

Table S1. *slds* mutations found in F0

<i>slds</i> mutations found in F0			
Name	Nucleotide Sequence Change	Ins/Del	Effect
sbdsnu129	189G>T+ 193G>A+195delGGCGAAG	Del	Truncation
sbdsnu130	190insC	Ins	Truncation
sbdsnu132	190delAAGTGGC	Del	Truncation
sbdsnu134	191delA	Del	Truncation
sbdsnu135	192delAGTGG + 199G>A	Del	Truncation
sbdsnu136	183delCAAGGGT	Del	Truncation
sbdsnu167	192G>A + 194insAGAAAGAAAGAAATGTGTCCA	Ins	Insertion 7 aa

Table S2. Primer for genotyping and sgRNA sequences

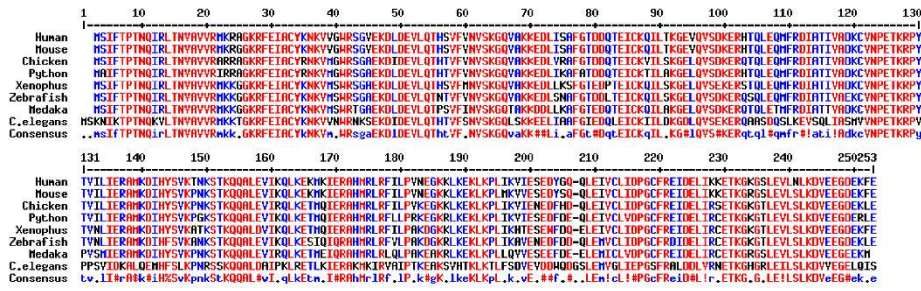
Primers for genotyping				
	Forward (5'-->3')	Reverse (5'-->3')	Size (bp)	Enzyme
<i>sbds</i>	TGACATGATTGGTTTAGGTTTG	CCCAGGTATATTATTTAGTCACAAGA	584	XcmI
<i>sbds</i>	TGATGAAGTCCTGCAAACCA	CAGGTCATCTGTTCCAAAAGC	100	
<i>sbds</i>	GCTTTGACCATTTCAGATCACC	TCCTGCAAACCAACACAGTC	130	
<i>p53</i>	ACATGAAATTGCCAGAGTATGTGTC	TCGGATAGCCTAGTGCGAGC	336	MboII
sgRNAs				
<i>sbds</i>	sgRNA XcmI	GAATGTGTCCAAGGGTCAAG		
<i>sbds</i>	sgRNA BbsI	AAGACCTATCCAATGCTTTTG		

