



Figure S1: Knocking down *NPFR* in the PG does not alter PG size

Quantification of PG size from *phm>NPFRⁱ; dcrII* and *phm>dcrII/+* animals shows that there are no significant differences in size. *phm-GFP; UAS-dcrII* was used to both knock down *NPFR* and to visualize PGs. Error bars represent ± 1 SEM. Scale bar = 50 μ m.

Genotypes indicated by the same letter indicate that they are not significantly different from one another ($p = 0.528$, pairwise t test). $n = 9$ for *phm-GFP>dcrII* animals, and $n = 6$ for *phm-GFP>NPFRⁱ; dcrII*.