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Supplemental information

Quantifying the contribution of dominance deviation effects to complex trait variation in biobank-scale data

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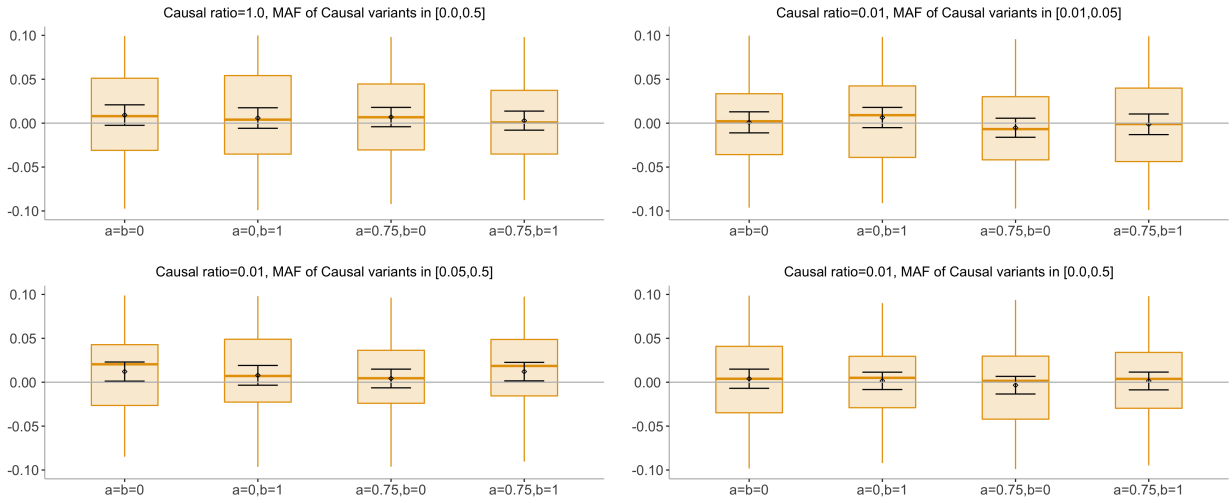
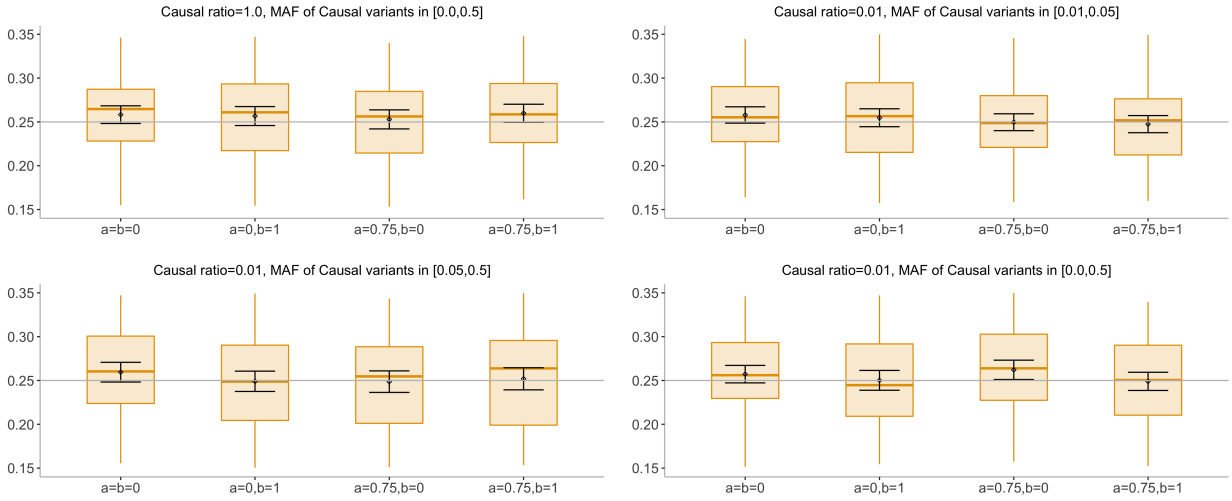


(a) The accuracy of estimates of dominance heritability



(b) The accuracy of estimates of additive heritability

Figure S1: **The accuracy of estimates of dominance and additive heritabilities in small-scale simulations with no true dominance heritability ($N = 10,000$ unrelated individuals, $M = 459,792$ array SNPs)**. In **a** and **b**: We plot estimates from our method in the absence of dominance deviation effects under 16 different genetic architectures. We varied the MAF range of causal variants (MAF of CV), the coupling of MAF with effect size (a), and the effect of local LD on effect size ($b = 0$ indicates no LDAK weights and $b = 1$ indicates LDAK weights. We ran 100 replicates where the true additive and dominance heritabilities of the phenotype are 0.5 and 0.0 respectively. We run our method using single dominance bin and 24 additive bins formed by the combination of 6 bins based on MAF as well as 4 bins based on quartiles of the LDAK score of a SNP. Black points and error bars represent the mean and ± 2 SE respectively. Box plot whiskers extend to the minimum and maximum estimates located within $1.5\times$ interquartile range (IQR) from the first and third quartiles respectively. Each box plot represents estimates from 100 simulations.

