Online Supplementary Material

An X-linked meiotic drive allele has strong, recessive fitness costs in female *Drosophila pseudoobscura*, by Larner et al. *Proceedings of the Royal Society B*

The figures and tables in this document, along with the with the R code used to generate them, can also be viewed online at https://lukeholman.github.io/cost_of_SR_Dpseudo/
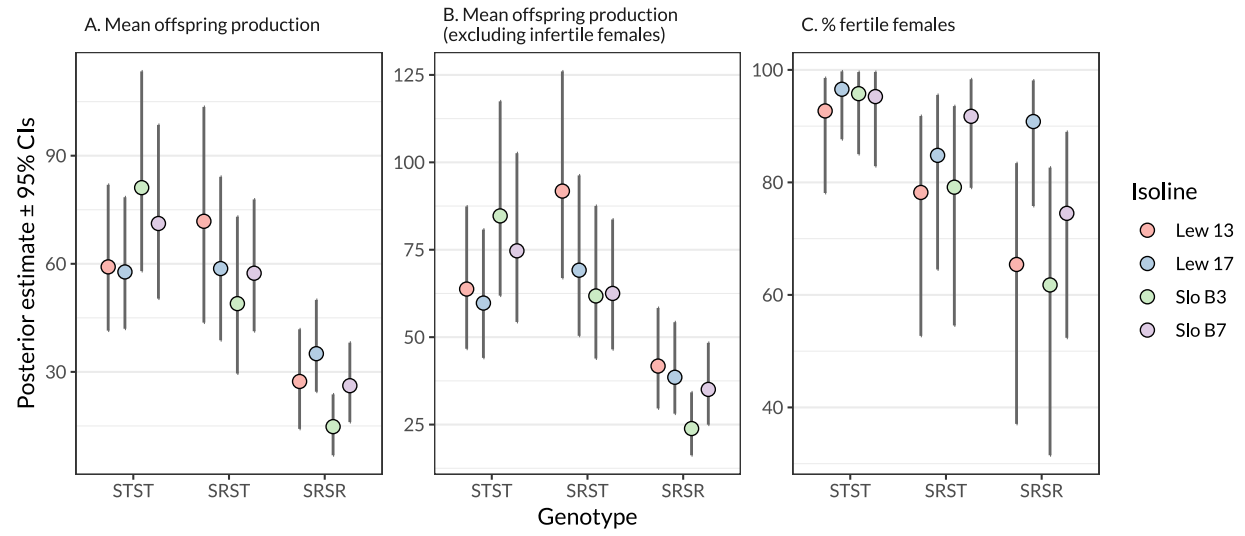
Figure S1: The same information as in Figure 1, except split by isoline. See Table S1 for sample sizes.
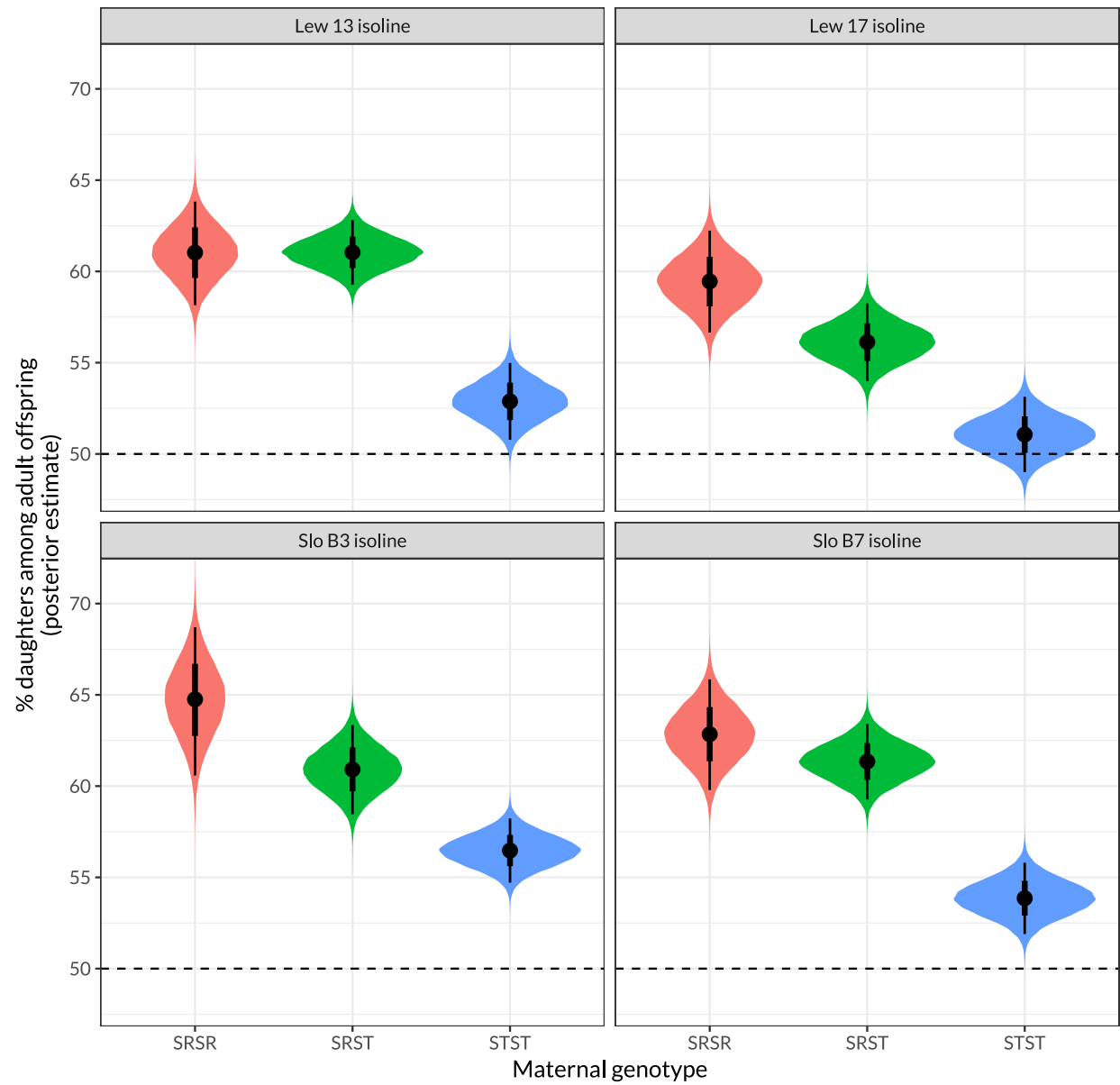
Figure S2: The same information as in Figure 3, except split by isoline.

