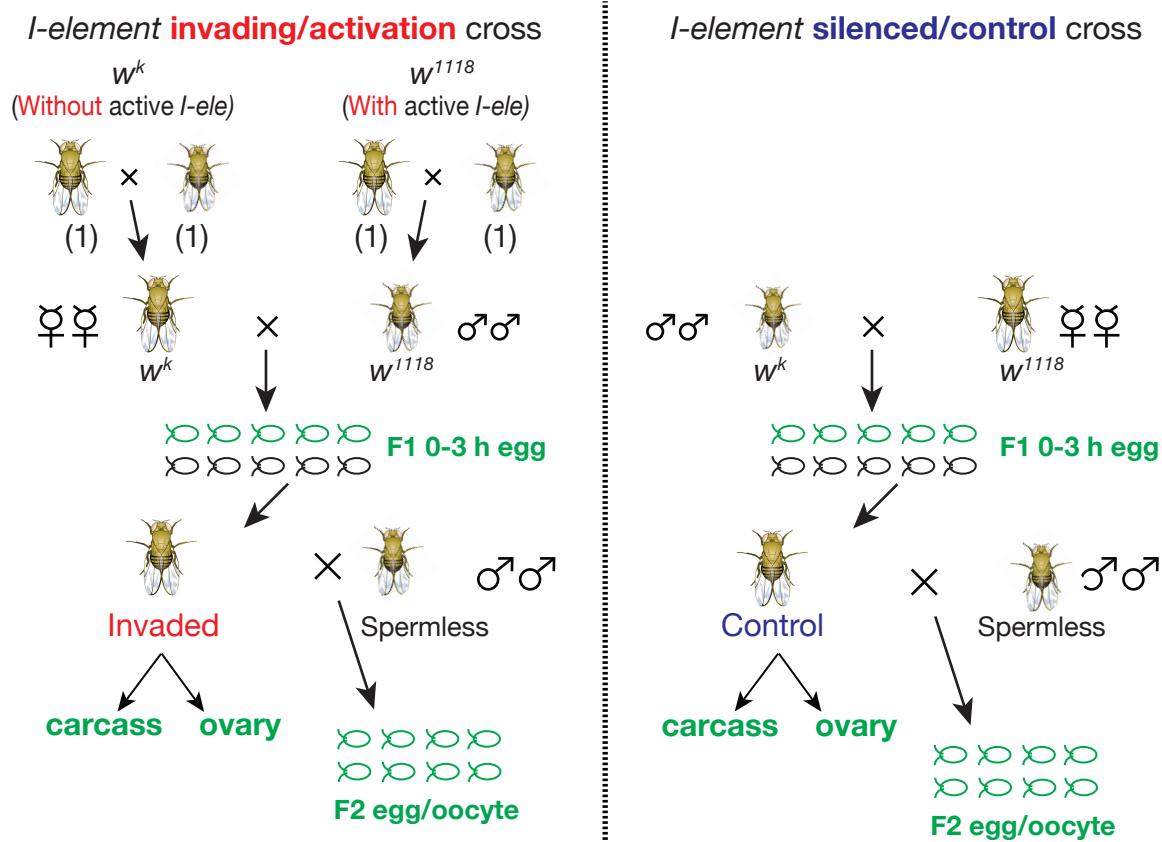
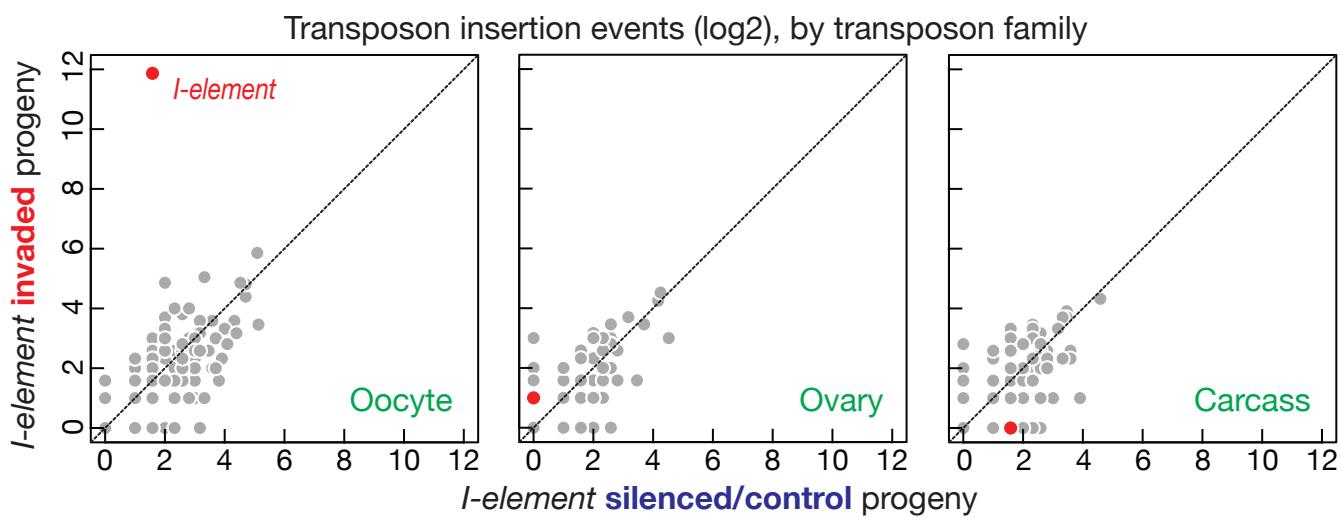
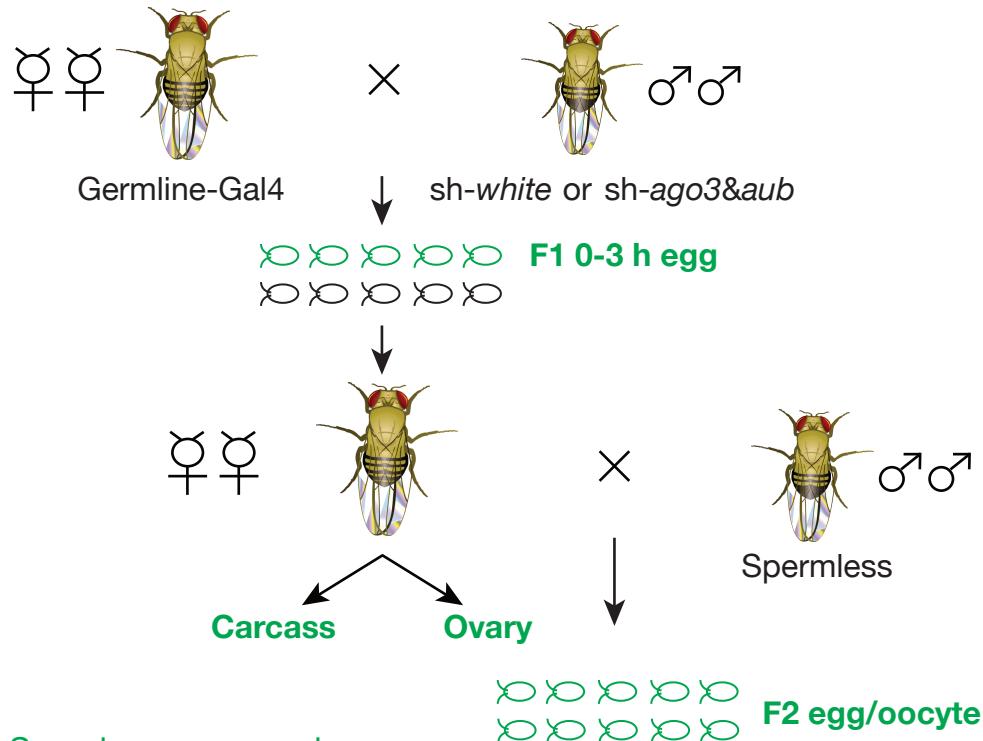


