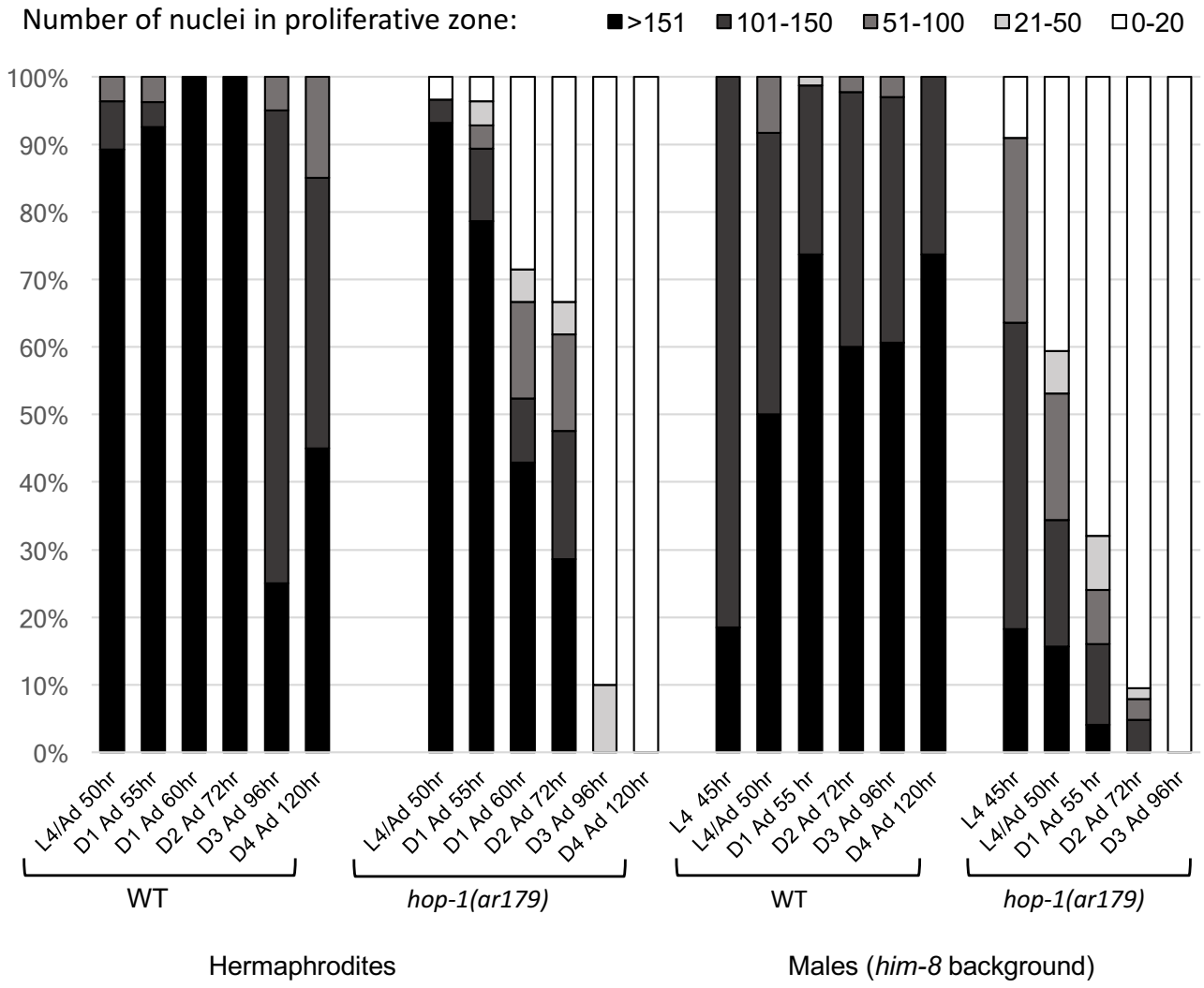

Figure S1 Time course for penetrance of proliferative zone defect in hermaphrodites and males.

Penetrance of gonad proliferation defect is plotted at six different ages for *hop-1(ar179)* hermaphrodites and males with corresponding wild type controls. Calculated averages from all gonads at each time point were used to generate the graphs shown in Figure 2B and 2C. Gonads are categorized here by severity of phenotype according to size of the proliferation zone (number of nuclei distal to the meiotic transition zone). All non-black categories represent gonads with reduced proliferative zones. Gonads in which fewer than 20 nuclei are present distal to the Transition zone (white category) are considered to lack a proliferative zone (see Methods). A subset of the data for male gonads is also shown in Figure 5. Ages are indicated in hours post-hatch at 20°; n $\geq$ 20 dissected gonads for each data point except *hop-1(ar179)* D4 Ad, for which n = 15.

