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Figure S1 Distribution of litter sizes for each cross. For each of the 62 crosses, we plot the distribution of litter sizes (ranging from 1 to 16). The red line indicates the mean litter size for each cross. The “X” symbol indicates crosses for which no offspring are produced. The y-axis is scaled to the individual maximum frequency for each plot.

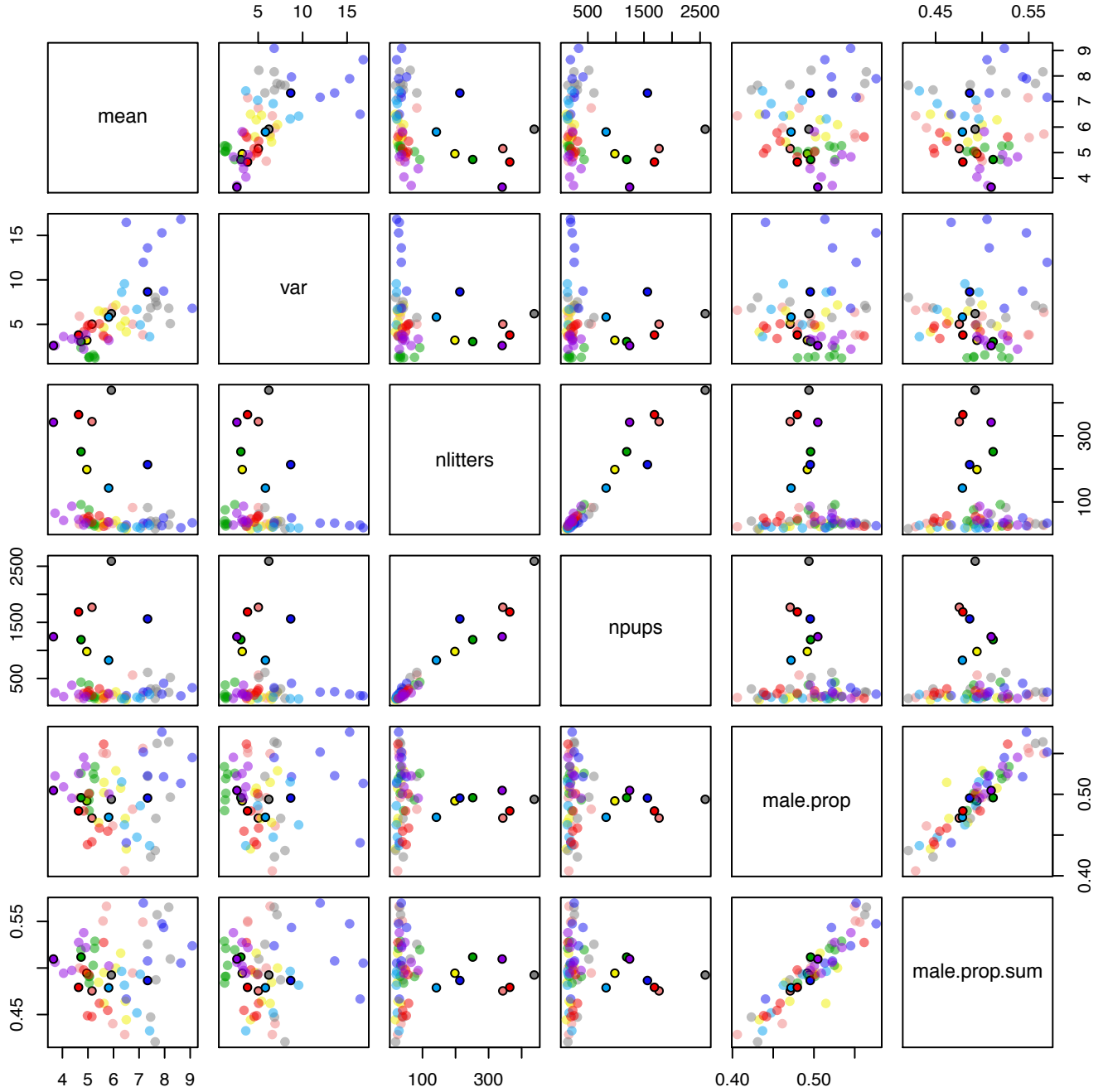


Figure S2 Phenotype relationships by cross. For each of the 62 crosses, we plot the mean, variance, total number of litters (nlitters), total number of pups (npups), and male proportion (male.prop=mean(males/total); male.prop.sum=sum(males)/sum(total)). The colors indicate maternal strain identity, and the circles outlined in black indicate the inbred founder genotypes.

