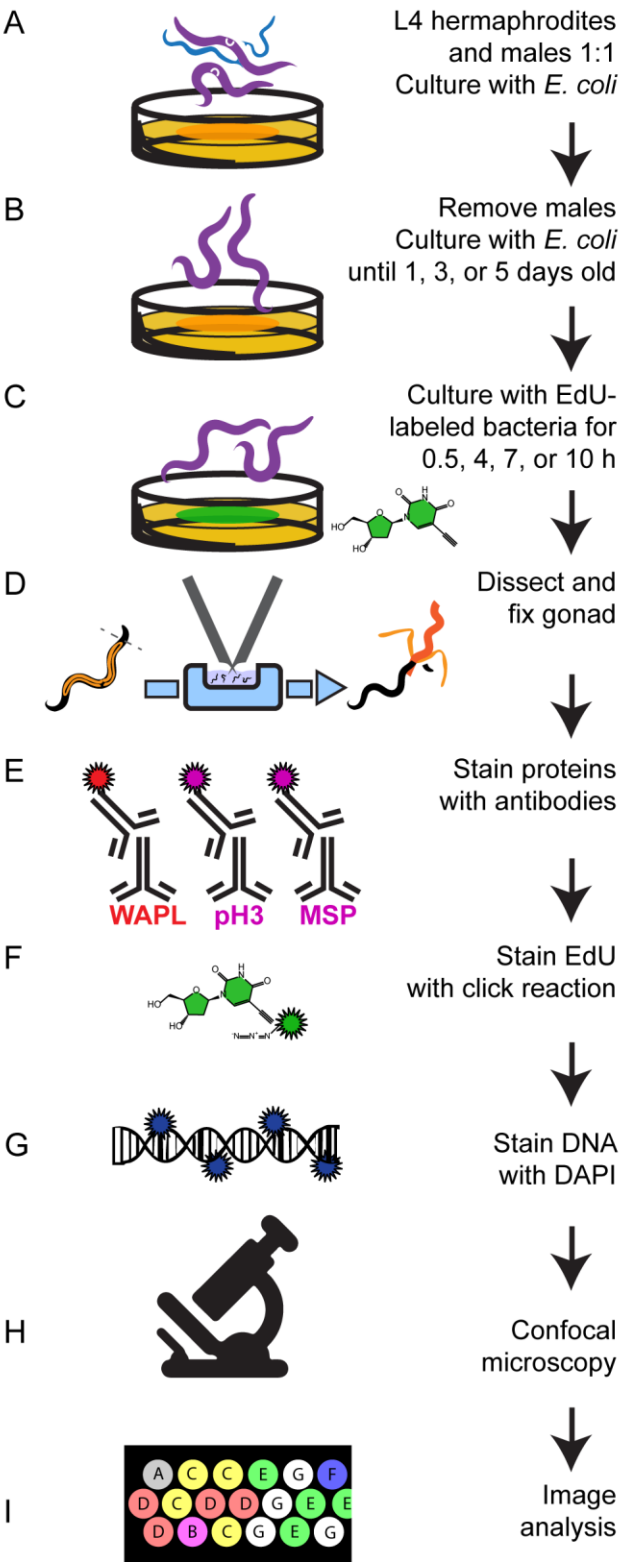

Figure S1. Experimental Workflow.

Experimental workflow used to assay the relationship between S-phase (EdU labeling), M-phase (pH3 antibody staining), progenitor zone cells, as well as the somatic gonadal DTC and sheath cell nuclei (WAPL-1 antibody staining), sperm presence (Major Sperm Protein antibody staining), and DNA morphology of each individual *C. elegans* germline. Hermaphrodites were mated to males **(A)**, cultured to the appropriate age **(B)**, EdU labeled by feeding **(C)**, dissected **(D)**, and stained with antibodies **(E)**. A click reaction was used to attach a dye to EdU **(F)**, DNA was stained with DAPI **(G)**, and germlines were imaged on a spinning disc confocal microscope **(H)** and analyzed in FIJI **(I)**. Diagram modified with permission from Kocsisova et al. (2018a).

