

Legends for figures in Additional file 1

Figure S1

Mapping of reads. Two different short-read aligner programs were used to map RNA-seq reads onto the zebrafish genome at pre- and post-MBT stages of development (representing pre- and post-ZGA transcriptomes). These two aligners map more reads when combined than when used individually.

Figure S2

IGV screenshot. TopHat and Bioscope complement each other; some reads were only mapped by TopHat, others only by Bioscope. Using both results in better coverage and improvement of the accuracy of the assembled isoforms. The arrows indicate Tophat (grey arrow) and Bioscope (white arrow) specific reads. In 'both' reads mapped by the two aligners are merged. The visualized area is on chromosome 1:396600-402000.

Figure S3

dazl isoform expression. *dazl* has two isoforms expressed maternally which exhibit differential degradation kinetics; isoform 2 is degraded more rapidly than isoform 1 and becomes the minor isoform after the 256-cell stage.

Figure S4

H3K4me3 marking of TSSs post-ZGA. **(a)** H3K4me3 post-translational modification marks (black bar) multiple alternative *dazl* TSSs (black arrows) at the post-ZGA stage. **(b)** Different

Sall4 TSSs are used pre-ZGA and post-ZGA. The maternal RNAs were transcribed from a TSS (black arrow) different from the zygotic transcripts (grey arrow). The H3K4me3 marks both TSSs (black bar). (c) *Actl6a* is transcribed from different promoters. Maternal isoform (black arrow) and post-ZGA (grey arrow). Only the post-ZGA TSS is marked by K3K4me3 (black bar).

Figure S5

qPCR validation of *f11r*. qPCR results for *f11r* confirms the onset of expression of the isoform with exon 8 skipped at 5.5 hpf (red asterix).

Figure S6

Novel isoforms of *dnmt1*. Numerous novel isoforms for *dnmt1* were detected; several were produced due to skipping of multiple exons.

Figure S7

Novel isoforms of *pou5f1*. We detected several new AS events which led to the assembly of four isoforms (grey arrow) different from the annotated version. We also observed a longer 3' UTR than in the annotated version (black arrow), in particular at the post-ZGA stage (white arrow).

Figure S8

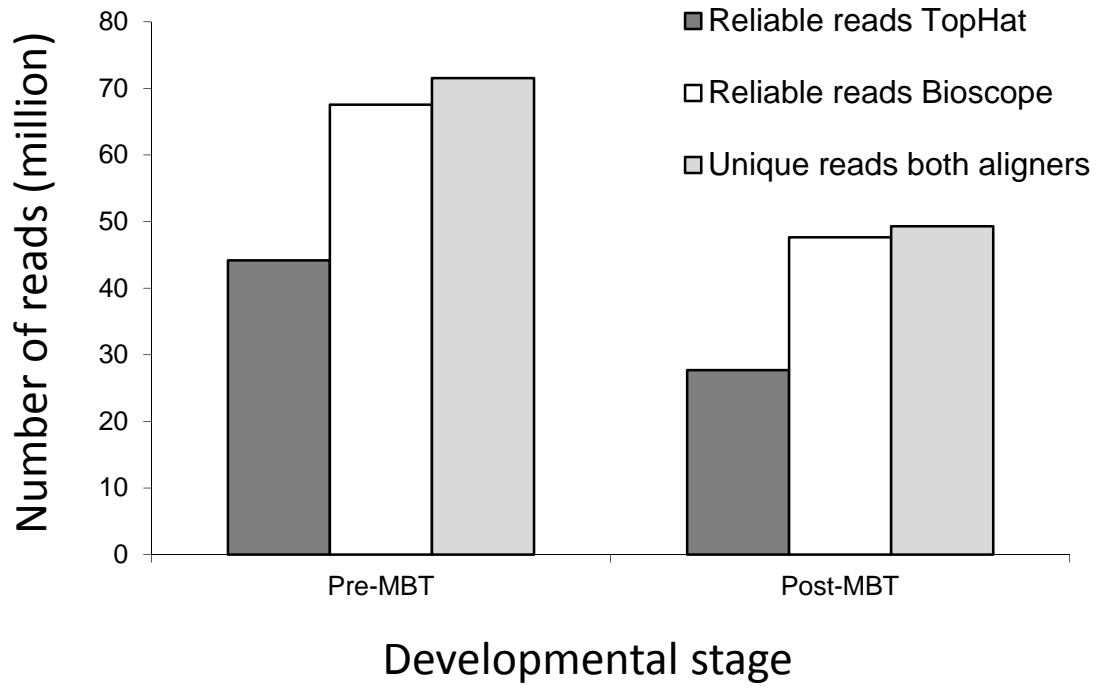
Metagene of skipped exons calculated from RNA-seq reads. Red line = skipped exons. Blue line = random set of exons.

