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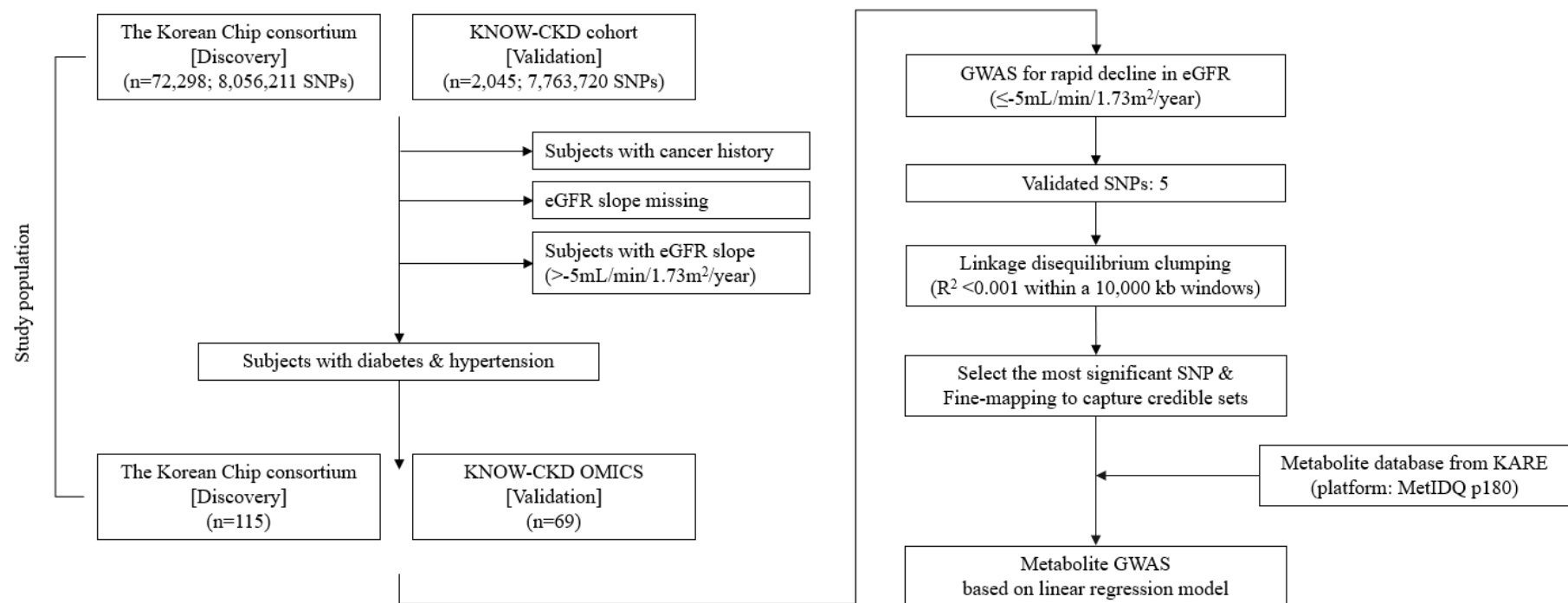


Figure S1. Study population and workflow for the genome-metabolomics integrative analysis (GMIA).

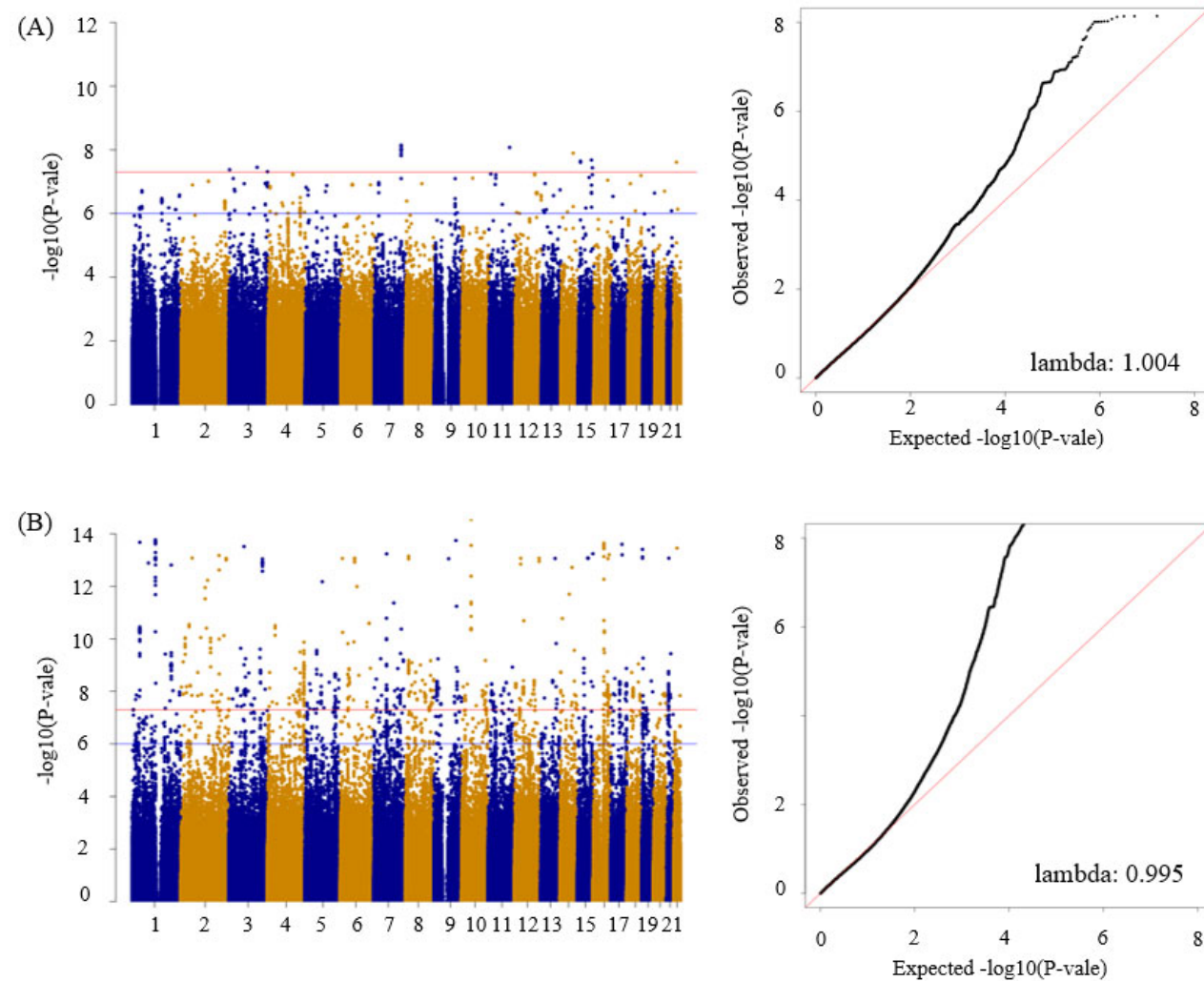


Figure S2. Manhattan and quantile-quantile plots of GWAS for the rapid decline in the estimated glomerular filtration rate. (A) K-CHIP consortium: discovery dataset. (B) KNOW-CKD cohort: validation dataset. GWAS, genome-wide association study; K-CHIP, Korean Chip; KNOW-CKD, The KoreaN Cohort Study for Outcomes in Patients With Chronic Kidney Disease.

