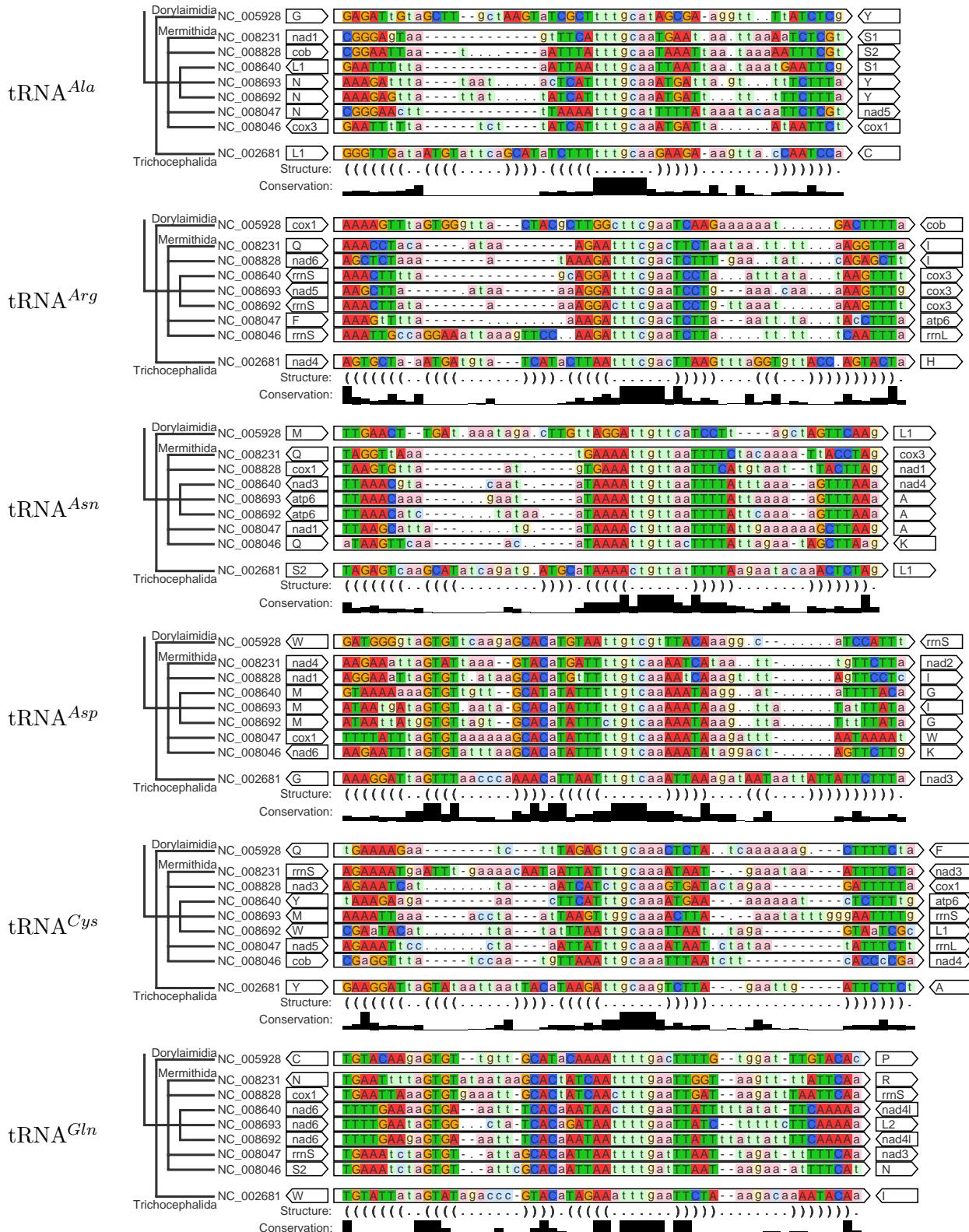


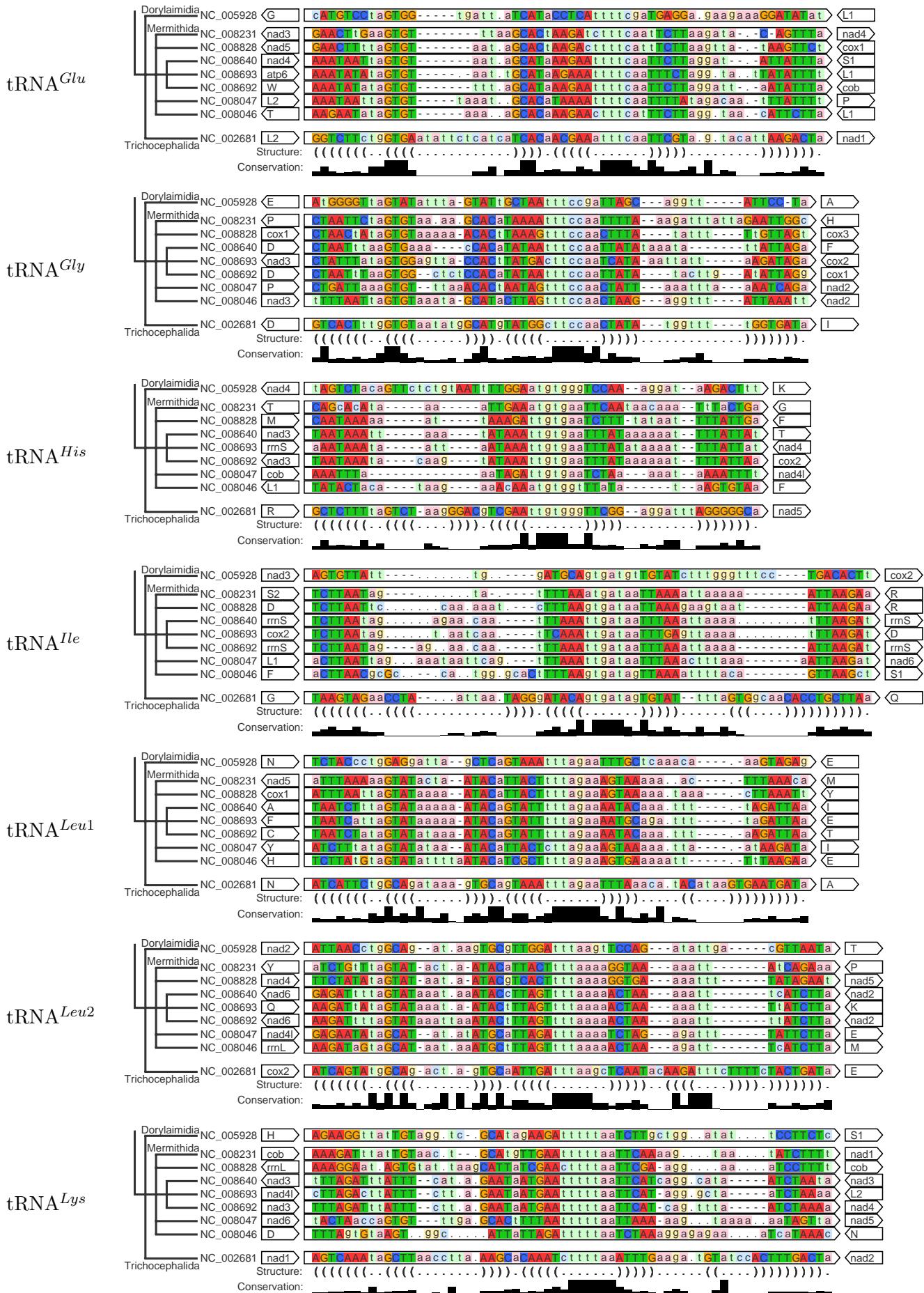
Supplementary Material

