Supplementary Material

**Interplay between Nrf2 and B-crystallin in the lens and heart of zebrafish under proteostatic stress**

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**Supplementary Figure 1. Transcription changes of *nrf2* target genes in WT and nrf2fh318/f318.** The relative expressional changes of *gstp, prdx* and *nqo-1* between WT and nrf2fh318/f318 in lens **(A)**, heart **(B)**, and Brain **(C)** tissues were measured using qRT-PCR. Data are expressed as mean ± SD. *n*=3 for lens, heart, and brain tissues. Statistical significance was calculated using two-tailed t-test.

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**Supplementary Figure 2. Relative *cryaba, cryabb* and *nrf2* transcripts in different tissues.** The relative level of *cryaba*, *cryabb* (**A**) and *nrf2* (**B**) mRNA were compared using qRT-PCR analysis in different tissues. Statistical significance was calculated using ANOVA.

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**Supplementary Figure 3. Tissue-specific upregulation of *cryabb* in response to Nrf2 deficiency.** Relative mRNA expression of *cryabb* **(A)** in whole embryos at 4 dpf, **(B)** eyes, **(C)** heart, and **(D)** brain tissues of WT, *nrf2*fh318/fh318, *cryaba*-/-, and *cryaba*-/-;*nrf2*fh318/fh318. Data are expressed as mean ± SD. Statistical significance was calculated using one-way ANOVA.

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**Supplementary Figure 4. Upregulation of *cryabb* transcript in response to tBHP treatment. (A)** Relative mRNA expression of *cryaba* and *cryabb* at 4 dpf were measured by qRT-PCR after treatment of 800 uM tBHP for two hours. Statistical significance was calculated using two-tailed t-test.

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**Supplementary Figure 5. Changes in the transcription of Nrf2 target genes in *cryab* mutants.** Relative levels of *nrf2, gpx1a, gstp1, prdx1, hmox1a, nqo1*, *gadd45bb*, and *gclc* in *cryaba-/-, cryabb-/-*, and *cryaba-/-;cryabb-/-* mutated embryos at 4 dpf were measured by qRT-PCR. Data are expressed as mean ± SD from 3 independent measurements. *P*-values were calculated using one-way ANOVA.

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**Supplementary Figure 6. Percentage of lens defect in *cryaba* and *cryabb* KO embryos. (A)** Lens of embryos from *cryaba*+/- incross were screened at 4 dpf for lens abnormalities, and the genotype of *cryaba* was determined. **(B)** The percentage of lens defect at 4 dpf was compared among WT, *cryaba*-/-, and *cryabb*-/-. Statistical significance was calculated using one-way ANOVA.

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**Supplementary Figure 7. Gene Ontology analysis of lens transcriptomics.** Lens RNA-seq data were compared between WT vs *cryaba*-/- (A) and *cryaba*-/- vs *cryaba*-/-;*nrf2*fh318/ fh318 (B) through ingenuity pathway analysis ([www.ingenuity.com](http://www.ingenuity.com/)).

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**Supplementary Figure 8. The level of *cryaba*, *cryabb*, and *nrf2* mRNA in lens and heart tissues**. Normalized count values of *cryaba*, *cryabb*, and *nrf2* from lens RNA seq **(A-C)** and heart RNA-seq **(E-F)** are plotted as bar graphs. \* Indicate False Discovery Rate (FDR) < 0.05.

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**Supplementary Figure 9.** Heatmaps for the heart extracellular region GO cluster from *cryaba*-/- versus *cryaba*-/-;*nrf2*fh318/ fh318 **(A)** and WT versus *cryaba*-/-;*nrf2*fh318/ fh318 **(B)**. **(C)** Venn-diagram analysis between the two GO clusters identifies significantly changed genes associated with ECM region in *cryaba*-/-;*nrf2*fh318/ fh318 compared with WT and *cryaba*-/-

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**Supplementary Figure 10. Expression of genes in the tight junction GO cluster.** Normalized count values of each gene associated with tight junction are illustrated as bar charts from heart RNA seq data. \* Indicate False Discovery Rate (FDR) < 0.05.

**Supplementary Table 1. Oligomer sequences for nrf2 pathway**

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**Supplementary Table 2. Oligomer sequences for cholesterol biosynthesis pathway**

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**Supplementary Table 3. Normalized counts (cpm) of genes in extracellular region part GO cluster from heart RNA-seq. Comparison between *cryaba*-/- *versus* *cryaba*-/-;*nrf2*fh318/ fh318**

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**Supplementary Table 4. Normalized counts (cpm) of genes in the extracellular region GO cluster from heart RNA-seq. Comparison between WT *versus* *cryaba*-/-;*nrf2*fh318/ fh318**

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