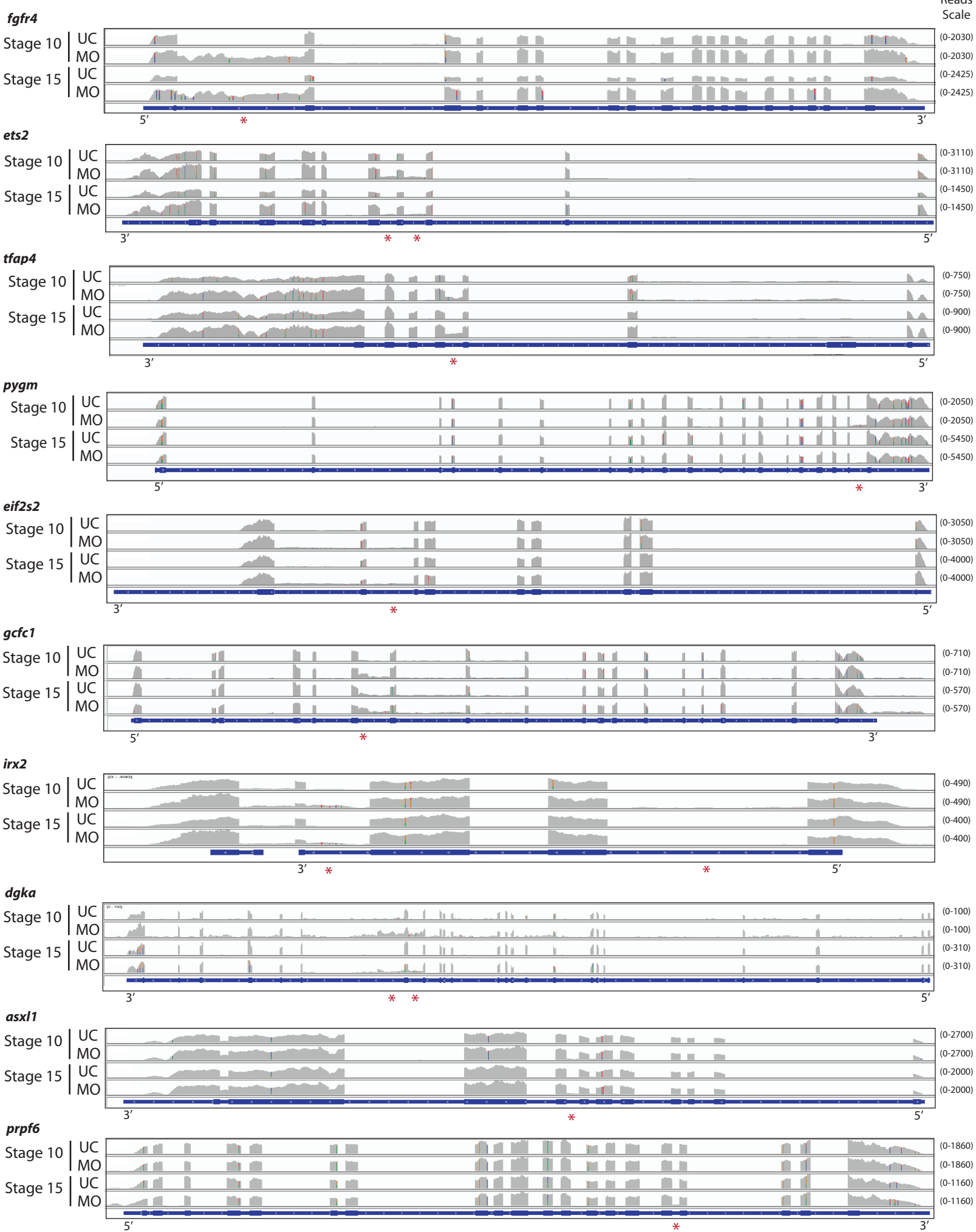
