Figure 1 - figure supplement 1
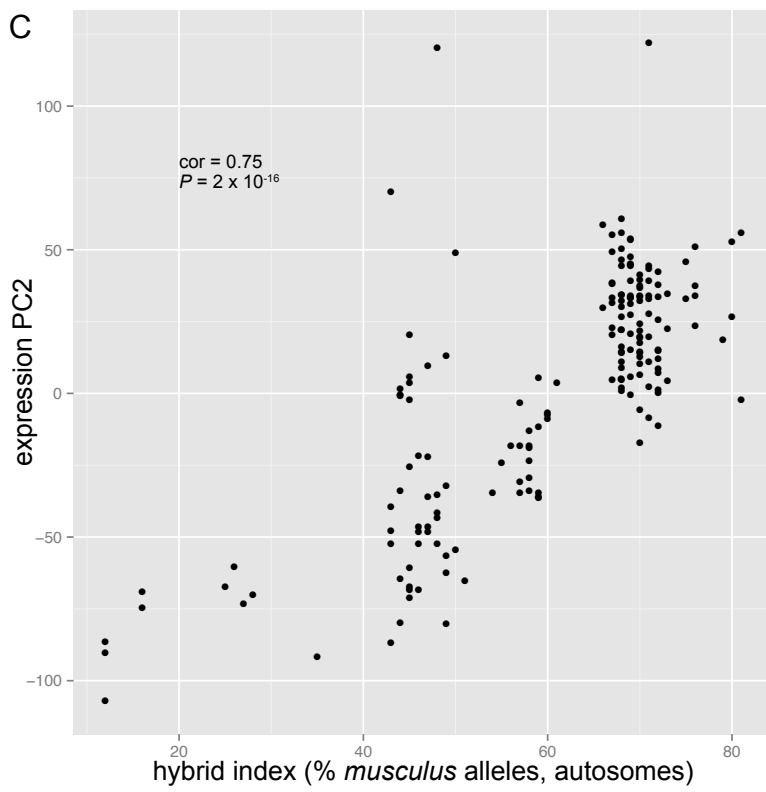