

SUPPLEMENTARY MATERIALS

Table S1 Correlation between Type 2 diabetes status and various traits related to cardiovascular disease in the KARE cohort.

Trait	correlation
Height	0.017
BMI	0.096
Log TG	0.154
TCHL	0.114
HDL	-0.047
LDL	0.070
SBP	0.112
DBP	0.076

Table S2 Estimates of heritability for height. Heritability of height in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population			ALL
	HTK		S.A.G.E.	ASF		KARE		GCTA w/o cutoff	GCTA w/ cutoff	
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff			GCTA w/ cutoff
h^2 (s.e.)	0.76(0.04)	0.78(0.46)	0.81(0.06)	0.66(0.07)	0.79(0.64)	0.67(0.09)	0.36(0.03)	0.32(0.04)	0.60(0.02)	0.32(0.04)
σ_a^2 (s.e.)	21.81(1.71)	22.30(13.38)	23.31(2.21)	19.86(2.87)	23.60(21.49)	19.14(3.12)	10.29(1.01)	8.98(1.22)	17.34(0.75)	9.12(1.06)
σ^2 (s.e.)	6.86(1.04)	6.32(13.15)	0.50(2.87)	10.34(1.90)	6.33(18.69)	3.84(3.55)	18.03(0.96)	19.37(1.19)	11.51(0.57)	19.24(1.03)
σ_m^2 (s.e.)	NA	NA	4.83(2.05)	NA	NA	3.05(2.25)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	0.28(0.91)	NA	NA	2.49(1.54)	NA	NA	NA	NA
σ_p^2 (s.e.)	28.67(1.10)	28.62(1.53)	28.92(1.15)	30.20(1.75)	29.93(3.57)	28.51(1.63)	28.32(0.43)	28.35(0.48)	28.85(0.41)	28.36(0.45)
n	1,791	717	1,799	784	342	784	8,842	7,178	11,421	8,172

Table S3 Estimates of heritability for BMI. Heritability of BMI in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population		ALL	
	HTK		S.A.G.E.	ASF		KARE		GCTA w/o cutoff	GCTA w/ cutoff	
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff			GCTA w/ cutoff
h^2 (s.e.)	0.43(0.05)	0(0.43)	0.38(0.06)	0.41(0.08)	0.95(0.65)	0.43(0.09)	0.18(0.03)	0.15(0.04)	0.32(0.02)	0.14(0.04)
σ_a^2 (s.e.)	4.31(0.55)	0(4.31)	3.73(0.68)	4.53(1.04)	10.84(8.57)	4.53(1.03)	1.71(0.32)	1.43(0.4)	3.14(0.23)	1.32(0.34)
σ^2 (s.e.)	5.77(0.46)	9.96(4.33)	4.70(0.91)	6.55(0.83)	0.63(7.43)	5.22(1.52)	7.84(0.33)	8.21(0.41)	6.71(0.22)	8.27(0.36)
σ_m^2 (s.e.)	NA	NA	0.43(0.71)	NA	NA	0.73(1.04)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	0.94(0.42)	NA	NA	NA	NA	NA	NA	NA
σ_p^2 (s.e.)	10.08(0.36)	9.96(0.53)	9.81(0.36)	11.08(0.61)	11.47(1.41)	10.48(0.56)	9.56(0.14)	9.63(0.16)	9.86(0.13)	9.58(0.15)
<i>n</i>	1,789	717	1,789	784	342	784	8,838	7,177	11,415	8,171

Table S4 Estimates of heritability for log(TG). Heritability of log(TG) in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population		ALL	
	HTK		S.A.G.E.	ASF		KARE		GCTA w/o cutoff	GCTA w/ cutoff	
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff			GCTA w/ cutoff
h^2 (s.e.)	0.37(0.05)	0.16(0.42)	0.29(0.07)	0.27(0.08)	0.39(0.66)	0.27(0.10)	0.19(0.03)	0.21(0.04)	0.24(0.02)	0.19(0.04)
σ_a^2 (s.e.)	0.10(0.02)	0.05(0.13)	0.08(0.02)	0.07(0.02)	0.10(0.18)	0.07(0.03)	0.05(0.01)	0.05(0.01)	0.06(0.01)	0.05(0.01)
σ^2 (s.e.)	0.17(0.01)	0.25(0.13)	0.17(0.01)	0.20(0.02)	0.15(0.15)	0.15(0.04)	0.19(0.01)	0.19(0.01)	0.19(0.01)	0.2(0.01)
σ_m^2 (s.e.)	NA	NA	NA	NA	NA	0.02(0.03)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	0.03(0.01)	NA	NA	0.02(0.02)	NA	NA	NA	NA
σ_p^2 (s.e.)	0.27(0.01)	0.3(0.02)	0.27(0.01)	0.27(0.01)	0.25(0.03)	0.26(0.01)	0.24(0)	0.24(0)	0.24(0.00)	0.24(0.00)
<i>n</i>	1,769	710	1,765	776	339	776	8,841	7,177	11,386	8,164

Table S5 Estimates of heritability for TCHL. Heritability of TCHL in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population			ALL
	HTK		S.A.G.E.	ASF		KARE				
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff	GCTA w/ cutoff	GCTA w/o cutoff	GCTA w/ cutoff
h^2 (s.e.)	0.47(0.05)	0.58(0.44)	0.42(0.06)	0.50(0.08)	1.00(0.64)	0.48(0.10)	0.24(0.03)	0.18(0.04)	0.30(0.02)	0.14(0.04)
σ_a^2 (s.e.)	591.91(68.92)	790.29(607.99)	516.78(86.65)	641.03(126.02)	1477.97(1083.31)	594.55 (136.58)	303.82(43.32)	226.86(53.05)	380.53(29.70)	184.49(45.92)
σ^2 (s.e.)	667.42(54.90)	571.5(600.76)	460.95(101.97)	645.15(94.74)	0.00(939.87)	515.27(107.30)	986.61(43.57)	1067.44(54.19)	901.60(28.39)	1115.85(47.84)
σ_m^2 (s.e.)	NA	NA	104.29(70.80)	NA	NA	NA	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	151.28(49.75)	NA	NA	123.25(80.79)	NA	NA	NA	NA
σ_p^2 (s.e.)	1259.33(44.95)	1361.8(72.37)	1233.30(45.60)	1286.18(72.90)	1477.98(179.48)	1233.06(68.31)	1290.43(19.53)	1294.30(21.68)	1282.14(17.33)	1300.34(20.39)
n	1,797	718	1,793	784	342	784	8,841	7,177	11,422	8,172

