

| Gene | Conservation at the second codon position (%) | Major groups ("All" or "More conserved" or "Less conserved") | Four groups for codon bias 1: 90%-100% 2: 80%-90% 3: 70%-80% 4: 60%-70% | Two groups for codon bias 1: 80%-100% 2: 60%-80% |
|-------|---|--|---|--|
| atp1 | 86.0 | More conserved | 2 | 1 |
| atp6 | 86.1 | More conserved | 2 | 1 |
| atp8 | 73.4 | Less conserved* | 3 | 2 |
| atp9 | 81.8 | Less conserved | 2 | 1 |
| cox1 | 92.7 | More conserved | 1 | 1 |
| cox2 | 97.0 | More conserved | 1 | 1 |
| cytb | 96.2 | More conserved | 1 | 1 |
| nad4L | 91.7 | More conserved | 1 | 1 |
| nad6 | 86.3 | More conserved | 2 | 1 |
| nad7 | 91.7 | More conserved | 1 | 1 |
| rpL2 | 77.3 | Less conserved | 3 | 2 |
| rpL16 | 76.9 | Less conserved | 3 | 2 |
| rpS3 | 71.9 | Less conserved | 3 | 2 |
| rpS7 | 60.9 | Less conserved | 4 | 2 |
| rpS12 | 82.8 | Less conserved | 2 | 1 |
| rpS19 | 78.0 | Less conserved | 3 | 2 |

Table S1 Conservation at the second position and group division for the 16 known genes. The group division depends on the conservation at the second codon position. Genes with a background frequency at the 2nd codon position less of than 85.0% are assigned to the "less conserved" group while the other genes are assigned to the "more conserved" group. For the codon bias analysis a more fine grained division into four groups is also used.

* Since we could not create a *Physarum* based PSSM for atp8, we excluded it in the RNA editing site prediction.