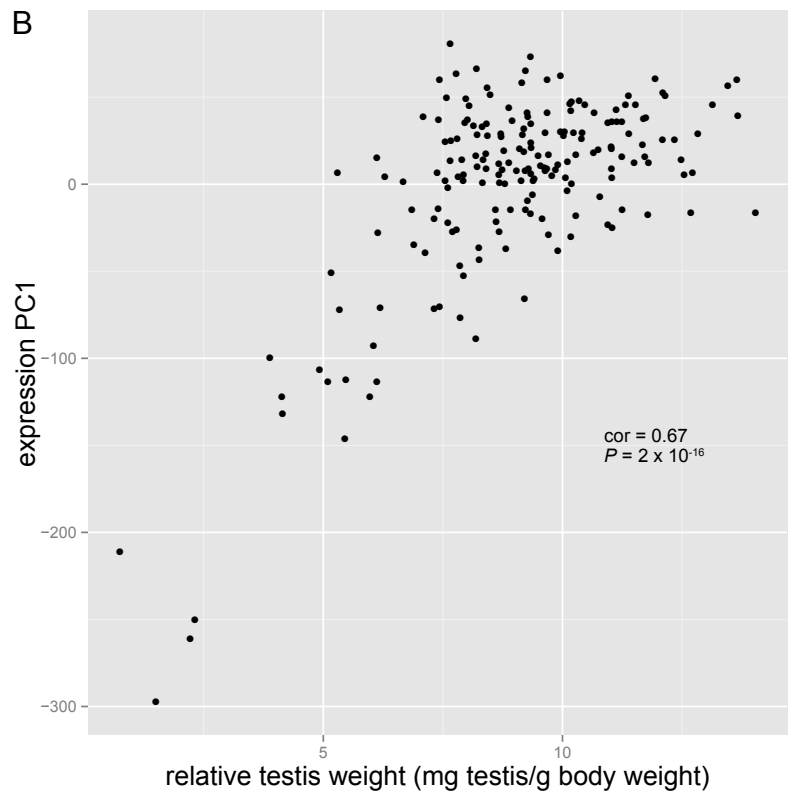