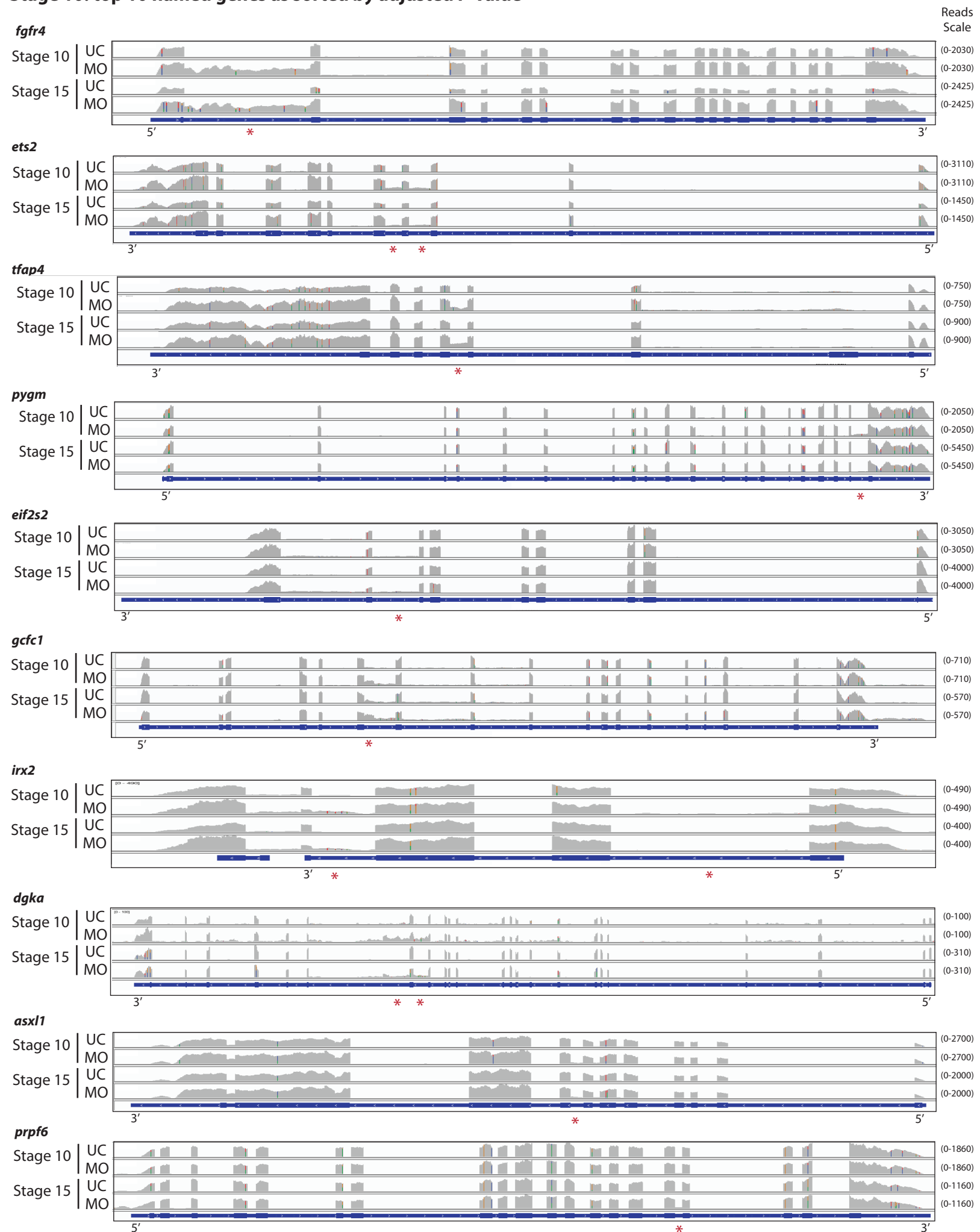


**Figure S1. Taf15 depletion by splice-blocking morpholino specifically targets zygotic *taf15*.**

Western blot analysis of Taf15 in 2-cell (pre-zygotic genome activation) through stage 11 (postzygotic genome activation) embryos from the following conditions: uninjected, splice-blocking morpholino (Z Taf15 depletion), and mismatch morpholino.

