

Supplemental Data

Table 1. Odds table for two-locus model 1, 2, 3 and 4.

Model 1	BB	Bb	bb
AA	μ	μ	μ
Aa	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)^3$
aa	μ	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$

Model 2	BB	Bb	bb
AA	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)$
Aa	$\mu(1 + \theta)$	μ	μ
aa	$\mu(1 + \theta)$	μ	μ

Model 3	BB	Bb	bb
AA	μ	μ	$\mu(1 + \theta)$
Aa	μ	$\mu(1 + \theta)$	μ
aa	$\mu(1 + \theta)$	μ	μ

Model 4	BB	Bb	bb
AA	μ	$\mu(1 + \theta)$	μ
Aa	$\mu(1 + \theta)$	μ	$\mu(1 + \theta)$
aa	μ	$\mu(1 + \theta)$	μ

Table 2: Numerical solutions for Table 1.

Model 1	$p(D) = 0.1, h^2 = 0.03$		
MAF	0.1	0.2	0.4
μ	0.100	0.091	0.075
θ	3.448	1.300	0.624
Model 2	$p(D) = 0.1, h^2 = 0.02$		
MAF	0.1	0.2	0.4
μ	0.077	0.064	0.065
θ	1.532	1.700	1.640
Model 3	$p(D) = 0.1, h^2 = 0.02$		
MAF	0.1	0.2	0.4
μ	0.0996	0.0893	0.0743
θ	3.0151	1.7876	1.5315
Model 4	$p(D) = 0.1, h^2 = 0.02$		
MAF	0.1	0.2	0.4
μ	0.078	0.067	0.061
θ	1.537	1.601	1.717

Table 3: Two-locus models with different odds patterns of two loci, the prevalence $p(D) = 0.1$ and the heritability $h^2 = 0.02$, MAF = 0.1, 0.2, 0.4.

Model 5 (mix of Model 1 and Model 2)		
Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_1	μ_2
AABb	μ_1	$\mu_2(1 + \theta)$
AAbb	μ_1	$\mu_2(1 + \theta)$
AaBB	μ_1	$\mu_2(1 + \theta)$
AaBb	$\mu_1(1 + \theta_1)$	μ_2
Aabb	$\mu_1(1 + \theta_1)^2$	μ_2
aaBB	μ_1	$\mu_2(1 + \theta)$
aaBb	$\mu_1(1 + \theta_1)^2$	μ_2
aabb	$\mu_1(1 + \theta_1)^4$	μ_2

Model 6 (mix of Model 1 and Model 3)		
Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_1	μ_2
AABb	μ_1	μ_2
AAbb	μ_1	$\mu_2(1 + \theta)$
AaBB	μ_1	μ_2
AaBb	$\mu_1(1 + \theta_1)$	$\mu_2(1 + \theta)$
Aabb	$\mu_1(1 + \theta_1)^2$	μ_2
aaBB	μ_1	$\mu_2(1 + \theta)$
aaBb	$\mu_1(1 + \theta_1)^2$	μ_2
aabb	$\mu_1(1 + \theta_1)^4$	μ_2

Model 7 (mix of Model 1 and Model 4)		
Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_1	μ_2
AABb	μ_1	$\mu_2(1 + \theta)$
AAbb	μ_1	μ_2
AaBB	μ_1	$\mu_2(1 + \theta)$
AaBb	$\mu_1(1 + \theta_1)$	μ_2
Aabb	$\mu_1(1 + \theta_1)^2$	$\mu_2(1 + \theta)$
aaBB	μ_1	μ_2
aaBb	$\mu_1(1 + \theta_1)^2$	$\mu_2(1 + \theta)$
aabb	$\mu_1(1 + \theta_1)^4$	μ_2

Model 8 (mix of Model 2 and Model 3)		
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Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_2	μ_2
AABb	$\mu_2(1 + \theta)$	μ_2
AAbb	$\mu_2(1 + \theta)$	$\mu_2(1 + \theta)$
AaBB	$\mu_2(1 + \theta)$	μ_2
AaBb	μ_2	$\mu_2(1 + \theta)$
Aabb	μ_2	μ_2
aaBB	$\mu_2(1 + \theta)$	$\mu_2(1 + \theta)$
aaBb	μ_2	μ_2
aabb	μ_2	μ_2