Figure S9

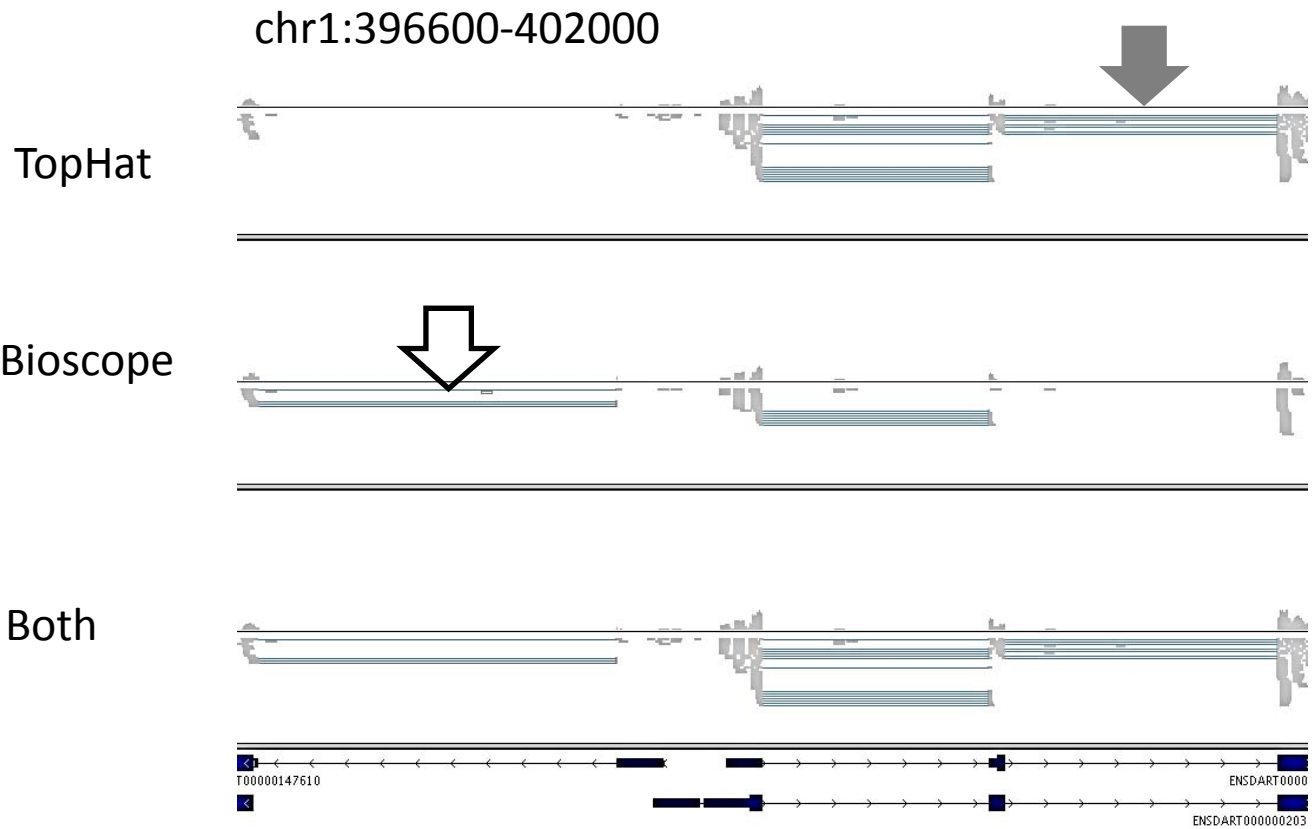
qPCR validation of *magil* expression.

magil expresses a post-ZGA specific isoform (red asterisk).