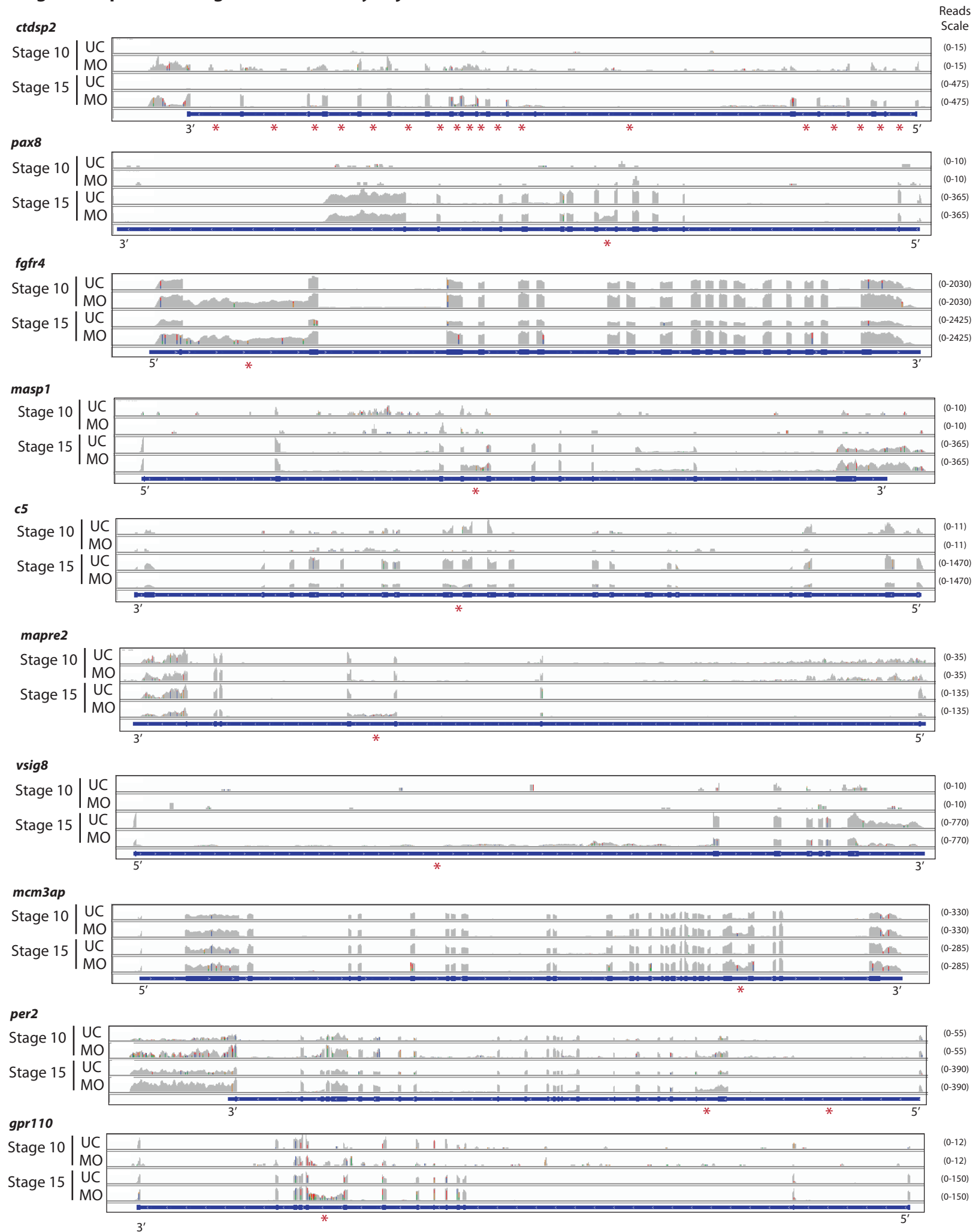
### Stage 10: top 10 named genes as sorted by adjusted P-value