Table S3. RT-qPCR primer sequences

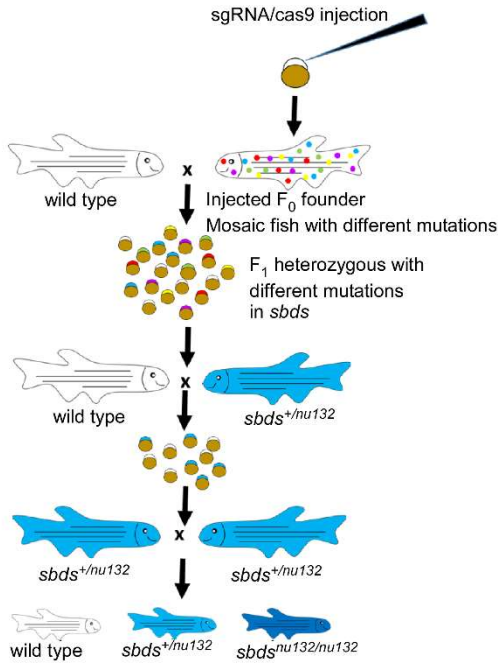
ZDB-GENE	Gene name	Gene	Forward (5'-->3')	Reverse (5'-->3')
ZDB-GENE-000329-1	Actin	<i>β-act</i>	TGCTGTTTTCCCTCCATTG	TTCTGTCCCATGCCAACCA
ZDB-GENE-000511-6	Bcl2-associated X protein	<i>bax</i>	GGAGATGAGCTGGATGGAAA	AGATCTCACGGGCCACTCT
ZDB-GENE-030825-5	Caspase 9, apoptosis-related cysteine peptidase	<i>casp9</i>	CTGTCAAAGGGGGTCTTAC	TCGTCTCCAGGTCTTTCACC
ZDB-GENE-020322-1	Cyclin G1	<i>ccng1</i>	CTTCTGTGCGGAGACGTTTT	ACAGCGATGTAGAAGCAGCA
ZDB-GENE-990415-153	E3 ubiquitin protein ligase	<i>mdm2</i>	TAACCGAGGCAGACTACTGGAAG	TTTCCCAGTTGGAGTGTGTTCT
ZDB-GENE-070705-7	Cyclin Dependent Kinase Inhibitor 1A	<i>p21 (cdk1a)</i>	AGAGCTCGCTGGAGTCAG	CCGAAAAGACTCCGCCTA
ZDB-GENE-070119-4	BCL2 binding component 3	<i>puma (bbc3)</i>	ACT GCC CCA CAT CCC CTC AC	CGT CCC CGA TTG TCC TCA GTT G
ZDB-GENE-040426-1116	Shwachman-Bodian-Diamond Syndrome	<i>sbds</i>	CCAACACAGTCTTTGTGAATG	CGCTTGGTCTCAGGATTC
ZDB-GENE-990415-270	Tumor protein p53	<i>tp53</i>	CTCTCCCACCAACATCCACT	ACGTCCACCACCATTGTAAC
ZDB-GENE-090812-3	Sterol regulatory element binding transcription factor 1	<i>srebp1 (sreb1)</i>	CTCTGGGTACCCGCTTCTTT	CAGATGCTCACGAAACCCT
ZDB-GENE-030131-7802	Fatty acid synthase	<i>fasn</i>	GAGAAAGCTTGCCAAACAGG	GAGGGTCTTGCAGGAGACAG
ZDB-GENE-990415-213	Peroxisome proliferator-activated receptor gamma	<i>pparg</i>	CACTCTCCGCTGATATGGTGG	GTAGATGGGCTCGTGTGCC

Figure S1

A



B



C

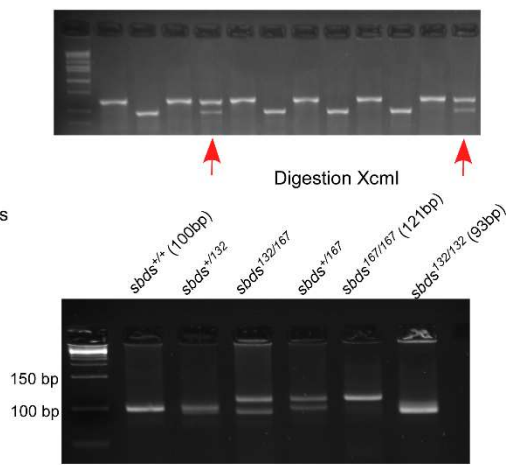
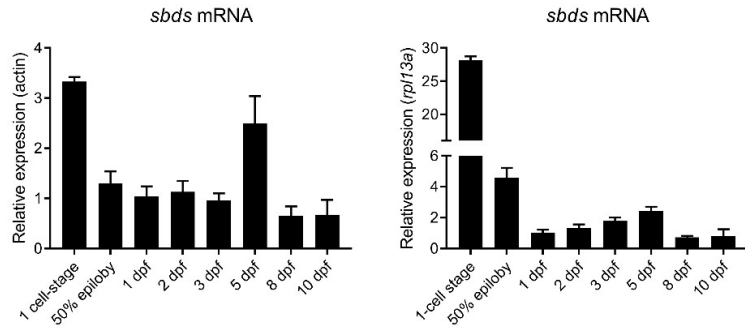