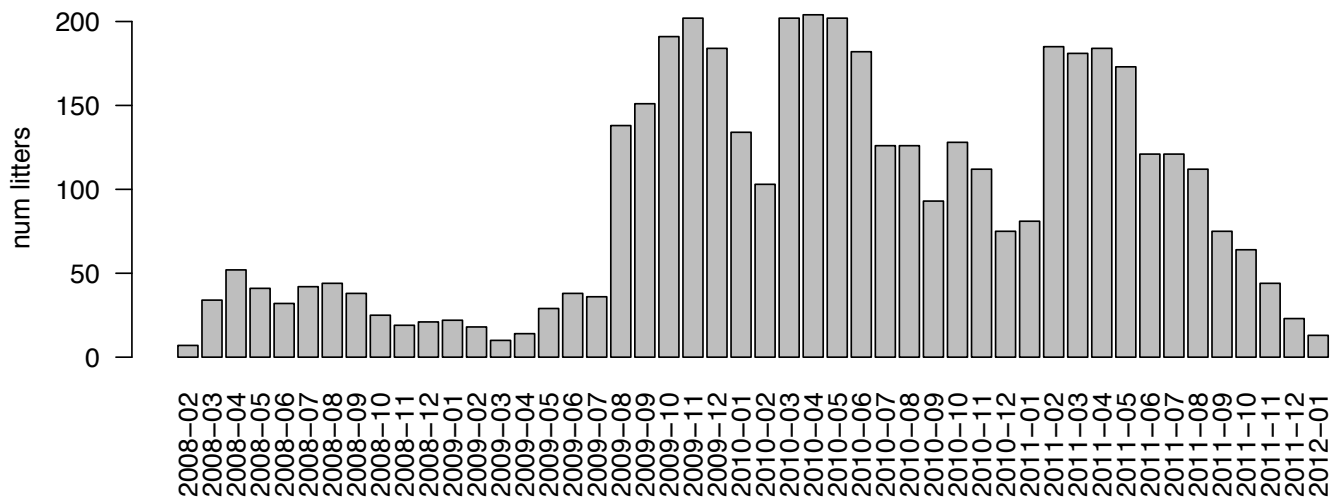


Figure S3 Overview of litter data collected over time.

