SUPPLEMENTAL INFORMATION APPENDIX

Table S1. Genotypes, phenotypes, abbreviations.

Phenotype	*♂ genotypes*	*♀ genotypes*
Ry	D	D/D, D/r2
R	none	D/+, D/r1
y	r2	r2/r2
WT	+, r1	+/+, +/r1, +/r2, r1/r1, r1/r2, +/r2m, r1/r2m
Rm	none	D/r2m
m	r2m	r2/r2m, r2m/r2m

R – dsRed phenotype
y – yellow phenotype
WT – wild-type phenotype
m – mosaic for eye phenotype
D – drive allele with disrupted target gene
r1 – type 1 resistance allele, preserves gene function
r2 – type 2 resistance allele, disrupts gene function
r2m – mosaic for type 2 resistance allele
+ – wild-type allele
♀ / ♂ – female / male
w - white-eye phenotype (used in Data S1-S3 and S6)

Drive parameter calculations

The listed equations show how different drive parameters were calculated for gene drive flies after phenotyping the progeny resulting from a cross of D/+ drive heterozygotes together with wild-type individuals. Numbers of flies in equations refer to the counts of progeny with the listed phenotypes. See the Supplemental Data Sets for specific individual rate calculations.

$$\text{Drive inheritance rate} = \frac{\text{dsRed Flies}}{\text{total flies}}$$

$$\text{Drive conversion rate (for D/+ flies)} = 2 * \frac{\text{dsRed Flies}}{\text{total flies}} - 1$$

$$\text{r2 inheritance rate (based on male progeny)} = \frac{\text{y } \male}{\text{total } \male}$$

$$\text{Germline r2 formation rate (based on male progeny)} = 2 * \frac{\text{y } \male}{\text{total } \male}$$

$$\text{Male (progeny) wild-type (phenotype) rate} = 2 * \frac{\text{WT } \male}{\text{total } \male}$$

$$\text{Embryo r2 allele formation rate in flies inheriting a drive allele} = \frac{\text{Ry}\female}{\text{R}\female + \text{Ry}\female + \text{Rm}\female}$$

$$\text{Embryo r2 allele mosaicism rate in flies inheriting a drive allele} = \frac{\text{Rm}\female}{\text{R}\female + \text{Ry}\female + \text{Rm}\female}$$

$$\text{Embryo r2 allele formation rate in flies not inheriting a drive allele} = \frac{\text{y}\female}{\text{WT}\female + \text{y}\female + \text{m}\female}$$

$$\text{Embryo r2 allele mosaicism rate in flies not inheriting a drive allele} = \frac{\text{m}\female}{\text{WT}\female + \text{y}\female + \text{m}\female}$$
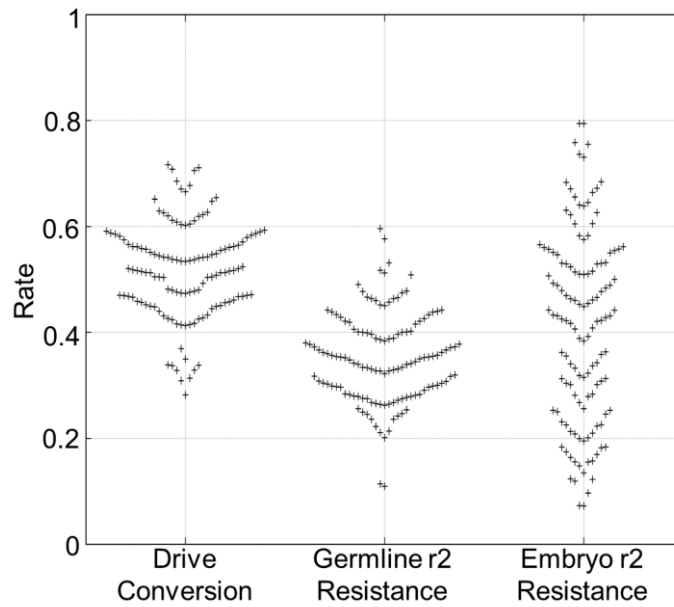
Figure S1 Variation in drive performance parameters among the DGRP lines. Each symbol on the plot represents the average rate for a single DGRP line.
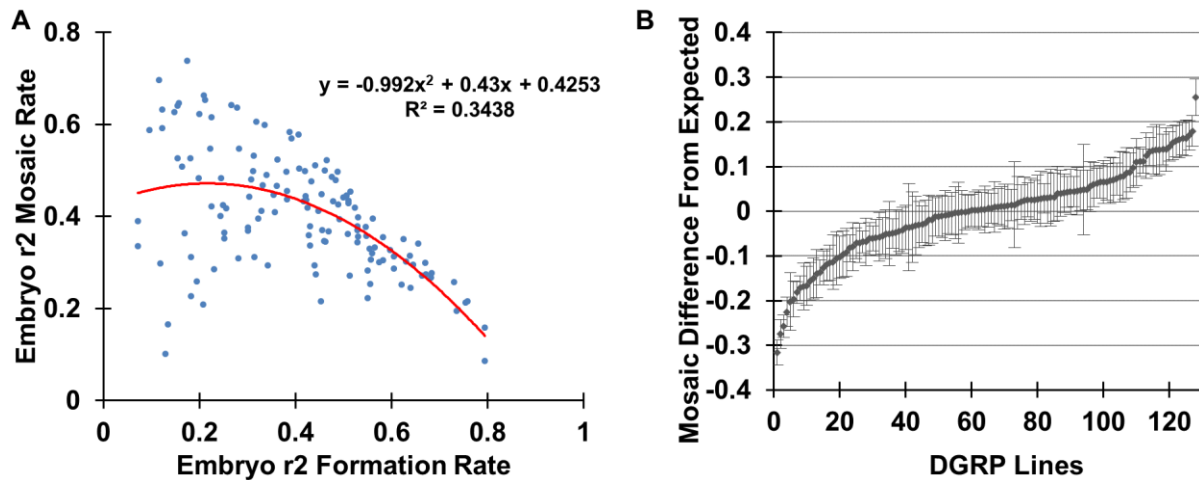