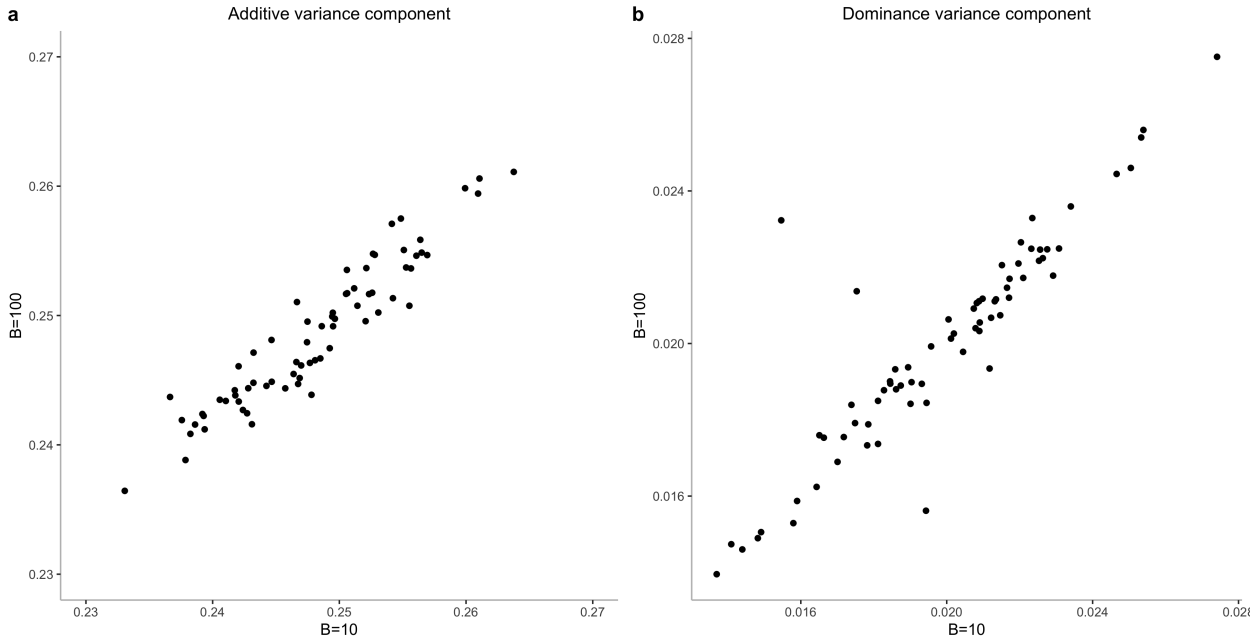


Figure S2: Comparison of estimates with B=10 and B=100 on large scale data (M=459,792 array SNPs and N=291,273k individuals): We simulated phenotypes such that $h^2_A = 0.25$, $h^2_D = 0.02$, $p_{causal}(A) = 1$ and $p_{causal}(D) = 0.02$. The Pearson's correlation coefficients between estimates with $B = 10$ and estimates with $B = 100$ are 0.94 and 0.91 for additive heritability and dominance heritability respectively.

Genetic architecture				P(rejection at $p < 0.05$)
Percentage of causal SNPs	MAF of causal SNPs	MAF and LD coupling	True h^2_D	
0.01	[0.01,0.05]	a=b=0	0.0	2%
0.01	[0.01,0.05]	a=0,b=1	0.0	2%
0.01	[0.01,0.05]	a=0.75,b=0	0.0	5%
0.01	[0.01,0.05]	a=0.75,b=1	0.0	4%
0.01	[0.0,0.5]	a=b=0	0.0	3%
0.01	[0.0,0.5]	a=0,b=1	0.0	6%
0.01	[0.0,0.5]	a=0.75,b=0	0.0	8%
0.01	[0.0,0.5]	a=0.75,b=1	0.0	7%
0.01	[0.05,0.5]	a=b=0	0.0	8%
0.01	[0.05,0.5]	a=0,b=1	0.0	3%
0.01	[0.05,0.5]	a=0.75,b=0	0.0	7%
0.01	[0.05,0.5]	a=0.75,b=1	0.0	7%
1.0	[0.0,0.5]	a=b=0	0.0	2%
1.0	[0.0,0.5]	a=0,b=1	0.0	4%
1.0	[0.0,0.5]	a=0.75,b=0	0.0	3%
1.0	[0.0,0.5]	a=0.75,b=1	0.0	5%

Table S1: **Calibration of tests of non-zero dominance heritability in small-scale simulations**. We assess calibration of our method in the absence of dominance deviation effects under 16 different genetic architectures. We varied the MAF range of causal variants (MAF of CV), the coupling of MAF with effect size (a), and the effect of local LD on effect size ($b = 0$ indicates no LDAK weights and $b = 1$ indicates LDAK weights. Probability of rejection is computed from 100 replicates.

