

Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design

Jia Wen^{1,2}, Xinwang Zhao¹, Guorong Wu², Dan Xiang², Qing Liu², Su-Hong Bu², Can Yi²,
Qijian Song³, Jim M. Dunwell⁴, Jinxing Tu¹, Tianzhen Zhang² & Yuan-Ming Zhang¹

Table S1 | Simulated parameters in all the simulation experiments

Simulation study	Case	NCII design			Genome length (cM)	Marker Density (cM)	QTL	Effect type of QTL	Heritability (%)	Position(cM)	Sample for analysis			
		maternal	paternal	F ₁							Trait phenotype	GCA	SCA	MPH
Part I	1	120	120	240	100	Equal, 5	1	<i>a</i>	5	25	240 F ₁	240 parents	240 F ₁	240 F ₁
							2	<i>a</i>	10	75				
							3	<i>a</i>	5	135				
							4	<i>a</i>	15	175				
							5	<i>a</i>	10	220				
							6	<i>a</i>	15	270				
	2	120	120	240	100	Equal, 5	1	<i>d</i>	5	25	240 F ₁	240 parents	240 F ₁	240 F ₁
							2	<i>d</i>	10	75				
							3	<i>d</i>	5	135				
							4	<i>d</i>	15	175				
							5	<i>d</i>	10	220				
							6	<i>d</i>	15	270				
	3	120	120	240	100	Equal, 5	1	<i>aa</i>	5	20 × 60	240 F ₁	240 parents	240 F ₁	240 F ₁
							2	<i>aa</i>	10	90 × 125				
							3	<i>aa</i>	5	155 × 205				
							4	<i>aa</i>	15	180 × 235				
							5	<i>aa</i>	10	40 × 275				
							6	<i>aa</i>	15	75 × 220				
	4	120	120	240	100	Equal, 5	1	<i>ad</i>	5	20 × 60	240 F ₁	240 parents	240 F ₁	240 F ₁
							2	<i>ad</i>	10	90 × 125				
							3	<i>ad</i>	5	155 × 205				
							4	<i>ad</i>	15	180 × 235				
							5	<i>ad</i>	10	40 × 275				
							6	<i>ad</i>	15	75 × 220				
5	120	120	240	100	Equal, 5	1	<i>da</i>	5	20 × 60	240 F ₁	240 parents	240 F ₁	240 F ₁	
						2	<i>da</i>	10	90 × 125					
						3	<i>da</i>	5	155 × 205					
						4	<i>da</i>	15	180 × 235					
						5	<i>da</i>	10	40 × 275					
						6	<i>da</i>	15	75 × 220					
6	120	120	240	100	Equal, 5	1	<i>dd</i>	5	20 × 60	240 F ₁	240 parents	240 F ₁	240 F ₁	
						2	<i>dd</i>	10	90 × 125					
						3	<i>dd</i>	5	155 × 205					

							4	dd	15	180×235			
							5	dd	10	40×275			
							6	dd	15	75×220			
Part II	7	120	120	240	100	Equal, 5	1	$d=0.5a$	5	25			
							2	$d=0.5a$	10	75			
							3	$d=0.5a$	5	135	240 F ₁	240 parents	240 F ₁ 240 F ₁
							4	$d=0.5a$	15	175			
							5	$d=0.5a$	10	220			
							6	$d=0.5a$	15	270			
	8	120	120	240	100	Equal, 5	1	$d=a$	5	25			
							2	$d=a$	10	75			
							3	$d=a$	5	135	240 F ₁	240 parents	240 F ₁ 240 F ₁
							4	$d=a$	15	175			
							5	$d=a$	10	220			
							6	$d=a$	15	270			
	9	120	120	240	100	Equal, 5	1	$d=2a$	5	25			
							2	$d=2a$	10	75			
							3	$d=2a$	5	135	240 F ₁	240 parents	240 F ₁ 240 F ₁
							4	$d=2a$	15	175			
							5	$d=2a$	10	220			
							6	$d=2a$	15	270			
Part III	10	80	80	80	100	Equal, 5	1	a	5	20			
							2	d	5	85			
							3	aa	5	10×30	160 parents+		
							4	ad	5	40×55	80 F ₁		
							5	da	5	45×80			
							6	dd	5	65×95			
	11	60	60	120	100	Equal, 5	1	a	5	20			
							2	d	5	85			
							3	aa	5	10×30	120 parents+		
							4	ad	5	40×55	120 F ₁		
							5	da	5	45×80			
							6	dd	5	65×95			
	12	48	48	144	100	Equal, 5	1	a	5	20			
							2	d	5	85			
							3	aa	5	10×30	96 parents+		
							4	ad	5	40×55	144 F ₁		
							5	da	5	45×80			