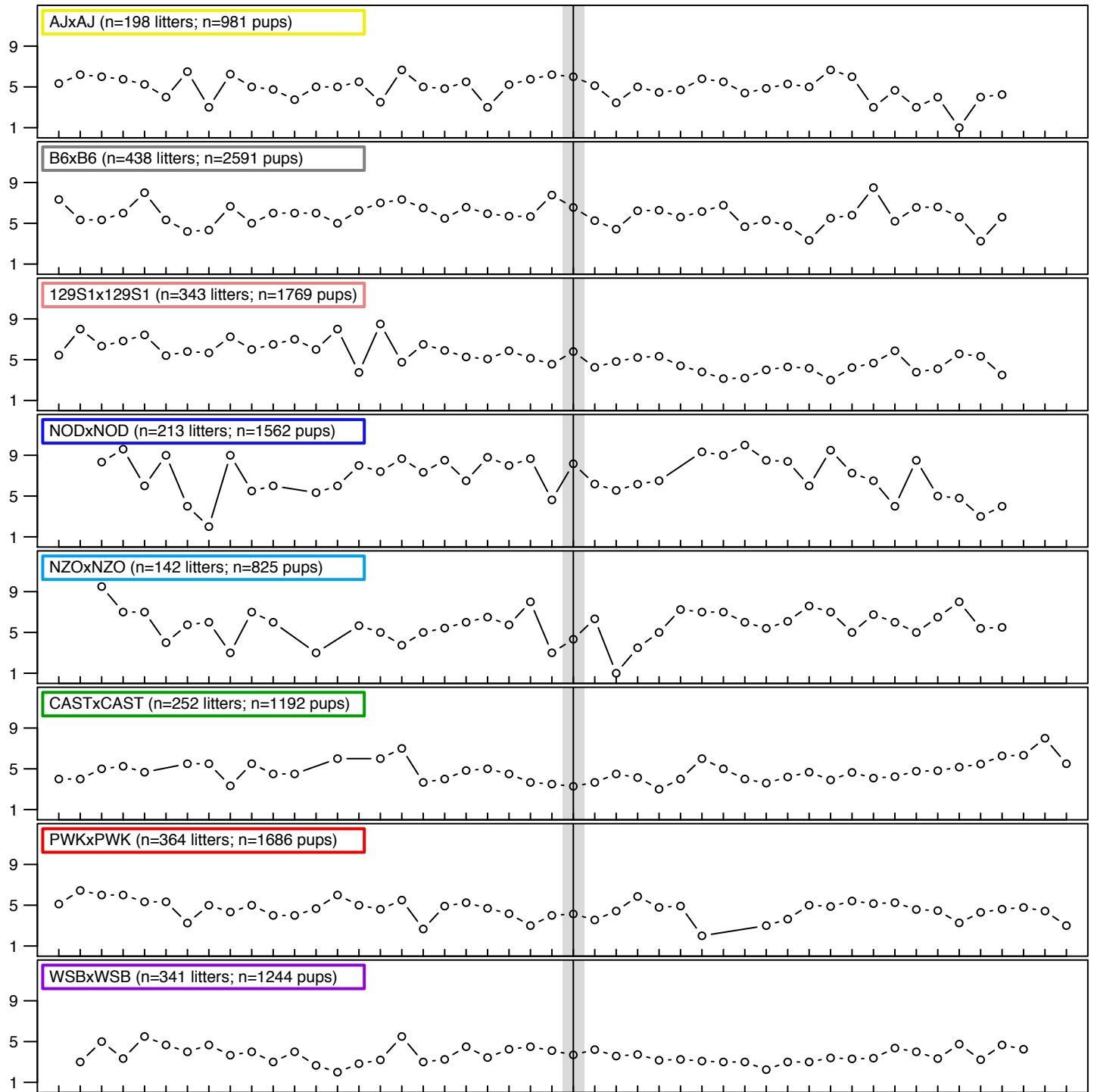


Figure S4 Average number of pups weaned per litter for eight inbred founders over time. The y-axis represents the average litter size for litters born in each month across four years of data collection (03/2008 to 02/2012). Each tick on the x-axis represents a consecutive month during this study. The vertical black line in the center of each figure indicates the month (03/2010) during which mice were transferred from the Hillsborough, NC vivarium facility to the UNC GMB facility, and the grey shaded rectangle indicates the period between the first and second supplementation of mouse chow with Fenbendazole.