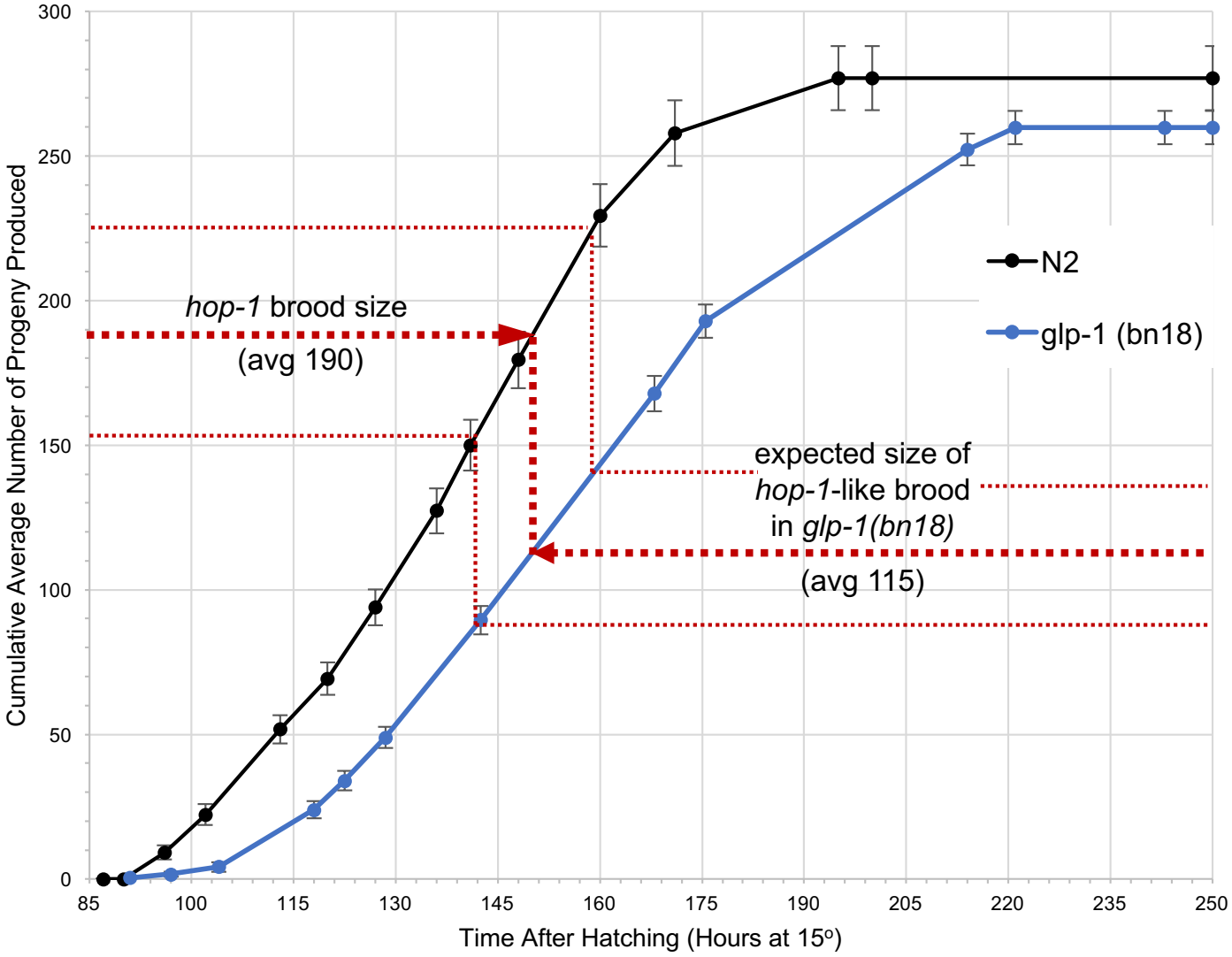

Figure S2 Cumulative progeny production is plotted for N2 and *glp-1(bn18)*^{ts} over the course of adulthood at 15°.

This graph was generated using the data plotted in Figure 7 in order to estimate the cumulative brood size of *glp-1(bn18)*^{ts} animals that would be expected after the amount of time by which N2 would produce a *hop-1*-like brood. The mean 15° *hop-1* brood size of 190+/-38(n = 8) is superimposed on the graph (thick red dashed line = Mean; thin red lines = Standard Deviation). Given the slower rate of progeny production, this graph allows us to estimate that *glp-1(bn18)*^{ts} animals would produce broods of 88-140 (mean 115) in the same amount of time in which N2 would produce *hop-1*-like broods in the range of 152-228 (mean 190). Error bars are standard error of the mean. These values were used to interpret the temperature shift experiment in which *glp-1(bn18)*^{ts} fecundity was plotted as a function temperature shift time (Figure 4).