

Supplementary Information

Evolutionary simulations of *Z*-linked suppression gene drives

Supplementary Figures and Supplementary Tables

The R code used to generate these figures and tables can be viewed at https://lukeholman.github.io/W_shredder/.

Supplementary tables

Table S1: The number and percentage of simulation runs (out of 5,657,700 total) that ended with the five possible outcomes, for the subset of simulation runs focusing on a *W*-shredder gene drive.

Outcome	Number of simulations	%
Z* fixed without causing extinction	2,330,324	41.2
Z* went extinct	1,584,409	28.0
Population went extinct	917,328	16.2
Wr fixed	689,487	12.2
Timer expired	136,152	2.4

Table S2: The number and percentage of simulation runs (out of 629,954 total) that ended with the five possible outcomes, for the subset of simulation runs focusing on a female-sterilising *Z*-linked gene drive.

Outcome	Number of simulations	%
Z* went extinct	539,978	85.7
Timer expired	69,942	11.1
Population went extinct	12,992	2.1
Wr fixed	7,042	1.1

Supplementary figures

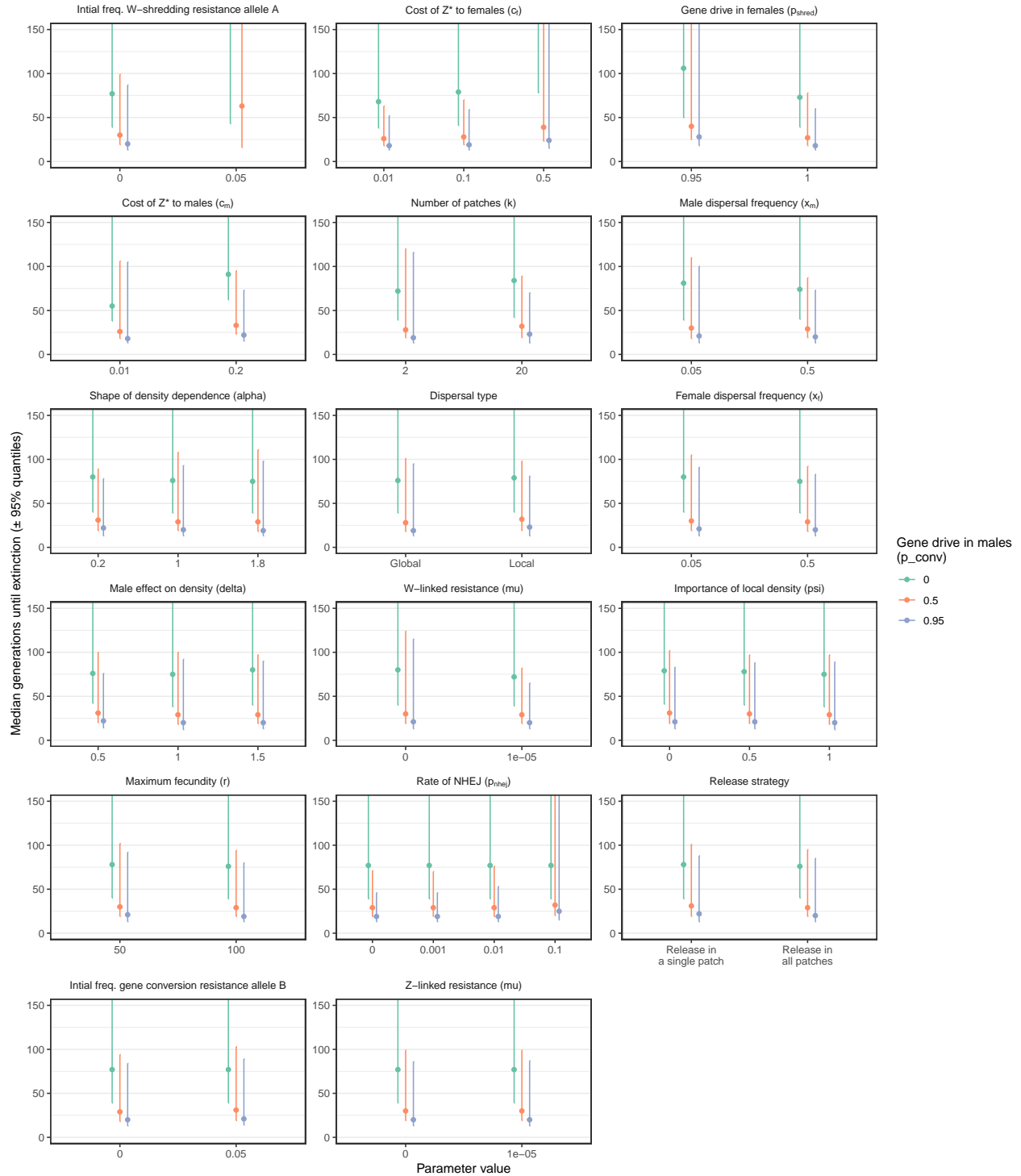


Figure S1: Similar plot to Figure 3, except that the y -axis shows the median number of generations until the W -shredder caused extinction, among just the subset of simulations in which extinction actually occurred. The median was only calculated if at least 40 simulation runs reached extinction, and the y -axis is truncated at 150 generations.

