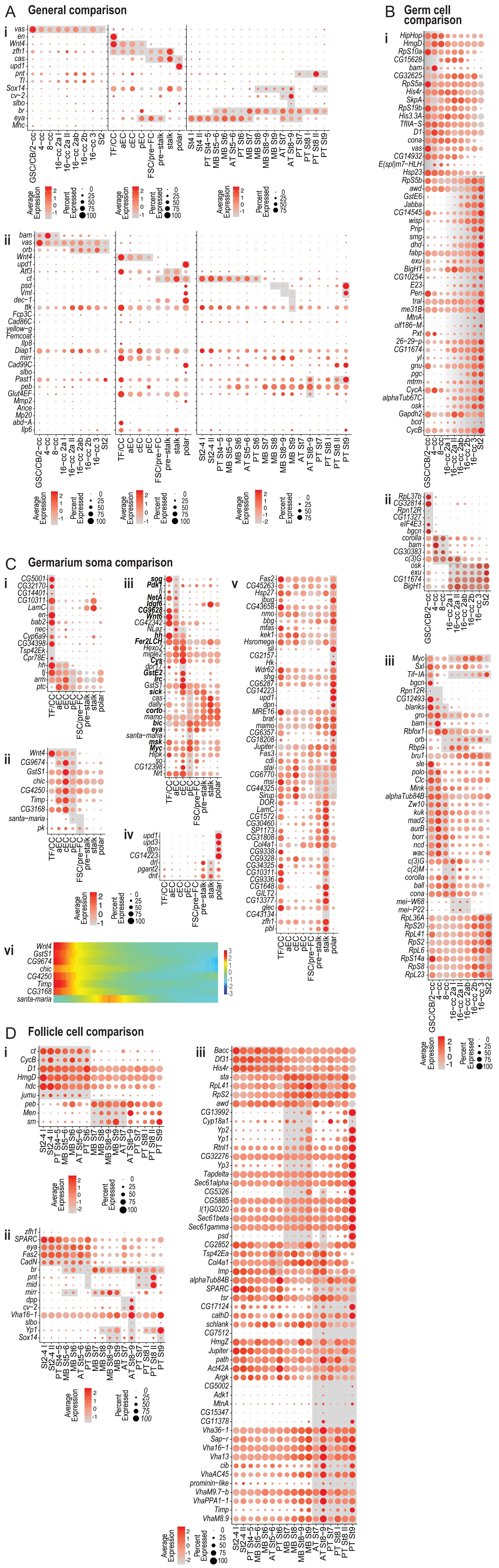

Supplemental Figure 10.

A-D - Dot plots visualizing expression of marker genes from Jevitt et al. and Rust et al. in our dataset. Dot diameter represents the fraction of cells expressing each gene in each cluster, as shown in scale. Color intensity represents the average normalized expression level. Gray background marks expected expression pattern according to Rust et al. and Jevitt et al. A - General markers from Rust et al. (i) and Jevitt et al. (ii). B - GC markers from Jevitt et al. pseudotime analyses (i), Rust et al. clustering (ii) and pseudotime analyses (iii). C - germarium soma markers. TF and CC markers (i), FSC markers (ii), EC markers (iii), polar and stalk cell markers (iv) from Rust et al., polar and stalk cell markers from Jevitt et al. pseudotime analyses (v). (vi) - Heatmap visualizing expression of putative FSC markers from Rust et al. in our FSC differentiation pseudotime analyses. Red indicates high and blue low expression as shown in scale. Early timepoints are on the left and late on the right. D - Follicle cell markers. Mitotic and endocycling FC markers from Jevitt et al. (i), all FC markers from Rust et al. (ii), and MB and terminal FC enriched genes from Jevitt et al. pseudotime analyses (iii).