococcaceae													
genus	rs11758312	C	A	C	A	0.237	2.536E-02	8.815E-21	0.037	2.347E-02	1.162E-01	87.411	
Ruminococcaceae													
genus	rs11773159	A	C	A	C	0.153	3.224E-02	1.963E-06	-0.001	2.779E-02	9.934E-01	22.631	
Ruminococcaceae													
genus	rs12130556	G	A	G	A	0.130	2.772E-02	2.718E-06	0.001	2.420E-02	9.748E-01	22.006	
Ruminococcaceae													
genus	rs12203031	C	T	C	T	-0.164	3.296E-02	6.608E-07	-0.007	3.235E-02	8.551E-01	24.726	
Ruminococcaceae													
genus	rs12458499	A	C	A	C	-0.143	3.178E-02	7.209E-06	0.009	2.902E-02	6.879E-01	20.137	
Ruminococcaceae													
genus	rs12485562	T	C	T	C	-0.136	3.001E-02	6.092E-06	0.002	2.852E-02	9.693E-01	20.459	
Ruminococcaceae													
genus	rs13181047	T	G	T	G	-0.115	2.540E-02	5.959E-06	-0.025	2.361E-02	2.919E-01	20.501	
Ruminococcaceae													
genus	rs16839196	T	C	T	C	-0.173	3.271E-02	1.286E-07	0.023	3.198E-02	4.391E-01	27.887	
Ruminococcaceae													
genus	rs1812491	G	A	G	A	0.132	2.612E-02	4.298E-07	-0.020	2.497E-02	4.278E-01	25.556	
Ruminococcaceae													
genus	rs1832741	C	T	C	T	0.120	2.527E-02	2.215E-06	0.006	2.350E-02	7.936E-01	22.399	
Ruminococcaceae													
genus	rs2250140	T	C	T	C	0.128	2.523E-02	4.162E-07	0.023	2.353E-02	3.405E-01	25.618	
Ruminococcaceae													
genus	rs2523589	G	T	G	T	-0.293	2.493E-02	6.369E-32	-0.044	2.350E-02	6.121E-02	138.268	
Ruminococcaceae													
genus	rs2546890	A	G	A	G	-0.228	2.592E-02	1.235E-18	-0.006	2.354E-02	7.980E-01	77.643	

Ruminococcaceae													
genus	rs28998802	G	A	G	A	0.210	3.123E-02	1.855E-11	0.036	3.372E-02	2.559E-01	45.117	
Ruminococcaceae													
genus	rs34473406	T	G	T	G	0.223	4.772E-02	3.112E-06	0.046	4.459E-02	2.978E-01	21.746	
Ruminococcaceae													
genus	rs4713636	G	A	G	A	0.139	2.636E-02	1.233E-07	0.024	2.716E-02	3.649E-01	27.969	
Ruminococcaceae													
genus	rs493090	G	A	G	A	-0.113	2.538E-02	8.552E-06	0.008	2.379E-02	7.431E-01	19.810	
Ruminococcaceae													
genus	rs57922664	G	A	G	A	0.158	3.557E-02	9.482E-06	-0.001	4.406E-02	9.449E-01	19.613	
Ruminococcaceae													
genus	rs62443225	G	A	G	A	0.234	4.502E-02	2.036E-07	-0.018	4.325E-02	6.322E-01	26.999	
Ruminococcaceae													
genus	rs674451	T	C	T	C	0.170	2.607E-02	7.145E-11	-0.025	2.483E-02	3.222E-01	42.479	
Ruminococcaceae													
genus	rs6966660	C	T	C	T	-0.151	2.537E-02	2.704E-09	0.018	2.371E-02	4.443E-01	35.386	
Ruminococcaceae													
genus	rs7177110	G	A	G	A	-0.134	2.869E-02	3.120E-06	-0.018	2.766E-02	5.031E-01	21.742	
Ruminococcaceae													
genus	rs7194171	C	T	C	T	-0.156	3.378E-02	3.634E-06	-0.011	2.954E-02	7.029E-01	21.449	
Ruminococcaceae													
genus	rs75257908	C	T	C	T	0.309	4.314E-02	7.437E-13	-0.013	4.104E-02	8.278E-01	51.425	
Ruminococcaceae													
genus	rs7627880	A	G	A	G	0.127	2.560E-02	6.698E-07	-0.020	2.347E-02	4.088E-01	24.700	
Ruminococcaceae													
genus	rs7989997	A	G	A	G	-0.136	2.969E-02	4.795E-06	0.022	2.689E-02	4.258E-01	20.917	