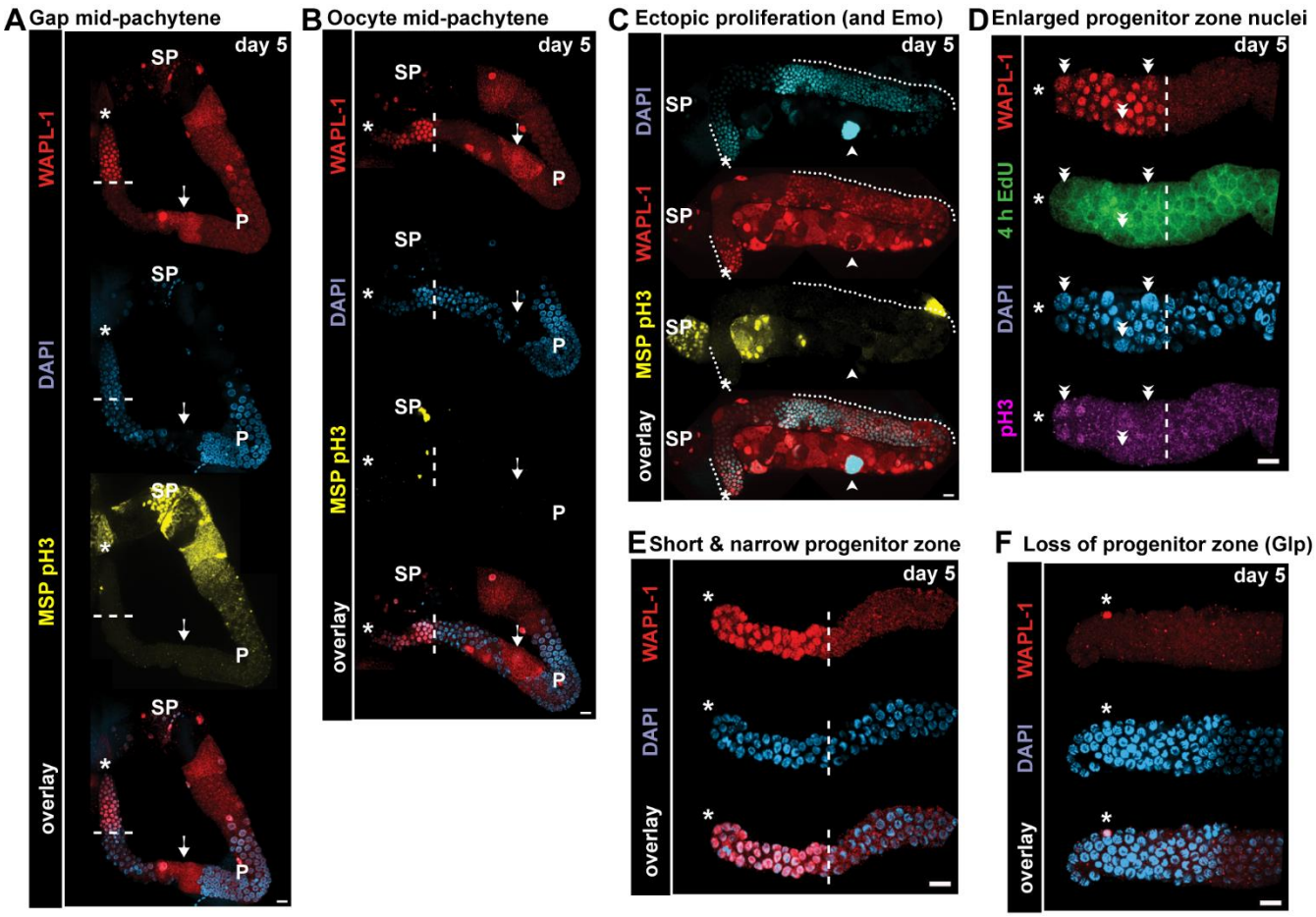

Figure S2. Very low frequency germline defects displayed by day 5 mated hermaphrodites. Representative confocal fluorescence micrographs of germlines displaying defects observed at very low frequency in mated day 5 wild-type hermaphrodites. Germlines were stained for WAPL-1 (red), DAPI (blue), MSP (Major Sperm Protein) and pH3 (both yellow), EdU (green), pH3 (violet), or a combination of markers (overlay). Asterisk indicates the position of the DTC nucleus, and white dashed line indicates the proximal boundary of WAPL-1-positive cells. P indicates pachytene region. SP indicates sperm in spermatheca. Scale bar = 10 μm **(A)** Arrow points to a gap in the middle of the pachytene region that lacks germ cell nuclei. **(B)** Arrow points to oocyte-like formations in the middle of the pachytene region. **(C)** Ectopic proliferation indicated by two WAPL-1-positive regions, one at the normal distal position and another more proximal, highlighted by dotted white lines; this germline also contained an endomitotic oocyte in the proximal germline, indicated with an arrowhead. **(D)** Double arrowheads indicate enlarged progenitor zone nuclei, suggestive of a mitotic cell cycle abnormality. **(E)** A germline that displayed an unusually short and narrow progenitor zone. **(F)** Apparent premature meiotic entry (Glp) phenotype, as the distal germline lacks WAPL-1-positive cells; note that DTC nucleus (asterisk) is displaced 7 c.d. from the distal end and may be nonfunctional.

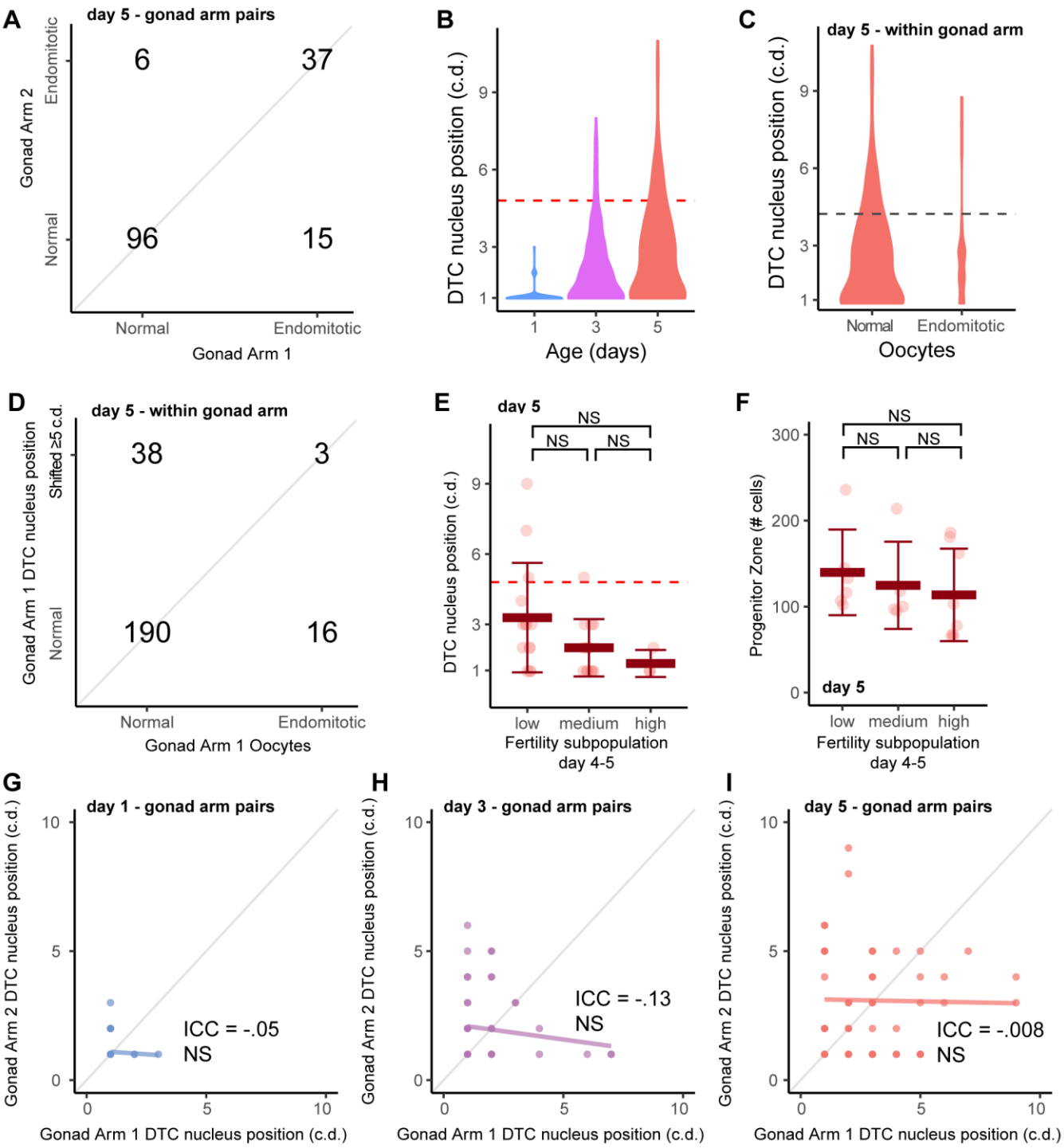

Figure S3. Endomitotic oocytes and a shifted DTC nucleus occurred at a low frequency.
A) To investigate co-occurrence of endomitotic oocytes in the two gonad arms in day 5 adults, we took advantage of a subset of animals in which both gonad arms were visible after dissection by comparing within-pair variation to between-pair variation using an intraclass correlation analysis. 96 animals displayed two normal germlines, 37 animals displayed two Emo germlines, and 21 animals displayed discordant germlines. There was a significant intraclass correlation (intraclass correlation coefficient = 0.68, P<.0000001). This result indicates the existence of a systemic process that uncouples oocyte meiotic

maturation from ovulation, leading to the generation of endomitotic oocytes in both gonad arms in a small number of animals.

B) Violin plots show the distribution of the position of the DTC nucleus (in cell diameters, c.d.) in day 1, 3 and 5 mated hermaphrodites. The same data are displayed in **Fig.2G**. The DTC nucleus was identified by its position at the exterior of the distal gonad and bright WAPL-1 staining, and its position was determined by counting the number of cell diameters from the tip of the gonad.

C) Violin plots show the distribution of the position of the DTC nucleus in day 5 mated hermaphrodites in germlines with and without endomitotic oocytes. The same data are displayed in **Fig.2H**.