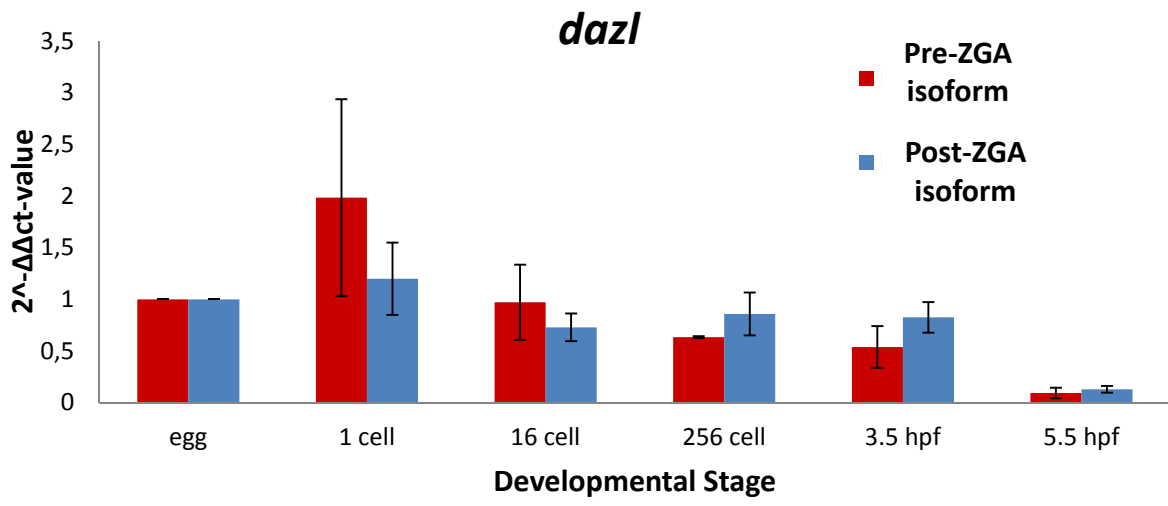
S1



S2



S3



S4

(a)

