Supplementary Table 1. Power of MDR to detect any correct model loci in the presence of locus heterogeneity with 250 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	24	98	98	100	32	35	66	95	100
	2	26	**NA**	98	93	98	45	31	67	98	99
	3	21	21	**NA**	96	99	40	36	64	98	97
	4	18	24	98	**NA**	100	31	35	60	95	98
0.1	**5**	22	20	99	94	**NA**	34	38	69	94	99
	8	33	33	100	96	99	**NA**	36	66	94	96
	9	33	30	98	96	99	50	**NA**	79	93	99
	10	56	46	99	94	98	51	47	**NA**	93	96
	11	65	58	99	96	96	64	61	76	**NA**	98
	12	32	41	98	96	98	37	51	66	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	16	96	70	98	28	33	54	79	91
	2	20	**NA**	98	84	96	31	31	57	84	92
	3	19	23	**NA**	80	99	32	27	57	91	89
	4	22	27	98	**NA**	100	36	43	59	83	92
0.25	**5**	28	18	100	82	**NA**	36	47	59	81	94
	8	26	27	96	89	98	**NA**	36	69	83	94
	9	32	33	99	79	100	45	**NA**	58	79	93
	10	52	49	95	88	97	48	42	**NA**	85	94
	11	65	48	97	76	100	52	55	52	**NA**	92
	12	38	37	98	83	100	49	45	45	77	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	16	**NA**								
	3	73	67	**NA**							
	4	47	48	70	**NA**						
	5	59	69	78	73	**NA**					
0.5	**8**	31	23	74	52	80	**NA**				
	9	29	36	69	50	79	45	**NA**			
	10	45	44	87	56	73	53	56	**NA**		
	11	60	52	80	70	78	55	53	53	**NA**	
	12	74	65	84	70	79	63	72	54	68	**NA**

Supplementary Table 2. Power of MDR to detect either correct model in the presence of locus heterogeneity with 250 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	97	98	100	1	6	59	92	98
	2	1	**NA**	98	88	98	6	3	59	97	98
	3	1	0	**NA**	95	99	5	8	56	95	96
	4	1	1	98	**NA**	100	4	3	53	93	98
0.1	**5**	0	2	98	94	**NA**	6	8	61	92	99
	8	3	3	99	94	99	**NA**	4	48	94	95
	9	3	2	98	94	99	5	**NA**	55	92	98
	10	2	7	99	92	98	7	7	**NA**	92	96
	11	4	3	99	95	96	3	4	49	**NA**	98
	12	3	3	98	93	97	7	18	55	96	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	96	68	97	1	5	37	75	87
	2	0	**NA**	98	74	95	3	6	36	78	88
	3	2	5	**NA**	76	97	12	8	41	86	86
	4	1	2	98	**NA**	100	3	2	42	79	86
0.25	**5**	3	4	99	79	**NA**	7	14	45	77	92
	8	2	2	96	86	98	**NA**	1	46	78	92
	9	1	3	99	72	98	3	**NA**	33	71	92
	10	4	4	94	79	97	2	7	**NA**	75	90
	11	9	5	95	66	98	8	13	23	**NA**	90
	12	11	8	98	75	100	11	13	36	71	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	1	**NA**								
	3	60	59	**NA**							
	4	33	25	64	**NA**						
0.5	**5**	48	58	73	68	**NA**					
	8	4	2	69	24	70	**NA**				
	9	1	4	56	29	64	11	**NA**			
	10	12	14	68	32	62	16	15	**NA**		
	11	38	31	67	57	70	27	29	29	**NA**	
	12	60	49	80	59	71	47	49	39	52	**NA**

Supplementary Table 3. Power of MDR to detect both models in the presence of locus heterogeneity with 250 cases and controls.

Proportion of data **0.9**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	1	1	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data **0.75**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	1	1	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data **0.5**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	0	**NA**						
0.5	**5**	0	0	0	0	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	1	0	0	1	0	**NA**		
	11	0	0	0	0	1	0	0	0	**NA**	
	12	0	0	1	0	0	0	0	1	0	**NA**

Supplementary Table 4. Power of MDR to detect any correct model locus in the presence of locus heterogeneity with 250 cases and 500 controls.

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	17	99	99	98	24	36	73	98	98
	2	11	**NA**	99	100	100	34	35	74	99	98
	3	15	13	**NA**	100	100	39	27	78	100	99
	4	14	27	99	**NA**	100	42	35	76	98	99
0.1	**5**	20	25	99	98	**NA**	34	37	75	97	97
	8	27	31	97	99	100	**NA**	30	71	98	98
	9	23	17	99	98	100	43	**NA**	75	97	99
	10	45	55	98	100	100	58	53	**NA**	97	97
	11	77	81	99	96	99	80	78	78	**NA**	99
	12	39	37	98	96	99	48	31	75	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	19	100	92	98	36	31	70	97	99
	2	13	**NA**	99	92	100	38	35	63	95	96
	3	22	17	**NA**	94	100	34	39	67	94	99
	4	31	18	100	**NA**	100	40	34	73	96	96
0.25	**5**	27	27	100	94	**NA**	39	44	60	92	97
	8	26	22	99	97	98	**NA**	41	72	94	98
	9	25	22	99	96	98	39	**NA**	74	96	99
	10	53	46	98	91	100	57	47	**NA**	96	98
	11	65	70	99	88	100	65	60	76	**NA**	99
	12	39	38	99	93	98	53	51	69	92	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	18	**NA**								
	3	77	87	**NA**							
	4	61	46	83	**NA**						
0.5	**5**	87	69	84	77	**NA**					
	8	29	31	83	61	89	**NA**				
	9	23	29	86	71	84	34	**NA**			
	10	49	42	93	65	88	49	58	**NA**		
	11	75	66	92	81	84	67	65	69	**NA**	
	12	79	79	87	76	88	82	82	78	75	**NA**