D) To investigate co-occurrence of endomitotic oocytes and a shifted DTC nucleus, we categorized day 5 mated wild-type hermaphrodites as (i) not displaying endomitotic nuclei (normal) or displaying endomitotic nuclei, and (ii) not displaying a shifted DTC nucleus (<5 c.d., defined as normal) or displaying a shifted DTC nucleus (≥5 c.d., defined as shifted). 190 animals displayed two normal germlines, 3 animals displayed an Emo germline and a shifted DTC nucleus, and 54 animals displayed discordant germlines. There was not a significant relationship between endomitotic oocytes and shift of the DTC nucleus (Pearson's Chi-squared $P>0.99$), indicating one systemic process does not cause both defects.

E) Each data point indicates the position of one DTC nucleus in the three fertility subpopulations of day 5 animals defined in **Fig.2B** (n=14, 13, 3). Bars represent the average, and whiskers represent the standard deviation. Position 1 means the DTC nucleus is at the distal tip. Dashed line represents cutoff for a nucleus to be designated as "shifted". Comparison by Kruskal-Wallis test. The position of the DTC nucleus at day 5 did not correlate with the number of progeny produced between day 4 and 5.

F) Each data point indicates the size of the progenitor zone measured as total number of cells in the three fertility subpopulations of day 5 animals defined in **Fig.2B**. Bars represent the average, and whiskers represent the standard deviation. Comparison by Kruskal-Wallis test. The size of the progenitor zone at day 5 did not correlate with the number of progeny produced between day 4 and 5.

E,F) We hypothesize that an effect of the shifted DTC nucleus and progenitor zone size on progeny production would be delayed by 2-3 days, as cells in the distal germline require 2-3 days to progress through meiosis, mature, be ovulated, fertilized, and deposited. Thus, the absence of a correlation was expected, and does not rule out the possibility that changes in distal germline morphology affect progeny production on later days that could not be measured in this experiment.

G-I) To investigate correlation of the DTC nucleus position in the two gonad arms in day 1, 3, and 5 adults, we took advantage of a subset of animals in which both gonad arms were visible after dissection by comparing the within-pair variation to the between-pair variation using an intraclass correlation analysis. There was no significant correlation in the degree of DTC nucleus shift within a pair of germlines in the same animal. Thus, the shifted DTC nucleus appears to result from local rather than systemic conditions. NS indicates $P>0.05$, * $P<0.05$, ** $P<.001$, *** $P<.0001$. (See Supplemental Table S3 for statistics)

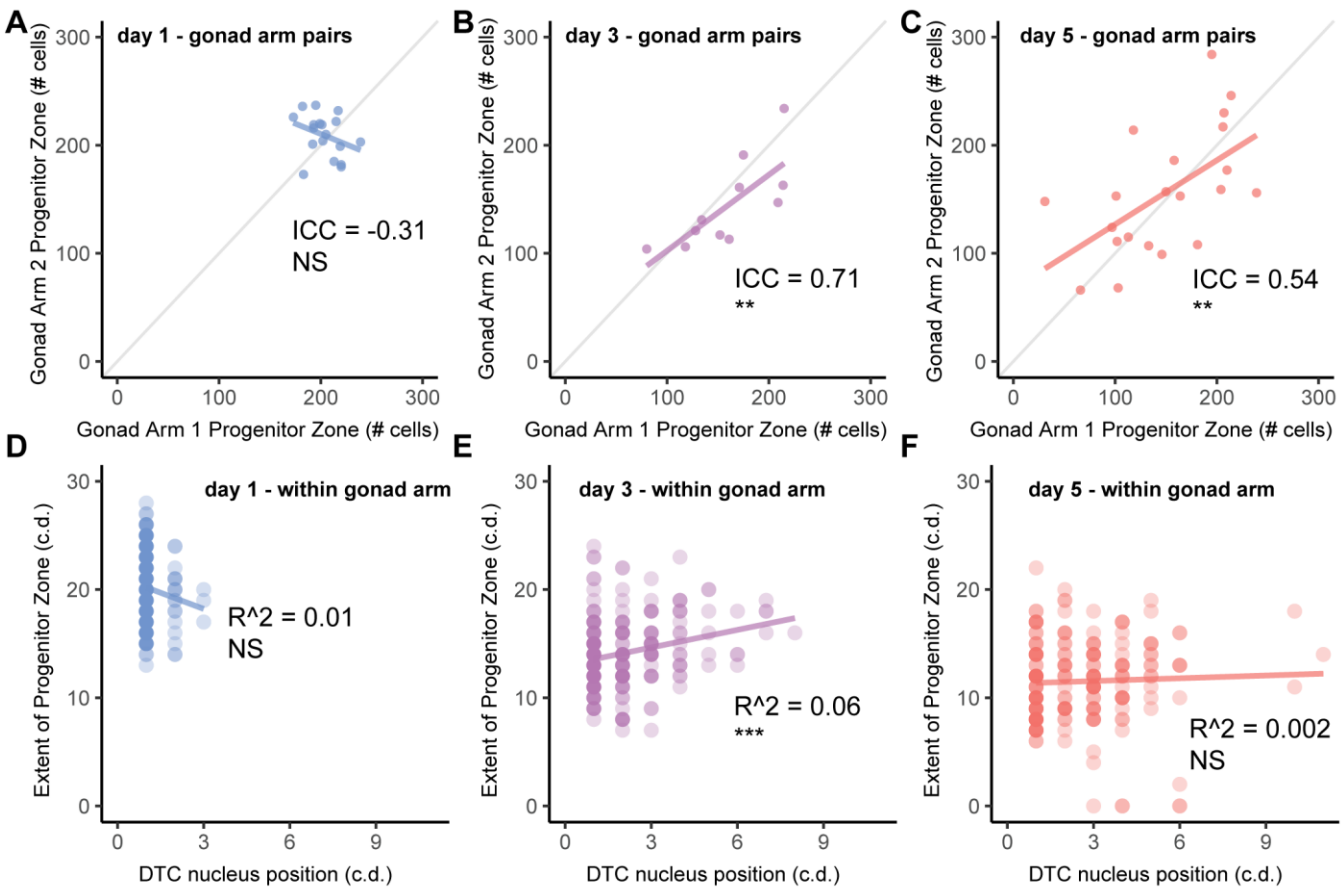

Figure S4. Correlational analysis of distal phenotypes

A-C) To investigate the relationship between the progenitor zone size in the two gonad arms in day 1, 3, and 5 adults, we took advantage of a subset of animals in which both germlines were visible after dissection by comparing the within-pair variation to the between-pair variation using an intraclass correlation analysis. Each data point indicates total number of progenitor zone cells in the two gonad arms of one animal. The line is a best fit, and statistical comparisons are shown. These data indicate that the age-related decrease in progenitor size appears to be result from systemic conditions.

