**SUPPLEMENTAL FIGURE LEGENDS**

**Fig. S1: Biological samples show correlation in germline-expressed genes**. Correlation level in gene expression between sections and biological repeats of hermaphrodite (A) and male (B) gonads.

**Fig. S2: Replicate sections show high level of correlation**. Sections correlation coefficient of the same section from duplicate gonads versus non-replicate section. Boxplots indicate 25th, median, and 75th quantile. \*\*\*, *p*<0.00005. (A) Hermaphrodite gonads. (B) Male gonads.

**Fig. S3: Comparison of the results obtained with two different collection protocols.** (A) Experimental work-through of the IR collection method. Worms were dissected, and gonads were transferred to glass slides. Following dehydration, the slides were mounted on the LCM, caps were placed on the gonad and attached to sections equivalent to 1/10 of the total gonad length via IR laser. The caps were removed and RNA from the caps were analyzed by CEL-Seq. (B) Pairwise profile correlation coefficients among gonad sections collected by the IR method. (C) Profile correlation coefficients among gonad sections between the IR (set 1) and UV (set 2) methods. (D) Representative normalized expression plots of genes from the IR and UV methods. The correlation coefficient (r) is indicated at each plot. (E) Distribution of correlation coefficients among the profiles derived by the two methods across all dynamic genes.

**Fig. S4:** Quantitative RT-PCR analysis of the expression levels of four genes in two gonad sections (sections 2 and 9). Based on the sequencing data, *C48B4.10* and *C01G5.2* belong to group 2 genes, which show high expression only in the first half of the gonad sections. *F08F3.6* and *R04D3.3* belong to the group 4 genes, which show high expression only in the second half of the gonad sections (Table S3). (A) analysis of gene expression levels in gonad sections dissected and collected through the UV method (left) and corresponding levels of expression detected by CEL-seq (right). (B) analysis of gene expression levels in gonad sections dissected and collected through the IR method. Gene expression levels for qRT-PCR were normalized to *gpd-1*. Error bars represent the SEM for two biological replicates each performed in duplicate; *P* values were determined using the two-tailed unpaired *t-test*. \* *P*<0.05, \*\* *P*<0.01.

**Fig. S5: Verification of dynamic germline gene expression via comparison with the NEXTDB RNA *in situ* data.** Representative examples of normalized expression of genes and the corresponding NEXTDB images. Gonads are outlined in red on the *in situ* images for ease of identification. Asterisks on the NEXTDB images indicate the distal tip and are also placed under gonad section 1 on the x-axes of the expression analysis to orient the direction in which the sections are located along these gonads.

**Fig. S6**: **Extended panel of gene ontology terms associated with genes expressed at specific developmental patterns.** For each of the indicated expression profiles (columns), the enrichment was computed for the genes expressed with that profile and the genes annotated to the indicated gene ontology categories (rows). All gene ontology terms with enrichment of less than P≤10-5 for at least one profile are shown in the plot. (A) Hermaphrodite. (B) Male. Genes were assigned to selected expression profiles by correlating their levels with a binary vector representing either high (1) or low (0) expression in the profile. Profiles are indicated as cartoons of gonads with red covering the high expression region. Gene cluster numbers are indicated below the gonad cartoons. Lines with numbers above the cartoons show a binary representation of expression (top line): high (1) or low (0) expression, and the corresponding section in the gonad where this was detected (bottom line). Color in the plot indicates the P-value of the enrichment with blue indicating low and red indicating high levels of enrichment.