

A

B

C

Transposon family

- LTR-Gypsy 37.438%
- LTR-ERV1 23.469%
- DNA-MULE 11.276%
- DNA-PIF-Harbinger 8.986%
- DNA-hAT 6.492%
- DIRS 5.529%
- LINE-RTE 2.321%
- RC-Helitron 1.808%
- DNA-TcMar 1.072%
- PLE 0.462%
- LINE-L1 0.372%
- LTR-ERVL 0.258%
- LTR-ERV 0.168%
- DNA-Kolobok-T2 0.123%
- LTR 0.081%
- LINE-RTE-X 0.073%
- DNA 0.031%
- DNA-Crypton-H 0.02%
- LTR-BEL-Pao 0.017%
- LINE-I 0.006%

Log10(active copy number)

- 2.5
- 3.0
- 3.5
- 4.0

Transposon class

- LTR
- DNA
- LINE
- DIRS
- RC
- PLE

(A) Distribution of substitution rate and sequence length for every single copy in each transposon family. Defined potentially active copies are highlighted in red. (B) Composition of potentially active copies. (C) Scatter plot of percentage of potentially active copy number and total copy number for transposon classes. Transposon classes without potentially active copies are omitted.

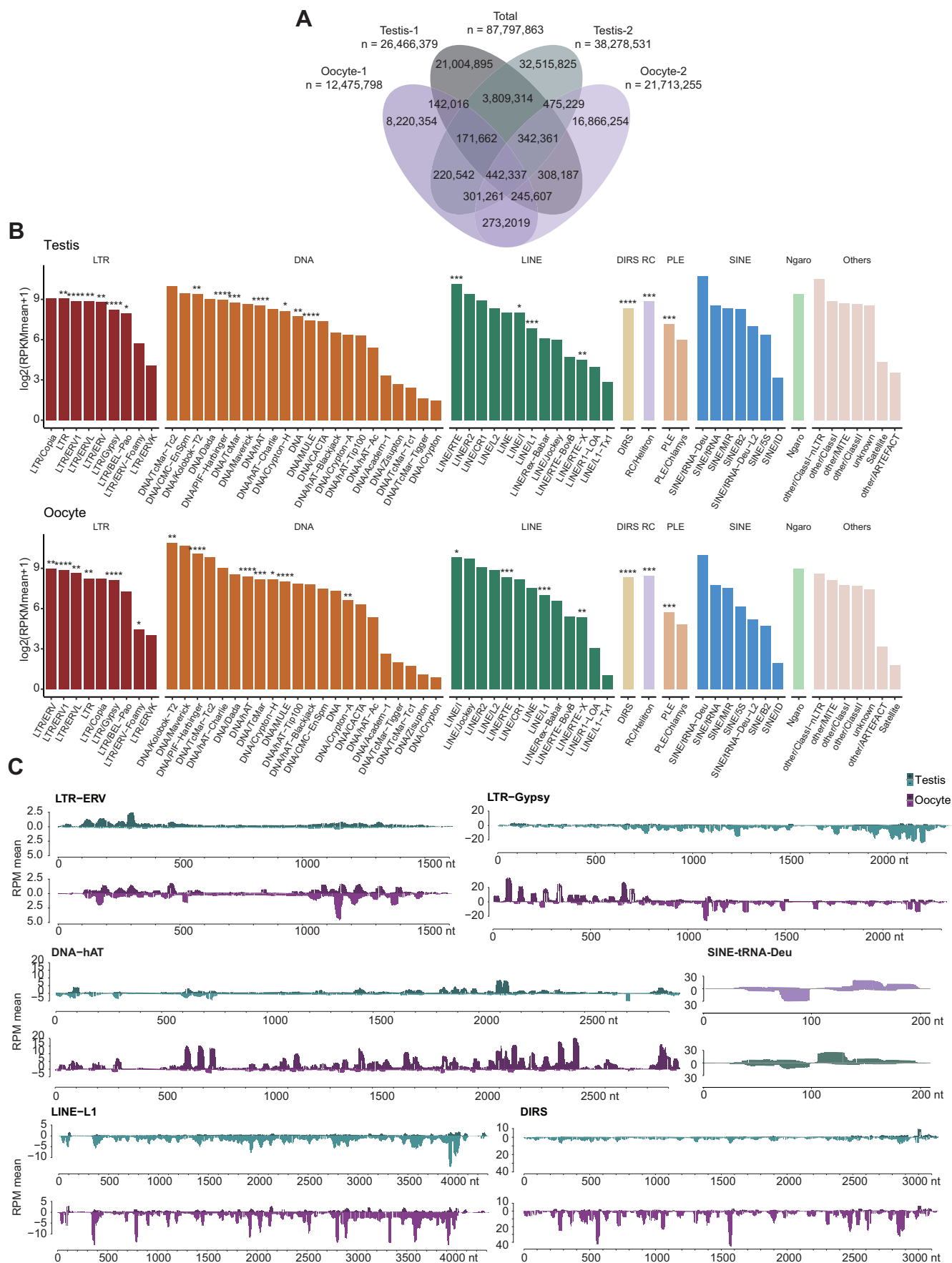


