



**Supplementary information, Fig. S12 Quality control of Ribosome profiling. a,** FPKM correlation of Ribosome profiling sequencing data between biological replicates for *ddx3xb* mutants and wild-type embryos at 4 hpf. **b,** Bar chart illustrating the proportion of Ribosome profiling sequencing data in three transcripts regions for *ddx3xb* mutant and wild-type embryos at 4 hpf. **c,** FPKM correlation of Ribosome profiling sequencing data between biological replicates for *ddx3xb<sub>FL</sub>* and *ddx3xb<sub>ΔN</sub>* mRNAs injected *ddx3xb* mutant embryos at 4 hpf. **d,** Bar chart illustrating the proportion of Ribosome profiling sequencing data in three transcripts regions for *ddx3xb<sub>FL</sub>* and *ddx3xb<sub>ΔN</sub>* mRNAs injected *ddx3xb* mutant embryos at 4 hpf. **e,** Boxplots

of the translation efficiency of wild-type, *ddx3xb* mutant, *ddx3xb<sub>FL</sub>* and *ddx3xb<sub>ΔN</sub>* mRNAs injected *ddx3xb* mutant embryos at 4 hpf. *P* values were calculated by the Kruskal Wallis test. **f**, Bar chart illustrating the proportion of Ribosome profiling sequencing data that belong to maternal decay, maternal stable, and zygotic groups for wild-type embryos, *ddx3xb* mutant embryos, *ddx3xb<sub>FL</sub>* and *ddx3xb<sub>ΔN</sub>* mRNAs injected *ddx3xb* mutant embryos at 4 hpf.