

# Origins and implications of mitochondrial genes expansion in bivalves

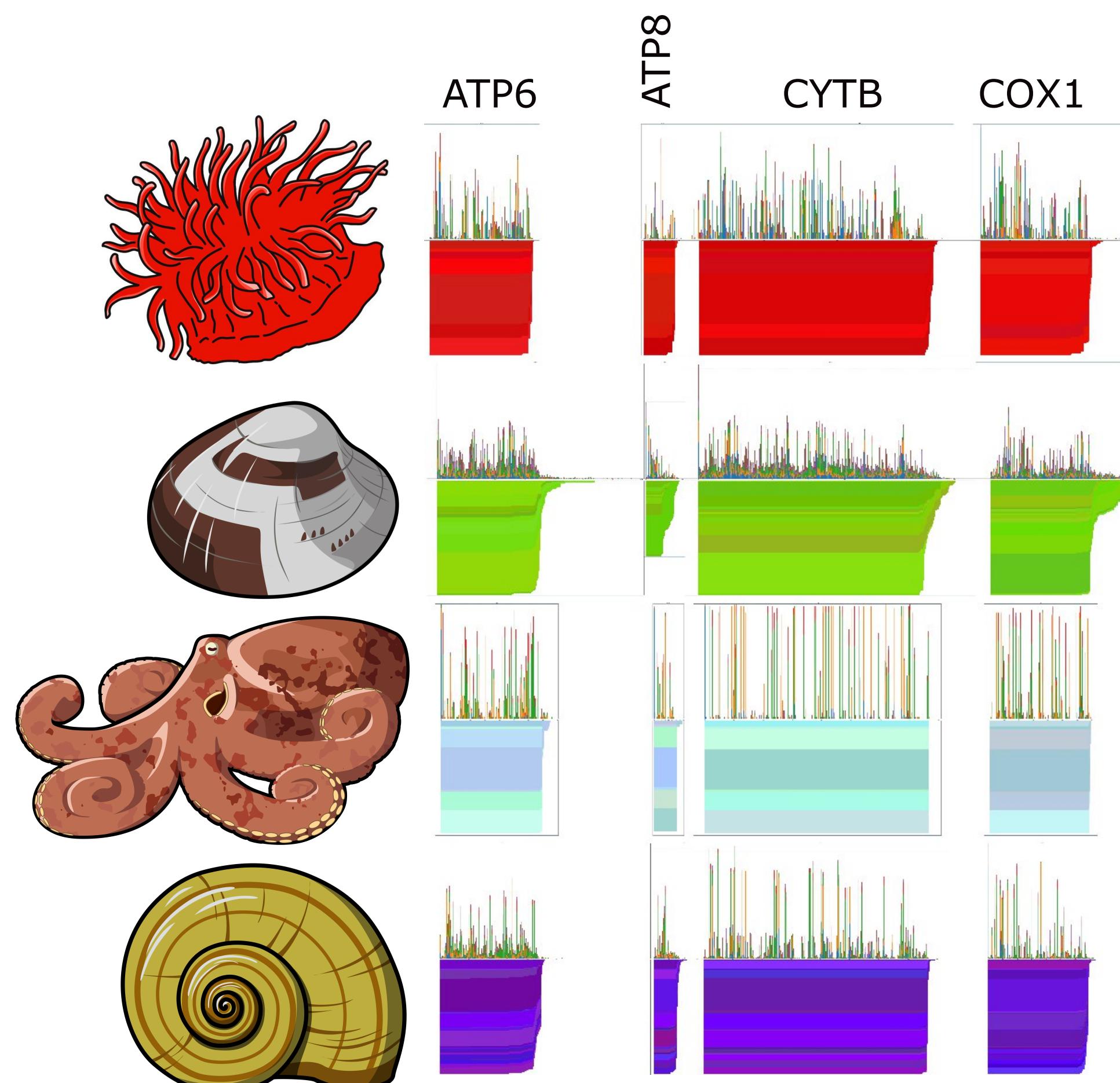


Diego Carli, Federico Pazzini, Enrico Negrisolo, Marco Passamonti

University of Bologna, Department of Biological, Geological and Environmental Sciences, Bologna

## Introduction

Mitochondrial genomes are typically considered stable elements in metazoans, exhibiting consistent size and gene content across species. However, bivalves present notable exception to this rule, as scattered reports in the literature suggest considerable variability. This study aims to investigate the extent of mitochondrial genome variability in bivalves compared to other animal classes. Specifically, we seek to determine whether this observed discrepancy is due to challenges in gene annotation or if it stems from inherent biological differences.



**Figure 2: Start codons frequency along mitochondrial genes.**

For each classes: Upper part of plots are the analyses on the start codon presence along genes, considering only in frame partitions. Lower part are gene's length. Shadows of the same color represent different order in the respective class.