Model 9 (mix of Model 2 and Model 4)		
Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_2	μ_2
AABb	$\mu_2(1 + \theta)$	$\mu_2(1 + \theta)$
AAbb	$\mu_2(1 + \theta)$	μ_2
AaBB	$\mu_2(1 + \theta)$	$\mu_2(1 + \theta)$
AaBb	μ_2	μ_2
Aabb	μ_2	$\mu_2(1 + \theta)$
aaBB	$\mu_2(1 + \theta)$	μ_2
aaBb	μ_2	$\mu_2(1 + \theta)$
aabb	μ_2	μ_2

Model 10 (mix of Model 3 and Model 4)		
Genotype	Odds of disease 1	Odds of disease 2
AABB	μ_2	μ_2
AABb	μ_2	$\mu_2(1 + \theta)$
AAbb	$\mu_2(1 + \theta)$	μ_2
AaBB	μ_2	$\mu_2(1 + \theta)$
AaBb	$\mu_2(1 + \theta)$	μ_2
Aabb	μ_2	$\mu_2(1 + \theta)$
aaBB	$\mu_2(1 + \theta)$	μ_2
aaBb	μ_2	$\mu_2(1 + \theta)$
aabb	μ_2	μ_2

Table 4. Odds table for three-locus models 11, 12, and 13. Model 11 with multiplicative effect between and within loci, Model 12 with multiplicative effect between loci, and Model 13 with threshold effect

(11)	BBCC	BBCc	BBcc	BbCC	BbCc	Bbcc	bbCC	bbCc	bbcc
AA	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)^2$	$\mu(1 + \theta)$	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$
Aa	$\mu(1 + \theta)$	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^5$
aa	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^3$	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^5$	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^5$	$\mu(1 + \theta)^6$
(12)	BBCC	BBCc	BBcc	BbCC	BbCc	Bbcc	bbCC	bbCc	bbcc
AA	μ	μ	μ	μ	μ	μ	μ	μ	μ
Aa	μ	μ	μ	μ	$\mu(1 + \theta)^1$	$\mu(1 + \theta)^2$	μ	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^4$
aa	μ	μ	μ	μ	$\mu(1 + \theta)^2$	$\mu(1 + \theta)^4$	μ	$\mu(1 + \theta)^4$	$\mu(1 + \theta)^7$
(13)	BBCC	BBCc	BBcc	BbCC	BbCc	Bbcc	bbCC	bbCc	bbcc
AA	μ	μ	μ	μ	μ	μ	μ	μ	μ
Aa	μ	μ	μ	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)$	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)$
aa	μ	μ	μ	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)$	μ	$\mu(1 + \theta)$	$\mu(1 + \theta)$

Table 5: Numerical solutions for Table 4.

Model 11	$p(D) = 0.1, h^2 = 0.03$	
MAF	0.2	0.4
μ	0.053	0.032
θ	0.690	0.592
Model 12	$p(D) = 0.1, h^2 = 0.03$	
MAF	0.2	0.4
μ	0.100	0.085
θ	1.719	0.462
Model 13	$p(D) = 0.1, h^2 = 0.03$	
MAF	0.2	0.4
μ	0.097	0.074
θ	4.187	2.108

Table 6: Three-locus models with different odds patterns of three loci, the prevalence $p(D) = 0.1$ and the heritability $h^2 = 0.03$, MAF = 0.2, 0.4.

Model 14 (mix of Model 11 and Model 12)		
Genotype	Odds of disease 1	Odds of disease 2
AABBCC	μ_1	μ_2
AABBcc	$\mu_1(1 + \theta_1)$	μ_2
AABBcc	$\mu_1(1 + \theta_1)^2$	μ_2
AABbCC	$\mu_1(1 + \theta_1)$	μ_2
AABbCc	$\mu_1(1 + \theta_1)^2$	μ_2
AABbcc	$\mu_1(1 + \theta_1)^3$	μ_2
AAbbCC	$\mu_1(1 + \theta_1)^2$	μ_2
AAbbCc	$\mu_1(1 + \theta_1)^3$	μ_2
AAbbcc	$\mu_1(1 + \theta_1)^4$	μ_2
AaBBCC	$\mu_1(1 + \theta_1)$	μ_2
AaBBcc	$\mu_1(1 + \theta_1)^2$	μ_2
AaBBcc	$\mu_1(1 + \theta_1)^3$	μ_2
AaBbCC	$\mu_1(1 + \theta_1)^2$	μ_2
AaBbCc	$\mu_1(1 + \theta_1)^3$	$\mu_2(1 + \theta_2)$
AaBbcc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)^2$
AabbCC	$\mu_1(1 + \theta_1)^3$	μ_2
AabbCc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)^2$
Aabbcc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)^4$
aaBBCC	$\mu_1(1 + \theta_1)^2$	μ_2
aaBBcc	$\mu_1(1 + \theta_1)^3$	μ_2
aaBBcc	$\mu_1(1 + \theta_1)^4$	μ_2
aaBbCC	$\mu_1(1 + \theta_1)^3$	μ_2
aaBbCc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)^2$
aaBbcc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)^4$
aabbCC	$\mu_1(1 + \theta_1)^4$	μ_2
aabbCc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)^4$
aabbcc	$\mu_1(1 + \theta_1)^6$	$\mu_2(1 + \theta_2)^7$