						6	<i>dd</i>	5	65 × 95	
13	40	40	160	100	Equal, 5	1	<i>a</i>	5	20	
						2	<i>d</i>	5	85	
						3	<i>aa</i>	5	10 × 30	80 parents+
						4	<i>ad</i>	5	40 × 55	160 F ₁
						5	<i>da</i>	5	45 × 80	
						6	<i>dd</i>	5	65 × 95	
14	34	34	172	100	Equal, 5	1	<i>a</i>	5	20	
						2	<i>d</i>	5	85	
						3	<i>aa</i>	5	10 × 30	68 parents+
						4	<i>ad</i>	5	40 × 55	172 F ₁
						5	<i>da</i>	5	45 × 80	
						6	<i>dd</i>	5	65 × 95	
15	30	30	180	100	Equal, 5	1	<i>a</i>	5	20	
						2	<i>d</i>	5	85	
						3	<i>aa</i>	5	10 × 30	60 parents+
						4	<i>ad</i>	5	40 × 55	180 F ₁
						5	<i>da</i>	5	45 × 80	
						6	<i>dd</i>	5	65 × 95	
16	26	26	188	100	Equal, 5	1	<i>a</i>	5	20	
						2	<i>d</i>	5	85	
						3	<i>aa</i>	5	10 × 30	52 parents+
						4	<i>ad</i>	5	40 × 55	188 F ₁
						5	<i>da</i>	5	45 × 80	
						6	<i>dd</i>	5	65 × 95	
17	15	15	225	100	Equal, 5	1	<i>a</i>	5	20	
						2	<i>d</i>	5	85	
						3	<i>aa</i>	5	10 × 30	30 parents+
						4	<i>ad</i>	5	40 × 55	225 F ₁
						5	<i>da</i>	5	45 × 80	
						6	<i>dd</i>	5	65 × 95	

Table S2 | Comparisons of trait phenotype, general combining ability (GCA), specific combining ability (SCA) and mid-parental heterosis (MPH) in the genetic dissection of heterosis under additive, dominance, *aa*, *ad*, *da* and *dd* genetic models using Monte Carlo simulation experiments

QTL	True value			Estimate																	
	Posi (cM)	Effect	r^2	Trait phenotype						GCA											
				Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power(%)	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power(%)		
<i>a</i>	25	1.5811	0.05	24.99 (0.34)	1.6386 (0.4046)	-0.0189 (0.4530)						85.0	25.00 (0.000)	0.7744 (0.0592)	-0.0001 (0.0349)						100.0
	75	2.2361	0.10	75.00 (0.00)	2.2179 (0.3593)	-0.0104 (0.4303)						99.5	75.00 (0.00)	1.0917 (0.0806)	-0.0001 (0.0349)						100.0
	135	1.5811	0.05	135.01 (0.17)	1.6444 (0.3250)	-0.0175 (0.4260)						85.7	135.00 (0.00)	0.7707 (0.0596)	-0.0001 (0.0349)						100.0
	175	2.7386	0.15	174.99 (0.16)	2.7093 (0.3594)	0.0135 (0.4181)						99.8	175.00 (0.00)	1.3406 (0.0855)	-0.0001 (0.0349)						100.0
	220	2.2361	0.10	219.97 (0.69)	2.2096 (0.4437)	-0.0059 (0.4475)						99.4	220.00 (0.00)	1.0922 (0.0787)	-0.0001 (0.0349)						100.0
	270	2.7386	0.15	270.00 (0.06)	2.7117 (0.3871)	0.0147 (0.4641)						100.0	270.00 (0.00)	1.3363 (0.0915)	-0.0001 (0.0349)						100.0
<i>d</i>	25	2.2361	0.05	25.00 (0.07)	0.0096 (0.2978)	2.2850 (0.4158)						87.2	25.01 (0.66)	0.0095 (0.1252)	-0.0108 (0.0059)						26.9
	75	3.1623	0.10	75.00 (0.22)	0.0113 (0.2985)	3.1371 (0.4813)						99.9	75.00 (0.77)	-0.0076 (0.1563)	-0.0107 (0.0061)						42.3
	135	2.2361	0.05	135.00 (0.07)	0.0107 (0.3253)	2.3163 (0.3983)						86.6	134.87 (0.92)	-0.0038 (0.1264)	-0.0109 (0.0060)						26.1
	175	3.8730	0.15	175.00 (0.14)	-0.0005 (0.3411)	3.8639 (0.4689)						100.0	175.01 (0.24)	-0.0044 (0.1721)	-0.0107 (0.0062)						51.5
	220	3.1623	0.10	220.00 (0.01)	0.0005 (0.3885)	3.1456 (0.4544)						99.9	220.01 (0.25)	0.00005 (0.1498)	-0.0108 (0.0063)						40.0
	270	3.8730	0.15	270.02 (0.50)	0.0079 (0.3046)	3.8482 (0.4921)						100.0	269.96 (0.63)	0.0075 (0.1733)	-0.0108 (0.0064)						51.0
<i>aa</i>	20	60	2.2361	0.05	19.91 (2.59)	60.01 (0.22)		2.3059 (0.4438)	0.0001 (0.6016)	-0.0080 (0.5968)	0.0147 (0.8694)	85.4	19.99 (0.33)	60.00 (0.00)		0.5477 (0.0415)	-0.0009 (0.0686)	0.0014 (0.0698)	0.0001 (0.0178)		100.0
	90	125	3.1623	0.10	90.00 (0.87)	125.01 (0.35)		3.1540 (0.5016)	-0.0245 (0.6219)	-0.0145 (0.6010)	0.0093 (0.8707)	99.4	90.00 (0.07)	125.00 (0.03)		0.7780 (0.0443)	-0.0013 (0.0788)	-0.0031 (0.0796)	0.0001 (0.0178)		100.0
	155	205	2.2361	0.05	155.00 (0.00)	205.03 (0.84)		2.3237 (0.4190)	0.0139 (0.5825)	0.0090 (0.6114)	0.0115 (0.8336)	85.2	155.00 (0.01)	205.00 (0.03)		0.5498 (0.0319)	-0.0044 (0.0702)	-0.0030 (0.0709)	0.0001 (0.0178)		100.0
	180	235	3.8730	0.15	179.99 (0.46)	234.97 (0.67)		3.8299 (0.5308)	0.0150 (0.6070)	0.0022 (0.6013)	0.0020 (0.8225)	100.0	180.00 (0.04)	235.00 (0.05)		0.9514 (0.0538)	0.0009 (0.0787)	-0.0007 (0.0758)	0.0001 (0.0178)		100.0
	40	275	3.1623	0.10	40.00 (0.02)	274.93 (2.09)		3.1298 (0.5024)	-0.0411 (0.6111)	0.0064 (0.6223)	-0.0126 (0.8590)	99.1	40.00 (0.04)	275.00 (0.07)		0.7769 (0.0472)	0.0011 (0.0767)	-0.0031 (0.0753)	-0.0001 (0.0178)		100.0
	75	220	3.8730	0.15	74.99 (0.61)	220.01 (0.21)		3.8575 (0.5159)	0.0101 (0.5753)	0.0087 (0.6172)	-0.0055 (0.8637)	99.9	75.00 (0.06)	220.00 (0.05)		0.9522 (0.0543)	-0.0050 (0.0770)	0.0024 (0.0806)	0.0001 (0.0178)		100.0
<i>ad</i>	20	60	3.1623	0.05	20.07 (3.00)	60.00 (0.08)		-0.0124 (0.4217)	3.2726 (0.5721)	-0.0136 (0.6072)	0.0126 (0.8662)	86.1	19.92 (1.53)	60.19 (1.51)		0.0087 (0.1182)	-0.0154 (0.0489)	0.0086 (0.0771)	-0.0001 (0.0037)		12.9
	90	125	4.4721	0.10	89.97 (0.77)	124.99 (0.21)		0.0159 (0.4183)	4.4339 (0.6949)	-0.0177 (0.5989)	0.0349 (0.8546)	99.8	89.96 (0.66)	125.00 (0.93)		-0.0004 (0.1341)	-0.0206 (0.0515)	0.0046 (0.0826)	0.000003 (0.0038)		23.2
	155	205	3.1623	0.05	155.01 (0.51)	204.99 (0.16)		-0.0231 (0.4475)	3.2707 (0.6015)	0.0204 (0.5946)	-0.0071 (0.8541)	88.5	155.04 (0.42)	205.19 (1.39)		0.0035 (0.1143)	-0.0148 (0.0487)	-0.0047 (0.0738)	-0.0002 (0.0036)		13.9
	180	235	5.4772	0.15	180.02 (0.49)	235.01 (0.34)		-0.0049 (0.4535)	5.4358 (0.7158)	0.0136 (0.6194)	0.0151 (0.8421)	100.0	179.99 (0.67)	235.04 (0.68)		0.0066 (0.1472)	-0.0228 (0.0529)	-0.0041 (0.0808)	0.0001 (0.0039)		33.4

