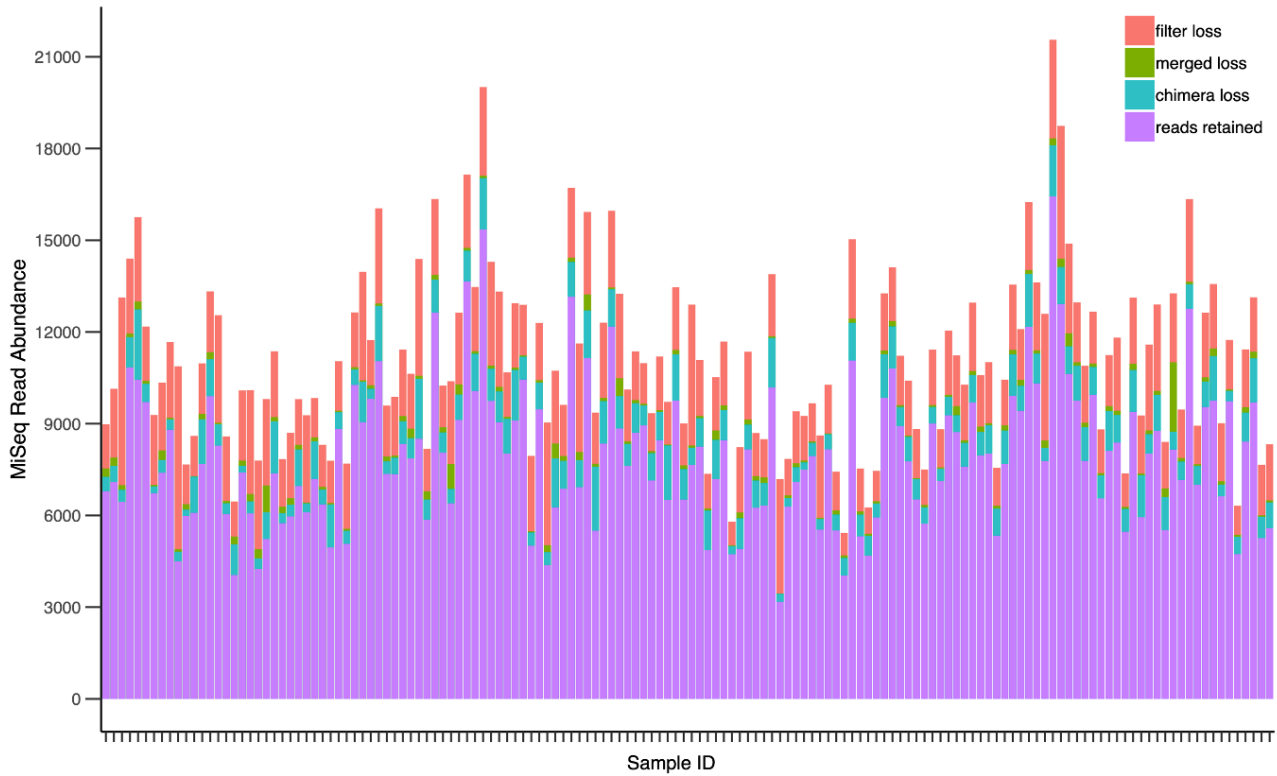
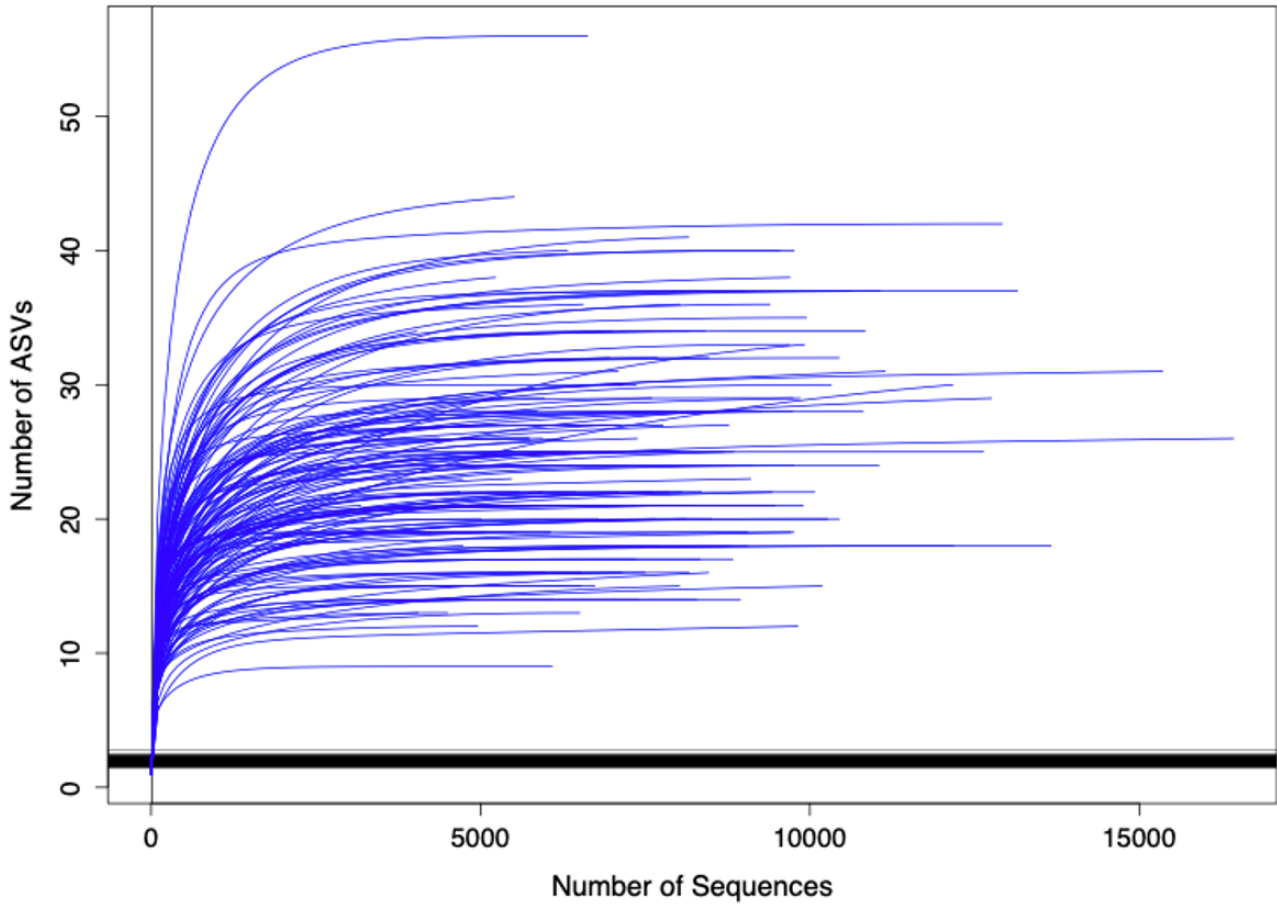


## SUPPLEMENTARY DATA

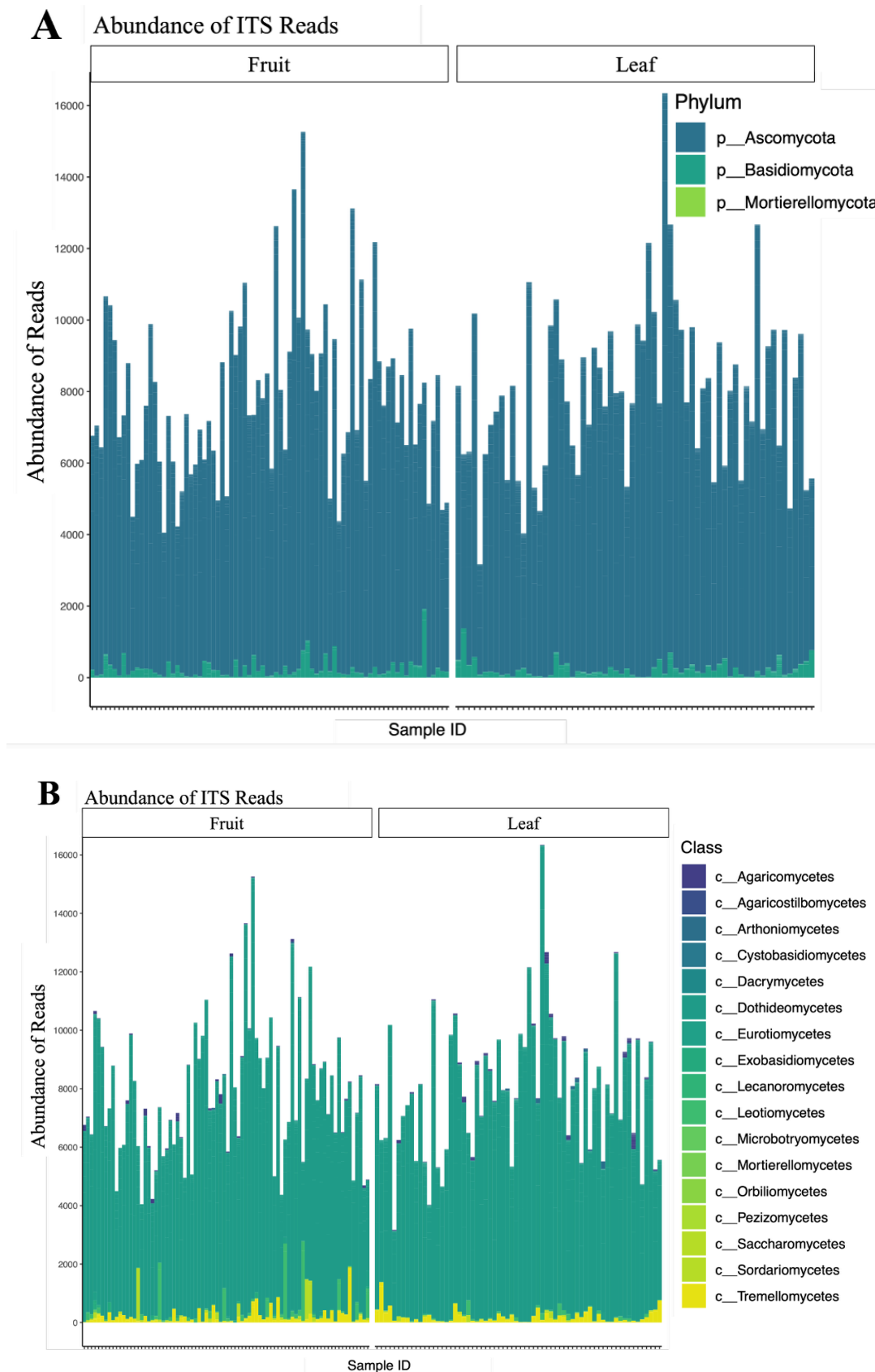
### DADA2 Workflow



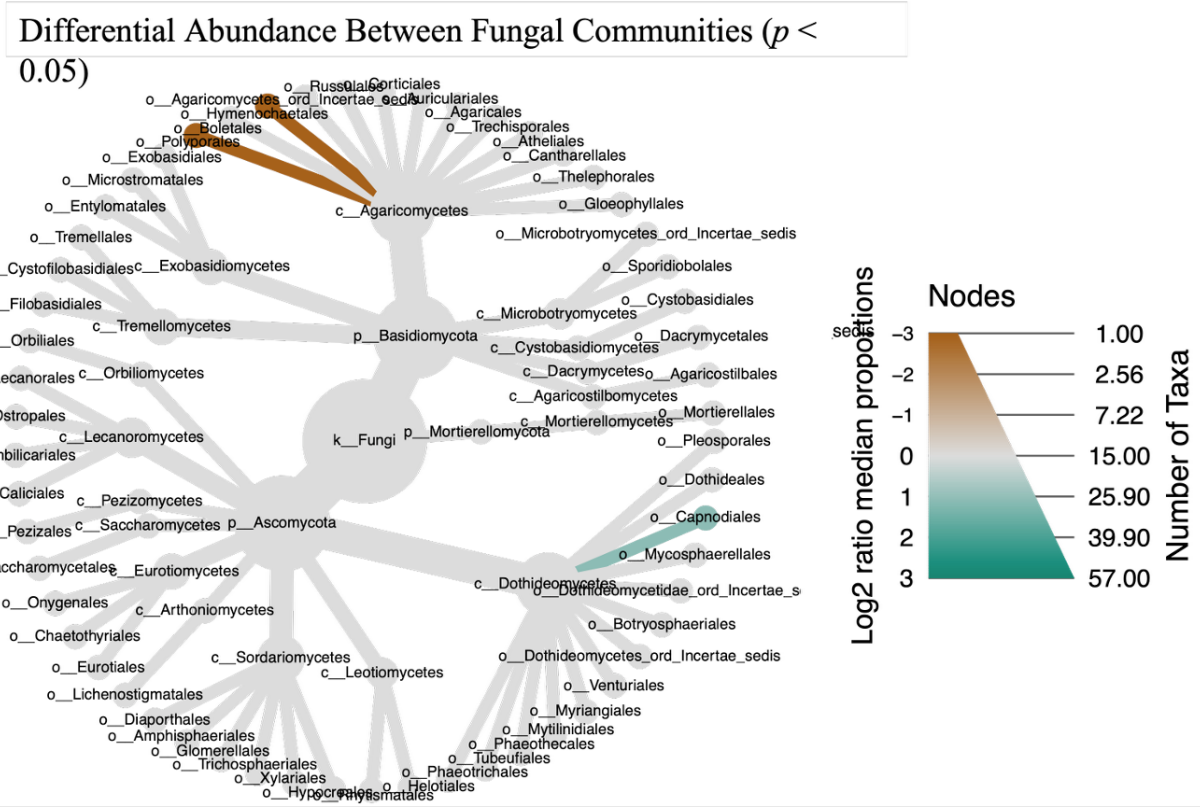
**Figure S1.** The DADA2 workflow processed 1,616,465 raw ITS reads from *Vitis* sp. grown during the 2020 season in Wolfville, Nova Scotia, produced from one lane of sequencing via Illumina’s MiSeq at Génome Québec, and retained 1,160,088 reads which were used to infer amplicon sequence variants (ASVs).



**Figure S2.** Rarefaction curves illustrated that the majority of the fungal communities were identified from our Illumina MiSeq sequencing depth in the samples harvested from the leaves and fruits of *Vitis* sp. grown during the 2020 season in Wolfville, Nova Scotia.



**Figure S3.** Fungal community composition, represented here as phyla (A) and class (B) from the leaves and fruits of *Vitis* sp. cv. L'Acadie blanc sampled across the 2020 season in Wolfville, Nova Scotia. High-quality MiSeq reads from the ITS amplicons were retained through the DADA2 pipeline, inferred as amplicon sequence variants (ASVs), and assigned taxonomy using the UNITE database. The total dataset shows that the fungal leaf and fruit communities were dominated by Ascomycetes (A), of the class *Dothideomycetes* (B).



**Figure S4.** The fungal communities of the *Vitis* sp. leaves (green) were enriched in taxa from the *Capnodiales* order, while the fruit (brown) communities were enriched in *Polysporales* and *Agaricomycetes*. Samples were grown and harvested during the 2020 season in Wolfville, Nova Scotia.