Supplementary Material

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Supplementary Table 1 GWAS data sources and information included in the current study.

Category	Traits	Sample size	SNPs	Consortium	Link
Dietary intake	pork intake	460,162	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-5640/
	Bacon intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-4414/
	Processed meat intake	461,981	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-6324/
	Cooked vegetable intake	448,651	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-8089/
	Salad / raw vegetable intake	435,435	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-1996/
	Fresh fruit intake	446,462	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-3881/
	Dried fruit intake	421,764	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-16576/
	Salted nuts intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-15960/
	Unsalted nuts intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-12217/
	Salted peanuts intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-1099/
	Unsalted peanuts intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-15555/
	Average weekly red wine intake	327,026	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-5239/
	Average weekly beer plus cider intake	327,634	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-5174/
	Coffee intake	428,860	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-5237/
	Tea intake	447,485	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-6066/
	Milk intake	64,943	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-2966/
	Yogurt intake	64,949	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-7753/
	Cheese intake	451,486	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-1489/
	Cereal intake	441,640	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-15926/
	Non-oily fish intake	460,880	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-17627/
	Oily fish intake	460,443	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-2209/
	Lamb intake	64,942	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-530/
	Beef intake	461,053	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-2862/
	Bread intake	452,236	9,851,867	MRC-IEU	https://gwas.mrcieu.ac.uk/datasets/ukb-b-11348/
Esophageal diseases	Gastroesophageal reflux disease	602,604	2,320,781	Ong JS	https://gwas.mrcieu.ac.uk/datasets/ebi-a-GCST90000514/
Risk factors	Body mass index	339,224	2,555,511	GIANT	https://gwas.mrcieu.ac.uk/datasets/ieu-a-2/
	Major depressive disorder	173,005	13,554,55	PGC	https://gwas.mrcieu.ac.uk/datasets/ieu-a-1188/

		0		
Smoking	249,752	12,003,613	GSCAN	https://gwas.mrcieu.ac.uk/datasets/ieu-b-142/
Alcohol drinking	335,394	11,887,865	GSCAN	https://gwas.mrcieu.ac.uk/datasets/ieu-b-73/

Supplementary Table 2 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Pork intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10972033	N		0.00897557	0.00279636	0.00482189	0.00147851	Pork intake	4.00E-05	24.08973689	TRUE
2	rs11211124	N		-0.00995273	-0.0131608	0.00570984	0.00175408	Pork intake	3.52E-05	21.18244591	TRUE
3	rs12721051	N		-0.0123637	-0.0206635	0.00614259	0.00188666	Pork intake	4.67E-05	28.17006783	TRUE
4	rs1355171	N		-0.0109832	-0.0183803	0.00481526	0.001477	Pork intake	6.03E-05	36.33023253	TRUE
5	rs2387807	Y	horizontal pleiotropic outliers SNP	-0.0150846	0.0187502	0.00909201	0.00274837	Pork intake	3.27E-05	19.69801597	TRUE
6	rs254152	N		-0.0104266	-0.0069774	0.0056959	0.00174217	Pork intake	3.91E-05	23.55410188	TRUE
7	rs34161520	N		0.0115919	0.0123242	0.00665382	0.0020206	Pork intake	3.62E-05	21.80823247	TRUE
8	rs3964074	N		-0.00895091	-0.012991	0.00485635	0.00148347	Pork intake	3.97E-05	23.92816642	TRUE

9	rs4146837	N		0.00879226	-0.00456659	0.00486716	0.0014944	Pork intake	3.83E-05	23.10862399	TRUE
10	rs7641973	N		0.00844615	0.0108042	0.00502059	0.00154097	Pork intake	3.26E-05	19.64594776	TRUE

Supplementary Table 3 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Processed meat intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10454812	Y	horizontal pleiotropic outliers SNP	-0.0199599	-0.0257294	0.00793908	0.00344207	Processed meat intake	7.36E-05	34.02125285	TRUE
2	rs11032380	N		-0.0133229	-0.00323047	0.00512169	0.00222295	Processed meat intake	7.89E-05	36.44881457	TRUE
3	rs11887120	N		0.0119621	0.000814544	0.00495807	0.00216043	Processed meat intake	6.85E-05	31.67078528	TRUE
4	rs1422192	N		0.0169681	0.00507484	0.0066129	0.00287128	Processed meat intake	7.66E-05	35.40712091	TRUE
5	rs2029401	N		0.0146312	-0.0112856	0.00490416	0.0021292	Processed meat intake	0.000103854	47.98335033	TRUE
6	rs203319	N		-0.016423	0.0140829	0.00600021	0.00260186	Processed meat intake	8.78E-05	40.55806349	TRUE
7	rs2873054	N		0.0139958	0.0108042	0.00502059	0.00218986	Processed meat intake	8.95E-05	41.35419445	TRUE
8	rs3762621	Y	horizontal pleiotropic outliers SNP	-0.0149895	-0.00855146	0.00605392	0.00271965	Processed meat intake	6.73E-05	31.09984026	TRUE

9	rs4077924	Y	horizontal pleiotropic outliers SNP	0.0124987	0.0160599	0.00523914	0.00228468	Processed meat intake	6.54E-05	30.20329725	TRUE
10	rs4240672	N		0.0171201	-0.0142787	0.00481478	0.00209412	Processed meat intake	0.000146528	67.70277926	TRUE
11	rs4778053	Y	horizontal pleiotropic outliers SNP	0.0164667	-0.00421737	0.00664802	0.00289872	Processed meat intake	7.15E-05	33.02166243	TRUE
12	rs6010651	N		-0.0124059	-0.0236132	0.00498384	0.00216796	Processed meat intake	7.25E-05	33.48624919	TRUE
13	rs6484504	N		0.0154728	-0.00887972	0.00537316	0.0023479	Processed meat intake	9.55E-05	44.14427853	TRUE
14	rs6765179	N		-0.0127603	0.00603966	0.00520604	0.00226606	Processed meat intake	6.97E-05	32.18032614	TRUE
15	rs6786550	Y	horizontal pleiotropic outliers SNP	0.0121871	0.00700087	0.00491799	0.00217408	Processed meat intake	6.88E-05	31.80736504	TRUE
16	rs7531118	N		-0.0140719	0.0174398	0.00483488	0.00211347	Processed meat intake	9.86E-05	45.56731156	TRUE
17	rs8096167	N		-0.0145937	-0.00474819	0.00613152	0.00267084	Processed meat intake	6.62E-05	30.60249965	TRUE

Supplementary Table 4 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Cooked vegetable intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10156602	Y	horizontal pleiotropic outliers SNP	0.0110063	-0.0176584	0.00502931	0.00163687	Cooked vegetable intake	2.80E-05	12.54305129	TRUE
2	rs10161952	N		-0.0095798	-8.87E-05	0.00519595	0.00168589	Cooked vegetable intake	1.97E-05	8.849776087	TRUE
3	rs11138705	N		0.0103715	0.00132208	0.0056428	0.00183004	Cooked vegetable intake	1.98E-05	8.87265809	TRUE

4	rs12550717	N		0.00918737	0.0029723	0.00499081	0.00161897	Cooked vegetable intake	1.97E-05	8.85107722	TRUE
5	rs1421085	Y	horizontal pleiotropic outliers SNP	0.0103316	0.032968	0.00492405	0.00159054	Cooked vegetable intake	2.57E-05	11.52640299	TRUE
6	rs2052063	N		-0.00945755	-0.00434821	0.00482265	0.0015679	Cooked vegetable intake	2.23E-05	10.02245931	TRUE
7	rs2102738	N		-0.0121578	-0.000813732	0.00643629	0.00208302	Cooked vegetable intake	2.11E-05	9.462162101	TRUE
8	rs2252508	N		0.0091021	0.00510836	0.00481352	0.00156216	Cooked vegetable intake	2.07E-05	9.278163461	TRUE
9	rs28450747	N		-0.0101604	-0.00938224	0.0056899	0.0018547	Cooked vegetable intake	1.84E-05	8.266644735	TRUE
10	rs28711392	N		-0.0107461	-0.0156964	0.0050196	0.00163223	Cooked vegetable intake	2.68E-05	12.03802431	TRUE
11	rs349062	N		-0.00890406	-0.0136772	0.00492571	0.00159767	Cooked vegetable intake	1.89E-05	8.483484892	TRUE
12	rs4851029	Y	horizontal pleiotropic outliers SNP	0.0101744	0.0227364	0.00481794	0.00156423	Cooked vegetable intake	2.58E-05	11.57737214	TRUE

Supplementary Table 5 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Salad / raw vegetable intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not**	**remove or not(YES or NO)**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs1052352	N		0.00816444	-0.00430515	0.00481674	0.00142564	Salad / raw vegetable intake	1.66E-05	7.24032614	TRUE
2	rs10819082	Y	horizontal pleiotropic outliers SNP	-0.00916475	0.0248468	0.00511603	0.00151342	Salad / raw vegetable intake	1.86E-05	8.119278654	TRUE
3	rs12908495	N		-0.00935	0.00704071	0.00563012	0.00166573	Salad / raw vegetable intake	1.61E-05	6.993384014	TRUE
4	rs13102393	Y	ambiguous palindromic SNPs	0.00797933	0.00488961	0.00481053	0.00143029	Salad / raw vegetable intake	1.59E-05	6.931071559	TRUE

5	rs17460017	Y	horizontal pleiotropic outliers SNP	0.0111744	-0.0269158	0.00611493	0.00181338	Salad / raw vegetable intake	1.92E-05	8.372100629	TRUE
6	rs1890012	N		-0.0104258	-0.0039026	0.00593363	0.00180794	Salad / raw vegetable intake	1.70E-05	7.421994905	TRUE
7	rs2194027	Y	ambiguous palindromic SNPs	-0.00860795	-0.000537916	0.0048298	0.00143565	Salad / raw vegetable intake	1.85E-05	8.058620584	TRUE
8	rs4083969	N		0.017133	-0.00532438	0.010537	0.00311517	Salad / raw vegetable intake	1.58E-05	6.894973017	TRUE
9	rs4291983	N		-0.00839985	-0.000927045	0.00481395	0.00142481	Salad / raw vegetable intake	1.76E-05	7.671419573	TRUE
10	rs62461186	N		-0.0113438	-0.00256488	0.00635519	0.00185732	Salad / raw vegetable intake	1.90E-05	8.264326844	TRUE
11	rs6482190	Y	horizontal pleiotropic outliers SNP	0.0112719	-0.0262908	0.00537941	0.00159025	Salad / raw vegetable intake	2.56E-05	11.1680543	TRUE
12	rs7619139	N		0.0124765	0.00463997	0.00489566	0.00145086	Salad / raw vegetable intake	3.77E-05	16.40660147	TRUE
13	rs7821179	N		-0.0108184	0.00576883	0.00667272	0.00197644	Salad / raw vegetable intake	1.52E-05	6.619291829	TRUE
14	rs790561	N		0.012474	-0.00267738	0.00526947	0.00156199	Salad / raw vegetable intake	3.24E-05	14.11554079	TRUE
15	rs8130508	N		0.0087404	-0.0121705	0.00535278	0.00157797	Salad / raw vegetable intake	1.57E-05	6.844940187	TRUE
16	rs9427220	Y	ambiguous palindromic SNPs	-0.00800801	-0.0055023	0.00481171	0.00144212	Salad / raw vegetable intake	1.58E-05	6.897585698	TRUE

Supplementary Table 6 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Fresh fruit intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**

		NO)									
1	rs10064431	N		-0.00757392	-0.00844975	0.00481861	0.00122365	Fresh fruit intake	1.43E-05	6.389826971	TRUE
2	rs10192394	N		-0.00766096	2.97E-05	0.00482951	0.0012287	Fresh fruit intake	1.46E-05	6.529081875	TRUE
3	rs10249294	N		0.0195637	-0.00263959	0.00495999	0.00126299	Fresh fruit intake	8.95E-05	39.96567613	TRUE
4	rs1051547	N		-0.00757523	0.013413	0.00488299	0.00124161	Fresh fruit intake	1.41E-05	6.307988526	TRUE
5	rs10828266	Y	horizontal pleiotropic outliers SNP	0.0123642	-0.0258804	0.00535758	0.00135696	Fresh fruit intake	3.11E-05	13.88980271	TRUE
6	rs10838724	N		0.00901088	-0.00136373	0.00503315	0.00128277	Fresh fruit intake	1.89E-05	8.431154501	TRUE
7	rs11032362	N		0.0123929	-0.0166555	0.00838063	0.00212339	Fresh fruit intake	1.27E-05	5.670694423	TRUE
8	rs11085749	N		-0.00773361	0.00352034	0.00493456	0.00125477	Fresh fruit intake	1.42E-05	6.335134062	TRUE
9	rs11248509	N		0.00732973	0.00205022	0.00488961	0.00126801	Fresh fruit intake	1.25E-05	5.598901843	TRUE
10	rs11896330	N		-0.00844567	0.0186939	0.00501021	0.0012744	Fresh fruit intake	1.66E-05	7.399572094	TRUE
11	rs12044599	N		0.00942073	-0.0121832	0.00591334	0.0015033	Fresh fruit intake	1.47E-05	6.57547043	TRUE
12	rs12536253	N		-0.00815943	-0.0102045	0.00557216	0.00141599	Fresh fruit intake	1.25E-05	5.558496203	TRUE
13	rs12641371	N		0.00791271	-0.0105016	0.00491162	0.00123354	Fresh fruit intake	1.54E-05	6.863490446	TRUE
14	rs12780952	N		0.00747457	-0.0131757	0.00534863	0.00135361	Fresh fruit intake	1.14E-05	5.097649192	TRUE
15	rs12885598	N		0.00751549	-0.00959818	0.00490902	0.00124738	Fresh fruit intake	1.36E-05	6.068723979	TRUE
16	rs13072255	N		0.00898012	-0.0168901	0.00481176	0.00122355	Fresh fruit intake	2.02E-05	8.999788157	TRUE

17	rs1356292	N		0.00917471	0.0137005	0.00611685	0.00155324	Fresh fruit intake	1.31E-05	5.840710775	TRUE
18	rs1375566	N		-0.00783382	-0.00289018	0.00498803	0.001266	Fresh fruit intake	1.43E-05	6.404962399	TRUE
19	rs149449	N		0.00728855	-0.00670532	0.00482208	0.00122061	Fresh fruit intake	1.33E-05	5.926611943	TRUE
20	rs1620977	N		-0.0131742	-0.00909179	0.00543953	0.00137761	Fresh fruit intake	3.42E-05	15.25485398	TRUE
21	rs17049185	N		0.00804043	0.00855971	0.00546273	0.00139033	Fresh fruit intake	1.27E-05	5.660559524	TRUE
22	rs1866823	Y	horizontal pleiotropic outliers SNP	0.00743079	-0.0205822	0.00486904	0.0012406	Fresh fruit intake	1.37E-05	6.114353436	TRUE
23	rs2048522	Y	ambiguous palindromic SNPs	0.0095625	-0.0209007	0.00489323	0.00124771	Fresh fruit intake	2.25E-05	10.03378895	TRUE
24	rs2093654	N		0.00712915	1.36E-05	0.00495066	0.00125874	Fresh fruit intake	1.21E-05	5.388926537	TRUE
25	rs2143081	N		0.00832073	0.00632883	0.00482718	0.00122891	Fresh fruit intake	1.72E-05	7.678708313	TRUE
26	rs2790688	N		0.0114466	-0.00374464	0.00664312	0.00169613	Fresh fruit intake	1.71E-05	7.624149031	TRUE
27	rs28479795	N		0.0112324	0.0138598	0.0057772	0.00147345	Fresh fruit intake	2.18E-05	9.712502126	TRUE
28	rs2867113	Y	horizontal pleiotropic outliers SNP	-0.0138606	-0.032439	0.00659849	0.00196025	Fresh fruit intake	2.19E-05	9.760766557	TRUE
29	rs329274	N		0.0068183	0.00341116	0.00482434	0.00122813	Fresh fruit intake	1.16E-05	5.18466625	TRUE
30	rs4302893	N		0.00738857	-0.00707425	0.00511271	0.00129959	Fresh fruit intake	1.21E-05	5.423170849	TRUE
31	rs559734	N		0.00776806	-0.0136873	0.00534335	0.00136078	Fresh fruit intake	1.24E-05	5.526484226	TRUE
32	rs60452247	N		0.00796969	-0.00829462	0.00499641	0.00126932	Fresh fruit intake	1.47E-05	6.557790094	TRUE
33	rs647572	N		0.0077216	0.0032464	0.005526	0.001374	Fresh fruit	1.18E-	5.279675	TRUE

	4			3	6	95	06	intake	05	165	
34	rs73455661	N		0.0102938	0.0127334	0.00535407	0.0013622	Fresh fruit intake	2.13E-05	9.523686057	TRUE
35	rs7554485	N		-0.00801014	-0.0101167	0.00493373	0.00125414	Fresh fruit intake	1.52E-05	6.805180985	TRUE
36	rs7818437	N		-0.00804815	0.00645441	0.00570215	0.00145251	Fresh fruit intake	1.17E-05	5.212704591	TRUE
37	rs7869969	Y	horizontal pleiotropic outliers SNP	0.00756738	-0.0201674	0.00511266	0.00129919	Fresh fruit intake	1.27E-05	5.660113053	TRUE
38	rs7982441	N		-0.00841258	0.00702854	0.00543559	0.00137614	Fresh fruit intake	1.39E-05	6.200299357	TRUE
39	rs8095324	N		-0.00694613	0.00981321	0.00490881	0.00124903	Fresh fruit intake	1.16E-05	5.186987896	TRUE
40	rs817223	Y	horizontal pleiotropic outliers SNP	-0.00726908	-0.0208835	0.00480996	0.00122339	Fresh fruit intake	1.32E-05	5.889510135	TRUE
41	rs862227	N		-0.0101452	-0.00827951	0.0048196	0.00122398	Fresh fruit intake	2.55E-05	11.40667473	TRUE
42	rs9517948	N		0.00695315	-0.0162827	0.00484005	0.00123287	Fresh fruit intake	1.20E-05	5.345172405	TRUE
43	rs9919429	Y	horizontal pleiotropic outliers SNP	-0.00672322	0.0225549	0.00481557	0.00122289	Fresh fruit intake	1.13E-05	5.04130466	TRUE
44	rs994270	N		0.0132585	-0.00962045	0.00568968	0.00144389	Fresh fruit intake	3.16E-05	14.11483267	TRUE

Supplementary Table 7 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Dried fruit intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs100267	N		0.0108465	-0.019605	0.005322	0.001842	Dried fruit	2.42E-	10.22519	TRUE

	92				6	53	3	intake	05	276	
2	rs10129747	N		0.00935902	-0.00406643	0.00482965	0.00168126	Dried fruit intake	2.18E-05	9.202035378	TRUE
3	rs10740991	N		0.016739	-0.0254456	0.00536316	0.00185722	Dried fruit intake	5.68E-05	23.94930145	TRUE
4	rs11037497	Y	ambiguous palindromic SNPs	0.0104396	-0.0103011	0.00484195	0.00168442	Dried fruit intake	2.69E-05	11.35860961	TRUE
5	rs11152349	Y	horizontal pleiotropic outliers SNP	0.00991215	0.00258304	0.00524934	0.0018176	Dried fruit intake	2.07E-05	8.7492546	TRUE
6	rs11586016	N		0.00987818	-0.0265372	0.00495766	0.00173034	Dried fruit intake	2.28E-05	9.60411902	TRUE
7	rs11632215	N		-0.0141434	0.00237207	0.0074293	0.00258382	Dried fruit intake	2.12E-05	8.920876747	TRUE
8	rs11720884	Y	horizontal pleiotropic outliers SNP	0.0111797	-0.0157853	0.00582004	0.00193554	Dried fruit intake	2.34E-05	9.887767074	TRUE
9	rs11772627	N		0.0183338	-0.0496497	0.00627641	0.00217099	Dried fruit intake	5.00E-05	21.10843091	TRUE
10	rs1582322	N		0.00994346	-0.0142504	0.00493285	0.00171571	Dried fruit intake	2.36E-05	9.96735731	TRUE
11	rs1622515	N		0.00991719	-0.0150637	0.00481418	0.00167077	Dried fruit intake	2.46E-05	10.36071151	TRUE
12	rs1648404	N		0.00941595	-3.18E-05	0.00481641	0.00167357	Dried fruit intake	2.21E-05	9.327219839	TRUE
13	rs17175518	N		0.0114962	0.00400272	0.0056501	0.00197514	Dried fruit intake	2.36E-05	9.955083456	TRUE
14	rs17184707	N		-0.0114381	0.0156208	0.00585871	0.00204011	Dried fruit intake	2.19E-05	9.243960354	TRUE
15	rs1797235	N		-0.0100206	0.00337892	0.0049288	0.00174235	Dried fruit intake	2.35E-05	9.922057935	TRUE
16	rs2533273	N		-0.00987659	0.00829771	0.00481289	0.00167714	Dried fruit intake	2.44E-05	10.27580666	TRUE
17	rs261809	Y	horizontal pleiotropic outliers SNP	-0.00962858	-0.00169799	0.00484454	0.00167902	Dried fruit intake	2.30E-05	9.710998406	TRUE

18	rs3101339	N		0.0142595	0.0205941	0.00490156	0.00170546	Dried fruit intake	4.87E-05	20.52570919	TRUE
19	rs3764002	N		0.0131215	-0.0246737	0.00546781	0.00190081	Dried fruit intake	3.32E-05	14.02105809	TRUE
20	rs4140799	N		0.0094566	-0.0169764	0.00482466	0.00167846	Dried fruit intake	2.23E-05	9.391203974	TRUE
21	rs4149513	N		0.01173	-0.0274123	0.00481254	0.00167139	Dried fruit intake	3.44E-05	14.50594848	TRUE
22	rs4269101	N		-0.0138099	0.0140382	0.00531885	0.00185921	Dried fruit intake	3.85E-05	16.2536046	TRUE
23	rs4800488	N		0.0119836	-0.0224589	0.00481369	0.00167202	Dried fruit intake	3.59E-05	15.13627391	TRUE
24	rs57499472	N		0.00991231	-0.00576697	0.00492745	0.00171869	Dried fruit intake	2.37E-05	9.979293739	TRUE
25	rs62084586	N		0.0133946	-0.0109594	0.00636728	0.00226174	Dried fruit intake	2.48E-05	10.4626986	TRUE
26	rs72720396	Y	horizontal pleiotropic outliers SNP	0.0114265	-0.00333956	0.00553968	0.00198541	Dried fruit intake	2.31E-05	9.727532238	TRUE
27	rs75641275	N		-0.0141613	0.0471749	0.00651075	0.00238518	Dried fruit intake	2.46E-05	10.38821174	TRUE
28	rs7582086	N		-0.00962821	0.016612	0.00481766	0.00167381	Dried fruit intake	2.31E-05	9.735461729	TRUE
29	rs7808471	N		-0.0115362	0.00866325	0.00514415	0.00178604	Dried fruit intake	2.91E-05	12.25709733	TRUE
30	rs7829800	Y	horizontal pleiotropic outliers SNP	-0.0104463	0.00528983	0.00513327	0.00178709	Dried fruit intake	2.41E-05	10.15998521	TRUE
31	rs7916868	Y	ambiguous palindromic SNPs	0.00960741	0.0197052	0.00481905	0.00167167	Dried fruit intake	2.31E-05	9.732171834	TRUE
32	rs862227	N		-0.0091646	-0.00827951	0.0048196	0.00167238	Dried fruit intake	2.09E-05	8.794595901	TRUE
33	rs893856	Y	horizontal pleiotropic outliers SNP	-0.013361	-0.000729791	0.00676324	0.00234923	Dried fruit intake	2.26E-05	9.546461537	TRUE
34	rs938526	N		0.0120673	-0.032415	0.004831	0.001681	Dried fruit	3.63E-	15.31772	TRUE

	9				9	41	83	intake	05	903	

Supplementary Table 8 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Average weekly red wine intake and risk of Gastroesophageal reflux disease.