<i>da</i>	40	275	4.4721	0.10	40.00 (0.01)	275.00 (0.07)	-0.0032 (0.4406)	4.4584 (0.6939)	-0.0228 (0.6141)	-0.0270 (0.8724)	99.9	40.02 (0.89)	274.93 (0.72)	0.0079 (0.1253)	-0.0188 (0.0447)	0.0028 (0.0858)	-0.00002 (0.0039)	22.0
	75	220	5.4772	0.15	75.00 (0.09)	220.02 (0.55)	0.0222 (0.4497)	5.4846 (0.7634)	-0.0172 (0.5926)	0.0378 (0.8372)	100.0	74.92 (0.88)	220.04 (1.00)	0.0132 (0.1464)	-0.0183 (0.0493)	0.0076 (0.0816)	-0.0002 (0.0040)	31.7
	20	60	3.1623	0.05	19.96 (1.21)	59.86 (3.92)	-0.0052 (0.4819)	-0.0184 (0.6150)	3.2686 (0.6652)	-0.0221 (0.8392)	85.8	20.37 (2.84)	60.17 (4.39)	-0.0032 (0.1105)	0.0085 (0.0806)	-0.0102 (0.0468)	0.0002 (0.0038)	11.9
	90	125	4.4721	0.10	90.00 (0.00)	124.91 (2.24)	0.0067 (0.4562)	0.0101 (0.5995)	4.4312 (0.7386)	-0.0007 (0.8136)	99.7	90.31 (8.57)	124.98 (0.57)	0.0078 (0.1247)	-0.0056 (0.0788)	-0.0171 (0.0500)	0.0002 (0.0037)	23.5
	155	205	3.1623	0.05	155.02 (0.27)	204.99 (0.58)	-0.0089 (0.4576)	-0.0047 (0.6128)	3.2314 (0.6205)	-0.0059 (0.8847)	85.4	155.04 (0.46)	204.83 (1.71)	-0.0022 (0.1108)	-0.0143 (0.0734)	-0.0103 (0.0462)	0.0004 (0.0037)	11.8
	180	235	5.4772	0.15	179.98 (0.53)	234.88 (3.83)	-0.0067 (0.4559)	0.0055 (0.6162)	5.4453 (0.8243)	0.0495 (0.8552)	100.0	180.13 (2.16)	235.01 (0.90)	0.0116 (0.1422)	-0.0053 (0.0796)	-0.0195 (0.0503)	0.0002 (0.0037)	34.1
	40	275	4.4721	0.10	39.99 (1.29)	275.00 (0.34)	-0.0069 (0.4541)	0.0197 (0.6136)	4.4347 (0.7244)	0.0110 (0.8279)	99.8	39.96 (0.64)	275.06 (0.84)	0.0001 (0.1260)	-0.0021 (0.0724)	-0.0215 (0.0474)	0.000008 (0.0037)	24.7
	75	220	5.4772	0.15	75.00 (0.32)	220.01 (0.34)	0.0081 (0.4607)	0.0098 (0.6022)	5.4277 (0.8416)	0.0388 (0.8625)	100.0	74.96 (0.82)	220.02 (0.33)	0.0006 (0.1464)	0.0033 (0.0801)	-0.0168 (0.0473)	0.0003 (0.0040)	31.8
	20	60	4.4721	0.05	19.98 (0.41)	59.99 (0.34)	0.0110 (0.4179)	0.0095 (0.5991)	-0.0073 (0.5998)	4.5834 (0.8441)	86.0	19.92 (0.75)	59.94 (1.65)	0.0035 (0.1271)	-0.0006 (0.0438)	-0.0018 (0.0482)	-0.0077 (0.0046)	26.5
	90	125	6.3246	0.10	89.98 (1.26)	124.99 (0.32)	0.0100 (0.4351)	0.0102 (0.6171)	-0.0082 (0.5954)	6.2686 (0.9940)	99.8	90.00 (0.59)	124.98 (0.60)	-0.0023 (0.1512)	0.0026 (0.0500)	-0.0006 (0.0470)	-0.0072 (0.0045)	42.5
<i>dd</i>	155	205	4.4721	0.05	155.04 (1.18)	205.00 (0.04)	-0.0088 (0.4223)	-0.0012 (0.6051)	-0.0051 (0.5773)	4.6106 (0.8283)	88.2	155.00 (0.86)	205.07 (1.97)	-0.0075 (0.1277)	-0.0005 (0.0482)	-0.0002 (0.0478)	-0.0079 (0.0048)	27.4
	180	235	7.7460	0.15	180.00 (0.10)	235.01 (0.36)	-0.0029 (0.4341)	-0.0017 (0.6236)	0.0198 (0.6123)	7.6976 (1.0334)	100.0	180.00 (0.09)	235.00 (0.33)	0.0130 (0.1705)	0.00001 (0.0472)	0.0022 (0.0465)	-0.0076 (0.0047)	47.3
	40	275	6.3246	0.10	40.01 (0.25)	274.99 (0.23)	0.00002 (0.4429)	0.0342 (0.6207)	-0.0021 (0.6138)	6.3201 (0.9553)	99.6	40.01 (0.94)	275.04 (0.55)	-0.0088 (0.1520)	0.0015 (0.0468)	-0.0057 (0.0464)	-0.0074 (0.0044)	42.3
	75	220	7.7460	0.15	75.00 (0.15)	220.00 (0.13)	0.0090 (0.4405)	-0.0296 (0.6035)	0.0148 (0.6101)	7.6949 (1.0650)	100.0	75.03 (0.50)	219.92 (1.13)	0.0058 (0.1679)	-0.0004 (0.0486)	0.0021 (0.0487)	-0.0073 (0.0048)	48.2

