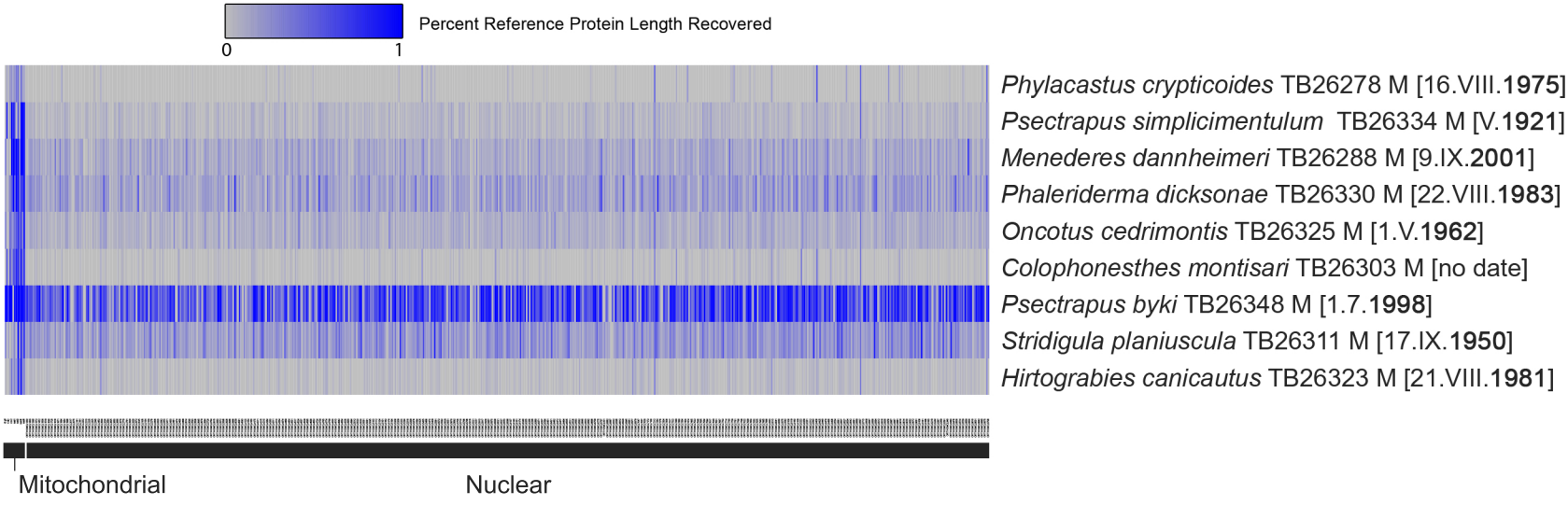

Heat map showing raw recovery efficiency obtained with HybPiper v. 2.0 pipeline for processed museum specimens representing Eurynotina. 620 nuclear genes were targeted, plus 12 mitochondrial loci were sequenced as bycatch. Each column corresponds to a gene and each row is a sample. The shading of each box represents the proportion of the target gene length recovered; darker colors indicate a higher percentage of the gene was recovered.