Figure S2 The relation between the full embryo r2 resistance allele formation rate and the mosaic embryo rate. (**A**) Each point represents values from a single DGRP line. A second-order polynomial was fitted to the data to determine the average expected rate of mosaic daughters (also inheriting the drive) from crosses between drive/wild-type heterozygote females and wild-type males based on the rate of daughters with full embryo r2 alleles (and also inheriting the drive). (**B**) The difference between the observed rate of mosaicism and the expected rate based on the full embryo r2 rate was plotted. Each point represents the difference value ± standard error in a single DGRP line.
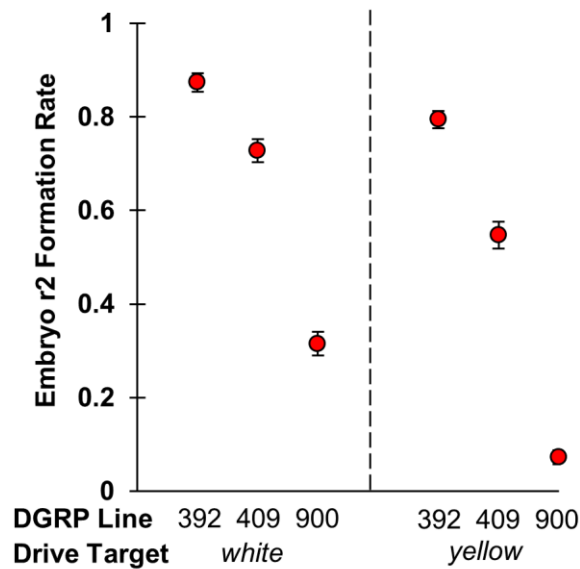
Figure S3 Effects of genetic background are similar between drives with different target sites. The rate of full embryo r2 resistance allele formation is shown (± standard error) for three DGRP lines with both the drive targeting *yellow* and a similar drive targeting *white*. The drive targeting *white* produces overall more embryo r2 resistance allele formation, but the pattern between the lines is similar.
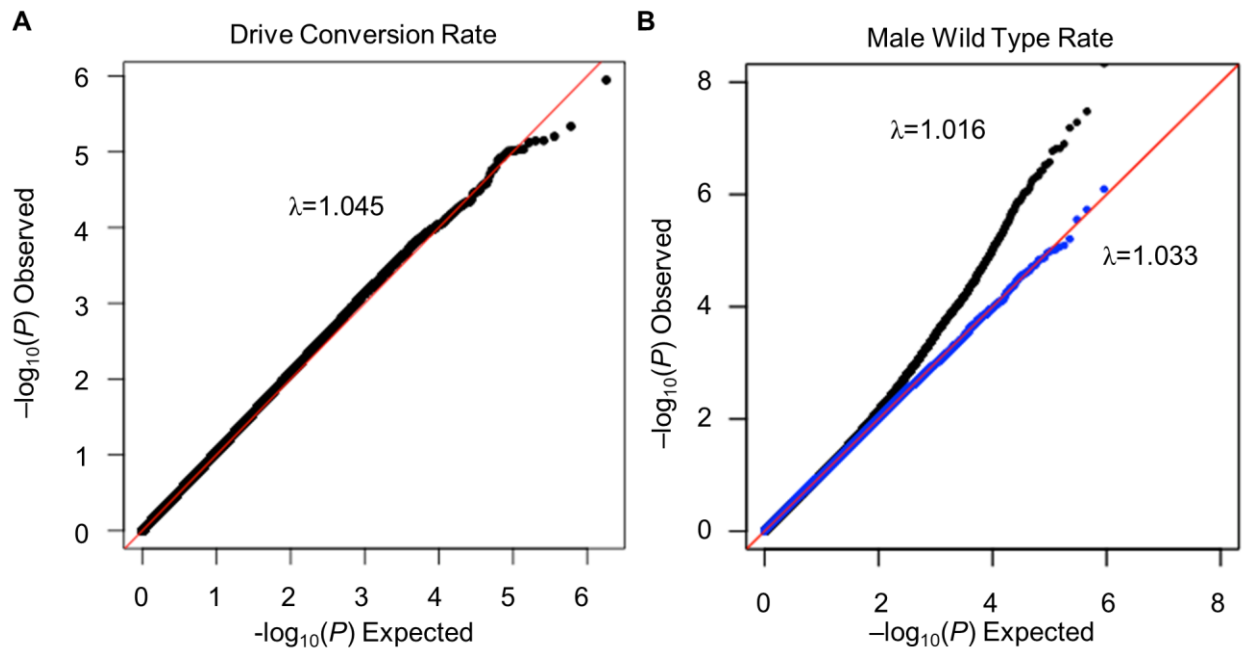

