Supplemental Figure S3. **Validation of the RNA-seq data**

(A) **Top panel:** Hierarchical clustering based on the Euclidian distance between the rlog-transformed read counts in the slow mutants and wild-type strain. **Bottom panel:** principal component (PC) analysis of the rlog-transformed read counts in the slow mutants and wild-type strain.

(B) Correlation between the log2 fold change (FC) of expression of the slow mutant as measured by RNA-seq and RT-qPCR. Identity (y=x) is indicated as a dashed red line. Detailed RT-qPCR measurement of relative expression are shown in Fig. S3C below.

(C) Gene expression changes in the slow mutant relative to the wild-type using nda2 as internal control for five down-regulated and five up-regulated genes (left and right panels, respectively). Error bars represent the standard deviation of the mean from three independent experiments.