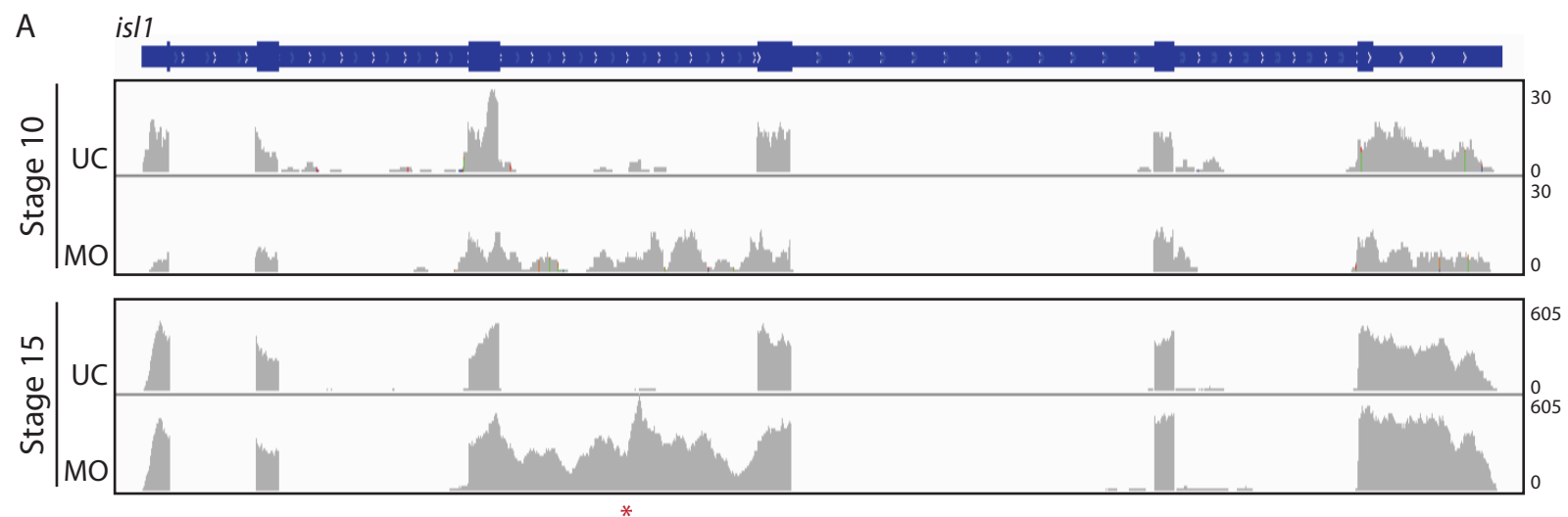
**Figure S2. Taf15 depletion by translation-blocking morpholino leads to various types of intron retentions at stage 10.**

Visualization of RNAseq reads with Integrative Genomics Viewer aligned with gene model in blue. Top 10 genes with differential exon usage (DEU) as sorted by their adjusted P value at stage 10. UC = uninjected control; MO = M+Z Taf15-depleting morpholino. \* = intron with affected DEU according to DEXseq and does not indicate the number of DEU within an intron.

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



**Figure S3. Taf15 depletion by translation-blocking morpholino leads to various types of intron retentions at stage 15.** Visualization of RNAseq reads with Integrative Genomics Viewer aligned with gene model in blue. Top 10 genes with differential exon usage (DEU) as sorted by their adjusted P value at stage 15. UC = uninjected control; MO = M+Z Taf15-depleting morpholino. \* = intron with affected DEU according to DEXseq and does not indicate the number of DEU within an intron.



**Figure S4. Taf15 depletion by translation-blocking morpholino leads to single intron retention in *isl1*.** (A) Visualization of *isl1* RNA-seq reads with Integrative Genomics Viewer aligned with gene model in blue. UC = uninjected control; MO = M+Z Taf15-depleting morpholino. \* = intron with affected DEU according to DEXseq and does not indicate the number of DEU within an intron.

**Table S1. Differential Exon Usage, stage 10.** DEXseq analysis of sequenced RNA from M+Z Taf15-depleted X. *tropicalis* embryos, stage 10; two-fold increase in expression cutoff; sorted by padj value.

[Click here to download Table S1](#)

**Table S2. Differential Exon Usage, stage 15.** DEXseq analysis of sequenced RNA from M+Z Taf15-depleted X. *tropicalis* embryos, stage 15; two-fold increase in expression cutoff; sorted by padj value.

[Click here to download Table S2](#)

**Table S3. Stage-persistent Differential Exon Usage, Stage 10 and 15.** Genes with conserved differential exon usage from stage 10 to 15. DEXseq analysis of sequenced RNA from M+Z Taf15-depleted X. *tropicalis* embryos; two-fold increase in expression cutoff; sorted by gene name.

[Click here to download Table S3](#)

**Table S4. Increased Gene Expression, stage 15.** DESeq analysis of sequenced RNA from M+Z Taf15-depleted X. *tropicalis* embryos, stage 15; two-fold increase in expression cutoff; sorted by padj value.

[Click here to download Table S4](#)

**Table S5. All changes in Gene Expression, stage 10.** DESeq analysis of sequenced RNA from M+Z Taf15-depleted *X. tropicalis* embryos, stage 10; sorted by padj value.

[Click here to download Table S5](#)

**Table S6. Increased and Decreased Gene Expression, stage 15.** DESeq analysis of sequenced RNA from M+Z Taf15-depleted *X. tropicalis* embryos, stage 15; two-fold increase or decrease in expression cutoff; sorted by fold change.

[Click here to download Table S6](#)

**Table S7. Differential Exon Usage Characteristics, stages 10 and 15.** Number and location of retained introns within the top 10 genes with differential exon usage (DEU) following DEXseq analysis, as sorted by adjusted P value.