Trait	Heritability	
	Additive	Dominance
Age first birth	0.20125 ± 0.00815	-0.00187 ± 0.00632
Alanine aminotransferase	0.14268 ± 0.00903	-0.00018 ± 0.00265
Albumin	0.16201 ± 0.01128	0.00333 ± 0.00283
Alcohol intake frequency	0.11322 ± 0.00415	-0.00197 ± 0.00235
Alkaline phosphatase	0.31743 ± 0.07676	0.01605 ± 0.01909
Apolipoprotein A	0.27997 ± 0.03758	-0.00256 ± 0.00244
Aspartate aminotransferase	0.16841 ± 0.02172	0.00686 ± 0.00267
Basal metabolic rate	0.32489 ± 0.00868	0.00253 ± 0.00263
BMD Heel T-score	0.34912 ± 0.02914	-0.00087 ± 0.00694
BMI	0.26371 ± 0.00874	0.00395 ± 0.00257
C-reactive protein	0.25196 ± 0.0488	-0.00119 ± 0.00252
Calcium	0.14078 ± 0.01216	0.00449 ± 0.0029
Cholesterol	0.15793 ± 0.03074	0.00188 ± 0.00295
Corneal Hysteresis	0.29504 ± 0.02625	-0.00917 ± 0.01182
Creatinine	0.23893 ± 0.00985	-0.00178 ± 0.00225
Creatinine in urine	0.07615 ± 0.00352	0.00175 ± 0.00234
Cystatin-C	0.27628 ± 0.04872	0.00542 ± 0.00278
Diastolic Blood Pressure	0.14413 ± 0.00511	0.00181 ± 0.00239
Eosinophil count	0.22676 ± 0.01476	$-4e-04 \pm 0.00262$
FEV1-FVC ratio	0.21179 ± 0.01061	0.0027 ± 0.00263
FVC	0.27173 ± 0.00726	-0.00473 ± 0.00241
Gamma glutamyltransferase	0.2542 ± 0.03487	0.00222 ± 0.00259
Glucose	0.09337 ± 0.01063	0.00649 ± 0.00295
Hair color	0.25831 ± 0.05408	-0.00202 ± 0.00345
HDL cholesterol	0.32793 ± 0.05241	$-9e-04 \pm 0.003$
Height	0.49507 ± 0.0192	-0.00045 ± 0.00285
Hemoglobin A1c	0.25886 ± 0.02513	0.00219 ± 0.00283
High light scatter reticulocyte count	0.23626 ± 0.01749	0.00215 ± 0.00265
IGF-1	0.26427 ± 0.01478	0.00368 ± 0.00288
LDL direct	0.15062 ± 0.04315	0.00225 ± 0.00306
Lymphocyte count	0.2214 ± 0.01295	0.00314 ± 0.00257
Mean corpuscular hemoglobin	0.27188 ± 0.03247	0.00075 ± 0.00273
Mean platelet volume	0.41688 ± 0.04684	0.00698 ± 0.00292
Mean sphered cell volume	0.23819 ± 0.02096	0.00607 ± 0.00254
Microalbumin in urine	0.03864 ± 0.012	-0.00642 ± 0.00915
Monocyte count	0.2569 ± 0.02192	0.00145 ± 0.00265
Overall health rating	0.14046 ± 0.00363	-0.00322 ± 0.00233
Phosphate	0.13263 ± 0.01091	-0.00026 ± 0.00299
Platelet count	0.31935 ± 0.02465	0.00515 ± 0.0028
Platelet distribution width	0.2824 ± 0.03317	0.00358 ± 0.00275
Potassium in urine	0.04415 ± 0.00261	0.0021 ± 0.00212
RBC count	0.26032 ± 0.0218	0.00232 ± 0.00296
RBC distribution width	0.2216 ± 0.01688	0.00292 ± 0.0031
SHBG	0.27094 ± 0.04282	0.00016 ± 0.0026
Sodium in urine	0.08761 ± 0.00355	-0.00068 ± 0.00247
Systolic Blood Pressure	0.14555 ± 0.00466	0.00232 ± 0.00257
Testosterone	0.13135 ± 0.00794	-0.00447 ± 0.00288
Vitamin D	0.10642 ± 0.01868	0.0049 ± 0.0024
Waist-hip Ratio	0.16782 ± 0.00813	-0.00173 ± 0.00232
White blood cell count	0.22091 ± 0.01219	0.00038 ± 0.00268

Table S2: **Estimate the proportions of variance explained by additive and dominance variation from our method for 50 quantitative phenotypes in the UK Biobank ($N = 291,273$ unrelated white British individuals, $M = 459,792$ common SNPs)**. We run our method partitioning the additive component into 8 bins defined based on two MAF bins (MAF≤ 0.05, MAF> 0.05) and quartiles of the LD-scores and a single dominance bin.