Table S6 Estimates of heritability for HDL. Heritability of HDL in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population			ALL
	HTK		S.A.G.E.	ASF		KARE		GCTA w/o cutoff	GCTA w/ cutoff	
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff			GCTA w/ cutoff
h^2 (s.e.)	0.72(0.04)	0(0.44)	0.74(0.06)	0.50(0.07)	0.74(0.63)	0.52(0.09)	0.18(0.03)	0.16(0.04)	0.38(0.02)	0.15(0.04)
σ_a^2 (s.e.)	105.26(8.6)	0(66.16)	110.21(11.51)	63.73(11.24)	106.88(101.72)	58.86(11.73)	18.15(3.41)	16.5(4.17)	42.01(2.59)	15.17(3.77)
σ^2 (s.e.)	41.31(5.45)	151.13(66.27)	14.99(14.28)	62.48(8.46)	38.17(88.58)	35.32(14.10)	82.63(3.5)	83.63(4.27)	68.27(2.34)	89.28(3.91)
σ_m^2 (s.e.)	NA	NA	13.14(10.03)	NA	NA	1.24(9.39)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	9.63(5.04)	NA	NA	17.57(7.30)	NA	NA	NA	NA
σ_p^2 (s.e.)	146.57(5.54)	151.13(8.02)	147.98(5.89)	126.21(7.03)	145.06(17.03)	112.99(6.27)	100.78(1.52)	100.14(1.68)	110.28(1.51)	104.45(1.64)
<i>n</i>	1,791	715	1,787	784	342	784	8,841	7,177	11,416	8,169

Table S7 Estimates of heritability for LDL. Heritability of LDL in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population		ALL	
	HTK		S.A.G.E.	ASF		S.A.G.E.	KARE		GCTA w/o cutoff	GCTA w/ cutoff
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff		
h^2 (s.e.)	0.43(0.05)	1.00(0.45)	0.33(0.06)	0.47(0.08)	0.54(0.67)	0.52(0.11)	0.22(0.03)	0.16(0.04)	0.29(0.02)	0.15(0.04)
σ_a^2 (s.e.)	377.20(48.08)	932.96(426.29)	291.25(62.08)	488.50(101.10)	639.35(849.86)	518.66(128.85)	225.08(35.58)	168.85(43.55)	292.71(24.13)	151.57(37.55)
σ^2 (s.e.)	508.98(39.87)	0(416.46)	436.39(75.66)	549.83(77.66)	539.27(743.94)	309.48(147.15)	812.75(36.06)	866.91(44.61)	725.57(23.19)	877.79(38.97)
σ_m^2 (s.e.)	NA	NA	17.70(55.51)	NA	NA	103.76(85.81)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	141.50(39.31)	NA	NA	66.17(66.35)	NA	NA	NA	NA
σ_p^2 (s.e.)	886.18(31.40)	932.96(49.98)	886.84(32.43)	1038.33(58.45)	1178.61(139.22)	998.07(56.25)	1037.84(15.93)	1035.76(17.56)	1018.28(13.91)	1029.35(16.33)
n	1,791	715	1,787	784	342	784	8,578	6,998	11,156	7,989

Table S8 Estimates of heritability for SBP. Heritability of SBP in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family			Population			ALL			
	HTK		S.A.G.E.	ASF		KARE		GCTA w/o cutoff	GCTA w/ cutoff	
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	S.A.G.E.	GCTA w/o cutoff			GCTA w/ cutoff
h^2 (s.e.)	0.37(0.05)	0.89(0.46)	0.35(0.06)	0.23(0.08)	0(0.76)	0.22(0.08)	0.22(0.03)	0.26(0.04)	0.23(0.02)	0.20(0.04)
σ_a^2 (s.e.)	87.87(12.76)	228.84(120.42)	79.82(15.84)	45.21(16.38)	0(155.97)	42.00(14.98)	62.03(9.43)	74.54(11.81)	61.71(6.10)	57.85(10)
σ^2 (s.e.)	148.45(11.09)	28.46(118)	124.22(19.50)	151.14(15.33)	205.73(138)	147.29(15.20)	222.16(9.56)	208.42(11.72)	212.42(6.16)	224.36(10.19)
σ_m^2 (s.e.)	NA	NA	2.47(13.91)	NA	NA	NA	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	23.27(9.90)	NA	NA	NA	NA	NA	NA	NA
σ_p^2 (s.e.)	236.32(8.29)	257.3(13.75)	229.78(8.31)	196.35(10.36)	205.73(24.44)	189.29(9.69)	284.19(4.30)	282.96(4.76)	274.13(3.67)	282.21(4.43)
<i>n</i>	1,791	717	1,787	784	342	784	8,841	7,177	11,416	8,171

Table S9 Estimates of heritability for DBP. Heritability of DBP in three Korean populations were estimated. S.A.G.E. estimates the heritability with FRM and GCTA does it with GRM. The additive polygenic variance, random error variance and phenotypic variance are denoted by σ_a^2 , σ^2 and σ_p^2 , respectively. Contrary to GCTA, S.A.G.E. can also estimate the relative proportion of variance explained by common sibling effects and common marital effects, and those are denoted by σ_m^2 and σ_s^2 , respectively. The standard errors of each estimate are shown in parenthesis. If the variance components are not estimable, the results are denoted as NA.

Cohort	Family						Population			ALL
	HTK		S.A.G.E.	ASF		S.A.G.E.	KARE			
Program	GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff		GCTA w/o cutoff	GCTA w/ cutoff	GCTA w/o cutoff	GCTA w/ cutoff
h^2 (s.e.)	0.53(0.05)	0.12(0.44)	0.60(0.06)	0.21(0.08)	0.24(0.67)	0.18(0.09)	0.21(0.03)	0.21(0.04)	0.24(0.02)	0.14(0.03)
σ_a^2 (s.e.)	55.52(5.97)	12.51(44.62)	62.54(7.77)	16.78(6.76)	19.34(56.18)	13.90(7.13)	25.61(4.21)	26.99(5.41)	28.78(2.75)	17.78(4.45)
σ^2 (s.e.)	50.1(4.52)	89.96(44.69)	21.39(9.28)	63.10(6.39)	61.88(49.6)	59.24(10.17)	98.78(4.28)	101.66(5.45)	91.12(2.73)	108.50(4.64)
σ_m^2 (s.e.)	NA	NA	16.95(6.85)	NA	NA	0.96(6.70)	NA	NA	NA	NA
σ_s^2 (s.e.)	NA	NA	3.72(3.66)	NA	NA	3.97(5.96)	NA	NA	NA	NA
σ_p^2 (s.e.)	105.61(3.83)	102.47(5.43)	104.60(3.94)	79.88(4.21)	81.23(9.23)	78.07(4.01)	124.38(1.88)	128.65(2.16)	119.90(1.61)	126.28(1.98)
n	1,792	717	1,788	784	342	784	8,841	7,177	11,417	8,171

1 **Table S10 Missing rates for each phenotype**

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	Cohort		
	KARE	HTK	ASF
Height	0%	0.11%	0%
BMI	0.05%	0.22%	0%
LogTG	0.01%	1.56%	1.02%
TCHL	0.01%	0%	0%
HDL	0.01%	0.33%	0%
LDL	2.95%	0.33%	0%
SBP	0.01%	0.33%	0%
DBP	0.01%	0.28%	0%

21 **Table S11 Empirical correlations between family members.** The mother-father, parent-offspring
 22 and sibling correlations, and their 95% confidence intervals were estimated with FCOR in S.A.G.E.