Ruminococcaceae													
genus	rs847	T	C	T	C	0.186	2.671E-02	3.528E-12	0.021	2.863E-02	4.684E-01	48.371	
Ruminococcaceae													
genus	rs8904	G	A	G	A	-0.170	2.616E-02	8.582E-11	0.013	2.412E-02	6.114E-01	42.121	
Ruminococcaceae													
genus	rs9461693	G	A	G	A	0.609	2.597E-02	1.219E-121	0.065	2.664E-02	1.662E-02	550.064	
Ruminococcaceae													

SNP: single nucleotide polymorphism; EAE: effect allele exposure; OAE: other allele exposure; EAO: effect allele outcome; OAO: other allele outcome;
 SE: standard error; F: F value;

Supplementary Table 2 Instrumental variables used in MR analysis of the association between gut microbiota and PSA

Bacterial taxa (exposure)	SNP	EAE	OAE	EAO	OAO	Exposure (Bacteria)			Outcome (psoriatic arthritis)			F
						Beta	Se	pval	Beta	Se	pval	
class Methanobacteria	rs10202904	G	T	G	T	0.122	2.354E-02	3.014E-07	-0.030	2.589E-02	2.539E-01	26.762
class Methanobacteria	rs10424197	A	G	A	G	0.111	2.475E-02	9.279E-06	0.002	2.927E-02	9.573E-01	20.211
class Methanobacteria	rs4257531	G	A	G	A	0.164	3.650E-02	7.443E-06	0.029	4.158E-02	4.904E-01	20.316
class Methanobacteria	rs6508769	C	T	C	T	-0.154	3.445E-02	8.225E-06	0.058	3.576E-02	1.068E-01	19.856
class Methanobacteria	rs6776814	T	C	T	C	-0.200	4.118E-02	1.631E-06	0.076	8.950E-02	3.944E-01	23.483
class Methanobacteria	rs73068003	G	T	G	T	-0.158	3.518E-02	8.446E-06	0.023	4.285E-02	5.983E-01	20.206
class Methanobacteria	rs73457410	A	G	A	G	0.215	4.367E-02	1.409E-06	-0.024	5.217E-02	6.422E-01	24.316
class Methanobacteria	rs75208022	C	T	C	T	-0.227	4.876E-02	5.921E-06	0.027	4.320E-02	5.281E-01	21.717
class Methanobacteria	rs894996	C	A	C	A	0.217	4.491E-02	1.876E-06	-0.091	4.928E-02	6.404E-02	23.349
order Methanobacteriales	rs10202904	G	T	G	T	0.122	2.354E-02	3.014E-07	-0.030	2.589E-02	2.539E-01	26.762
order Methanobacteriales	rs10424197	A	G	A	G	0.111	2.475E-02	9.279E-06	0.002	2.927E-02	9.573E-01	20.211
order Methanobacteriales	rs4257531	G	A	G	A	0.164	3.650E-02	7.443E-06	0.029	4.158E-02	4.904E-01	20.316
order Methanobacteriales	rs6508769	C	T	C	T	-0.154	3.445E-02	8.225E-06	0.058	3.576E-02	1.068E-01	19.856
order Methanobacteriales	rs6776814	T	C	T	C	-0.200	4.118E-02	1.631E-06	0.076	8.950E-02	3.944E-01	23.483
order Methanobacteriales	rs73068003	G	T	G	T	-0.158	3.518E-02	8.446E-06	0.023	4.285E-02	5.983E-01	20.206