Trait	Heritability	
	Additive	Dominance
Age first birth	0.20954 ± 0.00893	-0.00519 ± 0.00402
Alanine aminotransferase	0.15026 ± 0.00933	0.00037 ± 0.00163
Albumin	0.17477 ± 0.01302	0.00026 ± 0.00157
Alcohol intake frequency	0.11771 ± 0.00436	0.00042 ± 0.00155
Alkaline phosphatase	0.31876 ± 0.06188	0.00265 ± 0.00399
Apolipoprotein A	0.28728 ± 0.04033	-0.00254 ± 0.00147
Aspartate aminotransferase	0.1693 ± 0.01576	0.00379 ± 0.00177
Basal metabolic rate	0.3396 ± 0.0104	0.00398 ± 0.00138
BMD Heel T-score	0.36517 ± 0.02759	-0.00018 ± 0.0049
BMI	0.28143 ± 0.0089	0.00142 ± 0.00151
C-reactive protein	0.25389 ± 0.04917	-0.00143 ± 0.00176
Calcium	0.15274 ± 0.01237	0.0048 ± 0.00183
Cholesterol	0.16889 ± 0.03858	-0.00087 ± 0.00153
Corneal Hysteresis	0.30444 ± 0.02675	-0.00028 ± 0.00743
Creatinine	0.24341 ± 0.01095	-0.001 ± 0.00156
Creatinine in urine	0.08243 ± 0.00365	0.00078 ± 0.0012
Cystatin-C	0.28918 ± 0.05443	0.00168 ± 0.00152
Diastolic Blood Pressure	0.14725 ± 0.00659	$-5e-05 \pm 0.00153$
Eosinophil count	0.24544 ± 0.01602	-0.00063 ± 0.00149
FEV1-FVC ratio	0.22161 ± 0.01022	0.00183 ± 0.00161
FVC	0.27073 ± 0.00878	-0.00011 ± 0.00154
Gamma glutamyltransferase	0.26184 ± 0.03161	0.00108 ± 0.00147
Glucose	0.10327 ± 0.01324	0.0049 ± 0.002
Hair color	0.25466 ± 0.05171	0.00042 ± 0.00181
HDL cholesterol	0.3419 ± 0.05838	-0.00141 ± 0.0015
Height	0.50749 ± 0.0229	0.00079 ± 0.00141
Hemoglobin A1c	0.26891 ± 0.02624	-0.00138 ± 0.00176
High light scatter reticulocyte count	0.25615 ± 0.01887	0.00397 ± 0.00147
IGF-1	0.27632 ± 0.01504	0.00169 ± 0.00171
LDL direct	0.17004 ± 0.05658	0.00015 ± 0.00152
Lymphocyte count	0.23694 ± 0.0155	0.00101 ± 0.00136
Mean corpuscular hemoglobin	0.29132 ± 0.036	-0.00114 ± 0.00142
Mean platelet volume	0.42801 ± 0.0491	0.00034 ± 0.00162
Mean sphered cell volume	0.25593 ± 0.02494	0.00206 ± 0.00159
Microalbumin in urine	0.04201 ± 0.0081	0.00181 ± 0.00441
Monocyte count	0.26996 ± 0.02427	-0.00086 ± 0.00152
Overall health rating	0.13942 ± 0.00426	0.00021 ± 0.00147
Phosphate	0.14328 ± 0.01327	0.00176 ± 0.00169
Platelet count	0.33832 ± 0.0261	0.00184 ± 0.00171
Platelet distribution width	0.30071 ± 0.03937	$8e-04 \pm 0.00149$
Potassium in urine	0.04449 ± 0.0032	0.00239 ± 0.00147
RBC count	0.27218 ± 0.0208	0.00097 ± 0.00153
RBC distribution width	0.23468 ± 0.01997	0.00012 ± 0.00146
SHBG	0.29273 ± 0.05944	-0.00036 ± 0.00156
Sodium in urine	0.08935 ± 0.00354	-0.00217 ± 0.00125
Systolic Blood Pressure	0.15109 ± 0.00554	0.00107 ± 0.00142
Testosterone	0.12642 ± 0.00934	-0.00082 ± 0.00186
Vitamin D	0.11467 ± 0.02034	0.00079 ± 0.0017
Waist-hip Ratio	0.17866 ± 0.00949	0.00019 ± 0.00135
White blood cell count	0.22953 ± 0.01254	-0.00078 ± 0.00158