Cohorts	Types	Height	BMI	LogTG	TCHL	HDL	LDL	SBP	DBP
HTK	Mother – Father	0.172 ±0.142	0.212 ±0.136	-0.085 ±0.149	0.084 ±0.147	0.106 ±0.143	0.069 ±0.152	0.046 ±0.153	0.227 ±0.152
	Parent – offspring	0.413 ±0.063	0.197 ±0.068	0.114 ±0.062	0.169 ±0.068	0.363 ±0.064	0.164 ±0.069	0.175 ±0.074	0.297 ±0.075
	Sibling	0.517 ±0.056	0.331 ±0.591	0.290 ±0.060	0.367 ±0.060	0.480 ±0.058	0.382 ±0.060	0.283 ±0.057	0.374 ±0.060
	Mother – Father	0.144 ±0.181	0.075 ±0.222	0.033 ±0.209	-0.091 ±0.218	0.052 ±0.187	-0.007 ±0.226	0.134 ±0.179	0.039 ±0.184
ASF	Parent – offspring	0.298 ±0.102	0.215 ±0.090	0.118 ±0.099	0.219 ±0.090	0.237 ±0.100	0.190 ±0.091	0.161 ±0.116	0.140 ±0.108
	Sibling	0.353 ±0.128	0.168 ±0.123	0.245 ±0.175	0.264 ±0.129	0.350 ±0.130	0.236 ±0.127	0.177 ±0.156	0.080 ±0.115

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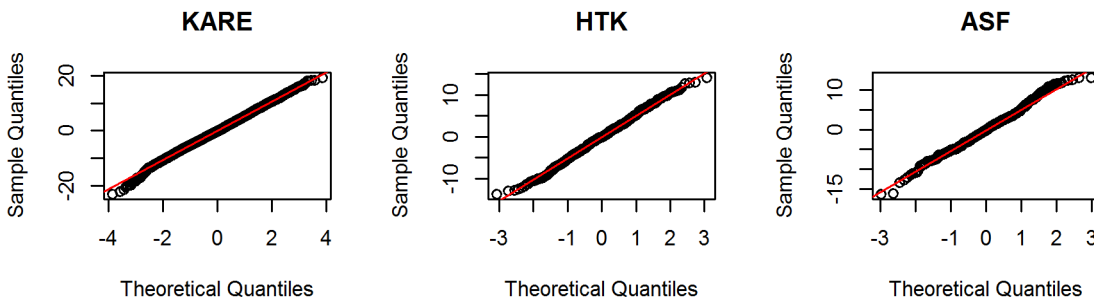
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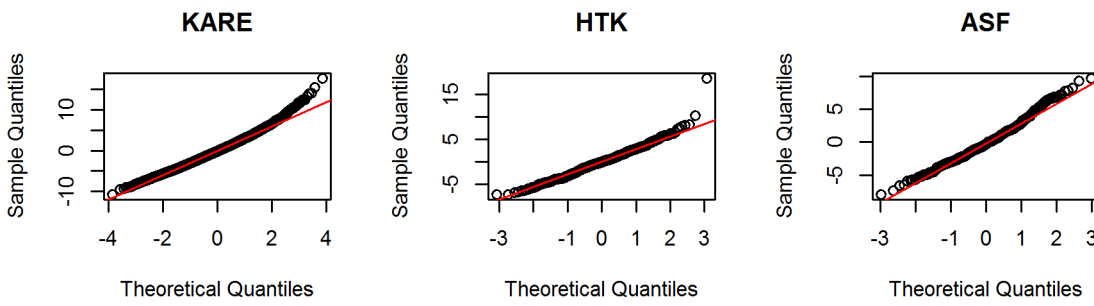
41 **Figure S1** Q-Q plots for HEIGHT, BMI, LOGTG and HDL in each cohort.

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A.HEIGHT

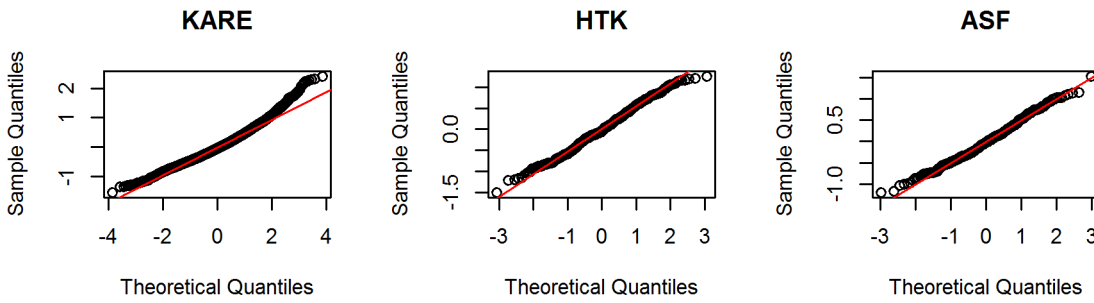


B.BMI



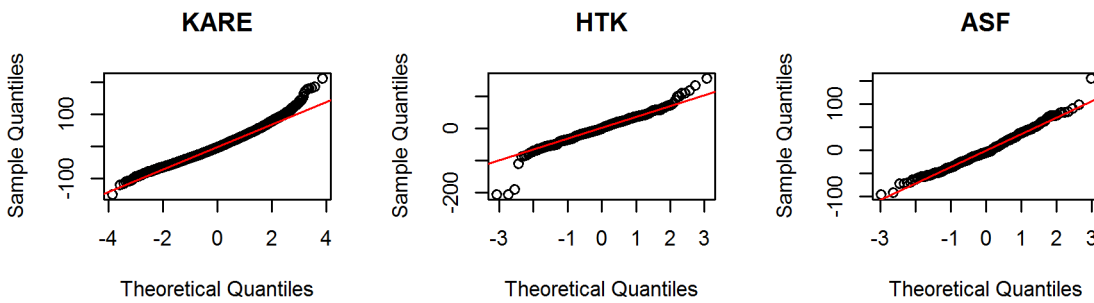
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C.LOGTG



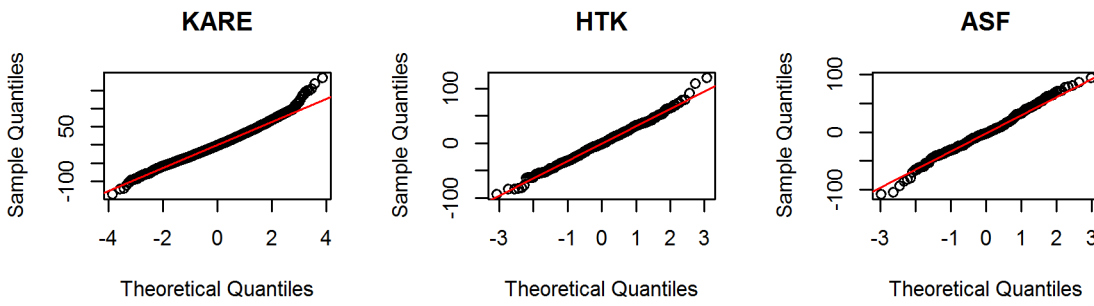
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D.TCHL

