

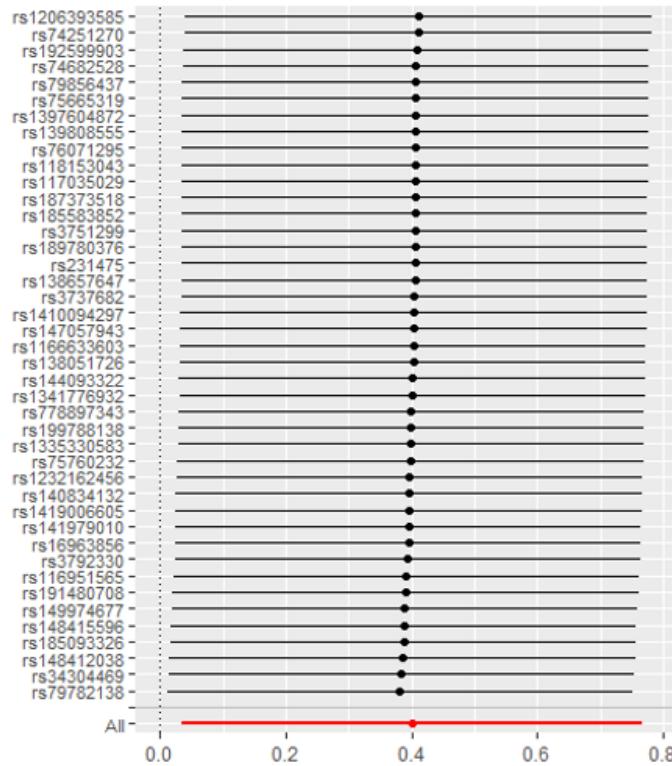
**Supplemental Table S1.** Genetic variants associated with V-C intake in city cohort and their magnitude in city hospital-based cohort and their association with fasting serum glucose concentrations at a fasting state in Ansan/Ansung+rural cohort

CHR	SNP	EA	NA	Beta for V-C intake	SE for V-C intake	p-value	Beta for fasting serum glucose	SE for fasting serum glucose	p-value	Gene name
1	rs74682528	C	T	0.0569	0.0320	4.19E-05	0.0212	0.1095	0.6554	KAZN
1	rs778897343	G	C	-0.0404	0.0223	2.93E-05	0.0048	0.0764	0.8902	NME7
1	rs3737682	A	G	-0.0565	0.0292	8.06E-06	-0.0559	0.1087	0.2361	SLC19A2
3	rs34304469	G	C	-0.1004	0.0557	3.32E-05	0.0846	0.1885	0.3008	FANCD2
3	rs141979010	T	C	-0.1047	0.0572	2.49E-05	-0.0931	0.2123	0.3124	ACP3
3	rs3792330	C	G	-0.1003	0.0567	4.55E-05	-0.1013	0.212	0.2711	ACP3
3	rs1410094297	G	A	0.0934	0.0502	1.83E-05	-0.1201	0.1934	0.1526	ENSG00000240478
4	rs138657647	G	A	0.0952	0.0494	9.59E-06	0.1007	0.1523	0.1274	ANK2
4	rs147057943	G	C	0.0803	0.0429	1.71E-05	-0.0584	0.15	0.3697	ARHGAP10
4	rs148412038	G	T	-0.1085	0.0553	6.28E-06	0.0204	0.1958	0.8117	FSTL5
5	rs79856437	G	T	-0.0534	0.0290	2.19E-05	0.0346	0.0978	0.4154	ENSG00000248752
5	rs79782138	A	G	-0.0488	0.0274	4.07E-05	-0.0489	0.0987	0.2541	GRAMD2B
5	rs144093322	A	G	0.0630	0.0322	6.71E-06	-0.0065	0.1106	0.8928	LINC01184
5	rs1335330583	G	A	0.0438	0.0239	2.54E-05	-0.0438	0.0830	0.2238	LOC102724404
7	rs185093326	C	T	-0.0925	0.0510	2.94E-05	-0.0083	0.1753	0.9127	GRID2IP
7	rs189780376	A	T	-0.1076	0.0582	2.05E-05	-0.036	0.2148	0.7007	Unknown
7	rs187373518	A	G	-0.1090	0.0581	1.56E-05	-0.0364	0.2147	0.6967	Unknown
7	rs185583852	C	T	-0.1090	0.0581	1.56E-05	-0.0364	0.2147	0.6967	Unknown
9	rs75760232	A	G	-0.1228	0.0655	1.56E-05	-0.2047	0.2703	0.0811	Unknown
9	rs140834132	G	C	-0.1344	0.0638	1.22E-06	-0.1967	0.262	0.0838	Unknown
9	rs199788138	C	T	0.1261	0.0676	1.75E-05	-0.0534	0.2344	0.5998	HACD4
10	rs1232162456	C	T	0.0580	0.0328	4.42E-05	-0.0754	0.1135	0.126	KCNMA1
10	rs138051726	G	A	0.1106	0.0625	4.53E-05	0.0107	0.2018	0.9037	CYP2C60P
10	rs1419006605	CA	C	-0.0490	0.0268	2.55E-05	0.0082	0.0920	0.8358	TDRD1
11	rs149974677	T	A	0.0878	0.0487	3.35E-05	0.0671	0.158	0.328	Unknown
12	rs3751299	A	G	0.0398	0.0222	3.89E-05	-0.0316	0.0753	0.3338	FBRSL1
14	rs1397604872	G	C	-0.1229	0.0691	4.16E-05	0.1222	0.2097	0.1795	EIF5
15	rs117035029	A	G	0.0959	0.0492	6.98E-06	0.0803	0.1598	0.2484	SORD
15	rs76071295	A	G	0.0959	0.0492	6.98E-06	0.0803	0.1598	0.2484	SORD
15	rs118153043	C	T	0.0959	0.0492	6.98E-06	0.0803	0.1598	0.2484	SORD
15	rs139808555	G	T	0.0959	0.0492	6.98E-06	0.0803	0.1598	0.2484	SORD
16	rs1166633603	C	A	0.0678	0.0376	3.28E-05	0.0871	0.1192	0.0932	CDH13
17	rs16963856	A	G	0.0438	0.0235	1.77E-05	-0.0123	0.0806	0.7246	LOC105371740
17	rs231475	G	A	0.0430	0.0235	2.41E-05	0.0354	0.0773	0.2884	MPP2
17	rs75665319	C	T	0.0523	0.0264	4.55E-06	-0.0253	0.0902	0.5181	SMURF2,
17	rs74251270	T	C	0.0527	0.0266	5.41E-06	-0.0177	0.0903	0.6512	SMURF2
18	rs1206393585	T	C	0.0414	0.0204	2.73E-06	0.0082	0.0696	0.7887	LAMA1
18	rs1341776932	C	CT	-0.0302	0.0163	2.05E-05	-0.0283	0.0565	0.2491	MIR4527HG
19	rs148415596	G	C	-0.0775	0.0430	3.29E-05	-0.052	0.1586	0.4487	CLASRP