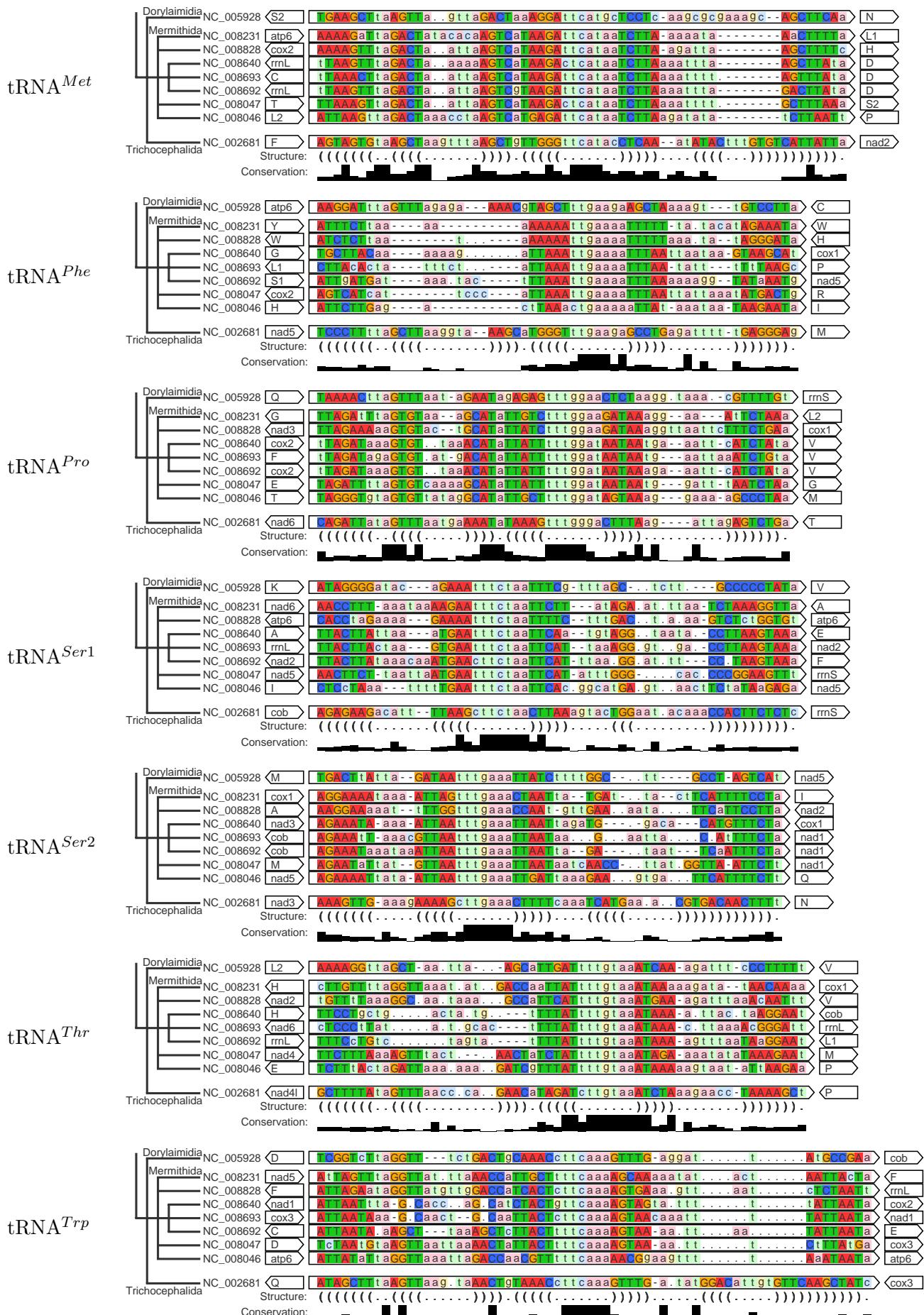
Suppl. Table 1: The mitochondrial genomes of Chromadorea analyzed within this study. All genomes are listed in the curated RefSeq database.

