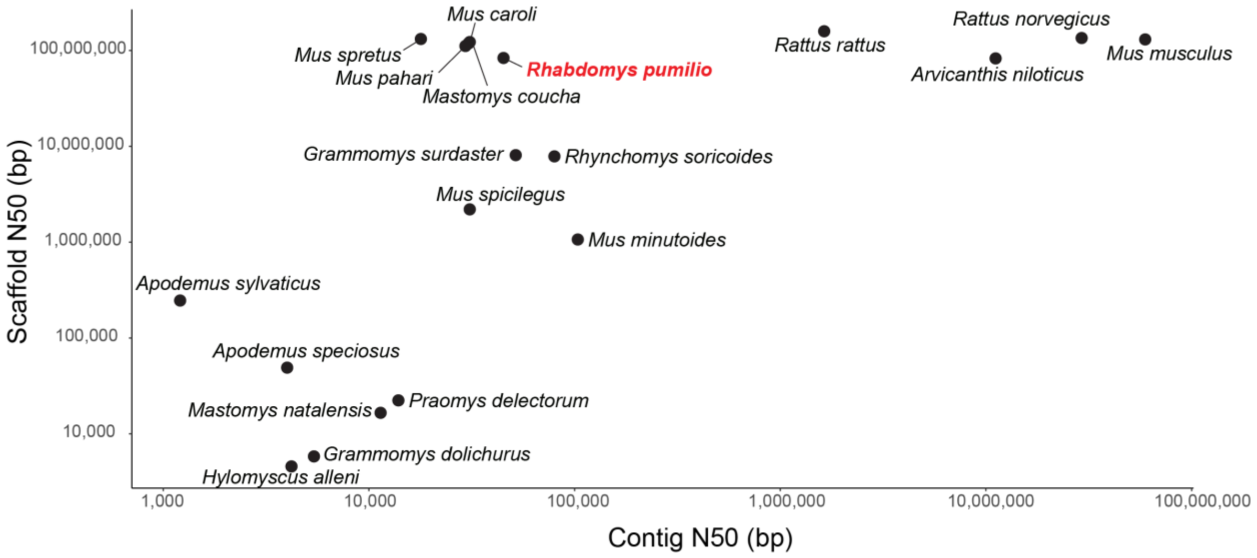

Figure S1. Comparison of assembly contiguity among sequenced murine genomes. Related to Figure 1.

Scaffold N50 in basepairs (bp) is plotted against contig N50 to indicate genome assembly contiguity. The African striped mouse genome has a high scaffold N50, comparable to that of other chromosome-scale murine genomes such as laboratory mice and rats. While contig N50 is somewhat less, the low gap percentage (~1%) indicates that only small breaks in contiguity are present within chromosome-scale scaffolds.