Table S3 | Comparisons of trait phenotype, general combining ability (GCA), specific combining ability (SCA) and mid-parental heterosis (MPH) in the genetic dissection of heterosis under partial-, complete-, and over-dominance models using Monte Carlo simulation experiments

QTL1		$d=0.5a$				$d=a$				$d=2a$			
		Posi (cM)	a	d	r^2	Posi (cM)	a	d	r^2	Posi (cM)	a	d	r^2
True value		25	1.4907	0.7454	0.05	25	1.2910	1.2910	0.05	25	0.9129	1.8257	0.05
Trait phenotype	Estimate	24.99	1.5632	0.6934		25.02	1.0888	1.0545		25.09	0.7256	1.7099	
	SD	0.18	0.4009	0.4647		0.49	1.0466	0.8710		0.99	0.9099	0.8784	
	Power(%)	66.3				43.2				50.5			
GCA	Estimate	25.00	0.7298	-0.0024		24.99	0.6350	-0.0029		25.00	0.4496	-0.0051	
	SD	0.00	0.0543	0.0323		0.09	0.0662	0.0271		0.00	0.0633	0.0200	
	Power (%)	100.0				100.0				100.0			
SCA	Estimate	24.52	0.0051	1.6513		25.27	0.0676	1.7220		24.99	0.0232	1.9997	
	SD	2.18	0.3768	0.3858		1.55	0.3031	0.6905		0.11	0.3094	0.4000	
	Power (%)	2.1				9.2				54.9			
Mid-parent heterosis	Estimate	25.38	-0.0511	1.4640		25.18	-0.1152	2.2374		24.94	-0.0547	2.4434	
	SD	3.20	1.1177	1.1086		1.44	0.4359	0.5727		1.04	0.4413	0.7005	
	Power (%)	1.3				4.9				21.2			
QTL2		Posi (cM)	a	d	r^2	Posi (cM)	a	d	r^2	Posi (cM)	a	d	r^2
True value		75	2.1082	1.0541	0.10	75	1.8257	1.8257	0.10	75	1.2910	2.5820	0.10
Trait phenotype	Estimate	75.00	2.0283	0.9304		74.96	1.3947	1.2668		75.01	0.7923	1.9952	
	SD	0.14	0.4816	0.4264		0.53	0.7438	0.6092		0.53	0.6763	0.9143	
	Power (%)	95.7				79.3				81.3			