Supplementary Table 5. Power of MDR to detect either correct model in the presence of locus heterogeneity with 250 cases and 500 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	98	98	3	4	66	97	98
	2	0	**NA**	99	100	100	1	9	68	99	97
	3	0	2	**NA**	99	100	6	6	73	98	97
	4	0	3	99	**NA**	100	4	13	72	97	99
0.1	**5**	0	1	99	98	**NA**	2	12	73	97	97
	8	1	3	96	99	100	**NA**	5	68	98	98
	9	4	1	99	97	100	1	**NA**	67	97	98
	10	3	7	98	100	100	6	10	**NA**	97	96
	11	4	5	99	95	99	5	5	56	**NA**	99
	12	8	5	97	96	99	5	9	64	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	100	89	98	1	7	57	96	98
	2	0	**NA**	99	89	100	5	6	50	93	95
	3	6	6	**NA**	90	100	8	19	51	92	99
	4	8	4	100	**NA**	100	7	8	61	94	95
0.25	**5**	5	5	100	92	**NA**	14	14	49	92	96
	8	2	1	97	92	98	**NA**	6	50	94	97
	9	3	3	99	94	97	7	**NA**	55	92	99
	10	6	6	97	88	100	8	7	**NA**	90	97
	11	9	11	99	84	99	15	10	51	**NA**	99
	12	7	14	99	91	97	12	14	56	87	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	72	85	**NA**							
	4	45	34	81	**NA**						
0.5	**5**	79	60	81	76	**NA**					
	8	1	2	80	41	77	**NA**				
	9	3	2	76	46	77	3	**NA**			
	10	15	19	87	49	82	14	16	**NA**		
	11	54	46	88	69	80	50	50	48	**NA**	
	12	67	70	84	67	87	71	69	71	68	**NA**

Supplementary Table 6. Power of MDR to detect both models in the presence of locus heterogeneity with 250 cases and 500 controls.

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	2	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	1	**NA**	0	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	1	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	1	**NA**	0
	12	0	0	1	0	0	0	0	1	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	0	**NA**						
0.5	**5**	0	0	1	1	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	1	**NA**			
	10	0	0	0	1	0	0	0	**NA**		
	11	0	0	0	0	1	0	0	0	**NA**	
	12	0	0	1	0	1	0	1	0	0	**NA**

Supplementary Table 7. Power of MDR to detect any correct model locus in the presence of locus heterogeneity with 250 cases and 1000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	18	100	99	98	22	29	80	99	99
	2	12	**NA**	99	99	100	30	28	87	99	99
	3	17	10	**NA**	98	100	27	22	79	98	99
	4	21	9	100	**NA**	100	27	29	82	97	97
0.1	**5**	12	25	98	100	**NA**	32	30	81	98	100
	8	22	23	99	99	100	**NA**	39	81	100	98
	9	31	27	100	98	99	38	**NA**	88	95	97
	10	66	58	100	99	100	65	64	**NA**	97	98
	11	79	75	97	98	100	77	70	82	**NA**	100
	12	28	36	99	100	99	48	44	86	99	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	12	100	94	100	25	24	71	95	100
	2	11	**NA**	98	98	97	33	27	70	97	98
	3	20	20	**NA**	95	99	42	23	64	95	99
	4	30	23	99	**NA**	99	29	37	67	95	98
0.25	**5**	22	22	99	97	**NA**	38	42	74	96	99
	8	24	21	99	97	99	**NA**	20	75	98	97
	9	27	19	99	98	98	39	**NA**	76	98	100
	10	64	59	98	100	99	48	53	**NA**	96	100
	11	65	58	100	96	99	57	74	82	**NA**	98
	12	45	38	100	98	100	44	46	76	95	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	14	**NA**								
	3	80	84	**NA**							
	4	63	59	90	**NA**						
0.5	**5**	88	89	93	91	**NA**					
	8	21	19	80	69	94	**NA**				
	9	26	29	86	75	89	29	**NA**			
	10	45	47	94	71	89	51	56	**NA**		
	11	83	73	94	82	95	76	73	75	**NA**	
	12	80	83	93	84	92	85	91	87	85	**NA**

Supplementary Table 8. Power of MDR to detect either correct model in the presence of locus heterogeneity with 250 cases and 1000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	99	99	98	2	6	79	99	99
	2	0	**NA**	99	99	100	5	5	84	99	97
	3	0	1	**NA**	97	99	2	10	74	98	99
	4	1	2	99	**NA**	100	1	9	79	96	97
0.1	**5**	0	1	98	100	**NA**	5	9	79	98	99
	8	0	0	99	98	100	**NA**	4	79	100	98
	9	4	0	99	97	99	5	**NA**	77	95	96
	10	4	7	100	97	100	11	11	**NA**	97	97
	11	3	2	96	97	100	3	4	69	**NA**	99
	12	5	3	99	100	99	9	10	81	98	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	100	91	100	3	4	60	95	100
	2	0	**NA**	98	97	96	1	5	60	95	96
	3	6	7	**NA**	94	99	14	7	55	95	99
	4	9	1	99	**NA**	99	4	7	60	93	98
0.25	**5**	5	11	99	95	**NA**	13	18	64	91	99
	8	1	0	99	96	99	**NA**	3	61	96	97
	9	1	0	99	97	98	3	**NA**	58	98	100
	10	8	7	98	99	99	7	14	**NA**	95	100
	11	9	11	100	93	98	11	8	57	**NA**	98
	12	17	13	100	95	100	13	15	70	92	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	79	83	**NA**							
	4	54	54	87	**NA**						
0.5	**5**	85	83	91	87	**NA**					
	8	1	0	75	53	92	**NA**				
	9	1	2	82	60	82	1	**NA**			
	10	20	25	93	59	86	21	23	**NA**		
	11	66	58	91	73	88	62	58	60	**NA**	
	12	76	80	91	81	88	78	82	80	79	**NA**

Supplementary Table 9. Power of MDR to detect both models in the presence of locus heterogeneity with 250 cases and 1000 controls.

Proportion of data **0.9**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data **0.75**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	1	1
	4	0	0	0	**NA**	1	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	1
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	2	0	0	**NA**

Proportion of data **0.5**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	1	**NA**						
0.5	**5**	0	0	5	2	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	1	0	0	0	0	**NA**		
	11	0	0	1	1	0	0	0	1	**NA**	
	12	0	0	4	0	1	0	0	1	2	**NA**