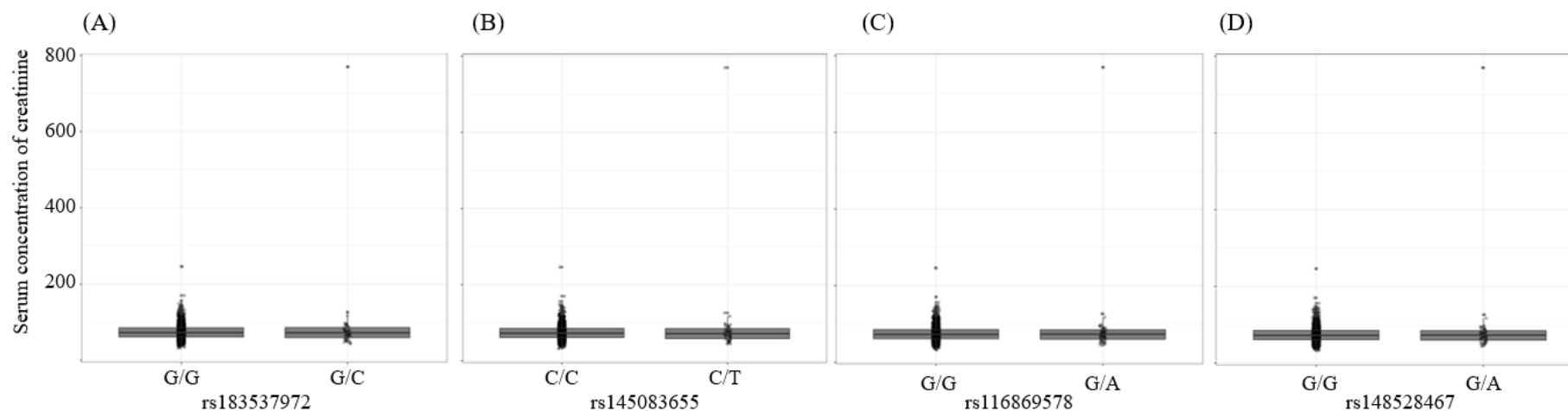


Figure S3. Associations between SNPs and the serum creatine concentration using a linear regression model from GMIA. (A) G: reference allele; C: effect allele of rs183537972 (HYAL6P). (B) C: reference allele; T: effect allele of rs145083655 (HYAL4). (C) G: reference allele; A: effect allele of rs116869578 (LMOD2). (D) G: reference allele; A: effect allele of rs148528467 (WASL). GMIA, genome-metabolomics integrative analysis; SNP, single nucleotide polymorphism.

Table S1. List of 135 serum metabolites in the KARE cohort

<b>Acylcarnitine</b>	<b>Amino acids</b>	<b>Biogenic amines</b>	<b>Sugar</b>	<b>Lyso Phosphatidylcholine</b>	<b>Phosphatidylcholine diacyl</b>
Carnitine	Alanine	Acetylornithine	Hexose	Lyso Phosphatidylcholine acyl C16:0	Phosphatidylcholine diacyl C28:1
Acetylcarnitine	Arginine	Asymmetric dimethylarginine		Lyso Phosphatidylcholine acyl C16:1	Phosphatidylcholine diacyl C30:0
Propionylcarnitine	Asparagine	Creatinine		Lyso Phosphatidylcholine acyl C17:0	Phosphatidylcholine diacyl C32:0
Butyrylcarnitine	Aspartate	Kynurenine		Lyso Phosphatidylcholine acyl C18:0	Phosphatidylcholine diacyl C32:1
Valerylcarnitine	Citrulline	Putrescine		Lyso Phosphatidylcholine acyl C18:1	Phosphatidylcholine diacyl C32:3
Pimelylcarnitine	Glutamine	Sarcosine		Lyso Phosphatidylcholine acyl C18:2	Phosphatidylcholine diacyl C34:1
Octanoylcarnitine	Glutamate	Serotonin		Lyso Phosphatidylcholine acyl C20:3	Phosphatidylcholine diacyl C34:2
Tetradecenoylcarnitine	Glycine	Spermidine		Lyso Phosphatidylcholine acyl C20:4	Phosphatidylcholine diacyl C34:3
Tetradecadienylcarnitine	Histidine	Spermine			Phosphatidylcholine diacyl C34:4
Hexadecanoylcarnitine	Isoleucine	Taurine			Phosphatidylcholine diacyl C36:0
Ocatdecanoylcarnitine	Leucine				Phosphatidylcholine diacyl C36:1
Octadecenoylcarnitine	Lysine				Phosphatidylcholine diacyl C36:2
Octadecadienylcarnitine	Methionine				Phosphatidylcholine diacyl C36:3
	Ornithine				Phosphatidylcholine diacyl C36:4
	Phenylalanine				Phosphatidylcholine diacyl C36:5
	Proline				Phosphatidylcholine diacyl C36:6
	Serine				Phosphatidylcholine diacyl C38:0
	Threonine				Phosphatidylcholine diacyl C38:1
	Tryptophan				Phosphatidylcholine diacyl C38:3
	Tyrosine				Phosphatidylcholine diacyl C38:4
	Valine				Phosphatidylcholine diacyl C38:5
					Phosphatidylcholine diacyl C38:6
					Phosphatidylcholine diacyl C40:1
					Phosphatidylcholine diacyl C40:2
					Phosphatidylcholine diacyl C40:3
					Phosphatidylcholine diacyl C40:4
					Phosphatidylcholine diacyl C40:5
					Phosphatidylcholine diacyl C40:6
					Phosphatidylcholine diacyl C42:0
					Phosphatidylcholine diacyl C42:1
					Phosphatidylcholine diacyl C42:2
					Phosphatidylcholine diacyl C42:4
					Phosphatidylcholine diacyl C42:5
					Phosphatidylcholine diacyl C42:6