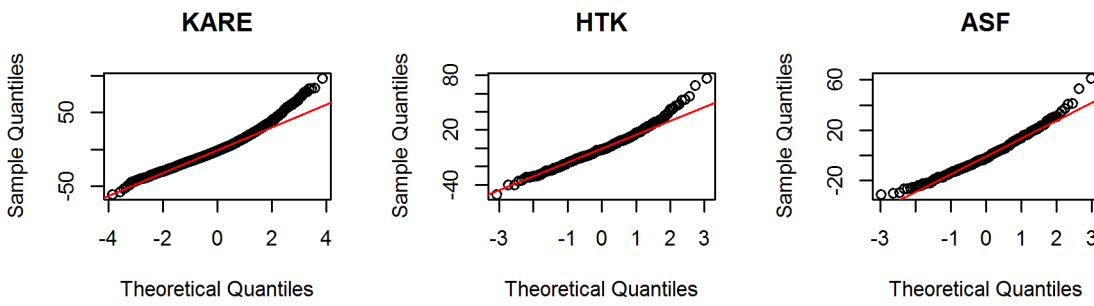


54 **Figure S2** Q-Q plots for LDL, SBP, DBP and TCHL in each cohort.
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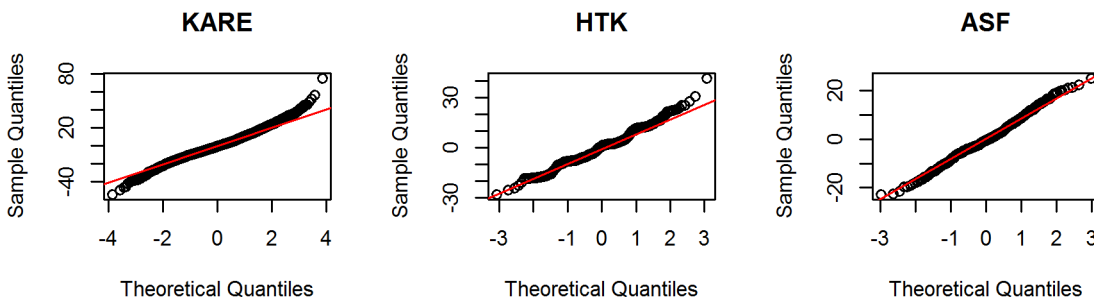
A.LDL



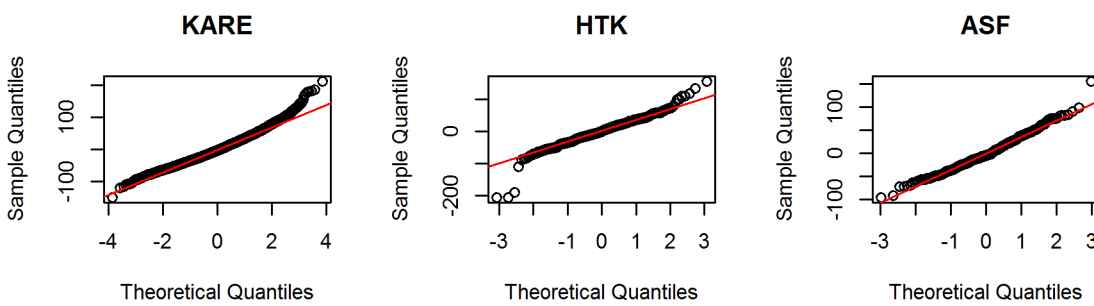
B.SBP



C.DBP



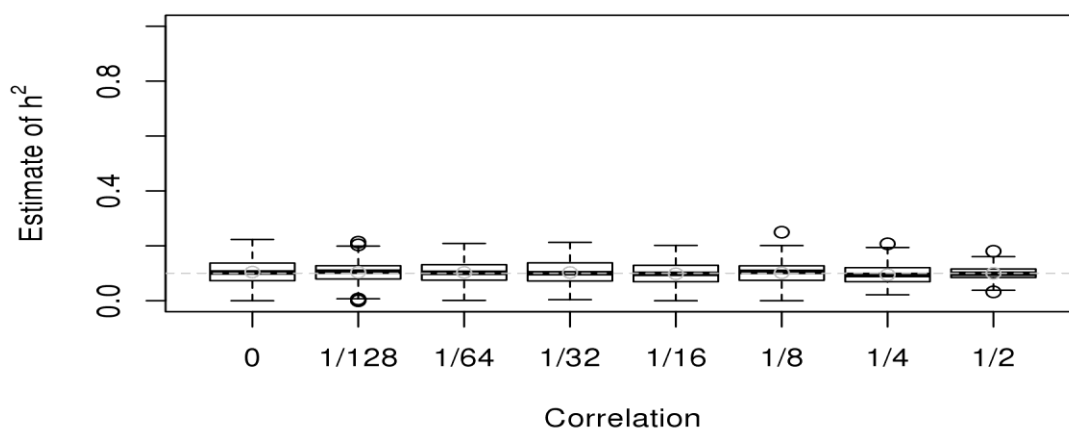
D.TCHL



66 **Figure S3 Heritability estimates for various levels of genetic correlation with 10,000**
 67 **individuals when h^2 was set at 0.1.** We generated 5,000 pairs of individuals with 100,000
 68 SNPs, and each box-plot was generated with results from 200 replicates. The dashed
 69 horizontal line indicates the proportion of the total phenotypic variance explained by the
 70 SNPs used for calculating the GRM, and the estimates of heritability with GCTA are
 71 plotted against the correlation between family members. In **a**, all causal variants were
 72 generated from $U(0, 0.1)$ and 100 causal SNPs were used to estimate the GRM, in **b**, all
 73 causal variants were generated from $U(0, 0.1)$ and 50 causal SNPs were used, in **c**, all
 74 causal variants were generated from $U(0.1, 0.4)$ and 100 causal SNPs were used, and in **d**,
 75 all causal variants were generated from $U(0.1, 0.4)$ and 50 causal SNPs were used. The
 76 horizontal dotted line indicates the relative proportion of variance explained by the SNPs.