order	rs73457410	A	G	A	G	0.215	4.367E-02	1.409E-06	-0.024	5.217E-02	6.422E-01	24.316
Methanobacteriales												
order	rs75208022	C	T	C	T	-0.227	4.876E-02	5.921E-06	0.027	4.320E-02	5.281E-01	21.717
Methanobacteriales												
order	rs894996	C	A	C	A	0.217	4.491E-02	1.876E-06	-0.091	4.928E-02	6.404E-02	23.349
Methanobacteriales												
family	rs10202904	G	T	G	T	0.122	2.354E-02	3.014E-07	-0.030	2.589E-02	2.539E-01	26.762
Methanobacteriaceae												
family	rs10424197	A	G	A	G	0.111	2.475E-02	9.279E-06	0.002	2.927E-02	9.573E-01	20.211
Methanobacteriaceae												
family	rs4257531	G	A	G	A	0.164	3.650E-02	7.443E-06	0.029	4.158E-02	4.904E-01	20.316
Methanobacteriaceae												
family	rs6508769	C	T	C	T	-0.154	3.445E-02	8.225E-06	0.058	3.576E-02	1.068E-01	19.856
Methanobacteriaceae												
family	rs6776814	T	C	T	C	-0.200	4.118E-02	1.631E-06	0.076	8.950E-02	3.944E-01	23.483
Methanobacteriaceae												
family	rs73068003	G	T	G	T	-0.158	3.518E-02	8.446E-06	0.023	4.285E-02	5.983E-01	20.206
Methanobacteriaceae												
family	rs73457410	A	G	A	G	0.215	4.367E-02	1.409E-06	-0.024	5.217E-02	6.422E-01	24.316
Methanobacteriaceae												
family	rs75208022	C	T	C	T	-0.227	4.876E-02	5.921E-06	0.027	4.320E-02	5.281E-01	21.717
Methanobacteriaceae												
family	rs894996	C	A	C	A	0.217	4.491E-02	1.876E-06	-0.091	4.928E-02	6.404E-02	23.349
Methanobacteriaceae												
family Rikenellaceae	rs10217435	C	T	C	T	-0.088	1.975E-02	6.508E-06	-0.082	3.645E-02	2.387E-02	20.022
family Rikenellaceae	rs10832801	A	C	A	C	-0.053	1.227E-02	7.504E-06	-0.057	2.835E-02	4.493E-02	19.005

family Rikenellaceae	rs1939881	G	A	G	A	-0.106	2.062E-02	5.644E-07	-0.028	5.442E-02	6.017E-01	26.218
family Rikenellaceae	rs2447496	A	G	A	G	0.055	1.219E-02	6.086E-06	-0.011	2.879E-02	7.007E-01	20.297
family Rikenellaceae	rs2833282	G	A	G	A	0.071	1.570E-02	4.311E-06	-0.076	3.559E-02	3.168E-02	20.526
family Rikenellaceae	rs36021379	A	G	A	G	-0.066	1.449E-02	7.195E-06	0.003	3.489E-02	9.218E-01	20.496
family Rikenellaceae	rs4264350	T	C	T	C	-0.053	1.086E-02	1.348E-06	-0.030	2.538E-02	2.451E-01	23.514
family Rikenellaceae	rs59663348	G	A	G	A	0.057	1.250E-02	6.122E-06	-0.002	2.943E-02	9.529E-01	20.844
family Rikenellaceae	rs62532512	A	C	A	C	0.050	1.074E-02	2.764E-06	0.014	2.563E-02	5.968E-01	22.045
family Rikenellaceae	rs6744030	C	T	C	T	0.070	1.571E-02	9.315E-06	0.010	3.107E-02	7.545E-01	19.669
family Rikenellaceae	rs6837275	A	G	A	G	0.057	1.189E-02	1.447E-06	0.024	2.777E-02	3.868E-01	23.022
family Rikenellaceae	rs74474130	T	G	T	G	0.138	2.957E-02	3.614E-06	0.053	6.901E-02	4.402E-01	21.702
family Rikenellaceae	rs77885767	C	T	C	T	-0.156	3.365E-02	2.847E-06	-0.155	6.055E-02	1.042E-02	21.552
family Rikenellaceae	rs7832304	T	G	T	G	-0.072	1.606E-02	8.709E-06	0.022	3.809E-02	5.661E-01	20.330
family Rikenellaceae	rs8130320	A	G	A	G	-0.049	1.068E-02	4.727E-06	-0.005	2.552E-02	8.544E-01	20.968
family Rikenellaceae	rs9389714	C	T	C	T	-0.064	1.434E-02	8.791E-06	-0.041	4.486E-02	3.553E-01	19.718
family Rikenellaceae	rs9578457	G	A	G	A	-0.141	3.158E-02	3.994E-06	0.026	5.935E-02	6.628E-01	20.064
family Rikenellaceae	rs9603208	G	T	G	T	0.082	1.596E-02	1.918E-07	0.042	4.238E-02	3.264E-01	26.474
genus Eubacterium fissicatena group	rs10147907	T	G	T	G	0.172	3.960E-02	8.272E-06	0.030	4.840E-02	5.311E-01	18.922
genus Eubacterium fissicatena group	rs11818408	G	A	G	A	0.106	2.371E-02	8.200E-06	-0.042	2.600E-02	1.027E-01	19.928
genus Eubacterium fissicatena group	rs11876297	T	C	T	C	0.131	2.817E-02	2.666E-06	-0.040	2.863E-02	1.604E-01	21.779
genus Eubacterium fissicatena group	rs15125769	A	G	A	G	0.210	4.548E-02	3.097E-06	0.045	4.933E-02	3.581E-01	21.217
genus Eubacterium fissicatena group	rs1768152	C	T	C	T	-0.139	3.162E-02	8.701E-06	0.012	4.142E-02	7.654E-01	19.462