Table S3: **Estimate the proportions of variance explained by additive and dominance variation from our method for 50 quantitative phenotypes in the UK Biobank ($N = 291,273$ unrelated white British individuals, $M = 4,824,392$ common SNPs)**. We run our method partitioning the additive component into 8 bins defined based on two MAF bins (MAF≤ 0.01, MAF> 0.01) and quartiles of the LD-scores and a single dominance bin.

Trait	Heritability	
	Additive	Dominance
Age first birth	0.23543 ± 0.00899	-0.00169 ± 0.00684
Alanine aminotransferase	0.18688 ± 0.01278	0.00073 ± 0.00276
Albumin	0.19454 ± 0.01269	0.00398 ± 0.00298
Alcohol intake frequency	0.12065 ± 0.00415	-0.00163 ± 0.00248
Alkaline phosphatase	0.45369 ± 0.11643	0.01733 ± 0.01916
Apolipoprotein A	0.38251 ± 0.06958	-0.00108 ± 0.00288
Aspartate aminotransferase	0.20966 ± 0.02106	0.00652 ± 0.00273
Basal metabolic rate	0.37079 ± 0.01332	0.00289 ± 0.00269
Eosinophil count	0.29185 ± 0.02304	-0.00043 ± 0.00278
Lymphocyte count	0.2791 ± 0.01718	0.00383 ± 0.00263
Mean corpuscular hemoglobin	0.37601 ± 0.05787	0.00135 ± 0.00284
Monocyte count	0.31017 ± 0.02943	0.00231 ± 0.00268
Mean platelet volume	0.54575 ± 0.06504	0.00834 ± 0.00289
Mean sphered cell volume	0.31017 ± 0.02992	0.0067 ± 0.00253
Platelet distribution width	0.37263 ± 0.04053	0.00406 ± 0.0027
Platelet count	0.40919 ± 0.03245	0.00687 ± 0.00271
RBC count	0.33508 ± 0.04016	0.0015 ± 0.00291
RBC distribution width	0.30012 ± 0.02638	0.00361 ± 0.00283
High light scatter reticulocyte count	0.32716 ± 0.03077	0.00165 ± 0.00252
White blood cell count	0.28163 ± 0.02257	0.00018 ± 0.00266
BMD Heel T-score	0.4293 ± 0.04375	0.00147 ± 0.00758
Body mass index	0.3309 ± 0.01475	0.00403 ± 0.0027
Diastolic Blood Pressure	0.17511 ± 0.00616	0.00242 ± 0.00246
Systolic Blood Pressure	0.17209 ± 0.00683	0.00239 ± 0.00257
Calcium	0.18503 ± 0.02218	0.00456 ± 0.00296
Cholesterol	0.2319 ± 0.06188	0.00209 ± 0.00304
Corneal Hysteresis	0.3403 ± 0.02555	-0.01101 ± 0.01152
C-reactive protein	0.38925 ± 0.10749	-0.00119 ± 0.00262
Creatinine	0.29748 ± 0.01585	-0.00193 ± 0.00226
Creatinine in urine	0.08572 ± 0.00321	0.00176 ± 0.00229
Cystatin-C	0.35118 ± 0.07187	0.00659 ± 0.00247
FEV1-FVC ratio	0.26591 ± 0.0155	0.00266 ± 0.00267
FVC	0.28646 ± 0.00968	-0.00366 ± 0.00238
Gamma glutamyltransferase	0.31742 ± 0.03892	0.00196 ± 0.00249
Glucose	0.11364 ± 0.01132	0.0067 ± 0.00301
Hair color	0.31134 ± 0.08947	-0.0012 ± 0.00366
Hemoglobin A1c	0.31881 ± 0.02474	0.00203 ± 0.00298
HDL cholesterol	0.46776 ± 0.10752	0.00149 ± 0.00302
Height	0.58529 ± 0.02597	-0.00195 ± 0.00294
IGF-1	0.33406 ± 0.01849	0.00345 ± 0.00281
LDL direct	0.24028 ± 0.09232	0.00321 ± 0.00334
Microalbumin in urine	0.04627 ± 0.00672	-0.00675 ± 0.00922
Overall health rating	0.1394 ± 0.00374	-0.00295 ± 0.00218
Phosphate	0.1578 ± 0.01356	0.00058 ± 0.00294
Potassium in urine	0.05076 ± 0.00239	0.00211 ± 0.00202
SHBG	0.37452 ± 0.07941	0.00036 ± 0.00277
Sodium in urine	0.09989 ± 0.00398	-0.00082 ± 0.00246
Testosterone	0.13937 ± 0.0144	-0.00394 ± 0.00303
Vitamin D	0.1347 ± 0.02674	0.00558 ± 0.00233
Waist-hip ratio	0.1955 ± 0.00974	-0.00173 ± 0.0024

Table S4: **Estimate the proportions of variance explained by additive and dominance variation from our method for 50 quantitative phenotypes in the UK Biobank ($N = 291,273$ unrelated white British individuals, $M = 459,792$ common SNPs)**. We run our method with a single additive component and a single dominance component.