Supplementary Table 10. Power of MDR to detect any correct model loci in the presence of locus heterogeneity with 500 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	13	97	99	100	30	19	89	99	99
	2	13	**NA**	99	100	100	24	21	90	98	98
	3	8	15	**NA**	100	100	24	29	84	97	98
	4	18	13	100	**NA**	100	33	34	86	99	100
0.1	**5**	14	12	97	98	**NA**	31	27	95	98	98
	8	18	24	99	100	98	**NA**	18	85	97	98
	9	20	29	99	100	100	36	**NA**	92	100	98
	10	70	65	100	98	100	71	73	**NA**	100	100
	11	92	89	97	100	99	88	88	89	**NA**	97
	12	33	28	99	99	99	46	50	92	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	12	100	100	99	20	30	79	97	100
	2	8	**NA**	98	98	97	14	18	79	99	99
	3	19	18	**NA**	99	100	30	23	74	98	99
	4	31	20	98	**NA**	95	32	25	82	99	98
0.25	**5**	35	24	99	100	**NA**	38	42	76	98	99
	8	20	27	99	99	100	**NA**	23	82	93	100
	9	22	22	99	98	100	33	**NA**	88	97	99
	10	66	60	99	99	99	44	62	**NA**	98	97
	11	79	79	100	100	100	79	82	88	**NA**	98
	12	53	47	98	97	100	43	43	84	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	16	**NA**								
	3	83	90	**NA**							
	4	68	73	96	**NA**						
0.5	**5**	89	97	94	96	**NA**					
	8	23	20	93	68	90	**NA**				
	9	20	19	91	77	93	29	**NA**			
	10	57	62	95	87	92	61	59	**NA**		
	11	78	78	97	87	95	77	77	77	**NA**	
	12	95	93	92	92	91	92	93	90	93	**NA**

Supplementary Table 11. Power of MDR to detect either model in the presence of locus heterogeneity with 500 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	95	99	99	3	6	87	99	99
	2	0	**NA**	97	100	100	0	3	87	97	98
	3	0	1	**NA**	100	100	1	8	80	97	98
	4	1	1	100	**NA**	100	6	14	85	97	100
0.1	**5**	1	3	97	98	**NA**	4	8	93	98	96
	8	2	3	99	100	98	**NA**	3	85	96	98
	9	2	0	99	99	99	3	**NA**	89	100	98
	10	2	3	100	98	100	5	11	**NA**	99	100
	11	6	2	96	100	99	4	5	70	**NA**	97
	12	5	4	98	99	98	6	18	89	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	100	99	1	7	78	96	100
	2	0	**NA**	97	96	97	0	1	76	99	99
	3	8	6	**NA**	99	100	9	14	70	96	98
	4	7	7	98	**NA**	94	7	8	79	99	97
0.25	**5**	14	12	99	100	**NA**	19	17	69	98	99
	8	1	1	99	99	99	**NA**	4	72	93	99
	9	3	1	98	97	100	0	**NA**	69	96	99
	10	11	7	99	99	99	5	10	**NA**	94	96
	11	12	12	100	100	99	13	15	64	**NA**	98
	12	26	22	98	97	100	18	18	78	99	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	80	89	**NA**							
	4	67	63	95	**NA**						
0.5	**5**	87	95	94	95	**NA**					
	8	2	1	92	54	89	**NA**				
	9	4	0	89	70	88	1	**NA**			
	10	36	32	94	83	90	29	33	**NA**		
	11	74	70	94	83	95	60	71	61	**NA**	
	12	93	92	91	90	87	86	89	87	90	**NA**

Supplementary Table 12. Power of MDR to detect both models in the presence of locus heterogeneity with 500 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	1	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	1	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	1	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	1	**NA**	0
	12	0	0	1	0	2	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	1	**NA**						
0.5	**5**	0	0	7	7	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	1	0	0	0	0	**NA**		
	11	0	0	0	1	3	1	0	3	**NA**	
	12	0	0	10	3	4	0	1	1	5	**NA**

Supplementary Table 13. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 500 cases and 1000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	9	98	99	100	19	17	92	99	96
	2	3	**NA**	100	100	100	20	18	94	98	99
	3	12	9	**NA**	100	100	13	12	90	98	98
	4	10	6	99	**NA**	100	23	23	89	97	99
0.1	**5**	10	11	100	100	**NA**	28	21	95	100	98
	8	10	18	100	99	100	**NA**	18	98	99	99
	9	11	17	98	100	99	24	**NA**	93	99	99
	10	81	80	98	100	98	67	72	**NA**	99	100
	11	94	93	100	100	100	92	95	94	**NA**	99
	12	37	29	98	100	99	32	46	96	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	10	97	99	100	17	11	87	100	100
	2	4	**NA**	100	100	100	15	12	86	99	97
	3	15	16	**NA**	100	99	22	27	83	99	99
	4	22	19	99	**NA**	100	43	34	81	99	99
0.25	**5**	24	25	100	100	**NA**	45	43	82	98	98
	8	10	12	100	100	100	**NA**	20	84	98	100
	9	10	10	98	99	98	21	**NA**	90	100	98
	10	64	61	99	99	99	55	67	**NA**	99	100
	11	90	89	99	100	100	84	89	87	**NA**	100
	12	46	41	100	100	100	43	59	85	98	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	4	**NA**								
	3	93	96	**NA**							
	4	85	83	93	**NA**						
0.5	**5**	98	99	92	96	**NA**					
	8	13	19	99	85	99	**NA**				
	9	10	16	94	90	99	11	**NA**			
	10	62	64	99	91	99	72	58	**NA**		
	11	88	91	99	87	97	93	96	88	**NA**	
	12	96	99	95	91	95	97	97	92	94	**NA**

Supplementary Table 14. Power of MDR to detect either model in the presence of genetic heterogeneity with 500 cases and 1000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	97	99	100	1	13	92	98	96
	2	0	**NA**	99	98	100	3	6	94	98	98
	3	0	0	**NA**	100	100	3	5	89	98	98
	4	0	1	99	**NA**	100	3	7	87	97	98
0.1	**5**	0	3	99	100	**NA**	2	13	93	100	98
	8	0	0	100	99	100	**NA**	2	97	98	99
	9	0	1	97	100	99	1	**NA**	90	99	99
	10	2	4	98	100	98	2	14	**NA**	97	100
	11	1	0	100	100	100	4	5	82	**NA**	98
	12	2	2	97	100	99	7	19	94	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	97	99	100	0	4	84	100	100
	2	0	**NA**	100	100	100	2	3	85	98	96
	3	11	11	**NA**	100	99	13	16	83	98	98
	4	5	6	99	**NA**	100	20	9	78	98	98
0.25	**5**	18	17	99	99	**NA**	25	26	79	98	98
	8	1	0	100	100	100	**NA**	6	79	98	100
	9	0	0	98	99	98	2	**NA**	82	100	97
	10	7	10	98	99	99	7	15	**NA**	99	99
	11	17	17	99	99	100	14	15	65	**NA**	100
	12	29	26	100	100	100	17	30	80	98	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	90	95	**NA**							
	4	83	79	93	**NA**						
0.5	**5**	98	99	91	96	**NA**					
	8	0	0	97	77	98	**NA**				
	9	1	1	93	83	99	0	**NA**			
	10	45	44	97	88	98	46	41	**NA**		
	11	85	87	96	83	97	84	94	83	**NA**	
	12	95	99	93	88	92	95	96	89	91	**NA**