genus Eubacterium fissicatena group	rs2733072	G	A	G	A	0.110	2.283E-02	1.491E-06	-0.044	2.546E-02	8.353E-02	23.064
genus Eubacterium fissicatena group	rs3771393	T	C	T	C	-0.131	2.667E-02	7.379E-07	0.078	3.209E-02	1.499E-02	24.074
genus Eubacterium fissicatena group	rs6934739	A	G	A	G	0.111	2.528E-02	9.753E-06	-0.022	2.692E-02	4.079E-01	19.442
genus Eubacterium fissicatena group	rs7104872	G	A	G	A	0.139	2.919E-02	2.731E-06	-0.078	4.047E-02	5.349E-02	22.548
genus Butyricicoccus	rs10084203	G	A	G	A	-0.055	1.236E-02	8.586E-06	0.004	3.767E-02	9.080E-01	19.791
genus Butyricicoccus	rs12034718	G	A	G	A	-0.070	1.582E-02	9.577E-06	-0.059	3.044E-02	5.307E-02	19.643
genus Butyricicoccus	rs12585793	T	C	T	C	-0.262	5.647E-02	5.792E-06	-0.016	7.607E-02	8.365E-01	21.558
genus Butyricicoccus	rs2017189	T	G	T	G	0.051	1.102E-02	3.873E-06	0.061	2.535E-02	1.644E-02	21.148
genus Butyricicoccus	rs4962426	T	G	T	G	-0.061	1.360E-02	7.385E-06	-0.125	3.257E-02	1.315E-04	20.403
genus Butyricicoccus	rs56221232	T	C	T	C	0.083	1.674E-02	7.619E-07	0.027	4.218E-02	5.146E-01	24.467
genus Butyricicoccus	rs62478070	T	G	T	G	0.224	4.950E-02	5.938E-06	0.011	8.008E-02	8.884E-01	20.488
genus Butyricicoccus	rs7322368	C	T	C	T	-0.082	1.832E-02	5.518E-06	-0.027	4.415E-02	5.483E-01	19.834
genus Methanobrevibacter	rs10202904	G	T	G	T	0.113	2.391E-02	3.085E-06	-0.030	2.589E-02	2.539E-01	22.260
genus Methanobrevibacter	rs1334944	T	C	T	C	0.115	2.555E-02	7.614E-06	0.002	2.831E-02	9.478E-01	20.330
genus Methanobrevibacter	rs4802933	G	A	G	A	0.136	3.081E-02	9.738E-06	-0.025	3.008E-02	4.060E-01	19.373
genus Methanobrevibacter	rs6776814	T	C	T	C	-0.189	4.199E-02	8.049E-06	0.076	8.950E-02	3.944E-01	20.250
genus Methanobrevibacter	rs76029318	T	C	T	C	0.223	4.543E-02	1.076E-06	-0.036	5.247E-02	4.898E-01	24.060

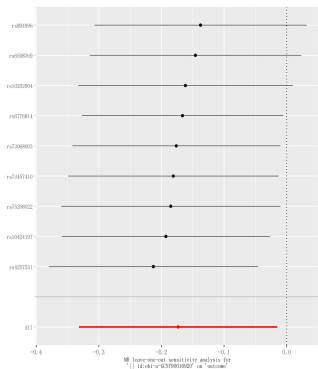
genus	rs894996	C	A	C	A	0.214	4.560E-02	3.816E-06	-0.091	4.928E-02	6.404E-02	22.064
Methanobrevibacter												
genus	rs10274562	C	T	C	T	0.111	2.446E-02	6.496E-06	0.008	2.606E-02	7.691E-01	20.570
Ruminococcaceae												
genus	rs12636310	G	A	G	A	0.133	2.820E-02	2.812E-06	0.000	2.934E-02	9.919E-01	22.146
Ruminococcaceae												
genus	rs12724320	C	T	C	T	-0.121	2.492E-02	1.520E-06	-0.029	2.608E-02	2.665E-01	23.524
Ruminococcaceae												
genus	rs1416041	A	C	A	C	-0.182	3.399E-02	7.044E-08	-0.041	3.126E-02	1.915E-01	28.778
Ruminococcaceae												
genus	rs2729556	T	C	T	C	0.109	2.337E-02	3.187E-06	0.075	2.539E-02	2.985E-03	21.793
Ruminococcaceae												
genus	rs4490371	T	C	T	C	-0.112	2.490E-02	7.746E-06	-0.028	2.584E-02	2.749E-01	20.172
Ruminococcaceae												
genus	rs79113084	C	T	C	T	-0.152	3.175E-02	2.061E-06	0.004	4.117E-02	9.320E-01	22.967
Ruminococcaceae												
genus	rs9729514	G	A	G	A	-0.185	3.946E-02	2.368E-06	-0.002	4.356E-02	9.616E-01	21.963
Ruminococcaceae												

