

Fig. S1. Both *Drosophila* wild type (dWT) and *sugarkill* (dM80T) enzymes follow traditional Michaelis-Menten kinetics. Michaelis-Menten nonlinear regression fits are shown, and all enzyme concentrations are indicated.



Fig. S2. Genomic engineering of the *TPI* locus. A) The target gene is replaced by the *attP* phiC31 integration site and a white minigene flanked by two *loxP* sites. B) The white minigene is removed by a CRE recombinase, leaving only the *attP* phiC31 integration site and a *loxP* site. C) *TPI* is cloned into the *pGE-attB* vector and modified, as desired. The construct is then injected into founder line embryos expressing the phiC31 integrase, which initiates specific and directional integration of the contruct into the *TPI* locus. D) The *white* minigene and plasmid construct are removed through the expression of CRE recombinase, leaving only an *attR* and a *loxP* site. E) Molecular analysis reveals the addition of an *attR* site 5' of the reconstituted *TPI* gene.



Fig. S3. Genomically engineered TPI^{sgk} displays abberant behavior and reduced longevity. A) Genomically engineered TPI^{*gk} (*GE-WT*) displays normal behavior, while the genomically engineered TPI^{*gk} (*GE-sgk*) displays marked mechanical stress sensitivity. B) *GE-sgk* exhibits reduced longevity compared to *GE-WT*. n > 20 for all lifespans and behavior. A Student's t test was used to assess behavioral differences between genotypes, and a Log-rank (Mantel-Cox) Test was used to assess lifespans. *** indicates p < 0.0001 compared to GE-WT. Error bars indicate ± s.e.m. Both genomically engineered alleles were assessed over $TPI^{/S10}$.



Fig. S4. The addition of the C-terminal CFP to TPI^{K11M} does not affect its capacity to genetically complement TPI^{sgk} A) mechanical stress sensitivity or B) thermal stress sensitivity. Mechanical stress sensitivity was assessed on Day 1 and thermal stress sensitivity was assessed on Day 5. n > 15. † indicates animals did not paralyze. A One-way ANOVA was performed to assess variance and data sets were compared using Tukey's post-hoc analysis. *** indicates that p < 0.001 and *ns* indicates no significant difference, both compared to WT. Error bars indicate ± s.e.m.

Table S1. The catalytically inactive allele complements TPI^{sgk} median lifespans. n > 150 animals per genotype for all lifespans.

| | +/+ | sgk/+ | sgk/sgk | sgk/JS10 | sgk/K11M |
|---------------------------|------|-------|---------|----------|----------|
| Median Lifespan (days) | 65.5 | 67 | 29 | 6 | 73 |