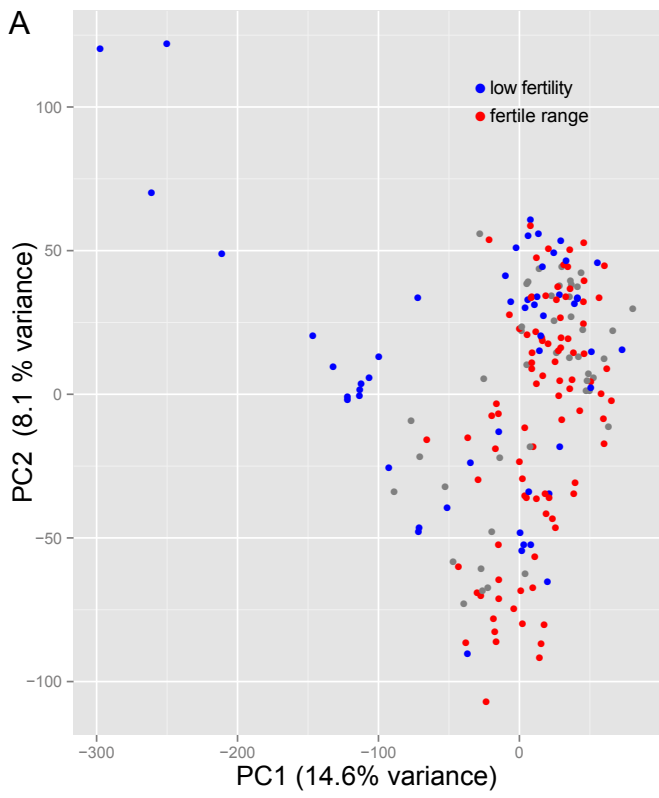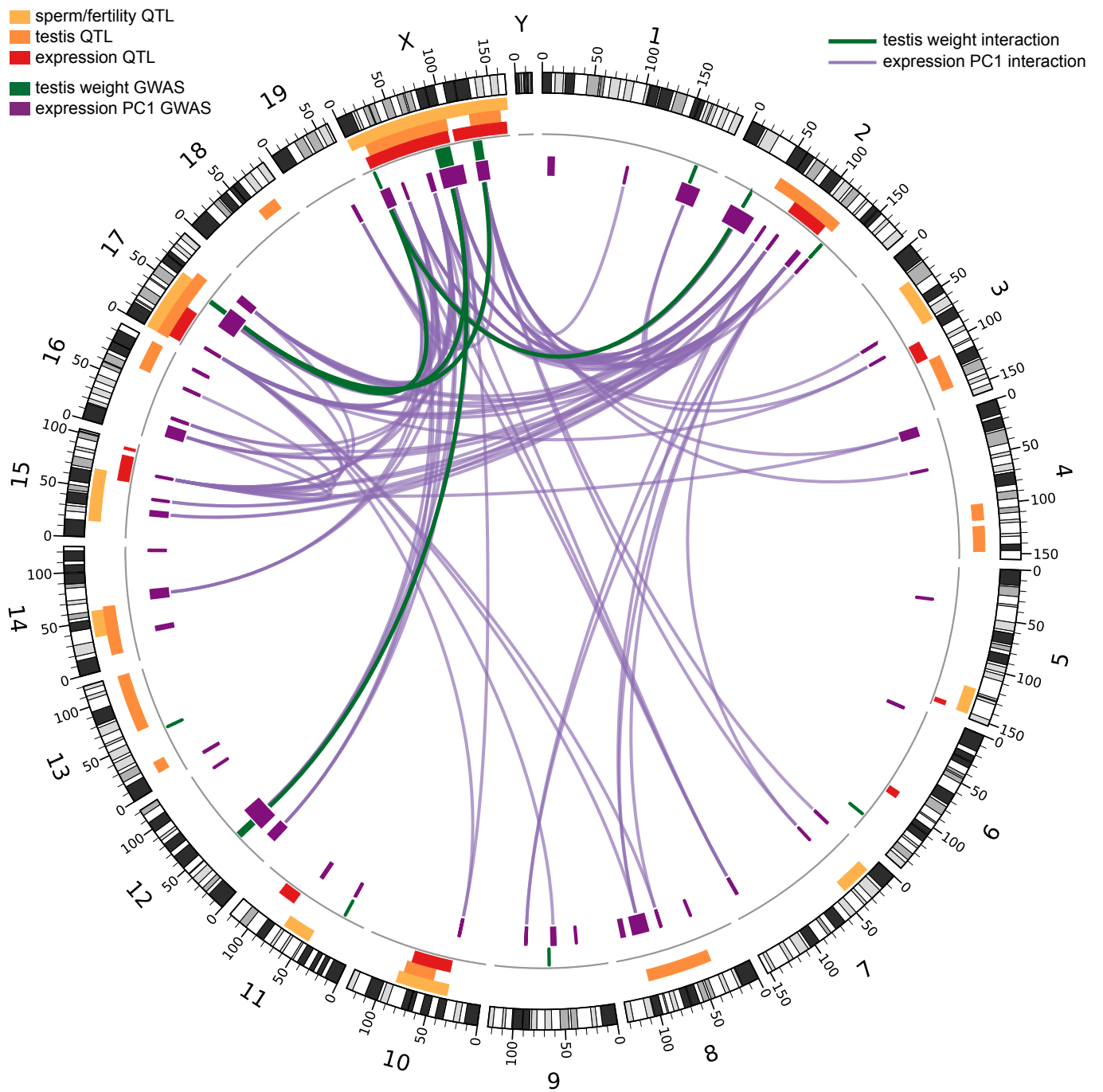
A