Genetic architecture		$\hat{h}^2_A$			$\hat{h}^2_D$		
Additive component	Dominance component	Mean	SE	Mean($\hat{SE}$)	Mean	SE	Mean($\hat{SE}$)
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 0.01$, $h^2_D = 0.05$	0.49831	0.01084	0.00909	0.04923	0.00336	0.00346
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 0.01$, $h^2_D = 0.02$	0.50048	0.01131	0.00923	0.02017	0.00279	0.00285
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 0.01$, $h^2_D = 0.002$	0.49977	0.01239	0.00929	0.00201	0.00268	0.00259
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 1$, $h^2_D = 0.002$	0.50057	0.0138	0.01035	0.0019	0.00264	0.00258
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 1$, $h^2_D = 0.01$	0.49982	0.01165	0.00934	0.00987	0.00248	0.00265
$p_c(A) = 1$, $h^2_A = 0.5$	$p_c(D) = 0.01$, $h^2_D = 0.01$	0.49766	0.01077	0.00938	0.01003	0.00229	0.00267
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 0.01$, $h^2_D = 0.01$	0.25011	0.00681	0.00542	0.00985	0.00292	0.0026
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 1$, $h^2_D = 0.01$	0.24867	0.00641	0.00524	0.00995	0.00303	0.00255
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 1$, $h^2_D = 0.002$	0.24985	0.0058	0.00531	0.00179	0.00255	0.00251
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 0.01$, $h^2_D = 0.002$	0.25026	0.00689	0.00518	0.00185	0.00268	0.00253
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 0.01$, $h^2_D = 0.05$	0.25049	0.00621	0.00521	0.0487	0.00363	0.0032
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 0.01$, $h^2_D = 0.02$	0.2502	0.00677	0.00554	0.02014	0.00263	0.0028
$p_c(A) = 1$, $h^2_A = 0.25$	$p_c(D) = 1$, $h^2_D = 0.02$	0.24853	0.00642	0.00501	0.01999	0.00282	0.00265

Table S5: **Accuracy of estimates and jackknife estimate of standard error in simulations ($N = 291,273$ unrelated individuals, $M = 459,792$ array SNPs)**. We assess jackknife estimation of SE of our method in the presence of dominance and additive heritability under 16 different genetic architectures. Mean and SE are computed from 100 replicates. Here $\hat{SE}$ denotes jackknife estimate of SE computed based on 100 jackknife blocks defined over SNPs. For every genetic architecture, we reported mean of $\hat{SE}$ computed from 100 replicates. Here, $p_c(A)$ and $p_c(D)$ denote proportion of additive and dominance causal variants respectively. h^2_A and h^2_D denotes total additive and dominance heritabilities.

Parameters		$\hat{h}^2_A$		$\hat{h}^2_D$	
Genetic architecture	Percentage of observed causal SNPs	Mean	SE	Mean	SE
$p_c(A) = 1.00$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	0%	0.250	0.005	0.002	0.002
$p_c(A) = 1.00$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	50%	0.249	0.005	0.011	0.002
$p_c(A) = 1.00$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	75%	0.249	0.005	0.016	0.002
$p_c(A) = 1.00$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	100%	0.250	0.006	0.020	0.002
$p_c(A) = 0.01$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	0%	0.183	0.008	0.003	0.003
$p_c(A) = 0.01$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	50%	0.216	0.008	0.007	0.003
$p_c(A) = 0.01$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	75%	0.233	0.008	0.014	0.003
$p_c(A) = 0.01$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	100%	0.251	0.009	0.020	0.003

Table S6: **The accuracy of estimates based on observed causal SNPs in simulations (**$N = 291,273$ **unrelated individuals,** $M = 459,792$ **array SNPs)**. Here, $p_c(A)$ and $p_c(D)$ denote proportion of additive and dominance causal variants respectively. h^2_A and h^2_D denotes total additive and dominance heritabilities. .Mean and SE are computed from 100 replicates.

