

Table S1: Design for the simulation II. ^a: Regression models used to simulate the core genes. We denote x_i^d as the i^{th} marker in module d . ^b: Number of genes in the module. ^c: Heritability of the core gene. ^d: Average correlation of the genes in the module with the core gene. ^e: Average percentage of variations for genes in the module explained by the true model.

Module	Model ^a	#Genes ^b	Heritability ^c	Cor. ^d	% of Var. ^e
A	$R = \beta I_{x_1^A=x_2^A} + \beta I_{x_3^A=1} + e$	60	0.85	0.5	23.66
B	$R = \beta I_{x_1^B=x_2^B} + e$	60	0.7	0.5	18.8
C	$R = \beta I_{x_1^C=1} + e$	40	0.65	0.5	15.6
D	$R = \beta I_{x_1^D=1} + \beta I_{x_2^D=1} + e$	40	0.7	0.5	18.6