Table S1: Sample sizes and summary statistics for the experiment. For each genotype and isoline combination (or across all the isolines), we give the sample size (i.e. number of females measured), their mean productivity (including the unproductive females), the associated standard error, the number of productive females (i.e. those who produced one or more offspring), and the % females that were productive.

Genotype	Isoline	n females	Mean productivity	SE	n productive	% productive
STST	Lew 13	37	57.81	6.46	35	94.59
STST	Lew 17	40	56.85	5.04	39	97.50
STST	Slo B3	40	76.67	5.59	39	97.50
STST	Slo B7	35	71.14	4.71	34	97.14
SRST	Lew 13	39	72.82	8.70	32	82.05
SRST	Lew 17	37	56.24	8.11	32	86.49
SRST	Slo B3	31	49.10	5.20	26	83.87
SRST	Slo B7	39	55.26	7.07	36	92.31
SRSR	Lew 13	36	28.58	5.92	25	69.44
SRSR	Lew 17	37	32.19	3.91	34	91.89
SRSR	Slo B3	31	17.19	4.56	22	70.97
SRSR	Slo B7	38	25.50	4.76	28	73.68
STST	Across all isolines	152	65.59	2.81	147	96.71
SRST	Across all isolines	146	58.89	3.83	126	86.30
SRSR	Across all isolines	142	26.21	2.45	109	76.76

Table S2: Parameter estimates from the Bayesian model plotted in Figure 1, showing the fixed effect estimates of genotype and female age, for both components of the hurdle model (n = 440 females). The Rhat and ESS (effective sample size) columns indicate that the model has converged and the posterior was well-sampled, respectively. The p column has the same interpretation as in Table 1. The final two rows show the standard deviation of the random intercepts associated with experimental block.

Parameter	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS	p	
Intercept	4.244	0.236	3.782	4.705	1.000	76247	51126	0.0000	*
Hurdle - Intercept	-2.304	0.940	-4.180	-0.486	1.000	79331	56507	0.0067	*
genotypeSRST	0.030	0.089	-0.143	0.206	1.000	74772	62501	0.3693	
genotypeSRSR	-0.669	0.094	-0.851	-0.482	1.000	77722	61179	0.0000	*
female_age	-0.010	0.053	-0.113	0.095	1.000	105585	57494	0.4280	
Hurdle - genotypeSRST	1.488	0.505	0.542	2.533	1.000	57326	49312	0.0007	*
Hurdle - genotypeSRSR	2.093	0.489	1.191	3.113	1.000	55547	49201	0.0000	*
Hurdle - female_age	-0.240	0.210	-0.651	0.170	1.000	101961	57083	0.1257	
sd(Block - Intercept)	0.137	0.125	0.006	0.453	1.000	17685	32248	NA	
sd(Block - Hurdle intercept)	0.328	0.344	0.011	1.176	1.000	25228	33771	NA	

Table S3: Parameter estimates from the Bayesian model plotted in Figure S1, showing the fixed effect estimates of genotype, isoline, the genotype-by-isoline interaction, and female age, for both components of the hurdle model (n = 440 females). The Rhat and ESS (effective sample size) columns indicate that the model has converged and the posterior was well-sampled, respectively. The p column has the same interpretation as in Table 1. The final two rows show the standard deviation of the random intercepts associated with experimental block.

