**Data Sharing Plan.** All raw data sequence data will be deposited to the NCBI Short Read Archive upon, or prior to, publication. All phenotypic / experimental data will be deposited onto Data Dryad upon, or prior to, publication. Scripts to analyze the data will be deposited onto GitHub (preferably) and/or DataDryad. Data will be retained on UVA’s High-Performance Computer.

**Sharing model organisms.** All stock lines generated from this proposed work will be available to the broader community. We often send inbred fly lines, as well as clonal Daphnia lines, to other researchers and will continue to do so.

**Genomic Data Sharing.** As mentioned above, all raw sequencing data will be deposited onto SRA. We will deposit final VCF files for specific publications on DataDryad. We also host data-sharing for population genomic data on a http pass-through site hosted by UVA (<http://berglandlab.uvadcos.io>). This site is used to share large files with collaborators.