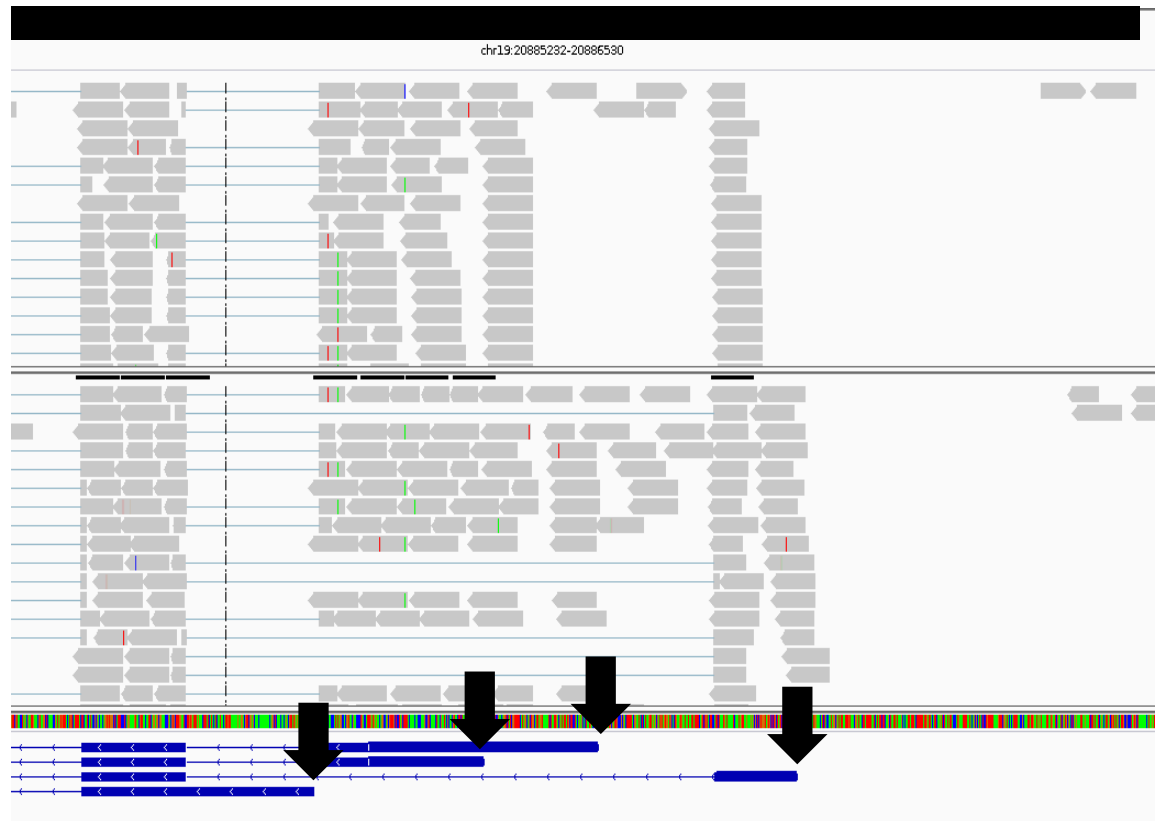
dazl

H3K4me3
peaks

Post-ZGA
reads

Pre-ZGA
reads

Ensembl
Annotation



(b)