Supplementary Table 15. Power of MDR to detect both models in the presence of locus heterogeneity with 500 cases and 1000 controls

Proportion of data **0.9**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data **0.75**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	3	0	0	0	0	0	0
	4	0	0	0	**NA**	1	0	0	0	0	0
0.25	**5**	0	0	1	0	**NA**	0	0	0	1	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	1	1	4	0	1	4	0	**NA**

Proportion of data **0.5**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	4	**NA**						
0.5	**5**	0	0	22	11	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	2	0	2	0	0	**NA**		
	11	0	0	6	1	6	0	0	0	**NA**	
	12	0	0	22	6	17	0	0	1	15	**NA**

Supplementary Table 16. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 500 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	2	99	100	99	15	13	93	100	98
	2	3	**NA**	99	100	100	17	8	96	99	100
	3	5	10	**NA**	100	99	19	11	95	100	99
	4	5	5	100	**NA**	99	19	17	96	98	99
0.1	**5**	7	8	98	100	**NA**	18	20	92	100	99
	8	6	10	100	100	100	**NA**	13	90	99	100
	9	11	8	100	100	100	19	**NA**	94	99	99
	10	83	89	99	98	100	83	81	**NA**	100	100
	11	98	94	100	100	100	93	92	95	**NA**	99
	12	27	32	98	100	99	27	49	92	99	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	5	99	100	99	14	3	93	97	100
	2	5	**NA**	100	100	99	14	8	92	99	100
	3	15	19	**NA**	97	99	30	25	89	99	99
	4	14	19	98	**NA**	100	35	27	81	96	100
0.25	**5**	33	37	97	100	**NA**	47	46	86	98	99
	8	11	7	100	99	100	**NA**	16	88	100	98
	9	6	4	100	100	100	18	**NA**	91	97	100
	10	69	74	100	99	100	63	75	**NA**	100	100
	11	94	98	100	99	100	87	89	93	**NA**	99
	12	51	46	100	99	100	49	57	90	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	8	**NA**								
	3	96	98	**NA**							
	4	90	90	94	**NA**						
0.5	**5**	99	99	95	96	**NA**					
	8	10	14	99	91	99	**NA**				
	9	7	7	98	94	99	19	**NA**			
	10	73	70	100	95	100	76	80	**NA**		
	11	94	93	100	85	97	92	95	93	**NA**	
	12	98	99	97	89	91	99	97	95	96	**NA**

Supplementary Table 17. Power of MDR to detect either model in the presence of genetic heterogeneity with 500 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	100	99	0	4	91	100	98
	2	0	**NA**	99	100	100	2	2	96	99	100
	3	0	0	**NA**	100	99	2	7	95	100	99
	4	0	0	98	**NA**	99	2	7	95	98	99
0.1	**5**	0	2	97	100	**NA**	5	10	92	100	99
	8	0	1	100	100	100	**NA**	2	88	99	99
	9	0	0	99	100	100	1	**NA**	94	97	99
	10	5	3	99	98	100	6	12	**NA**	100	100
	11	1	3	99	100	100	3	1	93	**NA**	98
	12	5	6	97	100	99	3	31	91	98	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	100	99	0	2	93	97	100
	2	0	**NA**	100	98	98	1	2	89	98	100
	3	15	11	**NA**	97	99	23	15	86	98	98
	4	8	7	98	**NA**	100	17	12	77	96	100
0.25	**5**	25	24	97	100	**NA**	25	30	86	98	98
	8	0	0	100	99	100	**NA**	3	85	98	97
	9	0	0	100	100	100	1	**NA**	83	96	99
	10	9	8	100	99	100	11	22	**NA**	100	100
	11	15	23	100	99	100	13	21	76	**NA**	99
	12	35	35	100	99	100	23	38	89	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	95	98	**NA**							
	4	89	89	93	**NA**						
0.5	**5**	99	98	94	93	**NA**					
	8	0	1	98	86	99	**NA**				
	9	1	1	98	91	99	0	**NA**			
	10	56	55	100	92	100	56	60	**NA**		
	11	89	91	100	83	96	89	89	88	**NA**	
	12	98	98	97	88	89	99	96	94	96	**NA**

Supplementary Table 18. Power of MDR to detect both models in the presence of locus heterogeneity with 500 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	1	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	1	0	0
	4	0	0	0	**NA**	1	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	1	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	3	2	0	1	1	4	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	16	**NA**						
0.5	**5**	0	0	45	11	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	8	3	6	0	0	**NA**		
	11	0	0	28	6	14	0	0	3	**NA**	
	12	0	0	48	14	30	0	0	4	20	**NA**

Supplementary Table 19. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 1000 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	3	99	100	100	12	10	96	99	97
	2	5	**NA**	100	100	100	14	13	97	100	100
	3	2	4	**NA**	99	100	5	16	96	98	100
	4	7	6	99	**NA**	99	12	11	97	100	98
0.1	**5**	6	12	100	100	**NA**	12	20	98	100	95
	8	6	7	100	100	100	**NA**	16	95	98	99
	9	2	4	100	100	100	10	**NA**	97	100	98
	10	94	96	99	100	100	88	86	**NA**	98	99
	11	96	99	100	100	100	99	97	98	**NA**	100
	12	25	21	99	98	100	19	32	92	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	3	100	99	96	2	8	100	98	99
	2	0	**NA**	100	97	99	3	8	97	100	98
	3	28	24	**NA**	98	99	33	26	95	100	99
	4	16	10	100	**NA**	100	33	29	99	99	97
0.25	**5**	33	39	100	98	**NA**	67	59	98	98	99
	8	1	3	100	99	100	**NA**	6	94	100	99
	9	3	5	100	100	97	8	**NA**	97	100	98
	10	93	95	100	99	100	91	97	**NA**	99	98
	11	97	97	100	99	100	100	99	100	**NA**	95
	12	57	71	98	99	99	64	70	96	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	5	**NA**								
	3	99	97	**NA**							
	4	96	93	94	**NA**						
0.5	**5**	100	100	98	98	**NA**					
	8	4	8	99	99	99	**NA**				
	9	5	5	97	99	100	8	**NA**			
	10	81	81	99	98	96	78	81	**NA**		
	11	95	98	97	94	98	100	95	97	**NA**	
	12	98	99	100	92	97	99	98	99	98	**NA**