	SNP	remove or not(YES or NO)	Reason for removing	beta.exposure	beta.outcome	se.outcome	se.exposure	exposure	R2	F	steiger_dir
1	rs10822129	N		0.01344	-0.022898	0.00493827	0.0021284	Average weekly red wine intake	4.36E-05	14.25232704	TRUE
2	rs10925183	N		-0.011922	0.0136976	0.00504712	0.00211168	Average weekly red wine intake	3.39E-05	11.08420011	TRUE
3	rs11714337	Y	horizontal pleiotropic outliers SNP	0.0123918	-0.0239611	0.00491478	0.00208811	Average weekly red wine intake	3.77E-05	12.32956396	TRUE
4	rs11715683	N		0.013978	-0.00598375	0.00517082	0.00217352	Average weekly red wine intake	4.41E-05	14.43753698	TRUE
5	rs12692596	N		-0.0116782	0.0198715	0.0049766	0.0021345	Average weekly red wine intake	3.18E-05	10.40306247	TRUE
6	rs1446577	N		0.0151328	-0.0275736	0.00549193	0.00236106	Average weekly red wine intake	4.37E-05	14.28055167	TRUE
7	rs17817497	Y	horizontal pleiotropic outliers SNP	0.014091	0.0328632	0.00492565	0.00211408	Average weekly red wine intake	4.73E-05	15.48329189	TRUE
8	rs303753	N		-0.0183206	0.0241635	0.0050911	0.0021899	Average weekly red wine intake	7.58E-05	24.79458297	TRUE
9	rs35698	N		-0.015348	0.014772	0.00626	0.00269	Average weekly red	3.48E-	11.38838	TRUE

	271			7	2	639	709	wine intake	05	603	
10	rs4643716	N		0.0115308	-0.00494447	0.00495813	0.00210517	Average weekly red wine intake	3.23E-05	10.56566923	TRUE
11	rs627685	N		-0.0125352	0.0137317	0.00525314	0.00226097	Average weekly red wine intake	3.32E-05	10.84980629	TRUE
12	rs6882046	N		0.0162857	-0.00291422	0.00548727	0.00234886	Average weekly red wine intake	5.21E-05	17.05093927	TRUE
13	rs6908328	N		0.0127108	-0.0174997	0.0048102	0.00206267	Average weekly red wine intake	4.04E-05	13.19899243	TRUE
14	rs713598	Y	horizontal pleiotropic outliers SNP	-0.0173682	-0.00231607	0.0049072	0.00210277	Average weekly red wine intake	7.24E-05	23.67926583	TRUE
15	rs898751	N		-0.012363	0.00834463	0.00482699	0.00206424	Average weekly red wine intake	3.82E-05	12.49318648	TRUE
16	rs9388171	Y	ambiguous palindromic SNPs	0.0145704	-0.0312521	0.00481844	0.00206677	Average weekly red wine intake	5.30E-05	17.3228229	TRUE

Supplementary Table 9 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Average weekly beer plus cider intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10822159			-0.0119112	-0.0195954	0.00481924	0.00173385	Average weekly beer plus cider intake	3.45E-05	11.30762583	TRUE
2	rs12046000			-0.0136389	-0.0159131	0.00483569	0.00172363	Average weekly beer plus cider intake	4.60E-05	15.06809549	TRUE
3	rs12513581			-0.0110019	-0.00765181	0.00481455	0.00171278	Average weekly beer plus cider intake	3.02E-05	9.898356627	TRUE
4	rs13130794			-0.0119638	-0.00549381	0.00500461	0.00177878	Average weekly beer plus cider intake	3.33E-05	10.91060722	TRUE
5	rs13876			0.009963	0.007121	0.00487	0.00173	Average weekly beer plus	2.43E	7.94893	TRUE

	95			78	24	914	417	cider intake	-05	8329	
6	rs1421085	Y	horizontal pleiotropic outliers SNP	-0.0154588	0.032968	0.00492405	0.00174549	Average weekly beer plus cider intake	5.74E-05	18.81623278	TRUE
7	rs1520929	Y	horizontal pleiotropic outliers SNP	0.0119855	-0.013317	0.00483965	0.00172587	Average weekly beer plus cider intake	3.55E-05	11.64379981	TRUE
8	rs2533273			0.0110845	0.00829771	0.00481289	0.00171533	Average weekly beer plus cider intake	3.07E-05	10.05582616	TRUE
9	rs2883059	Y	horizontal pleiotropic outliers SNP	0.0116948	0.0439648	0.00486238	0.00172733	Average weekly beer plus cider intake	3.34E-05	10.95120353	TRUE
10	rs34178057			0.0165482	0.0281511	0.00809122	0.00286516	Average weekly beer plus cider intake	2.44E-05	8.009520437	TRUE
11	rs75413320			0.0165527	0.0208139	0.0071257	0.00276055	Average weekly beer plus cider intake	2.64E-05	8.656135079	TRUE
12	rs7851830	Y	horizontal pleiotropic outliers SNP	-0.0132899	-0.00100258	0.00567289	0.00201723	Average weekly beer plus cider intake	3.17E-05	10.38524792	TRUE
13	rs8044722			-0.0100128	-0.0121318	0.00495386	0.00176015	Average weekly beer plus cider intake	2.36E-05	7.729807562	TRUE
14	rs9824301			-0.0103056	-0.0138127	0.00504614	0.00179806	Average weekly beer plus cider intake	2.42E-05	7.928525866	TRUE
15	rs9969466	Y	ambiguous palindromic SNPs	0.0103307	-0.00850177	0.00487876	0.00173331	Average weekly beer plus cider intake	2.62E-05	8.587230443	TRUE

Supplementary Table 10 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Coffee intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10119174	N		-0.00939786	-0.00696609	0.00494543	0.00164159	Coffee intake	2.16E-05	9.278243358	TRUE
2	rs105786	N		0.0199509	-0.001775	0.005364	0.001785	Coffee	8.11E-05	34.78659	TRUE

	8				02	39	17	intake		325	
3	rs12514566	N		-0.0113972	0.00529516	0.00509718	0.00170562	Coffee intake	2.90E-05	12.44899407	TRUE
4	rs12989746	N		0.01035	0.0102252	0.00535512	0.00186429	Coffee intake	2.01E-05	8.612327762	TRUE
5	rs13054099	Y	horizontal pleiotropic outliers SNP	-0.0107777	0.0143439	0.00546979	0.00183597	Coffee intake	2.24E-05	9.608692999	TRUE
6	rs13163336	N		0.0149472	0.00543504	0.00661344	0.00221005	Coffee intake	2.97E-05	12.7216351	TRUE
7	rs1338549	Y	horizontal pleiotropic outliers SNP	-0.00945121	0.0334763	0.00482175	0.0016218	Coffee intake	2.22E-05	9.533081959	TRUE
8	rs13387939	Y	horizontal pleiotropic outliers SNP	0.0165558	0.0321357	0.00638127	0.0021386	Coffee intake	3.90E-05	16.71329046	TRUE
9	rs1421085	Y	horizontal pleiotropic outliers SNP	0.0185426	0.032968	0.00492405	0.00164436	Coffee intake	8.28E-05	35.49513988	TRUE
10	rs1527961	N		-0.0133431	0.00732637	0.00708792	0.00236585	Coffee intake	2.08E-05	8.910739351	TRUE
11	rs17842490	N		-0.0451683	-0.0156455	0.0205293	0.00680848	Coffee intake	2.87E-05	12.28897792	TRUE
12	rs2189234	N		0.00998689	-0.00778133	0.00493985	0.00166052	Coffee intake	2.36E-05	10.10010108	TRUE
13	rs2465037	N		-0.0106317	-0.00307877	0.00507605	0.00170743	Coffee intake	2.55E-05	10.92444945	TRUE
14	rs2472297	N		0.0464708	0.011047	0.00543309	0.00182733	Coffee intake	0.000418465	179.537193	TRUE
15	rs34060476	N		0.0184292	0.000245375	0.00718048	0.00237033	Coffee intake	3.94E-05	16.8876349	TRUE
16	rs4410790	N		0.039072	0.0159406	0.00500264	0.00167288	Coffee intake	0.000354999	152.2982269	TRUE
17	rs442355	N		-0.0111372	0.00502404	0.00551808	0.00185374	Coffee intake	2.35E-05	10.09109464	TRUE
18	rs4615895	N		0.0122025	-0.00760799	0.00552519	0.00184972	Coffee intake	2.86E-05	12.25805549	TRUE

19	rs476828	N		0.0173461	0.00400272	0.0056501	0.00189543	Coffee intake	5.45E-05	23.36305492	TRUE
20	rs516636	N		0.0116767	0.0160648	0.00588799	0.00198419	Coffee intake	2.25E-05	9.663932392	TRUE
21	rs57918684	Y	horizontal pleiotropic outliers SNP	0.0128864	-0.0208647	0.00668953	0.00223845	Coffee intake	2.17E-05	9.315255408	TRUE
22	rs6062682	N		0.0103704	-0.00417581	0.00484414	0.00163929	Coffee intake	2.68E-05	11.47273015	TRUE
23	rs6063085	N		0.0104106	-0.0091147	0.00496589	0.00166919	Coffee intake	2.54E-05	10.87615759	TRUE
24	rs62064918	N		-0.0103075	-0.00563186	0.00559351	0.00187872	Coffee intake	1.96E-05	8.417747161	TRUE
25	rs630194	N		-0.0113533	0.00741232	0.00505881	0.00169853	Coffee intake	2.91E-05	12.46396208	TRUE
26	rs6469262	N		-0.00915347	-0.00186696	0.00485158	0.00162895	Coffee intake	2.06E-05	8.831611777	TRUE
27	rs7224815	N		-0.0108602	-0.0126517	0.00490561	0.00164162	Coffee intake	2.85E-05	12.21598212	TRUE
28	rs73075167	N		-0.0160639	-0.00359773	0.00722757	0.00244429	Coffee intake	2.90E-05	12.44950873	TRUE
29	rs75347775	N		0.0104504	0.0087632	0.00556685	0.00187898	Coffee intake	2.02E-05	8.652427599	TRUE
30	rs780093	N		0.0132935	-0.00396855	0.00494578	0.00165695	Coffee intake	4.18E-05	17.9304449	TRUE
31	rs7811609	N		0.00913864	0.00790417	0.0049613	0.00166468	Coffee intake	1.96E-05	8.392271997	TRUE
32	rs9398171	N		0.0108577	0.00426738	0.00530591	0.00177995	Coffee intake	2.42E-05	10.39649901	TRUE

Supplementary Table 11 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Tea intake and risk of Gastroesophageal reflux disease.

	SNP	remov	Reason for removing	beta.expos	beta.outco	se.outco	se.expos	exposur	R2	F	steiger_

		e or not(YES or NO)		ure	me	me	ure	e			dir
1	rs10752269	Y	horizontal pleiotropic outliers SNP	-0.0128727	-0.0218922	0.00483911	0.00211975	Tea intake	4.14E-05	18.53573736	TRUE
2	rs10764990	Y	horizontal pleiotropic outliers SNP	-0.0121906	-0.00219901	0.00492198	0.00216898	Tea intake	3.54E-05	15.86217892	TRUE
3	rs11164870	N		-0.0119604	-0.0157966	0.00496494	0.00218232	Tea intake	3.42E-05	15.30372599	TRUE
4	rs1156588	N		-0.015454	0.00484501	0.00591165	0.00260325	Tea intake	3.96E-05	17.73494638	TRUE
5	rs11587444	N		0.0140328	-0.0102044	0.00502847	0.00217078	Tea intake	4.70E-05	21.03036241	TRUE
6	rs13282783	Y	horizontal pleiotropic outliers SNP	-0.0135837	0.0154576	0.00524596	0.00235432	Tea intake	3.77E-05	16.85781189	TRUE
7	rs132904	N		0.0166007	-0.0105999	0.00580875	0.00255257	Tea intake	4.75E-05	21.25546763	TRUE
8	rs1453548	N		-0.0133414	-0.0057262	0.00501209	0.00224973	Tea intake	3.97E-05	17.74631335	TRUE
9	rs1481012	N		-0.0262435	-0.0103167	0.00759041	0.00335608	Tea intake	6.86E-05	30.70351244	TRUE
10	rs17245213	N		-0.0146481	-0.00213465	0.00594938	0.00260905	Tea intake	3.54E-05	15.82024679	TRUE
11	rs17685	N		0.0230655	-0.00177502	0.00536439	0.00236195	Tea intake	0.000106669	47.73765626	TRUE
12	rs2117137	N		0.0129948	0.00754158	0.00489815	0.0021557	Tea intake	4.07E-05	18.21191207	TRUE
13	rs2273447	N		0.0174715	-0.0107616	0.00597572	0.00263421	Tea intake	4.95E-05	22.16488607	TRUE
14	rs2279844	N		-0.0119879	-0.00763384	0.00495926	0.00218318	Tea intake	3.38E-05	15.14123386	TRUE
15	rs235118	N		0.0129023	-0.0076136	0.005134	0.002282	Tea	3.62E-05	16.18143	TRUE

	7				8	25	3	intake		615	
16	rs2472297	N		0.0533453	0.011047	0.00543309	0.00240098	Tea intake	0.000550304	246.3872727	TRUE
17	rs2478875	N		0.0218943	-0.00685702	0.00593391	0.00261129	Tea intake	7.92E-05	35.43442013	TRUE
18	rs2645929	N		-0.0149842	0.0044459	0.00615808	0.0027166	Tea intake	3.41E-05	15.27119175	TRUE
19	rs2783129	Y	ambiguous palindromic SNPs	-0.0117331	-0.00182613	0.0048301	0.00213314	Tea intake	3.44E-05	15.38718729	TRUE
20	rs34619	N		0.0117117	-0.00682396	0.00484581	0.0021375	Tea intake	3.36E-05	15.05208923	TRUE
21	rs4410790	N		0.0405506	0.0159406	0.00500264	0.00219507	Tea intake	0.000382772	171.3495507	TRUE
22	rs4808193	N		0.0151149	0.00605291	0.00508685	0.0022472	Tea intake	5.09E-05	22.78681566	TRUE
23	rs4817505	N		0.015068	0.00563789	0.00494397	0.0021746	Tea intake	5.40E-05	24.17116009	TRUE
24	rs56188862	N		-0.0157568	-0.0113626	0.0049357	0.0021747	Tea intake	5.89E-05	26.36922108	TRUE
25	rs56348300	N		0.0158824	0.0141565	0.00623493	0.00273191	Tea intake	3.80E-05	16.99269347	TRUE
26	rs57462170	N		0.0191505	0.0105076	0.00756101	0.00340563	Tea intake	3.56E-05	15.90970499	TRUE
27	rs57631352	N		-0.0131035	-0.00269781	0.00527763	0.00232117	Tea intake	3.58E-05	16.03832078	TRUE
28	rs6829	N		-0.0119163	-0.00482641	0.00494693	0.00216546	Tea intake	3.42E-05	15.29849008	TRUE
29	rs713598	N		0.0133969	-0.00231607	0.0049072	0.00215659	Tea intake	4.32E-05	19.31173851	TRUE
30	rs72797284	N		-0.0171147	0.002593	0.00538135	0.00238353	Tea intake	5.78E-05	25.88404811	TRUE
31	rs7757102	N		-0.0118039	0.00226435	0.00483898	0.00213302	Tea intake	3.44E-05	15.39618232	TRUE

32	rs9302428	Y	horizontal pleiotropic outliers SNP	0.0122457	0.0199642	0.0049922	0.00220122	Tea intake	3.47E-05	15.53889451	TRUE
33	rs9624470	N		0.0252071	-0.0090871	0.00488938	0.00215485	Tea intake	0.000154777	69.27079782	TRUE
34	rs9937354	Y	horizontal pleiotropic outliers SNP	-0.0140923	0.0331838	0.00486291	0.0021433	Tea intake	4.85E-05	21.70549973	TRUE

Supplementary Table 12 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Cheese intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs1024853	Y	ambiguous palindromic SNPs	-0.0128634	-0.0038253	0.00486933	0.00226242	Cheese intake	4.07E-05	18.38910536	TRUE
2	rs10896050	N		-0.0184695	0.0193613	0.0060891	0.00283438	Cheese intake	5.32E-05	24.00487459	TRUE
3	rs10938397	N		-0.0127071	0.0212978	0.00484971	0.00225751	Cheese intake	3.97E-05	17.91288689	TRUE
4	rs113367286	N		0.0151797	-0.022392	0.00547326	0.00249985	Cheese intake	4.63E-05	20.90350312	TRUE
5	rs11620149	N		-0.0176745	0.0169465	0.00697022	0.0032085	Cheese intake	3.84E-05	17.31602362	TRUE
6	rs11649653	N		0.0138485	-0.0187928	0.00494301	0.00229169	Cheese intake	4.53E-05	20.44344394	TRUE
7	rs12296440	N		0.0187942	-0.0104014	0.00643396	0.00297985	Cheese intake	4.98E-05	22.46930975	TRUE
8	rs12447542	N		0.0197476	-0.0102278	0.00732788	0.00340698	Cheese intake	4.28E-05	19.33436608	TRUE

9	rs12475594	N		0.0160073	-0.00934372	0.00630873	0.00292518	Cheese intake	3.76E-05	16.96144632	TRUE
10	rs12786959	N		-0.0160712	0.0218336	0.00605776	0.00281988	Cheese intake	4.07E-05	18.39569756	TRUE
11	rs1291145	N		-0.0202495	0.0071212	0.00518625	0.00241026	Cheese intake	8.83E-05	39.89118759	TRUE
12	rs13107325	Y	horizontal pleiotropic outliers SNP	-0.0291639	0.0701443	0.00918312	0.00425285	Cheese intake	5.88E-05	26.54146022	TRUE
13	rs1434511	N		0.0129646	-0.00750167	0.00484604	0.00225868	Cheese intake	4.17E-05	18.82053387	TRUE
14	rs1514755	N		0.0163749	-0.0217324	0.00560944	0.00261651	Cheese intake	4.89E-05	22.05692874	TRUE
15	rs17115145	N		-0.0128806	0.0147665	0.00491894	0.00228956	Cheese intake	3.99E-05	17.99714051	TRUE
16	rs1806771	Y	horizontal pleiotropic outliers SNP	-0.0221467	-0.00769522	0.00859767	0.004035	Cheese intake	3.93E-05	17.75011405	TRUE
17	rs2339928	N		0.0148578	-0.00660656	0.00526253	0.00244494	Cheese intake	4.60E-05	20.76714237	TRUE
18	rs2352974	Y	horizontal pleiotropic outliers SNP	-0.0144972	0.0448044	0.00483353	0.0022428	Cheese intake	5.25E-05	23.71332056	TRUE
19	rs26579	N		-0.0128007	0.001112	0.00492421	0.00229427	Cheese intake	3.97E-05	17.94562208	TRUE
20	rs2802530	Y	horizontal pleiotropic outliers SNP	0.0186266	-0.043946	0.00729169	0.00339704	Cheese intake	3.76E-05	16.95661508	TRUE
21	rs2854175	N		0.0169937	-0.0176239	0.00549133	0.00256857	Cheese intake	5.52E-05	24.92798852	TRUE
22	rs2960578	N		0.0170282	-0.0235972	0.00481449	0.00223594	Cheese intake	7.25E-05	32.72859644	TRUE
23	rs34198643	N		-0.0167006	0.010615	0.00578824	0.00267855	Cheese intake	4.85E-05	21.90106129	TRUE
24	rs35270670	N		0.0163794	0.00206538	0.00587314	0.00270974	Cheese intake	4.57E-05	20.64748813	TRUE
25	rs391101	N		0.0213573	-0.0093186	0.007862	0.003439	Cheese	4.85E-	21.89464	TRUE

	6			9	85	9	intake	05	96	
26	rs4296548	N	0.0130245	-0.00640946	0.00492208	0.00228781	Cheese intake	4.04E-05	18.2280028	TRUE
27	rs4503172	N	0.0129596	-0.0148557	0.0049274	0.002293	Cheese intake	4.00E-05	18.06816461	TRUE
28	rs4681981	N	-0.0124361	0.0134741	0.00487909	0.00224121	Cheese intake	3.85E-05	17.39016299	TRUE
29	rs4692708	N	0.0147298	0.0024396	0.00555593	0.00258904	Cheese intake	4.10E-05	18.49724461	TRUE
30	rs4776970	N	0.0154088	-0.0196256	0.00502929	0.00232683	Cheese intake	5.46E-05	24.63837489	TRUE
31	rs4860341	N	0.0243652	-0.003172	0.00931683	0.00435152	Cheese intake	3.93E-05	17.73896152	TRUE
32	rs524468	N	-0.0142421	0.00666328	0.00548888	0.00255161	Cheese intake	3.91E-05	17.64807067	TRUE
33	rs531358	N	0.0131666	-0.0201036	0.00504554	0.00233731	Cheese intake	3.95E-05	17.81233345	TRUE
34	rs6126641	N	0.013226	-0.0216605	0.00506579	0.00239492	Cheese intake	3.90E-05	17.62581077	TRUE
35	rs62034322	N	-0.0139355	0.0216349	0.00488153	0.00229986	Cheese intake	4.57E-05	20.65453193	TRUE
36	rs6685323	N	-0.0131886	-0.000819049	0.00520232	0.00241592	Cheese intake	3.72E-05	16.77722708	TRUE
37	rs67238148	N	0.0165432	0.000337327	0.00584297	0.00271432	Cheese intake	4.66E-05	21.02825973	TRUE
38	rs6873324	N	-0.0124766	0.00179167	0.00487991	0.00227073	Cheese intake	3.81E-05	17.18386416	TRUE
39	rs73096946	N	-0.0205914	0.0233328	0.00663909	0.00306664	Cheese intake	5.62E-05	25.38959205	TRUE
40	rs73335955	N	0.0277726	-0.0153235	0.0104941	0.00497824	Cheese intake	3.89E-05	17.58485798	TRUE
41	rs7936836	N	0.0159029	-0.00956642	0.00488885	0.00227272	Cheese intake	6.15E-05	27.77059266	TRUE

42	rs9504123	N		0.0141706	-0.00346615	0.00539749	0.00250387	Cheese intake	4.00E-05	18.06568125	TRUE
43	rs975303	N		0.0212756	-0.0114659	0.00623108	0.00290699	Cheese intake	6.72E-05	30.33765471	TRUE

Supplementary Table 13 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Cereal intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10057775	N		0.0200293	-0.00376221	0.00779449	0.00289378	Cereal intake	3.82E-05	16.85125252	TRUE
2	rs10837531	Y	ambiguous palindromic SNPs	0.0107836	-0.00704303	0.00488044	0.00179687	Cereal intake	2.88E-05	12.73544061	TRUE
3	rs10857964	N		0.0140866	-0.00987333	0.00596762	0.0022053	Cereal intake	3.24E-05	14.28886483	TRUE
4	rs11038810	N		0.0111343	-0.0136285	0.00502705	0.00186325	Cereal intake	2.84E-05	12.55135535	TRUE
5	rs1104608	Y	ambiguous palindromic SNPs	0.0108629	-0.00412846	0.00489755	0.00181843	Cereal intake	2.89E-05	12.7454222	TRUE
6	rs11097340	N		-0.0115334	0.0122281	0.00491305	0.00181501	Cereal intake	3.19E-05	14.09479662	TRUE
7	rs112780312	N		-0.0121483	0.010467	0.00523719	0.0020189	Cereal intake	2.94E-05	12.99421139	TRUE
8	rs11940694	N		-0.0126647	0.00510905	0.00494879	0.00183426	Cereal intake	3.84E-05	16.94259025	TRUE
9	rs12354267	N		0.0116473	-0.024468	0.00520899	0.00193279	Cereal intake	2.90E-05	12.79612518	TRUE

10	rs13234131	N		0.0170117	0.000134995	0.00717938	0.0026602	Cereal intake	3.24E-05	14.301099	TRUE
11	rs2450126	Y	horizontal pleiotropic outliers SNP	-0.0149019	-0.0112477	0.00650224	0.00245669	Cereal intake	2.94E-05	12.96333908	TRUE
12	rs2472297	N		-0.0158518	0.011047	0.00543309	0.00202189	Cereal intake	4.85E-05	21.42997803	TRUE
13	rs2504706	N		0.0181793	-0.00946495	0.00567149	0.00210238	Cereal intake	5.94E-05	26.21612788	TRUE
14	rs2817377	N		0.00990084	0.00466172	0.0048172	0.00178933	Cereal intake	2.44E-05	10.76099289	TRUE
15	rs3115230	N		-0.0114779	-0.00156796	0.00559095	0.00207131	Cereal intake	2.46E-05	10.85100311	TRUE
16	rs4410790	N		-0.0109143	0.0159406	0.00500264	0.00184697	Cereal intake	2.77E-05	12.25429295	TRUE
17	rs4739095	N		-0.0128656	0.00126672	0.00568085	0.00210523	Cereal intake	2.97E-05	13.11381403	TRUE
18	rs4797242	N		0.0114312	-0.00608249	0.00525438	0.00194889	Cereal intake	2.73E-05	12.05448492	TRUE
19	rs491711	N		0.0116885	-0.0172793	0.00521183	0.00193366	Cereal intake	2.93E-05	12.95150248	TRUE
20	rs56131196	N		0.0180024	-0.0206635	0.00614259	0.00227695	Cereal intake	4.96E-05	21.91516499	TRUE
21	rs62442924	Y	horizontal pleiotropic outliers SNP	0.0127309	-0.0498765	0.00620228	0.00225709	Cereal intake	2.54E-05	11.20472865	TRUE
22	rs627185	Y	ambiguous palindromic SNPs	-0.0108269	0.007907	0.00483449	0.00179076	Cereal intake	2.91E-05	12.8406007	TRUE
23	rs6545770	N		-0.013728	0.0141882	0.00556351	0.00206041	Cereal intake	3.55E-05	15.68493313	TRUE
24	rs67723420	N		0.0105252	-0.0216381	0.0049235	0.00184665	Cereal intake	2.60E-05	11.48323988	TRUE
25	rs68136852	N		-0.0141222	0.0106724	0.00670999	0.00247848	Cereal intake	2.58E-05	11.37710878	TRUE
26	rs6918737	N		0.0137325	-0.0148999	0.005682	0.002109	Cereal	3.39E-	14.95039	TRUE

						59	76	intake	05	402	
27	rs7040561	N		-0.0162685	0.0180025	0.00676856	0.00252002	Cereal intake	3.36E-05	14.85141627	TRUE
28	rs7619139	N		-0.016951	0.00463997	0.00489566	0.00181499	Cereal intake	6.96E-05	30.73214955	TRUE
29	rs79642906	N		-0.0181581	0.0192142	0.00879329	0.00322812	Cereal intake	2.52E-05	11.12134318	TRUE
30	rs8097544	N		-0.0246368	0.0353812	0.00683224	0.00254108	Cereal intake	7.53E-05	33.27467466	TRUE
31	rs9374896	Y	horizontal pleiotropic outliers SNP	0.0175265	-0.0338759	0.00482056	0.00179165	Cereal intake	7.64E-05	33.76368631	TRUE
32	rs9846396	N		0.0119674	-0.0105852	0.00484869	0.00180031	Cereal intake	3.53E-05	15.59721761	TRUE
33	rs9987289	N		0.0178679	0.00724211	0.00835764	0.0030947	Cereal intake	2.65E-05	11.69042314	TRUE

Supplementary Table 14 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Non-oily fish intake and risk of Gastroesophageal reflux disease.