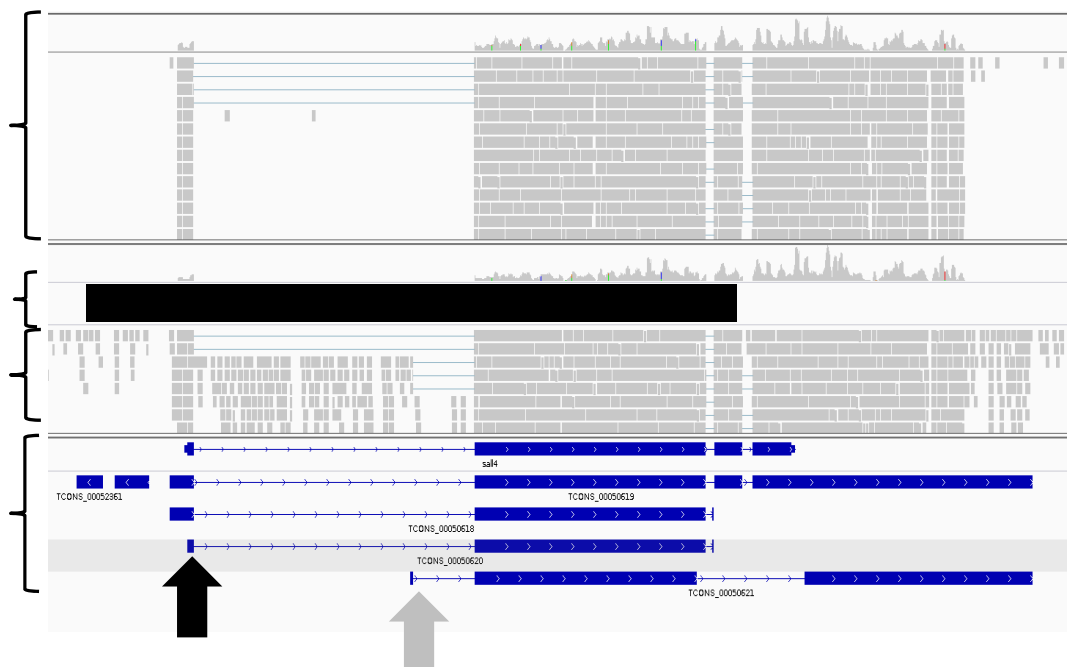
sall4

Pre-ZGA
reads

H3K4me3
peaks

Post-ZGA
reads

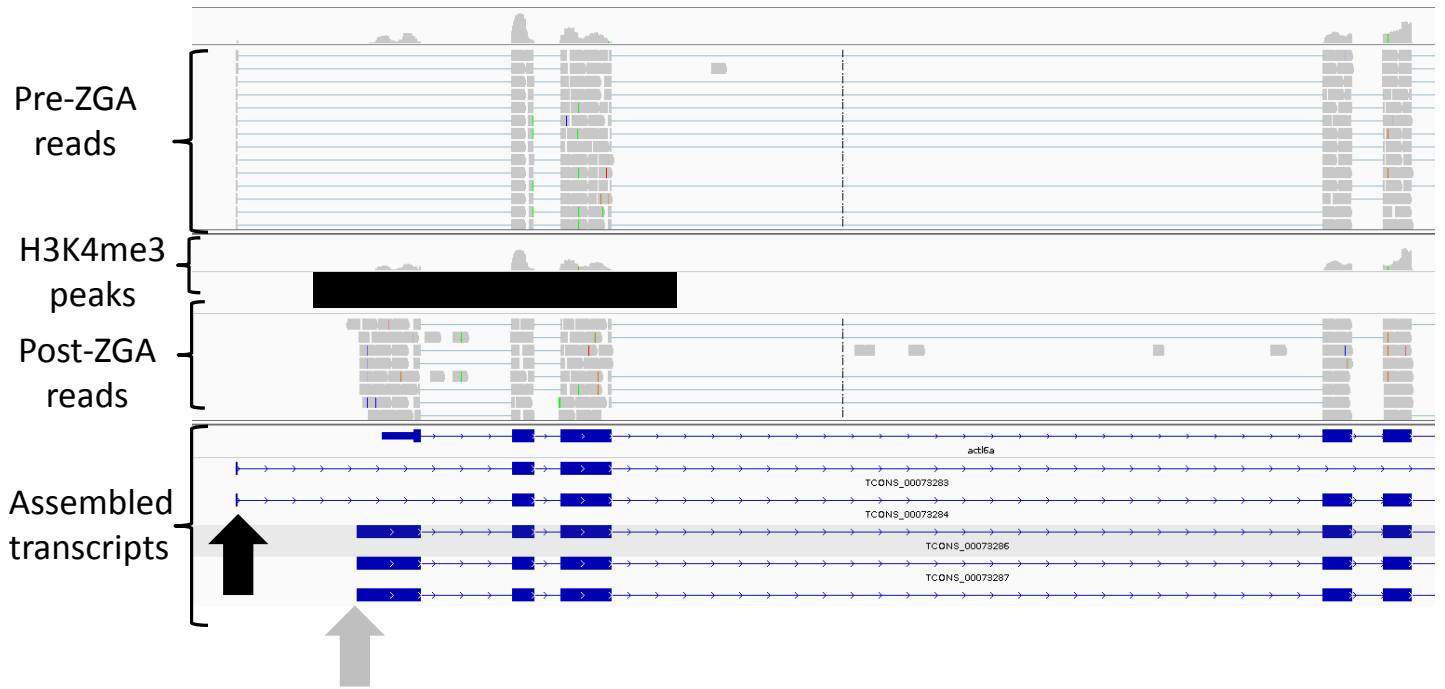
Assembled
transcripts



S4

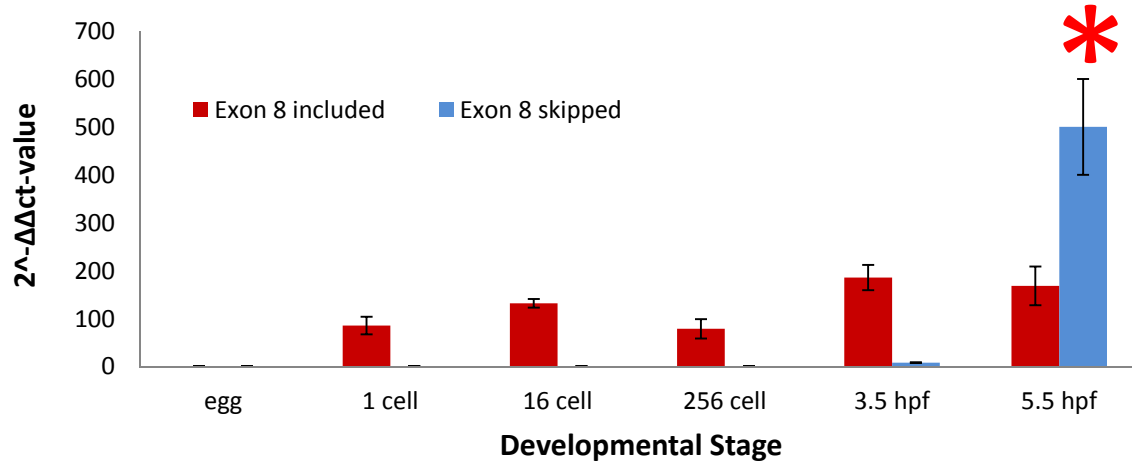
(c)