D-F) To investigate the relationship between the DTC nucleus position and the progenitor zone size in individual animals, we measured both values in the same gonad arm. Data points represent the two values expressed in cell diameters. There was no significant correlation in the degree of DTC nucleus shift and the extent of the progenitor zone in day 1 and 5 animals, and a slight positive correlation in day 3 animals. NS indicates P>0.05, * P<0.05, ** P<.001, *** P<.0001. (See Supplemental Table S4 for statistics)

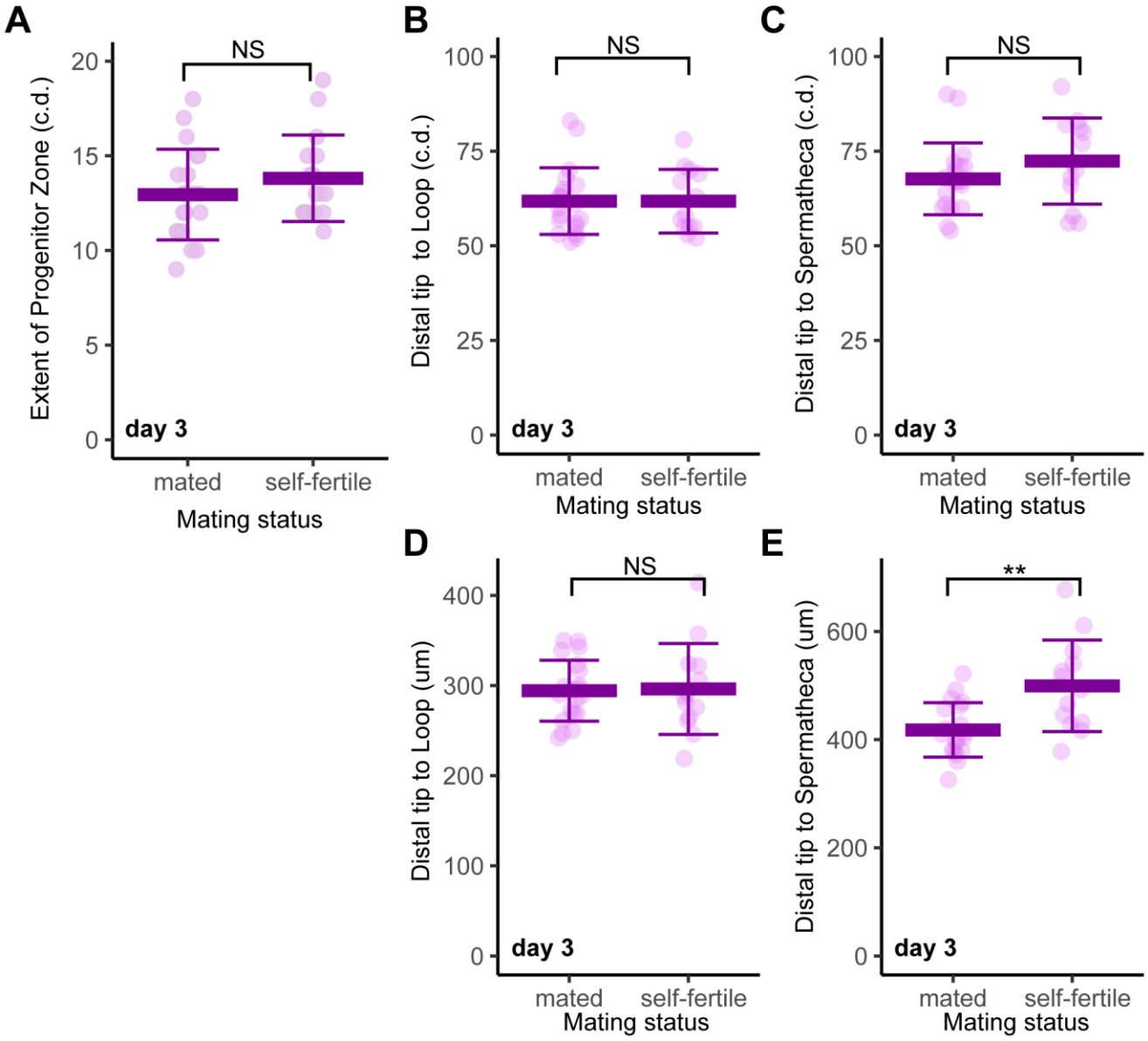

Figure S5. Evaluation of the effect of male mating on hermaphrodite germline size

To determine how mating influences the size of the germline, we analyzed day 3 adults that were self-fertile or mated to males for 24 hours. There was no significant difference in the length (measured in cell diameters) of the progenitor zone **(A)**, the distal germline **(B)**, or the entire germline **(C)** comparing self-fertile and mated animals. When the distal germline **(D)** or the entire germline **(E)** were measured using micrometers as the unit, the distal germline displayed no significant difference, whereas the entire germline was significantly longer in self-fertile animals. The likely reason for this difference is that some self-fertile hermaphrodites were sperm-depleted at day 3, resulting in diakinesis arrested oocytes that were stacked-up in the proximal germline, which extends the length of the tissue. NS indicates P>0.05, * P<0.05, ** P<.001, *** P<.0001. (See Supplemental Table S5 for statistics)

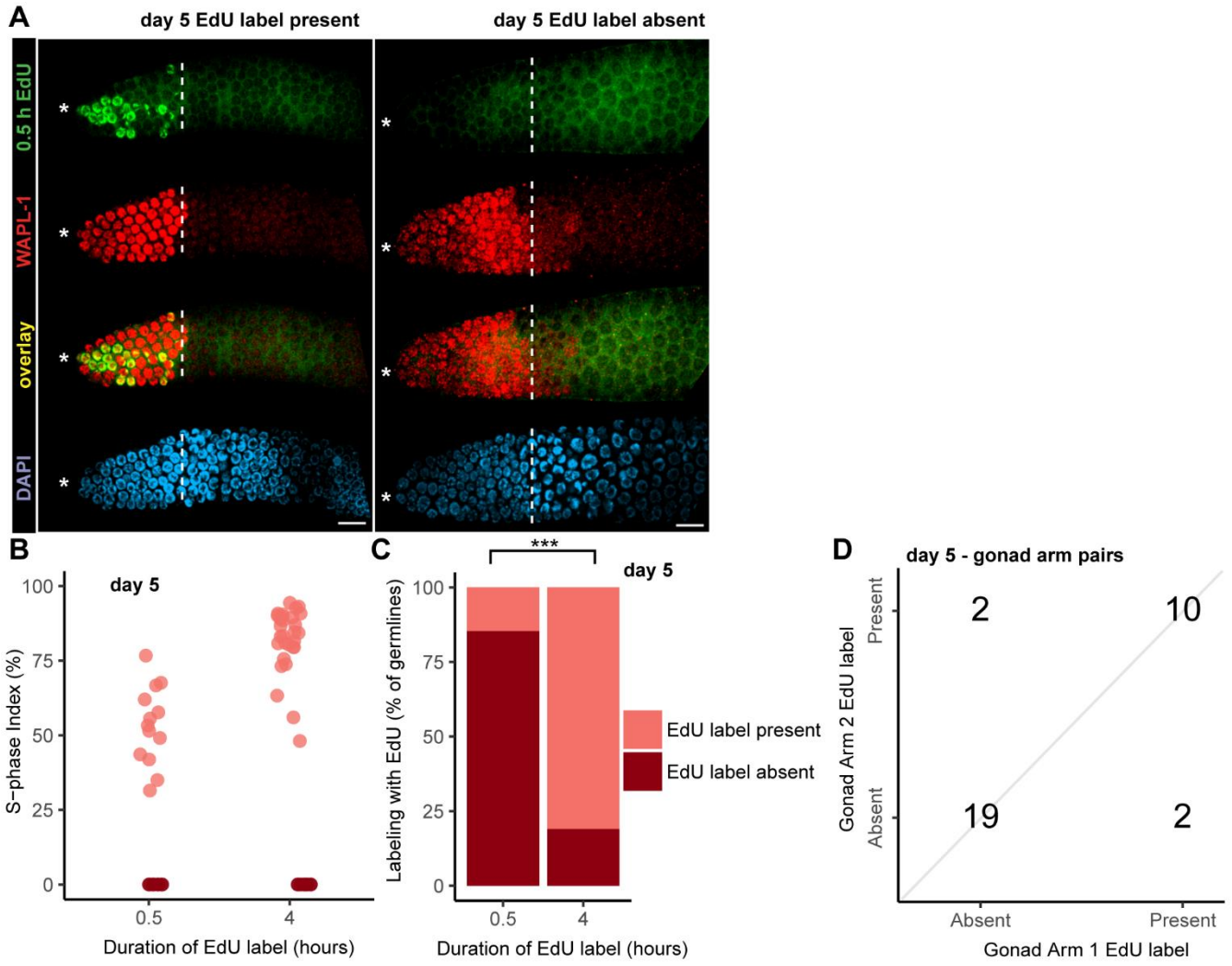

Figure S6. A fraction of sperm-replete day 5 animals displayed no EdU labeling.