a

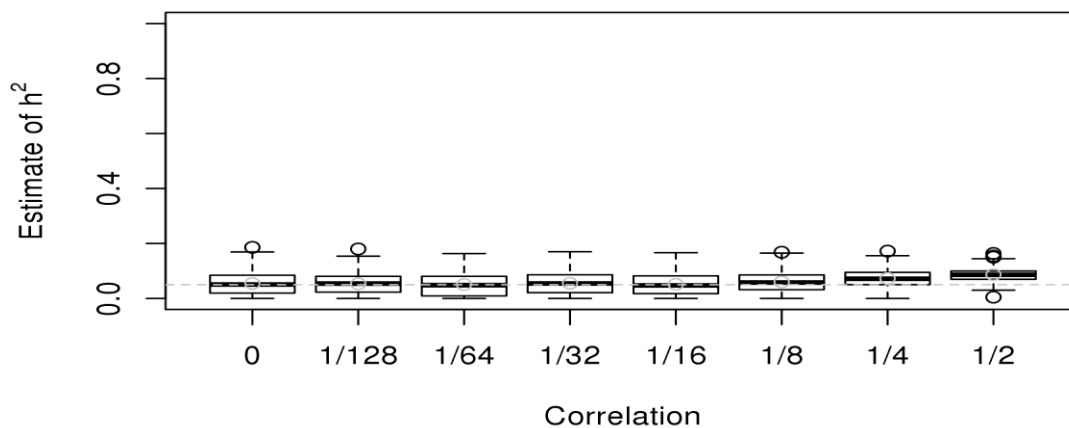
100 casual SNPs



77

b

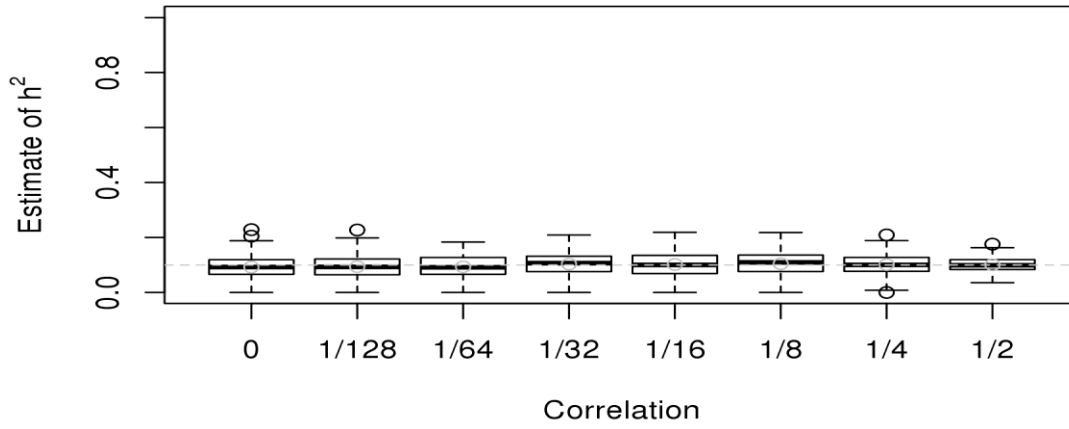
50 casual SNPs



78

c

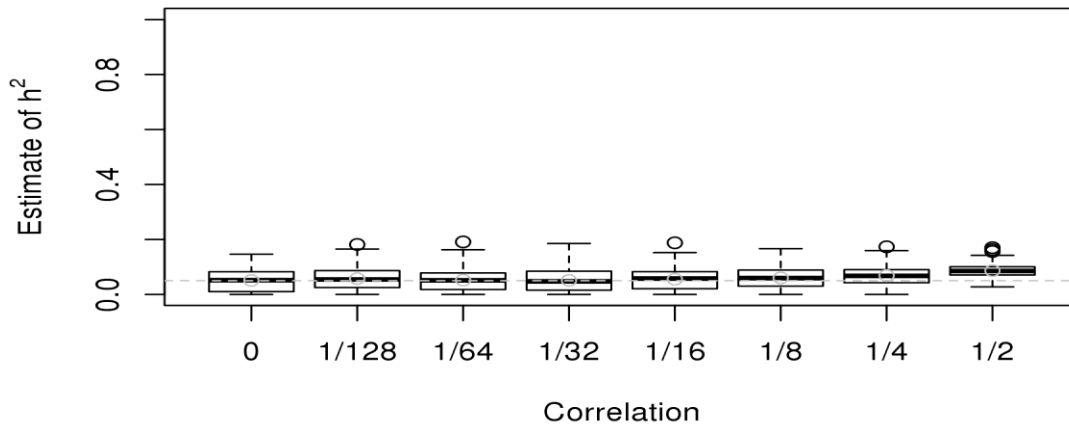
100 casual SNPs



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d

50 casual SNPs



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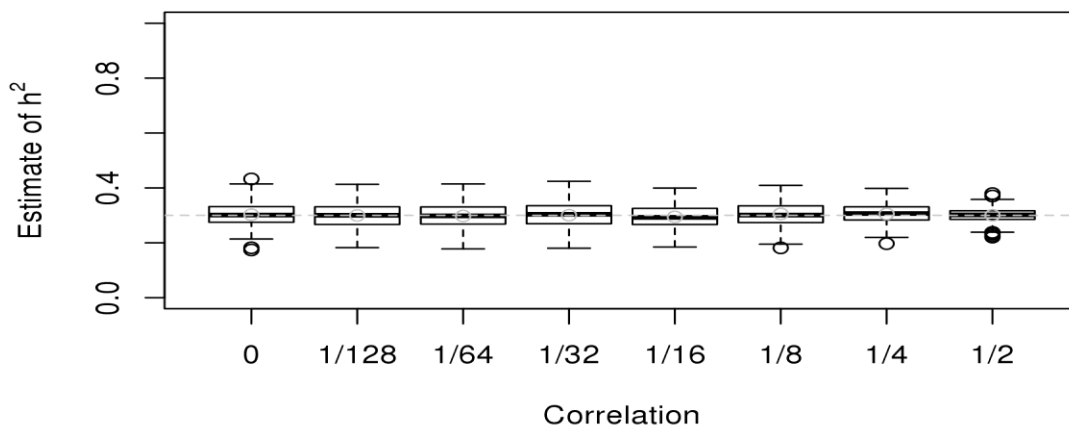
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94 **Figure S4 Heritability estimates for various levels of genetic correlation with 10,000**
 95 **individuals when h^2 was set at 0.3.** We generated 5,000 pairs of individuals with 100,000
 96 SNPs, and each box-plot was generated with results from 200 replicates. The dashed
 97 horizontal line indicates the proportion of the total phenotypic variance explained by the
 98 SNPs used for calculating the GRM, and the estimates of heritability with GCTA are
 99 plotted against the correlation between family members. In **a**, all causal variants were
 100 generated from $U(0, 0.1)$ and 100 causal SNPs were used to estimate the GRM, in **b**, all
 101 causal variants were generated from $U(0, 0.1)$ and 50 causal SNPs were used, in **c**, all
 102 causal variants were generated from $U(0.1, 0.4)$ and 100 causal SNPs were used, and in **d**,
 103 all causal variants were generated from $U(0.1, 0.4)$ and 50 causal SNPs were used. The
 104 horizontal dotted line indicates the relative proportion of variance explained by the SNPs.

