Supplemental Materials

smFISH in chips: a microfluidic-based pipeline to quantify *in situ* gene expression in whole organisms

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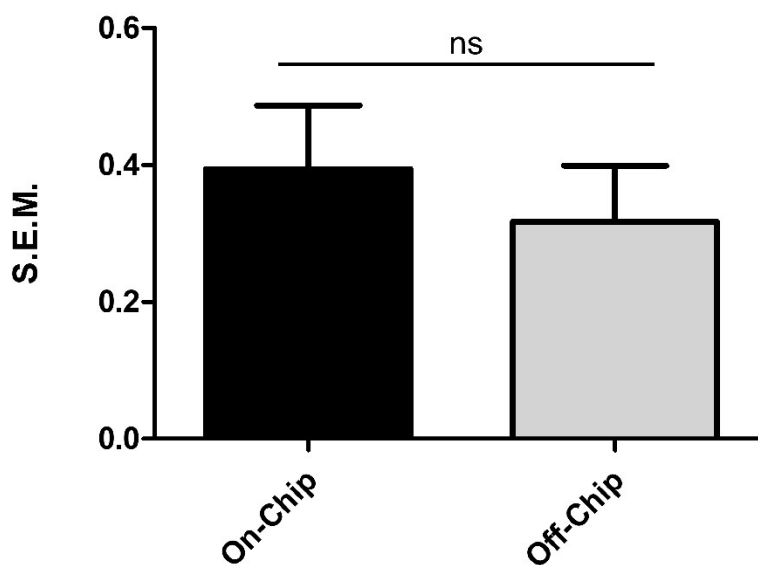*Author to whom correspondence should be addressed. Email: hang.lu@gatech.edu

FIG. S1. Standard error of the mean (S.E.M.) of *gpa-3* mRNA counts is not significantly different between on- and off-chip conditions. Each group represents the mean S.E.M. of the three independent experiments, and error bars represent S.E.M. An unpaired T-test was performed. (ns, not significant).
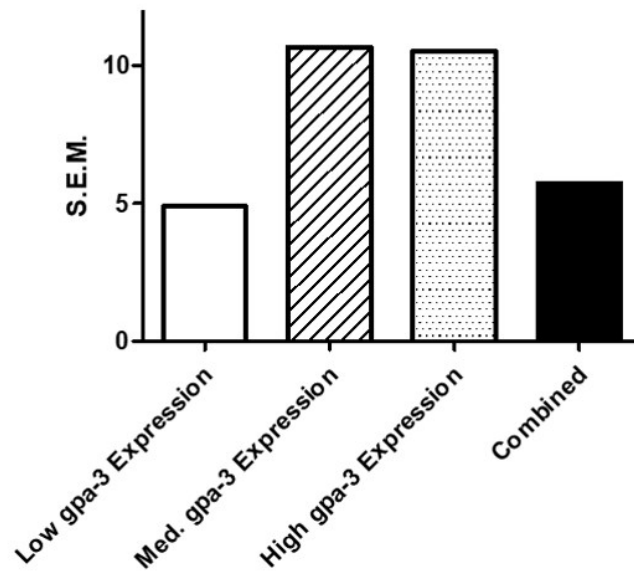
FIG. S2. Standard error of the mean (S.E.M.) of *Pdaf-7::Venus* expression in each population bin. S.E.M. increases as *gpa-3* expression increases, but this information is lost when considering the whole population (combined).
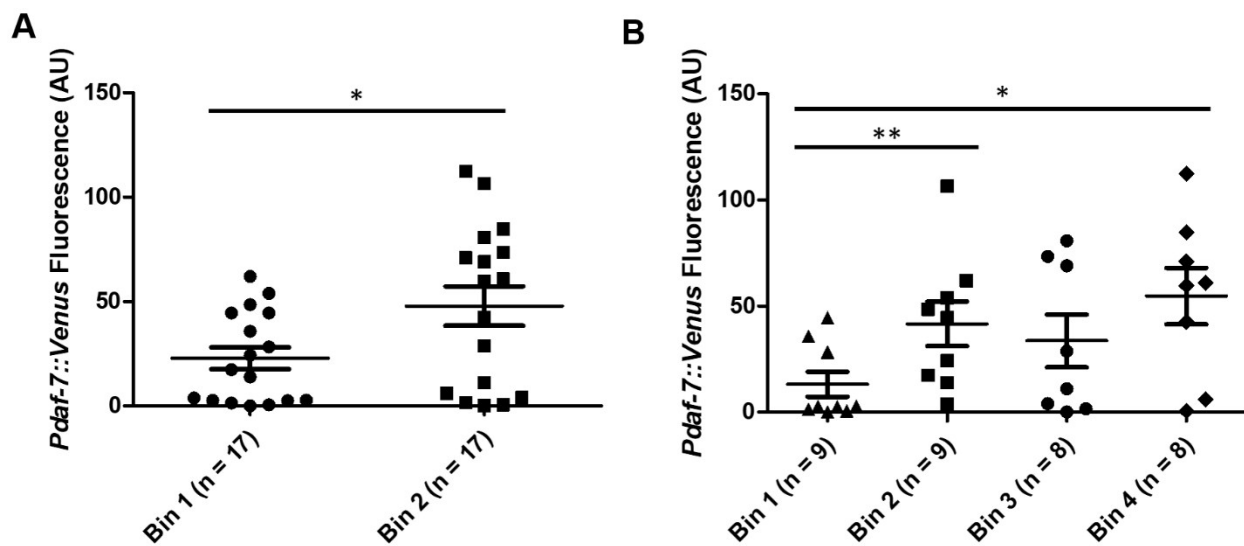

FIG. S3. The positive relationship between *gpa-3* and *daf-7* expression is consistent regardless of bin size. The binning is based on *gpa-3* mRNA expression. Higher *gpa-3* expression correlates with significantly higher *Pdaf-7::Venus* expression when the population is divided in (A) two bins or (B) four bins. The Mann-Whitney U test was performed. (**$P<0.01$; *$P<0.05$)