Parameters		$\hat{h}^2_A$		$\hat{h}^2_D$	
Genetic architecture	Percentage of observed causal SNPs	Mean	SE	Mean	SE
$p_c(A) = 0.01$, $h^2_A = 0.25$ $p_c(D) = 0.01$, $h^2_D = 0.02$	0%	0.246	0.02	0.021	0.009

Table S7: **The accuracy of estimates based on observed causal SNPs in simulations (**$N = 291,273$ **unrelated individuals,** $M = 4,824,392$ **imputed SNPs)**. Here, $p_c(A)$ and $p_c(D)$ denote proportion of additive and dominance causal variants respectively. h^2_A and h^2_D denotes total additive and dominance heritabilities Mean and SE are computed from 10 replicates.

Method	$\hat{h}^2_A$		$\hat{h}^2_D$	
	Mean	SE	Mean	SE
RHE-mc (B=10)	0.248	0.056	0.055	0.070
GCTA(REML)	0.247	0.054	0.052	0.062
GCTA(HE)	0.248	0.056	0.055	0.072

Table S8: **Comparison of heritability estimates in small-scale simulations ($N = 10,000$ unrelated individuals, $M = 459,792$ array SNPs)**. We compared the accuracy of our method with GCTA(HE) and GCTA(REML). We simulated phenotypes where $h^2_A = 0.25$, $h^2_D = 0.05$, $p_c(A) = 1$ and $p_c(D) = 0.05$. Here $p_c(A)$ and $p_c(D)$ denote proportion of additive and dominance causal variants respectively. Mean and SE are computed from 100 replicates.