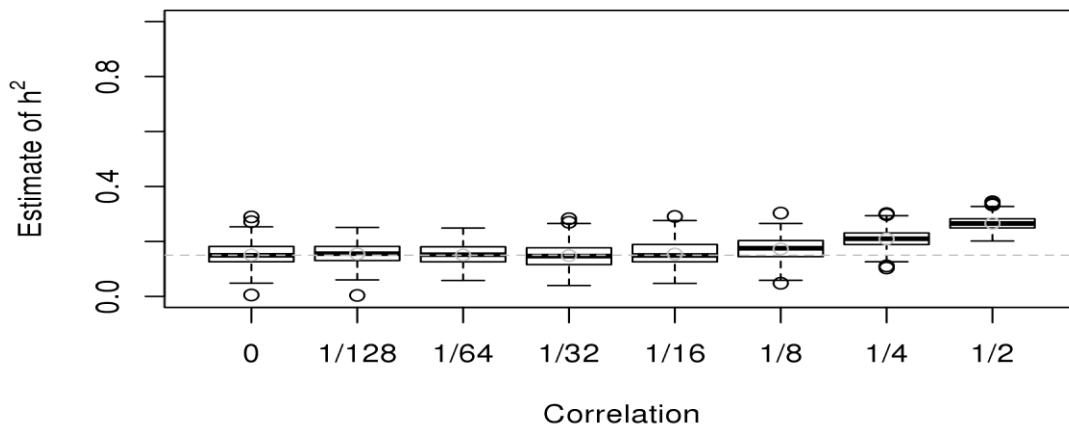
a

100 casual SNPs



b

50 casual SNPs

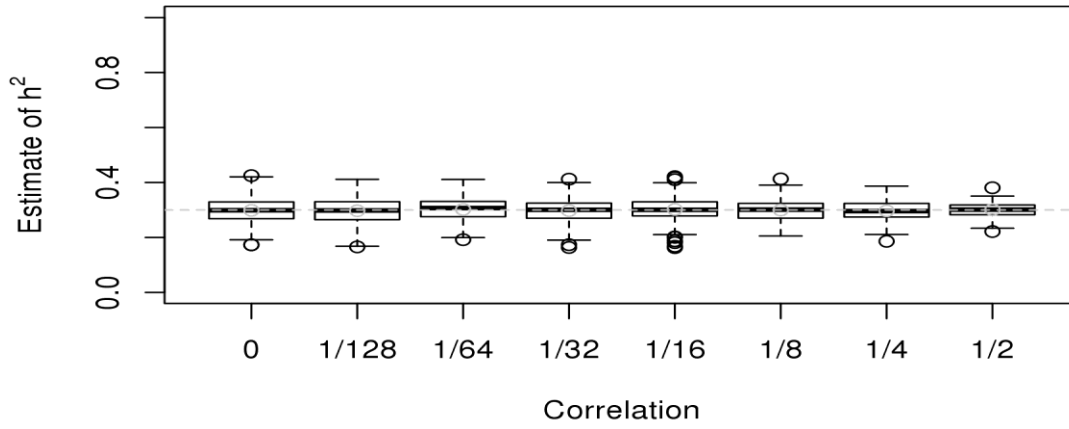


105

106

c

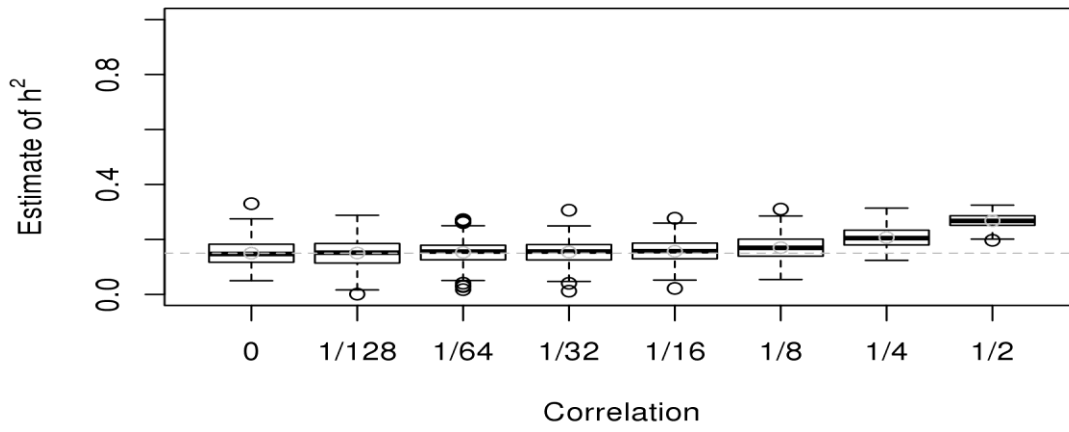
100 casual SNPs



107

d

50 casual SNPs



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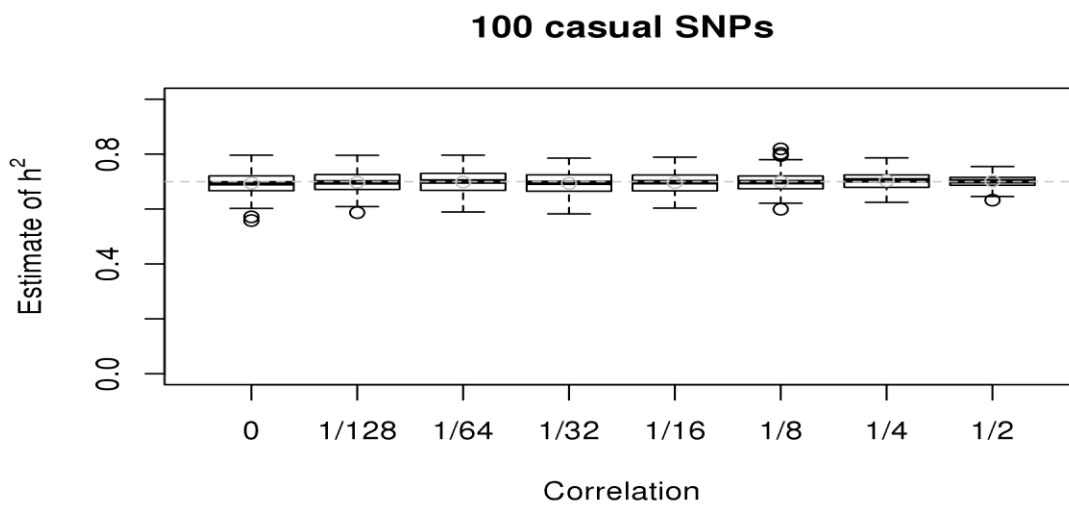
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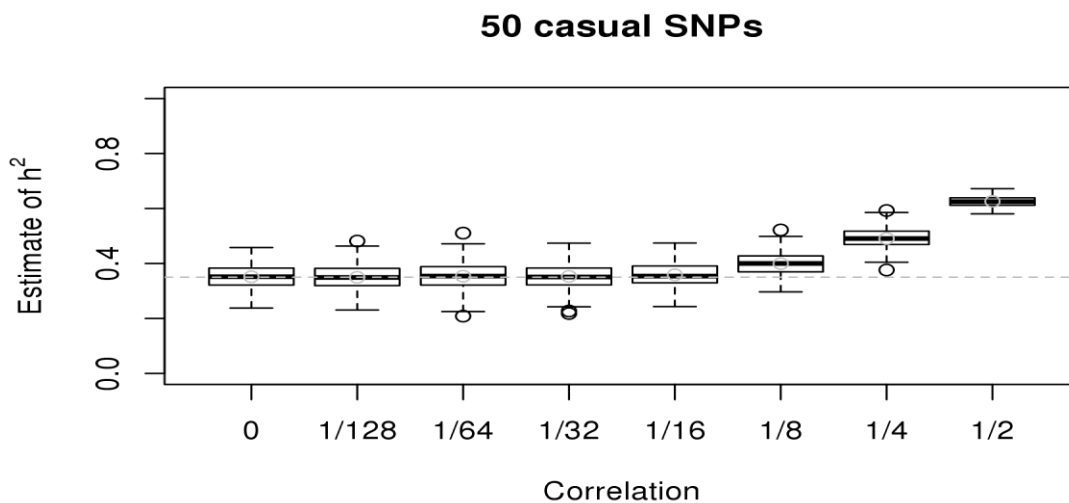
122 **Figure S5 Heritability estimates for various levels of genetic correlation with 10,000**
 123 **individuals when h^2 was set at 0.7.** We generated 5,000 pairs of individuals with 100,000
 124 SNPs, and each box-plot was generated with results from 200 replicates. The dashed
 125 horizontal line indicates the proportion of the total phenotypic variance explained by the
 126 SNPs used for calculating the GRM, and the estimates of heritability with GCTA are
 127 plotted against the correlation between family members. In **a**, all causal variants were
 128 generated from $U(0, 0.1)$ and 100 causal SNPs were used to estimate the GRM, in **b**, all
 129 causal variants were generated from $U(0, 0.1)$ and 50 causal SNPs were used, in **c**, all
 130 causal variants were generated from $U(0.1, 0.4)$ and 100 causal SNPs were used, and in **d**,
 131 all causal variants were generated from $U(0.1, 0.4)$ and 50 causal SNPs were used. The
 132 horizontal dotted line indicates the relative proportion of variance explained by the SNPs.