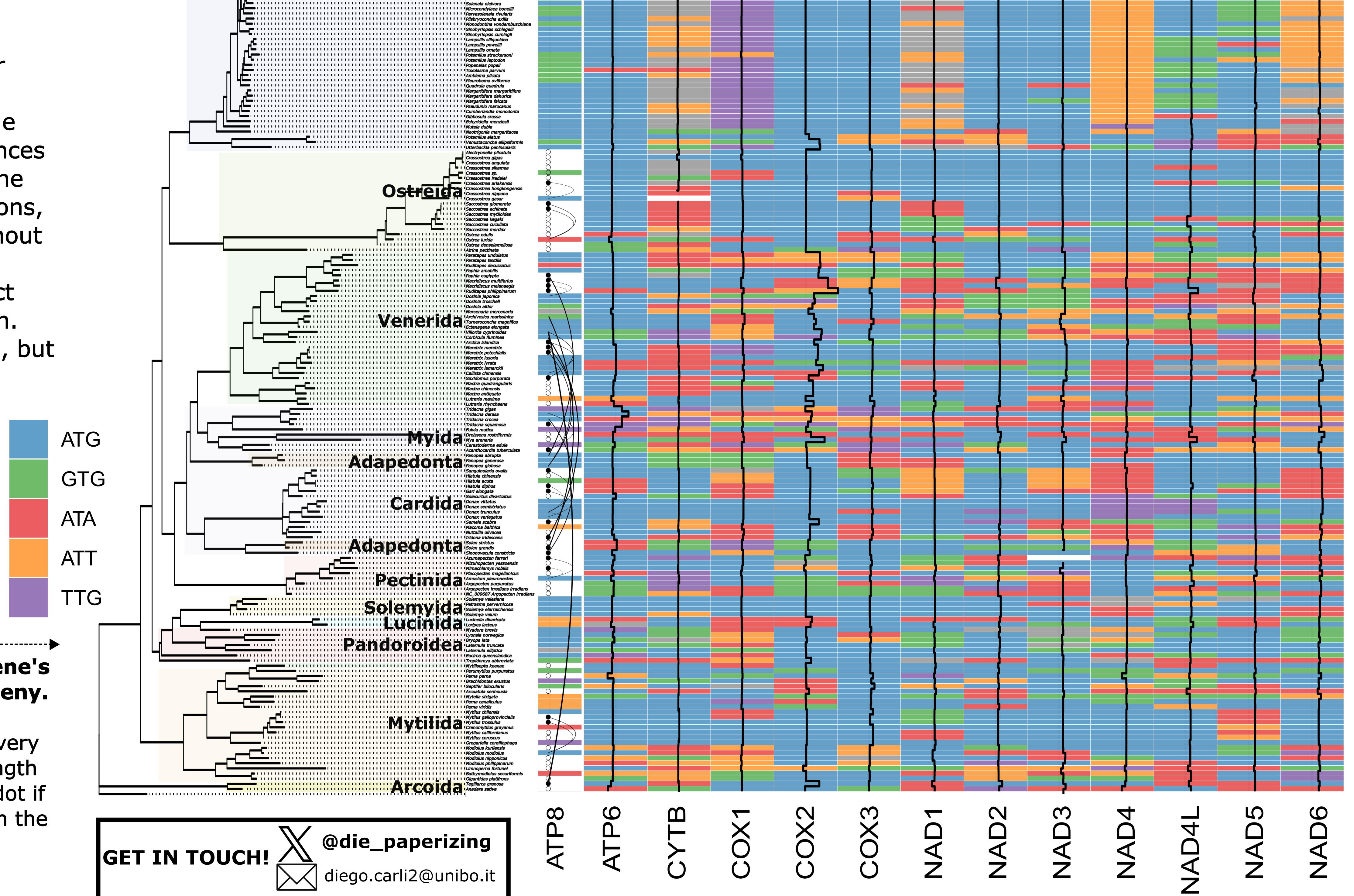
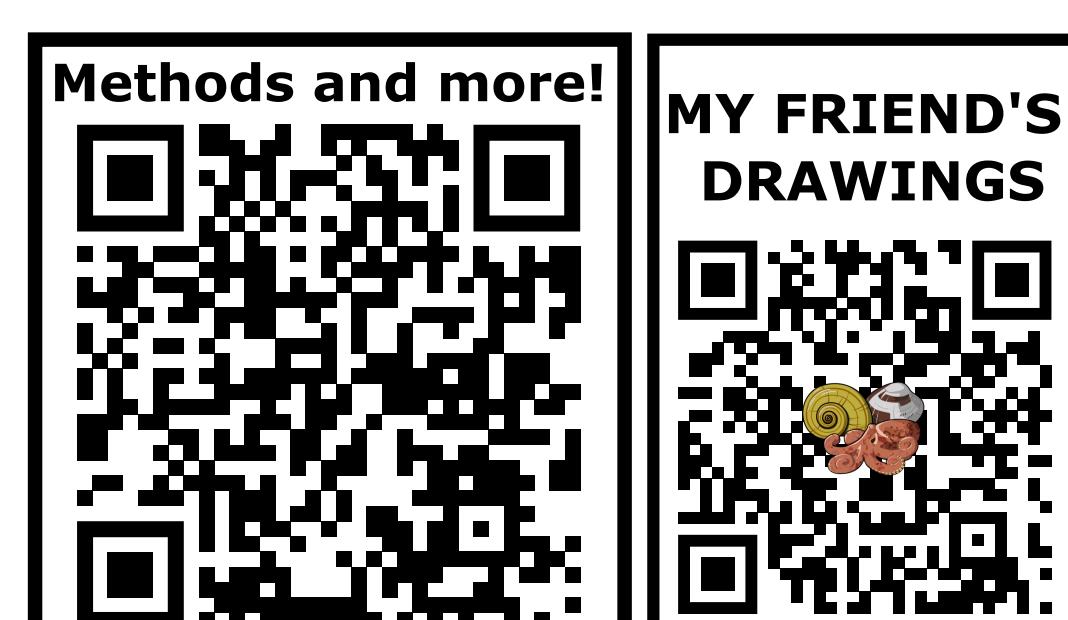
START	anthozoans	bivalves	cephalopods	gastropods
ATG	0.817	0.540	0.870	0.739
ATA	0.027	0.150	0.100	0.080
ATT	0.013	0.112	0.019	0.042
ATC	0.034	0.011	0.010	0.009
GTC	0.139	0.111	0.010	0.036
TTG	0.006	0.052	0.095	