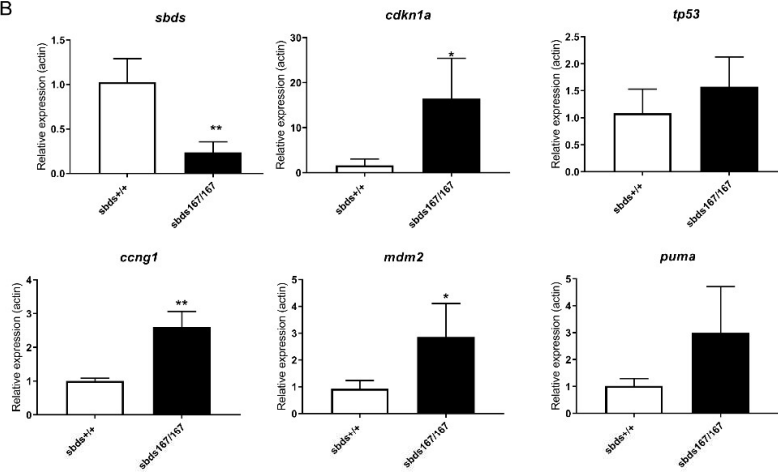
Figure S1. Generation and genotyping of zebrafish *sbds* mutants (A) Amino acid alignment of different species (alignment using Multalin). **(B)** Figure showing gRNA/cas9 injection and lines obtained. **(C)** Genotyping for the *sbds*⁺, *sbds*^{nu132} and *sbds*^{nu167}.

Figure S2

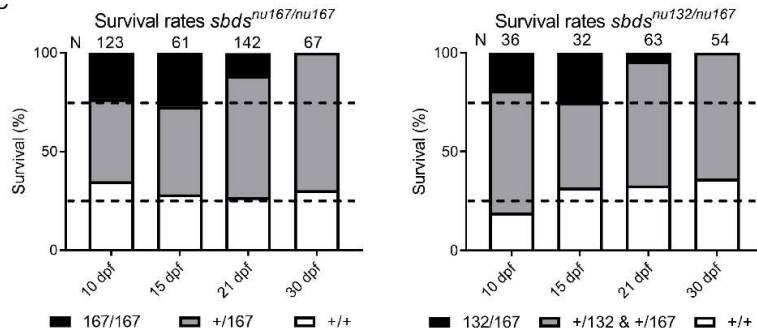
A



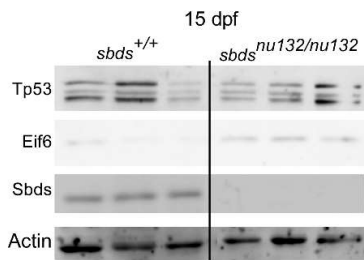
B



C



D



E

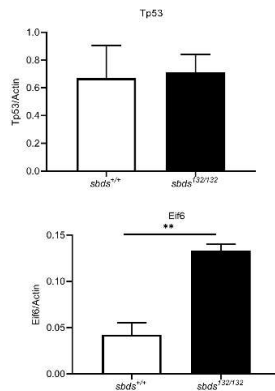


Figure S2. Transcriptional, protein, and survival analysis of mutant fish v. wild-type. (A) *sbds* mRNA levels in wildtype zebrafish at different ages respect to two different housekeeping genes *b-actin* and *rpl13a*. Gene expression normalized to 1dpf. Pool 25-30 embryo/larvae and three biological replicates by stage. (B) mRNA levels at 10 dpf of *sbds^{nu167}*. (C) Survival rates for siblings of *sbds^{nu167}* and compound heterozygotes (D) Western blot and (E) quantification at 15 dpf of *sbds^{nu132}* allele* p<0.05: **p<0.01

