



Supplemental Fig S5. pre-MBT Replication Timing Analysis, Related to Figure 4. (A) Replication timing for pre-MBT (blue line) and 28 hpf zebrafish embryos (green line). (B) Replication timing of the Genome overall (white), all genes (grey), the genes transcribed pre-MBT (blue), or the first genes transcribed after zygotic genome activation (First wave, red) after removal of sequences within 5 Mb of the chromosome ends. ANOVA with Bonferroni post-hoc correction, **** $p < 0.0001$. Box plots show the median (line), 95% confidence interval (notch), 25-75th percentile (box), and 10-90th percentile (whiskers). (C) Average repeat count in 100kb windows for all chromosomes plotted against distance from telomeres demonstrates that the chromosome ends (~15Mb) are enriched for repetitive elements. (D) Pearson's correlation between pre-MBT replication timing and repeat density shows a negative correlation. (E) Comparing replication timing in pre-MBT embryos and repeat density with 15Mb from the chromosome ends removed demonstrates that the correlation in Figure S4B is due to chromosome ends (Pearson's). (F) Average %GC content in 10kb windows for all chromosomes plotted against the distance from telomeres demonstrates that the chromosome ends have a higher %GC content. (G) Pearson's correlation between pre-MBT replication timing and %GC content shows a weak negative correlation. (H) Comparing replication timing in pre-MBT embryos and %GC content with 5Mb from the chromosome ends removed demonstrates that the correlation in Figure S5F is due to chromosome ends (Pearson's). Color bars represent fraction (percentage) of maximum density plotted