Trait	RHE-mc run with first 10 PCs		RHE-mc run with first 40 PCs	
	Additive	Dominance	Additive	Dominance
Age first birth	0.26042 ± 0.00986	-0.00121 ± 0.00637	0.22492 ± 0.0082	-0.00324 ± 0.00659
Alanine aminotransferase	0.18947 ± 0.01276	0.00016 ± 0.00273	0.18726 ± 0.01283	$-5e-04 \pm 0.00272$
Albumin	0.19846 ± 0.01298	0.00332 ± 0.00296	0.19343 ± 0.01262	0.00264 ± 0.00294
Alcohol intake frequency	0.122 ± 0.00428	-0.00167 ± 0.00242	0.1201 ± 0.00386	-0.00175 ± 0.00245
Alkaline phosphatase	0.45798 ± 0.11684	0.01612 ± 0.01916	0.45929 ± 0.11731	0.01605 ± 0.019
Apolipoprotein A	0.38402 ± 0.06944	-0.00093 ± 0.00277	0.38361 ± 0.06976	-0.00087 ± 0.00275
Aspartate aminotransferase	0.21089 ± 0.02085	0.00694 ± 0.00268	0.20951 ± 0.02089	0.00703 ± 0.00267
Basal metabolic rate	0.37306 ± 0.01369	0.0025 ± 0.00271	0.37165 ± 0.01376	0.00376 ± 0.00272
Eosinophil count	0.29562 ± 0.0231	0 ± 0.00286	0.2911 ± 0.02322	-0.00091 ± 0.00272
Lymphocyte count	0.28334 ± 0.01753	0.00333 ± 0.00258	0.27994 ± 0.01716	0.0024 ± 0.00267
Mean corpuscular hemoglobin	0.3797 ± 0.05788	0.00161 ± 0.00274	0.37329 ± 0.05729	0.00186 ± 0.00284
Monocyte count	0.31276 ± 0.02965	0.0017 ± 0.00277	0.30832 ± 0.02947	0.00098 ± 0.00272
Mean platelet volume	0.55001 ± 0.06527	0.00747 ± 0.0027	0.54579 ± 0.06551	0.00684 ± 0.00276
Mean sphered cell volume	0.31358 ± 0.02981	0.00633 ± 0.00251	0.31224 ± 0.02964	0.00615 ± 0.0025
Platelet distribution width	0.37879 ± 0.04064	0.00421 ± 0.00277	0.37446 ± 0.04095	0.00369 ± 0.00274
Platelet count	0.4039 ± 0.03225	0.00399 ± 0.00285	0.40368 ± 0.03196	0.00445 ± 0.00281
RBC count	0.34229 ± 0.04101	0.00258 ± 0.00305	0.33784 ± 0.04059	0.00186 ± 0.00293
RBC distribution width	0.30649 ± 0.0267	0.0033 ± 0.00284	0.29814 ± 0.02648	0.00218 ± 0.0029
High light scatter reticulocyte count	0.3283 ± 0.03062	0.00235 ± 0.00261	0.32501 ± 0.03013	0.0014 ± 0.00256
White blood cell count	0.28441 ± 0.02286	0.00068 ± 0.00259	0.27876 ± 0.02235	$-9e-05 \pm 0.00252$
BMD Heel T-score	0.43634 ± 0.04402	0.00093 ± 0.00764	0.42486 ± 0.04259	-0.00183 ± 0.00739
Body mass index	0.32683 ± 0.01444	0.00284 ± 0.00271	0.32441 ± 0.0138	0.00333 ± 0.00249
Diastolic blood pressure	0.17106 ± 0.00594	0.00163 ± 0.00242	0.16952 ± 0.00587	0.00175 ± 0.00242
Systolic blood pressure	0.17234 ± 0.0065	0.00189 ± 0.00252	0.17101 ± 0.00653	0.00192 ± 0.00257
Calcium	0.18188 ± 0.02174	0.00368 ± 0.00298	0.18303 ± 0.02202	0.00464 ± 0.00291
Cholesterol	0.23426 ± 0.06236	0.00195 ± 0.00305	0.23234 ± 0.06226	0.00248 ± 0.00297
Corneal Hysteresis	0.34781 ± 0.02558	-0.00591 ± 0.01224	0.33913 ± 0.02441	-0.01319 ± 0.01176
C-reactive protein	0.39271 ± 0.10826	-0.00155 ± 0.0025	0.38868 ± 0.10816	-0.00121 ± 0.00254
Creatinine	0.29764 ± 0.01562	-0.00163 ± 0.00232	0.29365 ± 0.01507	-0.00186 ± 0.00228
Creatinine in urine	0.08798 ± 0.00305	0.00184 ± 0.00235	0.08474 ± 0.00302	0.00175 ± 0.00234
Cystatin-C	0.35892 ± 0.07274	0.00573 ± 0.00274	0.35184 ± 0.07186	0.00638 ± 0.00271
FEV1-FVC ratio	0.26807 ± 0.0163	0.00219 ± 0.0026	0.26388 ± 0.0153	0.00259 ± 0.00268
FVC	0.295 ± 0.00893	-0.00428 ± 0.00242	0.28581 ± 0.00892	-0.00426 ± 0.00239
Gamma glutamyltransferase	0.322 ± 0.03908	0.00205 ± 0.00244	0.31658 ± 0.03942	0.00278 ± 0.00256
Glucose	0.11466 ± 0.01139	0.00665 ± 0.00302	0.11224 ± 0.0112	0.00598 ± 0.00292
Hair color	0.32007 ± 0.0914	-0.0022 ± 0.00351	0.31341 ± 0.09027	-0.00268 ± 0.00344
Hemoglobin A1c	0.31369 ± 0.02449	0.00062 ± 0.00295	0.32511 ± 0.0254	0.00251 ± 0.00287
HDL cholesterol	0.4724 ± 0.10795	-0.00021 ± 0.00297	0.47121 ± 0.10904	0.00036 ± 0.003
Height	0.59614 ± 0.02579	-0.00166 ± 0.00291	0.58163 ± 0.02495	-0.0034 ± 0.00301
IGF-1	0.32612 ± 0.01779	0.00204 ± 0.00282	0.32921 ± 0.01801	0.00289 ± 0.00286
LDL direct	0.24394 ± 0.09316	0.0024 ± 0.00322	0.24062 ± 0.0926	0.00159 ± 0.0031
Microalbumin in urine	0.0477 ± 0.00684	-0.00684 ± 0.00907	0.04555 ± 0.00675	-0.00674 ± 0.0093
Overall health rating	0.14251 ± 0.00361	-0.0039 ± 0.00217	0.13971 ± 0.00321	-0.00306 ± 0.00225
Phosphate	0.16069 ± 0.01349	$-8e-05 \pm 0.003$	0.1568 ± 0.01349	-0.00066 ± 0.00294
Potassium in urine	0.05298 ± 0.00234	0.00183 ± 0.00206	0.05034 ± 0.00233	0.002 ± 0.00205
SHBG	0.36544 ± 0.07724	-0.00185 ± 0.00283	0.37537 ± 0.07968	0.00088 ± 0.00278
Sodium in urine	0.1046 ± 0.00406	-0.00089 ± 0.00247	0.09896 ± 0.00373	-0.00087 ± 0.00242
Testosterone	0.13736 ± 0.01419	-0.00506 ± 0.00301	0.13885 ± 0.01419	-0.00419 ± 0.00305
Vitamin D	0.1404 ± 0.02702	0.00529 ± 0.00239	0.1345 ± 0.0267	0.00516 ± 0.00231
Waist-hip ratio	0.20162 ± 0.00943	-0.00219 ± 0.00237	0.19659 ± 0.00973	-0.0017 ± 0.00243

Table S9: **Effects of selected PCs on estimates of variance explained by additive and dominance variation from our method for 50 quantitative phenotypes in the UK Biobank ($N = 291,273$ unrelated white British individuals, $M = 459,792$ common SNPs)**. We run our method with a single additive component and a single dominance component.