B

C

Figure 1 - figure supplement 2
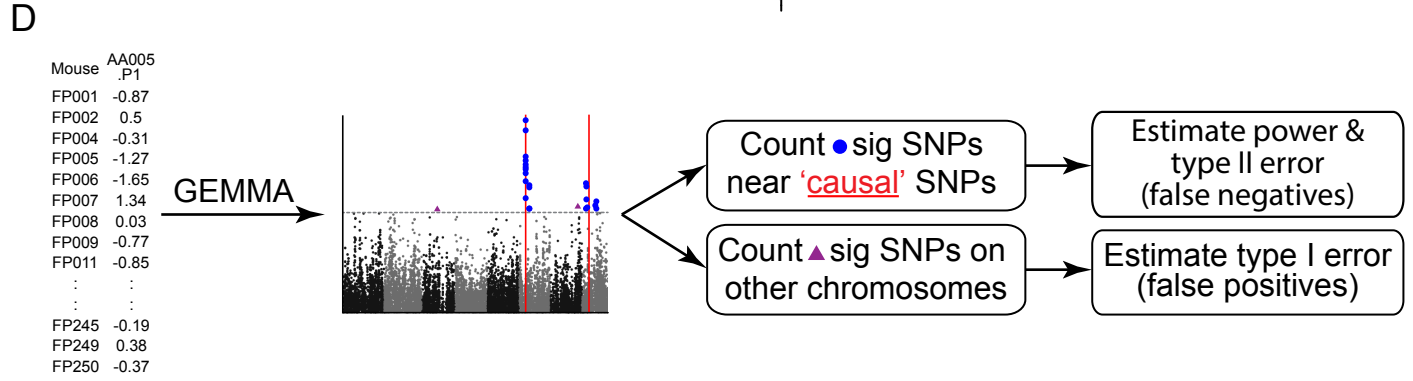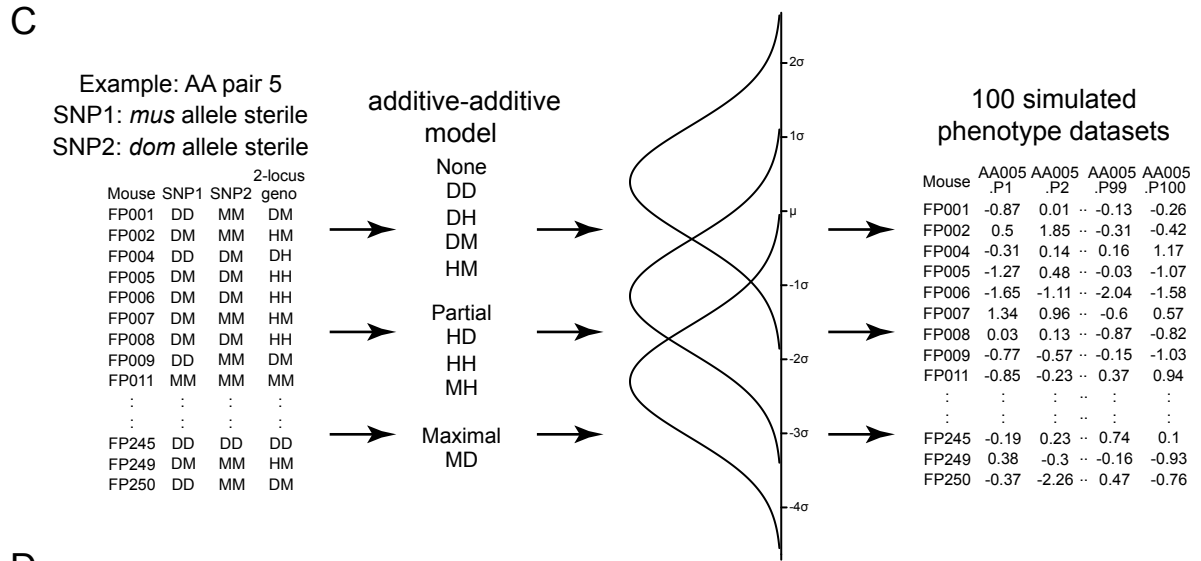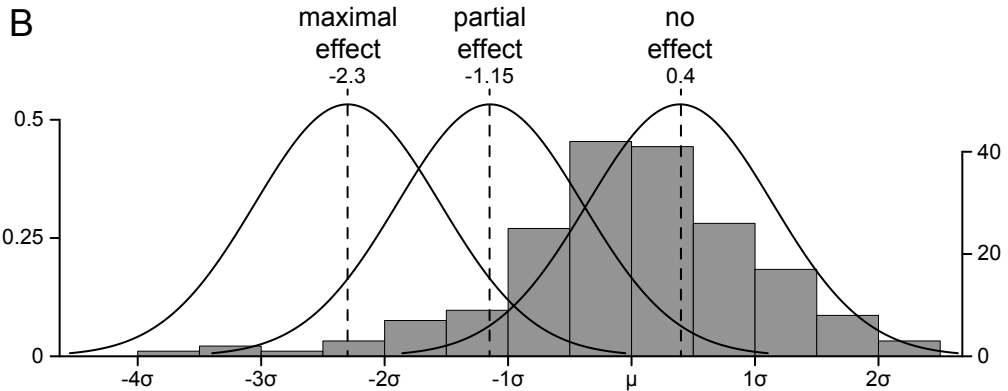
Figure 2 - figure supplement 1

A

144,506 possible
dom sterile SNPs
fixed *musculus*
(Kazakhstan, Czech Republic)

285,684 SNPs
MAF >5

124,390 possible
mus sterile SNPs
fixed *domesticus*
(France, Germany)

