### Estimation of variance components and heritability

We estimated variance components for donors and recipients using a full-sib/half-sib design, for sibling plants with at least one half-sib from each parent plant (ndonors =5?, nrecipients= 5?, nsibs=556 ) using a linear mixed model untransformed FFD as response variable donor and recipient identity included as random effects. Size was included as fixed effect to control for plant resource state. Including a covariate may increase the estimate of the additive genetic component and prevent comparisons between studies (Wilson 2008). Thus, we also estimated variance components for donors and recipients without controlling for plant size for comparison. We estimated the intra-class correlation coefficients (ICC) by dividing each variance component with the total phenotypic variance. Additive genetic variance (VA) is expected to be ¼ of the donor variance (Falconer and mckay ) and heritability was hence estimated as four times the donor ICC. The recipient variance component contains a combination of additive genetic and maternal effects on the offspring phenotype (REF). Thus, the maternal non-genetic effect, m2, was estimated by subtracting the additive genetic (donor) component from the recipient variance component and dividing the resulting estimate with the total phenotypic variance (m2 = (Vrecipient - Vdonor)/VP). The residual variance component represents the variance explained by environmental effects and measurement error. These models were fitted using Restricted Maximum Likelihood implemented in the lme4 package in R (Bates etal) and significance for the variance components was estimated using Likelihood Ratio Tests using the same package.

### Genotype analysis

To estimate genetic selection gradients for the sibling plants (n=556), we partitioned the (co)variance of FFD and relative fitness into additive genetic (donor), combined additive genetic and non-genetic maternal (recipient) and environmental (residual) effects, respectively. This was done in a Bayesian setting, using a Gibbs sampler in the R package MCMCglmm (Hadfield…). We used a bivariate model with relative number of intact seeds and FFD as Gaussian response variables. To fit the intercepts for both response variables, rather than the difference between them, we suppressed the model intercept. The (co)variances for donor and recipient ID, respectively, were included as random effects in the model. We used weakly informative parameter expanded priors for the random effects, and flat priors for the fixed effects. We ran one chain for one million iterations, of which the first 10000 iterations were used as burn-in and disregarded. After that every 500 iteration was sampled, which resulted in an effective sample size of 2000. Autocorrelation was within the -0.1 to 0.1 interval, indicating mixing of the chains. Selection gradients for additive genetic, non-genetic transgenerational and environmental effects were estimated by dividing the posterior covariance with the posterior FFD variance component for each group (). We calculated the highest posterior density intervals for the posterior distribution of each gradient. Estimates for which the 95% credible intervals do not overlap zero are considered significant in the frequentist sense. .