KARE, the Korea Association Resource

Table S1. List of 135 serum metabolites in the KARE cohort (Continued)

<b>Phosphatidylcholine acyl-alkyl</b>	<b>Sphingolipids</b>
Phosphatidylcholine acyl-alkyl C30:0	Hydroxysphingomyelin C14:1
Phosphatidylcholine acyl-alkyl C32:1	Hydroxysphingomyelin C16:1
Phosphatidylcholine acyl-alkyl C32:2	Hydroxysphingomyelin C22:1
Phosphatidylcholine acyl-alkyl C34:0	Hydroxysphingomyelin C22:2
Phosphatidylcholine acyl-alkyl C34:1	Hydroxysphingomyelin C24:1
Phosphatidylcholine acyl-alkyl C34:2	Sphingomyelin C16:0
Phosphatidylcholine acyl-alkyl C34:3	Sphingomyelin C16:1
Phosphatidylcholine acyl-alkyl C36:0	Sphingomyelin C18:0
Phosphatidylcholine acyl-alkyl C36:1	Sphingomyelin C18:1
Phosphatidylcholine acyl-alkyl C36:2	Sphingomyelin C24:0
Phosphatidylcholine acyl-alkyl C36:3	Sphingomyelin C24:1
Phosphatidylcholine acyl-alkyl C36:4	Sphingomyelin C26:1
Phosphatidylcholine acyl-alkyl C36:5	
Phosphatidylcholine acyl-alkyl C38:0	
Phosphatidylcholine acyl-alkyl C38:1	
Phosphatidylcholine acyl-alkyl C38:2	
Phosphatidylcholine acyl-alkyl C38:3	
Phosphatidylcholine acyl-alkyl C38:4	
Phosphatidylcholine acyl-alkyl C38:5	
Phosphatidylcholine acyl-alkyl C38:6	
Phosphatidylcholine acyl-alkyl C40:1	
Phosphatidylcholine acyl-alkyl C40:2	
Phosphatidylcholine acyl-alkyl C40:3	
Phosphatidylcholine acyl-alkyl C40:4	
Phosphatidylcholine acyl-alkyl C40:5	
Phosphatidylcholine acyl-alkyl C40:6	
Phosphatidylcholine acyl-alkyl C42:0	
Phosphatidylcholine acyl-alkyl C42:1	
Phosphatidylcholine acyl-alkyl C42:2	
Phosphatidylcholine acyl-alkyl C42:3	
Phosphatidylcholine acyl-alkyl C42:4	
Phosphatidylcholine acyl-alkyl C42:5	
Phosphatidylcholine acyl-alkyl C44:3	
Phosphatidylcholine acyl-alkyl C44:4	
Phosphatidylcholine acyl-alkyl C44:5	
Phosphatidylcholine acyl-alkyl C44:6	

KARE, the Korea Association Resource

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
7q33	135579485	rs12674250	intergenic	FAM180A;LUZP6	C/T	0.014	-6.632 (1.060)	7.20E-09
7q33	135578048	rs71539472	intergenic	FAM180A;LUZP6	G/C	0.014	-6.630 (1.060)	7.26E-09
7q33	135578725	rs11773428	intergenic	FAM180A;LUZP6	G/T	0.014	-6.631 (1.060)	7.28E-09
7q33	135572294	rs12670070	intergenic	FAM180A;LUZP6	C/T	0.014	-6.622 (1.060)	7.54E-09
11q22.3	105427302	rs117713934	intergenic	CARD18;GRIA4	T/G	0.035	-4.126 (0.663)	8.40E-09
7q33	135567068	rs2348907	intergenic	FAM180A;LUZP6	A/C	0.013	-6.576 (1.060)	9.43E-09
7q33	135570157	rs11762987	intergenic	FAM180A;LUZP6	A/G	0.013	-6.577 (1.061)	9.48E-09
7q33	135527463	rs71539459	intergenic	FAM180A;LUZP6	A/C	0.013	-6.562 (1.059)	9.65E-09
7q33	135531147	rs71539462	intergenic	FAM180A;LUZP6	T/C	0.013	-6.562 (1.059)	9.69E-09
7q33	135551217	rs79466054	intergenic	FAM180A;LUZP6	C/T	0.013	-6.562 (1.059)	9.71E-09
7q33	135537495	rs11975634	intergenic	FAM180A;LUZP6	A/G	0.013	-6.561 (1.059)	9.75E-09
7q33	135520471	rs56244135	intergenic	FAM180A;LUZP6	T/C	0.013	-6.542 (1.060)	1.10E-08
14q31.1	83299627	rs117363978	intergenic	LINC02301;NONE	G/A	0.029	-5.293 (0.862)	1.27E-08
7q33	135490878	rs11766426	intergenic	FAM180A;LUZP6	C/G	0.014	-6.504 (1.063)	1.38E-08
7q33	135539970	rs60112348	intergenic	FAM180A;LUZP6	A/G	0.012	-6.789 (1.113)	1.52E-08
15q26.1	89195127	rs111437463	UTR5	ISG20	G/A	0.008	-9.620 (1.595)	2.08E-08
15q13.3	33261838	rs7168080	intronic	FMN1	T/C	0.027	-4.511 (0.750)	2.26E-08
22q12.2	30757436	rs79247733	intronic	CCDC157	G/A	0.087	-2.734 (0.456)	2.44E-08
15q13.3	33262276	rs60847748	intronic	FMN1	G/C	0.028	-4.487 (0.748)	2.46E-08
3q24	143157268	rs13093275	intronic	SLC9A9	G/T	0.113	-2.304 (0.389)	3.53E-08
15q26.1	93906143	rs148163587	intergenic	LOC105370980;LINC02207	C/T	0.013	-6.334 (1.071)	3.65E-08
3p26.2	3175601	rs149885665	intronic	TRNT1	C/T	0.010	-7.688 (1.307)	4.19E-08