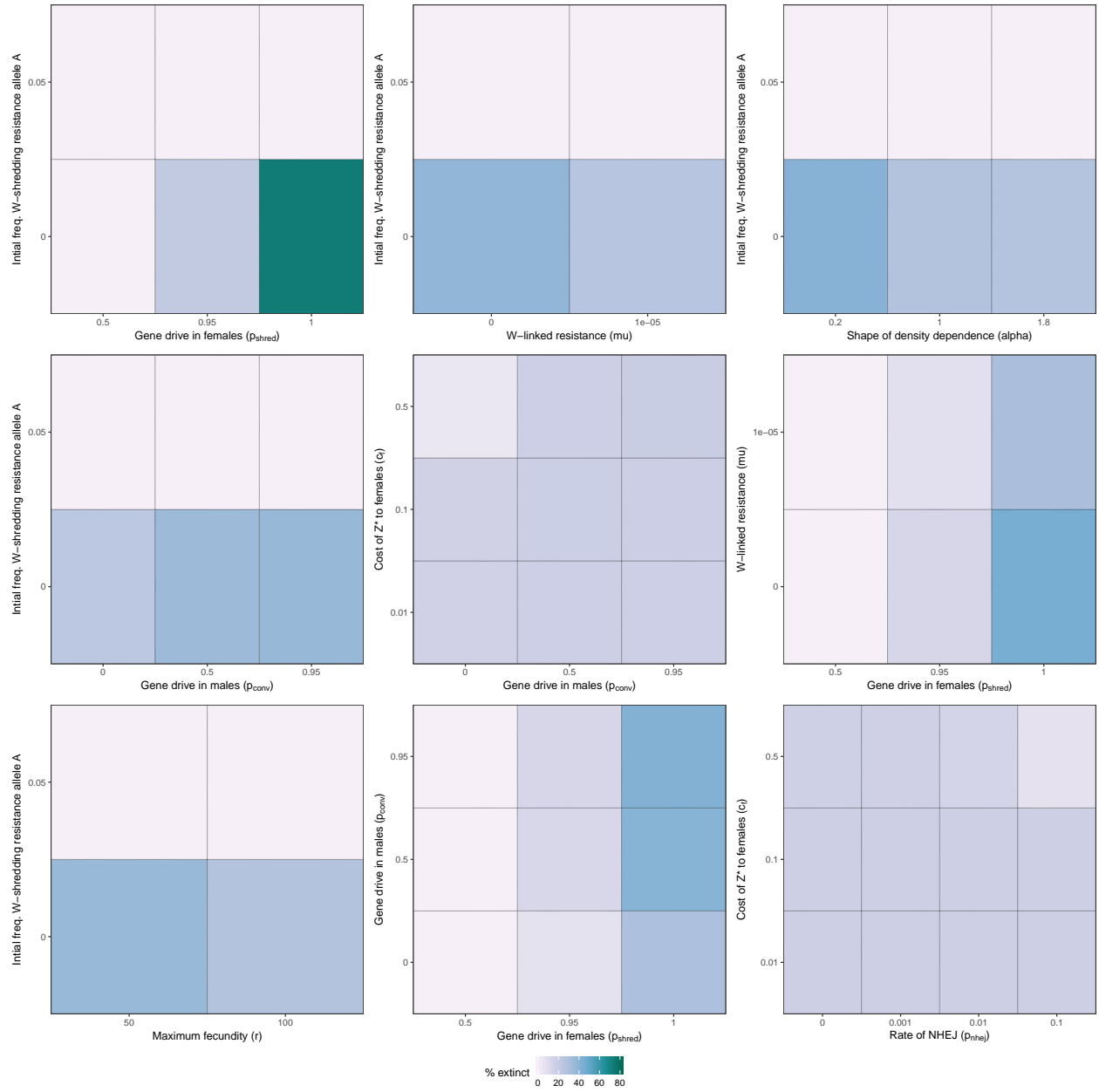


Figure S2: Heatmap showing the twelve strongest interactions between pairs of parameters in the model, as determined by the effect sizes from the GLM plotted in Figure 4.