Model 15 (mix of Model 11 and Model 13)		
Genotype	Odds of disease 1	Odds of disease 2
AABBCC	μ_1	μ_2
AABBcc	$\mu_1(1 + \theta_1)$	μ_2
AABBcc	$\mu_1(1 + \theta_1)^2$	μ_2
AABbCC	$\mu_1(1 + \theta_1)$	μ_2
AABbCc	$\mu_1(1 + \theta_1)^2$	μ_2
AABbcc	$\mu_1(1 + \theta_1)^3$	μ_2
AAbbCC	$\mu_1(1 + \theta_1)^2$	μ_2
AAbbCc	$\mu_1(1 + \theta_1)^3$	μ_2
AAbbcc	$\mu_1(1 + \theta_1)^4$	μ_2
AaBBCC	$\mu_1(1 + \theta_1)$	μ_2
AaBBcc	$\mu_1(1 + \theta_1)^2$	μ_2

AaBBcc	$\mu_1(1 + \theta_1)^3$	μ_2
AaBbCC	$\mu_1(1 + \theta_1)^2$	μ_2
AaBbCc	$\mu_1(1 + \theta_1)^3$	$\mu_2(1 + \theta_2)$
AaBbcc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
AabbCC	$\mu_1(1 + \theta_1)^3$	μ_2
AabbCc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
Aabbcc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)$
aaBBCC	$\mu_1(1 + \theta_1)^2$	μ_2
aaBBCc	$\mu_1(1 + \theta_1)^3$	μ_2
aaBBcc	$\mu_1(1 + \theta_1)^4$	μ_2
aaBbCC	$\mu_1(1 + \theta_1)^3$	μ_2
aaBbCc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
aaBbcc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)$
aabbCC	$\mu_1(1 + \theta_1)^4$	μ_2
aabbCc	$\mu_1(1 + \theta_1)^5$	$\mu_2(1 + \theta_2)$
aabbcc	$\mu_1(1 + \theta_1)^6$	$\mu_2(1 + \theta_2)$

Model 16 (mix of Model 12 and Model 13)		
Genotype	Odds of disease 1	Odds of disease 2
AABBCC	μ_1	μ_2
AABBcc	μ_1	μ_2
AABBcC	μ_1	μ_2
AABbCC	μ_1	μ_2
AABbCc	μ_1	μ_2
AABbcc	μ_1	μ_2
AAbbCC	μ_1	μ_2
AAbbCc	μ_1	μ_2
AAbbcc	μ_1	μ_2
AaBBCC	μ_1	μ_2
AaBBCc	μ_1	μ_2
AaBBcc	μ_1	μ_2
AaBbCC	μ_1	μ_2
AaBbCc	$\mu_1(1 + \theta_1)$	$\mu_2(1 + \theta_2)$
AaBbcc	$\mu_1(1 + \theta_1)^2$	$\mu_2(1 + \theta_2)$
AabbCC	μ_1	μ_2
AabbCc	$\mu_1(1 + \theta_1)^2$	$\mu_2(1 + \theta_2)$
Aabbcc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
aaBBCC	μ_1	μ_2
aaBBCc	μ_1	μ_2
aaBBcc	μ_1	μ_2
aaBbCC	μ_1	μ_2
aaBbCc	$\mu_1(1 + \theta_1)^2$	$\mu_2(1 + \theta_2)$
aaBbcc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
aabbCC	μ_1	μ_2
aabbCc	$\mu_1(1 + \theta_1)^4$	$\mu_2(1 + \theta_2)$
aabbcc	$\mu_1(1 + \theta_1)^7$	$\mu_2(1 + \theta_2)$