SNP: single nucleotide polymorphism; EAE: effect allele exposure; OAE: other allele exposure; EAO: effect allele outcome; OAO: other allele outcome;
SE: standard error; F: F value;

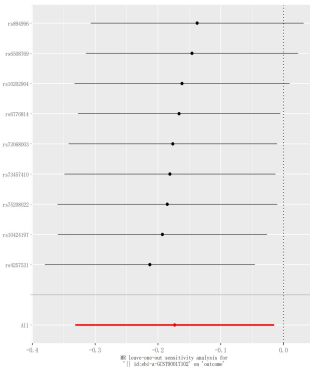
Supplementary Table 3 Sensitivity analysis of the MR analysis results of PSA on Gut microbes.

Gut microbes	Method	Heterogeneity		MR-PRESSO		Pleiotropy
		MR-IVW	MR-Egger	MR-PRESSO global test	Outlier-corrected	Egger intercept test
Family Clostridiaceae1	Statistics	Q=7.262 I ² = 0.0 %	Q=7.219 I ² = 0.0 %	7.650	NA	0.001
	<i>P</i>	1.000	1.000	1.000	NA	0.837
Family Defluviitaleaceae	Statistics	Q=12.432 I ² = 0.0 %	Q=12.428 I ² = 0.0 %	12.946	NA	4.518E-04
	<i>P</i>	1.000	1.000	1.000	NA	0.948
Genus Butyrivibrio	Statistics	Q=14.791 I ² = 0.0 %	Q=14.775 I ² = 0.0 %	16.684	NA	0.001
	<i>P</i>	0.987	0.981	0.984	NA	0.899
Genus Defluviitaleaceae	Statistics	Q=13.485 I ² = 0.0 %	Q=13.452 I ² = 0.0 %	14.042	NA	0.001
	<i>P</i>	1.000	0.999	0.999	NA	0.857
Genus Clostridium sensustricto1	Statistics	Q=8.515 I ² = 0.0 %	Q=8.652 I ² = 0.0 %	8.962	NA	0.002
	<i>P</i>	1.000	1.000	1.000	NA	0.713
Genus Ruminococcaceae UCG011	Statistics	Q=17.645 I ² = 0.0 %	Q=14.308 I ² = 0.0 %	15.136	NA	-0.020
	<i>P</i>	0.951	0.985	0.974	NA	0.078