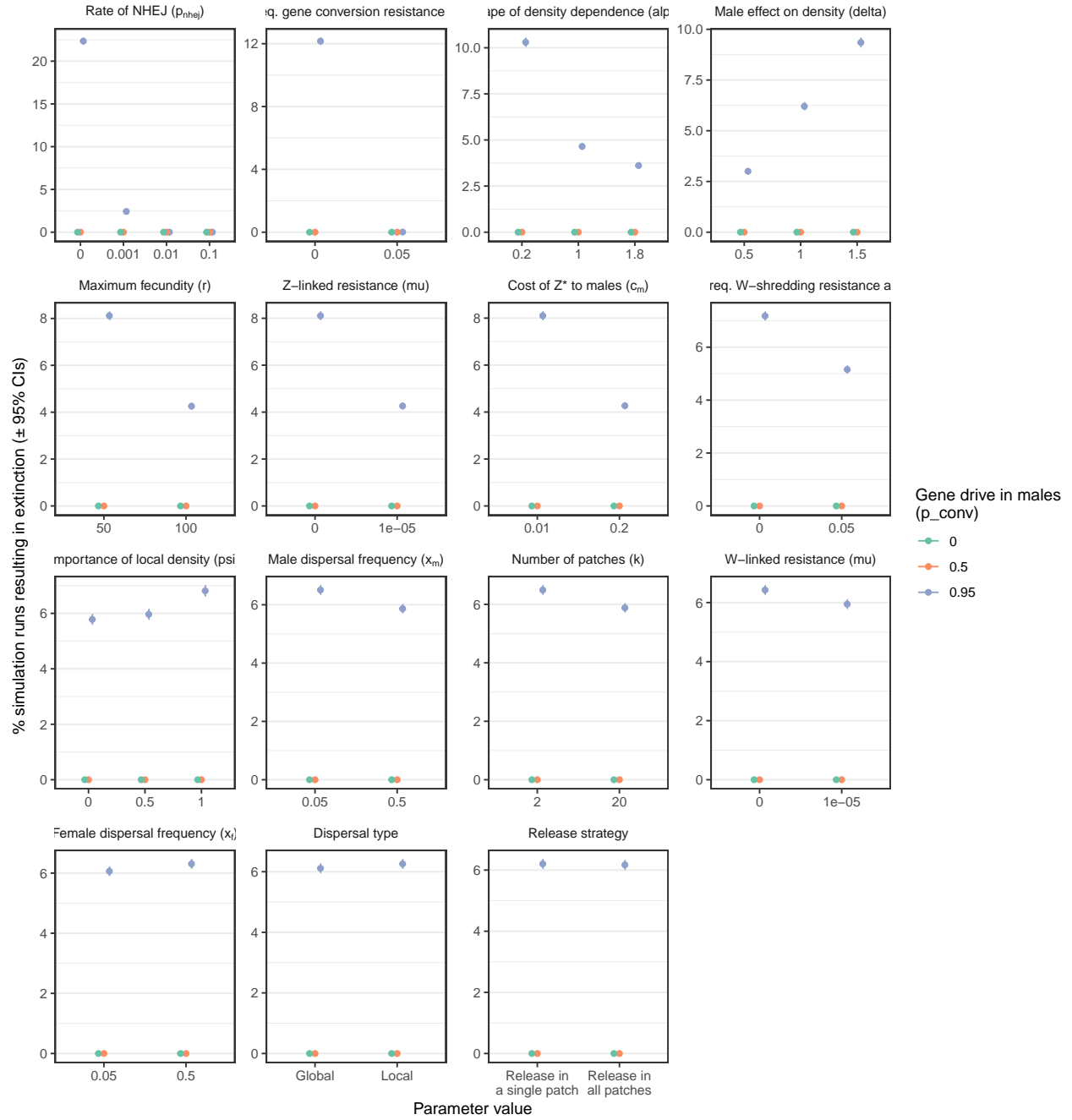


Figure S3: Analogous information to Figure 3, but showing the results for a female-sterilising Z^* allele instead of a W -shredder.