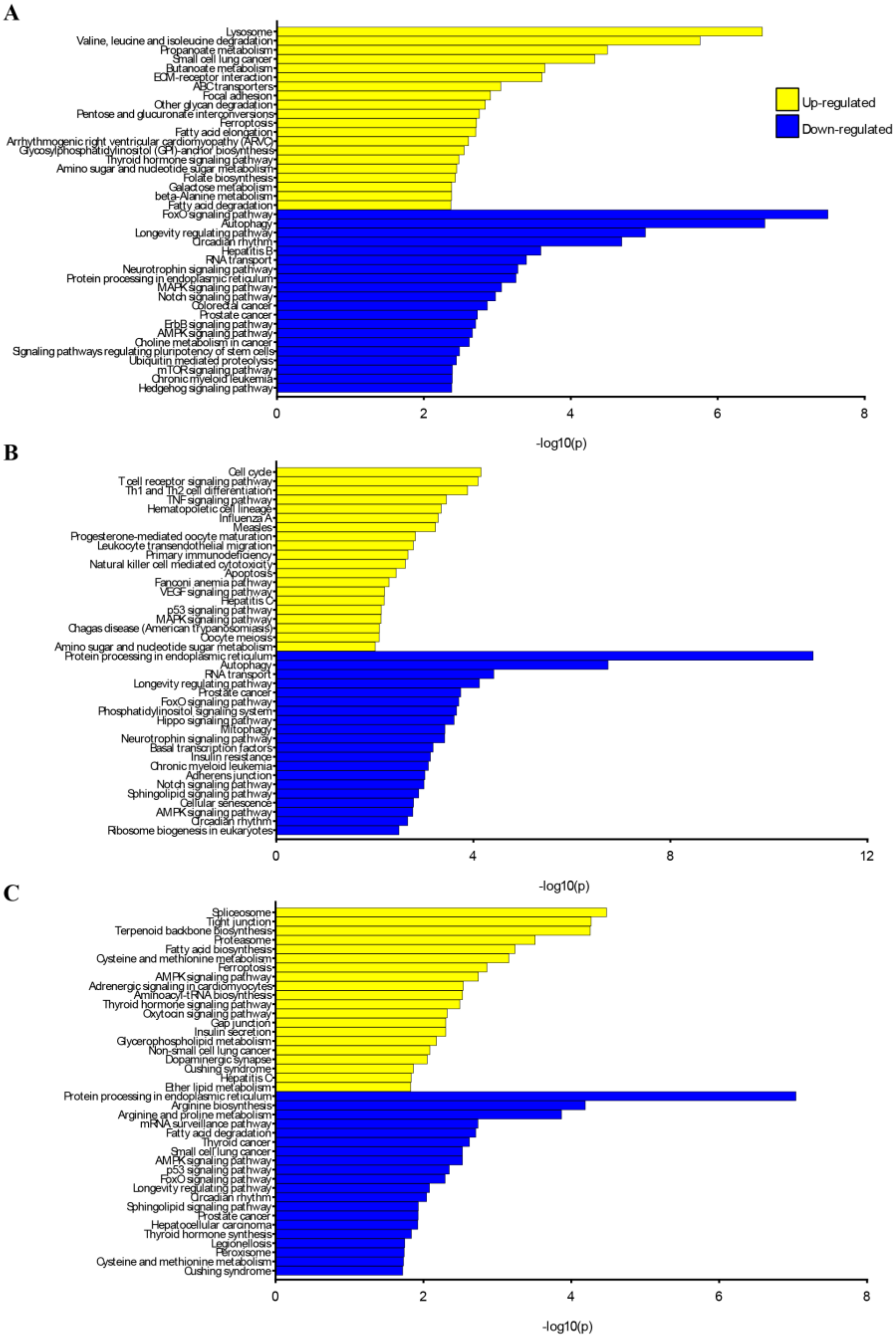

Figure S2. Enriched KEGG pathways of genes in peripheral tissues in the night versus the day. Related to Figure 2.

A-C, Overrepresentation analysis of up and down regulated DE genes (FDR < 0.05; log2FC < 0 or > 0) in night versus day for retina (**A**), liver (**B**) and (**C**) lung samples using KEGG. The top 20 most significant up and down regulated pathways are shown for each tissue. The x-axis represents the enrichment value as the logarithm of the p-value. All represented pathways are significantly enriched, with a p-value < 0.05.

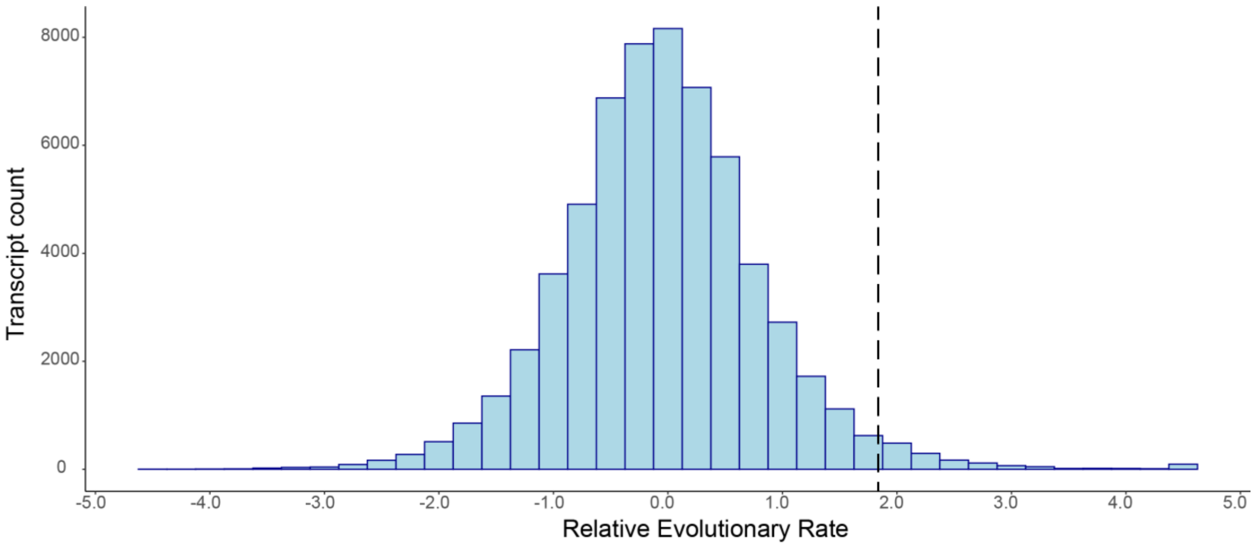

Figure S3. Distribution of relative evolutionary rates in the African striped mouse exome. Related to Figure 3.