Figure S3

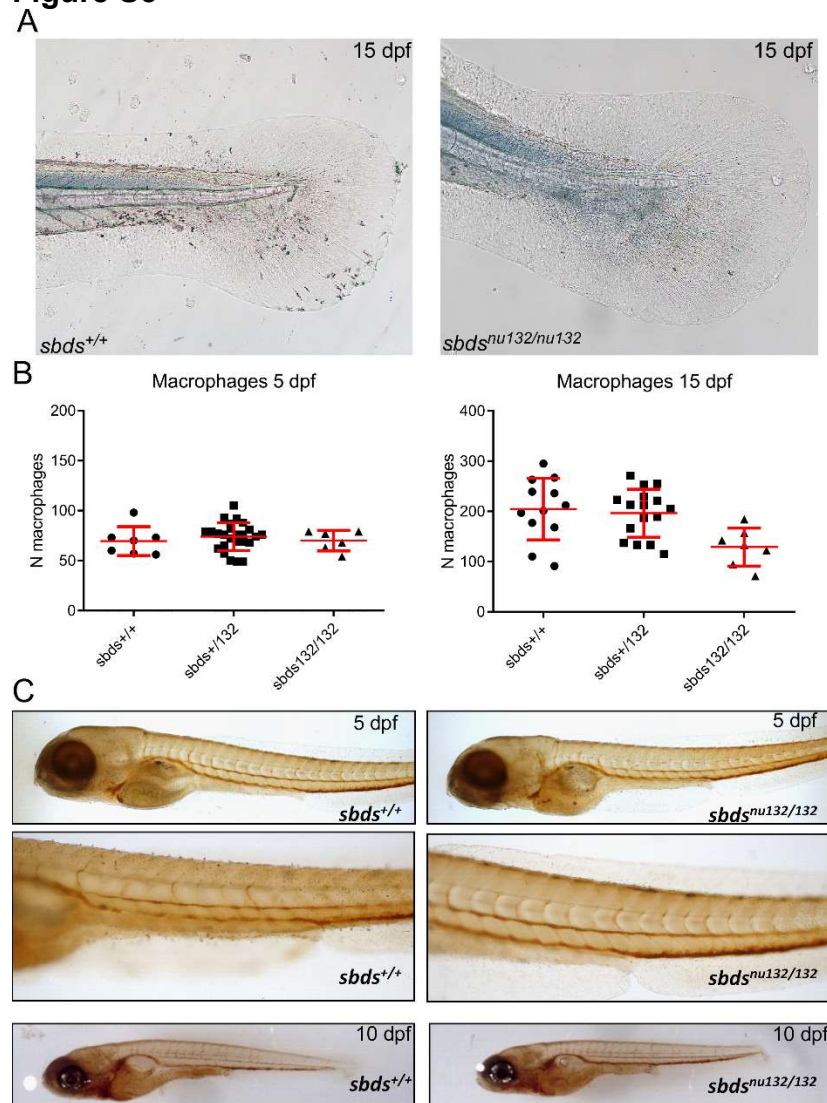


Figure S3. *sbds*^{nu132/nu132} mutants showed no changes in number of macrophages or hemoglobin appearance. (A) Sudan black staining for neutrophils at 15 dpf. **(B)** Number of macrophages at 5 and 15 dpf. The long horizontal lines denote the mean value. Statistical analysis was performed using ANOVA test. O-dianasidine staining for erythrocytes **(C)** at 5dpf and 10dpf.