A) Representative fluorescence micrographs of two germlines from day 5 adults fed EdU for 0.5 hours and subsequently stained for EdU (green, row 1), WAPL-1 (red, row 2), EdU and WAPL-1 (row 3) and DAPI (blue, row 4). Panels on the left show an animal that successfully labeled with EdU; panels on the right show an animal that failed to label with EdU. Asterisks indicate the position of the DTC nucleus, and white dashed lines indicate the proximal boundary of WAPL-1-positive cells. Scale bar = 10 μm.

B) Each data point indicates the S-phase index (number of EdU positive cells divided by the number of progenitor zone WAPL-1-positive cells) of day 5 animals fed EdU for either 0.5 or 4 hours. Both data sets display a bimodal distribution.

C) The proportion of day 5 adults that labeled with EdU in 0.5 or 4 hours. Dark red indicates germlines with no detectable EdU labeled cells, and light red indicates germlines with multiple EdU labeled cells. n=130, 63; three or more biological replicates. Comparison by Pearson's Chi-squared test.

D) To investigate co-occurrence of EdU labeling in the two gonad arms in day 5 adults, we took advantage of a subset of animals in which both gonad arms were visible after dissection following feeding EdU for 0.5 h. 19 animals displayed two germlines lacking EdU labeling, 10 animals displayed two germlines positive for EdU labeling, and 4 animals displayed discordant germlines. There was a significant intraclass correlation (intraclass correlation coefficient=0.75, $p<0.0001$), suggesting a systemic cause of germline non-labeling. (See Supplemental Table S6 for statistics)

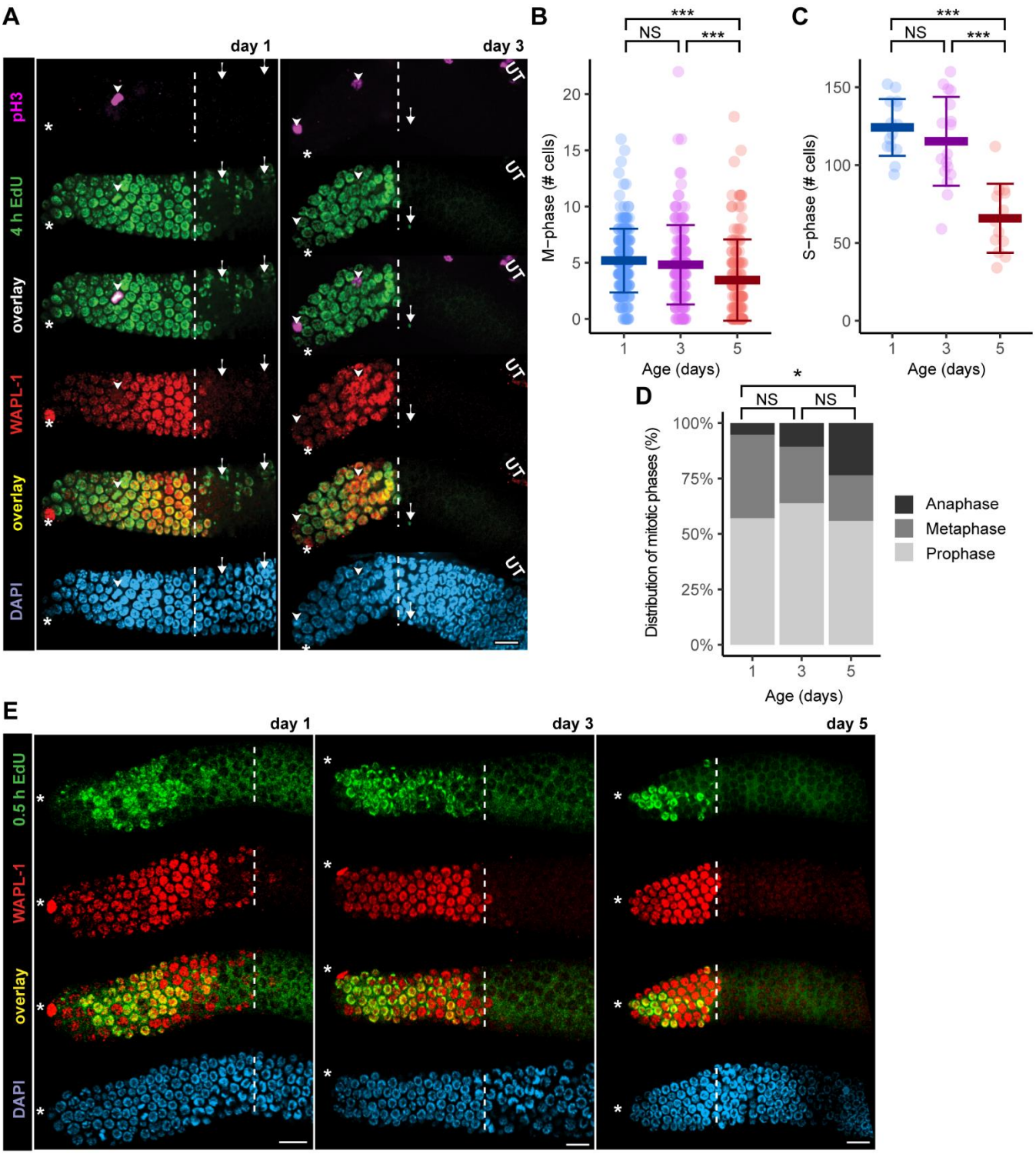

Figure S7. Age-related change in the numbers of M-phase and S-phase cells.

A) Representative fluorescence micrographs of germlines from day 1 (left) and day 3 (right) adults fed EdU for 4 hours and subsequently stained for pH3 (magenta, row 1), EdU (green, row 2), pH3 and EdU (overlay, row 3), WAPL-1 (red, row 4), EdU and WAPL-1 (overlay, row 5), and DAPI (blue, row 6). Asterisks indicate the position of the DTC nuclei, and white dashed lines indicate the proximal boundary of WAPL-1-

positive cells. Arrowheads indicate pH3-positive cells. Arrows indicate examples of EdU-positive, WAPL-1-negative cells. UT indicates the uterus, where Major Sperm Protein positive sperm are visible in magenta. Scale bar = 10 μm.

B) Each data point indicates the number of M-phase (pH3-positive) cells per gonad arm of day 1, 3, and 5 adults. Bars represent the average, and whiskers represent the standard deviation. n=213, 155, 134 in 4 or more biological replicates. Comparison by Kruskal-Wallis test.