GCA	Estimate	75.00	1.0329	-0.0024			75.00	0.8958	-0.0029			75.00	0.6359	-0.0051	
	SD	0.00	0.0774	0.0323			0.01	0.0844	0.0271			0.00	0.0884	0.0200	
	Power (%)	100.0					100.0					100.0			
SCA	Estimate	74.67	-0.0769	1.7465			75.04	-0.0010	2.0765			75.00	-0.0014	2.5790	
	SD	2.18	0.3788	0.3864			0.56	0.3084	0.4083			0.12	0.3184	0.4594	
	Power (%)	7.5					45.5					92.2			
Mid-parent heterosis	Estimate	74.47	-0.0743	1.9853			75.00	-0.0477	2.6145			75.00	-0.0779	3.0142	
	SD	2.26	0.5779	0.7917			0.00	0.4120	0.4394			0.10	0.4195	0.5689	
	Power (%)	3.8					22.1					63.4			
QTL3		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²
True value		135	1.4907	0.7454	0.05		135	1.2910	1.2910	0.05		135	0.9129	1.8257	0.05
Trait phenotype	Estimate	134.99	1.5813	0.6895			134.86	1.2246	1.0287			135.01	1.2290	1.8104	
	SD	0.12	0.4825	0.4773			1.19	1.0158	0.7531			0.56	0.8942	0.8360	
	Power (%)	64.9					44.8					45.1			
GCA	Estimate	135.00	0.7280	-0.0024			135.00	0.6306	-0.0029			135.00	0.4464	-0.0051	
	SD	0.00	0.0593	0.0323			0.00	0.0613	0.0271			0.00	0.0660	0.0200	
	Power (%)	100.0					100.0					100.0			
SCA	Estimate	135.00	0.4503	1.4810			135.08	0.0708	1.7970			135.01	0.0115	2.0433	
	SD	1.25	0.2604	0.4830			0.91	0.2916	0.5485			0.14	0.2931	0.3655	
	Power (%)	1.6					12.1					53.8			
Mid-parent heterosis	Estimate	136.82	-0.0433	1.7546			134.78	0.0125	2.4241			135.04	-0.0497	2.5849	
	SD	4.05	0.8944	1.0154			1.49	0.4098	0.4072			0.65	0.4336	0.5117	

	Power (%)	0.9					4.5					23.7			
QTL4		Posi (cM)	<i>a</i>	<i>d</i>	r^2		Posi (cM)	<i>a</i>	<i>d</i>	r^2		Posi (cM)	<i>a</i>	<i>d</i>	r^2
True value		175	2.5820	1.2910	0.15		175	2.2361	2.2361	0.15		175	1.5811	3.1623	0.15
Trait phenotype	Estimate	175.01	2.4041	1.0861			174.97	1.5055	1.4016			174.99	0.9701	2.1122	
	SD	0.17	05864	0.4060			1.40	0.7792	0.5759			0.50	0.5598	0.9275	
	Power (%)	99.4					92.2					95.7			
GCA	Estimate	175.00	1.2647	-0.0024			175.00	1.0934	-0.0029			175.00	0.7772	-0.0051	
	SD	0.00	0.0964	0.0323			0.02	0.1078	0.0271			0.00	0.1138	0.0200	
	Power (%)	100.0					100.0					100.0			
SCA	Estimate	175.00	-0.0170	1.8211			175.01	0.0219	2.3449			175.00	-0.0012	3.0905	
	SD	0.00	0.2900	0.2623			0.35	0.3328	0.4185			0.06	0.3449	0.5100	
	Power (%)	19.1					75.0					99.6			
Mid-parent heterosis	Estimate	174.87	-0.0386	2.1653			174.96	-0.0923	2.7376			175.00	-0.1102	3.4635	
	SD	0.80	0.4319	0.6966			0.74	0.4425	0.5311			0.17	0.4366	0.6505	
	Power (%)	7.7					50.0					88.3			
QTL5		Posi (cM)	<i>a</i>	<i>d</i>	r^2		Posi (cM)	<i>a</i>	<i>d</i>	r^2		Posi (cM)	<i>a</i>	<i>d</i>	r^2
True value		220	2.1082	1.0541	0.10		220	1.8257	1.8257	0.10		220	1.2910	2.5820	0.10
Trait phenotype	Estimate	219.87	2.0419	0.9348			219.70	1.3928	1.2705			220.00	0.8752	1.9730	
	SD	4.08	0.4727	0.4276			8.42	0.7582	0.5952			0.54	0.6397	0.9100	
	Power (%)	94.6					77.5					81.2			
GCA	Estimate	220.00	1.0317	-0.0024			220.00	0.8957	-0.0029			220.00	0.6337	-0.0051	
	SD	0.00	0.0801	0.0323			0.01	0.0787	0.0271			0.00	0.0902	0.0200	