**Table 1: Frequency of start codons usage.**

Only overall values are displayed. They can vary a lot between genes, and species of the same class. They are generally conserved at the order level in other classes (data not show), while in bivalves it change frequently, as in Figure 3.

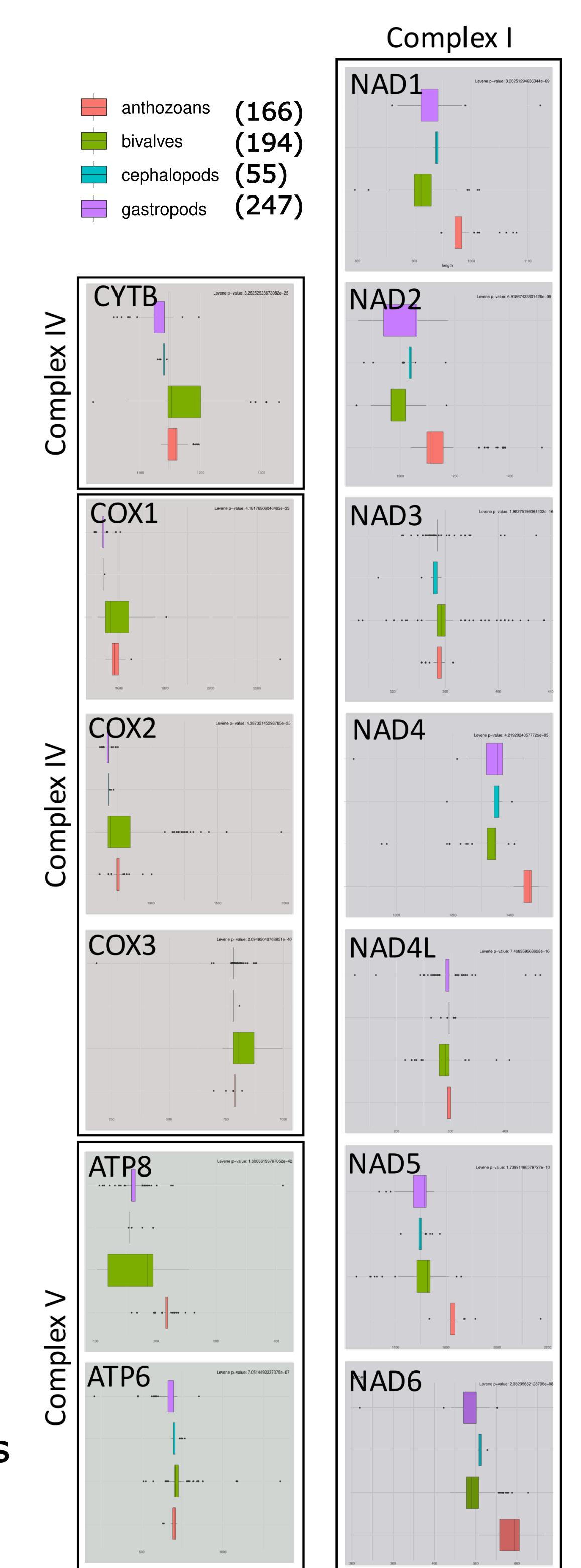
## Start codon usage

Bivalves exhibit a significantly higher usage of alternative start codons compared to other classes, with some genes displaying up to half of sequences initiating with codon different from the canonical one. Contrary to expectations, the presence of start codons throughout the genes is more frequent in other classes (figure 2), indicating no direct correlation with gene length variation. The causes for this are still unknown, but it may involve tRNA biochemistry.



**Figure 3: Start codons usage and gene's length throughout bivalve's phylogeny.**  
Mitochondrial topology inferred by ML analyses on concatenated genes. On every genes out of ATP8, black lines show length variation. ATP8 missing genes are full dot if a ATP8-like sequence has been found in the linked cell.

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diego.carli2@unibo.it



**Figure 1: Mitochondrial genes variation across the four classes.**

Bivalves show a wide degree of variability in terms of length, especially in genes of the third and forth complexes.