C) Each data point indicates the number of S-phase (EdU-positive) cells per gonad arm of day 1, 3, and 5 adults fed EdU for 0.5 hours. Bars represent the average, and whiskers represent the standard deviation. n= 14, 17, 13 in two or more biological replicates. Comparison by Kruskal-Wallis test.

D) Distribution of mitotic phases among pH3 immunoreactive cells was determined by DAPI morphology in day 1, 3, and 5 adults and characterized as anaphase (black), metaphase (dark gray) or prophase (light gray). n=77, 47, 34. Comparison by Pearson's Chi-squared test. NS indicates $P>0.05$, * $P<0.05$, ** $P<.001$.

E) Representative fluorescence microscope images of germlines from day 1, 3, and 5 adults fed EdU for 0.5 hours and subsequently stained for EdU (green, row 1), WAPL-1 (red, row 2), EdU and WAPL-1 (overlay, row 3) and DAPI (blue, row 4). Asterisks indicate the position of the DTC nuclei, and white dashed lines indicate the proximal boundary of WAPL-1-positive cells. Scale bar = 10 μm. Some of these images appear in **Fig.3A** and **Fig.4E**. (See Supplemental Table S7 for statistics)

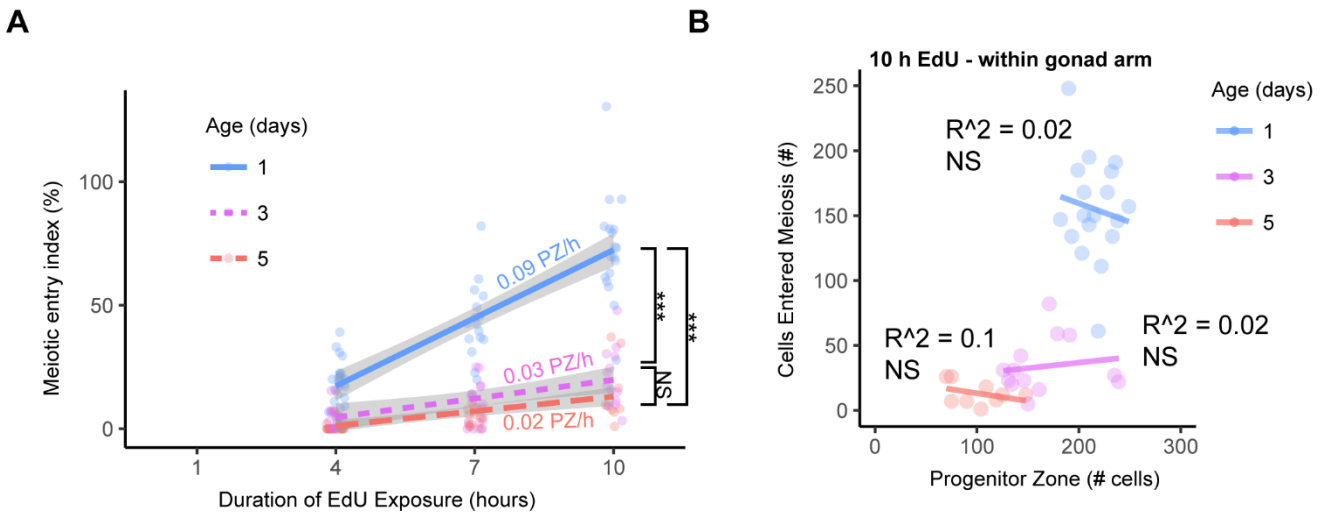

Figure S8. Age-related decrease in the rate of meiotic entry

A) Mated hermaphrodites at day 1 (blue), 3 (purple), or 5 (red) were exposed to EdU for 4, 7, or 10 hours, and germlines were dissected and stained with anti-WAPL-1 antibody and EdU click chemistry. The meiotic entry index was calculated by dividing the number of cells that entered meiosis (EdU positive, WAPL-1 negative) by the number of progenitor zone cells (WAPL-1-positive). The normalized rate of meiotic entry (% of progenitor zone per hour) was calculated from the slope of the linear regression of the meiotic entry index versus the duration of the EdU exposure. Gray range indicates 95% confidence interval on linear regression. Comparison by Kruskal-Wallis test compared the meiotic entry index at 10 hours. NS indicates P>0.05, *** P<.0001.

B) To investigate the relationship between the rate of cells entering meiosis and the progenitor zone size in individual animals, we measured both values in the same gonad arm. Data points represent the two values expressed as number of cells. There was no significant correlation between the number of cells that entered meiosis (in a 10 hour EdU label) and the number of progenitor zone cells within day 1, 3, or 5 adults. n=18, 13, 9. Comparison by Pearson Correlation. (See Supplemental Table S8 for statistics)

