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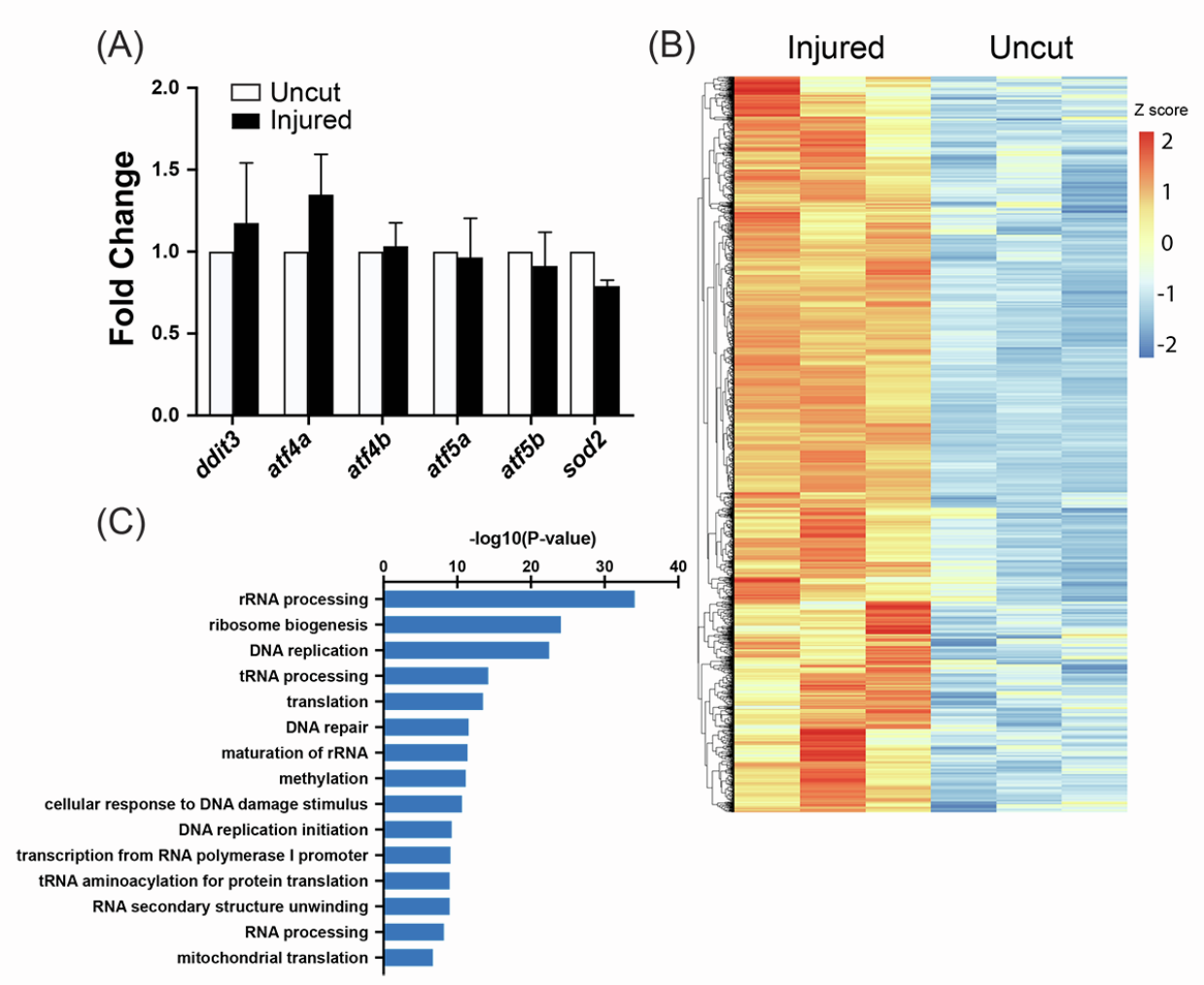
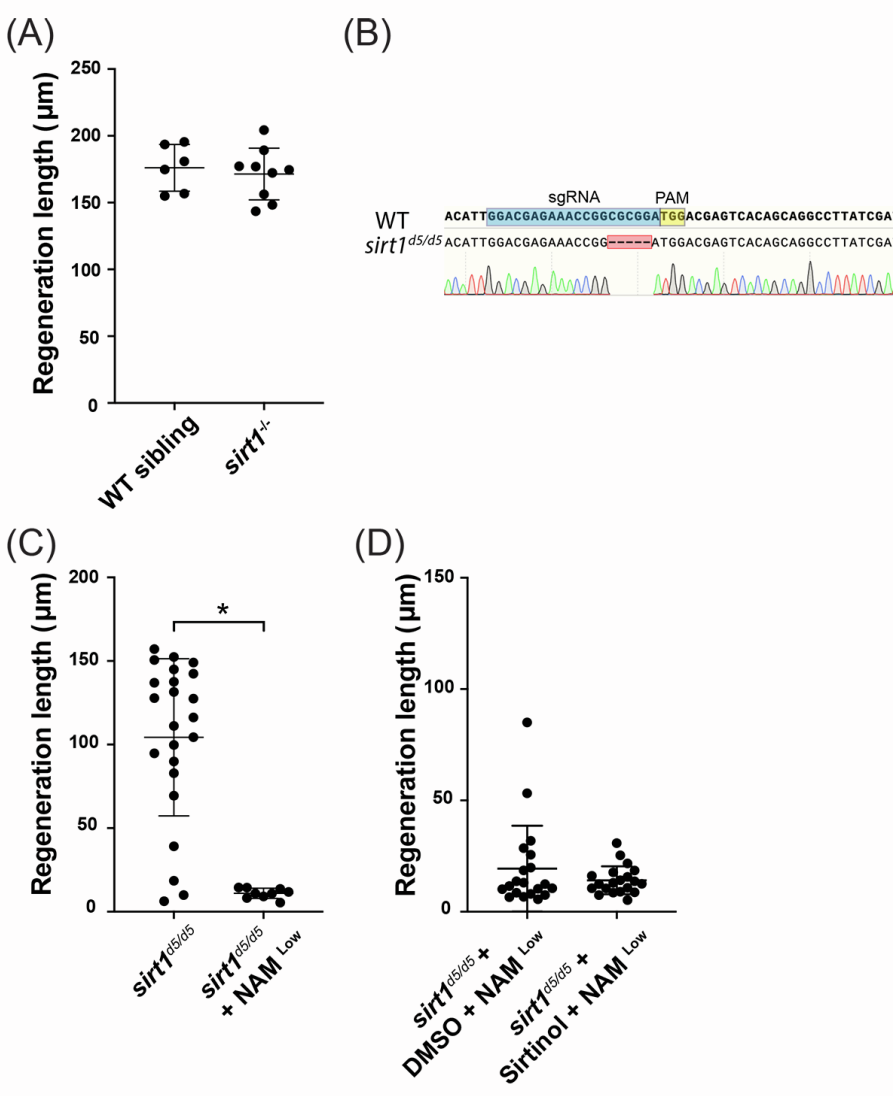
Supplemental information

