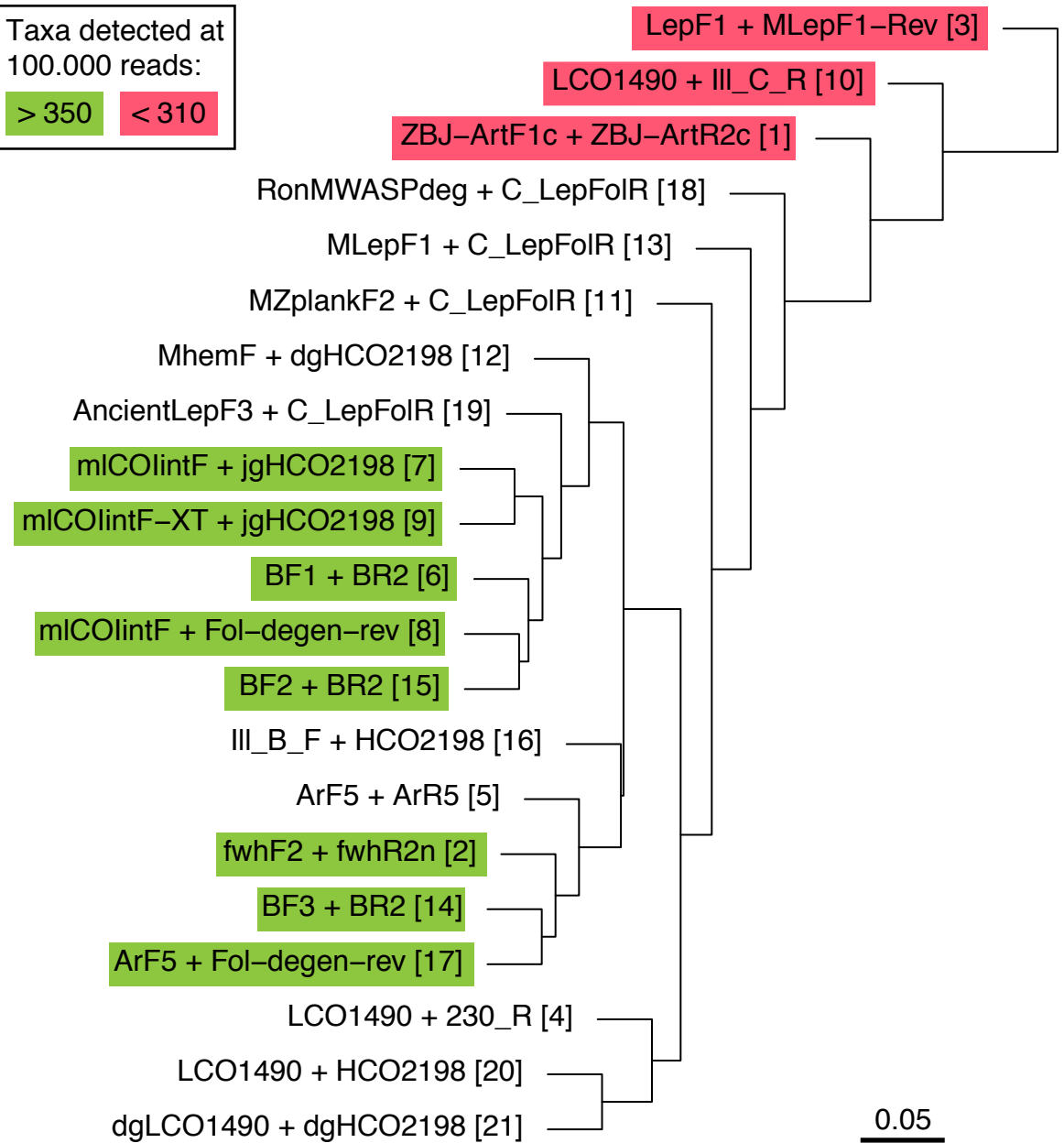


A Jaccard similarity (p/a based)

Taxa detected at 100.000 reads:
> 350 < 310



B Bray-Curtis dissimilarity (abundance is considered)