100 AA pairs
autosome-autosome
(different chromosomes)

50 XA pairs
X - autosome
dom X - *mus* auto

50 XA pairs
X - autosome
mus X - *dom* auto

B

maximal effect
-2.3

partial effect
-1.15

no effect
0.4

0.5

0.25

0

40

20

0

-4σ -3σ -2σ -1σ μ 1σ 2σ

C

Example: AA pair 5
SNP1: *mus* allele sterile
SNP2: *dom* allele sterile

Mouse	SNP1	SNP2	2-locus geno
FP001	DD	MM	DM
FP002	DM	MM	HM
FP004	DD	DM	DH
FP005	DM	DM	HH
FP006	DM	DM	HH
FP007	DM	MM	HM
FP008	DM	DM	HH
FP009	DD	MM	DM
FP011	MM	MM	MM
⋮	⋮	⋮	⋮
FP245	DD	DD	DD
FP249	DM	MM	HM
FP250	DD	MM	DM

additive-additive model

None
DD
DH
DM
HM

Partial
HD
HH
MH

Maximal
MD

2σ

1σ

μ

-1σ

-2σ

-3σ

-4σ

100 simulated phenotype datasets

Mouse	AA005 .P1	AA005 .P2	AA005 .P99	AA005 .P100
FP001	-0.87	0.01	-0.13	-0.26
FP002	0.5	1.85	-0.31	-0.42
FP004	-0.31	0.14	0.16	1.17
FP005	-1.27	0.48	-0.03	-1.07
FP006	-1.65	-1.11	-2.04	-1.58
FP007	1.34	0.96	-0.6	0.57
FP008	0.03	0.13	-0.87	-0.82
FP009	-0.77	-0.57	-0.15	-1.03
FP011	-0.85	-0.23	0.37	0.94
⋮	⋮	⋮	⋮	⋮
FP245	-0.19	0.23	0.74	0.1
FP249	0.38	-0.3	-0.16	-0.93
FP250	-0.37	-2.26	0.47	-0.76

D

Mouse	AA005 .P1
FP001	-0.87
FP002	0.5
FP004	-0.31
FP005	-1.27
FP006	-1.65
FP007	1.34
FP008	0.03
FP009	-0.77
FP011	-0.85
⋮	⋮
FP245	-0.19
FP249	0.38
FP250	-0.37

GEMMA

Count ● sig SNPs near 'causal' SNPs

Estimate power & type II error (false negatives)

Count ▲ sig SNPs on other chromosomes
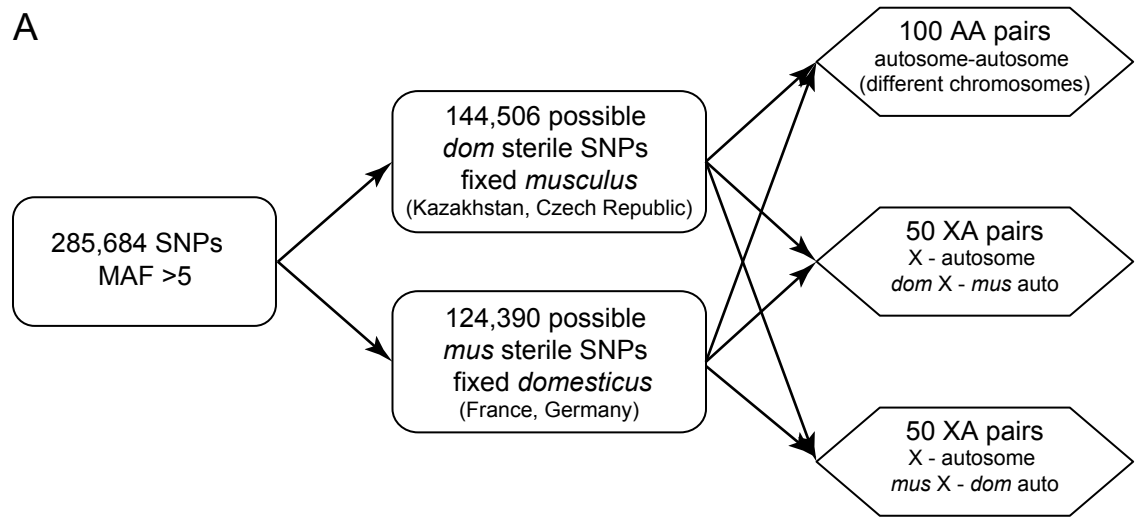
Estimate type I error (false positives)