	Power (%)	100.0					100.0					100.0			
SCA	Estimate	219.94	0.0414	1.7468			219.98	0.0143	2.1208			220.00	0.0122	2.5688	
	SD	1.21	0.3352	0.3899			0.28	0.3186	0.4026			0.00	0.3320	0.4536	
	Power (%)	8.6					43.4					91.8			
Mid-parent heterosis	Estimate	220.19	-0.0678	2.1797			220.03	-0.0569	2.5631			219.99	-0.0748	3.0314	
	SD	0.96	0.4954	0.3541			0.34	0.4653	0.5135			0.10	0.4218	0.5809	
	Power (%)	2.7					23.9					61.0			
QTL6		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²		Posi (cM)	<i>a</i>	<i>d</i>	<i>r</i> ²
True value		270	2.5820	1.2910	0.15		270	2.2361	2.2361	0.15		270	1.5811	3.1623	0.15
Trait phenotype	Estimate	270.00	2.3977	1.0645			269.92	1.4552	1.3944			269.98	0.9576	2.0999	
	SD	0.07	0.5897	0.4134			2.60	0.7785	0.5948			0.43	0.5729	0.9317	
	Power (%)	99.4					92.9					94.4			
GCA	Estimate	270.00	1.2662	-0.0024			270.00	1.0934	-0.0029			270.00	0.7725	-0.0051	
	SD	0.00	0.0975	0.0323			0.03	0.1053	0.0271			0.00	0.1106	0.0200	
	Power (%)	100.0					100.0					100.0			
SCA	Estimate	270.03	0.0325	1.8047			270.02	-0.0141	2.3334			270.00	0.0116	3.0958	
	SD	0.65	0.2968	0.4344			0.37	0.3271	0.4449			0.00	0.3432	0.5159	
	Power (%)	17.7					76.6					98.2			
Mid-parent heterosis	Estimate	269.87	-0.0325	2.2862			270.00	-0.0935	2.7613			270.00	-0.1000	3.4680	
	SD	1.13	0.4408	0.3967			0.67	0.4291	0.5139			0.00	0.4362	0.6241	
	Power (%)	7.8					47.7					88.5			

Table S4 | Genetic basis of heterosis from 2,160,000 simulated F₁ individuals

QTL	Heterosis			r^2	Power of QTL detection from phenotypic observation					
	Absolute of Mean (SD)	95% Confidence interval	CV		a	d	$a \times a$	$a \times d$	$d \times a$	$d \times d$
Additive (a)	0.0772 (0.2785)	-7.5097~7.9917	72.47	0.05	85.0					
				0.10	99.5					
				0.05	85.7					
				0.15	99.8					
				0.10	99.4					
Dominance (d)	10.28621 (0.4402)	-1.7238~22.6488	0.60	0.15	100.0					
				0.05	87.2					
				0.10	99.9					
				0.05	86.6					
				0.10	99.9					
$a \times a$	0.1851 (0.4317)	-10.1961~11.8511	-2.32	0.15	100.0					
				0.05	85.4					
				0.10	99.4					
				0.05	85.2					
				0.10	99.1					
$a \times d$	0.2008 (0.5303)	-12.7127~14.3138	-8.03	0.15	99.9					
				0.05	100.0					
				0.10	99.9					
				0.15	100.0					
				0.05	86.1					
$d \times a$	0.1689 (0.5141)	-12.7198~14.2701	-3.78	0.10	99.8					
				0.05	88.5					
				0.15	100.0					
				0.10	99.9					
				0.15	100.0					
$d \times d$	8.4467 (0.3425)	-18.1604~1.4647	-0.59	0.05					85.8	
				0.10					99.7	
				0.05					85.4	
				0.15					100.0	
				0.10					99.8	
$d=0.5a$	3.2542 (0.3184)	-5.0630~11.9028	1.3203	0.15					100.0	
				0.05					86.0	
				0.10					99.8	
				0.05					88.2	
				0.15					100.0	
$d=2a$	8.2501 (0.3945)	-2.4574~19.3589	0.6670	0.15	66.3	66.3				
				0.10	95.7	95.7				
				0.05	64.9	64.9				
				0.15	99.4	99.4				
				0.10	94.6	94.6				
$d=a$	5.7222 (0.3474)	-3.6537~15.4374	0.8410	0.15	99.4	99.4				
				0.05	50.5	50.5				
				0.10	81.3	81.3				
				0.05	45.1	45.1				
				0.15	95.7	95.7				
$d=0.5a$	3.2542 (0.3184)	-5.0630~11.9028	1.3203	0.10	81.2	81.2				
				0.15	94.4	94.4				
				0.05	43.2	43.2				
				0.10	79.3	79.3				
				0.05	44.8	44.8				
$d=2a$	8.2501 (0.3945)	-2.4574~19.3589	0.6670	0.15	92.2	92.2				
				0.10	77.5	77.5				
				0.05	43.2	43.2				
				0.10	79.3	79.3				
				0.15	92.9	92.9				

Table S5 | Comparison of trait phenotype and mid-parental heterosis (MPH) under additive, dominance, *aa*, *ad*, *da*, and *dd* effects in F₂