Relative evolutionary rates, taken as the residual length of branches in scaled gene trees relative to the average tree for the exome, are shown as a histogram. Striped mouse accelerated loci were defined as the 95th percentile of loci with positive relative evolutionary rates.

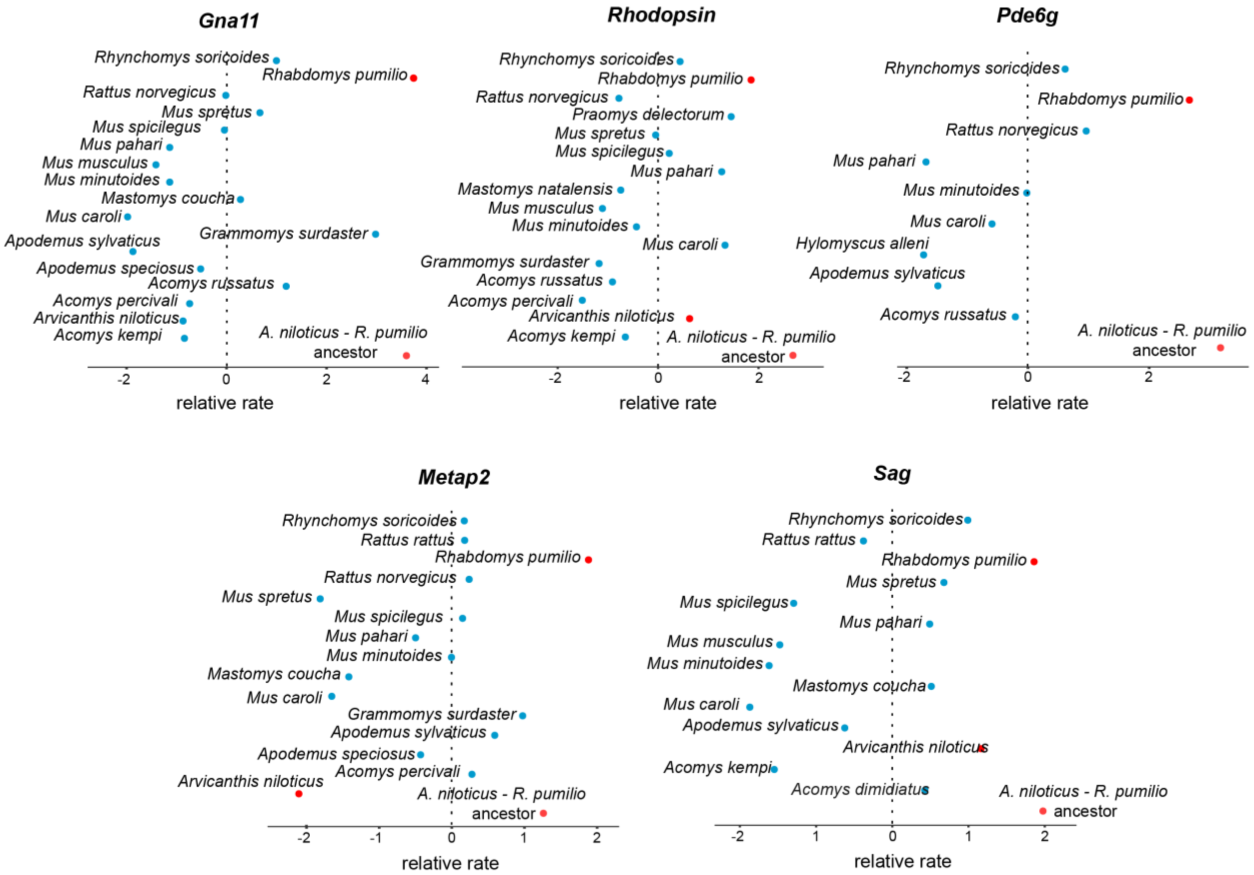

Figure S4. Relative evolutionary rates of additional phototransduction genes. Related to Figure 3.

Relative evolutionary rates of striped mouse accelerated loci (red) involved in rhodopsin-mediated phototransduction are compared to their orthologs in other murids (blue).