act16a



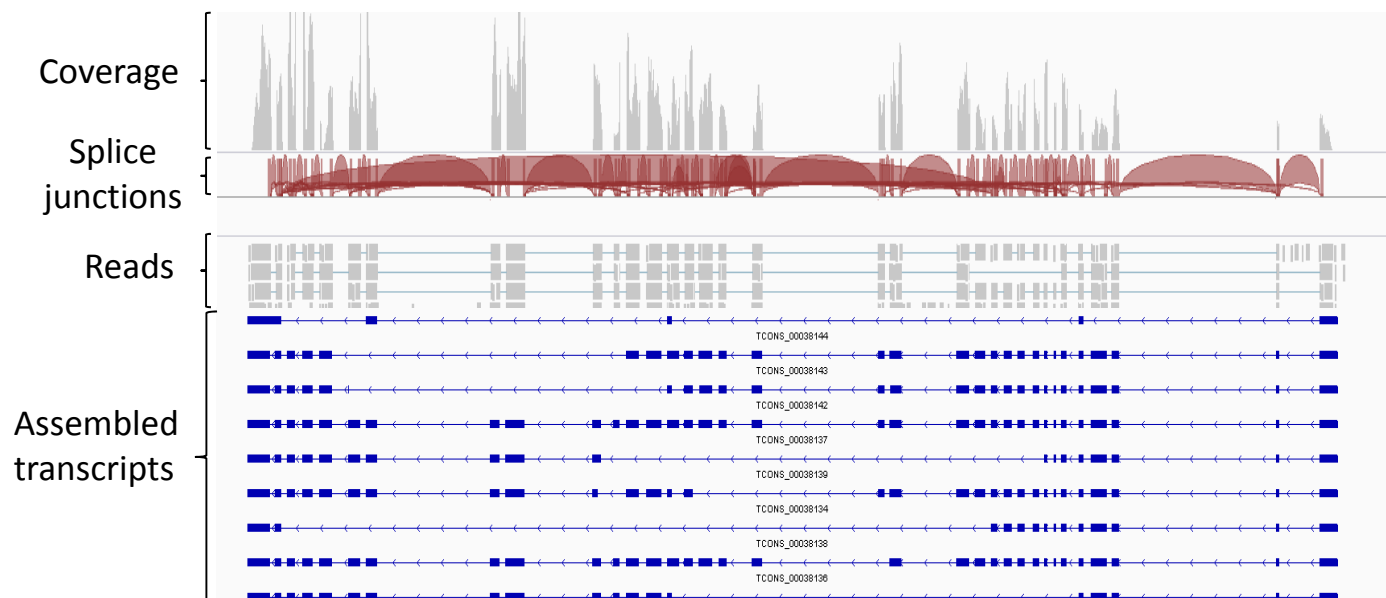
S5

f11r



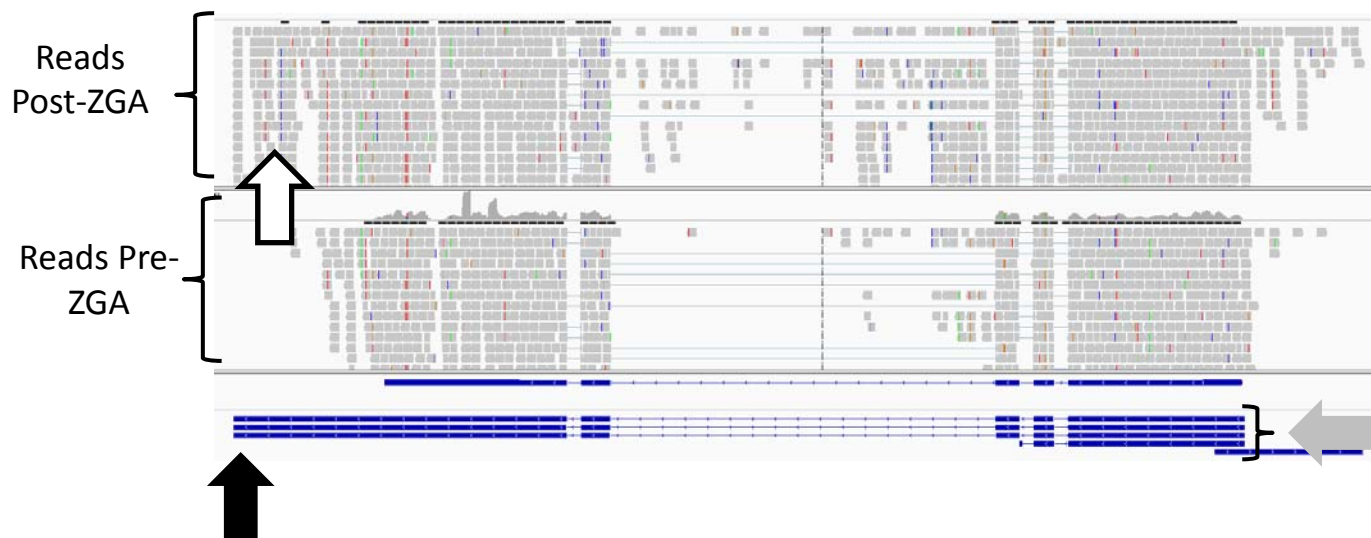