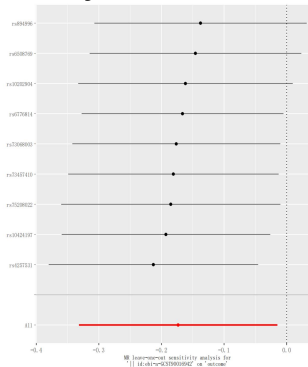
Class Methanobacteria



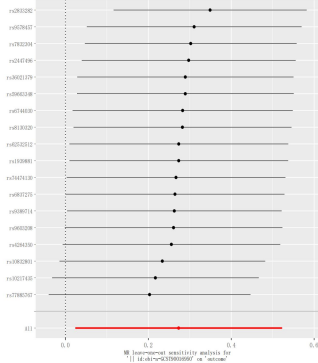
Order Methanobacteriales



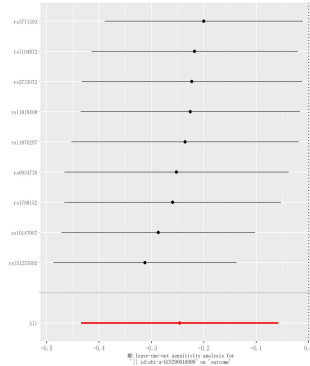
Family Methanobacteriaceae



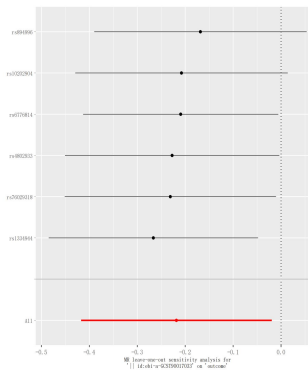
Family Rikenellaceae



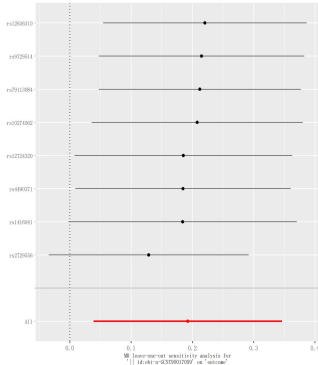
Genus Eubacterium fissicatena group



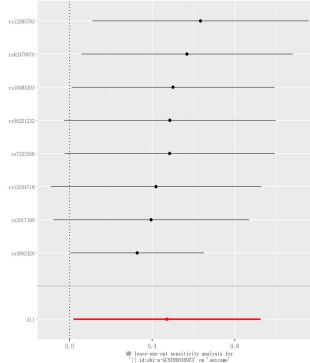
Genus Methanobrevibacter