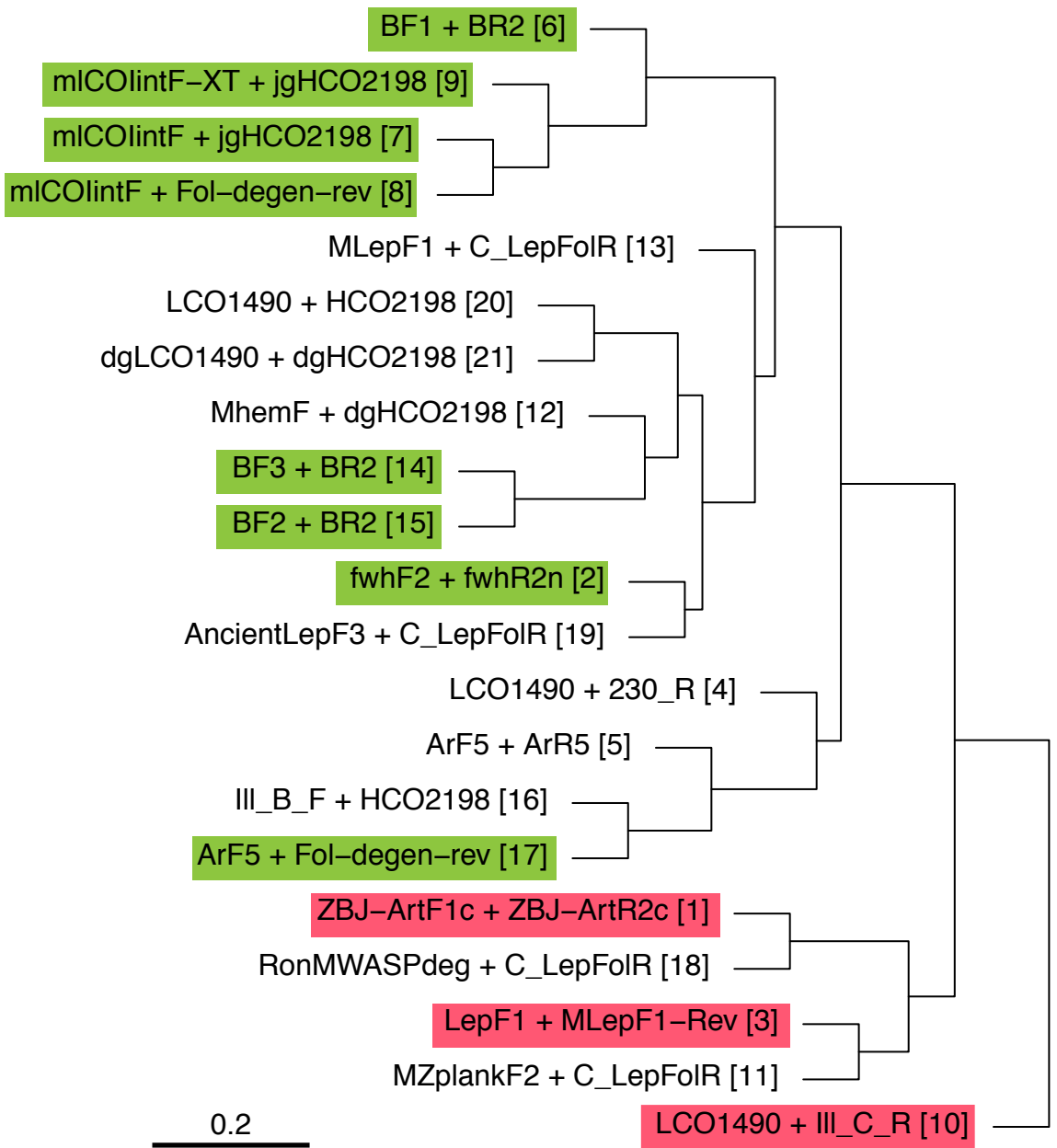


Figure S14: Cluster Dendrogram (UPGMA) for Jaccard similarity (A) and Bray-Curtis dissimilarity (B) for the mock sample metabarcoding data using 21 primer sets, generated with the R package *vegan* v2.5-2. If the number of taxa detected is above 350 or below 310 taxa, the primer set is highlighted in Green or Red respectively. Sequencing depth was normalised to 100.000 reads for each primer sets (reads below 0.001% abundance discarded).