Figure S4

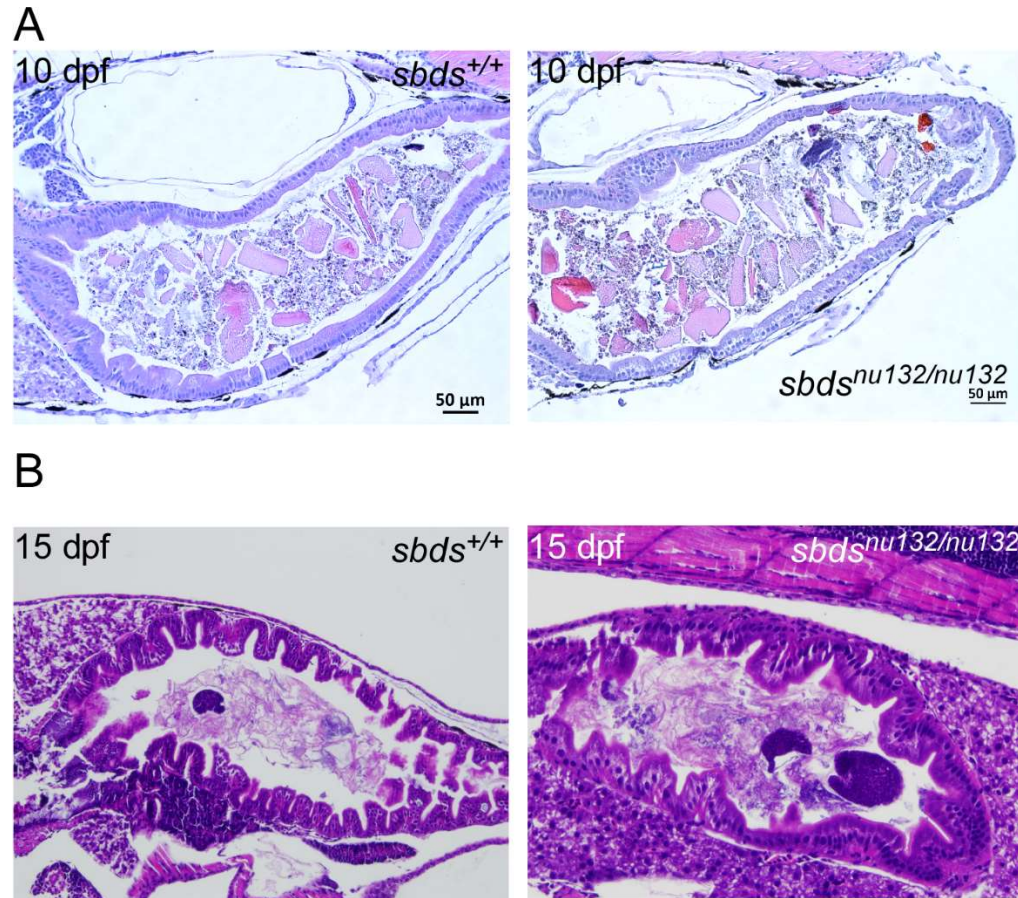


Figure S4. Comparable amounts of ingested food by *sbds* mutants and wild-type clutchmates. Histologic analysis of zebrafish intestine at **(A)** 10 dpf and **(B)** 15 dpf in mutants and siblings wildtype.