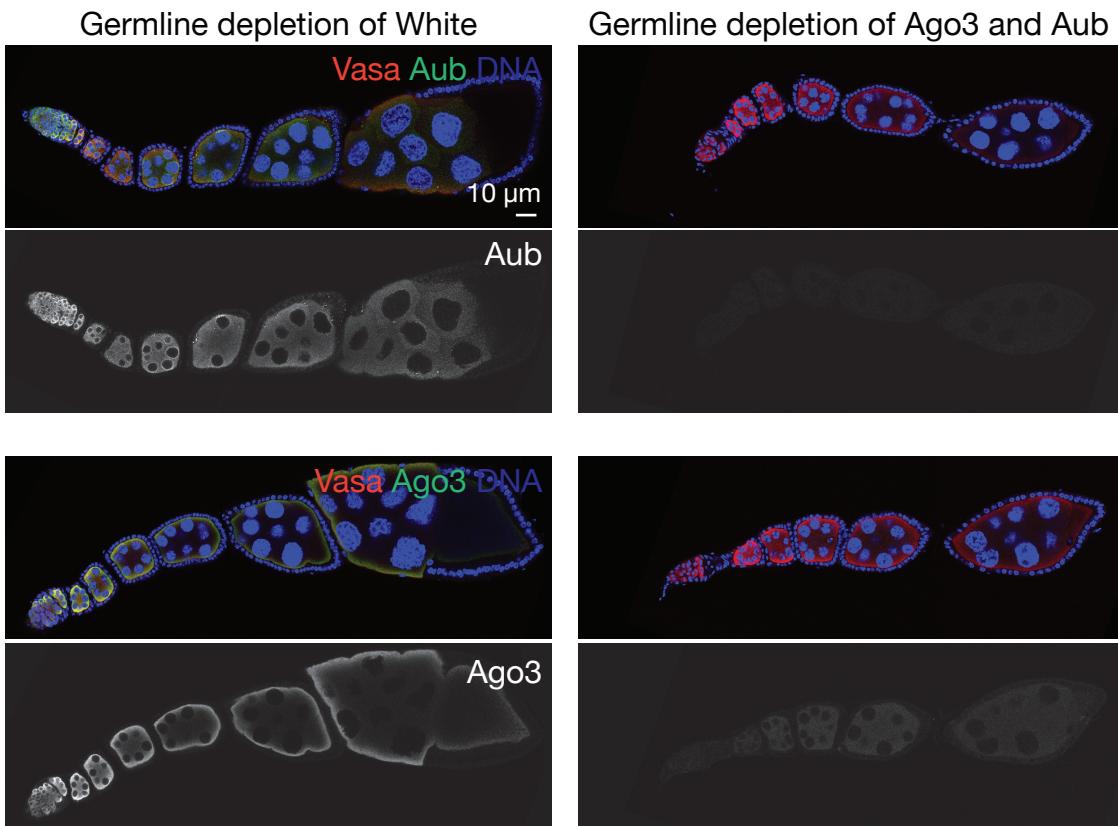
A

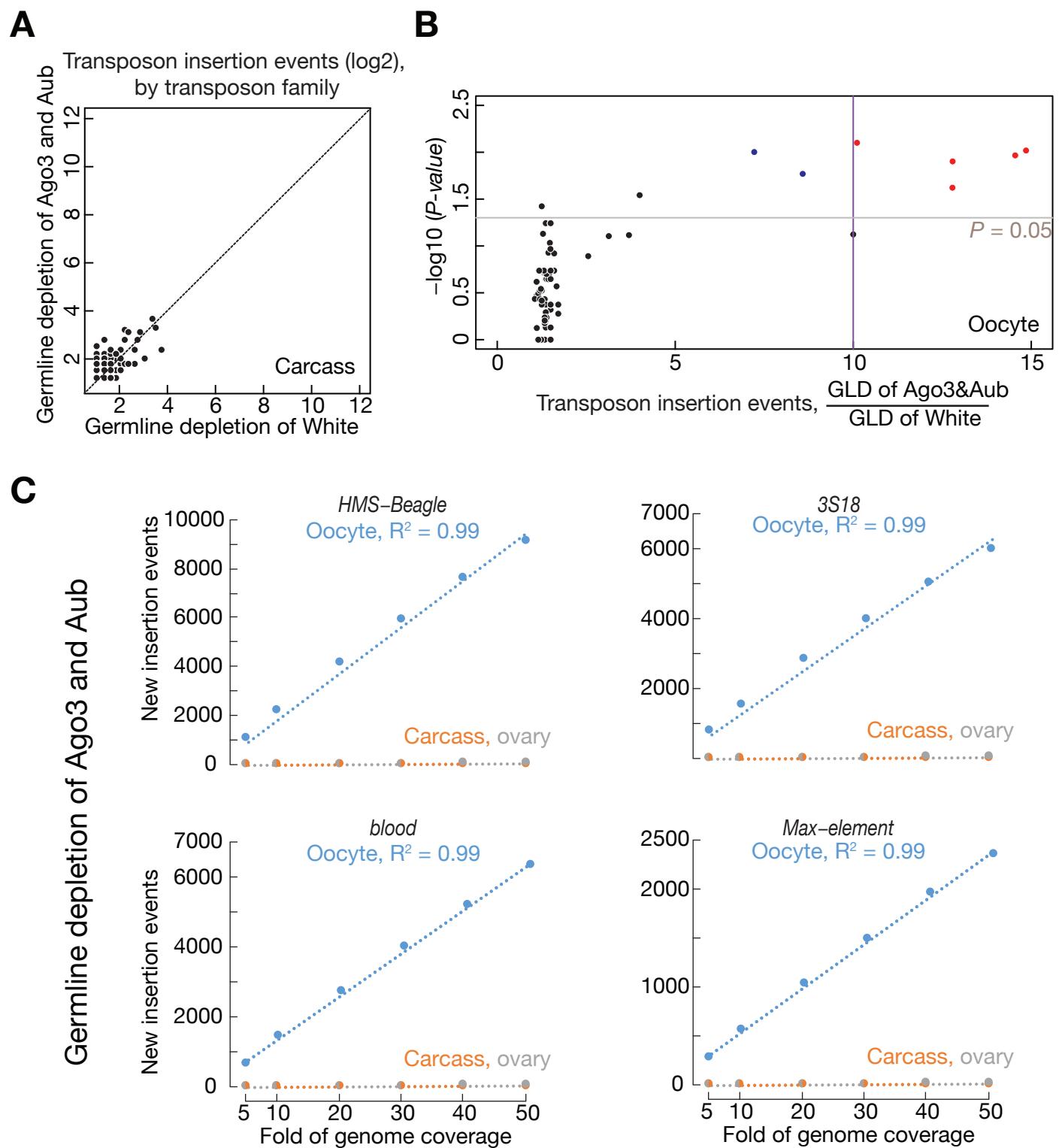
- Samples sequenced
- F1 egg DNA is used as reference to define new insertions