	SNP	remove or not(YES or NO)	Reason for removing	beta.exposure	beta.outcome	se.outcome	se.exposure	exposure	R2	F	steiger_dir
1	rs11680516	N		0.0122842	0.00602562	0.00599779	0.00202829	Non-oily fish intake	2.44E-05	11.22707722	TRUE
2	rs1260326	N		-0.00955354	-0.00380969	0.00492172	0.0016553	Non-oily fish intake	2.18E-05	10.05915842	TRUE
3	rs16822430	N		0.0116344	0.0203969	0.00570283	0.00191996	Non-oily fish intake	2.42E-05	11.15600638	TRUE
4	rs17317920	Y	horizontal pleiotropic outliers SNP	0.00906029	-0.00655142	0.00482553	0.0016312	Non-oily fish intake	2.05E-05	9.442108849	TRUE
5	rs37990	N		-0.0107346	-0.010668	0.00522	0.001757	Non-oily fish	2.46E-	11.35986	TRUE

	77				9	046	64	intake	05	268	
6	rs56094641	Y	horizontal pleiotropic outliers SNP	0.0125875	0.032968	0.00492405	0.00165108	Non-oily fish intake	3.82E-05	17.59229258	TRUE
7	rs7148387	N		-0.00930647	-0.0064767	0.00489784	0.00165022	Non-oily fish intake	2.09E-05	9.650941322	TRUE

Supplementary Table 15 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Oily fish intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10061973	N		-0.0108521	-0.00321905	0.00482133	0.00191598	Oily fish intake	2.94E-05	13.54625043	TRUE
2	rs10076975	N		0.0112394	0.00760154	0.00493957	0.0019672	Oily fish intake	2.98E-05	13.72362281	TRUE
3	rs10510554	N		0.0110446	0.00311625	0.00487017	0.00193636	Oily fish intake	2.99E-05	13.77238642	TRUE
4	rs10513136	N		-0.0233232	0.0146881	0.00970749	0.00386307	Oily fish intake	3.33E-05	15.31496122	TRUE
5	rs10828250	Y	horizontal pleiotropic outliers SNP	-0.0201462	0.0292335	0.00527625	0.00207341	Oily fish intake	8.67E-05	39.92936049	TRUE
6	rs11859365	N		0.0225669	-0.0043191	0.00553195	0.00219679	Oily fish intake	9.64E-05	44.40861418	TRUE
7	rs11986122	Y	ambiguous palindromic SNPs	0.0148173	0.00435317	0.00489541	0.00194936	Oily fish intake	5.36E-05	24.66792862	TRUE
8	rs1201289	N		-0.0107265	0.00163354	0.00492281	0.0019595	Oily fish intake	2.75E-05	12.65529244	TRUE
9	rs12663865	N		0.012772	-0.0116856	0.00561813	0.00223239	Oily fish intake	2.99E-05	13.77091292	TRUE

10	rs12855717	Y	horizontal pleiotropic outliers SNP	-0.0122298	0.0157426	0.00486018	0.00192275	Oily fish intake	3.73E-05	17.16809071	TRUE
11	rs12896749	N		-0.0109641	0.00542556	0.00494365	0.00196607	Oily fish intake	2.85E-05	13.10240567	TRUE
12	rs13070166	N		0.0142105	0.00118498	0.00574314	0.00227811	Oily fish intake	3.56E-05	16.39628929	TRUE
13	rs1361016	N		0.0149567	-0.020519	0.00666163	0.00265295	Oily fish intake	2.93E-05	13.50153899	TRUE
14	rs1421085	Y	horizontal pleiotropic outliers SNP	0.0184814	0.032968	0.00492405	0.00194873	Oily fish intake	8.22E-05	37.8531576	TRUE
15	rs16891727	Y	horizontal pleiotropic outliers SNP	-0.0237173	-0.0392019	0.00695861	0.00284003	Oily fish intake	6.35E-05	29.25943146	TRUE
16	rs17050031	N		-0.0120492	-0.00641469	0.00482289	0.0019207	Oily fish intake	3.62E-05	16.68620377	TRUE
17	rs1876245	Y	horizontal pleiotropic outliers SNP	0.0151162	-0.024205	0.00485541	0.00193122	Oily fish intake	5.61E-05	25.81013169	TRUE
18	rs1951286	N		-0.0145833	0.00200702	0.00502249	0.00199948	Oily fish intake	4.87E-05	22.42558185	TRUE
19	rs2374424	N		-0.0114437	0.00988763	0.00487805	0.00195609	Oily fish intake	3.14E-05	14.45355855	TRUE
20	rs2827161	N		0.0107114	-0.00450354	0.00488493	0.00193719	Oily fish intake	2.80E-05	12.89293923	TRUE
21	rs28533540	N		0.0146421	-0.00494901	0.00482083	0.00192478	Oily fish intake	5.33E-05	24.56445647	TRUE
22	rs28623270	N		-0.0178328	-0.000674339	0.00683376	0.00273746	Oily fish intake	4.03E-05	18.53842334	TRUE
23	rs2952140	N		-0.0106774	0.00498931	0.00481272	0.00191504	Oily fish intake	2.85E-05	13.10783918	TRUE
24	rs303817	N		0.0135799	0.00352675	0.0055755	0.00220965	Oily fish intake	3.45E-05	15.87273118	TRUE
25	rs3124402	N		-0.0220014	-0.00681836	0.00542443	0.00215651	Oily fish intake	9.47E-05	43.59743838	TRUE
26	rs400247	N		-0.0192439	0.0011052	0.004831	0.001924	Oily fish	9.18E-	42.24989	TRUE

	1				7	11	4	intake	05	076	
27	rs4278546	N		0.0125555	0.00340491	0.00496607	0.00193806	Oily fish intake	3.89E-05	17.89481403	TRUE
28	rs4869859	Y	horizontal pleiotropic outliers SNP	0.0140098	-0.0169259	0.0048355	0.00192207	Oily fish intake	4.86E-05	22.36779088	TRUE
29	rs510161	Y	horizontal pleiotropic outliers SNP	-0.0112998	-0.0163573	0.00520246	0.00206615	Oily fish intake	2.73E-05	12.58415041	TRUE
30	rs552234	N		-0.0116474	-0.00130875	0.00481724	0.00191252	Oily fish intake	3.39E-05	15.61532706	TRUE
31	rs59355765	N		-0.0162522	0.00818836	0.00654273	0.00260966	Oily fish intake	3.55E-05	16.35259033	TRUE
32	rs6033437	N		0.0124683	-0.00144338	0.00555899	0.00220977	Oily fish intake	2.97E-05	13.68001645	TRUE
33	rs6059844	N		0.0110001	0.00827102	0.0048128	0.00191451	Oily fish intake	3.02E-05	13.92770252	TRUE
34	rs631490	N		-0.0151398	0.0110502	0.00524153	0.00210253	Oily fish intake	4.73E-05	21.77114028	TRUE
35	rs6465487	N		-0.0123535	0.00493118	0.00491762	0.00195628	Oily fish intake	3.66E-05	16.86219714	TRUE
36	rs703987	N		0.0111218	0.00444296	0.00496375	0.00197362	Oily fish intake	2.93E-05	13.48560679	TRUE
37	rs7243428	Y	horizontal pleiotropic outliers SNP	-0.0129784	0.0350683	0.00576416	0.00229212	Oily fish intake	2.93E-05	13.5092288	TRUE
38	rs7254235	N		-0.0106304	-0.00173561	0.00487463	0.00194012	Oily fish intake	2.76E-05	12.69788558	TRUE
39	rs7683782	N		0.0144775	-0.0109928	0.00648055	0.00257399	Oily fish intake	2.91E-05	13.39959139	TRUE
40	rs790564	N		0.0146906	-7.92E-05	0.0053834	0.00214766	Oily fish intake	4.32E-05	19.90383698	TRUE
41	rs905575	N		0.0138824	-0.000367392	0.00633988	0.00251917	Oily fish intake	2.80E-05	12.87102101	TRUE
42	rs9597870	N		-0.0127449	-0.00144351	0.00559325	0.00223046	Oily fish intake	3.01E-05	13.86692064	TRUE

43	rs9606833	N		0.0169856	-0.00466521	0.00562804	0.00223087	Oily fish intake	5.32E-05	24.47820668	TRUE
44	rs973526	N		-0.011507	-0.0122067	0.00482866	0.00192962	Oily fish intake	3.31E-05	15.23156982	TRUE
45	rs9841174	N		0.0147781	-0.0043387	0.00496909	0.00198025	Oily fish intake	5.11E-05	23.54175621	TRUE
46	rs9886779	Y	ambiguous palindromic SNPs	-0.0107206	-0.0192422	0.00483541	0.00192877	Oily fish intake	2.83E-05	13.03457886	TRUE
47	rs9889161	N		-0.0133201	0.0130117	0.00502804	0.0020015	Oily fish intake	4.08E-05	18.77529338	TRUE
48	rs9958909	Y	horizontal pleiotropic outliers SNP	0.0157617	0.0332188	0.00695217	0.00277809	Oily fish intake	2.99E-05	13.74950114	TRUE

Supplementary Table 16 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Beef intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10789340	Y	horizontal pleiotropic outliers SNP	-0.0137797	0.0213429	0.00497311	0.00176936	Beef intake	4.44E-05	20.4813946	TRUE
2	rs10959890	Y	horizontal pleiotropic outliers SNP	-0.0126658	-0.0232612	0.00587596	0.00209611	Beef intake	2.68E-05	12.368947	TRUE
3	rs11165829	N		-0.0102001	-0.00252336	0.00501985	0.00177865	Beef intake	2.40E-05	11.05184181	TRUE
4	rs11878917	N		0.0150187	-0.00834413	0.00748301	0.00274812	Beef intake	2.20E-05	10.15602461	TRUE
5	rs12247907	Y	ambiguous palindromic SNPs	0.00984097	0.0225407	0.00481543	0.00171131	Beef intake	2.42E-05	11.15378509	TRUE
6	rs132901	N		0.0139249	-0.0116529	0.00581145	0.00209282	Beef intake	3.24E-05	14.95255327	TRUE

7	rs1421085	Y	horizontal pleiotropic outliers SNP	-0.0121232	0.032968	0.00492405	0.00174274	Beef intake	3.54E-05	16.30910339	TRUE
8	rs1470610	N		-0.0122159	0.00857517	0.0060706	0.00215779	Beef intake	2.35E-05	10.85007631	TRUE
9	rs4676964	N		0.0133533	-0.00771155	0.0048156	0.00172438	Beef intake	4.46E-05	20.54424144	TRUE
10	rs62169335	N		-0.00968628	-0.00655829	0.00488938	0.00173523	Beef intake	2.33E-05	10.7337938	TRUE
11	rs62396185	Y	horizontal pleiotropic outliers SNP	-0.0148447	-0.0209656	0.00541283	0.00195102	Beef intake	4.24E-05	19.55137398	TRUE
12	rs7791463	N		0.00954846	0.00508434	0.00481642	0.00171063	Beef intake	2.27E-05	10.45825706	TRUE
13	rs784251	N		-0.0103387	0.0071542	0.00482303	0.00171651	Beef intake	2.67E-05	12.29600483	TRUE
14	rs9407624	Y	ambiguous palindromic SNPs	-0.0137626	-0.0189829	0.00482308	0.00171589	Beef intake	4.73E-05	21.8206862	TRUE

Supplementary Table 17 Association of the SNPs used as candidate genetic instruments from the GWAS for Mendelian randomization analyses of Bread intake and risk of Gastroesophageal reflux disease.

	SNP	**remove or not(YES or NO)**	**Reason for removing**	**beta.exposure**	**beta.outcome**	**se.outcome**	**se.exposure**	**exposure**	**R2**	**F**	**steiger_dir**
1	rs10761661	N		-0.0114852	0.00741757	0.00483822	0.00200486	Bread intake	3.27E-05	14.78347003	TRUE
2	rs11060853	N		-0.012789	0.0164068	0.00489601	0.00202087	Bread intake	3.96E-05	17.9170451	TRUE
3	rs11183201	N		-0.016725	0.0108954	0.00481983	0.00199574	Bread intake	6.99E-05	31.61974377	TRUE
4	rs116286	N		-0.013495	0.0041866	0.005616	0.002322	Bread	3.35E-05	15.16454	TRUE

	39				4	44	26	intake		764	
5	rs1492988	N		0.0115447	0.00512259	0.00501969	0.00203549	Bread intake	3.20E-05	14.47701645	TRUE
6	rs17083079	N		0.0301138	-0.0244177	0.0111994	0.00467938	Bread intake	4.10E-05	18.52684134	TRUE
7	rs1940033	N		-0.011079	-0.00115668	0.00490278	0.00202843	Bread intake	2.96E-05	13.40040705	TRUE
8	rs1994315	N		-0.0168239	-0.00288703	0.00517103	0.00214445	Bread intake	6.11E-05	27.61364689	TRUE
9	rs2068650	N		-0.013938	0.00281897	0.00482844	0.00199929	Bread intake	4.84E-05	21.89619534	TRUE
10	rs28406095	N		-0.010949	0.00554171	0.0048212	0.00200012	Bread intake	2.98E-05	13.4745326	TRUE
11	rs4665972	N		-0.0142361	-0.00384079	0.0049459	0.00204335	Bread intake	4.85E-05	21.9125678	TRUE
12	rs4984685	N		0.0135849	-0.0126106	0.00602577	0.00248083	Bread intake	2.96E-05	13.40420604	TRUE
13	rs55745436	Y	horizontal pleiotropic outliers SNP	0.0134245	-0.0230249	0.00543251	0.00234263	Bread intake	3.26E-05	14.75022866	TRUE
14	rs656817	N		-0.0126883	0.00573926	0.00510194	0.00210929	Bread intake	3.58E-05	16.20661228	TRUE
15	rs73802707	Y	horizontal pleiotropic outliers SNP	-0.0159296	0.0277534	0.00661419	0.00276165	Bread intake	3.30E-05	14.92697331	TRUE
16	rs75287965	N		-0.0247475	0.0205929	0.0099506	0.00409745	Bread intake	3.61E-05	16.33392531	TRUE
17	rs7802468	N		-0.0233527	-0.00150964	0.00500044	0.00205629	Bread intake	0.000127332	57.59119289	TRUE
18	rs79436018	N		-0.0176147	0.01846	0.00751319	0.00311645	Bread intake	3.19E-05	14.41899112	TRUE
19	rs9323989	N		-0.0116143	0.00166494	0.00495978	0.00205547	Bread intake	3.18E-05	14.36051354	TRUE
20	rs9564268	N		-0.0121606	-0.00823305	0.00494613	0.00204932	Bread intake	3.50E-05	15.8256686	TRUE

21	rs9662365	N		0.0121661	-0.0160875	0.00482143	0.00198921	Bread intake	3.70E-05	16.73486007	TRUE
22	rs9832088	Y	ambiguous palindromic SNPs	0.0147289	0.00354653	0.00483326	0.00198902	Bread intake	5.41E-05	24.48242501	TRUE
23	rs9881332	Y	ambiguous palindromic SNPs	0.0113702	-0.010788	0.00488517	0.00202188	Bread intake	3.15E-05	14.22555838	TRUE

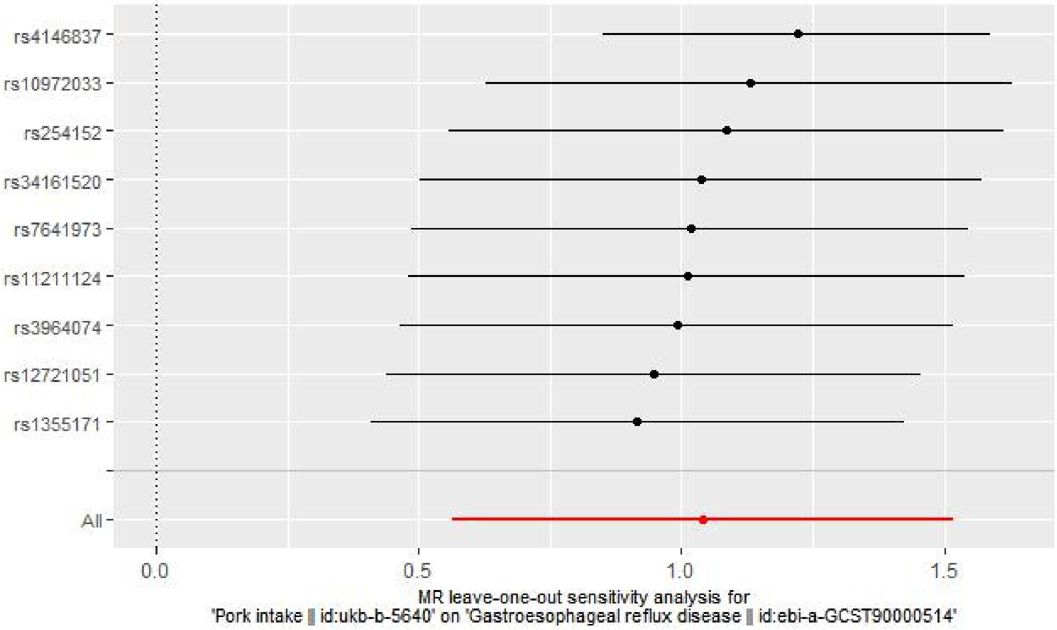
Supplementary Table 18 The complementary MVMR analysis results of the causal effects of dietary intake on GERD.

pork intake	risk factors	OR-IVW	95%CI	P
	BMI	1.76	1.07-2.89	0.025
	MDD	2.06	1.49-2.85	1.37E-05
	Smoking	2.39	1.15-4.99	0.020
	Alcoholic drinking	1.69	0.67-4.23	0.263
dried fruit intake		OR-IVW	95%CI	P
	BMI	0.39	0.29-0.52	5.77E-11
	MDD	0.36	0.25-0.53	1.04E-07
	Smoking	0.35	0.23-0.53	1.03E-06
	Alcoholic drinking	0.29	0.19-0.43	3.58E-09
red wine intake		OR-IVW	95%CI	P
	BMI	0.43	0.32-0.57	6.24E-09
	MDD	0.46	0.29-0.72	0.001
	Smoking	0.48	0.28-0.83	0.008
	Alcoholic drinking	0.42	0.24-0.74	0.003
beer intake		OR-IVW	95%CI	P
	BMI	1.85	1.23-2.76	0.003
	MDD	1.57	0.84-2.94	0.16
	Smoking	1.9	0.93-3.87	0.078
	Alcoholic drinking	2.59	1.1-6.06	0.029
cheese intake		OR-IVW	95%CI	P
	BMI	0.52	0.43-0.64	3.94E-10
	MDD	0.41	0.33-0.51	9.54E-16
	Smoking	0.4	0.32-0.51	2.25E-14

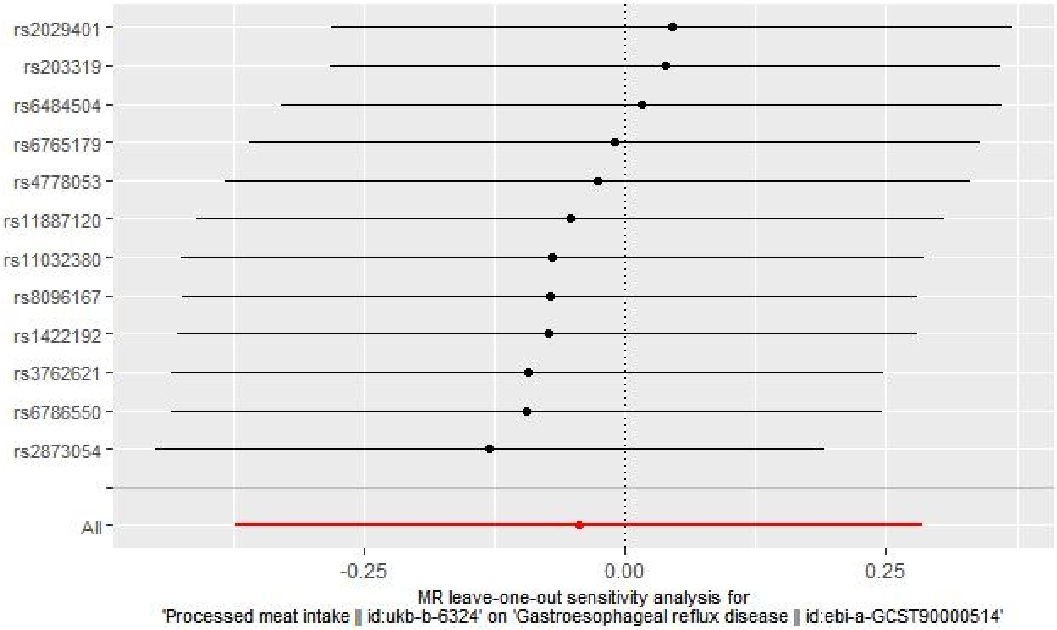
	Alcoholic drinking	0.41	0.33-0.53	4.63E-13
cereal intake		OR-IVW	95%CI	P
	BMI	0.48	0.37-0.64	2.36E-07
	MDD	0.52	0.4-0.69	2.76E-06
	Smoking	0.42	0.3-0.58	2.25E-07
	Alcoholic drinking	0.38	0.26-0.56	9.55E-07
non-oily fish intake		OR-IVW	95%CI	P
	BMI	1.16	0.67-2.02	0.594
	MDD	2.74	1.39-5.4	0.004
	Smoking	3.09	1.3-7.36	0.011
	Alcoholic drinking	2.53	0.91-7.02	0.076
coffee intake		OR-IVW	95%CI	P
	BMI	0.87	0.69-1.09	0.234
	MDD	1.26	0.99-1.59	0.056
	Smoking	1.24	0.89-1.74	0.209
	Alcoholic drinking	1.32	0.26-0.56	9.55E-07
bread intake		OR-IVW	95%CI	P
	BMI	0.77	0.58-1.01	0.059
	MDD	0.73	0.55-0.96	0.024
	Smoking	0.64	0.46-0.91	0.011
	Alcoholic drinking	0.61	0.4-0.92	0.018

Supplementary Figures

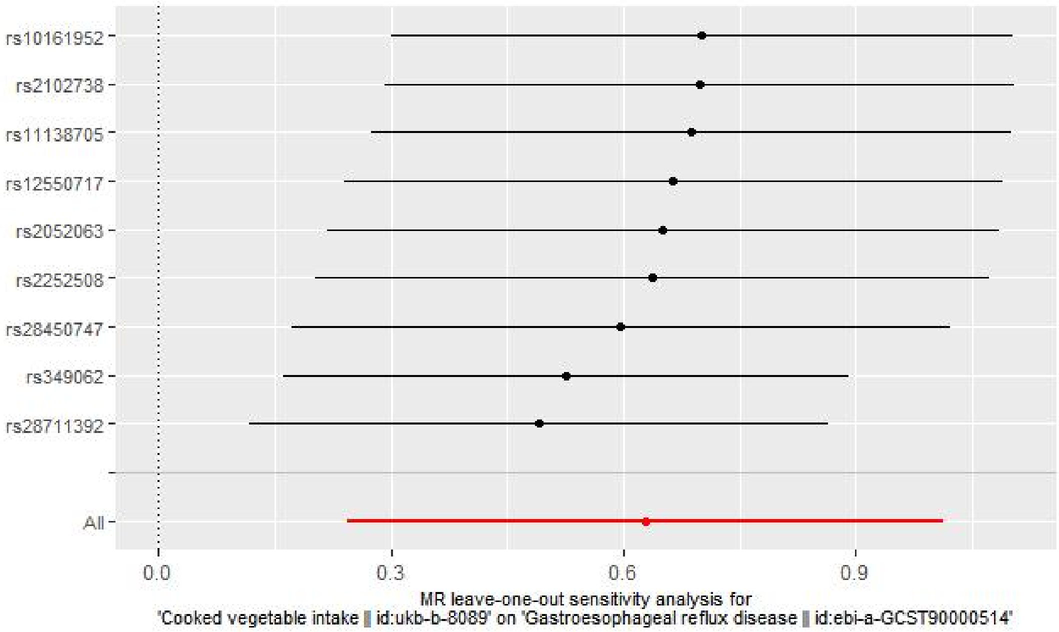
Supplementary Figure H1-16 leave-one-out sensitivity analysis



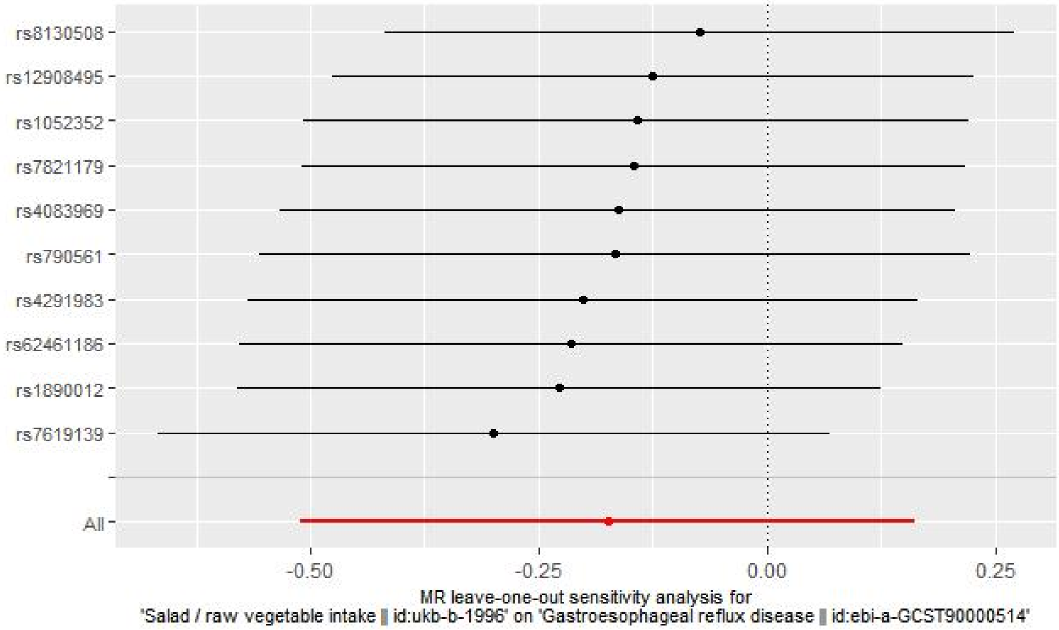
Supplementary Figure H1; MR, Mendelian Randomization.



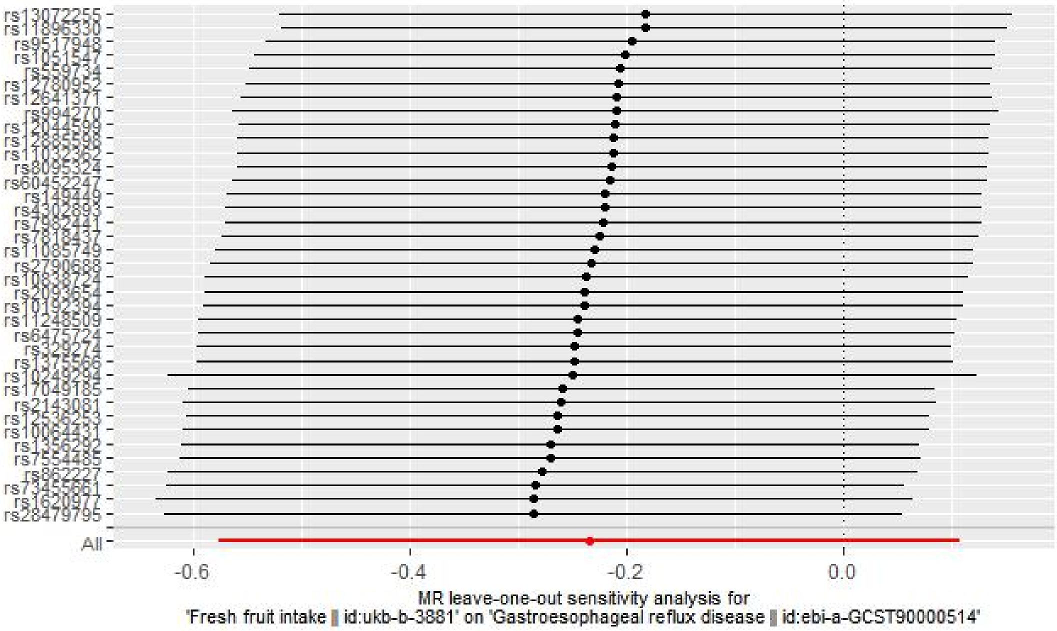
Supplementary Figure H2; MR, Mendelian Randomization.