Figure EV2. piRNA repertoires and transposon targeting in axolotl germlines.

(A) The overlap of unique piRNA sequences among the four samples. (B) Mean piRNA signal level over testis or oocyte for each transposon family. ****, active copy number >1000; ***, active copy number >100; **, active copy number >10; *, active copy number >0. (C) Tracks for piRNAs targeting both sense and antisense strands of representative transposon consensus sequence. For all panels, testis, $n = 2$; oocyte, $n = 2$.

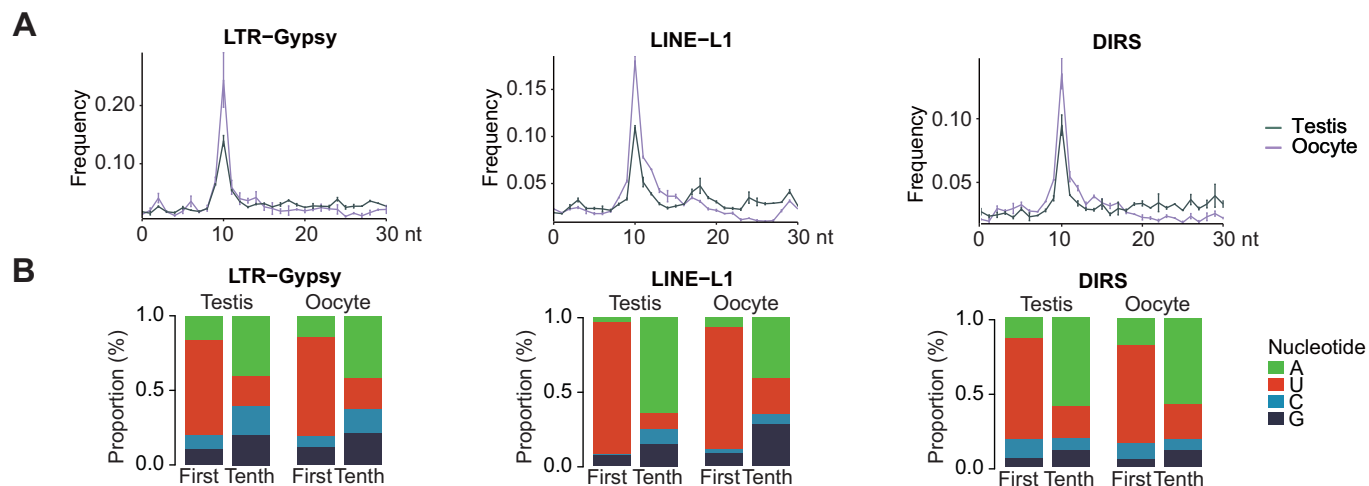


Figure EV3. Features of ping-pong cycle in axolotl germlines.

(A) Relative frequency of the nucleotide distance between 5' ends of complementary piRNA pairs over representative transposon families. Mean and S.E.M. are presented. (B) Nucleotide composition of the first and tenth position in piRNAs over representative transposon families. A, Adenine; U, Uracil; C, Cytosine; G, Guanine. For all panels, testis, $n = 2$; oocyte, $n = 2$.

