Supplementary Table S1: Minor allele frequencies and effect sizes of causal SNPs used in the simulations

MAF[a]	β				
	Set 1	**Set 2**	**Set 3**	**Set 4**	**Set 5**
0.01075	0.8	0.8	2	2	0.5
0.0795	0.15	0.15	0	0	0
0.00075	1.6	1.6	2	2 (major causative allele)	0.5
0.0085	1.6	1.6	2	2 (major causative allele)	0.5
0.0015	1.6	-1.6	2	2 (major causative allele)	0.5
0.00075	1.6	-1.6	2	2 (major causative allele)	0.5
0.2455	0.15	0.15	0	0	0
0.004	-	-	-	-	0.5
0.00425	-	-	-	-	0.5
0.00875	-	-	-	-	0.5
0.00075	-	-	-	-	0.5
0.00025	-	-	-	-	0.5
0.03075	-	-	-	-	0.5
0.099	-	-	-	-	0
0.03725	-	-	-	-	0.5
0.004	-	-	-	-	0.5
0.0085	-	-	-	-	0.5
5.00E-04	-	-	-	-	0.5
0.007	-	-	-	-	0.5
0.00025	-	-	-	-	0.5

[a] minor allele frequency;

Supplementary Table S2. The mean and variance of the percent of variability of a quantitative trait explained by CVs, LCVs, and RVs in the five models[1].

ρ	Model 1[a], mean (SD)			Model 2[b], mean (SD)			Model 3[c], mean (SD)			Model 4[d], mean (SD)			Model 5[e] (mean (sd))		
	CVs	LCVs	RVs	CVs	LCVs	RVs	CVs	LCVs	RVs	CVs	LCVs	RVs	CVs	LCVs	RVs
0	0.011 (2×10^{-7})	0.013 (4×10^{-6})	0.054 (6×10^{-5})	0.011 (3×10^{-7})	0.013 (4×10^{-6})	0.054 (5×10^{-5})	0	0.07 (1*10^{-4})	0.08 (1×10^{-4})	0	0.07 (1*10^{-4})	0.08 (1×10^{-4})	0	0.04 (5×10^{-6})	0.02 (3×10^{-6})
0.5	0.011 (2×10^{-7})	0.013 (3×10^{-6})	0.055 (7×10^{-5})	0.011 (2×10^{-7})	0.013 (3×10^{-6})	0.055 (6×10^{-5})	0	0.07 (9*10^{-5})	0.08 (1×10^{-4})	0	0.07 (9*10^{-5})	0.08 (1×10^{-4})	0	0.04 (7×10^{-6})	0.02 (4×10^{-6})

[1]CVs: common SNPs (MAFs 5%~50%); LCVs: less common SNPs (MAFs 1% ~5%); RVs: rare SNPs (MAFs < 1%).

Supplementary Table S3. The type one error rates of two-stage designs at a nominal level of 0.05 when CVs and LCVs are in LD

Test	Design	*l*												
		.001	.0025	.004	.0055	.007	.0085	.01	.0115	.013	.0145	.016	.0175	.019	.0205
Sum	OS[a]	.047													
	TS-E[b]	.056	.058	.047	.049	.052	.052	.053	.048	.059	.053	.050	.055	.049	.054
SSU	OS	.051													
	TS-E	.055	.052	.051	.052	.053	.054	.054	.053	.052	.050	.052	.052	.054	.052

[a] OS = one-stage design; [b] TS-E = two-stage design with extreme phenotype sampling.

Supplementary Table S4: The percent of variability of quantitative trait $Q_{2\text{-}10}$ explained by CVs, LCVs, and RVs within13 causal genes for GAW17 data

Gene	#(causal SNPs)			%		
	CVs	**LCVs**	**RVs**	**CVs**	**LCVs**	**RVs**
BCHE	0	0	13	0	0	0.05497
GCKR	0	1	0	0	0.03319	0
INSIG1	0	0	3	0	0	0.00225
LPL	0	1	2	0	0.03687	0.0157
PDGFD	0	0	4	0	0	0.06447
PLAT	0	0	8	0	0	0.01211
RARB	0	0	2	0	0	0.02238
SIRT1	0	0	9	0	0	0.03721
SREBF1	0	0	10	0	0	0.04033
VLDLR	0	0	8	0	0	0.02357
VNN1	1	0	1	0.07382	0	0.01244
VNN3	1	2	4	0.03431	0.00261	0.00659
VWF	0	0	2	0	0	0.01372