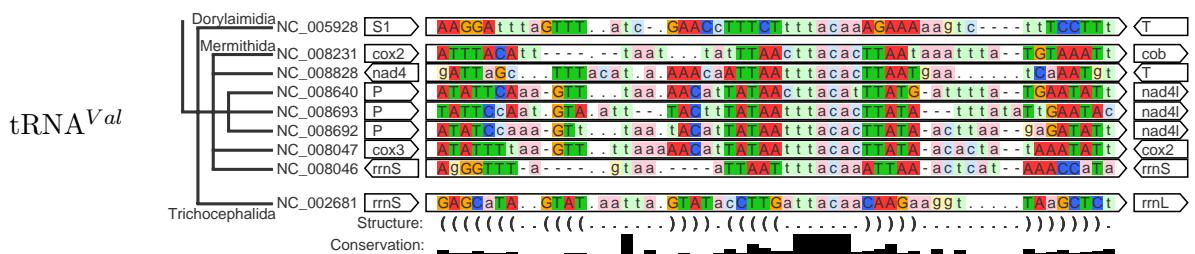
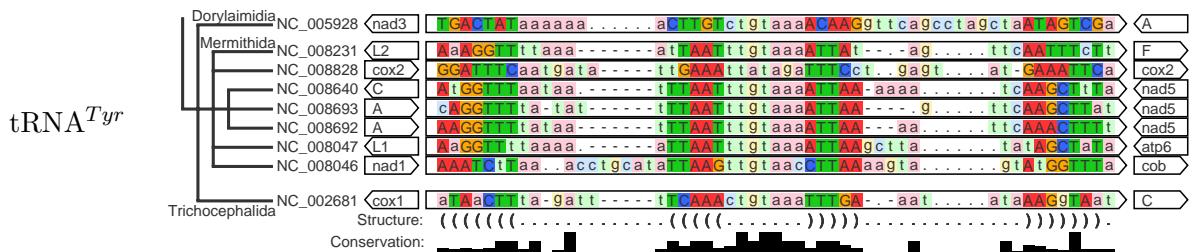
Taxonomy	Organism	Accession
Chromadorea		
Ascaridida	<i>Anisakis simplex</i>	NC_007934
	<i>Ascaris suum</i>	NC_001327
	<i>Toxocara canis</i>	NC_010690
	<i>Toxocara cati</i>	NC_010773
	<i>Toxocara malayensis</i>	NC_010527
Oxyuroidea	<i>Enterobius vermicularis</i>	NC_011300
Rhabditida	<i>Ancylostoma caninum</i>	NC_012309
	<i>Ancylostoma duodenale</i>	NC_003415
	<i>Angiostrongylus cantonensis</i>	NC_013065
	<i>Angiostrongylus costaricensis</i>	NC_013067
	<i>Bunostomum phlebotomum</i>	NC_012308
	<i>Caenorhabditis briggsae</i>	NC_009885
	<i>Caenorhabditis elegans</i>	NC_001328
	<i>Cooperia oncophora</i>	NC_004806
	<i>Haemonchus contortus</i>	NC_010383
	<i>Heterorhabditis bacteriophora</i>	NC_008534
	<i>Necator americanus</i>	NC_003416
	<i>Steinernema carpocapsae</i>	NC_005941
	<i>Strongyloides stercoralis</i>	NC_005143
Spirurida	<i>Brugia malayi</i>	NC_004298
	<i>Dirofilaria immitis</i>	NC_005305
	<i>Onchocerca volvulus</i>	NC_001861
Tylenchida	<i>Radopholus similis</i>	NC_013253

Suppl. Figure 1: The full set of detected mt-tRNAs in 9 Enoplea species. The NCBI taxonomy was used for sorting the sequences which were aligned with Infernal. The conservation scores plotted below the alignments were calculated using ClustalX, normalized and squared to improve the readability.