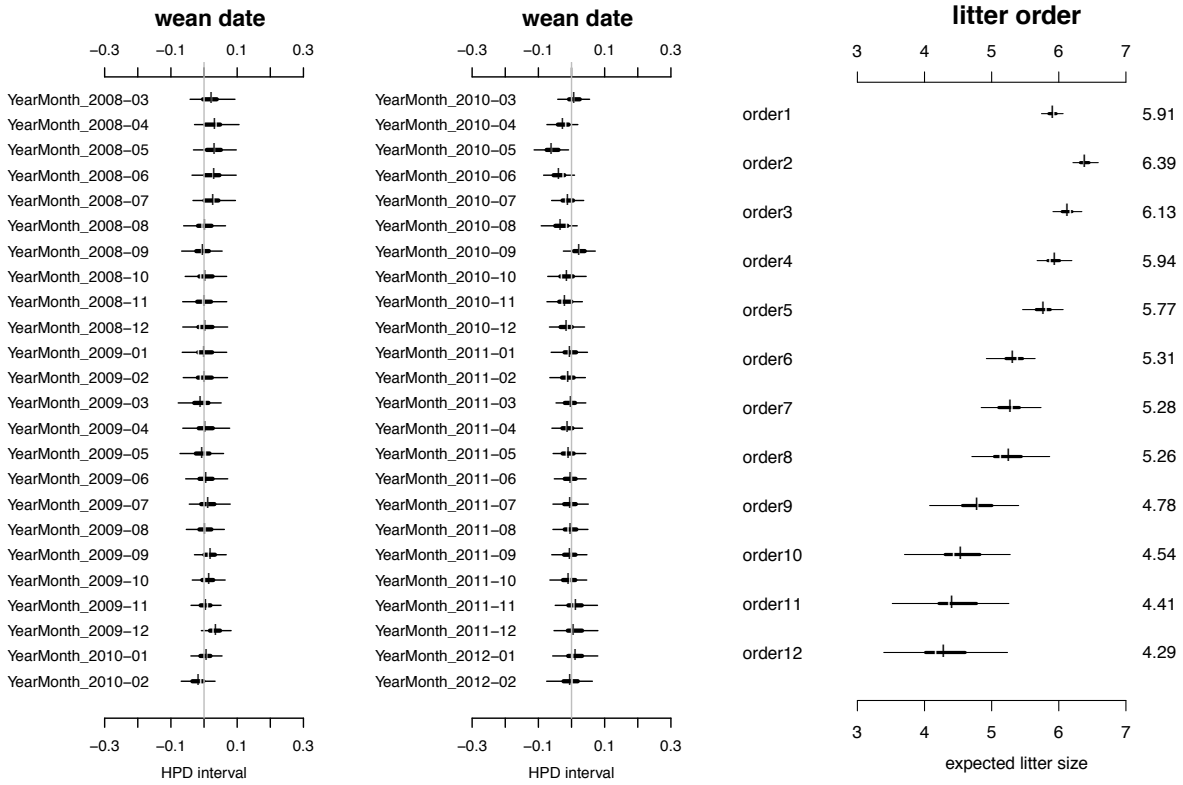


Figure S5 Wean date and birth order effects on litter size. The highest posterior densities of the effect estimates are shown on the latent scale for the wean date effects. For litter birth order 1 through 12, the posterior predictive confidence intervals (means printed to the right) are shown for expected litter size on the data scale (number of pups), and are based on the fixed and random effects estimates for litter order terms, and the overall μ .

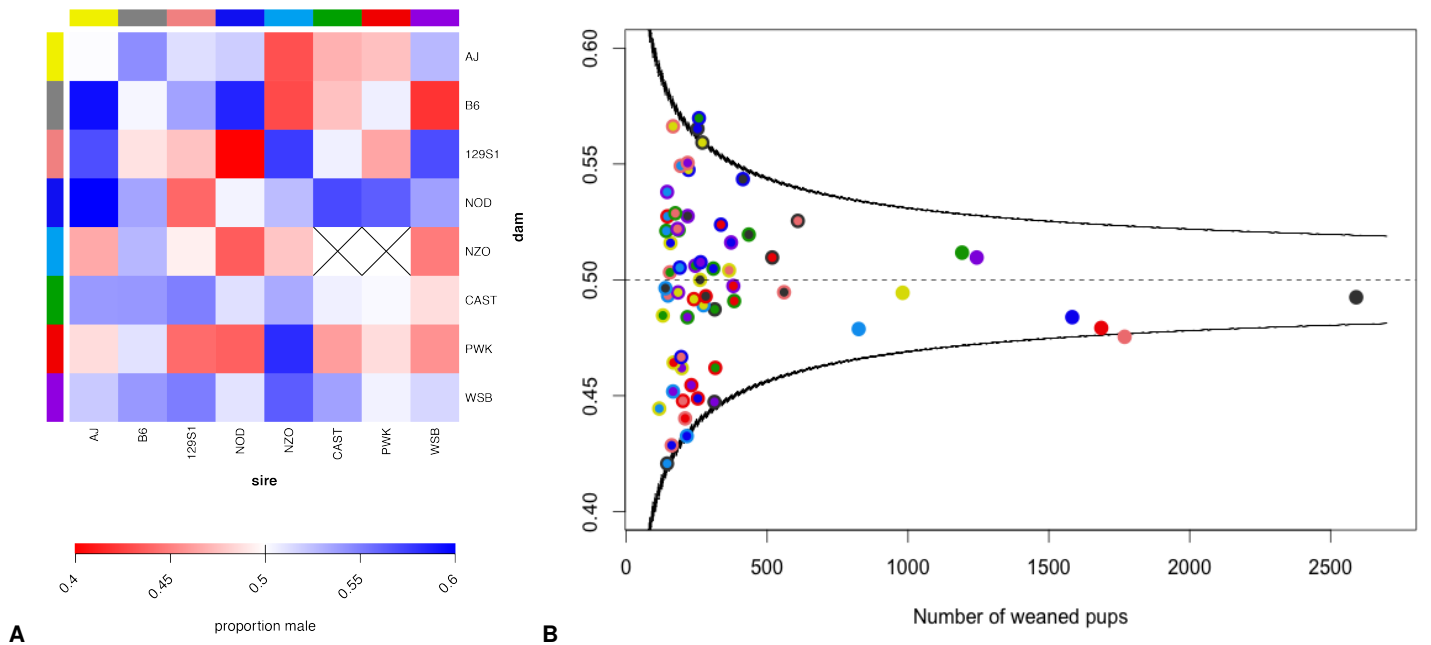


Figure S6 Examination of sex ratio distortion in the diallel. (A) Heatmap indicating overall proportion of males in each observed cross in the diallel. (B) Observed proportion of male pups to total pups across all 62 crosses, as a function of the total number of weaned pups per cross (zoomed in from npups vs. male.prop panel in Figure S2). The boundary lines indicate the expected 95% interval for random binomial data with increasing N. Solid dots indicate inbred litters, dots with a different color outline indicate F1s.