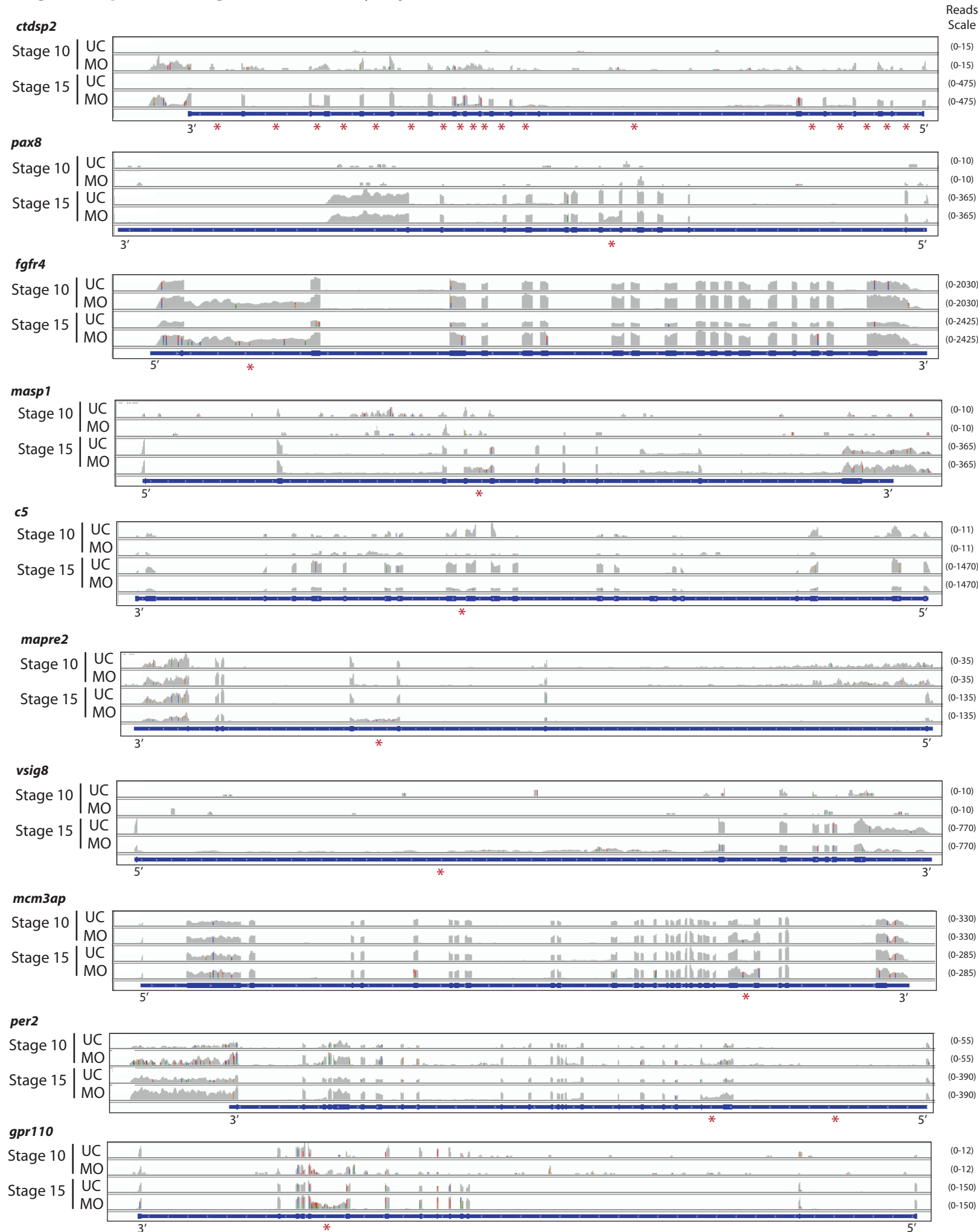