Sirt1 promotes tissue regeneration in zebrafish through regulating the mitochondrial unfolded protein response

Yi-Fan Lin, Jessica Sam, and Todd Evans



Supplemental Figure 1. Transcriptional analysis of larval fin tissue during regeneration, Related to Figure 2. (A) qRT-PCR assays show that none of the known UPR^{mt} transcriptional regulators, nor *sod2* is up-regulated in regenerating larval fin tissue. (B) A heatmap shows significantly up-regulated genes (2908 genes) in regenerating larval fin tissue. (C) Top enriched processes identified from the up-regulated genes in regenerating larval fin tissue.



Supplemental Figure 2. An independent *sirt1* mutant allele also shows a consistent fin regeneration defect, Related to Figure 3. (A) The *sirt1* mutant larval fish exhibit normal regeneration growth compared to wild type siblings. (B) An independent second *sirt1* mutant allele (indicated here as d5) carries a 5 bp deletion in exon1 of the *sirt1* gene. The official name for this mutant allele is *sirt1*$^{wcm19/wcm19}$. (C) The *sirt1*$^{d5/d5}$ mutant larval fish exhibit a strong regeneration defect when incubated in the low concentration of NAM. (D) The *sirt1*$^{d5/d5}$ mutant larval fish exhibit a similar regeneration defect when treated with Sirtinol and NAM compared to NAM alone.

Table 1. List of Primers, Related to STAR Methods

cloning		
hspd1 promoter	f:	TGTTTGTGGATCCTGGACCC
	r:	TCAGAGAGTGAGAGAGAGAG
ornithine decarboxylase d2 fragment	f:	AGCCATGGCTTCCCGCCGGAG
	r:	CTACACATTGATCCTAGCAGA
hspd1 in situ	f:	TGTTGAGGACCAGAGTGCTG
	r:	TGAGACAGATGAGGCCTGTG
lonp1 in situ	f:	CCCATGTCGCTCAGGTAAAT
	r:	GATCATCAGAGCCGGGATTA
qRT-PCR		
hspd1	f:	ACTCCAGAGGAAATCGCTCA
	r:	CATGCCCTCAATGATCTCAA
hspa9	f:	GTGGCTGTGATGGATGGAAA
	r:	ATTCCTACAAGCCGCTCTCC
clpp	f:	CAGAGAGCAACAATAAGCCGA
	r:	CAGGTGGAGATGGGATTTAGGA
lonp1	f:	GCTGTTGAGGAGGAAAGTGC
	r:	CGCAGTTTATCTCCGAGGTC
ddit3	f:	TGGGACAAAATATCGCCAAC
	r:	AATACGACACGCTCCCACTC
atf4a	f:	GACAGAGCAGAGCACAGCAG
	r:	TCACACGACCCAATCAGAGA
atf4b	f:	CGCAAACAACTCAGTGCATC
	r:	TAATTTCGTGCTGTCGGGTA
atf5a	f:	TGGTGAACGCAAACAGAAGA
	r:	GCTGTTCCTCCAATGAGTCC
atf5b	f:	TCAGCACGATGGAGTTTCAG
	r:	ATCTATGCCGCCACAATTTC
sod2	f:	TTCATCACAGCAAGCACCAT
	r:	ATTTCAATGCAGGCTGAAGG

polrmt	f:	TGTTGTCGCATGTGTCTCAG
	r:	GCCTTCGGTAAATCGTAGCC
tf2bm	f:	GTGTTGACTCGTGCTTTGCT
	r:	CCCTCCAGTCTGCTCTCCA
***sirt1* mutagenesis**		
gRNA to target sirt1 (PAM site underlined)		GGACGAGAAACCGGCGCGGATGG
sirt1 genotyping	f:	TGACGTCACGCCACGGCATTACCG
	r:	CGGAGATCTCGGGCTCCGGGTCGGCTG