Figure 4 - figure supplement 1

Figure 4 – figure supplement 2.

Z scores for simulation models.

	Locus 1 dominance[1]	Locus 1 sterile allele	Locus 2 dominance[1]	Locus 2 sterile allele	Mean Z score								
					DD	HD	MD	DH	HH	MH	DM	HM	MM
autosomal-autosomal	rec	M	rec	D	0.4	-0.03	-2.3	-0.44	0.44	0.23	-0.47	0.42	-0.08
	rec	M	add	D	0.4	-0.03	-2.3	-0.44	0.44	-1.15	-0.47	0.42	-0.08
	rec	M	dom	D	0.4	-0.03	-2.3	-0.44	0.44	-2.3	-0.47	0.42	-0.08
	add	M	add	D	0.4	-1.15	-2.3	-0.44	-1.15	-1.15	-0.47	0.42	-0.08
	add	M	dom	D	0.4	-1.15	-2.3	-0.44	-1.15	-2.3	-0.47	0.42	-0.08
	dom	M	dom	D	0.4	-2.3	-2.3	-0.44	-2.3	-2.3	-0.47	0.42	-0.08
X-autosomal	X	M	rec	D	0.4	-	-2.3	-0.3	-	0.3	-0.33	-	0
	X	M	add	D	0.4	-	-2.3	-0.3	-	-1.15	-0.33	-	0
	X	M	dom	D	0.4	-	-2.3	-0.3	-	-2.3	-0.33	-	0
	X	D	rec	M	0	-	-0.33	0.3	-	-0.3	-2.3	-	0.4
	X	D	add	M	0	-	0.27	-1.15	-	-0.3	-2.3	-	0.4
	X	D	dom	M	0	-	-0.33	-2.3	-	-0.3	-2.3	-	0.4