Supplementary Table 20. Power of MDR to detect either model in the presence of genetic heterogeneity with 1000 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	100	99	1	5	96	99	97
	2	0	**NA**	100	99	100	4	7	96	100	100
	3	0	1	**NA**	99	100	0	11	96	98	100
	4	0	0	99	**NA**	99	0	8	96	100	97
0.1	**5**	0	2	100	100	**NA**	3	8	98	99	94
	8	0	1	98	100	100	**NA**	4	94	98	98
	9	0	0	100	100	100	0	**NA**	95	100	98
	10	2	2	99	100	100	2	**11**	**NA**	96	98
	11	0	0	100	100	100	3	5	97	**NA**	100
	12	2	4	99	98	100	2	14	92	99	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	100	99	96	0	6	99	97	98
	2	0	**NA**	100	97	98	2	7	96	100	98
	3	24	22	**NA**	98	99	30	23	95	100	99
	4	14	10	100	**NA**	100	24	25	97	99	95
0.25	**5**	33	36	100	98	**NA**	62	51	98	98	99
	8	0	0	100	99	100	**NA**	5	94	100	97
	9	0	0	100	100	97	0	**NA**	97	99	97
	10	13	8	100	99	100	14	13	**NA**	99	98
	11	31	32	100	99	100	37	34	99	**NA**	95
	12	53	68	98	99	98	59	65	94	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	99	96	**NA**							
	4	96	91	93	**NA**						
0.5	**5**	100	100	97	98	**NA**					
	8	0	0	99	98	99	**NA**				
	9	0	0	96	98	100	**0**	**NA**			
	10	68	71	98	97	96	55	63	**NA**		
	11	93	97	96	90	96	99	92	96	**NA**	
	12	97	98	100	91	96	99	98	99	93	**NA**

Supplementary Table 21. Power of MDR to detect both models in the presence of locus heterogeneity with 1000 cases and controls

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	1	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	8	2	0	0	5	0	5
	4	0	0	0	**NA**	6	0	0	2	2	1
0.25	**5**	0	0	0	9	**NA**	0	0	6	3	6
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	1	0	0	**NA**	0	2
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	4	6	6	1	3	8	4	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	14	**NA**						
0.5	**5**	0	0	60	25	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	1	0	**NA**			
	10	0	0	10	8	7	0	0	**NA**		
	11	0	0	25	21	30	0	0	1	**NA**	
	12	0	0	72	28	53	0	0	11	30	**NA**

Supplementary Table 22. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 1000 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	4	99	99	100	3	9	100	99	98
	2	2	**NA**	100	100	99	6	13	94	99	100
	3	3	1	**NA**	100	100	6	13	95	100	99
	4	1	3	99	**NA**	99	6	15	97	100	98
0.1	**5**	3	4	100	99	**NA**	6	14	98	98	100
	8	3	4	100	99	100	**NA**	14	99	99	100
	9	1	1	99	100	99	8	**NA**	98	99	96
	10	91	92	100	97	99	92	98	**NA**	99	100
	11	100	100	100	99	100	100	97	100	**NA**	99
	12	12	16	97	100	99	8	31	98	98	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	1	99	98	99	6	6	96	98	99
	2	0	**NA**	100	98	100	4	5	97	99	98
	3	22	17	**NA**	99	100	28	26	95	99	99
	4	16	15	100	**NA**	100	29	27	96	98	98
0.25	**5**	31	35	98	99	**NA**	53	43	97	99	99
	8	4	3	100	100	100	**NA**	11	98	100	99
	9	4	4	100	99	100	6	**NA**	94	100	98
	10	92	89	99	100	99	85	94	**NA**	100	98
	11	94	98	100	100	100	94	98	97	**NA**	100
	12	59	57	100	99	99	52	70	96	99	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	3	**NA**								
	3	100	100	**NA**							
	4	97	100	100	**NA**						
0.5	**5**	99	100	99	100	**NA**					
	8	3	5	98	97	98	**NA**				
	9	5	1	100	99	100	5	**NA**			
	10	90	84	97	100	100	83	90	**NA**		
	11	99	99	99	96	100	100	98	94	**NA**	
	12	100	99	99	95	98	99	99	100	98	**NA**

Supplementary Table 23. Power of MDR to detect either model in the presence of genetic heterogeneity with 1000 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	99	100	0	3	100	99	98
	2	0	**NA**	100	100	99	1	6	94	99	100
	3	0	0	**NA**	100	100	2	10	95	99	98
	4	0	0	99	**NA**	99	0	10	96	100	97
0.1	**5**	0	2	100	99	**NA**	0	11	98	98	100
	8	0	1	100	99	99	**NA**	10	98	98	100
	9	0	0	98	100	98	0	**NA**	98	99	96
	10	1	2	99	97	99	1	14	**NA**	99	98
	11	0	2	100	99	99	1	3	100	**NA**	97
	12	4	6	97	99	99	1	23	95	97	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	99	98	99	0	1	96	96	99
	2	0	**NA**	100	98	98	0	3	95	99	98
	3	19	14	**NA**	99	100	22	21	95	98	99
	4	10	9	99	**NA**	100	17	22	95	98	97
0.25	**5**	28	32	98	99	**NA**	45	37	96	99	98
	8	0	0	100	100	100	**NA**	2	98	100	98
	9	0	0	100	99	100	2	**NA**	92	99	98
	10	8	8	99	100	98	14	12	**NA**	99	98
	11	20	26	100	100	99	21	25	94	**NA**	100
	12	49	49	100	99	98	46	66	95	98	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	100	100	**NA**							
	4	97	99	100	**NA**						
0.5	**5**	99	99	99	100	**NA**					
	8	0	0	98	96	98	**NA**				
	9	0	0	99	99	100	0	**NA**			
	10	78	72	97	99	100	73	79	**NA**		
	11	97	98	99	95	100	100	97	93	**NA**	
	12	99	99	99	94	98	99	98	99	98	**NA**