Figure S5

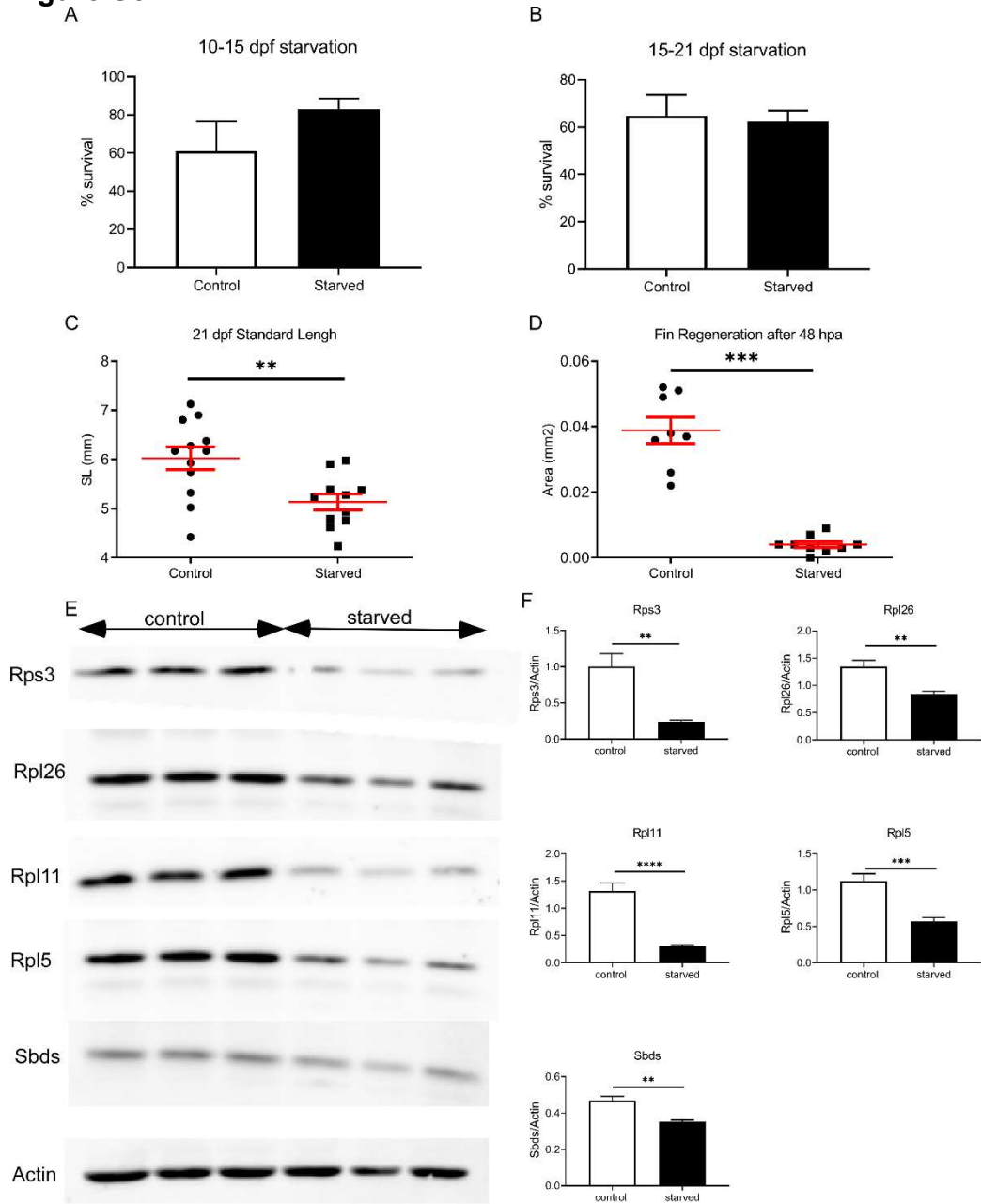


Figure S5. Phenotype of starved fish. Survival rates in wildtype fish after starvation from **(A)** 10 to 15 dpf and **(B)** 15 to 21 dpf. **(C)** Size distribution of starved fish and control group at 21 dpf. **(D)** Fin regeneration in wildtype starved fish is reduced compared to control group. **(E)** Western blot showing ribosomal proteins and Tp53 expression in 15 dpf larvae after 5 days of starvation. **(F)** Quantification of western blots. N=6

Figure S6

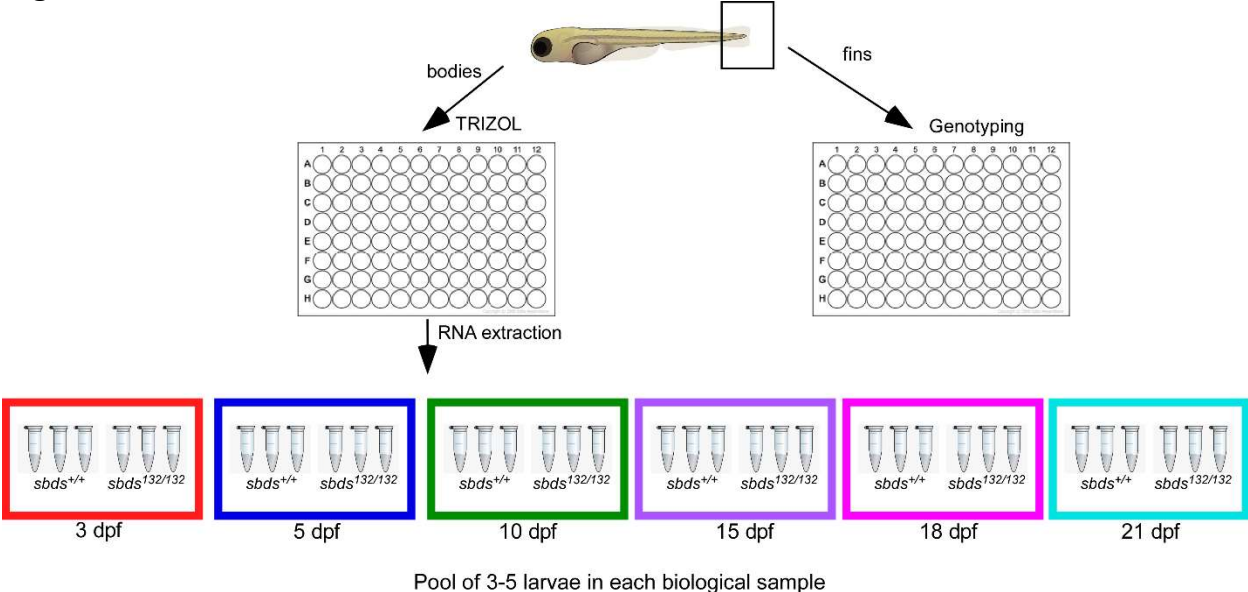


Figure S6. Schema showing the work flow for RNA extraction.