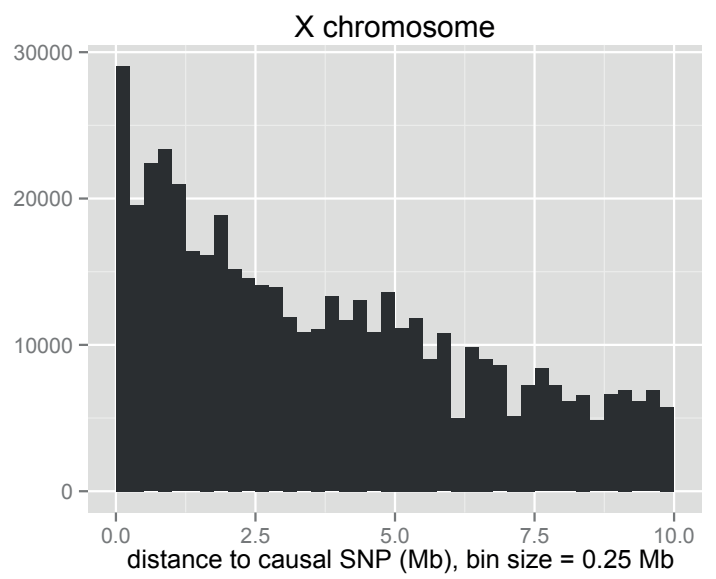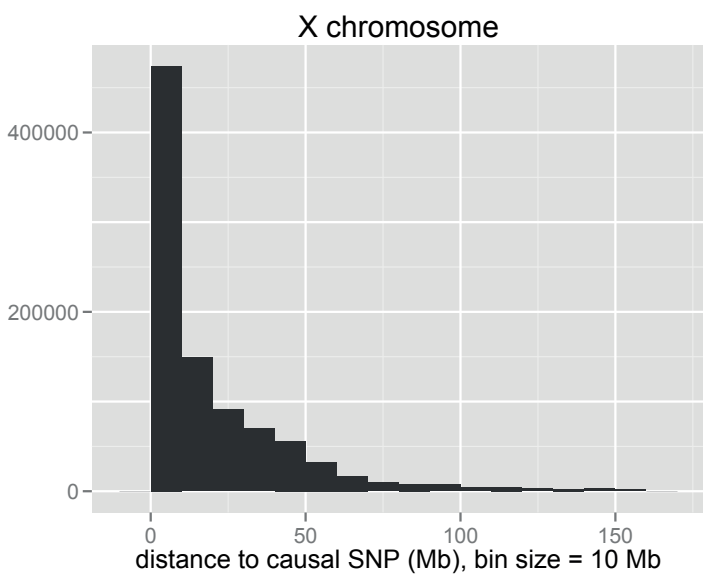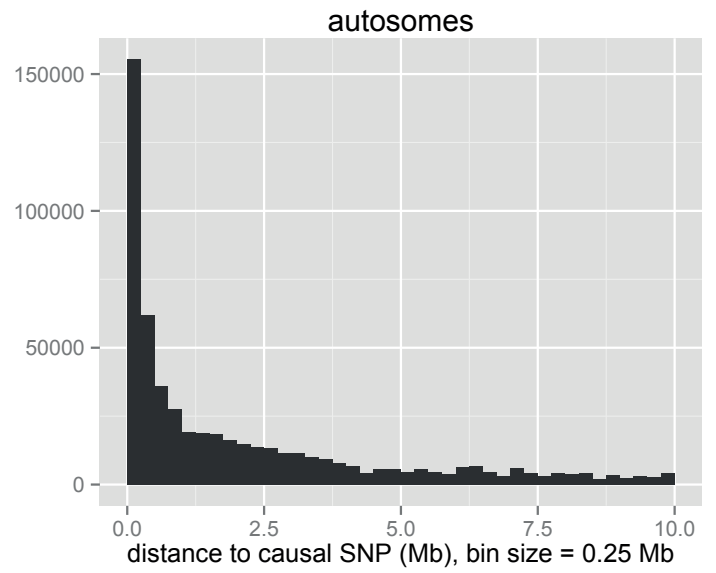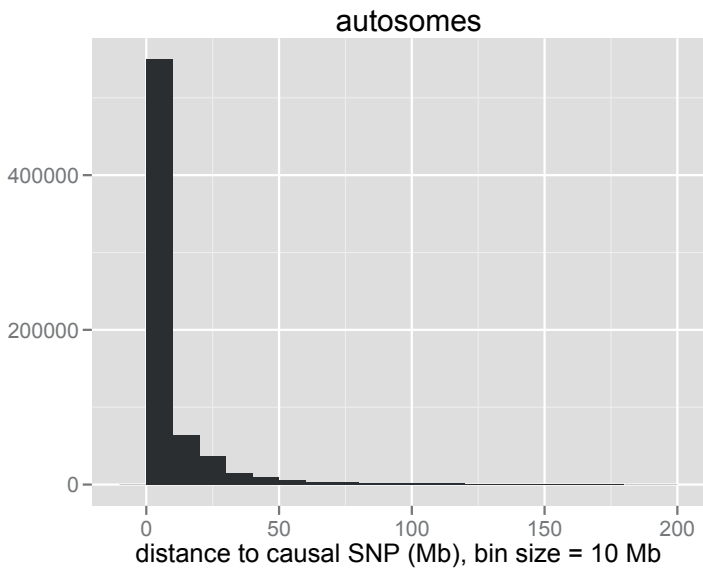[1]add – additive; dom – dominant; rec – recessive

Figure 4 - figure supplement 3

Figure 4 – figure supplement 4.