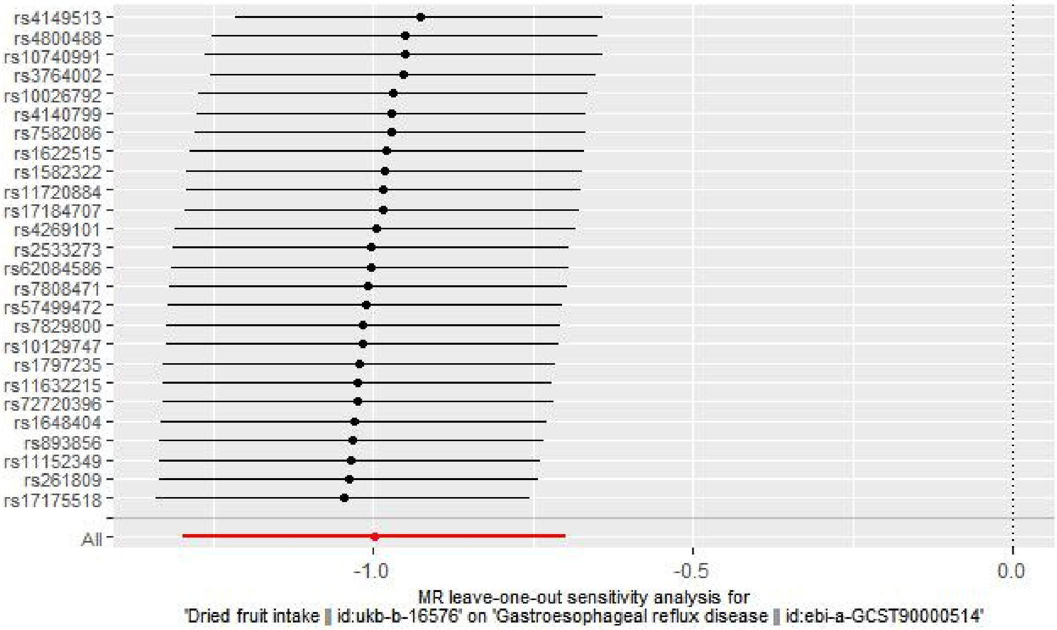
Supplementary Figure H3; MR, Mendelian Randomization.



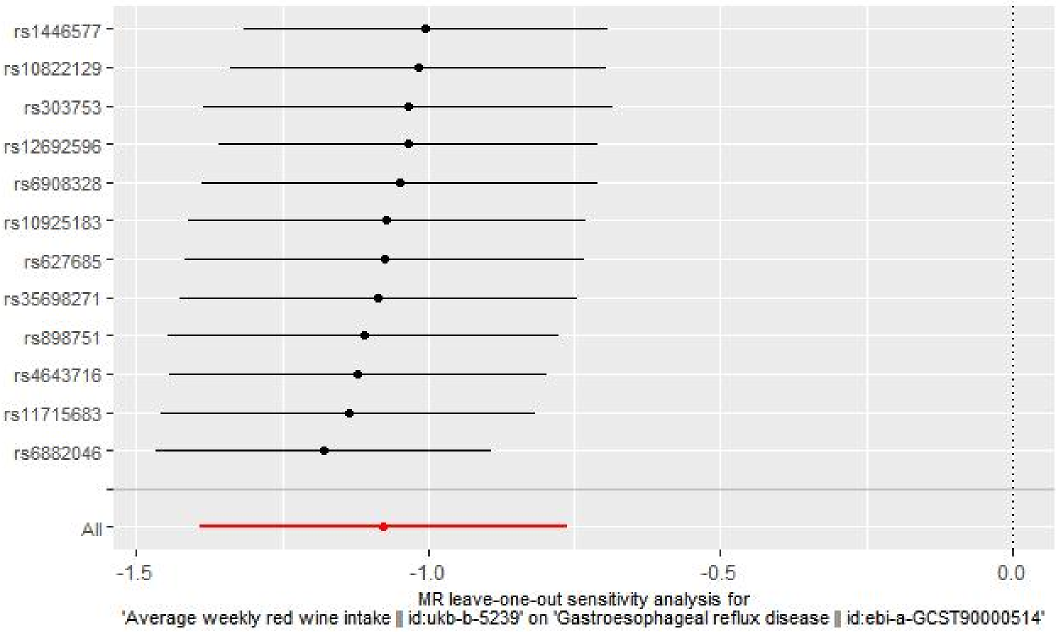
Supplementary Figure H4; MR, Mendelian Randomization.



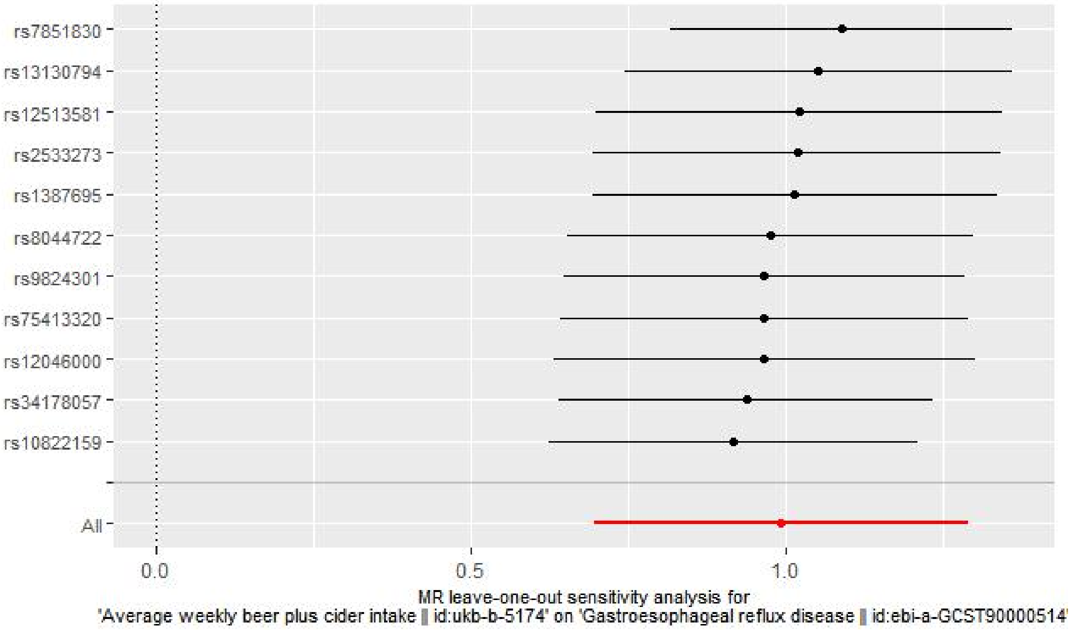
Supplementary Figure H5; MR, Mendelian Randomization.



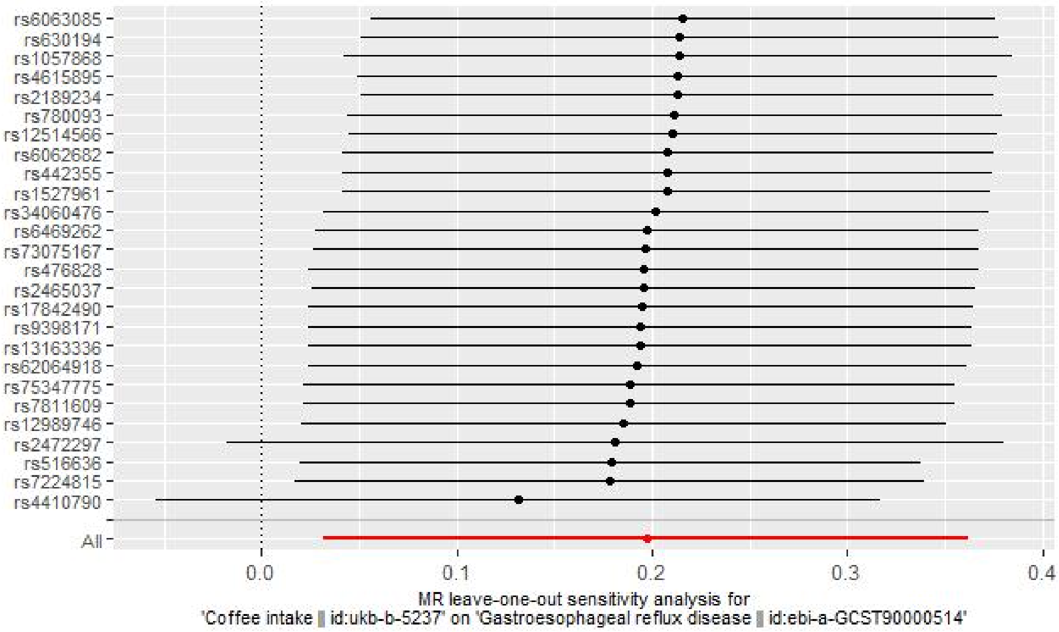
Supplementary Figure H6; MR, Mendelian Randomization.



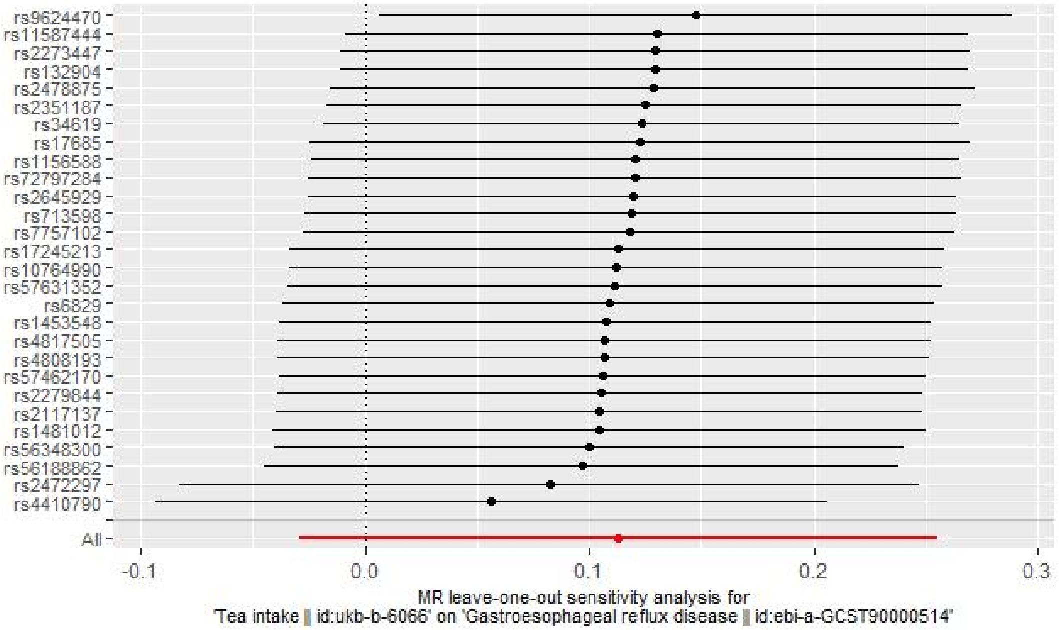
Supplementary Figure H7; MR, Mendelian Randomization.



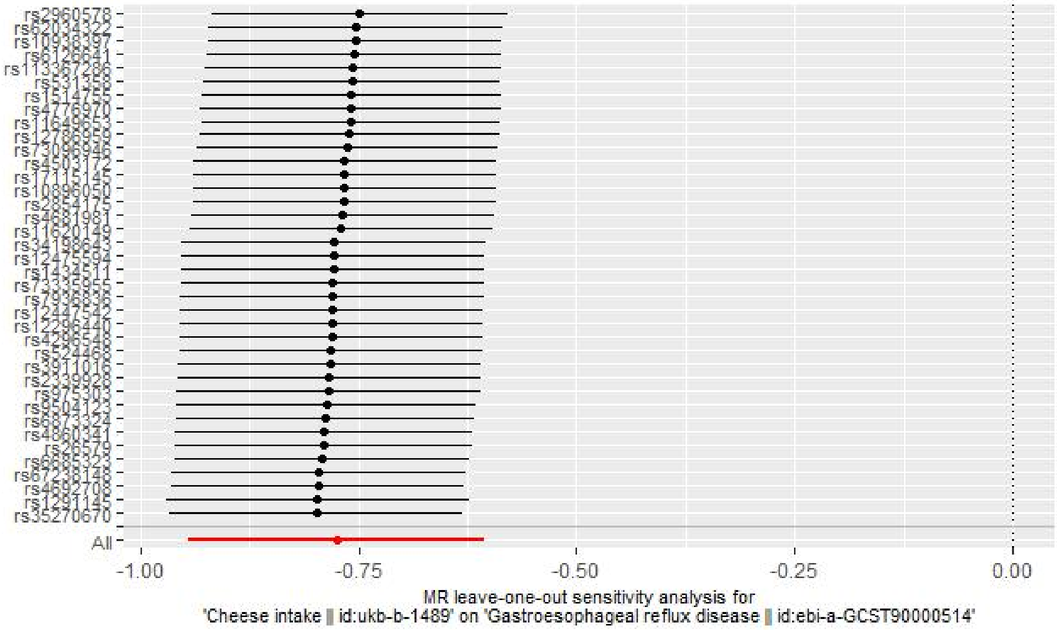
Supplementary Figure H8; MR, Mendelian Randomization.



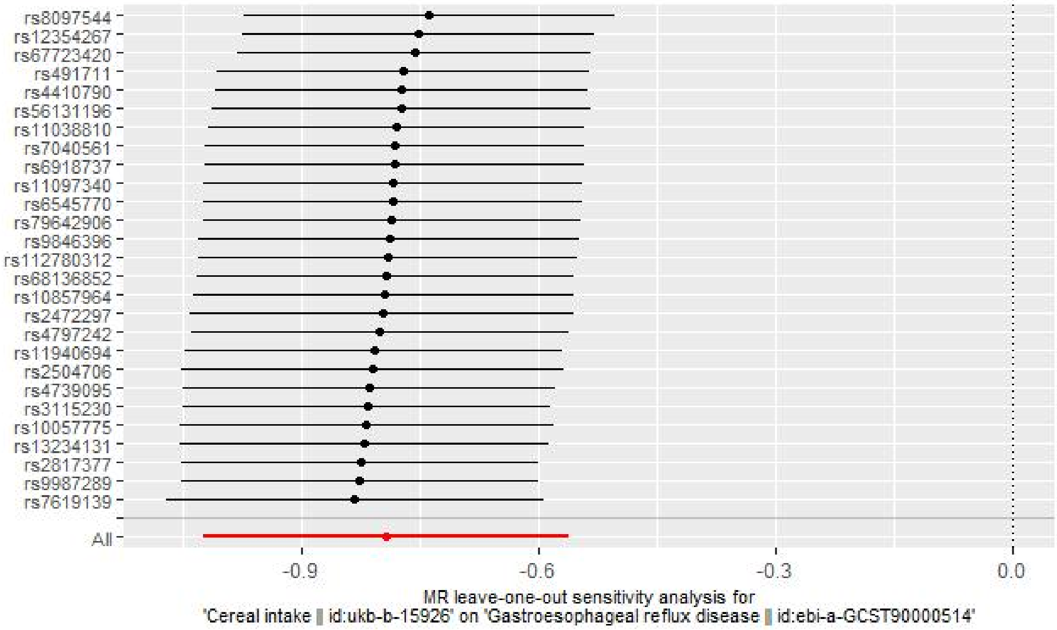
Supplementary Figure H9; MR, Mendelian Randomization.



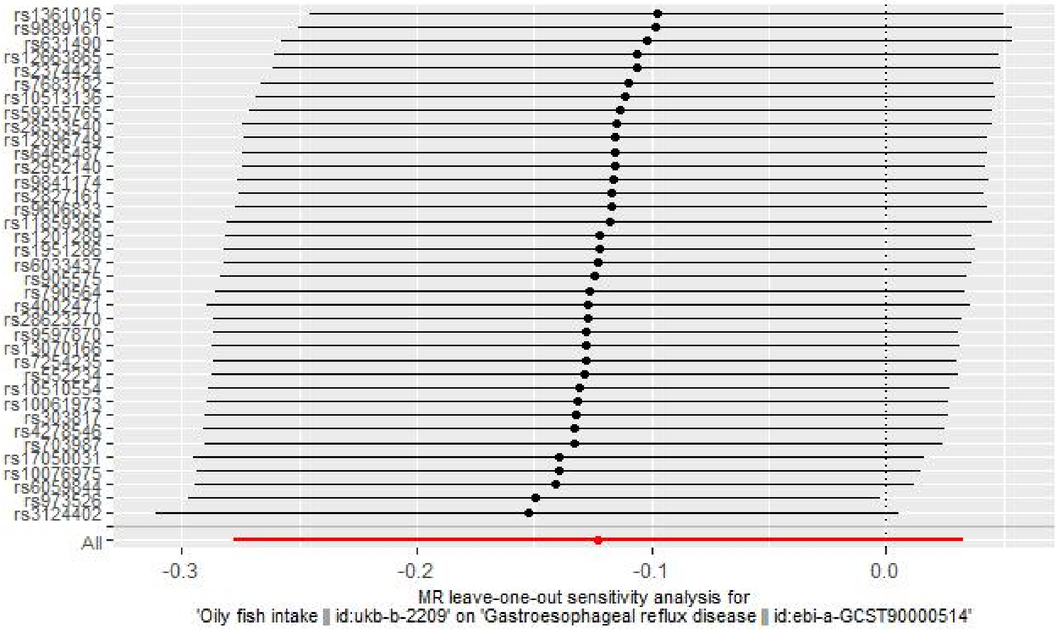
Supplementary Figure H10; MR, Mendelian Randomization.



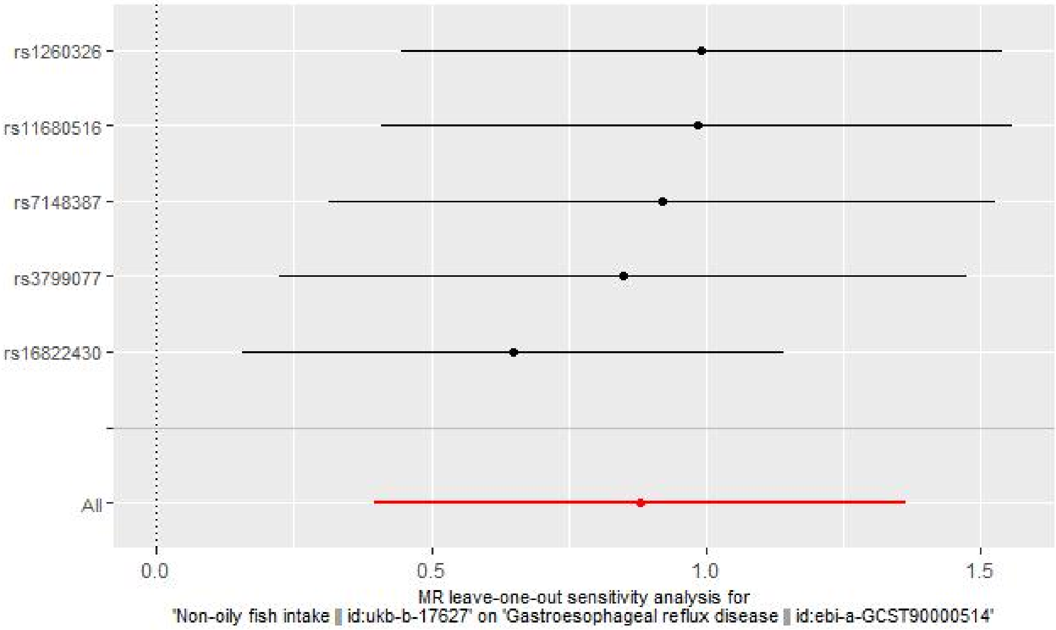
Supplementary Figure H11; MR, Mendelian Randomization.



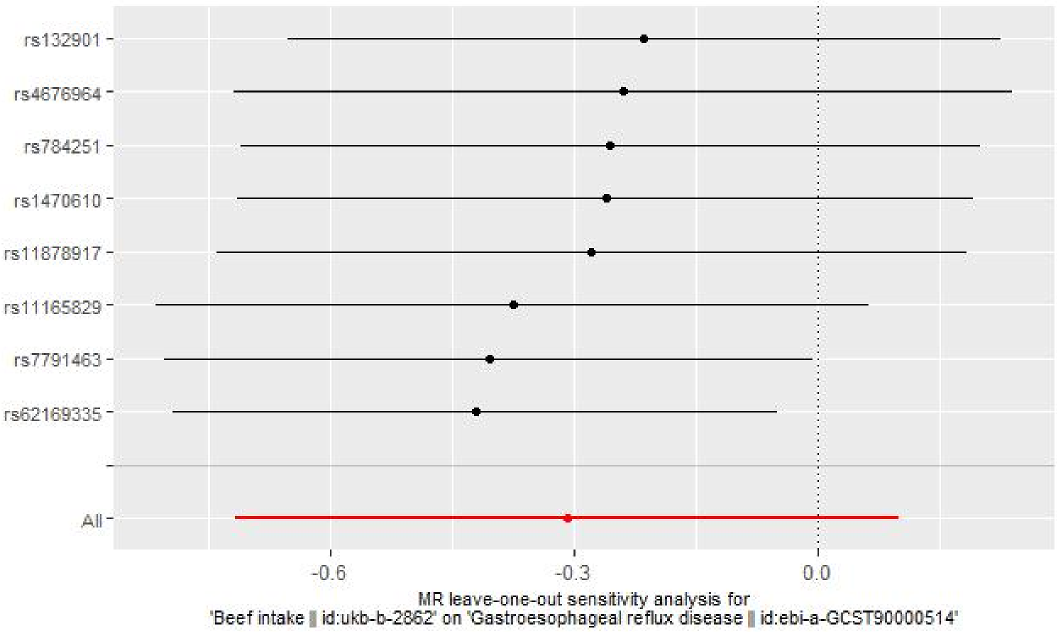
Supplementary Figure H12; MR, Mendelian Randomization.



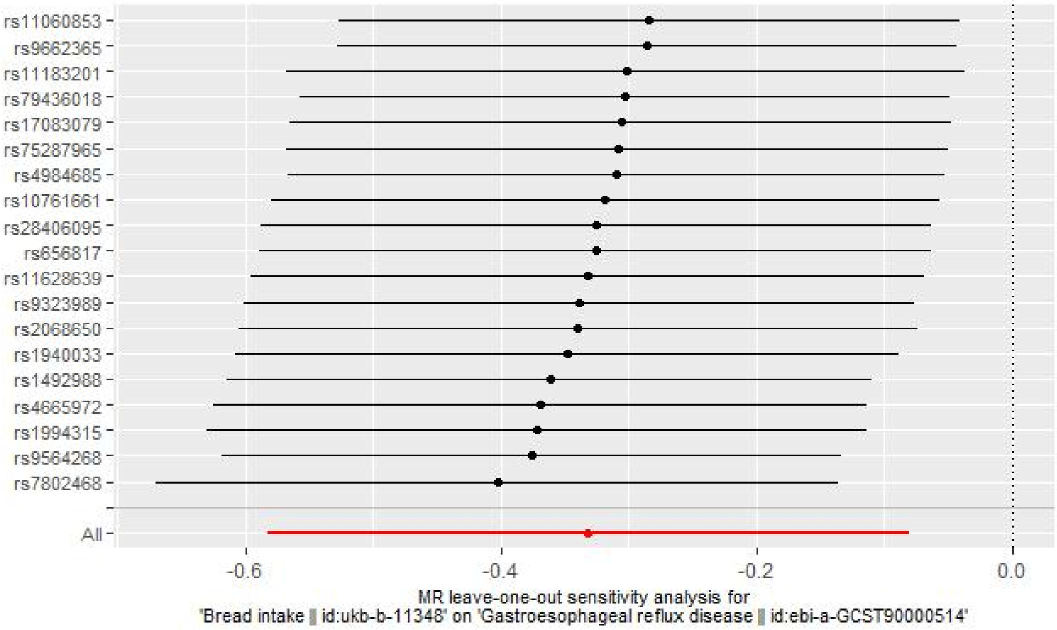
Supplementary Figure H13; MR, Mendelian Randomization.



Supplementary Figure H14; MR, Mendelian Randomization.

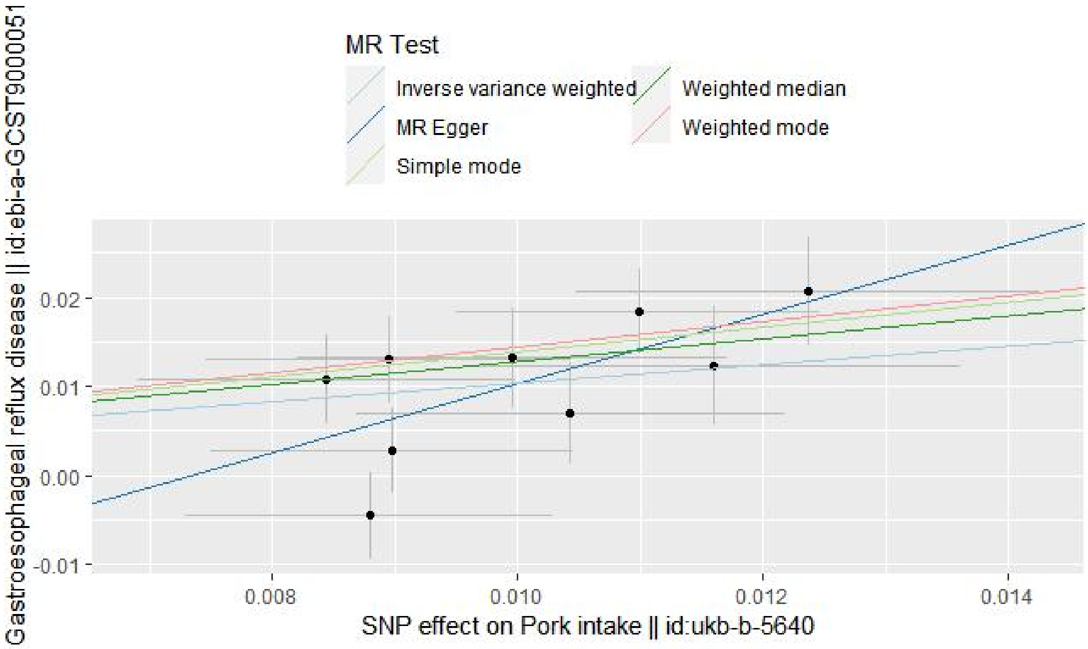


Supplementary Figure H15; MR, Mendelian Randomization.