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
3q29	195847118	rs145588336	intergenic	TFRC;LINC00885	C/T	0.048	-3.406 (0.582)	4.85E-08
11p15.4	9650309	rs117764660	intergenic	WEE1;SWAP70	A/G	0.009	-7.626 (1.311)	5.72E-08
12q23.1	98213754	rs139661669	intergenic	LOC643711;MIR4495	T/G	0.009	-7.626 (1.311)	5.72E-08
4q28.1	127056018	rs149461767	intergenic	MIR2054;INTU	C/G	0.013	-7.011 (1.206)	5.75E-08
15q26.1	93888877	rs955690599	intergenic	LOC105370980;LINC02207	C/T	0.014	-6.316 (1.089)	6.08E-08
11p13	34728253	rs184451962	intergenic	EHF;APIP	G/A	0.000	-541.650 ( 93.367)	6.10E-08
4q28.1	127191674	rs75153312	intergenic	MIR2054;INTU	T/A	0.011	-7.555 (1.303)	6.14E-08
12q23.1	98211000	rs79833465	intergenic	LOC643711;MIR4495	T/C	0.009	-7.612 (1.313)	6.15E-08
18q22.2	67318159	rs73463973	intronic	DOK6	A/G	0.115	-2.110 (0.364)	6.38E-08
15q24.3	77336133	rs118012826	UTR3	TSPAN3	G/A	0.027	-4.485 (0.779)	7.38E-08
10q21.1	53171297	rs117744777	intronic	PRKG1	C/T	0.000	-7739.970 (1346.350)	7.76E-08
11p13	34737478	rs187796610	intergenic	EHF;APIP	A/G	0.000	-540.784 ( 94.068)	7.76E-08
3p24.3	21653781	rs147909135	intronic	ZNF385D	G/A	0.009	-7.555 (1.315)	7.90E-08
7q33	135549647	rs11764776	intergenic	FAM180A;LUZP6	C/A	0.009	-7.558 (1.316)	7.91E-08
9q31.1	104899256	rs150890582	intergenic	GRIN3A;LINC00587	G/A	0.009	-7.553 (1.315)	7.96E-08
16q22.1	69186529	rs557474024	intronic	UTP4	C/T	0.008	-8.489 (1.485)	8.97E-08
2q22.1	138442200	rs549533033	intergenic	THSD7B;LOC101928273	G/A	0.008	-8.487 (1.489)	9.68E-08
2q22.1	138442195	rs567460414	intergenic	THSD7B;LOC101928273	A/G	0.008	-8.487 (1.489)	9.68E-08
7p15.3	21587183	rs201198710	intronic	DNAH11	ATAAT/A	0.011	-7.470 (1.315)	1.06E-07
3q29	195809725	rs17091661	upstream	TFRC	C/G	0.052	-3.234 (0.569)	1.07E-07
13q13.3	36255134	rs142727278	intergenic	NBEA;LINC00445	C/T	0.017	-5.902 (1.042)	1.15E-07
3q29	192624876	rs116204719	intronic	MB21D2	A/T	0.009	-7.474 (1.320)	1.15E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)



Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
3p12.3	77523031	rs145860157	intronic	ROBO2	A/C	0.009	-7.469 (1.319)	1.15E-07
8q21.13	81610194	rs148850681	intronic	ZNF704	T/C	0.009	-7.469 (1.319)	1.15E-07
18p11.21	13719612	rs184493441	intronic	FAM210A	T/C	0.009	-7.469 (1.319)	1.15E-07
3q27.2	185140359	rs76390866	intronic	MAP3K13	C/T	0.009	-7.469 (1.319)	1.15E-07
3q29	192617374	rs141743783	intronic	MB21D2	A/G	0.009	-7.472 (1.320)	1.16E-07
3q29	192621063	rs79926231	intronic	MB21D2	G/T	0.009	-7.472 (1.320)	1.16E-07
3q29	192623144	rs115525172	intronic	MB21D2	G/A	0.009	-7.471 (1.320)	1.16E-07
3q29	192627068	rs11921144	intronic	MB21D2	A/T	0.009	-7.471 (1.320)	1.16E-07
3q29	192626691	rs79654963	intronic	MB21D2	A/T	0.009	-7.471 (1.320)	1.16E-07
3q29	192614938	rs138060225	intronic	MB21D2	A/C	0.009	-7.468 (1.319)	1.17E-07
3q29	192621921	rs77225906	intronic	MB21D2	G/C	0.009	-7.470 (1.320)	1.17E-07
3q29	192630923	rs73198800	intronic	MB21D2	T/C	0.009	-7.464 (1.320)	1.19E-07
6p11.2	57281388	rs575341105	intronic	PRIM2	G/C	0.009	-7.712 (1.364)	1.20E-07
7p15.3	21580775	rs115451224	intergenic	SP4;DNAH11	G/T	0.009	-7.463 (1.321)	1.21E-07
11p13	32360746	rs55767723	intergenic	SNORA88;WT1	C/T	0.012	-7.120 (1.260)	1.22E-07
7p15.3	21583910	rs56688731	intronic	DNAH11	T/G	0.009	-7.458 (1.321)	1.24E-07
6q25.1	150329057	rs185234953	intergenic	RAET1K;RAET1L	A/G	0.024	-4.892 (0.867)	1.25E-07
2p16.1	57600654	rs147118782	intergenic	CCDC85A;VRK2	T/C	0.010	-8.573 (1.519)	1.25E-07
6p11.2	57324187	rs1192133075	intronic	PRIM2	A/C	0.009	-7.919 (1.404)	1.26E-07
6p11.2	57325078	rs994418306	intronic	PRIM2	G/A	0.009	-7.922 (1.404)	1.26E-07
6p11.2	57326277	rs1179007536	intronic	PRIM2	C/T	0.009	-7.926 (1.405)	1.27E-07
6p11.2	57325945	rs1397294397	intronic	PRIM2	A/G	0.009	-7.926 (1.405)	1.27E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
6p11.2	57328179	rs1218145796	intronic	PRIM2	A/G	0.009	-7.930 (1.406)	1.27E-07
6p11.2	57327372	rs1294551034	intronic	PRIM2	A/T	0.009	-7.930 (1.406)	1.27E-07
6p11.2	57327572	rs1319926816	intronic	PRIM2	G/T	0.009	-7.930 (1.406)	1.27E-07
6p11.2	57330616	rs1334057224	intronic	PRIM2	T/G	0.009	-7.937 (1.407)	1.27E-07
6p11.2	57330720	rs761503009	intronic	PRIM2	A/C	0.009	-7.937 (1.407)	1.27E-07
15q26.1	89197517	rs141786963	intronic	ISG20	C/T	0.022	-5.985 (1.062)	1.28E-07
5q21.3	108575881	rs80194513	ncRNA_intronic	LOC285638	T/C	0.003	-49.798 (8.840)	1.31E-07
4p16.1	11150684	rs375628754	intergenic	CLNK;MIR572	G/T	0.036	-3.913 (0.696)	1.38E-07
3q29	195804208	rs17091588	intronic	TFRC	A/G	0.052	-3.181 (0.566)	1.38E-07
3q29	195798320	rs41301381	exonic	TFRC	G/C	0.052	-3.172 (0.565)	1.44E-07
5p15.33	3278879	rs372457561	intergenic	LINC01377;LINC01019	T/C	0.022	-5.131 (0.915)	1.49E-07
3p24.1	27705156	rs536262664	intergenic	SLC4A7;EOMES	C/T	0.000	-312.603 (56.097)	1.73E-07
13q34	112170827	rs139027045	intergenic	TEX29;LINC02337	C/T	0.010	-7.885 (1.417)	1.80E-07
5p15.2	13361785	rs138135958	intergenic	LINC02220;DNAH5	G/T	0.017	-5.730 (1.030)	1.80E-07
1p33	49684590	rs185947935	intronic	AGBL4	C/T	0.013	-6.262 (1.128)	1.91E-07
3p24.1	29770237	rs79101590	intronic	RBMS3	T/C	0.024	-4.940 (0.891)	1.98E-07
20q13.2	50168870	rs188208200	intronic	NFATC2	C/T	0.010	-7.341 (1.325)	1.99E-07
5q21.1	102568853	rs75498191	intergenic	PPIP5K2;C5orf30	A/G	0.000	-777.631 (140.453)	2.03E-07
1p33	49659599	rs117205909	intronic	AGBL4	C/T	0.013	-6.291 (1.137)	2.07E-07
1p33	49657256	rs184839480	intronic	AGBL4	T/C	0.013	-6.295 (1.138)	2.10E-07
15q26.1	89180627	rs148556246	intronic	ISG20	C/T	0.017	-5.226 (0.946)	2.17E-07
12q23.3	108894982	rs11113949	intergenic	LINC01498;FICD	G/A	0.010	-7.266 (1.316)	2.19E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
12q23.3	108895133	rs11113950	intergenic	LINC01498;FICD	A/C	0.010	-7.266 (1.316)	2.19E-07
12q23.3	108894645	rs11113946	intergenic	LINC01498;FICD	C/A	0.010	-7.266 (1.316)	2.19E-07
12q23.3	108894695	rs11113947	intergenic	LINC01498;FICD	A/G	0.010	-7.266 (1.316)	2.19E-07
12q23.3	108894518	rs11113945	intergenic	LINC01498;FICD	T/C	0.010	-7.265 (1.316)	2.20E-07
12q23.3	108894433	rs12367034	intergenic	LINC01498;FICD	G/A	0.010	-7.265 (1.316)	2.20E-07
12q23.3	108895874	rs11113951	intergenic	LINC01498;FICD	A/G	0.010	-7.265 (1.317)	2.20E-07
7p15.3	21630394	rs143123989	intronic	DNAH11	A/T	0.009	-8.086 (1.466)	2.22E-07
12q23.3	108896797	rs11113953	intergenic	LINC01498;FICD	C/T	0.010	-7.263 (1.317)	2.22E-07
12q23.3	108893730	rs11113944	intergenic	LINC01498;FICD	T/C	0.010	-7.262 (1.316)	2.22E-07
12q23.3	108893870	rs77449249	intergenic	LINC01498;FICD	A/T	0.010	-7.262 (1.316)	2.22E-07
12q23.3	108893479	rs11113940	intergenic	LINC01498;FICD	T/A	0.010	-7.261 (1.316)	2.23E-07
12q23.3	108893524	rs11113941	intergenic	LINC01498;FICD	C/T	0.010	-7.261 (1.316)	2.23E-07
12q23.3	108893600	rs11113942	intergenic	LINC01498;FICD	G/T	0.010	-7.261 (1.316)	2.23E-07
12q23.3	108897590	rs11113956	intergenic	LINC01498;FICD	C/A	0.010	-7.263 (1.317)	2.23E-07
12q23.3	108893722	rs11113943	intergenic	LINC01498;FICD	G/A	0.010	-7.261 (1.316)	2.23E-07
12q23.3	108893341	rs11113939	intergenic	LINC01498;FICD	G/A	0.010	-7.260 (1.316)	2.24E-07
12q23.3	108893177	rs11113936	intergenic	LINC01498;FICD	T/G	0.010	-7.260 (1.316)	2.24E-07
12q23.3	108893204	rs11113937	intergenic	LINC01498;FICD	G/T	0.010	-7.260 (1.316)	2.24E-07
12q23.3	108893248	rs11113938	intergenic	LINC01498;FICD	T/G	0.010	-7.260 (1.316)	2.24E-07
12q23.3	108892840	rs11113935	intergenic	LINC01498;FICD	C/T	0.010	-7.259 (1.317)	2.25E-07
12q23.3	108892921	rs199953283	intergenic	LINC01498;FICD	A/AT	0.010	-7.259 (1.317)	2.25E-07
12q23.3	108892623	rs11113932	intergenic	LINC01498;FICD	A/G	0.010	-7.258 (1.317)	2.26E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
12q23.3	108892405	rs11113930	intergenic	LINC01498;FICD	C/T	0.010	-7.258 (1.317)	2.26E-07
12q23.3	108892085	rs11113927	intergenic	LINC01498;FICD	A/C	0.010	-7.258 (1.317)	2.26E-07
12q23.3	108892316	rs11113928	intergenic	LINC01498;FICD	T/A	0.010	-7.258 (1.317)	2.26E-07
12q23.3	108892317	rs11113929	intergenic	LINC01498;FICD	G/A	0.010	-7.258 (1.317)	2.26E-07
12q23.3	108892094	rs138719215	intergenic	LINC01498;FICD	A/AG	0.010	-7.258 (1.317)	2.26E-07
19q13.43	58196865	rs967336174	intronic	ZNF551	CCT/C	0.010	-7.257 (1.317)	2.27E-07
12q23.3	108891504	rs12368931	intergenic	LINC01498;FICD	A/G	0.010	-7.256 (1.317)	2.28E-07
12q23.3	108891644	rs11113926	intergenic	LINC01498;FICD	G/A	0.010	-7.255 (1.317)	2.28E-07
12q23.3	108891607	rs12372268	intergenic	LINC01498;FICD	C/A	0.010	-7.255 (1.317)	2.28E-07
12q23.3	108891441	rs57853417	intergenic	LINC01498;FICD	A/G	0.010	-7.255 (1.317)	2.29E-07
12q23.3	108898482	rs57507907	intergenic	LINC01498;FICD	T/A	0.010	-7.257 (1.317)	2.29E-07
12q23.3	108890795	rs200436713	intergenic	LINC01498;FICD	T/TA	0.010	-7.252 (1.317)	2.31E-07
12q23.3	108890835	rs11113924	intergenic	LINC01498;FICD	T/A	0.010	-7.251 (1.317)	2.32E-07
15q26.1	89173098	rs150509619	intronic	AEN	A/C	0.018	-5.277 (0.958)	2.32E-07
12q23.3	108890649	rs76473093	intergenic	LINC01498;FICD	G/C	0.010	-7.251 (1.317)	2.32E-07
12q23.3	108890651	rs77258936	intergenic	LINC01498;FICD	T/A	0.010	-7.251 (1.317)	2.32E-07
12q23.3	108898481	rs56999150	intergenic	LINC01498;FICD	C/A	0.011	-7.252 (1.318)	2.35E-07
12q23.3	108898892	rs60988999	intergenic	LINC01498;FICD	C/A	0.010	-7.251 (1.318)	2.36E-07
12q23.3	108890137	rs76822917	intergenic	LINC01498;FICD	A/G	0.010	-7.246 (1.317)	2.36E-07
12q23.3	108890022	rs77049190	intergenic	LINC01498;FICD	T/C	0.010	-7.246 (1.317)	2.36E-07
12q23.3	108890022	rs77049190	intergenic	LINC01498;FICD	T/C	0.010	-7.246 (1.317)	2.36E-07
12q23.3	108889920	rs79379950	intergenic	LINC01498;FICD	A/G	0.010	-7.243 (1.317)	2.39E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
1q43	240811124	rs565547003	intergenic	GREM2;RGS7	A/G	0.012	-6.624 (1.209)	2.62E-07
5p15.2	13341420	rs142344584	intergenic	LINC02220;DNAH5	A/G	0.017	-5.681 (1.037)	2.64E-07
12q24.33	130982880	rs55762517	intronic	RIMBP2	G/A	0.015	-6.217 (1.135)	2.64E-07
13q31.1	79187459	rs1180870680	ncRNA_intronic	OBI1-AS1	T/C	0.026	-4.123 (0.754)	2.74E-07
17p13.2	6091502	rs116979438	intergenic	WSCD1;AIPL1	T/C	0.013	-5.952 (1.091)	2.89E-07
1q43	239701246	rs16838444	intronic	CHRM3	T/G	0.013	-5.952 (1.091)	2.89E-07
12q24.33	130984960	rs60921151	intronic	RIMBP2	G/A	0.015	-6.146 (1.127)	2.97E-07
4q32.3	164687231	rs12505111	intronic	MARCHF1	A/G	0.027	-4.253 (0.782)	3.12E-07
1q21.3	151012068	rs115422057	intronic	BNIP1	G/A	0.010	-7.387 (1.362)	3.36E-07
9q31.1	104627355	rs10989665	intergenic	GRIN3A;LINC00587	A/C	0.045	-3.442 (0.635)	3.40E-07
12q24.33	130985984	rs66756436	intronic	RIMBP2	G/A	0.015	-6.064 (1.123)	3.76E-07
1q21.3	151013099	rs151070704	intronic	BNIP1	C/T	0.010	-7.363 (1.364)	3.78E-07
1q21.3	151014400	rs146753684	intronic	BNIP1	A/G	0.010	-7.363 (1.365)	3.81E-07
1q21.3	151015174	rs117770722	intronic	BNIP1	C/T	0.010	-7.362 (1.365)	3.84E-07
2q36.1	222176106	rs72952909	intergenic	MIR4268;EPHA4	A/G	0.086	-2.375 (0.441)	3.98E-07
8p23.2	4820233	rs146823031	intronic	CSMD1	T/C	0.012	-6.945 (1.290)	4.05E-07
1q21.3	151008914	rs115270318	upstream;downstream	BNIP1;PRUNE1	T/A	0.010	-7.359 (1.368)	4.12E-07
2q36.1	222178867	rs1430246	intergenic	MIR4268;EPHA4	A/G	0.086	-2.367 (0.440)	4.19E-07
2q36.1	222182550	rs16862493	intergenic	MIR4268;EPHA4	C/G	0.086	-2.355 (0.439)	4.44E-07
1q21.3	151007574	rs12070466	UTR3	PRUNE1	G/C	0.011	-7.347 (1.372)	4.58E-07
2q36.1	222190938	rs72952942	intergenic	MIR4268;EPHA4	C/T	0.087	-2.328 (0.435)	4.60E-07
2q36.1	222191045	rs16862504	intergenic	MIR4268;EPHA4	G/A	0.087	-2.328 (0.435)	4.61E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
4q13.3	72010245	rs375674565	intergenic	DCK;SLC4A4	T/G	0.028	-4.228 (0.790)	4.63E-07
4q32.3	164684385	rs13127646	intronic	MARCHF1	G/A	0.027	-4.205 (0.786)	4.65E-07
4q28.1	127035452	rs117610704	intergenic	MIR2054;INTU	A/G	0.010	-7.848 (1.467)	4.70E-07
2q36.1	222186825	rs16862499	intergenic	MIR4268;EPA4	A/T	0.087	-2.336 (0.437)	4.71E-07
2q36.1	222187315	rs16862501	intergenic	MIR4268;EPA4	G/A	0.087	-2.335 (0.437)	4.74E-07
2q36.1	222185906	rs72952930	intergenic	MIR4268;EPA4	C/T	0.087	-2.338 (0.438)	4.85E-07
9q31.1	104638232	rs10989675	intergenic	GRIN3A;LINC00587	G/A	0.044	-3.341 (0.625)	4.85E-07
3q27.2	184792192	rs79424017	intergenic	VPS8;C3orf70	C/T	0.014	-5.823 (1.092)	5.04E-07
9q31.1	104639683	rs12238882	intergenic	GRIN3A;LINC00587	C/T	0.044	-3.325 (0.624)	5.11E-07
11q13.2	68116010	rs112180284	intronic	LRP5	T/C	0.020	-5.100 (0.957)	5.15E-07
3q27.2	184908072	rs183410169	ncRNA_intronic	EHHADH-AS1	T/C	0.008	-8.731 (1.641)	5.33E-07
2q36.1	222191393	rs6748878	intergenic	MIR4268;EPA4	A/T	0.088	-2.324 (0.438)	5.74E-07
4q21.1	76527346	rs111466342	intronic	CDKL2	G/GT	0.052	-3.092 (0.583)	5.75E-07
9q31.1	104642966	rs9299352	intergenic	GRIN3A;LINC00587	C/T	0.044	-3.289 (0.621)	5.79E-07
1p33	49542012	rs190235218	intronic	AGBL4	C/T	0.012	-6.468 (1.222)	5.95E-07
14q31.1	83551687	rs77734808	intergenic	LINC02301;NONE	G/A	0.016	-6.224 (1.176)	5.98E-07
9q31.1	104645652	rs10989682	intergenic	GRIN3A;LINC00587	G/T	0.044	-3.286 (0.621)	6.13E-07
2q36.1	222184970	rs72952924	intergenic	MIR4268;EPA4	A/G	0.086	-2.332 (0.441)	6.26E-07
15q26.1	89124390	rs150320390	intergenic	DET1;LINC01586	G/T	0.010	-7.572 (1.434)	6.30E-07
1p34.3	38079825	rs117174295	intronic	RSPO1	C/T	0.026	-4.178 (0.792)	6.43E-07
4q32.3	164691345	rs10013393	intronic	MARCHF1	T/G	0.035	-3.645 (0.691)	6.51E-07
1p33	49501403	rs140975530	intronic	AGBL4	T/G	0.012	-6.463 (1.226)	6.54E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
1q25.3	185746647	rs61314460	intronic	HMCN1	G/A	0.070	-2.555 (0.485)	6.58E-07
3q21.3	126517078	rs138613194	intronic	CHCHD6	C/T	0.007	-11.763 (2.233)	6.66E-07
15q22.2	60473320	rs140501799	intergenic	FOXB1;ANXA2	A/G	0.030	-3.857 (0.732)	6.70E-07
1p34.3	38095804	rs12753021	intronic	RSPO1	C/T	0.027	-4.150 (0.788)	6.79E-07
1p33	49485775	rs146366723	intronic	AGBL4	T/C	0.012	-6.475 (1.231)	6.91E-07
2q36.1	222191389	rs200126617	intergenic	MIR4268;EPHA4	A/T	0.087	-2.322 (0.442)	7.13E-07
1p34.3	38097519	rs71640742	UTR5	RSPO1	A/C	0.026	-4.137 (0.788)	7.18E-07
4q32.3	164704667	rs10009600	intronic	MARCHF1	G/C	0.035	-3.615 (0.689)	7.26E-07
22q12.3	37122086	rs16997246	ncRNA_intronic	LOC105373021	T/C	0.013	-5.769 (1.099)	7.26E-07
4q32.3	164741639	rs28637179	intronic	MARCHF1	G/A	0.035	-3.619 (0.690)	7.29E-07
4q32.3	164744895	rs13103455	intronic	MARCHF1	T/C	0.035	-3.616 (0.689)	7.30E-07
4q32.3	164690172	rs13146066	intronic	MARCHF1	T/C	0.041	-3.437 (0.655)	7.31E-07
4q32.3	164716627	rs10030446	intronic	MARCHF1	C/G	0.035	-3.613 (0.689)	7.44E-07
1q41	221080599	rs74957276	intergenic	HLX;C1orf140	C/T	0.026	-4.132 (0.788)	7.46E-07
1q41	221083429	rs75369607	intergenic	HLX;C1orf140	T/G	0.026	-4.132 (0.788)	7.47E-07
13q14.11	42647779	rs78735820	intronic	DGKH	C/T	0.079	-2.694 (0.514)	7.49E-07
4q32.3	164680214	rs13136324	intronic	MARCHF1	C/T	0.026	-4.143 (0.791)	7.56E-07
4q32.3	164672601	rs13105978	intronic	MARCHF1	T/A	0.026	-4.138 (0.790)	7.68E-07
4q32.3	164672948	rs34162806	intronic	MARCHF1	A/C	0.026	-4.138 (0.790)	7.68E-07
4q32.3	164672979	rs139079372	intronic	MARCHF1	T/TGTGTGA	0.026	-4.138 (0.791)	7.71E-07
4q32.3	164707381	rs4691934	intronic	MARCHF1	G/A	0.035	-3.632 (0.694)	7.78E-07
4q32.3	164714927	rs7695742	intronic	MARCHF1	T/C	0.035	-3.632 (0.695)	7.93E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)

Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
13q12.13	27518236	rs11618475	intergenic	GPR12;USP12	A/G	0.017	-5.822 (1.114)	7.97E-07
4q32.3	164670165	rs13101998	intronic	MARCHF1	G/T	0.026	-4.134 (0.791)	7.99E-07
4q32.3	164674901	rs10009742	intronic	MARCHF1	C/T	0.027	-4.128 (0.790)	8.01E-07
4q32.3	164670444	rs1390835129	intronic	MARCHF1	CT/C	0.027	-4.129 (0.790)	8.01E-07
3p24.1	29471087	rs536791351	intronic	RBMS3	A/C	0.018	-5.590 (1.070)	8.04E-07
4q32.3	164670375	rs71600637	intronic	MARCHF1	C/CAT	0.027	-4.127 (0.790)	8.08E-07
4q32.3	164719589	rs7657245	intronic	MARCHF1	G/A	0.035	-3.631 (0.695)	8.09E-07
21q22.12	37599375	rs564113735	intronic	DOP1B	G/C	0.008	-8.378 (1.605)	8.20E-07
18q12.3	39023592	rs80352123	intergenic	LINC01477;KC6	T/A	0.190	-1.950 (0.374)	8.22E-07
4q32.3	164669428	rs12504820	intronic	MARCHF1	C/T	0.026	-4.135 (0.792)	8.26E-07
4q32.3	164668086	rs13139036	intronic	MARCHF1	G/A	0.026	-4.131 (0.792)	8.27E-07
4q32.3	164669328	rs34491561	intronic	MARCHF1	C/A	0.026	-4.135 (0.792)	8.27E-07
4q32.3	164668003	rs17474074	intronic	MARCHF1	G/T	0.026	-4.130 (0.792)	8.32E-07
4q32.3	164694482	rs2201374	intronic	MARCHF1	A/G	0.036	-3.606 (0.691)	8.34E-07
4q32.3	164667565	rs12502759	intronic	MARCHF1	G/A	0.026	-4.129 (0.792)	8.38E-07
4q32.3	164669067	rs12512360	intronic	MARCHF1	A/C	0.026	-4.132 (0.793)	8.45E-07
4q32.3	164666859	rs17577474	intronic	MARCHF1	G/A	0.026	-4.128 (0.792)	8.49E-07
4q32.3	164666401	rs62333006	intronic	MARCHF1	T/C	0.026	-4.127 (0.792)	8.53E-07
4q32.3	164665383	rs6852270	intronic	MARCHF1	C/T	0.027	-4.116 (0.790)	8.55E-07
4p16.1	11229217	rs140390646	intergenic	CLNK;MIR572	G/A	0.040	-3.521 (0.676)	8.55E-07
4q32.3	164665271	rs6847496	intronic	MARCHF1	G/T	0.026	-4.121 (0.791)	8.61E-07
4q32.3	164664668	rs17577453	intronic	MARCHF1	T/C	0.026	-4.120 (0.791)	8.66E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S2. Genome-wide association study-derived genetic variants in the K-CHIP consortium (Continued)