- Pairwise cross (single male and female) was used to minimize genetic background variation

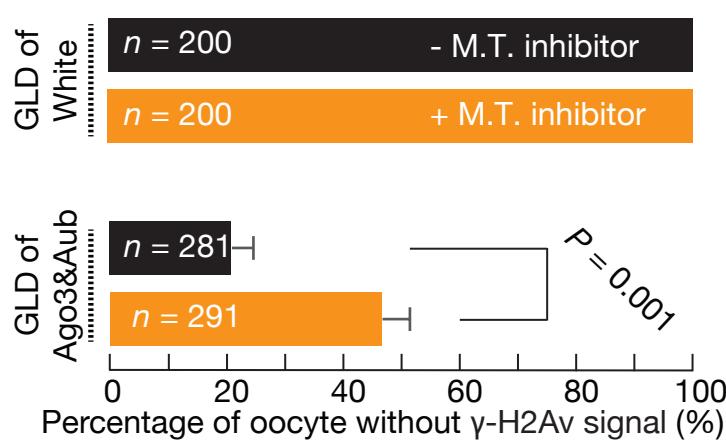
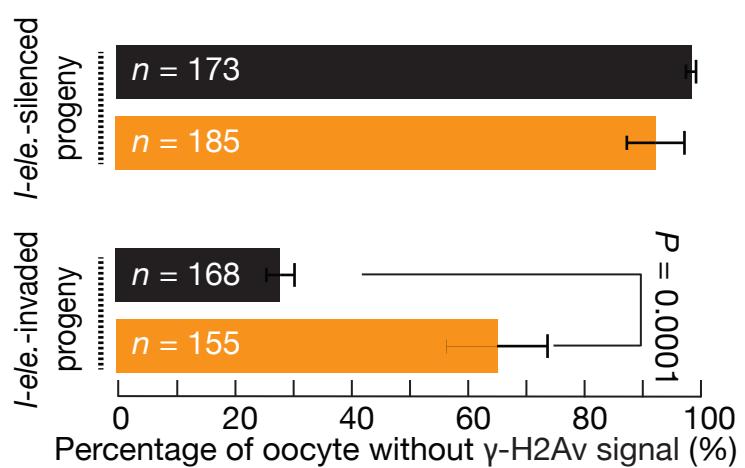
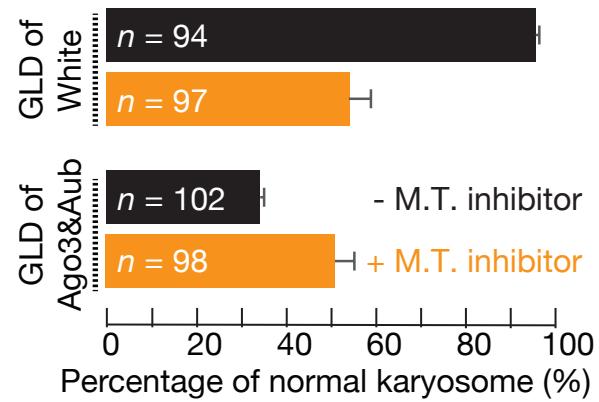
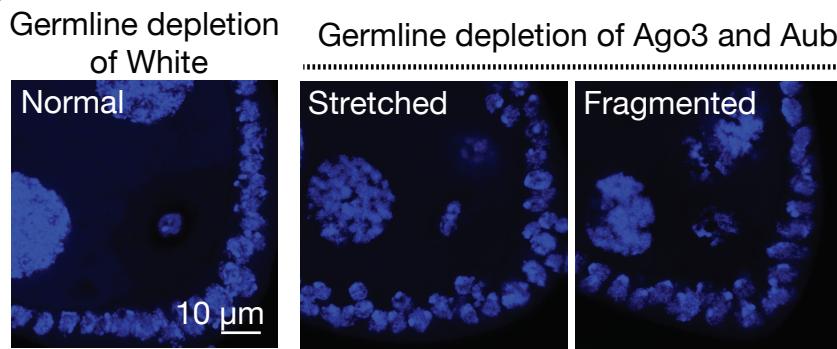
B

A

- Samples sequenced
- F1 egg DNA is used as reference to define new insertions
- Carcass DNA is used to estimate the false-positive insertion rate

B



A**B****C****D**