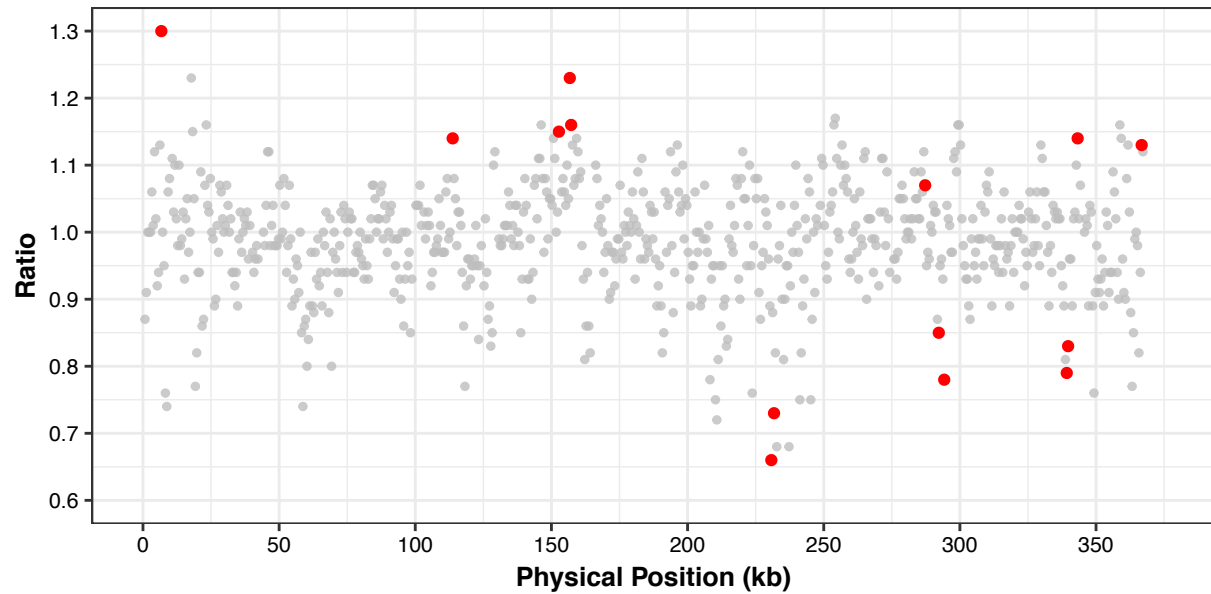**Figure S1**. Sequencing coverage variation across mitogenome of *Arabidopsis thaliana* mutation accumulation lines as measured by the residuals from a model accounting for sequencing bias due to nucleotide composition. Each panel represents an average of three biological replicates. Red vertical lines at the bottom of the figure represent the two pairs of large, identical repeats in the *A. thaliana* mitogenome.
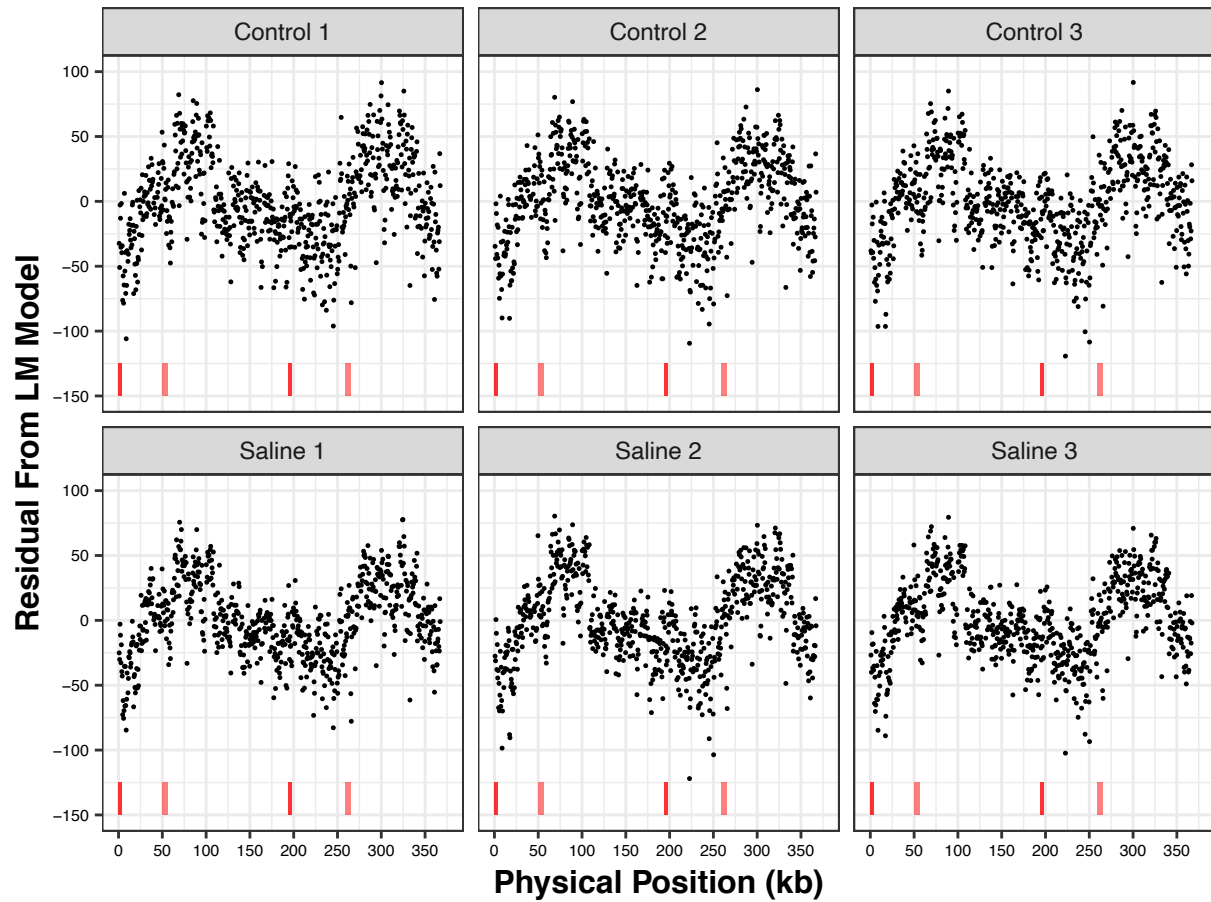
Figure S2. Divergence in region-specific mitogenome copy number in salt-stressed vs. control mutation accumulation lines. Values are expressed as a ratio of average values for all salt-stressed vs. all control lines. These are the same data depicted in Figure 2 except that value were calculated as the genome-wide mean CPMM plus the residual from a linear model that accounts for sequencing bias due to nucleotide composition. Windows