Supplementary Table 24. Power of MDR to detect both models in the presence of locus heterogeneity with 1000 cases and 2000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	4	1	0	0	1	3	7
	4	0	0	0	**NA**	3	0	0	0	0	0
0.25	**5**	0	0	0	2	**NA**	0	0	2	1	2
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	1	1	0	0	0	**NA**	0	0
	11	0	0	0	0	2	0	0	1	**NA**	0
	12	0	0	1	7	3	0	2	6	2	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	33	**NA**						
0.5	**5**	0	0	77	50	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	0	0	**NA**			
	10	0	0	27	22	24	0	0	**NA**		
	11	0	0	43	48	56	0	0	6	**NA**	
	12	0	0	82	54	80	0	0	18	59	**NA**

Supplementary Table 25. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 1000 cases and 4000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	2	100	99	99	4	10	96	99	99
	2	1	**NA**	100	99	100	3	14	99	99	99
	3	0	1	**NA**	99	96	3	9	99	99	98
	4	4	1	100	**NA**	95	3	19	94	100	96
0.1	**5**	0	1	100	99	**NA**	4	17	99	100	99
	8	3	1	100	99	98	**NA**	14	100	99	98
	9	2	6	100	98	100	8	**NA**	96	96	95
	10	96	97	100	99	97	96	98	**NA**	0	0
	11	96	98	100	99	99	97	96	0	**NA**	0
	12	11	9	99	98	100	8	35	100	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	5	100	99	99	36	26	99	98	99
	2	2	**NA**	100	99	99	29	28	96	99	97
	3	29	25	**NA**	100	99	61	42	96	98	100
	4	15	11	100	**NA**	99	8	6	98	99	100
0.25	**5**	36	46	100	100	**NA**	94	94	98	99	98
	8	1	2	100	100	100	**NA**	98	97	100	98
	9	1	3	100	100	98	96	**NA**	96	98	100
	10	97	95	100	99	100	57	61	**NA**	0	0
	11	95	97	100	0	0	0	0	0	**NA**	0
	12	61	69	100	100	6	5	100	100	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	1	**NA**								
	3	100	100	**NA**							
	4	99	99	98	**NA**						
0.5	**5**	100	100	100	99	**NA**					
	8	3	1	100	99	100	**NA**				
	9	6	2	99	96	100	99	**NA**			
	10	100	88	93	97	90	96	99	**NA**		
	11	100	98	100	0	0	0	0	0	**NA**	
	12	98	0	0	100	6	99	89	95	0	**NA**

Supplementary Table 26. Power of MDR to detect either model in the presence of genetic heterogeneity with 1000 cases and 4000 controls

Proportion of data **0.9**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**	0	100	99	99	0	9	95	99	99
	2	0	**NA**	100	99	100	1	10	99	99	99
	3	0	0	**NA**	98	96	0	5	98	99	98
	4	0	0	100	**NA**	95	1	12	93	98	96
0.1	**5**	0	0	99	99	**NA**	3	13	99	100	99
	8	0	0	100	99	98	**NA**	9	100	98	97
	9	0	1	100	98	100	0	**NA**	96	96	93
	10	0	3	100	99	96	7	10	**NA**	0	0
	11	2	5	100	99	99	1	2	0	**NA**	0
	12	1	2	99	98	100	3	24	100	100	**NA**

Proportion of data **0.75**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**	0	100	99	99	26	20	98	98	99
	2	0	**NA**	100	99	99	19	21	96	99	97
	3	22	23	**NA**	100	99	52	36	95	97	100
	4	9	8	99	**NA**	99	0	4	96	99	99
0.25	**5**	34	38	99	100	**NA**	20	27	98	98	98
	8	0	0	100	99	100	**NA**	28	96	100	98
	9	1	0	100	100	98	30	**NA**	96	96	100
	10	14	8	100	99	100	47	55	**NA**	0	0
	11	20	27	100	0	0	0	0	0	**NA**	0
	12	57	63	98	100	0	4	99	100	99	**NA**

Proportion of data **0.5**

	Model	1	2	3	4	5	8	9	10	11	12
	1	**NA**									
	2	0	**NA**								
	3	99	100	**NA**							
	4	99	99	98	**NA**						
0.5	**5**	100	99	100	99	**NA**					
	8	0	0	100	96	99	**NA**				
	9	1	2	98	92	100	99	**NA**			
	10	100	79	88	97	87	95	99	**NA**		
	11	100	98	100	0	0	0	0	0	**NA**	
	12	98	0	0	98	0	99	84	95	0	**NA**

Supplementary Table 27. Power of MDR to detect both models in the presence of locus heterogeneity with 1000 cases and 4000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	1	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	3	0	0	7	5	5
	2	0	**NA**	0	6	2	0	0	0	0	0
	3	0	0	**NA**	5	0	0	0	3	1	3
	4	0	0	0	**NA**	1	0	0	0	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	2	1	**NA**	0	0	0	0
	9	0	0	0	2	2	0	**NA**	3	5	0
	10	0	0	0	4	4	0	1	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	2	0	0	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	86	0	**NA**							
	4	63	0	0	**NA**						
0.5	**5**	0	0	0	0	**NA**					
	8	0	0	0	31	69	**NA**				
	9	0	0	57	57	90	0	**NA**			
	10	43	0	0	65	0	6	32	**NA**		
	11	0	0	95	0	0	0	0	0	**NA**	
	12	1	0	0	0	0	0	0	58	0	**NA**

Supplementary Table 28. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 2000 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	2	100	99	99	5	13	98	100	97
	2	1	**NA**	100	98	100	4	19	100	100	98
	3	2	6	**NA**	98	99	5	17	99	100	100
	4	3	4	99	**NA**	100	8	24	99	100	98
0.1	**5**	2	4	99	100	**NA**	3	26	99	100	95
	8	4	1	100	100	99	**NA**	17	98	100	99
	9	3	4	100	99	99	6	**NA**	100	98	98
	10	98	98	100	99	98	96	96	**NA**	99	99
	11	99	100	100	99	100	99	98	100	**NA**	100
	12	6	10	99	99	100	11	18	97	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	3	100	99	96	2	8	100	98	99
	2	0	**NA**	100	97	99	3	8	97	100	98
	3	28	24	**NA**	98	99	33	26	95	100	99
	4	16	10	100	**NA**	100	33	29	99	99	97
0.25	**5**	33	39	100	98	**NA**	67	59	98	98	99
	8	1	3	100	99	100	**NA**	6	94	100	99
	9	3	5	100	100	97	8	**NA**	97	100	98
	10	93	95	100	99	100	91	97	**NA**	99	98
	11	97	97	100	99	100	100	99	100	**NA**	95
	12	57	71	98	99	99	64	70	96	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	1	**NA**								
	3	100	100	**NA**							
	4	99	98	95	**NA**						
0.5	**5**	100	100	100	100	**NA**					
	8	1	5	100	99	99	**NA**				
	9	3	2	100	100	98	4	**NA**			
	10	95	94	99	98	100	93	95	**NA**		
	11	100	100	97	97	100	98	100	98	**NA**	
	12	98	99	100	99	100	99	99	99	99	**NA**