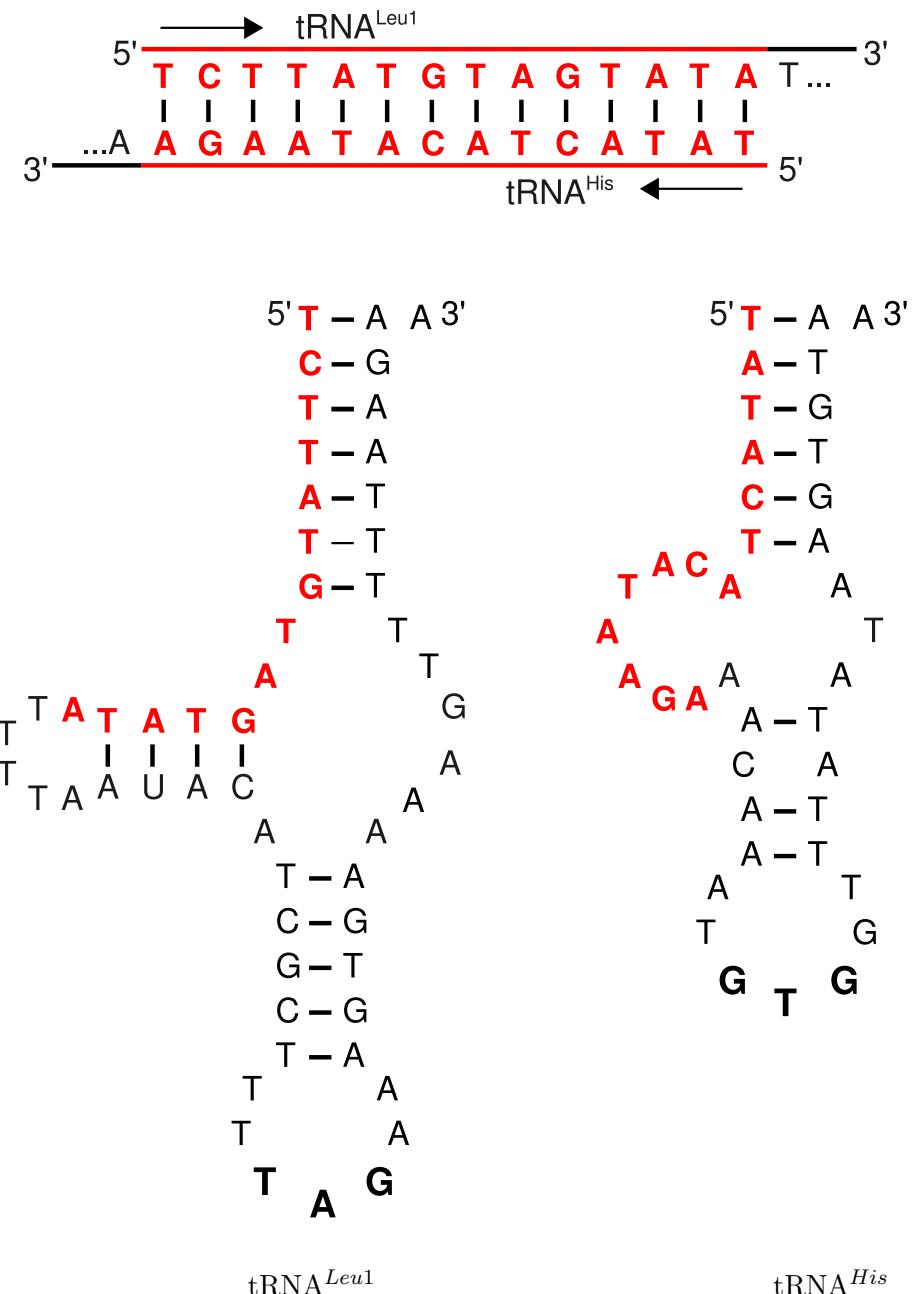








Suppl. Figure 2: Overlapping tRNA^{Leu1} and tRNA^{His} in *Thaumamermis cosgrovei*. Both mitochondrial tRNA genes overlap for 14 nt (red). The anticodons are highlighted in bold.



Suppl. Figure 3: Comparison of all armless mitochondrial tRNAs of *Romanomermis nielseni*. Anticodons are shown in bold.