that deviate significantly from a ratio of 1 after false-discovery-rate correction are highlighted in red. CPMM: counts per million mapped reads.

Figure S3. Sequencing coverage variation across the mitogenome for three purified mtDNA samples from *Arabidopsis thaliana* as measured by the residuals from a model accounting for sequencing bias due to nucleotide composition. Red vertical lines at the bottom of the figure represent the two pairs of large, identical repeats in the *A. thaliana* mitogenome.
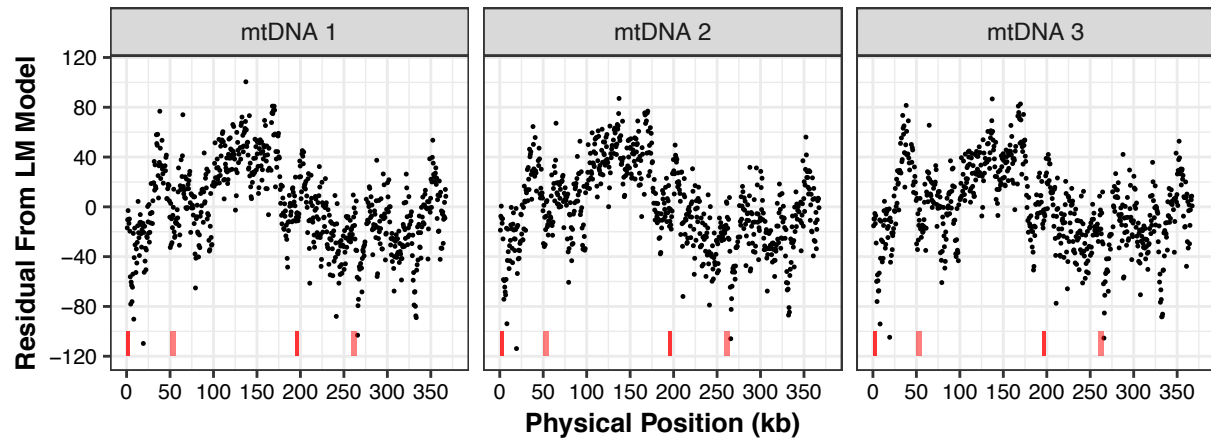
Figure S4. Correlation between mitogenome coverage from published Col-0 mutation accumulation lines (JIANG *et al.* 2014) and purified mtDNA from our Col-0 lab line. Each point represents a 500-bp window. Coverage is expressed as either (A) raw copies per million mapped reads (CPMM) or (B) residuals from a model that accounts for sequencing bias due to nucleotide composition.