Results of mapping simulations.

Architecture[1]	Med. Distance to Causal SNP (Mb) X chromosome/Autosome	Locus 1 detected[2,3]			Locus 2 detected[3,4]			Both loci detected[3]			Mean No. Sig. SNPs		
		0.2 Mb	1 Mb	10 Mb	0.2 Mb	1 Mb	10 Mb	0.2 Mb	1 Mb	10 Mb	10 Mb[5]	50 Mb[5]	Diff. Chr.[6]
Permutation *P*<0.05													
rec-rec	5.9	7.2	8.4	12.3	9.0	11.7	15.8	0.3	0.7	2.6	1.1	1.5	5.5
rec-add	2.6	18.3	22.2	28.0	12.6	15.8	21.0	3.2	4.4	7.2	3.5	2.3	4.4
rec-dom	2.0	27.4	31.8	39.2	19.1	22.2	26.4	5.5	7.8	12.9	6.9	8.5	5.0
add-add	1.4	6.7	7.7	10.5	47.5	51.9	55.8	2.7	3.1	4.7	7.9	9.2	6.1
add-dom	1.7	14.2	15.9	19.0	51.6	55.7	59.2	6.0	7.5	10.3	11.1	13.3	5.4
dom-dom	1.8	7.8	9.8	14.3	63.8	66.9	70.6	2.4	3.7	7.3	14.7	17.6	6.2
X-rec	12.2/4.8	10.3	14.0	26.2	10.0	12.7	18.8	0.1	1.3	4.9	5.6	9.9	4.8
X-add	9.1/2.0	33.9	39.1	48.5	24.3	25.6	31.0	3.8	5.3	11.4	21.9	35.7	5.7
X-dom	9.8/2.0	46.5	51.3	59.7	26.9	28.5	32.6	5.9	8.6	14.4	31.0	52.8	3.8
FDR <0.1													
rec-rec	10.0	16.6	21.4	34.7	18.5	23.5	35.5	3.5	5.4	15.0	5.1	8.3	34.7
rec-add	5.5	32.7	39.7	52.7	27.2	32.6	45.2	11.4	15.5	27.9	13.2	18.9	32.9
rec-dom	4.1	42.2	49.7	62.9	33.5	37.2	48.4	16.5	21.3	33.8	22.2	30.1	28.7
add-add	3.6	14.4	17.6	30.6	63.3	69.3	77.6	8.4	11.3	23.3	21.6	28.8	36.8
add-dom	3.5	26.5	31.1	42.0	65.5	70.6	78.1	18.2	22.8	33.5	29.2	39.3	29.1
dom-dom	3.6	16.4	22.1	35.3	76.8	79.8	85.9	9.4	15.1	29.3	35.5	48.0	26.5
X-rec	12.2/7.8	10.3	14.0	26.2	20.0	25.2	40.5	0.7	3.1	11.0	10.3	17.5	34.6
X-add	9.1/4.7	33.9	39.1	48.5	33.2	36.6	48.3	6.3	9.4	20.9	28.7	46.1	30.0
X-dom	9.8/5.0	46.5	51.3	59.7	37.0	41.2	50.9	11.4	16.3	27.2	38.8	65.5	21.6

[1]Architecture abbreviations: add – additive; dom – dominant; rec – recessive
[2]Locus 1 for autosomal pairs is *musculus* sterile allele; locus 1 for X-autosomal pairs is X-linked
[3]'detected' - ≥1 significant SNP within given distance criterion
[4]Locus 2 for autosomal pairs has a *domesticus* sterile allele; locus 2 for X-autosomal pairs is autosomal
[5]Mean number significant SNPs within distance criterion for either locus
[6]Mean number significant SNPs on chromosomes not containing 'causal' SNPs