



Figure S1. Analysis of *C. reinhardtii* mRNA-seq data. (A) Principal components analysis of gene expression for the triplicate mRNA-seq experiments done with the PL and EL populations of *C. reinhardtii*. These results demonstrate that the transcriptome data derived from both sets of triplicate cultures provided a consistent signal of gene expression. (B) Expression differences using mRNA-seq data from the PL-EL comparison. The Log₂ fold changes for points shown in red are significantly different (p -value < 0.05 with FDR correction) from the mean of normalized counts in that experiment.