a



133

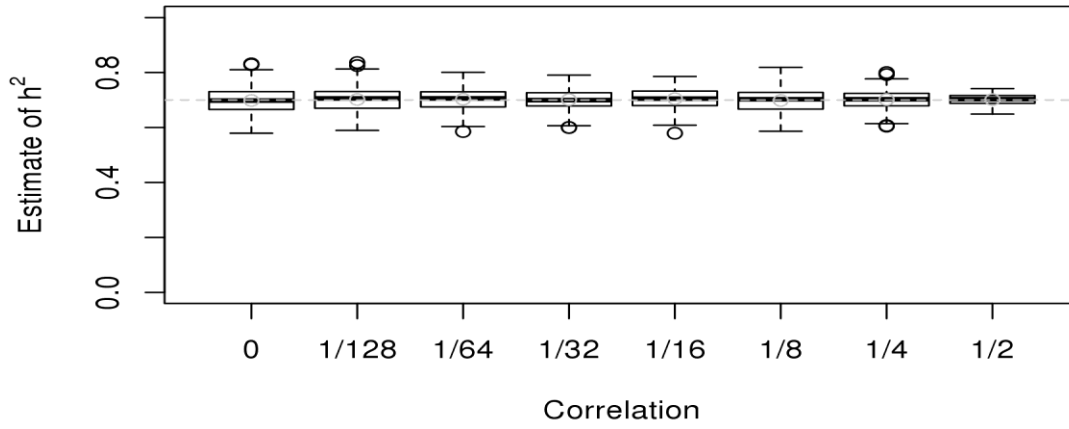
b



134

c

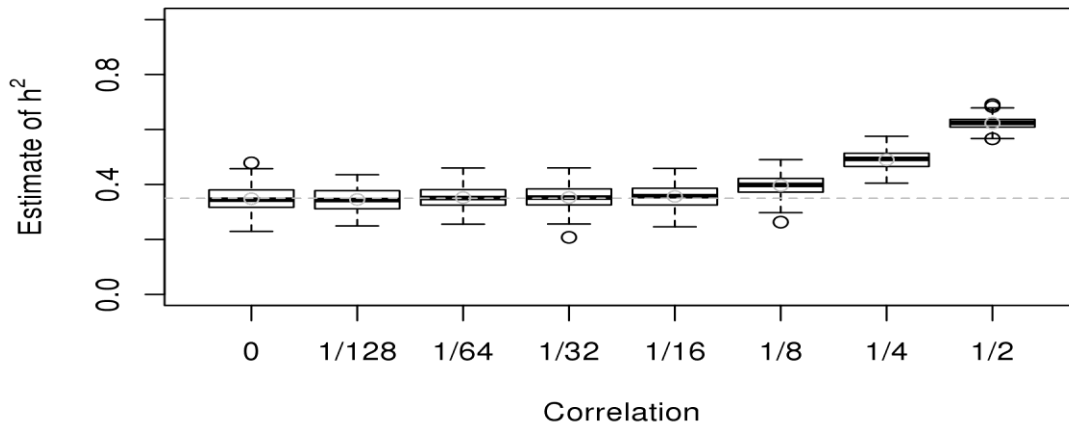
100 casual SNPs



135

d

50 casual SNPs



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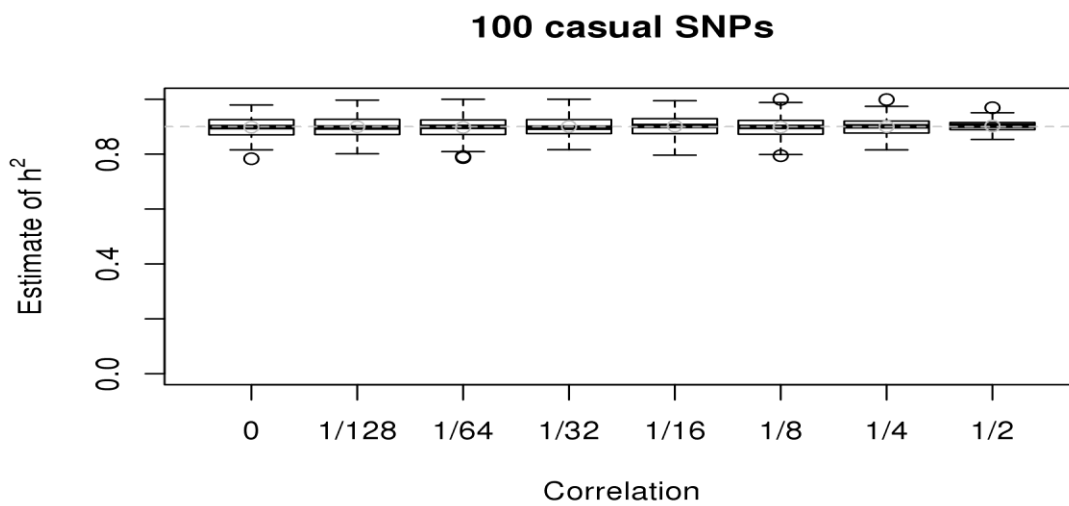
147