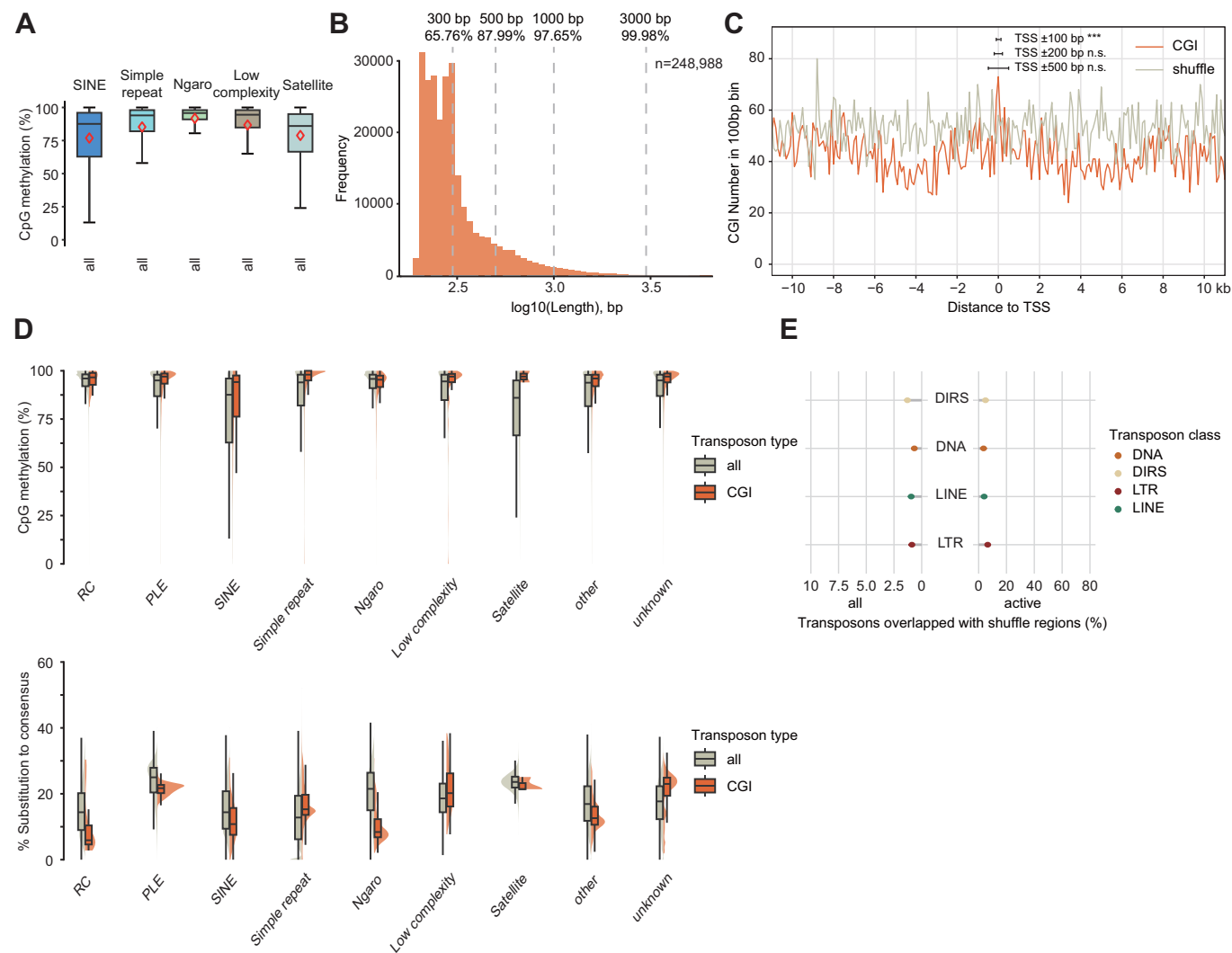


Figure EV4. DNA methylation landscape of minor transposon classes and CpG islands in axolotl spermatozoa.

(A) Percentages of CpG methylation levels over all copies of minor transposon classes in the axolotl. For boxplots, the middle line represents the median; boxes represent the 25th (bottom) and 75th (top) percentiles; whiskers represent median $\pm$ 1.5 $\times$ interquartile range; and outside values are not shown. Rhombus, mean level. (B) Length distribution of all CGI regions ($n = 248,988$). (C) CGI enrichment over TSS and adjacent regions. For statistical tests, *** P value < 0.001, n.s. not significant; Chi-square test. (D) Distribution of CpG methylation level and substitution rate for all transposon copies or copies overlapped with CGI of minor transposon classes. (E) Percentages of transposons overlapped with shuffled region. For all panels, spermatozoa, $n = 3$; pooled for analysis.