Genus Ruminococcaceae

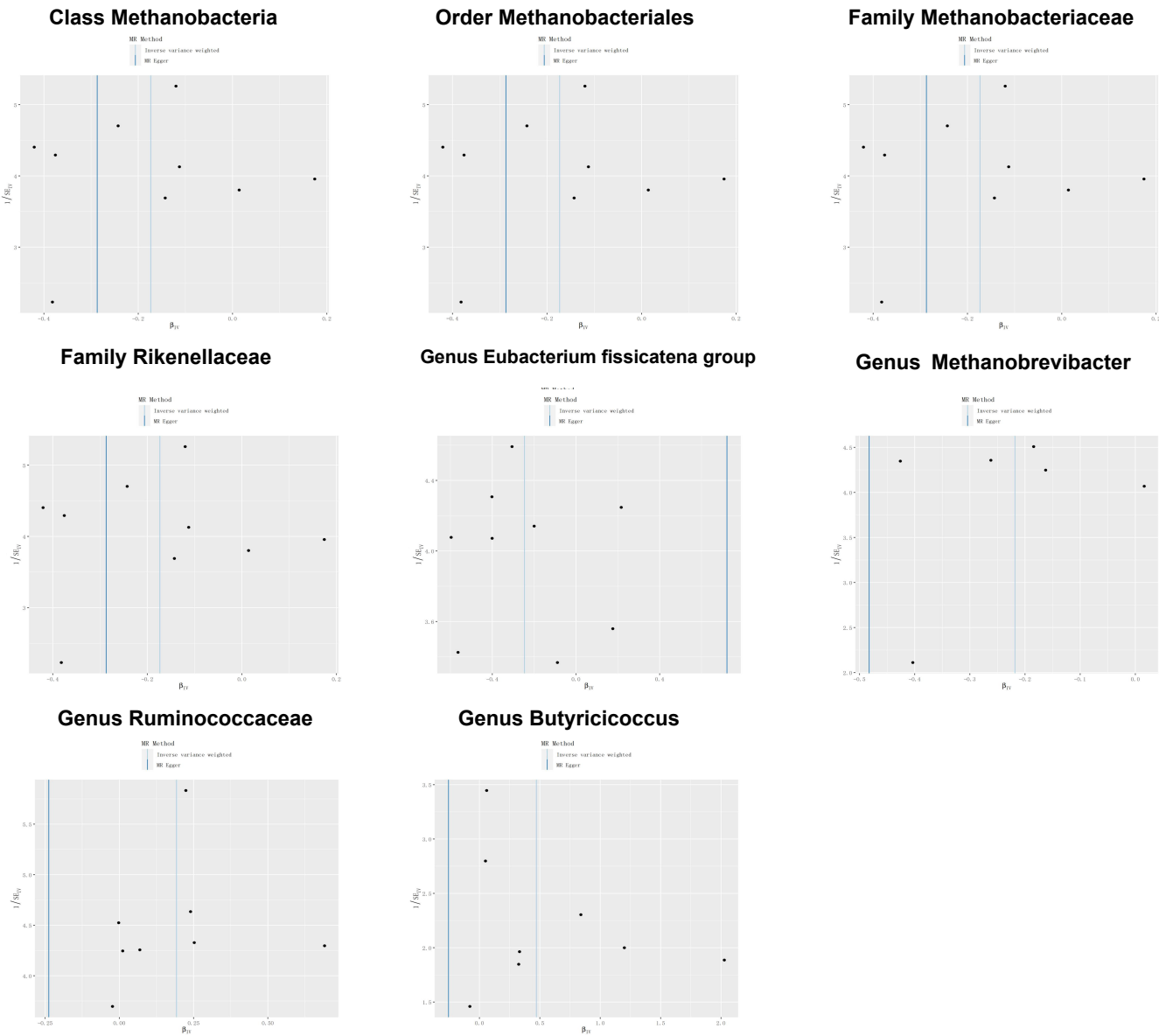


Genus Butyrivibrio



Supplementary Figure 1

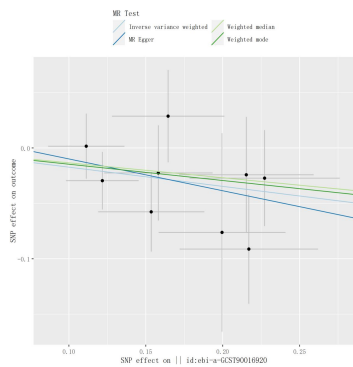
Leave one out test showing the causal relationship between the genetically identified 8 microbial taxa and PSA



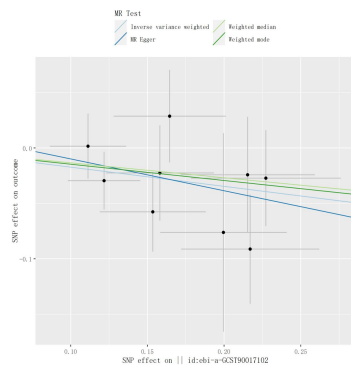
Supplementary Figure 2

Funnel plots showing the causal relationship between the genetically identified 8 microbial taxa and PSA