S6

dnmt1

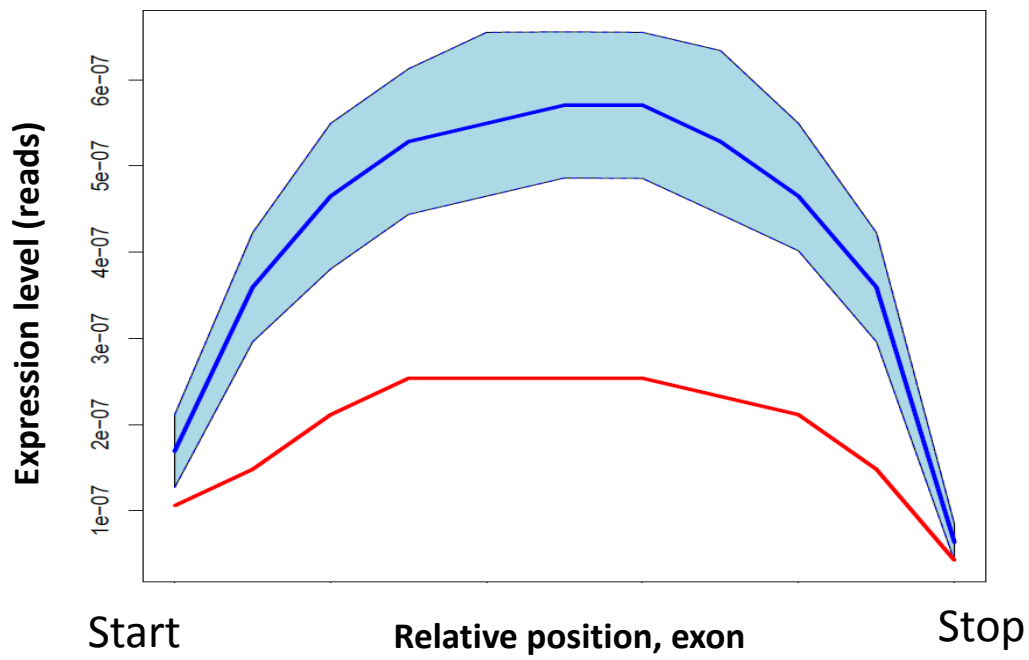


S7

pou5f1



S8



S9