QTL	Type	True value				Estimates from trait phenotype				Estimates from MPH			
		Posi. (cM)		Effect	r^2	Posi. (cM)		Effect	Power (%)	Posi. (cM)		Effect	Power (%)
1	Additive (<i>a</i>)	70		0.7071	0.10	70.10 (2.11)		0.7048 (0.0969)	83.9	70.09 (2.09)		0.6976 (0.0962)	83.9
2	Dominance (<i>d</i>)	145		1.000	0.10	144.96 (1.02)		0.9911 (0.1367)	100.0	144.97 (0.99)		0.9818 (0.1357)	100.0
3	<i>a</i> × <i>a</i>	35	285	1.000	0.10	34.93 (2.57)	284.98 (2.33)	0.9818 (0.1418)	97.0	34.93 (2.57)	284.98 (2.34)	0.9730 (0.1392)	96.9
4	<i>a</i> × <i>d</i>	95	170	1.4142	0.10	94.60 (1.69)	169.98 (1.23)	1.3981 (0.1977)	99.5	94.60 (1.69)	169.98 (1.20)	1.3834 (0.1966)	99.5
5	<i>d</i> × <i>a</i>	120	235	1.4142	0.10	120.00 (1.74)	235.00 (2.30)	1.3935 (0.1893)	99.0	120.00 (1.74)	235.00 (2.30)	1.3800 (0.1874)	98.9
6	<i>d</i> × <i>d</i>	195	255	2.000	0.10	194.93 (0.63)	254.98 (1.08)	1.9738 (0.2676)	99.7	194.93 (0.63)	254.98 (1.07)	1.9538 (0.1712)	99.7

*The sample size was equal to 300.

Table S6 | The true and estimated values for QTL parameters using real molecular marker dataset and the 0.01 significance level

QTL	QTL Type	True value					Estimate																	
							Trait phenotype						GCA											
		Marker	Posi (cM)	Effect	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)				
QTL1		A4-1	D2-1	18.34	23.60	0.40	18.34 (0.00)	23.60 (0.00)			-0.0199 (0.1193)	0.3395 (0.2209)	-0.0241 (0.2021)	-0.0573 (0.3857)	100.0	18.34 (0.00)	23.60 (0.00)			-0.0449 (0.0129)	-0.0102 (0.0130)	-0.0018 (0.0118)	0.0172 (0.0052)	8.5
	<i>ad</i>																							
QTL2		A5-1	A5-2	26.14	95.80	0.44	26.14 (0.00)	95.80 (0.00)			-0.0190 (0.1205)	0.3736 (0.2299)	-0.0245 (0.2093)	-0.0605 (0.4003)	99.9	26.14 (0.00)	95.80 (90.00)			-0.0460 (0.0147)	-0.0097 (0.0103)	-0.0008 (0.0094)	0.0167 (0.0053)	22.5
QTL	QTL Type	True value					SCA						MPH											
							Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)		
		Marker	Posi (cM)	Effect	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)	Posi (cM)	<i>a</i>	<i>d</i>	<i>aa</i>	<i>ad</i>	<i>da</i>	<i>dd</i>	Power (%)				
QTL1															18.34	4.1655 (0.9544)	-2.4131 (1.4016)							6.9
	False QTL																							
QTL2															26.14	4.4357 (0.8507)	-2.6822 (1.5639)							8.2
	<i>ad</i>																							
QTL1		A4-1	D2-1	18.34	23.60	0.40	18.34 (0.00)	23.60 (0.00)			0.2670 (0.1612)	0.1095 (0.0758)	0.0912 (0.0746)	-0.5172 (0.2113)	66.5	18.34 (0.00)	23.60 (0.00)			-0.5443 (2.4514)	5.6387 (2.2560)	-0.6636 (2.3172)	-3.5870 (3.4101)	57.8
QTL2		A5-1	A5-2	26.14	95.80	0.44	26.14 (0.00)	95.80 (0.00)			0.2897 (0.1681)	0.1175 (0.0749)	0.0965 (0.0736)	-0.5522 (0.2197)	74.0	26.14 (0.00)	95.80 (0.00)			-0.6112 (2.3727)	5.9524 (2.3402)	-0.5894 (2.4100)	-3.9025 (3.4834)	60.6

The software GAS_NCII (Genetic Analysis System for NC II mating design):

The Windows software in this study was attached (To first install JAVA Runtime Environment (jdk-7u71-windows-x64.exe) by default install directory, and to then install Matlab Runtime Environment (R2014b (8.4) For Windows). The two files are too large. Readers may download the first file at <http://www.oracle.com/technetwork/java/javase/downloads/jdk7-downloads-1880260.html> and the second file at <http://cn.mathworks.com/products/compiler/mcr/index.html>, respectively). If the readers want to use another jdk version please change your jdk directory in run.bat file. The above two files are also downloaded from <http://yun.baidu.com/share/link?shareid=2858238674&uk=3276116826>. EMS memory size in the running computer is more than 8 G. By running "run.dat" file, prior parameters a and b need to be determined by cross-validation experiments. Thus, our suggestion is to run the software several times and select the best results.

Maternal	Paternal									
	F ₁	F ₂	F ₃	F ₄	F ₅	F ₆	F ₇₉	F ₈₀
M ₁	*									
M ₂		*								
M ₃			*							
M ₄				*						
M ₅					*					
...						*				
...							...			
...								*		
M ₇₉									*	
M ₈₀										*

I

Maternal	Paternal									
	F ₁	F ₂	F ₃	F ₄	F ₅	F ₆	F ₃₃	F ₃₄
M ₁	*	*	*	*	*					
M ₂		*	*	*	*	*				
M ₃			*	*	*	*	*			
M ₄				*	*	*	*	*		
M ₅					*	*	*	*	*	
...						*	...			
...							...			
...							*	*	*	*
M ₃₃									...	
M ₃₄							*	*	*	*

