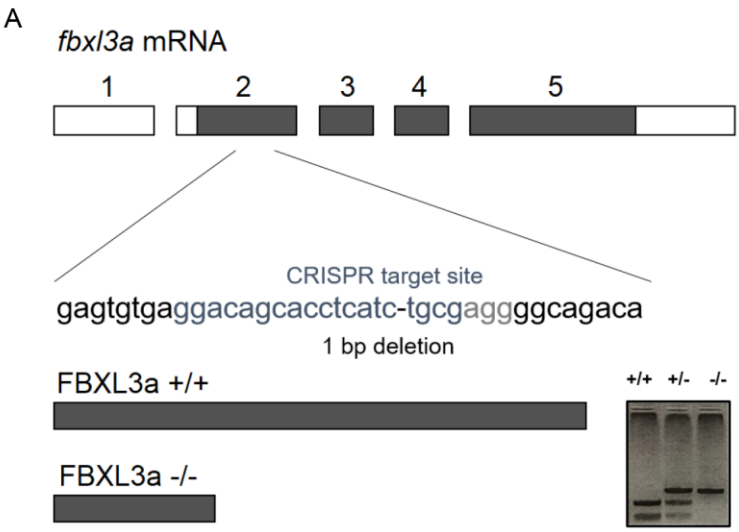

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Figure S1. Zebrafish *fbxl3a* genomic structure and loss-of-function mutation. Top, the genomic organization of *fbxl3a* with 5 exons, the first is non-coding. The target sequence in exon 2 and the predicted size of the resulting proteins are depicted. Mutants were identified using PCR amplification followed by enzymatic digestion with *NlaIII*, which recognizes a specific nucleotide sequence within the WT allele (5'-CATG-3'). The mutation is the deletion of the A in this restriction site. The observed *NlaIII*-digested PCR products for WT, heterozygous and homozygous mutant fish are shown (two clear bands of 230 bp and 133 bp are observed for WT, one undigested band of 363 bp for the homozygous mutant and all three bands for the heterozygotes). Bottom, partial *fbxl3a* genomic sequence. Blue letters represent coding sequence within exon 2. The deletion mutation of nucleotide A (red, bold) introduces an early stop codon (red-highlighted) after 80 codons, resulting in a 94 amino acid protein. The sites of PCR primers used for screening are highlighted in yellow. The underlined base sequence represents the *NlaIII* restriction site used in the process of screening. The grey-highlighted nucleotides represent the CRISPR target site.