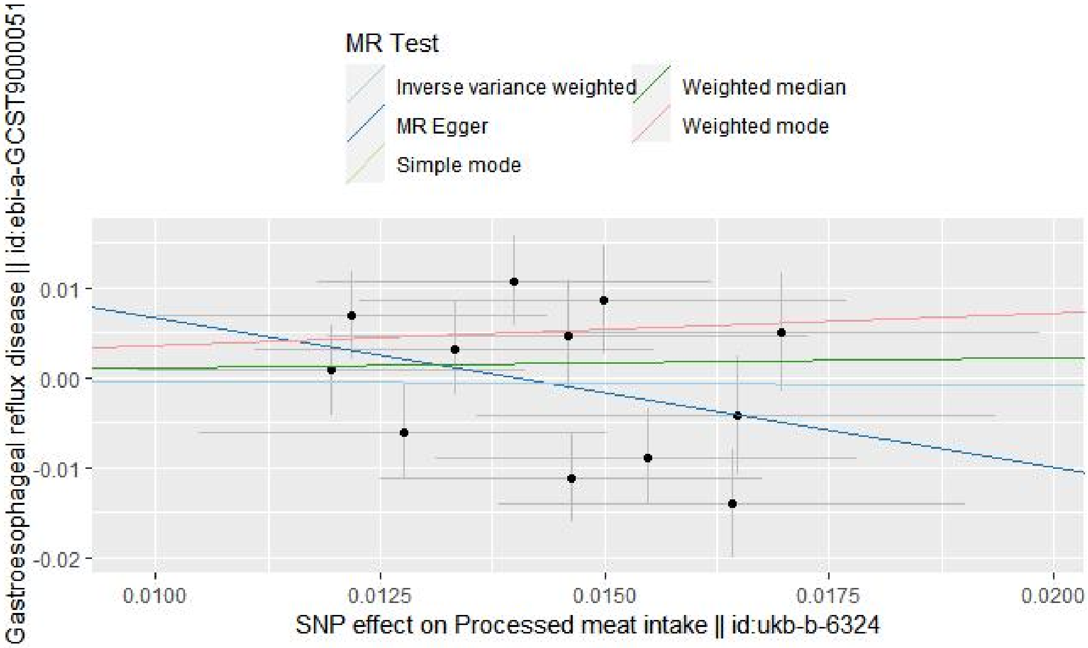


Supplementary Figure H16; MR, Mendelian Randomization.

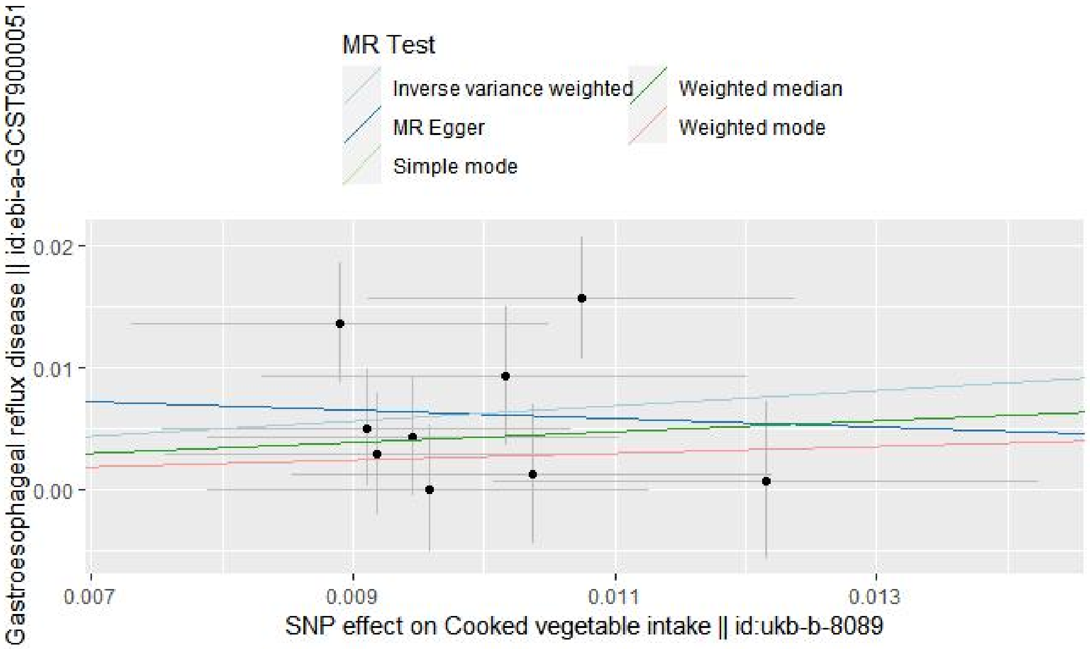
Supplementary Figure R1-16 Scatter plot figures



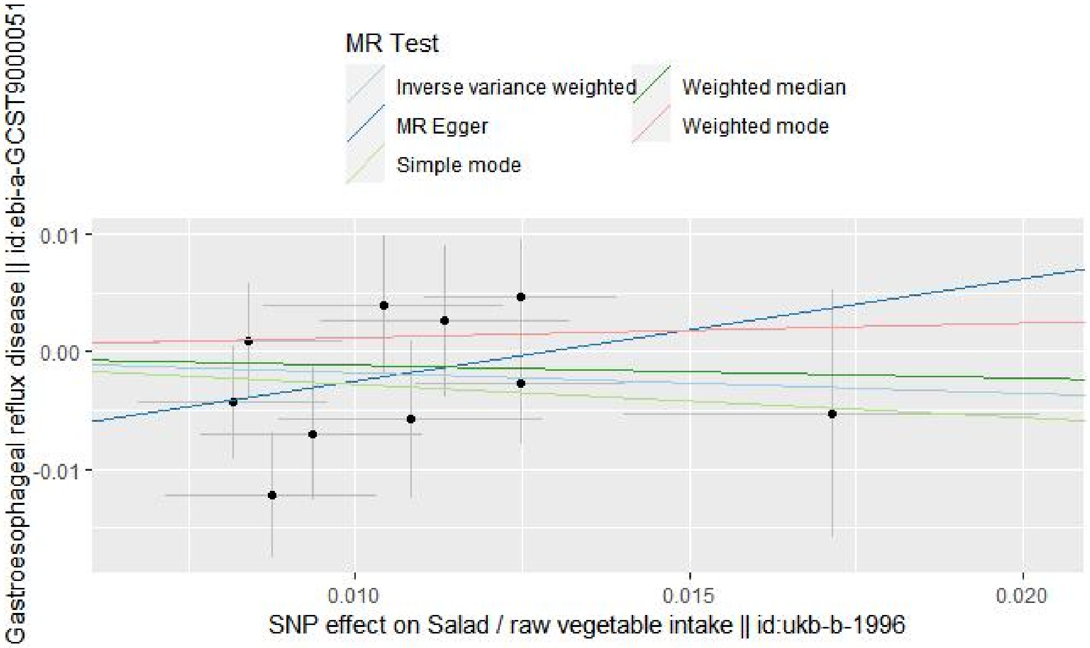
Supplementary Figure R1. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



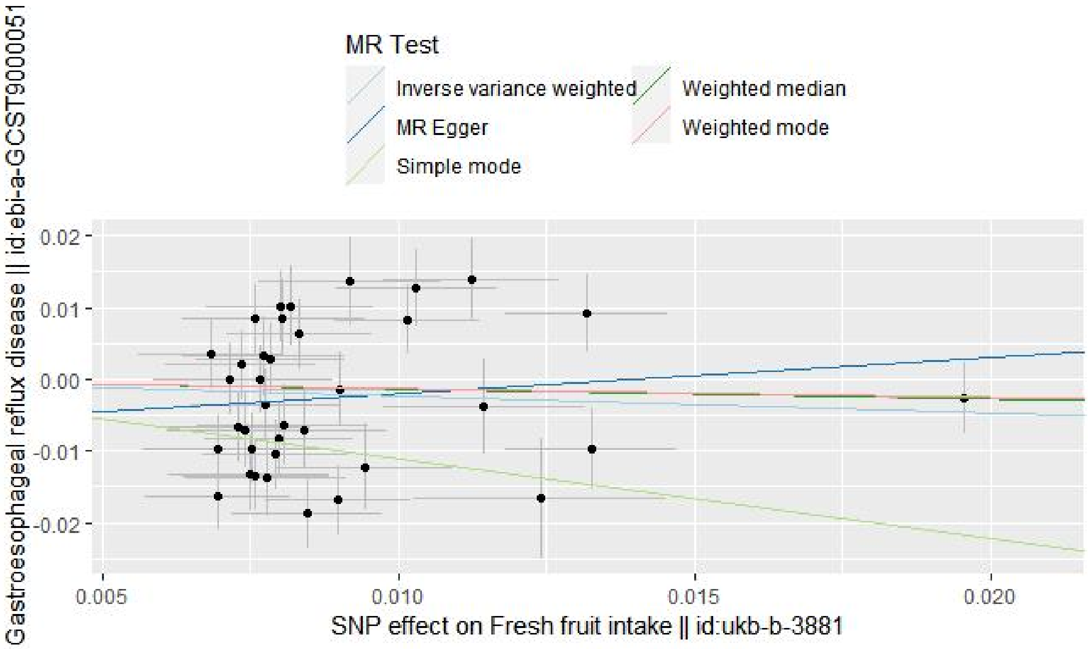
Supplementary Figure R2. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



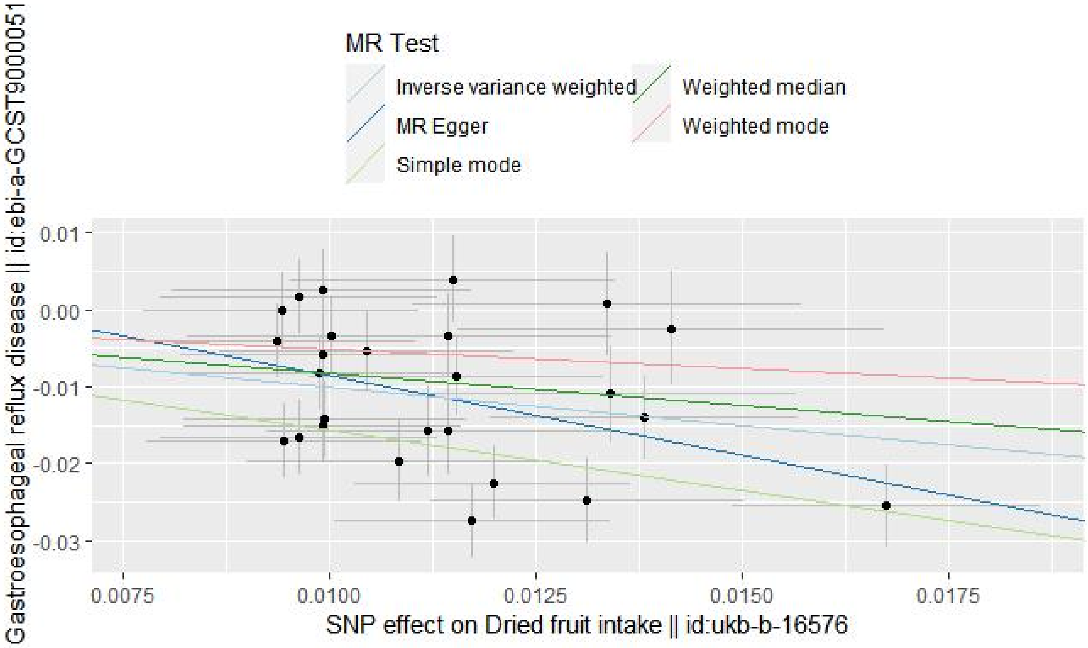
Supplementary Figure R3. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



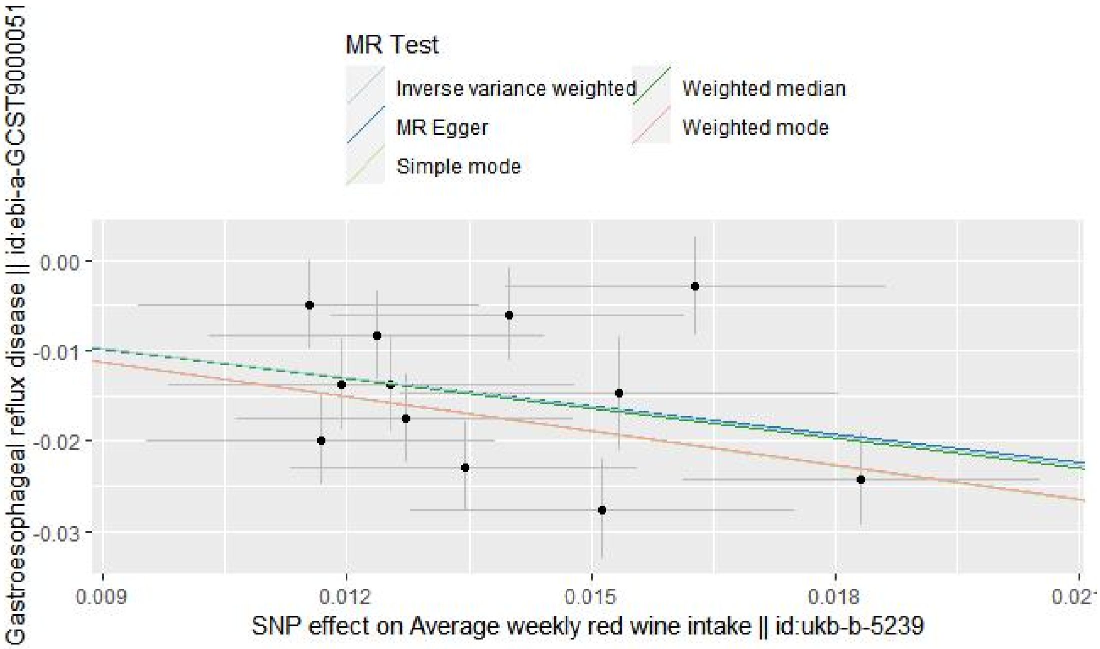
Supplementary Figure R4. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



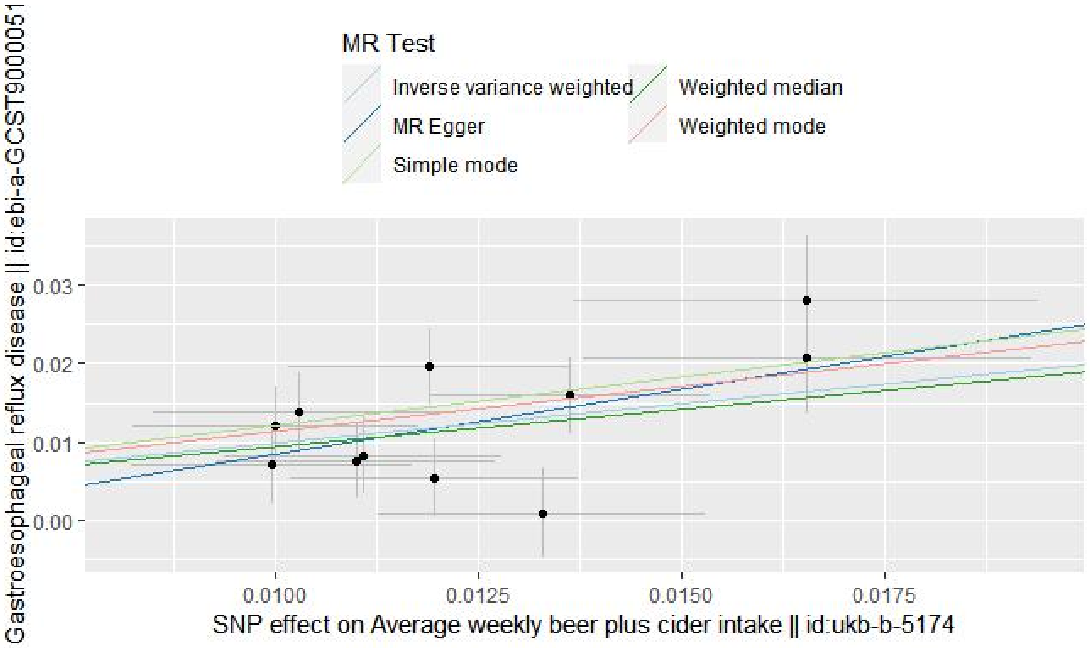
Supplementary Figure R5. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



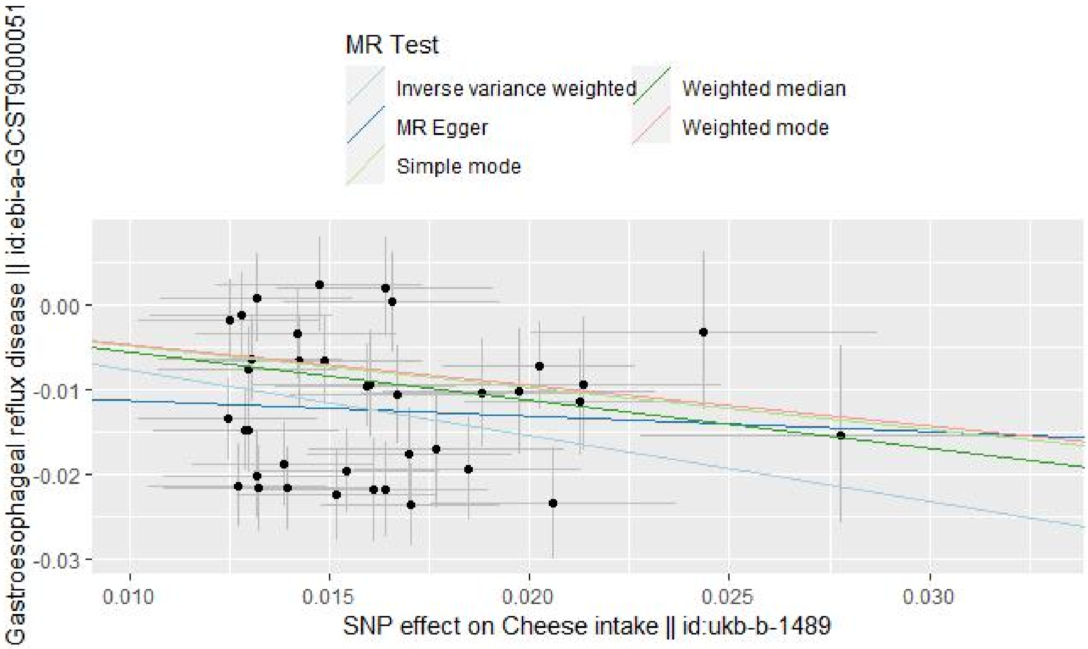
Supplementary Figure R6. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



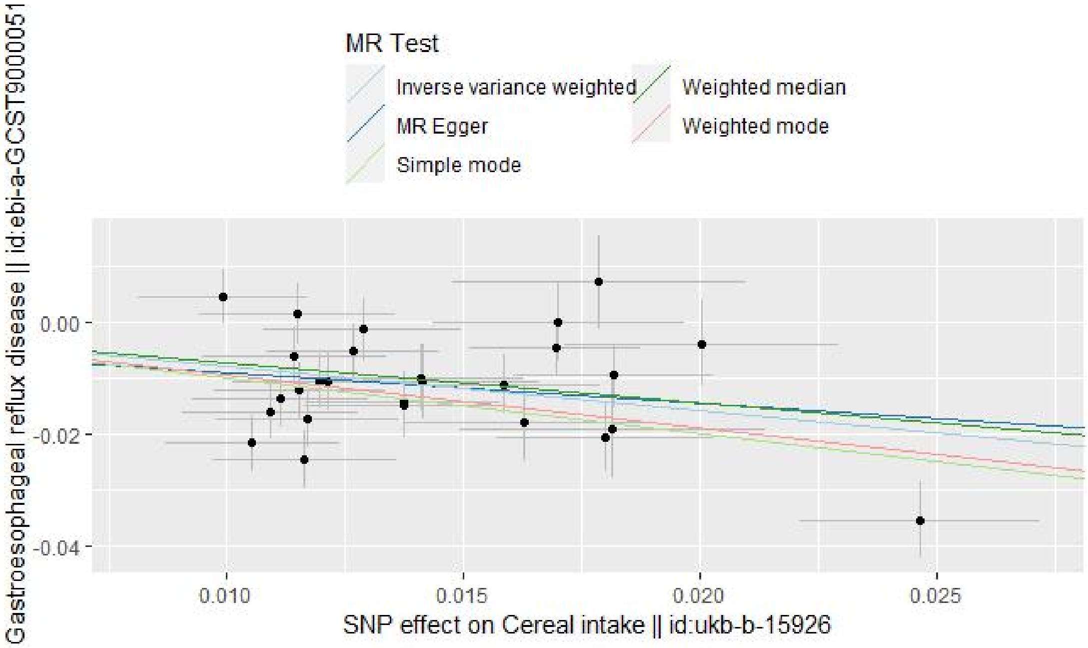
Supplementary Figure R7. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



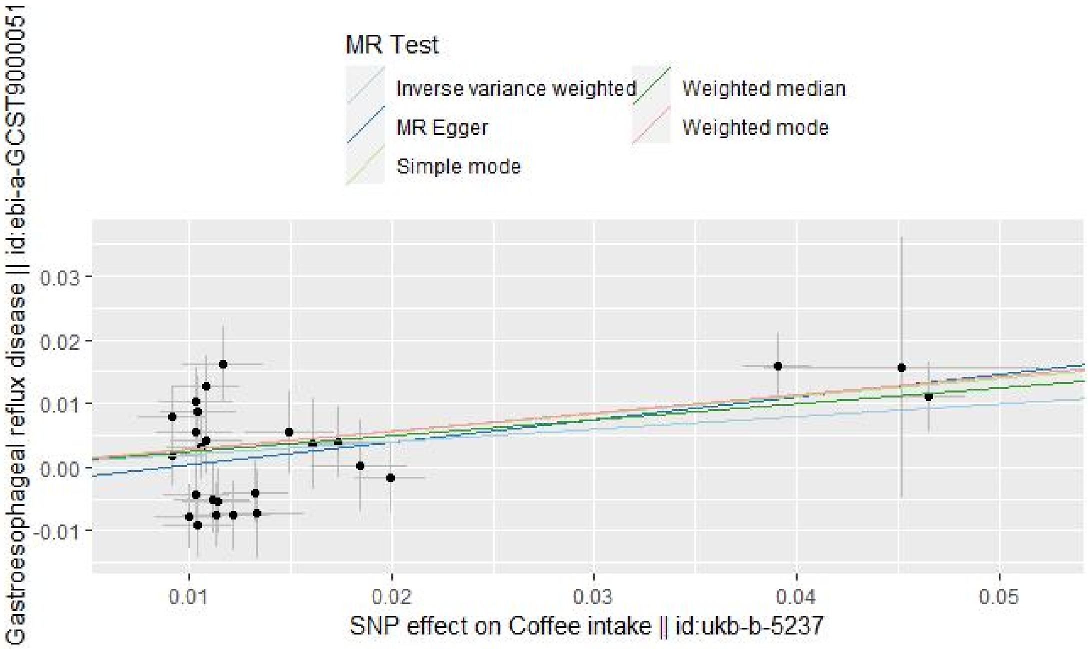
Supplementary Figure R8. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



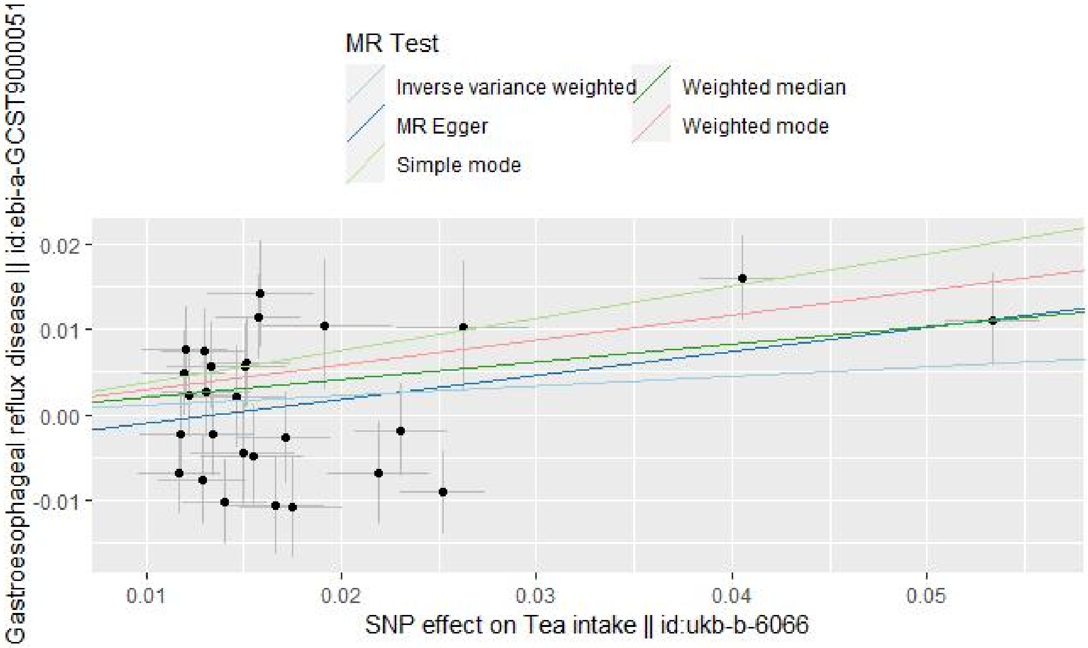
Supplementary Figure R9. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



