**Supplemental Tables**

**Table S1. Regression analysis statistics for data in Figure 3A.**

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| --- |
| ***tslΔ* vs *tslΔ*/+** |
|  | **Sum of squares** | **F value** | **Pr(>F)** |
| **log10(Weight)** | 0.638 | 9.695 | 0.004 \*\* |
| **Genotype** | 1.261 | 19.152 | <0.001 \*\*\* |
| **log10(Weight)\*Genotype** | 0.019 | 0.291 | 0.594 NS |

Data was fit with the linear model log10(total hemocyte number) = log10(weight) + genotype + log10(weight)\*genotype (F3, 29 = 25.55, Adjusted R2 = 0.70) using RStudio.

**Table S2. Regression analysis statistics for data in Figure 3C.**

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| ***tslcaki/+* vs *tslΔ/+* vs *tslΔ/tslcaki*** |
|  | **Sum of squares** | **F value** | **Pr(>F)** |
| **log10(Weight)** | 0.246 | 4.841 | 0.034 \* |
| **Genotype** | 0.568 | 5.584 | 0.007 \*\* |
| **log10(Weight)\*Genotype** | 0.021 | 0.203 | 0.817 NS |
| **Genotype Tukey post-hoc** |
|  |  | **T ratio** | **P value** |
| ***tslcaki/+* vs *tslΔ/+*** |  | 1.994 | 0.128 NS |
| ***tslcaki/+* vs *tslΔ/tslcaki*** |  | 2.994 | 0.069 NS |
| ***tslΔ/+* vs *tslΔ/tslcaki*** |  | 0.914 | 0.635 NS |

Data was fit with the linear model log10(total hemocyte number) = log10(weight) + genotype + log10(weight)\*genotype (F5, 38 = 14.67, Adjusted R2 = 0.61) using RStudio. This was followed with a Tukey posthoc test to determine which genotype(s) had significantly different effects on total hemocyte number compared to the others.

**Table S3. Regression analysis statistics for data in Figure 4C.**

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| --- |
| ***chico1/+* vs *+/chicodf* vs *chico1/chicodf*** |
|  | **Sum of squares** | **F value** | **Pr(>F)** |
| **log10(Weight)** | 0.806 | 22.041 | <0.001\*\*\* |
| **Genotype** | 0.086 | 1.173 | 0.322 NS |
| **log10(Weight)\*Genotype** | 0.152 | 2.076 | 0.141 NS |

Data was fit with the linear model log10(total hemocyte number) = log10(weight) + genotype + log10(weight)\*genotype (F5, 34 = 31.38, Adjusted R2 = 0.80) using RStudio.

**Table S4. Regression analysis statistics for data in Figure 4F.**

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| --- |
| **100% diet vs 25% diet** |
|  | **Sum of squares** | **F value** | **Pr(>F)** |
| **log10(Weight)** | 2.362 | 40.944 | <0.001\*\*\* |
| **Diet** | 0.011 | 0.194 | 0.663 NS |
| **log10(Weight)\*Diet** | 0.011 | 0.192 | 0.665 NS |

Data was fit with the linear model log10(total hemocyte number) = log10(weight) + diet + log10(weight)\*diet (F3, 29 = 24.31, Adjusted R2 = 0.69) using RStudio.