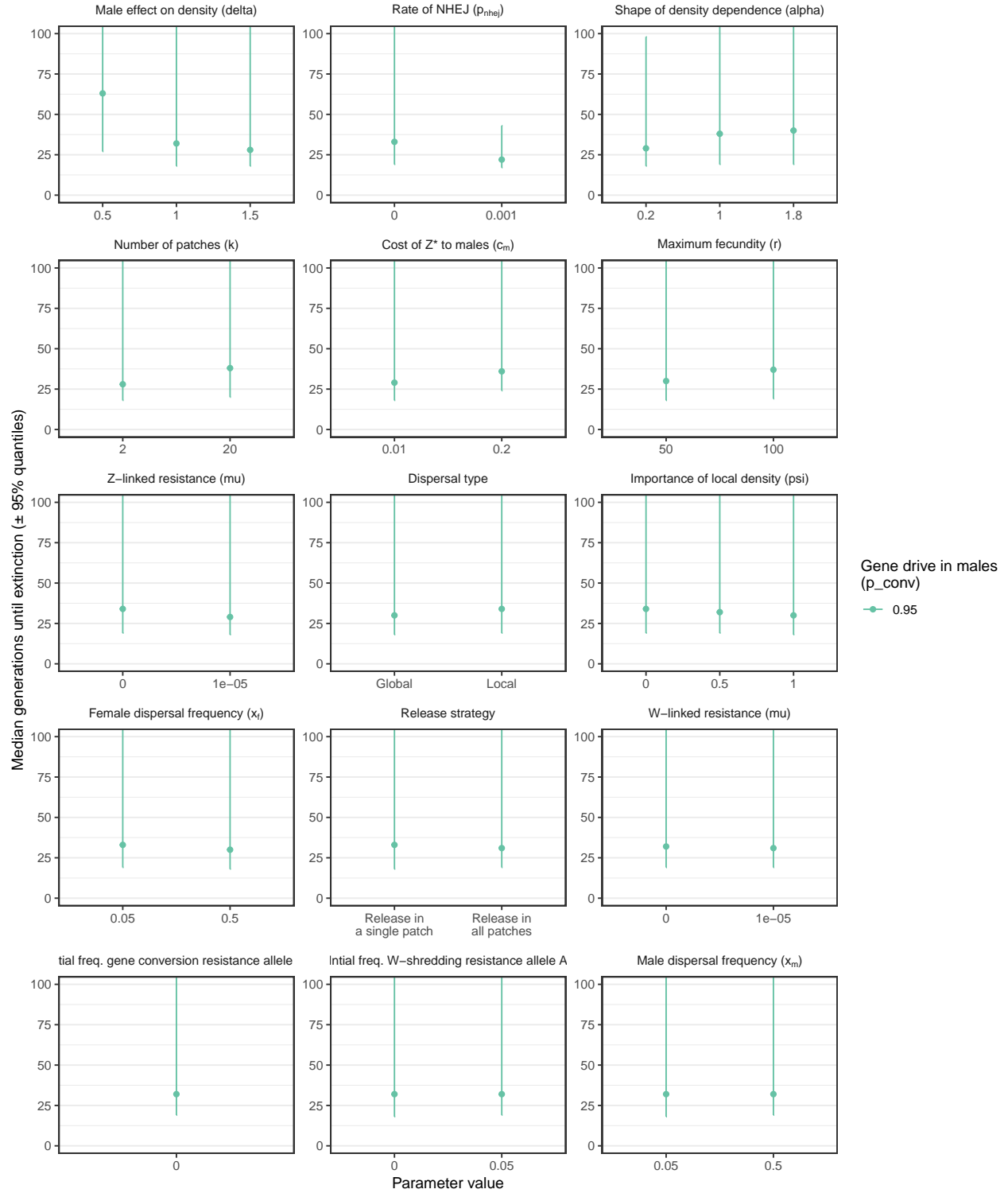


Figure S4: Analogous information to Figure S1, but showing the results for a female-sterilising Z^* allele instead of a W -shredder. Note that a median was only calculated if at least 40 simulation runs reached extinction, and extinction only occurred when gene drive in males was strong ($p_{conv} = 0.95$).

