A

B

Germ cells

	Cluster	Number of cells in cluster	Number of cells (literature)	Estimated coverage	References
GSC			2		
Cystoblast	GSC/CB/2-cc	35	1.3	7.1	
2-cell cyst			1.6 (3.2)		
4-cell cyst	4-cc	168	0.9 (3.6)	46.7	
8-cell cyst	8-cc	101	0.8 (6.4)	15.8	
16-cell cyst region 2A	16-cc 2a I	122	3.2 (51.2)		Drummond-Barbosa and Spradling (2001)
16-cell cyst region 2A	16-cc 2a II	107	2.3 (36.8)	3.6	
	16-cc 2ab	89			
16-cell cyst region 2B	16-cc 2b	146	1.9	4.8	
16-cell cyst region 3	16-cc 3	116	1	7.3	
	St2	167	NA	NA	

Somatic cells of germarium

	Cluster	Number of cells in cluster	Number of cells (literature)	Estimated coverage	References
TF	TF/CC	10	8	1.4	Godt and Laski (1995)
CC			6		Xie and Spradling (2000)
EC	aEC	112			
	cEC	113	35	9.1	Kirilly, et al. (2011)
	pEC	95			
FSC 2-16	FSC/pre-FC	135	2-16	~1.8-2.2	Reilein et al. (2017), Fadiga and Nystul (2019)
pre-FC			58		Nystul and Spradling (2010)
	pre-stalk	53	NA	NA	
stalk	stalk	39	NA	NA	
polar	polar	79	NA	NA	

C

D

	total cells	high quality cells	sequencing saturation	total genes detected	reads per cell
sample 1	1955	1450	78.0%	11,850	182,576
sample 2	1052	874	81.0%	11,724	337,747
sample 3	7192	3729	28.9%	12,788	22,991
sample 4	7794	3946	27.5%	12,846	21,762
sample 5	8559	5228	26.1%	12,777	19,906
total	26552	15227			

E

Supplemental Figure 1.

A - UMAP plot of the entire dataset visualizing integration of 5 samples. Each dot represents a transcriptome of a single cell, and is color-coded according to sample. B - A table showing number of recovered cells in germ cell and somatic cell of germarium clusters, and the number of corresponding cells per cell type in the ovary according to the literature. C - Violin plots visualizing number of transcripts detected, genes detected and fraction of mitochondrial reads in each sample. D - A table showing experiment statistics - total number of cells, number of high-quality cells, sequencing saturation, total genes detected and reads per cell. E - Feature plots visualizing select marker gene expression in somatic cells of the germarium. Left panel - fragment of UMAP plot from Figure 3A. Right panel - visualization of *AdamTS-A*, *en*, *kar*, *Lmx1a*, *peb*, *ptc*, *Wnt4* and *wun2* expression in somatic cells of the germarium. Each dot represents a cell, and is color-coded according to gene expression levels as indicated in the scale.