Parameter	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS	p	
Intercept	4.048	0.267	3.528	4.574	1.000	72473	57919	0.0000	*
Hurdle - Intercept	-1.472	1.135	-3.708	0.765	1.000	67580	60659	0.0947	
genotypeSRST	0.364	0.168	0.037	0.696	1.000	38432	53888	0.0145	*
genotypeSRSR	-0.426	0.183	-0.783	-0.064	1.000	39680	53807	0.0106	*
IsolineLew17	-0.064	0.162	-0.383	0.253	1.000	43018	54768	0.3465	
IsolineSloB3	0.283	0.165	-0.042	0.607	1.000	43390	55525	0.0434	*
IsolineSloB7	0.158	0.168	-0.171	0.487	1.000	43288	55837	0.1735	
female_age	0.023	0.057	-0.089	0.135	1.000	116292	59814	0.3422	
genotypeSRST:IsolineLew17	-0.220	0.243	-0.698	0.255	1.000	43855	58262	0.1831	
genotypeSRSR:IsolineLew17	-0.015	0.253	-0.512	0.480	1.000	42954	55722	0.4758	
genotypeSRST:IsolineSloB3	-0.682	0.251	-1.175	-0.190	1.000	47072	56573	0.0033	*
genotypeSRSR:IsolineSloB3	-0.845	0.267	-1.368	-0.318	1.000	47446	58737	0.0009	*
genotypeSRST:IsolineSloB7	-0.540	0.239	-1.011	-0.073	1.000	45584	55874	0.0117	*
genotypeSRSR:IsolineSloB7	-0.331	0.260	-0.843	0.175	1.000	45035	57432	0.1011	
Hurdle - genotypeSRST	1.412	0.712	0.056	2.865	1.000	49133	52278	0.0204	*
Hurdle - genotypeSRSR	2.104	0.700	0.788	3.540	1.000	49181	51113	0.0005	*
Hurdle - IsolineLew17	-0.978	1.021	-3.104	0.904	1.000	47749	49997	0.1673	
Hurdle - IsolineSloB3	-0.738	0.982	-2.768	1.080	1.000	46415	47553	0.2286	
Hurdle - IsolineSloB7	-0.644	1.030	-2.792	1.255	1.000	45448	51193	0.2709	
Hurdle - female_age	-0.324	0.234	-0.787	0.131	1.000	122902	58474	0.0825	
Hurdle - genotypeSRST:IsolineLew17	0.496	1.163	-1.702	2.858	1.000	50908	53025	0.3420	
Hurdle - genotypeSRSR:IsolineLew17	-0.836	1.203	-3.152	1.590	1.000	51879	54263	0.2373	
Hurdle - genotypeSRST:IsolineSloB3	0.661	1.147	-1.534	2.971	1.000	49960	52796	0.2843	
Hurdle - genotypeSRSR:IsolineSloB3	0.900	1.094	-1.160	3.121	1.000	48351	51616	0.2061	
Hurdle - genotypeSRST:IsolineSloB7	-0.591	1.231	-2.981	1.886	1.000	49704	56772	0.3100	
Hurdle - genotypeSRSR:IsolineSloB7	0.188	1.133	-1.958	2.496	1.000	46281	52320	0.4416	
sd(Block - Intercept)	0.180	0.152	0.010	0.556	1.000	20743	32454	NA	
sd(Block - Hurdle intercept)	0.559	0.516	0.023	1.882	1.000	22920	39935	NA	

Table S4: Parameters estimates from a model with the same formula as the top model (i.e. the one shown in Figure 1 and Table S2), with body size added as an additional predictor. Since not every female had a measure of body size, the sample size for this model is lower (n = 338 females). Details are as in Tables S2-S3; note that the parameter estimates are similar to those in Table S2.

Parameter	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS	p	
Intercept	2.501	0.841	0.860	4.172	1.000	78603	61911	0.0014	*
Hurdle - Intercept	-0.813	2.746	-6.253	4.498	1.000	97985	61318	0.3853	
genotypeSRST	0.046	0.118	-0.184	0.280	1.000	54937	56365	0.3480	
genotypeSRSR	-0.623	0.113	-0.842	-0.400	1.000	62405	59369	0.0000	*
female_age	-0.004	0.065	-0.131	0.123	1.000	89886	60265	0.4763	
body_size	1.072	0.539	0.005	2.124	1.000	72909	61737	0.0246	*
Hurdle - genotypeSRST	1.577	0.579	0.503	2.767	1.000	51814	50939	0.0018	*
Hurdle - genotypeSRSR	2.338	0.534	1.350	3.458	1.000	52524	47783	0.0000	*
Hurdle - female_age	-0.378	0.228	-0.827	0.065	1.000	91787	58967	0.0478	*
Hurdle - body_size	-0.594	1.708	-3.916	2.789	1.000	88482	60276	0.3627	
sd(Block - Intercept)	0.153	0.133	0.008	0.477	1.000	18485	26949	NA	
sd(Block - Hurdle intercept)	0.319	0.306	0.011	1.108	1.000	28166	39262	NA	