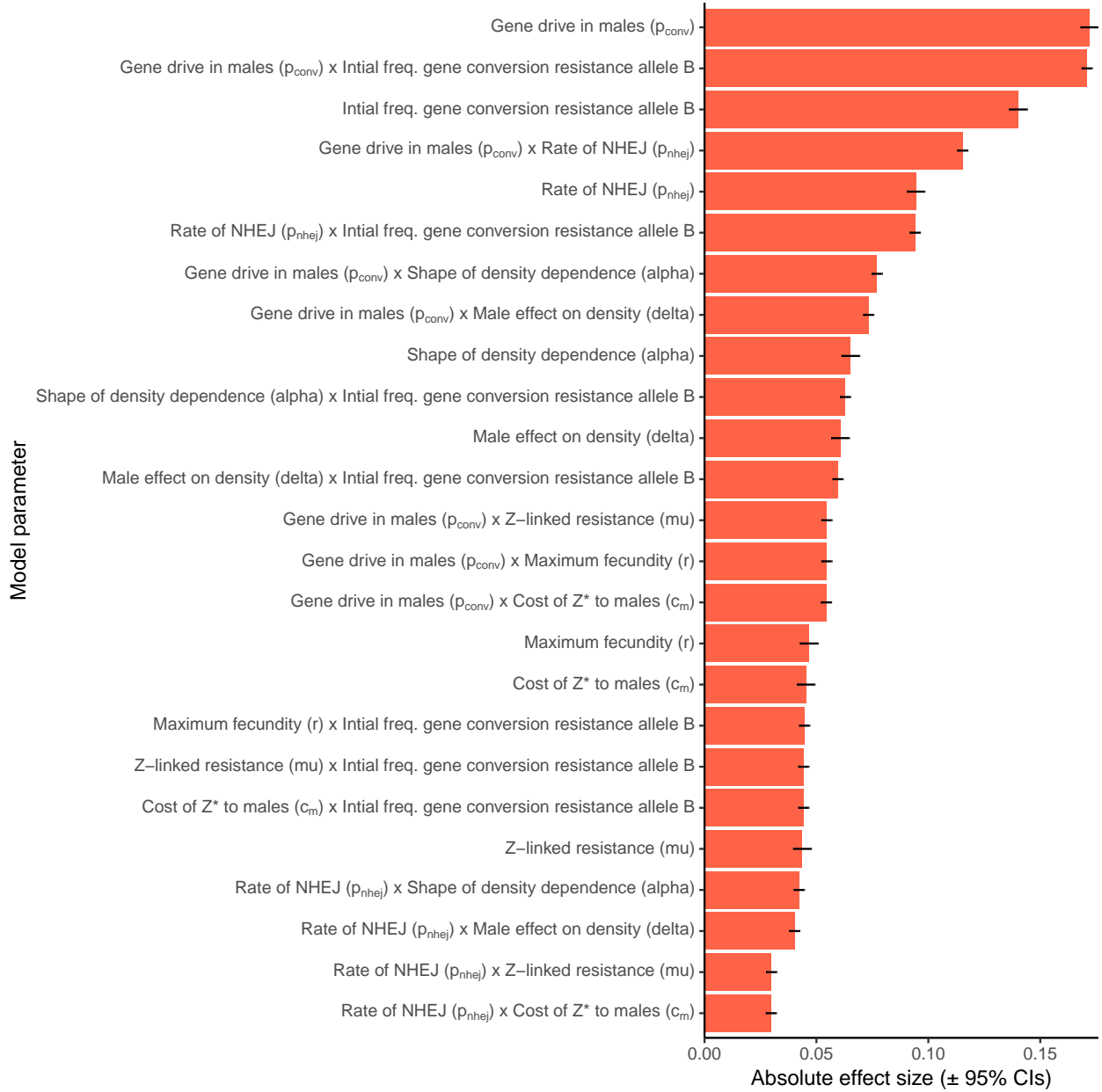


Figure S5: Relative parameter importance in the simulations of Z-linked female-sterilising gene drives, for the top 25 most important main effects or two-way interactions (from a binomial GLM that included all the main effects and all their two-way interactions). Each predictor variable was scaled before running the model, meaning that the absolute effect size indicates how important each parameter is to the extinction probability, given the range of values plotted in Figure S3.