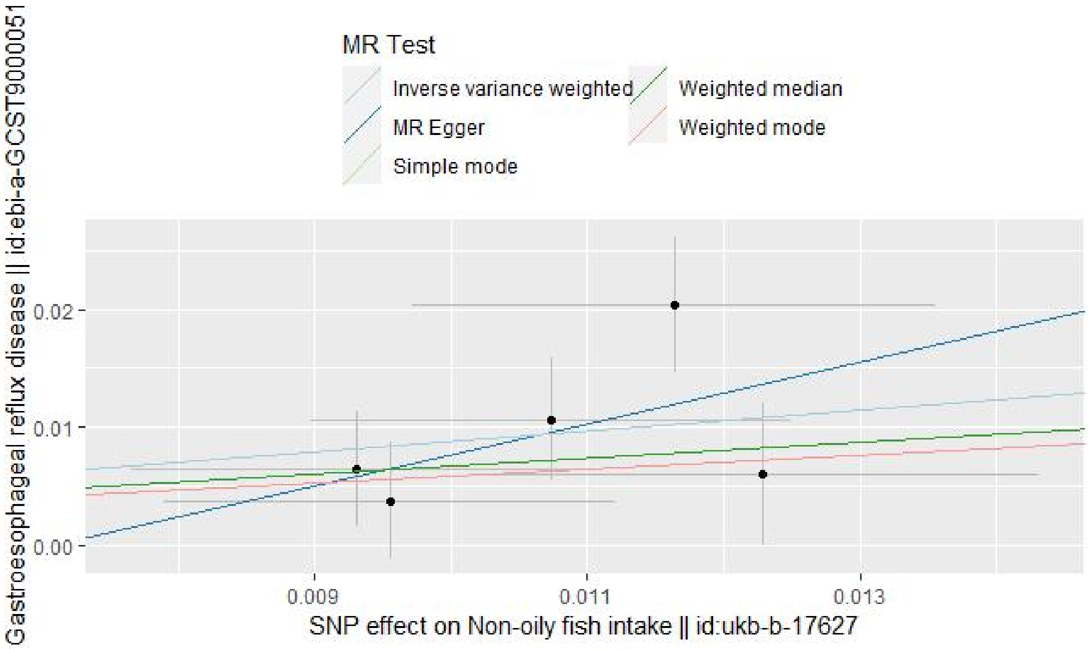
Supplementary Figure R10. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



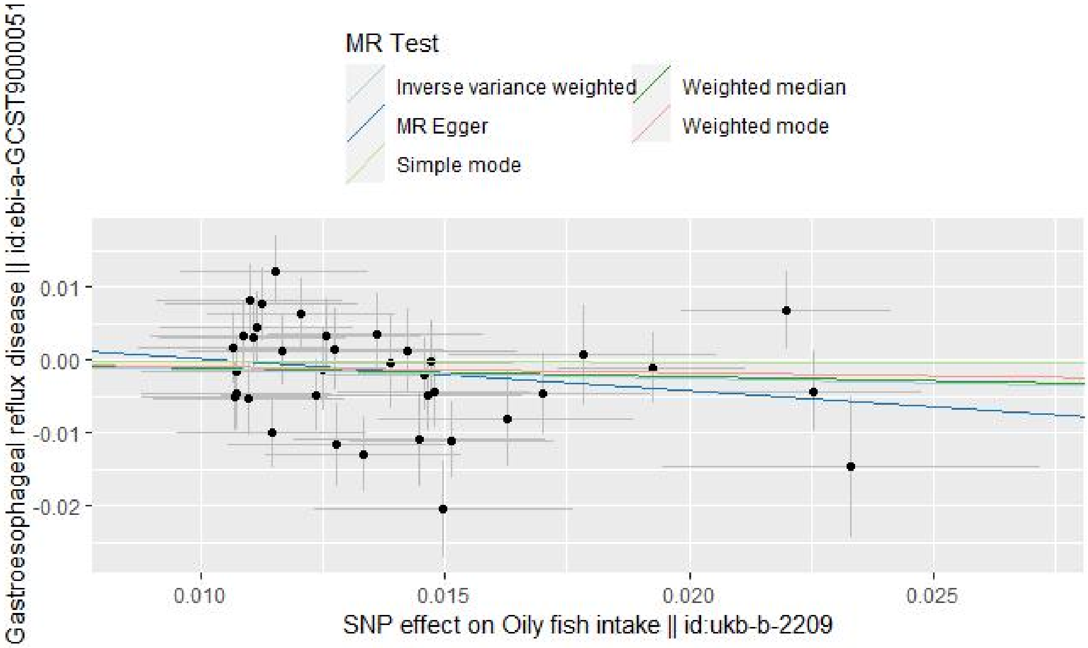
Supplementary Figure R11. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



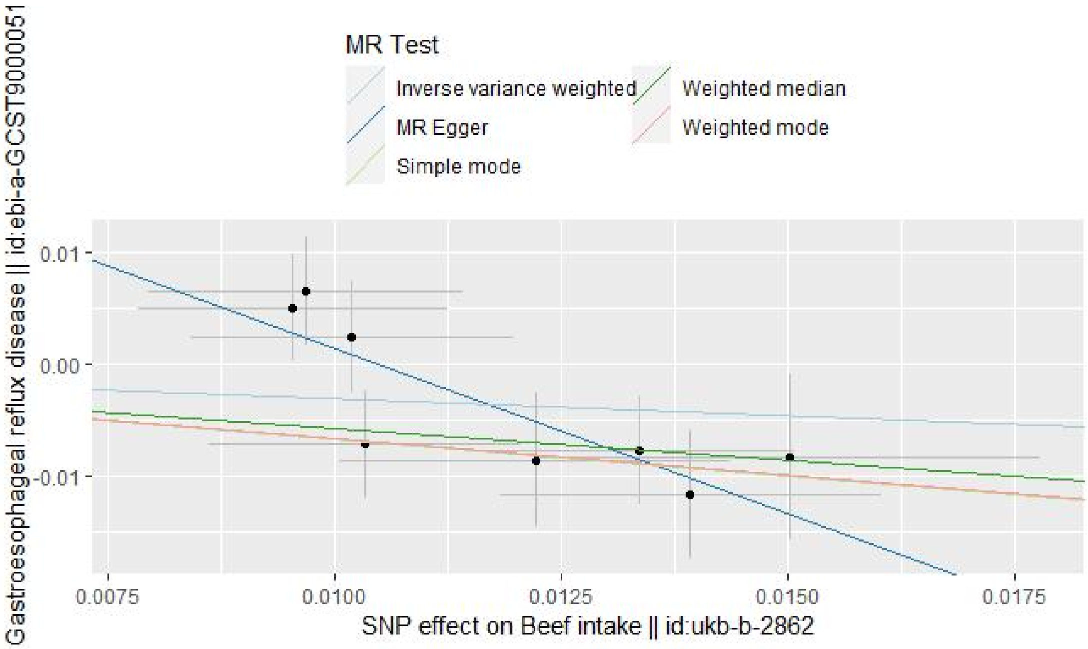
Supplementary Figure R12. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



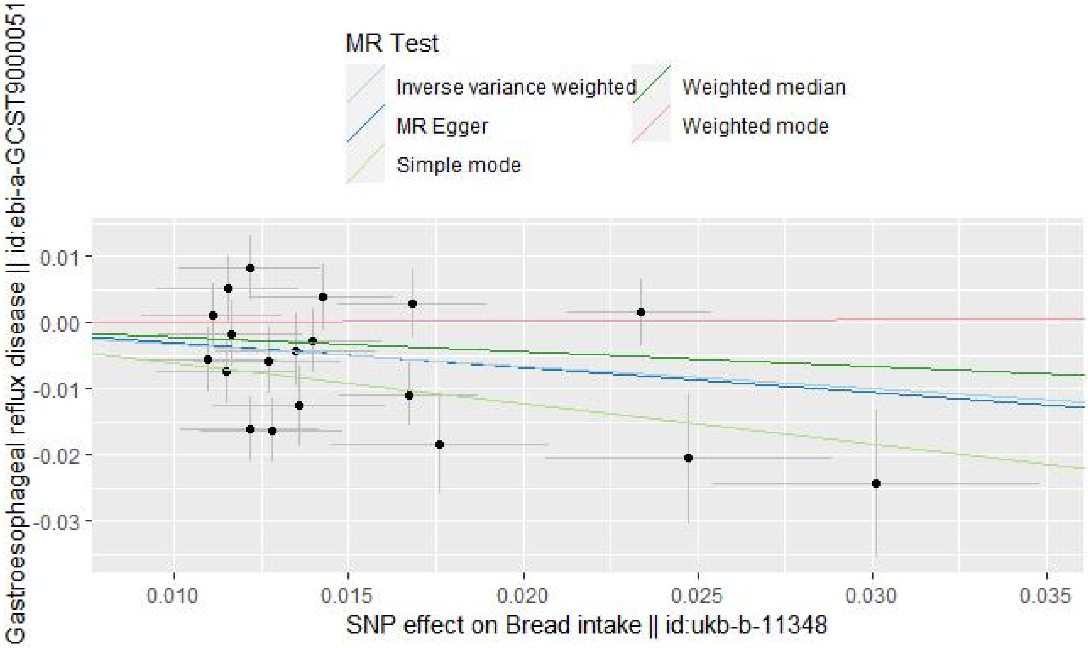
Supplementary Figure R13. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.



Supplementary Figure R14. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.

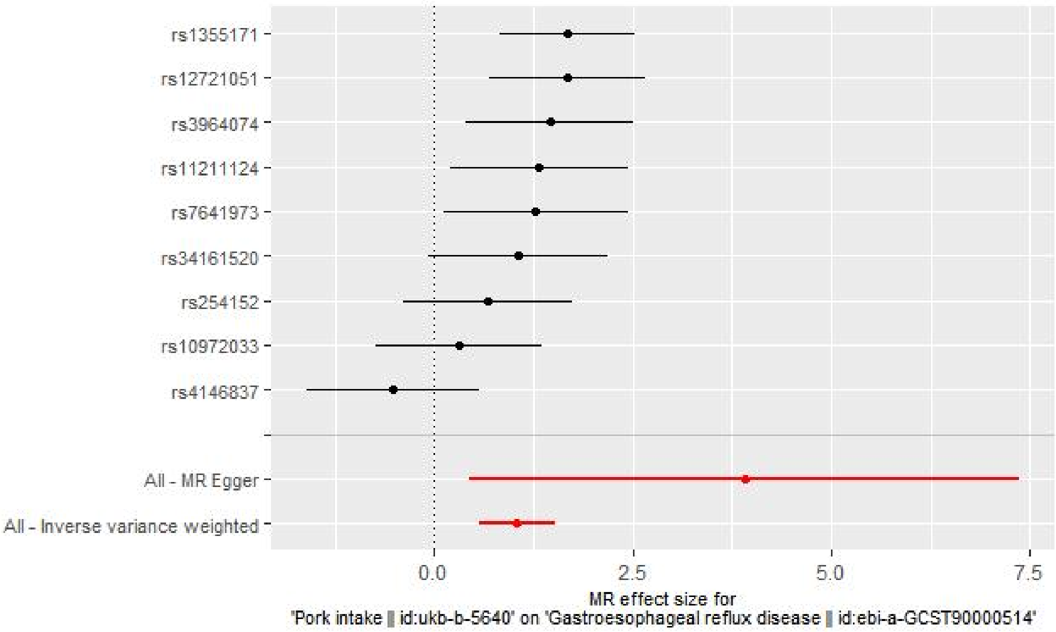


Supplementary Figure R15. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.

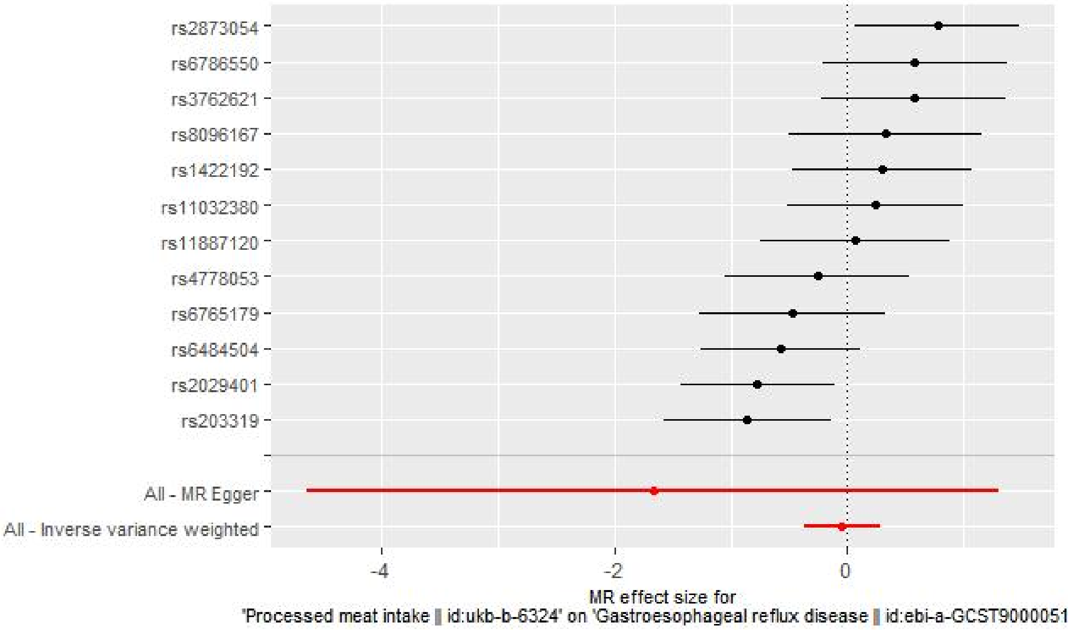


Supplementary Figure R16. SNP, single-nucleotide polymorphism; MR, Mendelian Randomization.

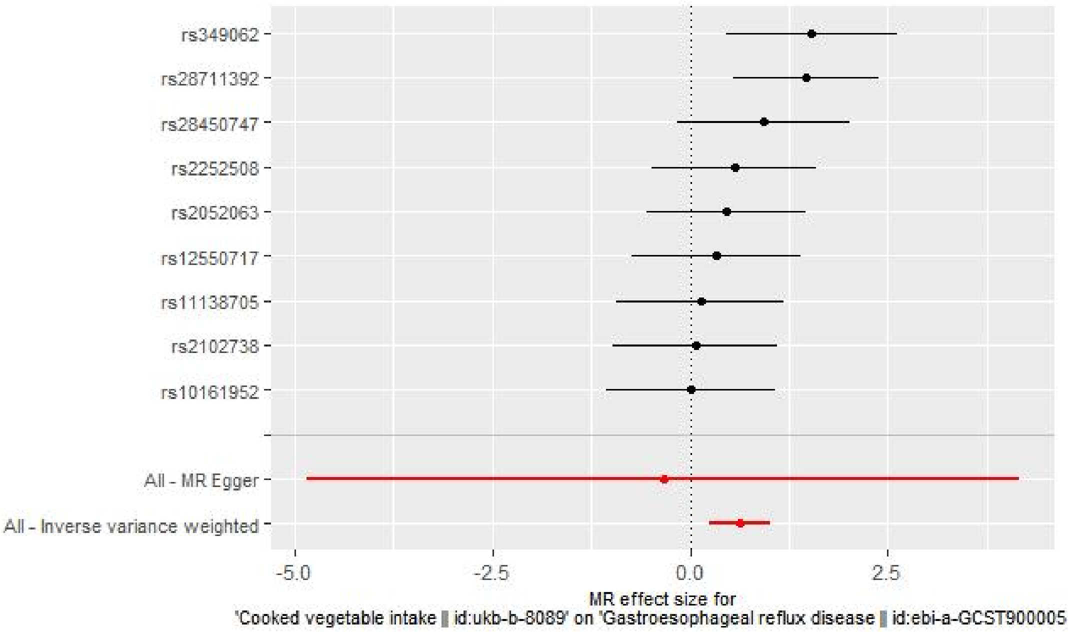
Supplementary Figure T1-16 Forest plot figure



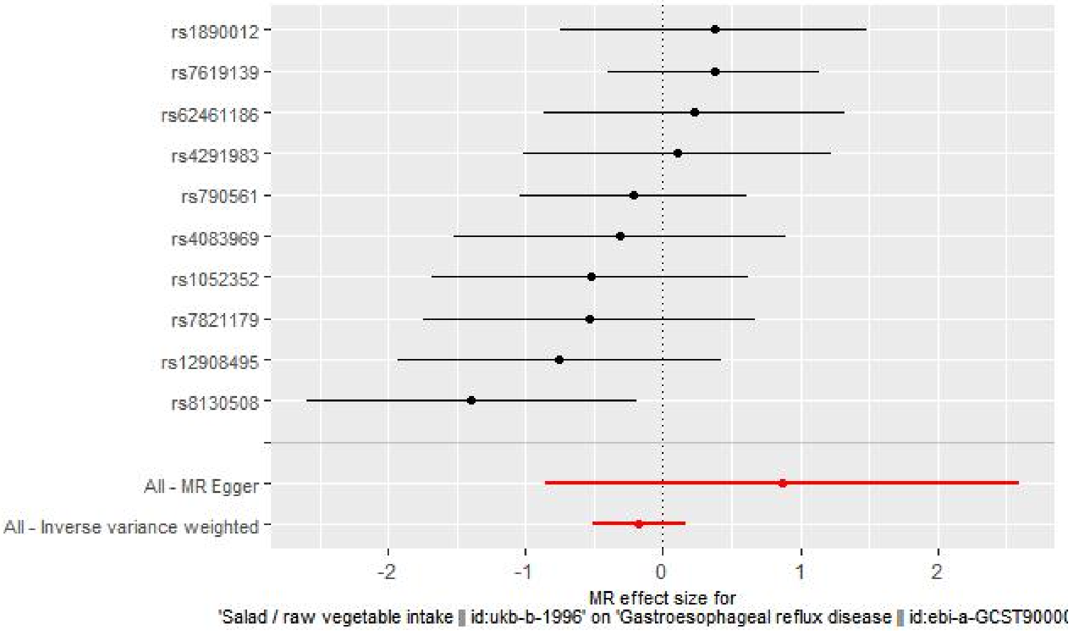
Supplementary Figure T1. MR, Mendelian Randomization.



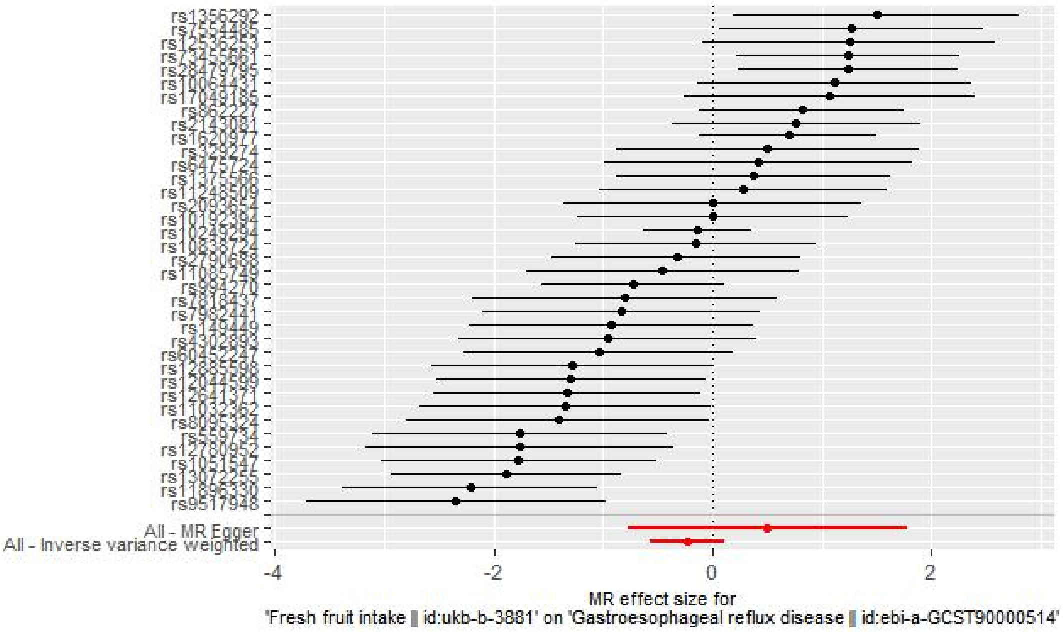
Supplementary Figure T2. MR, Mendelian Randomization.



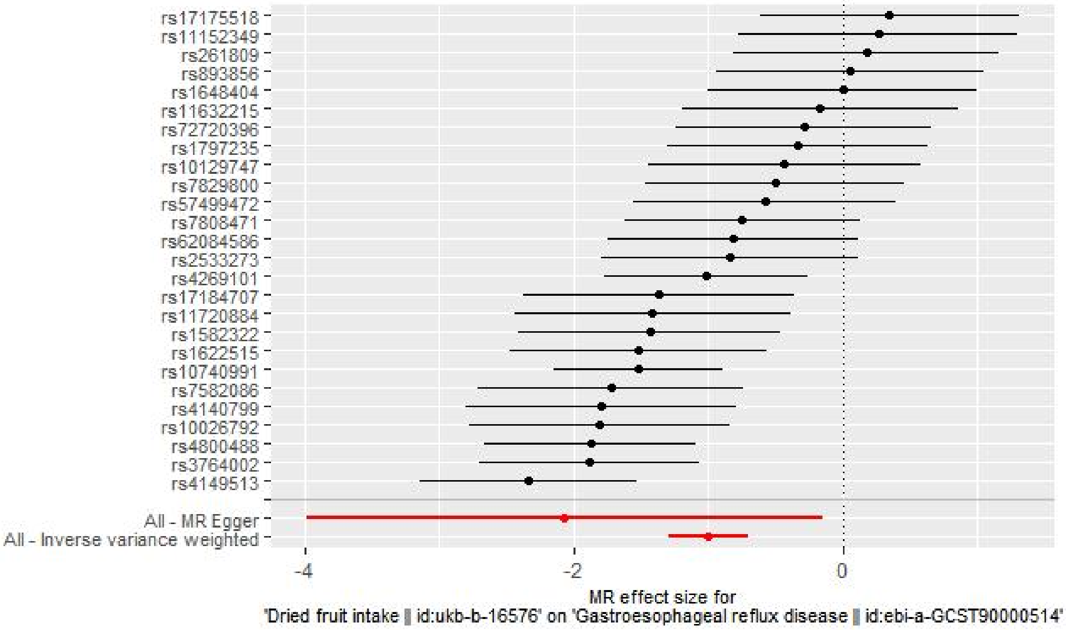
Supplementary Figure T3. MR, Mendelian Randomization.



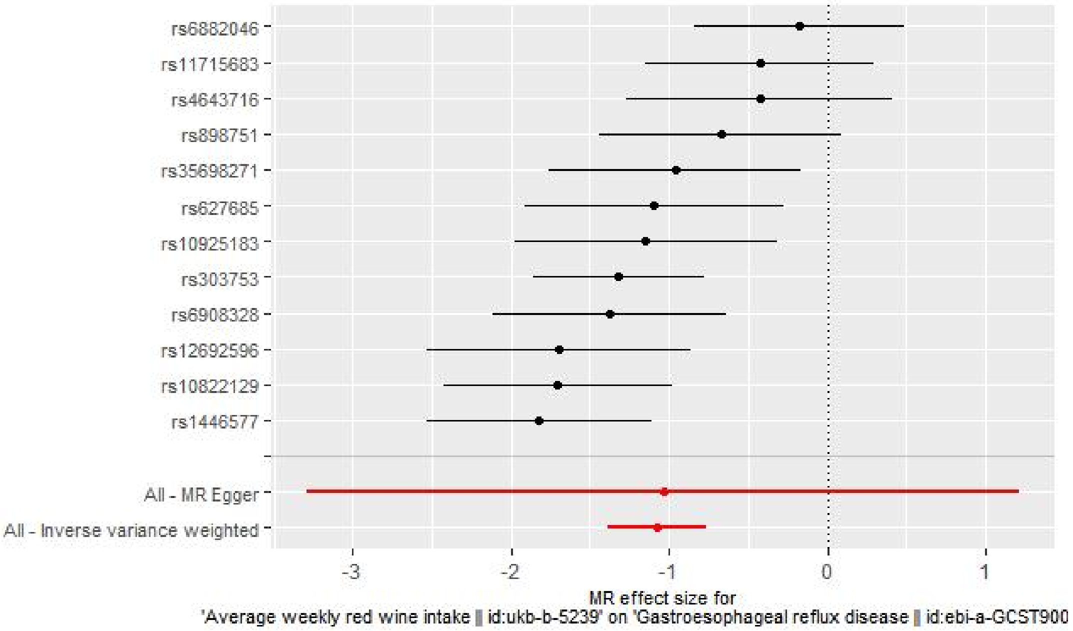
Supplementary Figure T4. MR, Mendelian Randomization.



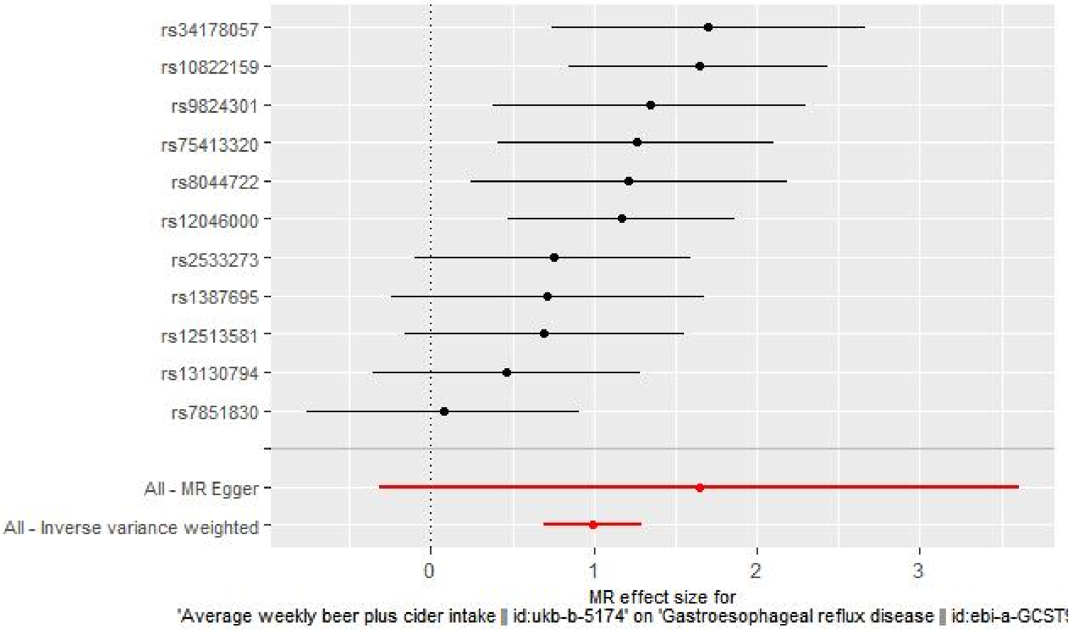
Supplementary Figure T5. MR, Mendelian Randomization.