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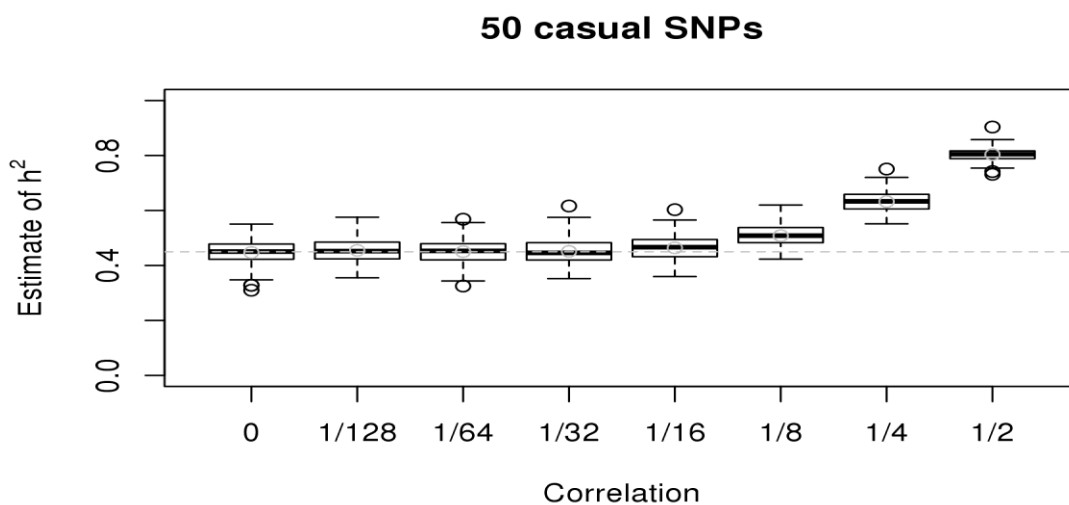
150 **Figure S6 Heritability estimates for various levels of genetic correlation with 10,000**
151 **individuals when h^2 was set at 0.9.** We generated 5,000 pairs of individuals with 100,000
152 SNPs, and each box-plot was generated with results from 200 replicates. The dashed
153 horizontal line indicates the proportion of the total phenotypic variance explained by the
154 SNPs used for calculating the GRM, and the estimates of heritability with GCTA are
155 plotted against the correlation between family members. In **a**, all causal variants were
156 generated from $U(0, 0.1)$ and 100 causal SNPs were used to estimate the GRM, in **b**, all
157 causal variants were generated from $U(0, 0.1)$ and 50 causal SNPs were used, in **c**, all
158 causal variants were generated from $U(0.1, 0.4)$ and 100 causal SNPs were used, and in **d**,
159 all causal variants were generated from $U(0.1, 0.4)$ and 50 causal SNPs were used. The
160 horizontal dotted line indicates the relative proportion of variance explained by the SNPs.

a



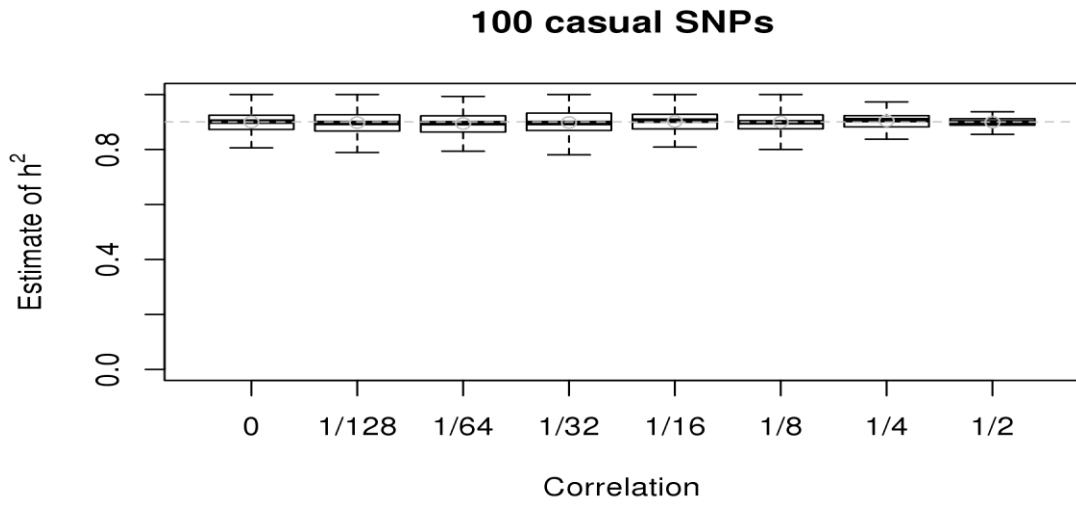
161

b



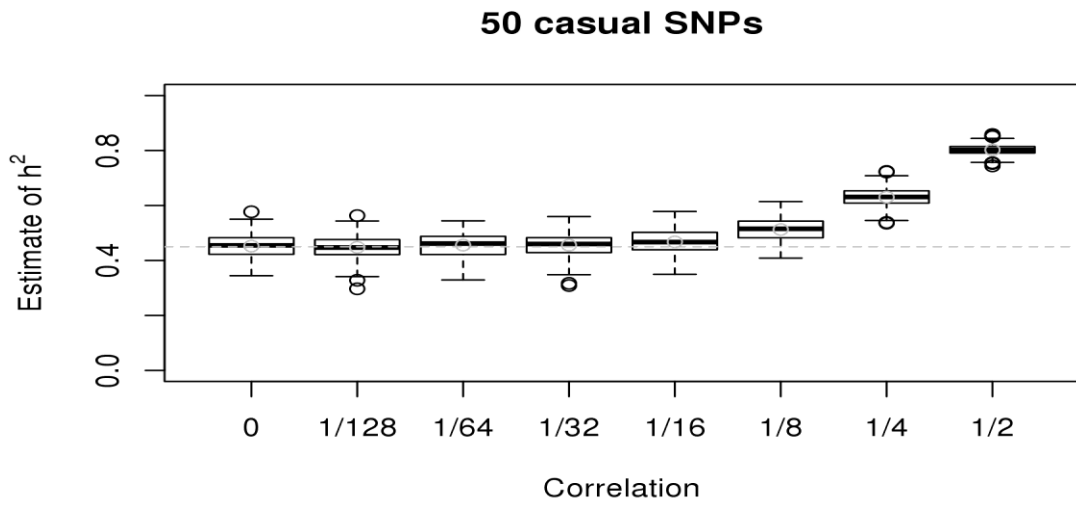
162

c



163

d



164