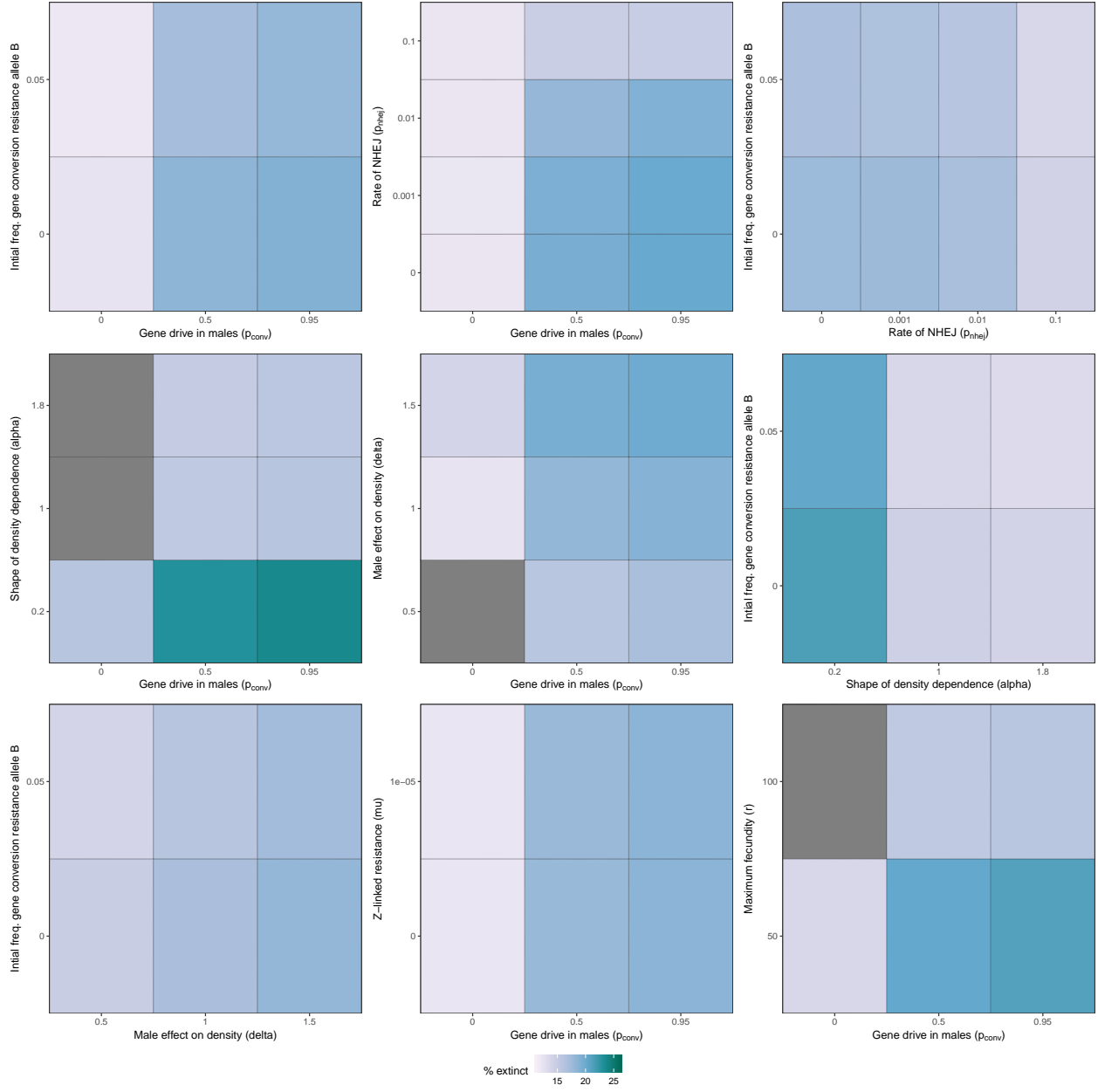


Figure S6: Heatmap illustrating the twelve strongest two-way interactions for simulations of a female-sterilising gene drive, as determined by the effect sizes from the GLM plotted in Figure S5.