Supplementary Table 29. Power of MDR to detect either model in the presence of genetic heterogeneity with 2000 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	100	99	98	2	12	98	100	97
	2	0	**NA**	100	98	100	1	14	100	99	98
	3	0	2	**NA**	98	99	1	17	99	98	100
	4	0	2	99	**NA**	100	2	19	99	100	97
0.1	**5**	0	1	99	100	**NA**	0	24	99	99	94
	8	0	1	100	100	98	**NA**	16	97	98	98
	9	0	1	100	99	99	1	**NA**	100	97	98
	10	1	1	99	99	98	4	16	**NA**	99	98
	11	4	5	100	99	100	3	9	100	**NA**	100
	12	1	5	98	98	100	2	16	96	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	100	99	96	0	6	99	97	98
	2	0	**NA**	100	97	98	2	7	96	100	98
	3	24	22	**NA**	98	99	30	23	95	100	99
	4	14	10	100	**NA**	100	24	25	97	99	95
0.25	**5**	33	36	100	98	**NA**	62	51	98	98	99
	8	0	0	100	99	100	**NA**	5	94	100	97
	9	0	0	100	100	97	0	**NA**	97	99	97
	10	13	8	100	99	100	14	13	**NA**	99	98
	11	31	32	100	99	100	37	34	99	**NA**	95
	12	53	68	98	99	98	59	65	94	100	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	100	100	**NA**							
	4	99	97	95	**NA**						
0.5	**5**	100	100	100	100	**NA**					
	8	0	0	100	98	99	**NA**				
	9	0	0	100	100	98	0	**NA**			
	10	90	90	99	96	100	91	91	**NA**		
	11	100	100	97	96	100	97	100	96	**NA**	
	12	98	99	100	99	100	99	97	99	97	**NA**

Supplementary Table 30. Power of MDR to detect both models in the presence of locus heterogeneity with 2000 cases and controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	1	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	1	0	0	**NA**	0	0	0
	10	0	0	0	1	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	8	2	0	0	5	0	5
	4	0	0	0	**NA**	6	0	0	2	2	1
0.25	**5**	0	0	0	9	**NA**	0	0	6	3	6
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	1	0	0	**NA**	0	2
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	4	6	6	1	3	8	4	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	43	**NA**						
0.5	**5**	0	0	94	71	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	1	0	**NA**			
	10	0	0	52	56	71	0	0	**NA**		
	11	0	0	55	82	87	0	0	17	**NA**	
	12	0	0	99	85	98	0	0	44	77	**NA**

Supplementary Table 31. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 2000 cases and 4000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	4	100	99	100	3	41	100	99	100
	2	3	**NA**	100	98	100	5	33	100	100	98
	3	2	5	**NA**	100	100	6	41	100	100	99
	4	2	3	100	**NA**	100	6	35	100	99	97
0.1	**5**	1	8	100	99	**NA**	7	27	100	99	99
	8	2	5	100	99	99	**NA**	99	100	100	99
	9	6	99	100	96	100	100	**NA**	100	100	98
	10	96	97	100	98	100	100	98	**NA**	100	0
	11	100	6	99	99	99	4	34	98	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	6	100	98	100	2	17	100	100	96
	2	2	**NA**	100	98	100	57	47	95	98	97
	3	48	50	**NA**	99	97	29	31	99	100	95
	4	19	17	100	**NA**	100	74	61	100	99	98
0.25	**5**	52	55	100	99	**NA**	5	12	98	100	95
	8	7	1	100	98	100	**NA**	96	99	99	97
	9	2	4	100	100	99	96	**NA**	100	100	98
	10	98	98	100	100	100	100	97	**NA**	97	0
	11	97	96	98	100	99	58	65	95	**NA**	0
	12	73	66	0	0	0	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	6	**NA**								
	3	100	100	**NA**							
	4	99	100	99	**NA**						
0.5	**5**	100	100	100	100	**NA**					
	8	7	4	100	99	99	**NA**				
	9	1	3	100	100	100	3	**NA**			
	10	95	98	100	99	99	98	95	**NA**		
	11	99	99	99	100	99	98	99	99	**NA**	
	12	99	98	100	100	100	98	98	99	99	**NA**

Supplementary Table 32. Power of MDR to detect either model in the presence of genetic heterogeneity with 2000 cases and 4000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	3	100	99	100	1	40	100	99	100
	2	0	**NA**	100	98	98	3	32	100	99	98
	3	0	3	**NA**	99	98	2	36	100	100	99
	4	0	2	100	**NA**	100	1	34	100	99	97
0.1	**5**	0	4	100	99	**NA**	3	27	99	99	98
	8	0	0	100	98	99	**NA**	25	100	100	98
	9	0	7	100	96	99	6	**NA**	100	100	98
	10	3	4	100	98	99	3	26	**NA**	100	0
	11	2	1	99	99	99	0	30	98	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	2	100	98	100	0	16	100	99	96
	2	0	**NA**	100	98	100	56	46	95	97	97
	3	46	46	**NA**	99	96	26	30	98	99	95
	4	17	13	100	**NA**	100	71	54	98	99	97
0.25	**5**	50	51	100	98	**NA**	1	8	97	100	95
	8	0	0	100	96	100	**NA**	16	98	99	97
	9	0	1	99	100	99	17	**NA**	100	99	98
	10	19	15	100	100	100	54	36	**NA**	96	0
	11	50	46	96	100	99	52	61	93	**NA**	0
	12	71	64	0	0	0	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	1	**NA**								
	3	100	100	**NA**							
	4	99	100	99	**NA**						
0.5	**5**	100	100	100	100	**NA**					
	8	1	0	100	99	99	**NA**				
	9	1	1	100	99	100	1	**NA**			
	10	92	96	100	98	98	98	90	**NA**		
	11	98	99	98	100	99	98	99	99	**NA**	
	12	99	98	100	100	100	98	98	98	98	**NA**