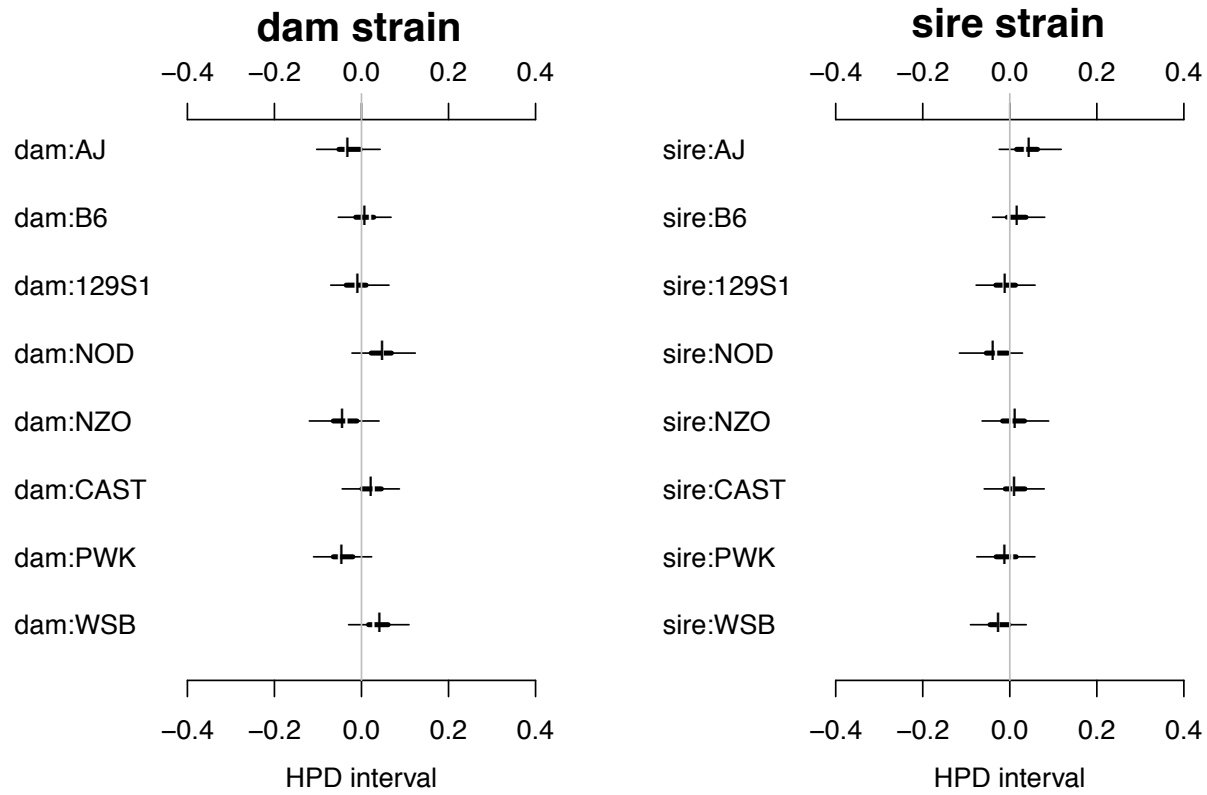


Figure S7 Estimated dam.strain and sire.strain effects on sex ratio distortion, using BayesDiallel. This shows the highest posterior density (HPD) intervals for the maternal (“dam.strain”) and paternal (“sire.strain”) effects on male pup proportion.

SUPPLEMENTAL TABLES

■ Table S1 Model parameters: random and fixed.

Parameter	Color	Description	Type	Levels
μ		mean (overall)	fixed	1
α		litter order (overall)	fixed	1
$u^{(\text{order})}$		litter order	random	12
$u^{(\text{batch})}$		experimental batch	random	48
a_j	light blue	strain-specific additive	random	8
m_j	light green	strain-specific parental sex (parent-of-origin)	random	8
β_{inbred}	pink	inbred penalty (overall)	fixed	1
b_j	light orange	strain-specific inbred penalty	random	8
v_{jk}	lavender	strain pair-specific symmetric epistasis	random	28
w_{jk}	tan	strain pair-specific asymmetric epistasis (parent-of-origin)	random	28
dam_j		strain-specific dam ($a_j + m_j$)		8
sire_j		strain-specific sire ($a_j - m_j$)		8

■ **Table S2** Model inclusion probabilities (MIPs) using the Gaussian model.

Parameter Class	MIP
mu	1.0000
inbred.overall	0.9989
litternum	0.9983
litterorder	0.9972
Year-Month	1.0000
additive	1.0000
parental.sex	0.3432
inbred	0.9998
symmetric.epistatic	1.0000
asymmetric.epistatic	0.9866