[Click here to download Table S7](#)

**Table S8. Primer set pairs used in these studies:**

<i>efl1a1</i>	F 5'-CCCTGCTGGAAGCTCTTGAC-3'	R 5'-GGACACCAGTCTCCACACGA-3'
<i>fgfr4 intron 1</i>	F 5'-AGGGCTAAGCAGTGCCTGTA-3'	R 5'-AATGCAAGAGCAGCTCCAAT-3'
<i>fgfr4 total</i>	F 5'-AGCCAGGAATGTTCTTGTGG-3'	R 5'-TCCCATGTCAAACTCCAAA-3'
<i>ventx2.1</i>	F 5'-AACAGCCAGCTGTCTCCAGT-3'	R 5'-GCTGTGTCCCTGTGTAGCAA-3'
<i>engrailed 2</i>	F 5'-GAAGACGACGACGACTGTCA-3'	R 5'-AACTTTGCCTCCTCTGCTCA-3'
<i>bmp7.1 intron 3</i>	F 5'-TCCCCTCCTCTATGGCTTTT-3'	R 5'-AGTGGTGCCCAAGATTCAAC-3'
<i>bmp7.1 total</i>	F 5'-CGGAAAGGTTTGGAAAATGA-3'	R 5'-ATATCGAACACCAGCCATCC-3'
<i>cpl1 5'UTR</i>	F 5'-TATGCCTCCCCTGTGGATAG-3'	R 5'-TACTTTGCCTGCCCTATGCT-3'
<i>cpl1 total</i>	F 5'-AGAGATCTGCCGCACTTTGT-3'	R 5'-TGAACCACGTGGACCATAGA-3'
<i>dgka intron 9</i>	F 5'-GAGGGTGATGTGACCATGTG-3'	R 5'-TCCATTTTAAGCCCAACAGC-3'
<i>dgka intron 11</i>	F 5'-GCGACCAATGAATGCTACCT-3'	R 5'-TAAACATGCTGCTGGGTCAG-3'
<i>dgka total</i>	F 5'-TGGATGAGAGGTGGATGTGA-3'	R 5'-CATCACACAGTGGGGATGAG-3'
<i>pdgfa intron 1</i>	F 5'-CCTCAGAGGCACTTTCCAAG-3'	R 5'-TTGTGCTACAGAACCAGCAAC-3'
<i>pdgfa total</i>	F 5'-CCAGAGAAGCGTTCTGTTCC-3'	R 5'-ACACACGGAGGCCAGATTAG-3'
<i>per2 intron 1</i>	F 5'-GGCCTGTAATTTGGAGCTTTC-3'	R 5'-CAAACCGGATGTGGGATTAT-3'
<i>per2 total</i>	F 5'-TGGACGGAATCAAGAAAAG-3'	R 5'-GAACCCTCTCAGCAAACAGC-3'
<i>rab15 intron 2</i>	F 5'-GGATGCTTTTGGTGGTGTTT-3'	R 5'-ATTGGATGGTTTTGCCTCTG-3'
<i>rab15 total</i>	F 5'-GGATGAAGCTTGCAGAGGAG-3'	R 5'-CTCCAGCTCCCTTTTGTGAG-3'
<i>srsf4 intron 5</i>	F 5'-TCTGATCCCCATTCAGTTGC-3'	R 5'-GTTTTGCCTGCATAGCCAGT-3'
<i>srsf4 total</i>	F 5'-GAGCAAGGATAGGGACCACA-3'	R 5'-TCTCTTTGCTACGGCTGGAT-3'
<i>zdhhc5 intron 6</i>	F 5'-GAAGCGGGCTATCTGAGTTG-3'	R 5'-CCTTGGGGTCTGAGATTTGA-3'
<i>zdhhc5 total</i>	F 5'-ACTGGCCAATTTTAGCATGG-3'	R 5'-AACCTGCACTCCCCTTACCT-3'

<i>gpr110 intron 9</i>	F 5'-GCCATTTAGTGATGGGCTGT-3'	R 5'-CCAAGGCACACATACATGCT-3'
<i>gpr110 total</i>	F 5'-GCTTGTCATATCCCGTTGCT-3'	R 5'-CTAGCCCACACGTAGCCATT-3'
<i>isl1 intron 3</i>	F 5'-CCCTCCTACCCTTTTCCAAG-3'	R 5'-GGCTGAAGTGC GGAATCTAA-3'
<i>isl1 total</i>	F 5'-ACTTTGCCCTGCAGAGTGAC-3'	R 5'-TGCCTCTATAGGGCTGGCTA-3'