Supplementary Table 33. Power of MDR to detect both models in the presence of locus heterogeneity with 2000 cases and 4000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	2	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	1	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	7	5	0	0	9	5	1
	3	0	0	**NA**	5	3	0	0	0	4	0
	4	0	0	0	**NA**	0	0	0	1	0	0
0.25	**5**	0	0	0	0	**NA**	0	0	0	0	1
	8	0	0	0	0	0	**NA**	0	0	0	1
	9	0	0	0	4	3	0	**NA**	0	1	1
	10	0	0	0	2	2	0	0	**NA**	3	0
	11	0	0	8	3	9	0	8	2	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	1	71	**NA**						
0.5	**5**	0	0	97	88	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	1	1	0	**NA**			
	10	0	0	67	80	84	0	0	**NA**		
	11	0	0	71	97	95	0	0	21	**NA**	
	12	0	0	100	97	99	0	1	58	88	**NA**

Supplementary Table 34. Power of MDR to detect any model locus in the presence of genetic heterogeneity with 2000 cases and 8000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	6	100	99	100	1	51	100	99	99
	2	4	**NA**	100	97	99	7	52	100	99	98
	3	2	10	**NA**	98	98	3	44	100	100	98
	4	2	2	100	**NA**	100	5	47	100	100	99
0.1	**5**	3	9	100	98	**NA**	7	48	100	99	98
	8	5	8	100	99	100	**NA**	37	100	99	99
	9	3	6	100	96	99	4	**NA**	100	99	99
	10	97	98	100	99	100	99	99	**NA**	100	96
	11	100	98	100	100	100	98	99	100	**NA**	100
	12	1	14	100	99	99	8	60	97	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	4	100	99	99	4	27	99	100	98
	2	2	**NA**	100	99	100	4	20	99	99	99
	3	62	61	**NA**	99	98	70	60	97	100	95
	4	25	25	100	**NA**	99	46	25	99	99	99
0.25	**5**	63	70	100	99	**NA**	65	78	99	100	99
	8	1	5	100	100	99	**NA**	15	99	100	100
	9	1	3	100	99	100	4	**NA**	100	100	100
	10	97	98	100	95	99	98	98	**NA**	100	100
	11	100	100	100	95	100	99	97	100	**NA**	100
	12	78	76	100	97	98	66	77	95	99	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	2	**NA**								
	3	100	100	**NA**							
	4	100	100	99	**NA**						
0.5	**5**	98	100	100	100	**NA**					
	8	3	4	100	99	100	**NA**				
	9	7	4	100	99	99	6	**NA**			
	10	96	97	98	100	100	97	100	**NA**		
	11	99	99	99	100	100	99	99	100	**NA**	
	12	99	100	100	100	100	100	99	100	100	**NA**

Supplementary Table 35. Power of MDR to detect either model in the presence of genetic heterogeneity with 2000 cases and 8000 controls

Proportion of data		0.9									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	4	100	98	100	0	49	100	99	99
	2	0	**NA**	100	97	99	3	50	100	99	97
	3	0	7	**NA**	98	98	0	43	100	100	98
	4	0	1	100	**NA**	100	1	45	100	100	99
0.1	**5**	0	5	100	98	**NA**	4	47	100	99	98
	8	0	5	100	98	100	**NA**	35	100	99	98
	9	0	3	100	96	98	1	**NA**	100	97	99
	10	2	5	100	99	99	8	40	**NA**	100	95
	11	4	5	100	99	100	3	37	100	**NA**	100
	12	1	11	100	99	99	3	58	94	100	**NA**

Proportion of data		0.75									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	2	100	99	99	1	25	99	100	98
	2	0	**NA**	100	99	100	0	20	99	99	99
	3	60	61	**NA**	99	98	68	58	96	100	95
	4	23	23	100	**NA**	99	38	23	99	99	98
0.25	**5**	62	70	100	98	**NA**	63	76	99	100	99
	8	0	1	100	100	99	**NA**	12	99	100	99
	9	0	1	100	99	100	1	**NA**	100	97	100
	10	11	9	100	94	99	15	32	**NA**	100	100
	11	54	59	100	95	100	57	52	100	**NA**	100
	12	76	74	99	97	98	58	73	94	99	**NA**

Proportion of data		0.5									
	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	100	100	**NA**							
	4	100	100	98	**NA**						
0.5	**5**	97	100	100	100	**NA**					
	8	0	0	100	99	100	**NA**				
	9	5	4	100	99	99	4	**NA**			
	10	94	97	98	100	100	94	98	**NA**		
	11	99	98	99	100	100	99	99	100	**NA**	
	12	99	99	100	100	100	100	99	100	99	**NA**

Supplementary Table 36. Power of MDR to detect both models in the presence of locus heterogeneity with 2000 cases and 8000 controls

Proportion of data **0.9**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	0	0	0	0	0	0
	3	0	0	**NA**	0	0	0	0	0	0	0
	4	0	0	0	**NA**	0	0	0	0	0	0
0.1	**5**	0	0	0	0	**NA**	0	0	0	0	0
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	0	0	0	0	**NA**	0	0
	11	0	0	0	0	0	0	0	0	**NA**	0
	12	0	0	0	0	0	0	0	0	0	**NA**

Proportion of data **0.75**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**	0	0	0	0	0	0	0	0	0
	2	0	**NA**	0	0	1	0	0	0	0	0
	3	0	0	**NA**	0	2	0	0	8	9	7
	4	0	0	0	**NA**	5	0	0	2	8	6
0.25	**5**	0	0	0	5	**NA**	0	1	5	3	6
	8	0	0	0	0	0	**NA**	0	0	0	0
	9	0	0	0	0	0	0	**NA**	0	0	0
	10	0	0	0	6	1	0	0	**NA**	1	1
	11	0	0	0	3	2	0	0	0	**NA**	0
	12	0	0	7	2	4	0	8	1	3	**NA**

Proportion of data **0.5**

	Model	**1**	**2**	**3**	**4**	**5**	**8**	**9**	**10**	**11**	**12**
	1	**NA**									
	2	0	**NA**								
	3	0	0	**NA**							
	4	0	0	66	**NA**						
0.5	**5**	0	0	100	95	**NA**					
	8	0	0	0	0	0	**NA**				
	9	0	0	0	0	1	0	**NA**			
	10	0	0	71	85	88	0	0	**NA**		
	11	0	0	75	99	97	0	0	22	**NA**	
	12	0	0	100	100	100	0	1	86	77	**NA**