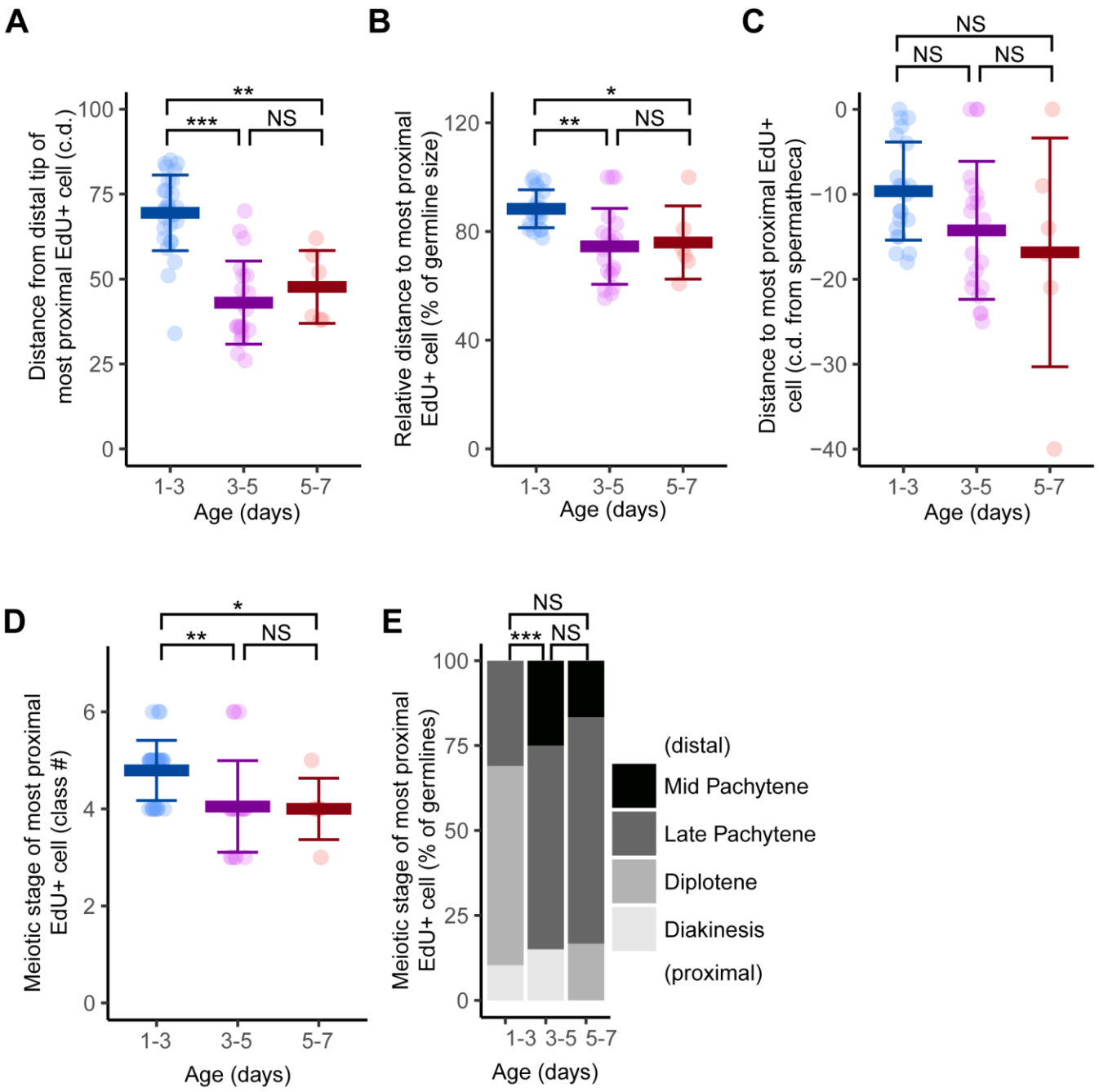

Figure S9. Age-related decrease in the rate of meiotic progression

Mated hermaphrodites at day 1 (blue), 3 (purple), or 5 (red) were exposed to EdU labeled bacteria for 4 hours ("pulse"), transferred to unlabeled bacteria for 48 hours ("chase"), and germlines were dissected and stained with anti-WAPL-1 antibody and EdU click chemistry. The most proximal EdU positive cells were identified, and their position and meiotic stage were determined.

A) Each data point indicates the distance from the distal tip of the gonad arm to the most proximal EdU positive cell in cell diameters.

B) Each data point indicates the distance from the distal tip of the gonad arm to the most proximal EdU positive cell, divided by the distance from the distal tip of the gonad arm to the spermatheca (size of the germline).
C) Each data point indicates the distance from the spermatheca to the most proximal EdU positive cell in cell diameters. We defined the position of the spermatheca as 0, and negative values indicate positions distal to the spermatheca. Comparison by Kruskal-Wallis test.
D) To facilitate statistical tests of an ordered categorical variable, we defined mid-pachytene = 3, late-pachytene = 4, diplotene = 5, and diakinesis = 6, similar to Jaramillo-Lambert et al., (2007). Each data point indicates the numeric meiotic stage of the most proximal EdU positive cell. Comparison by Kruskal-Wallis test.
E) In each germline, the most proximal EdU labeled cell was identified and categorized as mid pachytene, late pachytene, diplotene or diakinesis stage of meiosis. Comparison by Pearson's Chi-squared test. Only a small number of germlines were included in the day 5-7 data, which may contribute to the lack of significance in comparisons with that age (See Supplemental Table S9 for statistics).

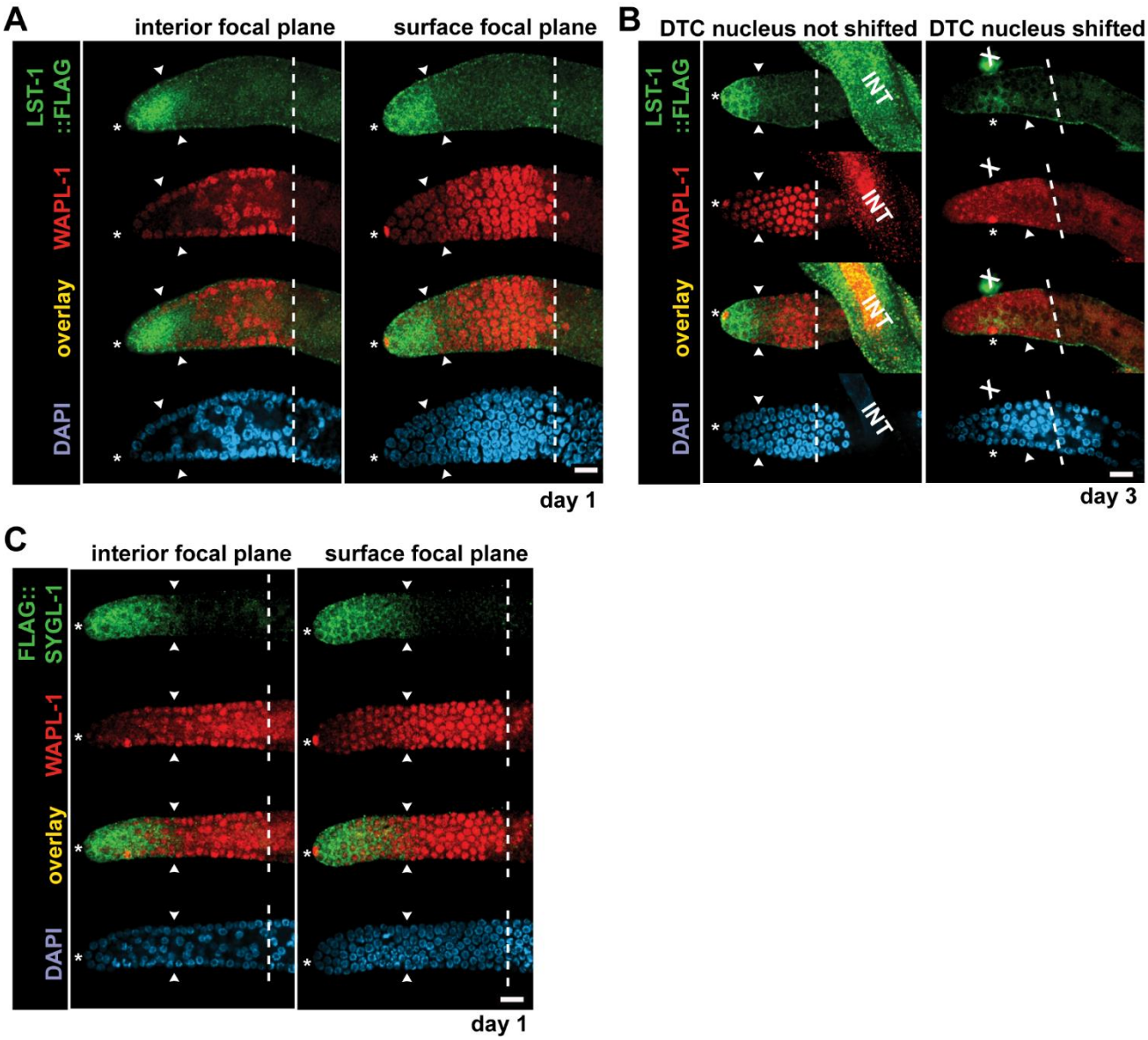

Figure S10. Distribution of LST-1::FLAG and FLAG::SYGL-1 in the surface and interior of germlines and relative to the position of the DTC nucleus.

A-C) Representative fluorescence microscope image of one germline stained for FLAG (green, row 1), WAPL-1 (red, row 2), FLAG and WAPL-1 (overlay, row 3) and DAPI (blue, row 4). Asterisk indicates the position of the DTC nucleus, white arrowheads indicate the proximal boundary of FLAG staining, and white dashed lines indicate the proximal boundary of WAPL-1-positive cells. Scale bar = 10 μm.

A) Day 1 germline with LST-1::FLAG. Panels on left display a focal plane from the interior of the germline, whereas panels on right display a focal plane from the surface of the germline.

