***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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For the transcriptomic study of the adult oviducts, we used 12 knockouts and 12 wildtypes in order to have at least minimum sample size for statistics (3 vs. 3) at each stage of estrous cycle, which can be found in the “Results” section “Knockout effect on the transcriptome”, Figure 4, and corresponding “Materials and Methods” section. For the fertility test, we were based on our observation on the data from the normal breeding of the knockout line as prior test. For the formal fertility test, we used 20 breeding pairs (10 knockouts vs. 10 wildtypes) which is generally considered to be the good sample size in this research community. All the information of the fertility test can be found in the “Results” section “Knockout phenotype”, Figure 5, and corresponding “Materials and Methods” section.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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The masking of the genotypes in the fertility test can be found in the corresponding “Materials and Methods” section.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

The source data files of Figure 1, Figure 3, and Figure 5 are provided as supplementary materials. The source data (sequencing data) of Figure 2, Figure 4, and Table 1 are deposited at ENA.