**TL;DR Reads were quantified and analyzed using FastQC [v0.11.7], FastP [v0.21.0], Salmon [v1.2.1]**

Sequencing was performed at the Joint Genomics Institute (JGI). All sequencing was performed using Illumina NovaSeq 6000, paired-end reads of 151bp each [Modi et al. 2021]. Raw reads were downloaded from the JGI online genome database (gold.jgi.doe.gov/projects; GOLD Project ID Gp0332996-Gp0332982) and are also available on the SRA database (PRJNA807682). The *Physcomitrella patens* genome version 3.3 CDS file 2018 [Ppatens\_318\_V3.3.cds.fa.gz; NCBI Taxonomy ID: 3218] (*P. patens* transcriptome), Filtered Mortierella GBAus27b CDS file [MorGBAus27b\_1\_GeneCatalog\_CDS\_20170422.fa.gz, NCBI Taxonomy ID: 1954212] (*B. eriona* transcriptome), and filtered Mortierella NVP64 CDS file [MoeNVP64\_1\_GeneCatalog­\_CDS\_20190403.fa.gz; NCBI Taxonomy ID: 2684331] (*L. elongata* transcriptome) were used as reference transcriptomes [Lang et al 2018]. Prior to mapping, meta-transcriptomes were created for their respective environmental conditions by concatenating all genes from the *P. patens* transcriptome with either the *B. eriona* transcriptome or *L. elongata* transcriptome. Supplemental bash script (Supplemental code 2a, 2b) was submitted to the Michigan State University High Performance Computing Center (MSU HPCC). The script indexed transcriptome and meta-transcriptomes (*P. patens*; *P. patens* x *B. eriona*; *P. patens* x *L. elongata*) for read quantification with Salmon [v1.2.1].Raw reads were split into separate forward and reverse read files, raw QC reports were generated with FastQC [v0.11.7], low-quality reads and adapters were removed using FastP [v0.21.0], trimmed QC reports were then again generated with FastQC, and filtered reads were mapped to their respective index again using Salmon. All quantified reads were merged using the Salmon -quantmerge function and were reduced to only included the *P. patens* gene list, which contained five experimental conditions in triplicate (*P. patens*: CUTON, CUTOO, CUTOP; *P. patens* x *B. eriona*+: CUTOZ, CUTPA, CUTPB; *P. patens* x *B. eriona*-: CUTPC, CUTPG, CUTPH; *P. patens* x *L. elongata*+: CUTOS, CUTOT, CUTOU; *P. patens* x *L. elongata*-: CUTOW, TUCOX, CWYAU)) (Supplemental Data physco\_quants).

**RAW READS:**

*Physcomitrium patens*: <https://www.ncbi.nlm.nih.gov/sra/?term=PRJNA807682>

*Chlamydomonas reinhardtii*:

*Arabidopsis thaliana*: <https://www.ncbi.nlm.nih.gov/sra?linkname=bioproject_sra_all&from_uid=704083>