Chr	BP	SNP	Function	Gene	Alleles	MAF	Beta (SE)	P-value
4q32.3	164664101	rs5012631	intronic	MARCHF1	C/G	0.027	-4.113 (0.790)	8.69E-07
4q32.3	164663804	rs146477132	intronic	MARCHF1	A/AT	0.026	-4.120 (0.791)	8.72E-07
14q22.2	54445014	rs189166361	intergenic	BMP4;CDKN3	G/A	0.033	-3.827 (0.735)	8.80E-07
4q32.3	164663966	rs954805	intronic	MARCHF1	C/T	0.026	-4.122 (0.792)	8.80E-07
5q11.2	56577733	rs140712449	intergenic	GPBP1;ACTBL2	G/C	0.020	-5.826 (1.120)	8.81E-07
4q32.3	164702553	rs28562031	intronic	MARCHF1	C/G	0.035	-3.591 (0.690)	8.88E-07
4q32.3	164660169	rs903300	intronic	MARCHF1	C/T	0.026	-4.115 (0.791)	8.99E-07
4q32.3	164659196	rs9683694	intronic	MARCHF1	G/T	0.026	-4.115 (0.791)	9.00E-07
4q32.3	164659625	rs2131863	intronic	MARCHF1	A/G	0.026	-4.114 (0.791)	9.02E-07
4q35.1	186557519	rs190229637	intronic	SORBS2	G/A	0.017	-4.980 (0.958)	9.02E-07
4q32.3	164656734	rs13142980	intronic	MARCHF1	G/A	0.026	-4.114 (0.791)	9.05E-07
4q32.3	164648499	rs2101769	intronic	MARCHF1	G/A	0.026	-4.114 (0.792)	9.06E-07
4q32.3	164646243	rs3921738	intronic	MARCHF1	G/A	0.026	-4.114 (0.792)	9.08E-07
13q13.1	32777632	rs150859875	intronic	FRY	G/A	0.018	-4.233 (0.815)	9.17E-07
12p13.31	6335550	rs141164457	intronic	CD9	G/A	0.006	-10.581 (2.037)	9.18E-07
4q32.3	164691710	rs2022557	intronic	MARCHF1	A/T	0.034	-3.693 (0.711)	9.25E-07
9q31.3	114650365	rs148002888	intergenic	SHOC1;UGCG	T/C	0.019	-5.027 (0.969)	9.38E-07
4q24	102711373	rs73834300	upstream	BANK1	G/C	0.048	-3.111 (0.600)	9.71E-07
12p12.1	21386509	rs34138322	intronic	SLCO1B1	A/C	0.141	-2.087 (0.403)	9.86E-07
1q21.3	151000257	rs72292296	intronic	PRUNE1	T/C	0.019	-5.813 (1.123)	9.87E-07
3p26.2	3168971	rs193122721	UTR5	TRNT1	G/C	0.014	-5.744 (1.110)	9.91E-07