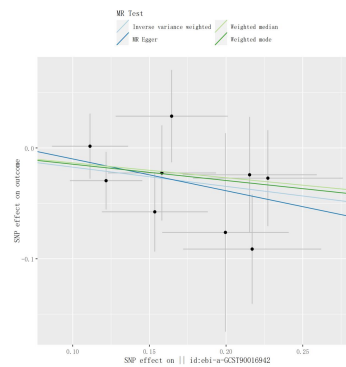
Class Methanobacteria



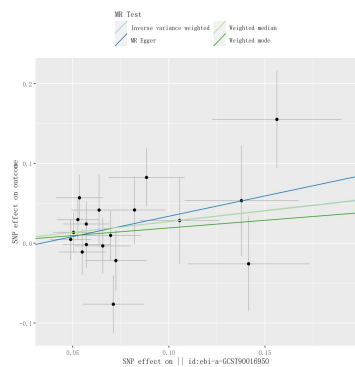
Order Methanobacteriales



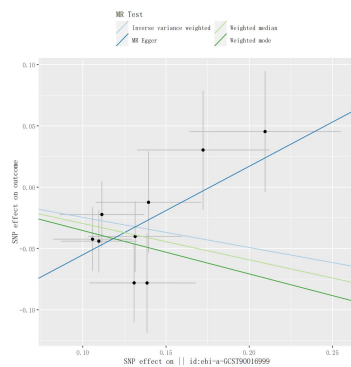
Family Methanobacteriaceae



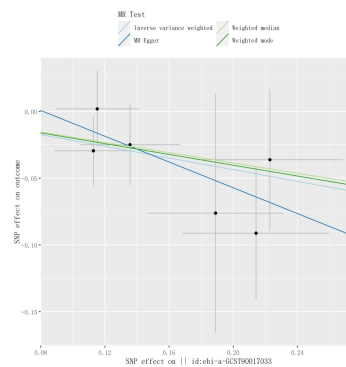
Family Rikenellaceae



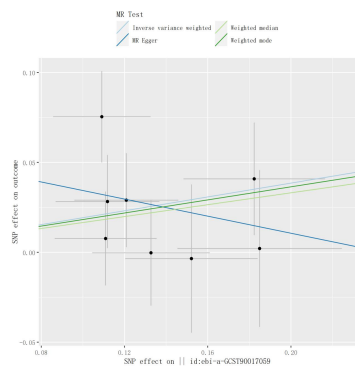
Genus Eubacterium fissicatena group



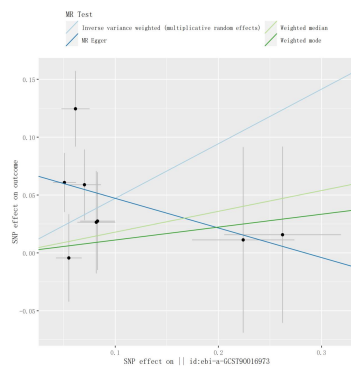
Genus Methanobrevibacter



Genus Ruminococcaceae



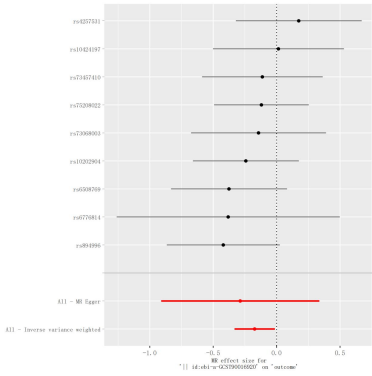
Genus Butyricicoccus



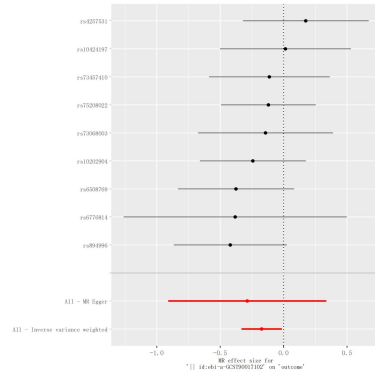
Supplementary Figure 3

Scatter plots showing the causal relationship between the genetically identified 8 microbial taxa and PSA

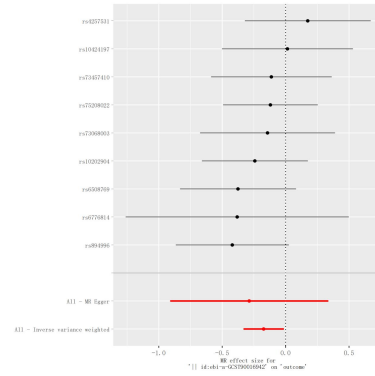
Class Methanobacteria



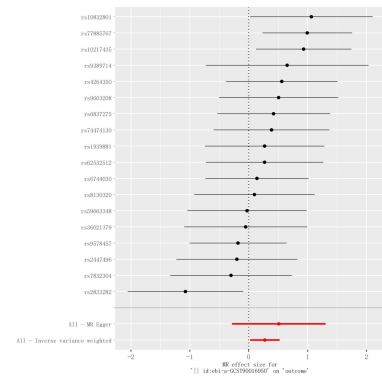
Order Methanobacteriales



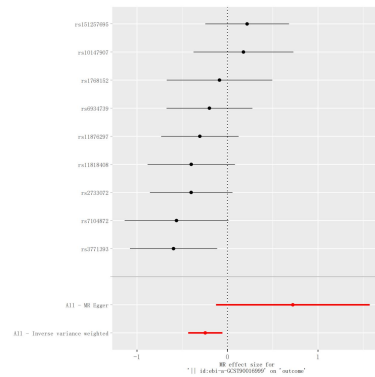
Family Methanobacteriaceae



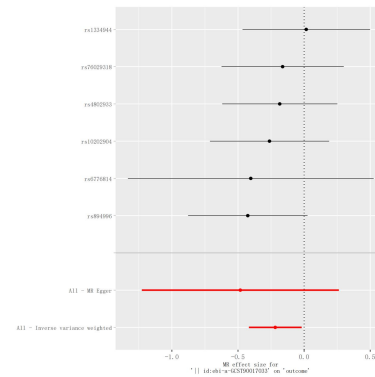
Family Rikenellaceae



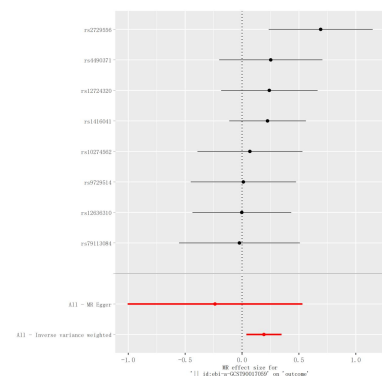
Genus Eubacterium fissicatena group



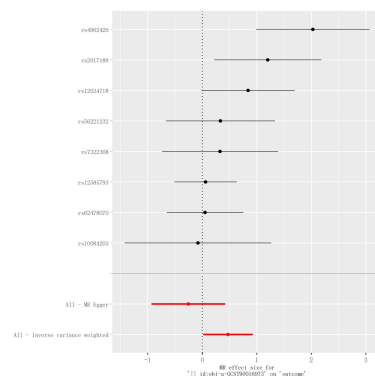
Genus Methanobrevibacter



Genus Ruminococcaceae



Genus Butyricicoccus



Supplementary Figure 4

Forest plots showing the causal relationship between the genetically identified 8 microbial taxa and PSA