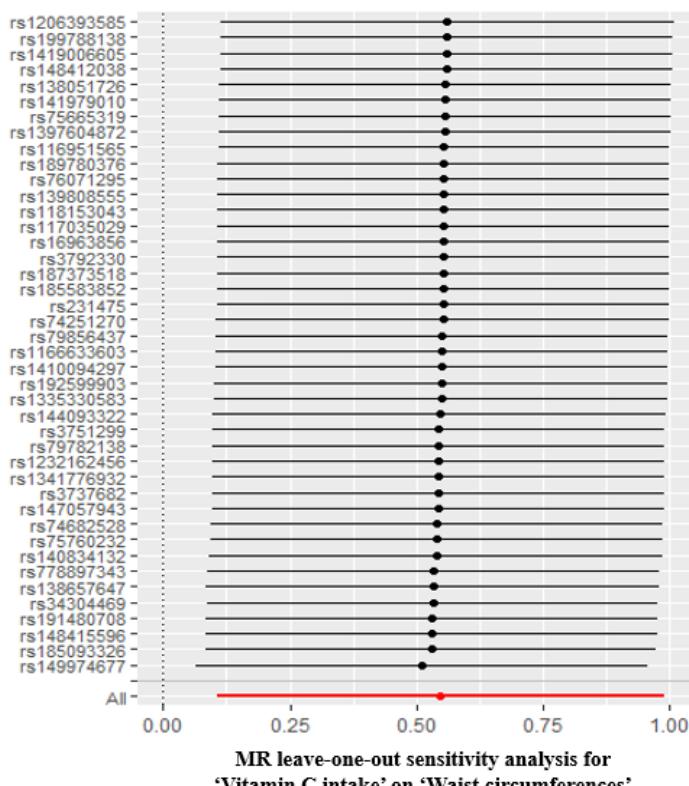
19	rs191480708	T	C	-0.0808	0.0427	1.29E-05		-0.0479	0.1571	0.4828	CLASRP
22	rs192599903	C	T	0.1326	0.0727	2.62E-05		0.0026	0.2393	0.9803	TTC28
22	rs116951565	G	A	-0.0856	0.0481	4.14E-05		-0.0727	0.1848	0.3649	BPIFC

CHR, chromosome; EA, effective allele; NA, non-effective allele; SE, standard errors