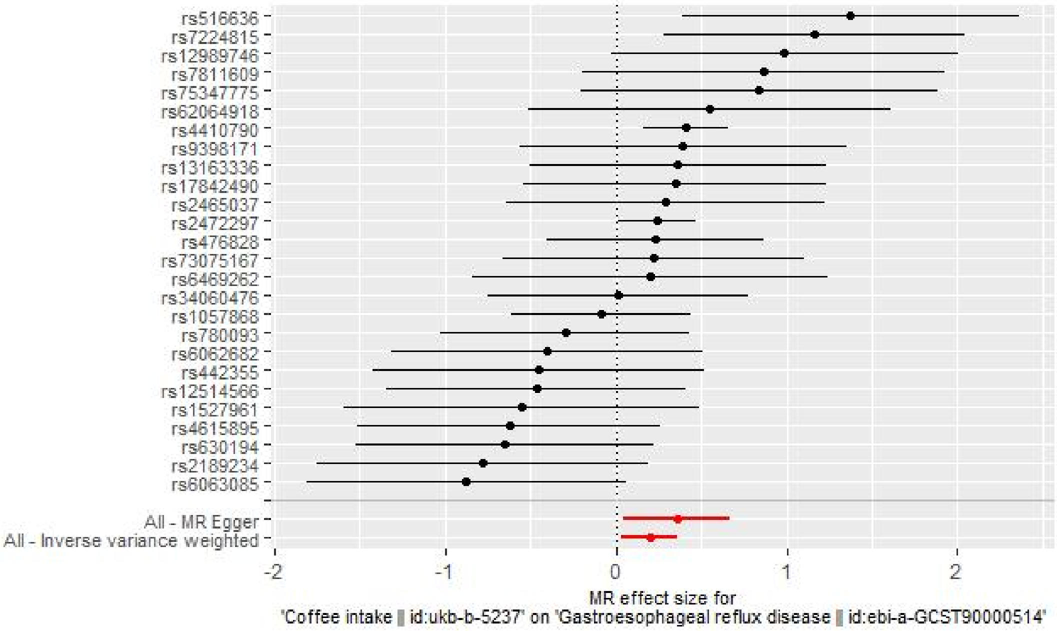
Supplementary Figure T6. MR, Mendelian Randomization.



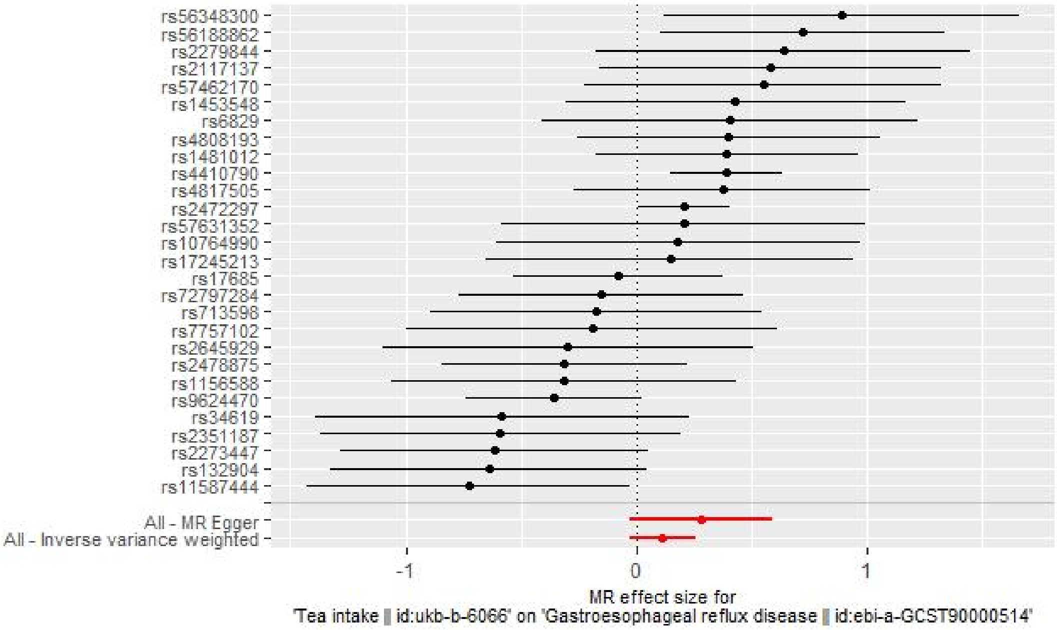
Supplementary Figure T7. MR, Mendelian Randomization.



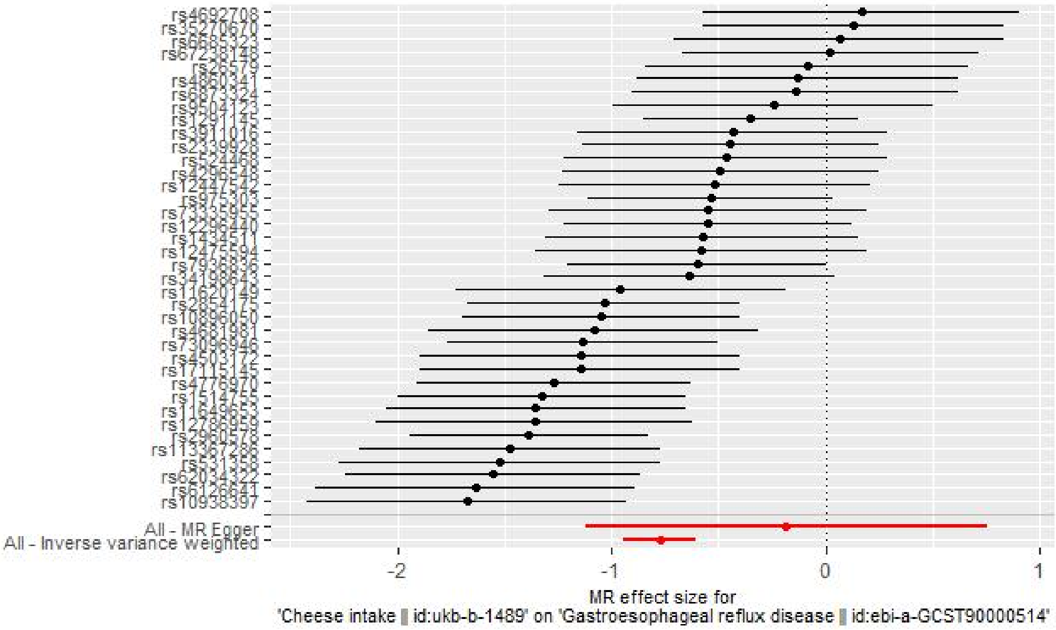
Supplementary Figure T8. MR, Mendelian Randomization.



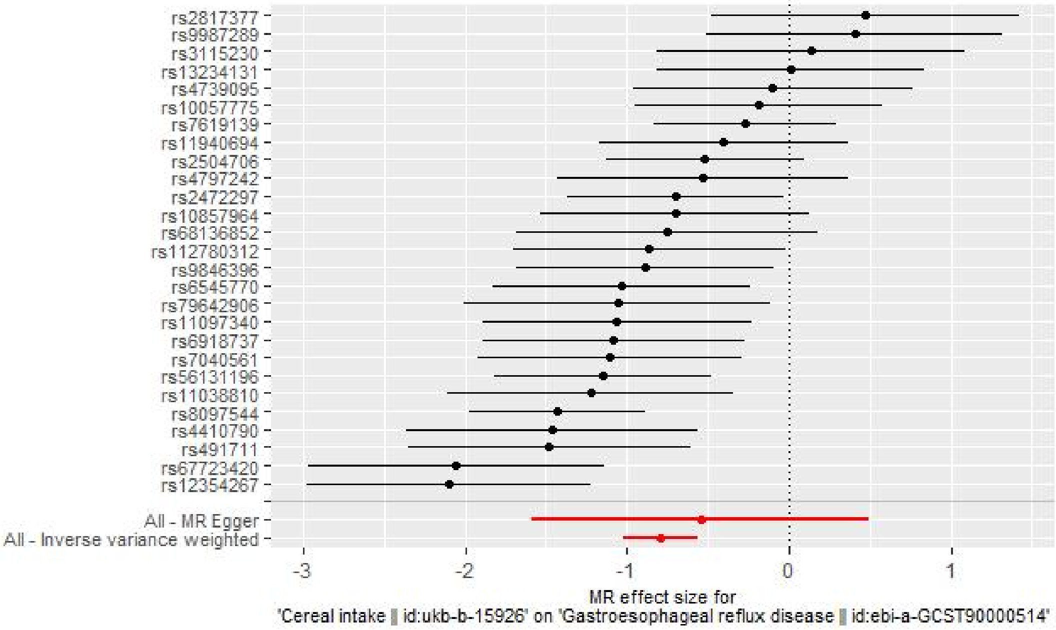
Supplementary Figure T9. MR, Mendelian Randomization.



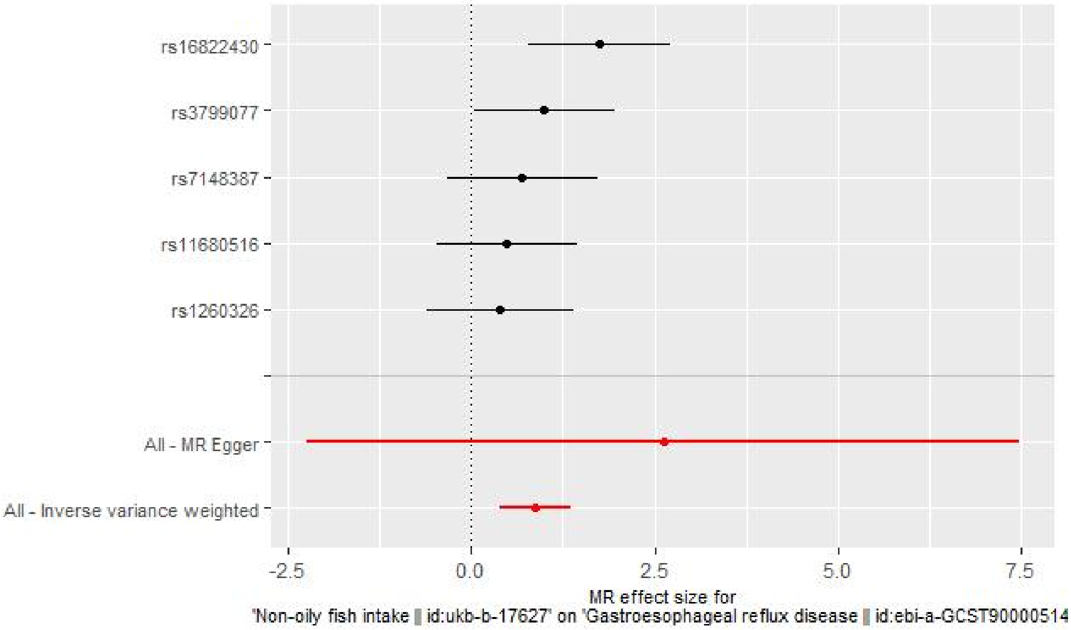
Supplementary Figure T10. MR, Mendelian Randomization.



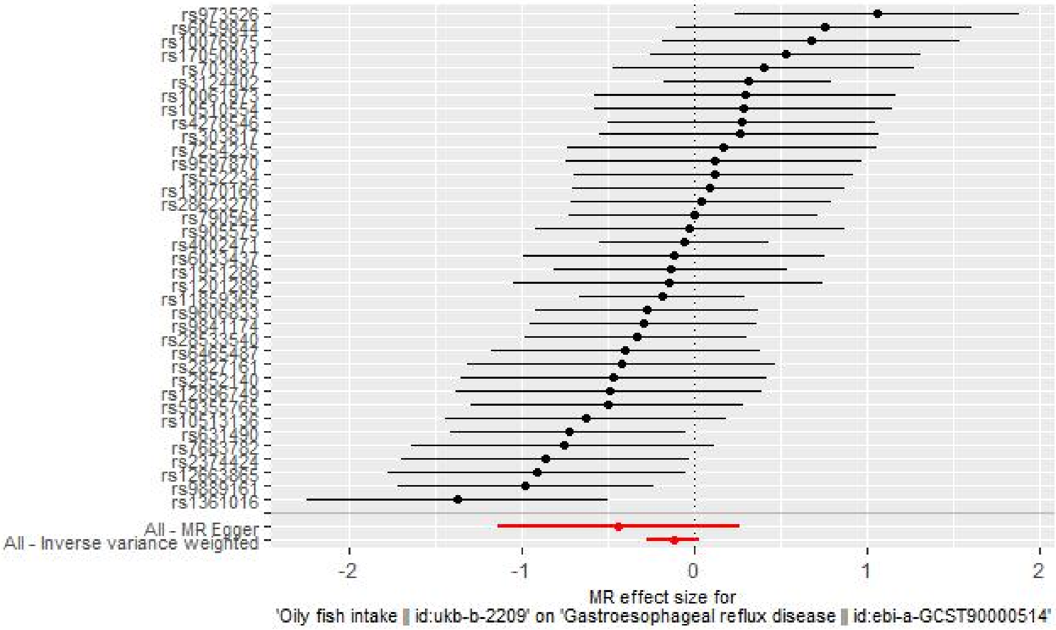
Supplementary Figure T11. MR, Mendelian Randomization.



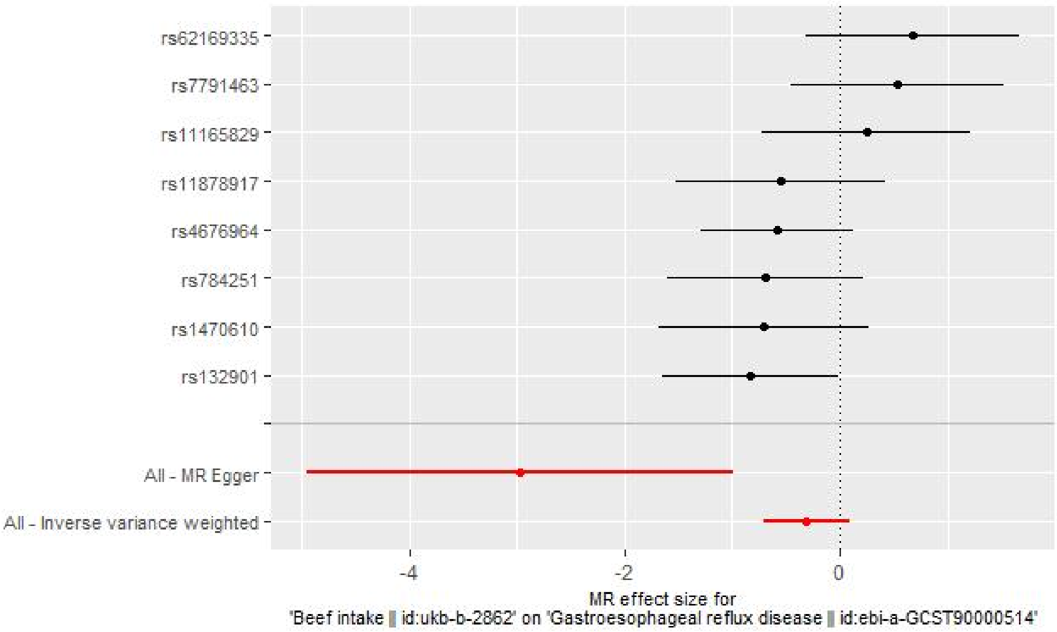
Supplementary Figure T12. MR, Mendelian Randomization.



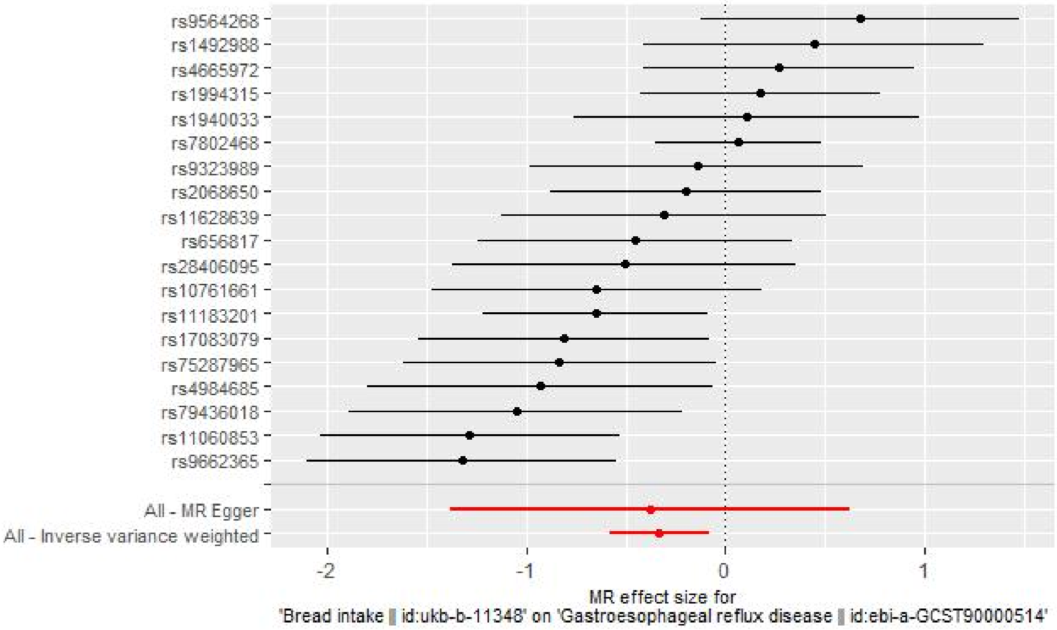
Supplementary Figure T13. MR, Mendelian Randomization.



Supplementary Figure T14. MR, Mendelian Randomization.

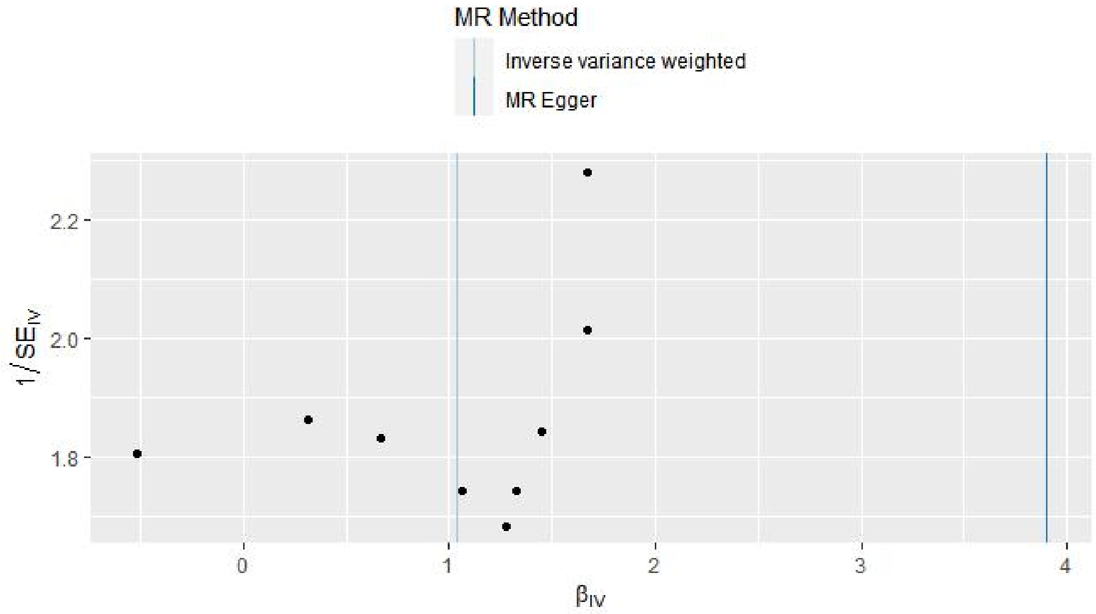


Supplementary Figure T15. MR, Mendelian Randomization.

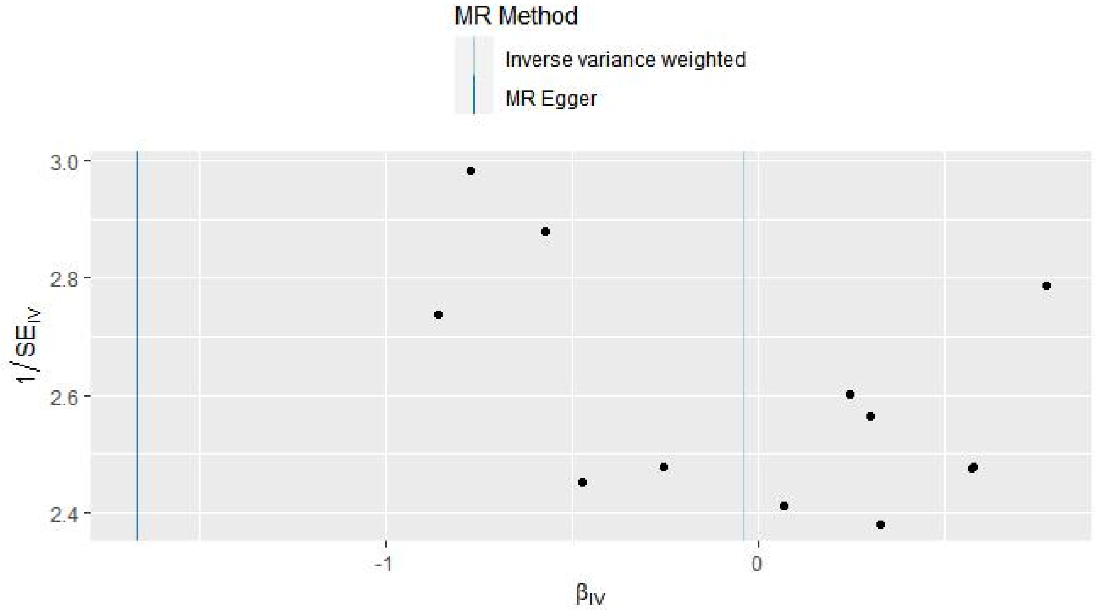


Supplementary Figure T16. MR, Mendelian Randomization.