Stage 10: top 10 named genes as sorted by adjusted P-value

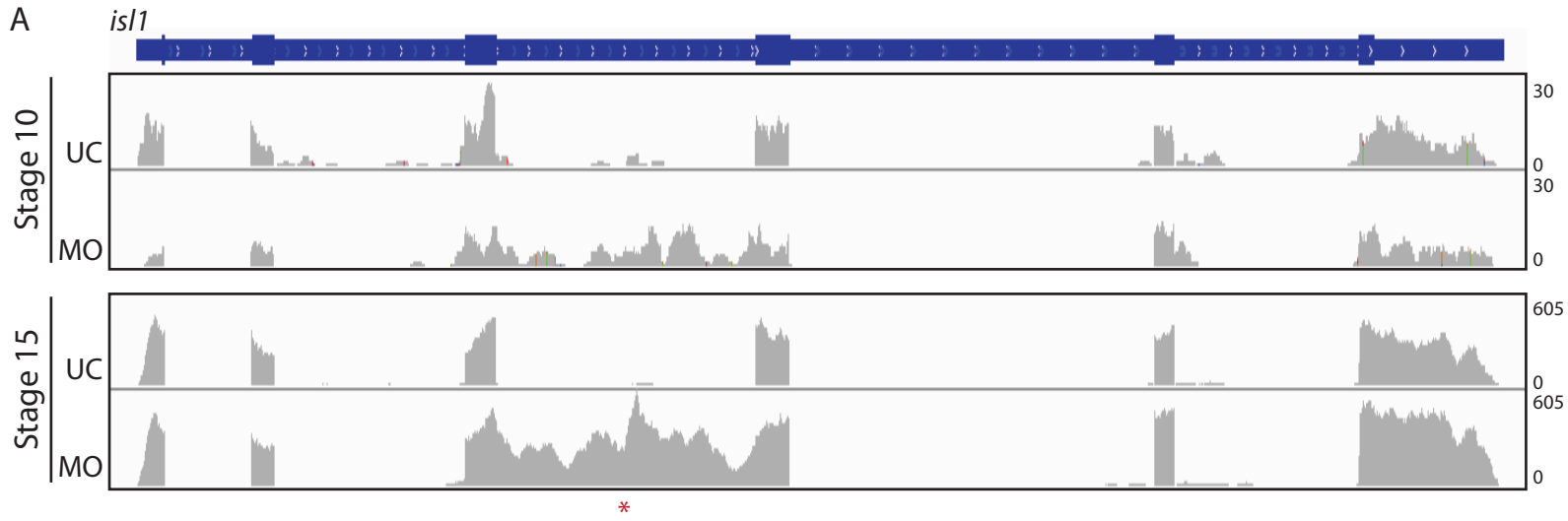
Reads
Scale



Stage 15: top 10 named genes as sorted by adjusted P-value



A



1 **SUPPLEMENTAL FIGURE AND TABLE LEGENDS**

2

3 **Supplemental Figure 1. TAF15 depletion by splice-blocking morpholino specifically targets**
4 **zygotic *taf15*.** Western blot analysis of TAF15 in 2-cell (pre-zygotic genome activation) through
5 stage 11 (post-zygotic genome activation) embryos from the following conditions: uninjected,
6 splice-blocking morpholino (Z TAF15 depletion), and mismatch morpholino.

7 **Supplemental Figure 2. TAF15 depletion by translation-blocking morpholino leads to**
8 **various types of intron retentions at stage 10.** Visualization of RNAseq reads with Integrative
9 Genomics Viewer aligned with gene model in blue. Top 10 genes with differential exon usage
10 (DEU) as sorted by their adjusted P value at stage 10. UC = uninjected control; MO = M+Z
11 TAF15-depleting morpholino. * = intron with affected DEU according to DEXseq and does not
12 indicate the number of DEU within an intron.

13 **Supplemental Figure 3. TAF15 depletion by translation-blocking morpholino leads to**
14 **various types of intron retentions at stage 15.** Visualization of RNAseq reads with Integrative
15 Genomics Viewer aligned with gene model in blue. Top 10 genes with differential exon usage
16 (DEU) as sorted by their adjusted P value at stage 15. UC = uninjected control; MO = M+Z
17 TAF15-depleting morpholino. * = intron with affected DEU according to DEXseq and does not
18 indicate the number of DEU within an intron.

19 **Supplemental Figure 4. TAF15 depletion by translation-blocking morpholino leads to**
20 **single intron retention in *ils1*.** (A) Visualization of *ils1* RNA-seq reads with Integrative
21 Genomics Viewer aligned with gene model in blue. UC = uninjected control; MO = M+Z
22 TAF15-depleting morpholino. * = intron with affected DEU according to DEXseq and does not
23 indicate the number of DEU within an intron.

24 **Supplemental Table 1. Differential Exon Usage, stage 10.** DEXseq analysis of sequenced
25 RNA from M+Z TAF15-depleted *X. tropicalis* embryos, stage 10; two-fold increase in
26 expression cutoff; sorted by padj value.

27 **Supplemental Table 2. Differential Exon Usage, stage 15.** DEXseq analysis of sequenced
28 RNA from M+Z TAF15-depleted *X. tropicalis* embryos, stage 15; two-fold increase in
29 expression cutoff; sorted by padj value.

30 **Supplemental Table 3. Stage-persistent Differential Exon Usage, Stage 10 and 15.** Genes
31 with conserved differential exon usage from stage 10 to 15. DEXseq analysis of sequenced RNA
32 from M+Z TAF15-depleted *X. tropicalis* embryos; two-fold increase in expression cutoff; sorted
33 by gene name.

34 **Supplemental Table 4. Increased Gene Expression, stage 15.** DESeq analysis of sequenced
35 RNA from M+Z TAF15-depleted *X. tropicalis* embryos, stage 15; two-fold increase in
36 expression cutoff; sorted by padj value.

37 **Supplemental Table 5. All changes in Gene Expression, stage 10.** DESeq analysis of
38 sequenced RNA from M+Z TAF15-depleted *X. tropicalis* embryos, stage 10; sorted by padj
39 value.

40 **Supplemental Table 6. Increased and Decreased Gene Expression, stage 15.** DESeq analysis
41 of sequenced RNA from M+Z TAF15-depleted *X. tropicalis* embryos, stage 15; two-fold
42 increase or decrease in expression cutoff; sorted by fold change.

43 **Supplemental Table 7. Differential Exon Usage Characteristics, stages 10 and 15.** Number
44 and location of retained introns within the top 10 genes with differential exon usage (DEU)
45 following DEXseq analysis, as sorted by adjusted P value.