B) Day 3 germlines with LST-1::FLAG. Panels on left show a germline with the DTC nucleus at position 1. Panels on right show a germline with the DTC nucleus shifted to position 6. Note that LST-1::FLAG signal is positioned near the shifted DTC nucleus, not near the distal tip of the germline. INT indicates intestine; X indicates a speck of green dust.

C) Day 1 germline with FLAG::SYGL-1. Panels on left display a focal plane from the interior of the germline, whereas panels on right display a focal plane from the surface of the germline.

Table S1. Data for Figure 1: The female reproductive system displayed rapid age-related decline in sperm-replete *C. elegans*

[1] Adult days. L4 stage = day 0.

[2] Mean value rounded to whole number. View data in spreadsheet for decimal values.

[3] Standard deviation.

[4] Number of animals in experiment producing one or more viable egg during a 24-hour period. Some animals died of matricidal hatching or vulval extrusion and were censored from the experiment.

[5] Number of animals in experiment producing no viable eggs during a 24-hour period, that were alive with no evidence of internal hatching of embryos or vulval extrusion.

[6] Progeny production on a given day, divided by peak progeny production on day 2, expressed as percent.

[7] Sample size (number of P0 "mother" animals).

[8] ND = Not determined, as animals were mated in groups on day 1.

Click here to Download Table S1

Table S2. Data for Figure 2: Endomitotic oocytes and a shifted DTC nucleus occurred at a low frequency

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S2

Table S3. Data for Figure 3: Population-wide, age-related decreases in the size of the germline and progenitor zone

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S3

Table S4. Data for Figure 4: An age-related increase in the duration of the cell cycle

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S4

Table S5. Data for Figure 5: Age-related decrease in the rate of meiotic entry

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S5

Table S6. Data for Figure 6: Age-related decrease in the rate of meiotic progression

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S6

Table S7. Data for Figure 7: Population-wide age-related decrease in the stem cell pool and GLP-1 (Notch) signaling

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S7

Table S3: Data for Supplemental Figure 3: Endomitotic oocytes and a shifted DTC nucleus occurred at a low frequency

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.

[2] Global comparisons were used to test overall differences between all groups.

[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).

[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

[5] Intraclass correlation was used to compare the pooled variance between pairs of germlines from one animal and pooled variance within pairs. Pearson's interclass correlation was used to test for linear relationships between variables.

Click here to Download Table S3

Table S4: Data for Supplemental Figure 4: Correlational analysis of distal phenotypes.

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Global comparisons were used to test overall differences between all groups.
[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).
[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.
[5] Intraclass correlation was used to compare the pooled variance between pairs of germlines from one animal and pooled variance within pairs. Pearson's interclass correlation was used to test for linear relationships between variables.

Click here to Download Table S4

Table S5: Data for Supplemental Figure 5: Effect of mating on germline size

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Global comparisons were used to test overall differences between all groups.
[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).
[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.
[5] Intraclass correlation was used to compare the pooled variance between pairs of germlines from one animal and pooled variance within pairs. Pearson's interclass correlation was used to test for linear relationships between variables.

Click here to Download Table S5

Table S6 : Data for Supplemental Figure 6: A fraction of day 5 animals displayed no EdU labeling

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Intraclass correlation was used to compare the pooled variance between pairs of germlines from one animal and pooled variance within pairs. Pearson's interclass correlation was used to test for linear relationships between variables.

Click here to Download Table S6

Table S7: Data for Supplemental Figure 7: Age-related change in the numbers of M-phase and S-phase cells

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Global comparisons were used to test overall differences between all groups.
[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).
[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S7

Table S8: Data for Supplemental Figure 8: Age-related decrease in the rate of meiotic entry

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Global comparisons were used to test overall differences between all groups.
[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).
[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

[5] Intraclass correlation was used to compare the pooled variance between pairs of germlines from one animal and pooled variance within pairs. Pearson's interclass correlation was used to test for linear relationships between variables.
[6] Sample size only includes cells which entered meiosis.

Click here to Download Table S8

Table S9: Data for Supplemental Figure 9: Age-related decrease in the rate of meiotic progression

[1] Summary of values, mean, standard deviation, and sample size (n). Sample size is expressed as the number of animals or germlines, as indicated. Mean and standard deviations rounded to whole number or one decimal. View data in spreadsheet for decimal values.
[2] Global comparisons were used to test overall differences between all groups.
[3] Post-hoc comparisons were used for pairwise tests and to correct for multiple comparisons (familywise error).
[4] Both parametric tests, which assume the data are normally distributed, and non-parametric tests were performed for all comparisons.

Click here to Download Table S9

Table S10. CRISPR/Cas9 plasmids and oligonucleotides specific to this study

Locus	Corresponding plasmid	Oligo name	Sequence	Notes
lst-1	pZK07	ZK034	TTTGGAAGAACATTTGAAGGGGG	g4
	pZK07	ZK035	AAACCCCCCTTCAAATGTTCTTC	g4
	pZK13	ZK073	TTTGTTGCTCAACTCGATCGTGC	g16
	pZK13	ZK074	AAACGCACGATCGAGTTGAGCAA	g16
	NA	ZK038	AAAAATCTTCTCAAATTATTATTATTTCAGATGTCCCCGTTTATGGTTC GCTCAATTGGACCGAGCAGGTTCAGAGATGGTGGAGCAGATGGGAC ACGCTCGAAATGTTCCAGTCGACTACAAAGACCATGACGGTGATTATA AAGATCATGATATCGATTACAAGGATGACGATGACAAGTAAGCAATA AAATTGGTTTAAATATCAATTAATTTATATTTTACGACCCGCTTGAATA GTTCTTCTTGTTTTACACTATCATCCAAAAAAATGCGGTTC	gblock
	NA	ZK039	AAAAATCTTCTCAAATTATTATTATTTCAGA	Amplify gblock
	NA	ZK040	GAACCGCATTTTTTTGGATG	Amplify gblock
	NA	ZK028	CACTTTATGATATGCAAGGACGAG	Genotyping
	NA	ZK029	CAAAAGAGCACATGGATATACAGC	Genotyping
sygl-1	pZK15	ZK041	TTTGGACGTCAGAGACGATGAGG	g1
	pZK15	ZK042	AAACCCTCATCGTCTCTGACGTC	g1
	pZK17	ZK043	TTTGTGGAATGGCATTATGCACG	g5
	pZK17	ZK044	AAACCGTGCATAATGCCATTCCA	g5
	pZK20	ZK045	TTTGAACTCTACATGGATCACCG	g6
	pZK20	ZK046	AAACCGGTGATCCATGTAGAGTT	g6
	NA	ZK049	TTCAGCGATCATCGAACCATTGTCATCACGCCACGTGCATAATGGACT ACAAAGACCATGACGGTGATTATAAAGATCATGATATCGATTACAAG GATGACGATGACAAGCCATTCCATTATCCAAAATTATATATGGACCAT CGCGGAAACATGTCTACGTCTTCGTCTCTGACGTCATCGACAACCGCC ACGTCATCA	Repair oligo
	NA	ZK047	ATCTACCCGCCGATTTTCTAAT	Genotyping
	NA	ZK048	ATCTCCAAGTGTTGCACATAACC	Genotyping

Supplementary Materials and Methods

Individual measurements and scripts used to analyze the data can be found here