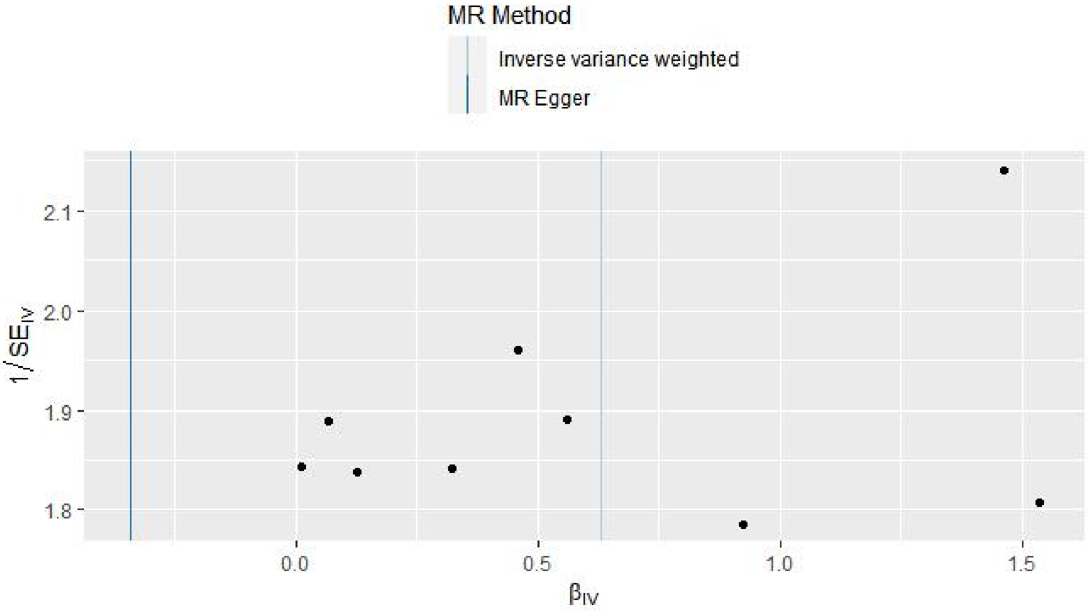
Supplementary Figure S1-16 Funnel plot figure



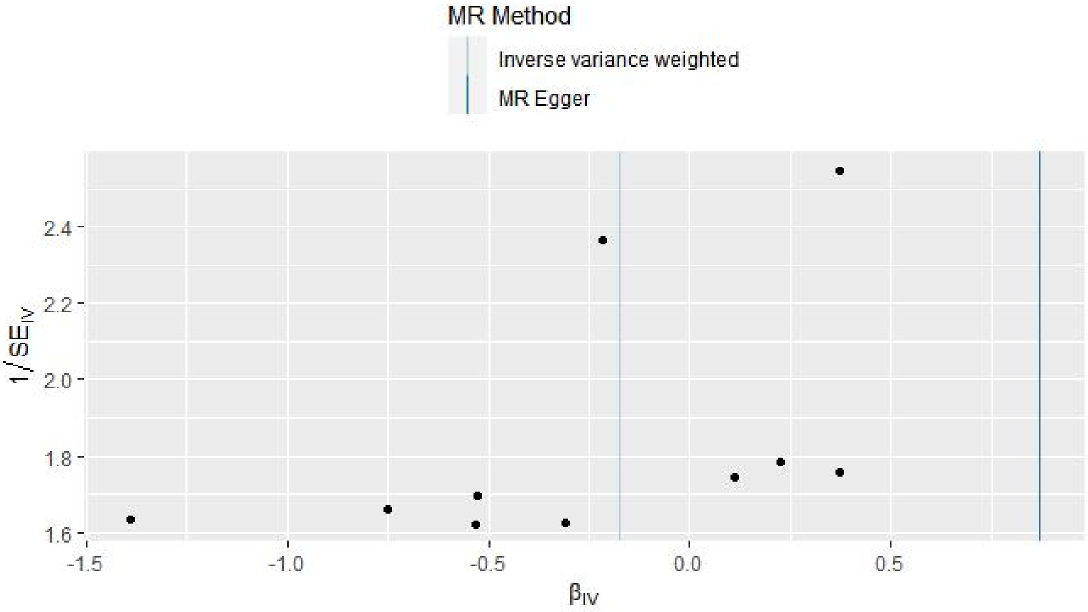
Supplementary Figure S1. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



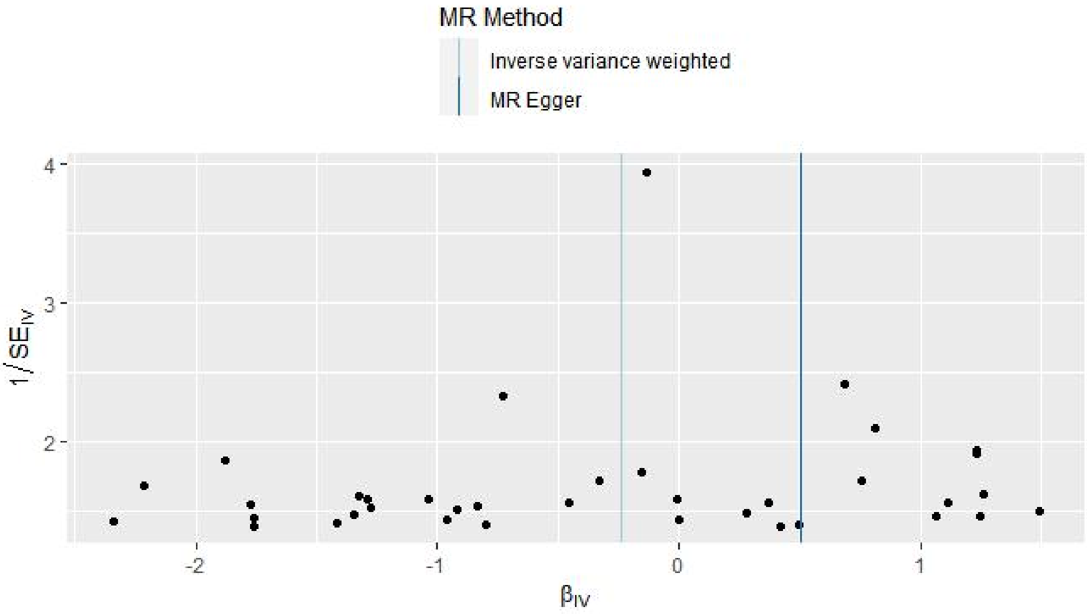
Supplementary Figure S2. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



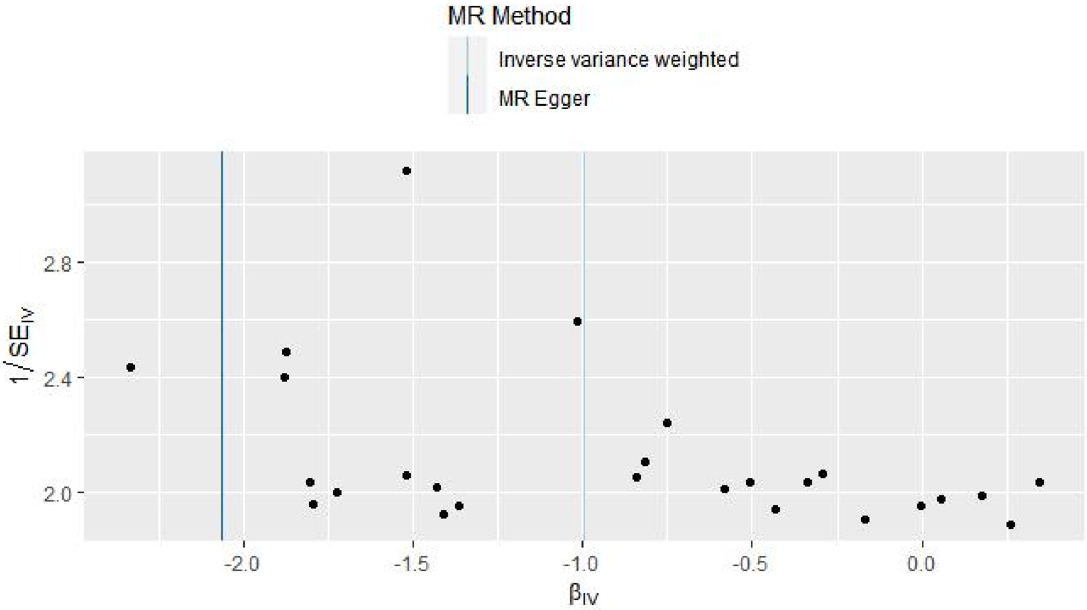
Supplementary Figure S3. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



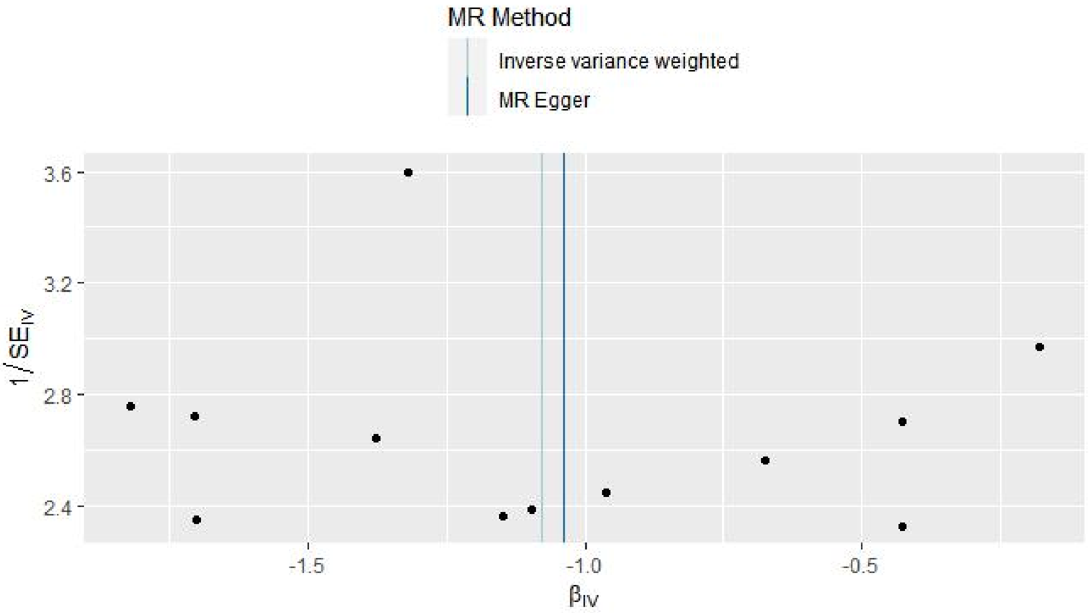
Supplementary Figure S4. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



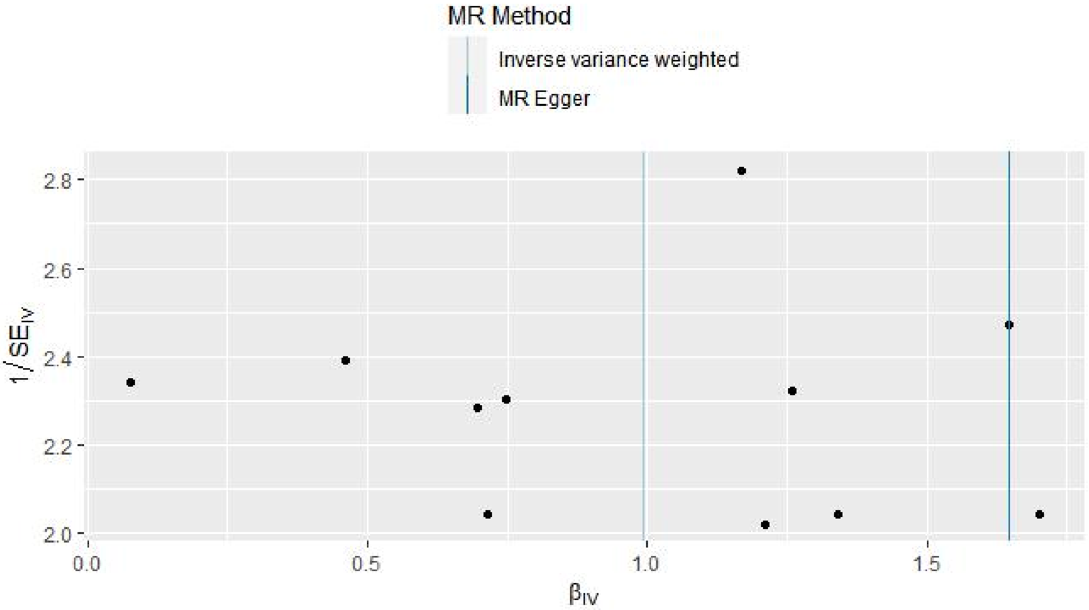
Supplementary Figure S5. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



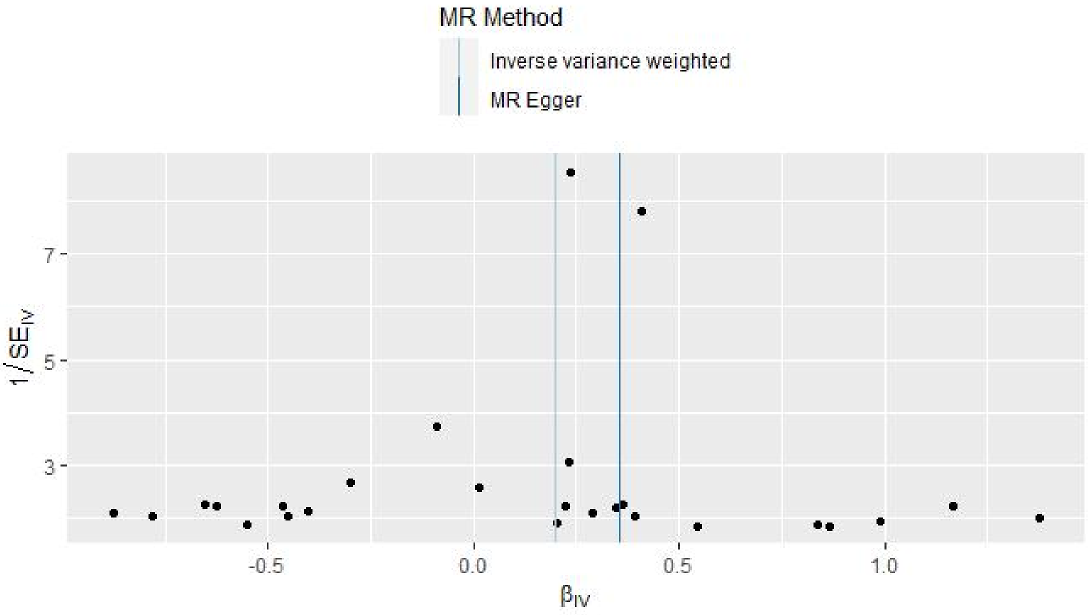
Supplementary Figure S6. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



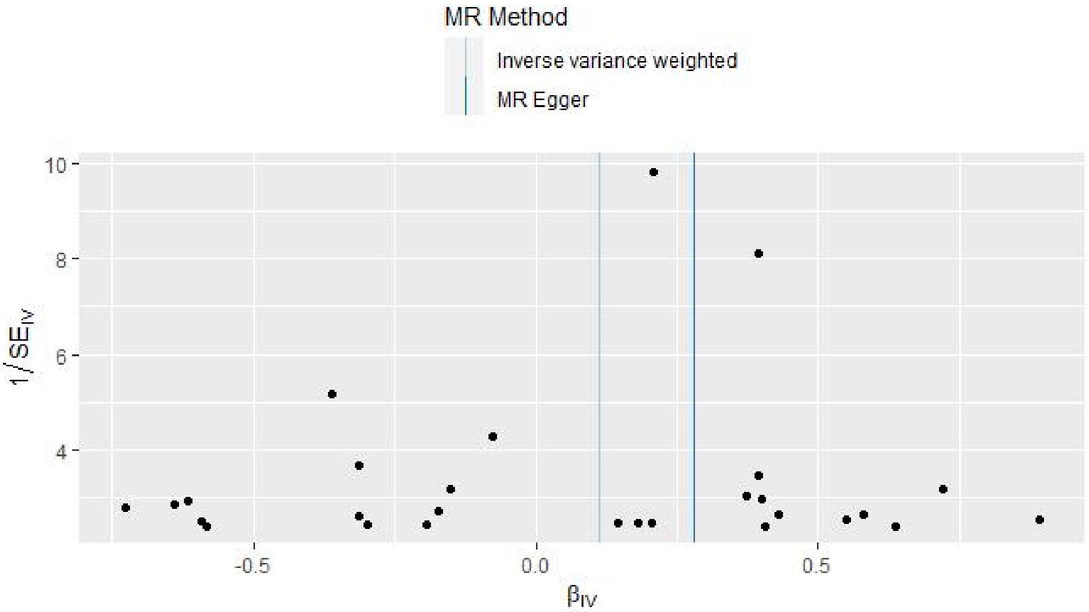
Supplementary Figure S7. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



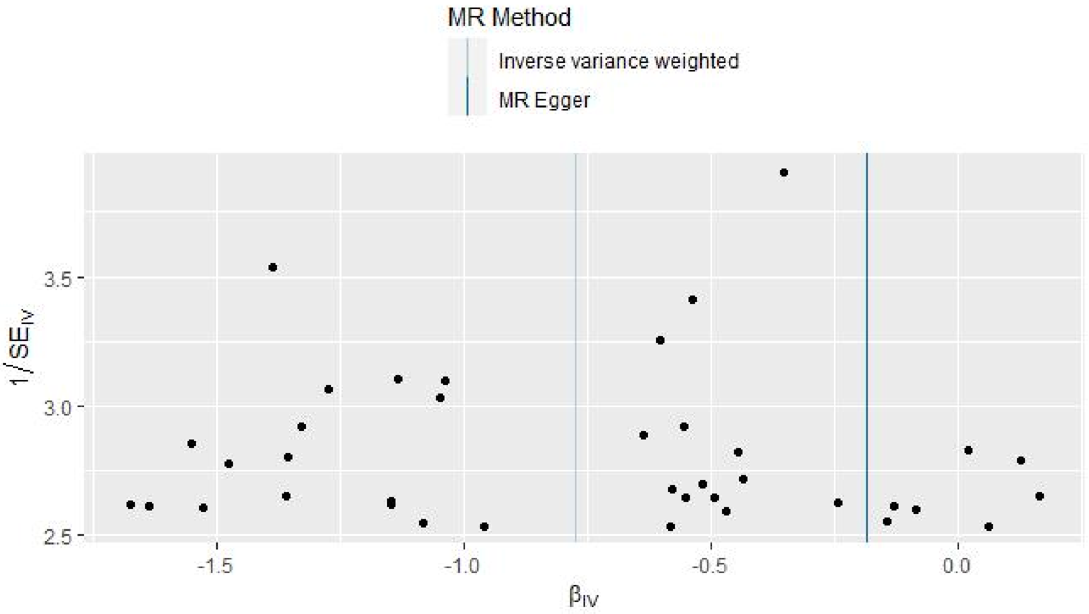
Supplementary Figure S8. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



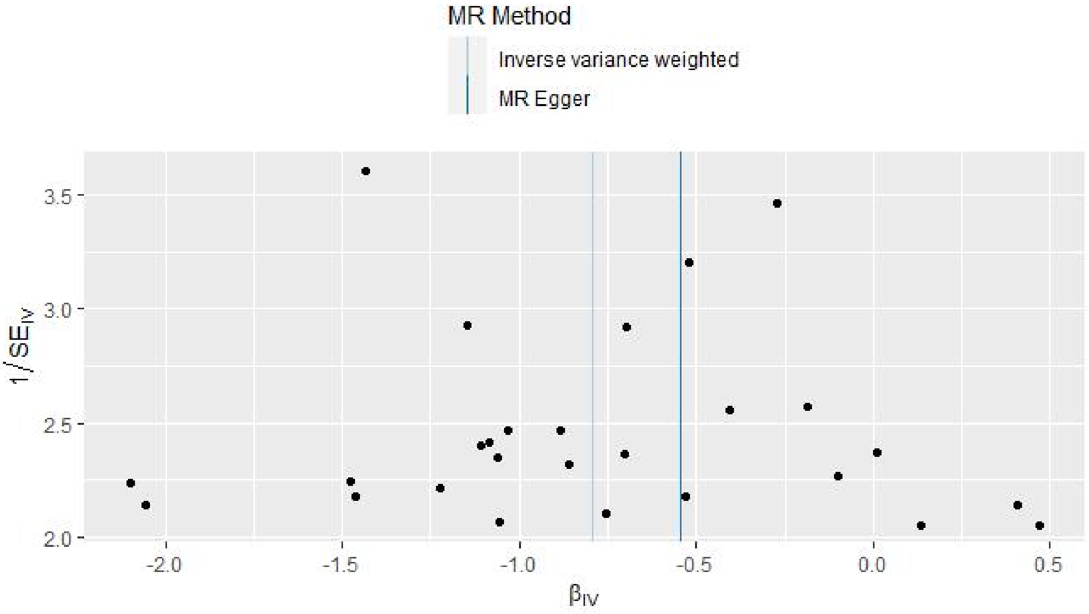
Supplementary Figure S9. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



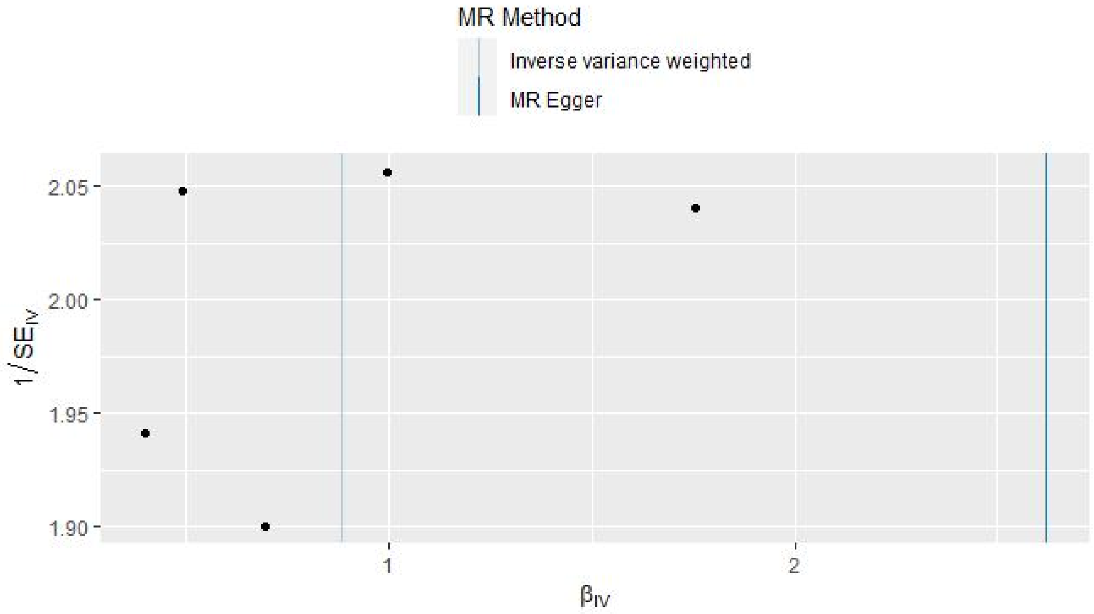
Supplementary Figure S10. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



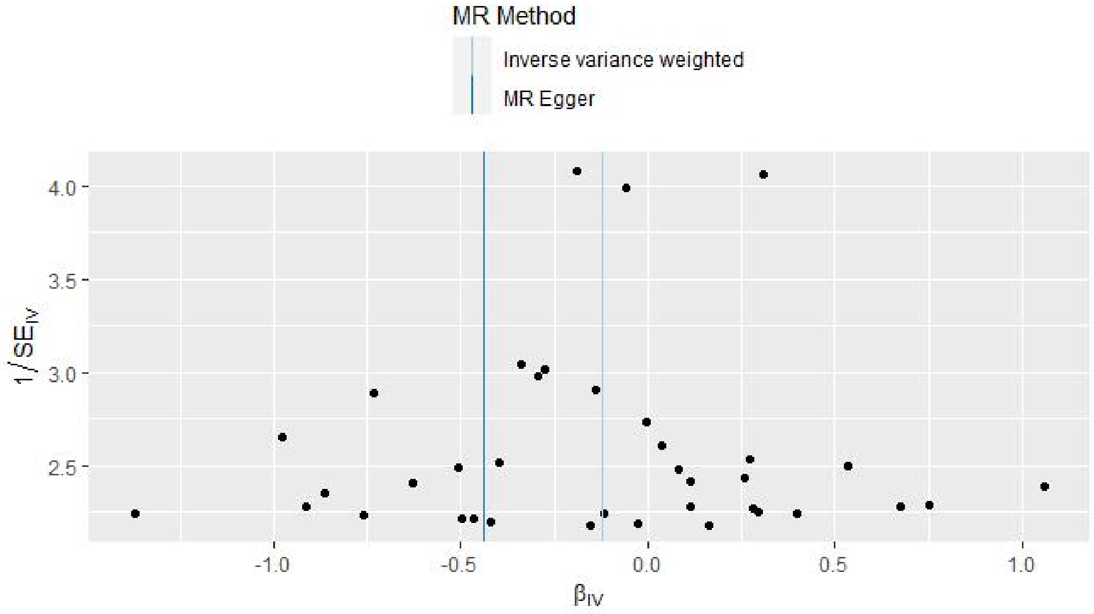
Supplementary Figure S11. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



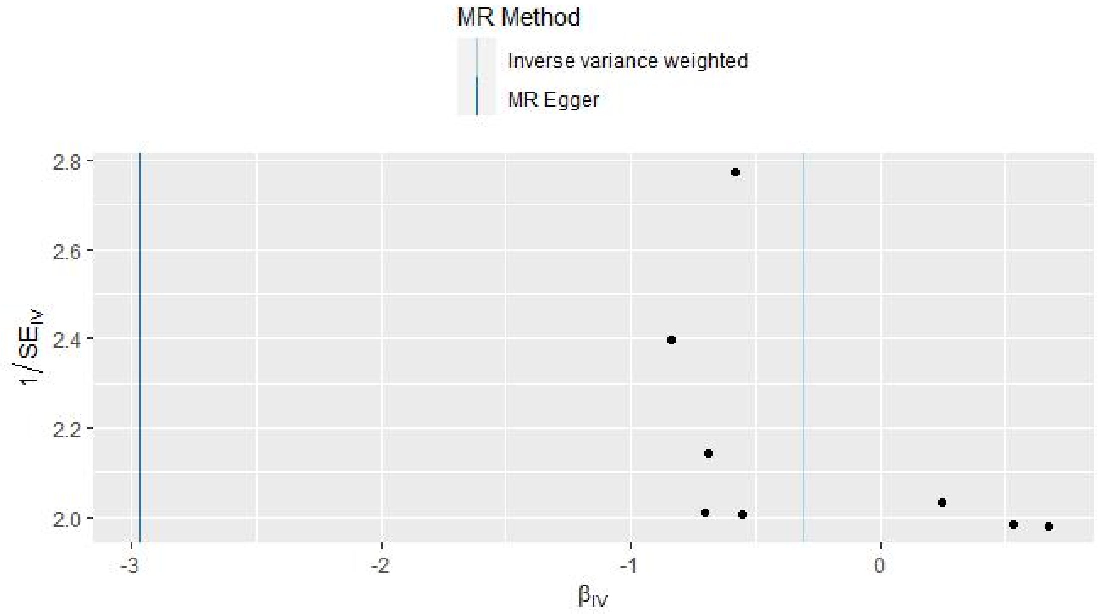
Supplementary Figure S12. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



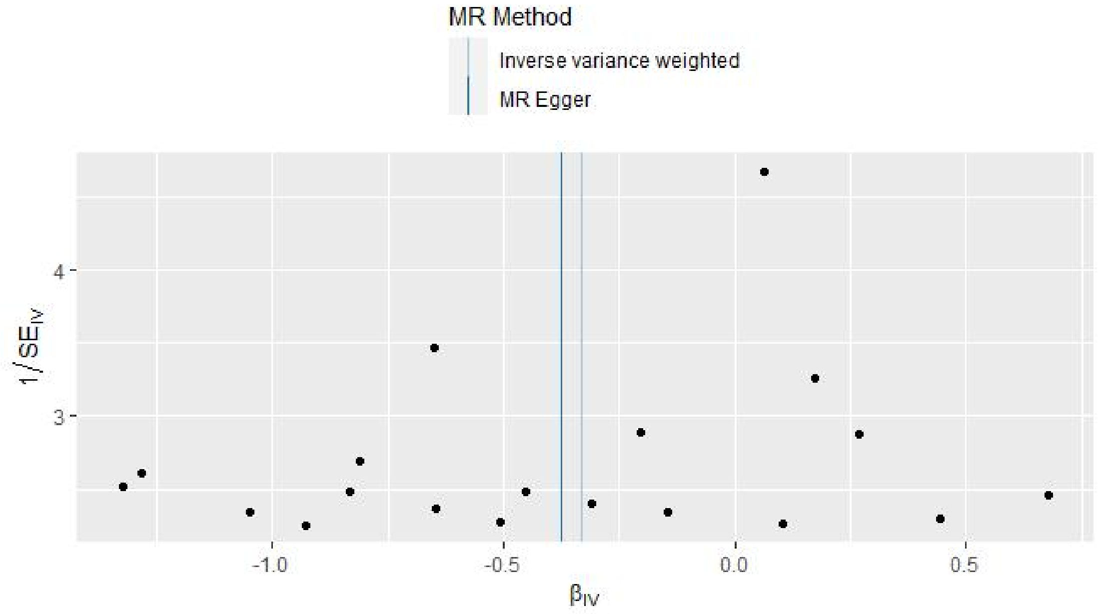
Supplementary Figure S13. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



Supplementary Figure S14. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



Supplementary Figure S15. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.



Supplementary Figure S16. SNP, single-nucleotide polymorphism; IV, Instrumental variable; SE: Standard Error; MR, Mendelian Randomization.