Figure S4 Q-Q analysis of GWAS for drive performance among the DGRP lines. A plot of expected vs. observed $-\log_{10}(P\text{-value})$ for each hit for (**A**) drive conversion efficiency in heterozygote females and (**B**) the rate of wild-type phenotype in male progeny, with rank-normalization corrected values shown in blue.
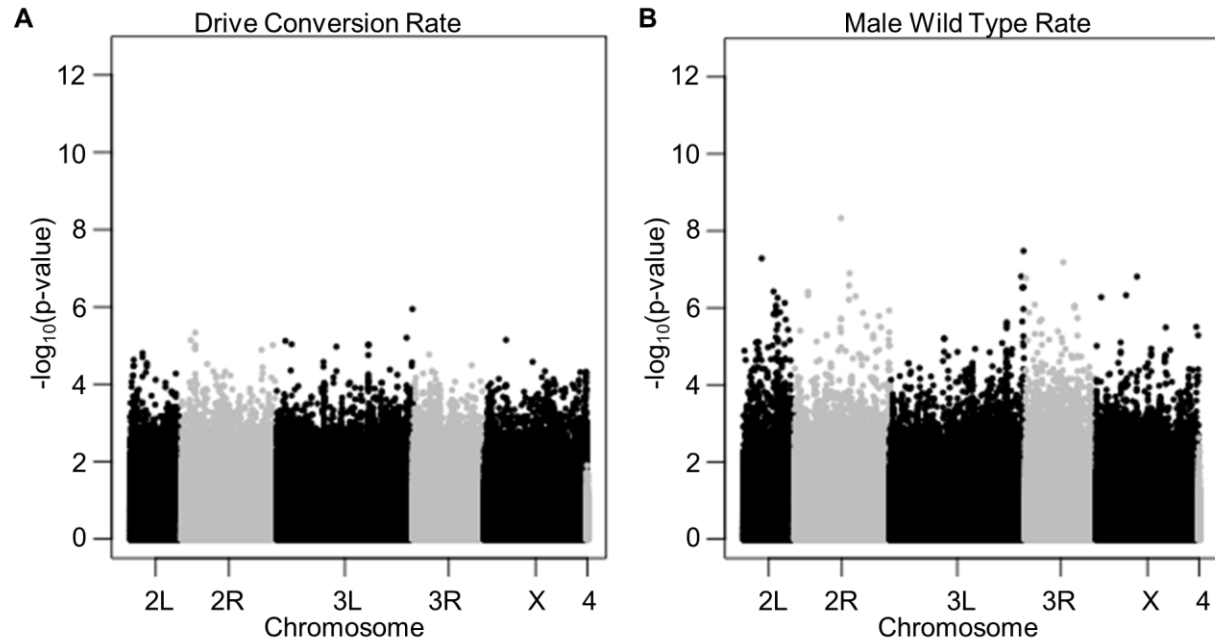
Figure S5 Manhattan plot from GWAS analysis. Each dot shows the location and *P*-value of a single polymorphism of the (**A**) drive conversion rate in heterozygote females and (**B**) the rate of wild-type phenotype in male progeny.