III

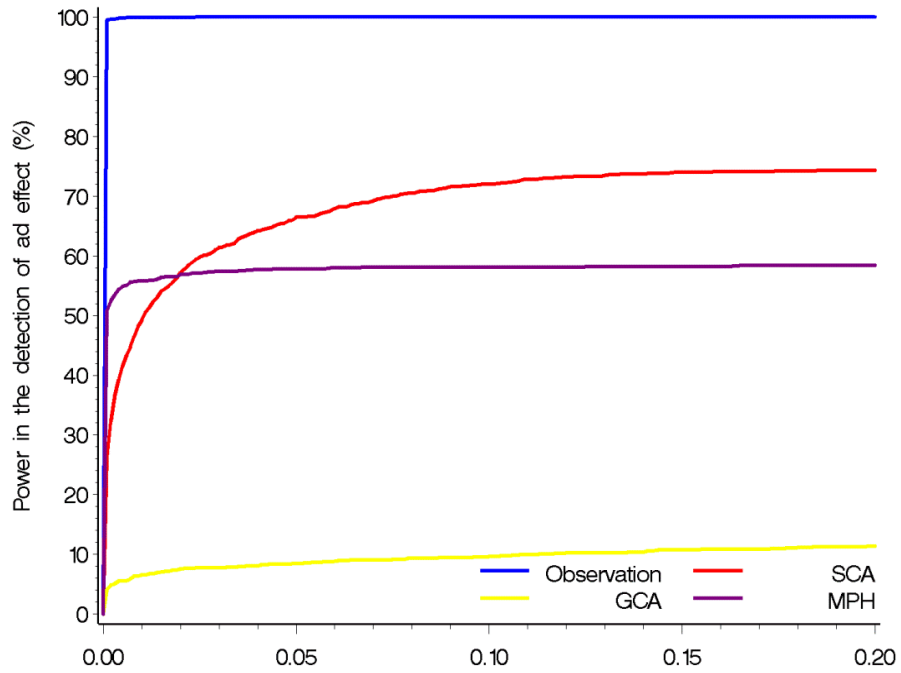
Maternal	Paternal									
	F ₁	F ₂	F ₃	F ₄	F ₅	F ₆	F ₄₇	F ₄₈
M ₁	*	*	*							
M ₂		*	*	*						
M ₃			*	*	*					
M ₄				*	*	*				
M ₅					*	*	*			
...						*	...			
...							...			
...								*	*	*
M ₄₇								*	*	*
M ₄₈								*	*	*

II

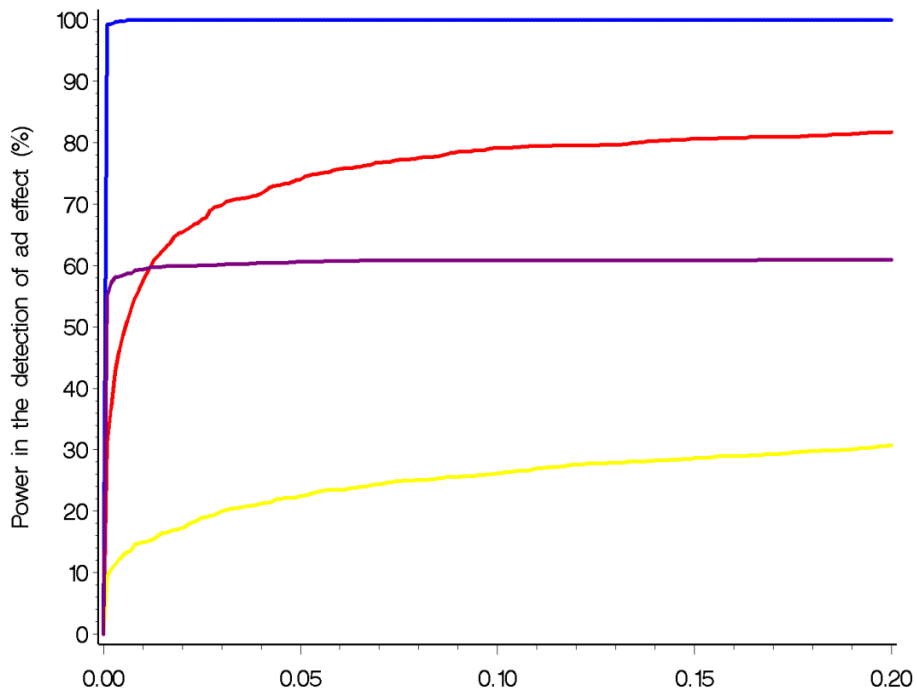
Maternal	Paternal									
	F ₁	F ₂	F ₃	F ₄	F ₅	F ₆	F ₇	F ₈	...	F ₁₅
M ₁	*	*	*	*	*	*	*	*	*	*
M ₂	*	*	*	*	*	*	*	*	*	*
M ₃	*	*	*	*	*	*	*	*	*	*
M ₄	*	*	*	*	*	*	*	*	*	*
M ₅	*	*	*	*	*	*	*	*	*	*
M ₆	*	*	*	*	*	*	*	*	*	*
M ₇	*	*	*	*	*	*	*	*	*	*
M ₈	*	*	*	*	*	*	*	*	*	*
...	*	*	*	*	*	*	*	*	*	*
M ₁₅	*	*	*	*	*	*	*	*	*	*

IV

Figure S1 | Mating strategies in NCII genetic mating design. In the NCII mating design, each maternal line was crossed with one (I), two, three (II), four, five (III), six, seven, and fifteen (IV) paternal lines.



A



B

Figure S2 | Statistical power in the detection of QTL1 (A) and QTL2 (B) under different false discovery rates for various phenotypic measures (trait phenotype(observation), GCA, SCA and MPH). The true and estimated values for simulated QTL are listed in Table S6.