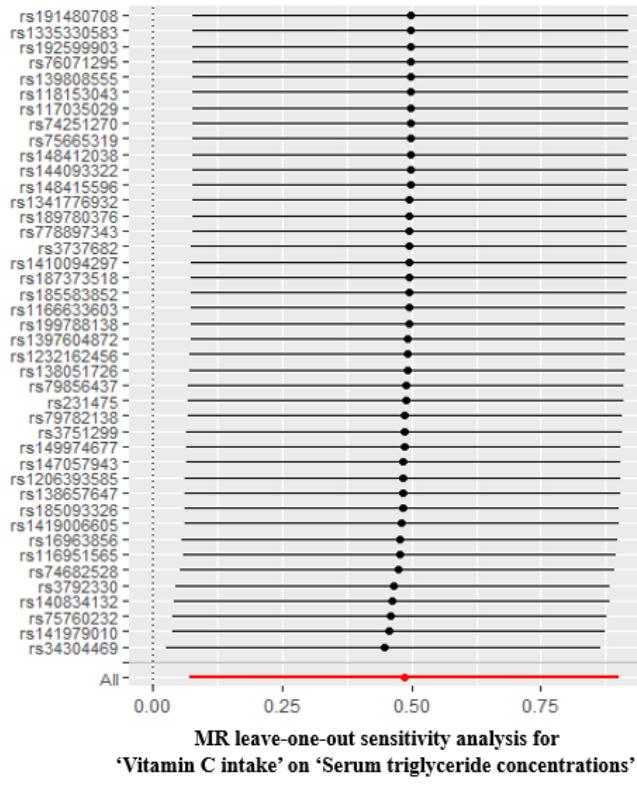
A



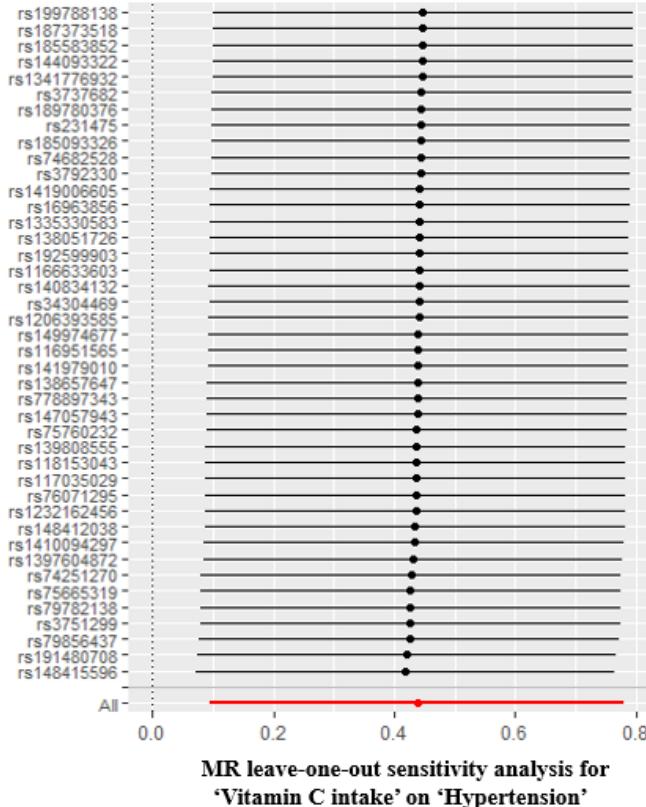
B



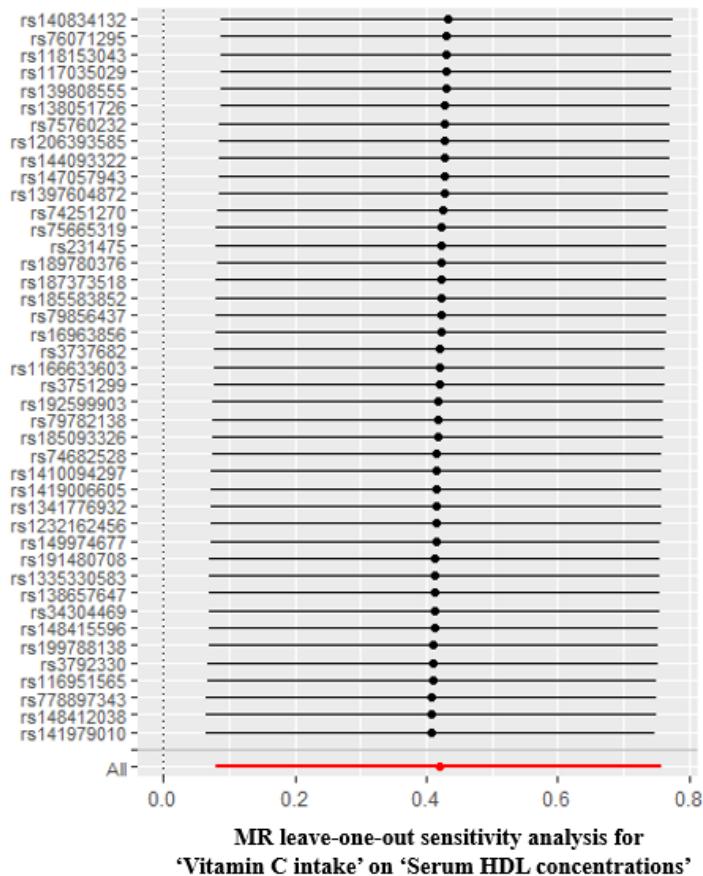
C



D



E



**Supplemental Figure S1.** Leave-one-out sensitivity analysis of MR for the dietary V-C intake on metabolic syndrome and its metabolic traits. A. Metabolic syndrome, B. Waist circumferences, C. serum triglyceride concentrations, D. Hypertension, E. Serum HDL concentrations