Chr, chromosome; SNP, single nucleotide polymorphisms; MAF, minor allele frequency; SE, standard error; K-CHIP, the Korea Biobank Array

Table S3. Fine-mapping of the lead SNPs from the results of GWAS

SNP	Position	Function	Alleles	MAF	Beta (SE)	P-value	PIP
rs10009742 on MARCHF1 gene							
rs6847496	164665271	intronic	G/T	0.026	-4.121 (0.791)	8.61E-07	0.16
rs62333006	164666401	intronic	T/C	0.026	-4.127 (0.792)	8.53E-07	0.16
rs17577474	164666859	intronic	G/A	0.026	-4.128 (0.792)	8.49E-07	0.16
rs12502759	164667565	intronic	G/A	0.026	-4.129 (0.792)	8.38E-07	0.16
rs17474074	164668003	intronic	G/T	0.026	-4.130 (0.792)	8.32E-07	0.16
rs13139036	164668086	intronic	G/A	0.026	-4.131 (0.792)	8.27E-07	0.16
rs12512360	164669067	intronic	A/C	0.026	-4.132 (0.793)	8.45E-07	0.16
rs34491561	164669328	intronic	C/A	0.026	-4.135 (0.792)	8.27E-07	0.16
rs12504820	164669428	intronic	C/T	0.026	-4.135 (0.792)	8.26E-07	0.16
rs13101998	164670165	intronic	G/T	0.026	-4.134 (0.791)	7.99E-07	0.16
rs13105978	164672601	intronic	T/A	0.026	-4.138 (0.790)	7.68E-07	0.16
rs34162806	164672948	intronic	A/C	0.026	-4.138 (0.790)	7.68E-07	0.16
rs139079372	164672979	intronic	T/TGTGTGA	0.026	-4.138 (0.791)	7.71E-07	0.16
rs13136324	164680214	intronic	C/T	0.026	-4.143 (0.791)	7.56E-07	0.17
rs71600637	164670375	intronic	C/CAT	0.027	-4.127 (0.790)	8.08E-07	0.18
rs10009742	164674901	intronic	C/T	0.027	-4.128 (0.790)	8.01E-07	0.18
rs6852270	164665383	intronic	C/T	0.027	-4.116 (0.790)	8.55E-07	0.18
rs1390835129	164670444	intronic	CT/C	0.027	-4.129 (0.790)	8.01E-07	0.18
rs13127646	164684385	intronic	G/A	0.027	-4.205 (0.786)	4.65E-07	0.20

GWAS, genome-wide association study; SNP, single nucleotide polymorphism; MAF, minor allele frequency; SE, standard error; PIP, posterior inclusion probability