

**Table S1.** Organization of the *C. magna* mitogenome.

Gene	Position (bp)	Size (bp)	Direction	Intergenic Nucleotides (IGN)	Anti- or Start/Stop Codons	A+T %
<i>trnIle</i> (I)	1–65	65	Forward	0	AAT	63.08
<i>trnGln</i> (Q)	63–131	69	Reverse	–3	TAT	65.22
<i>trnMet</i> (M)	144–213	70	Forward	12	AGA	58.57
<i>nad2</i>	214–1248	1035	Forward	0	ATG/TAA	58.72
<i>trnTrp</i> (W)	1247–1314	68	Forward	–2	AAG	70.59
<i>trnCys</i> (C)	1319–1388	70	Reverse	4	AGC	65.72
<i>trnTyr</i> (Y)	1389–1454	66	Reverse	0	GGT	54.55
<i>cox1</i>	1464–2996	1533	Forward	9	CAA/TAA	53.72
<i>trnLeu2</i> (UUR)	2992–3055	64	Forward	–5	TCT	67.19
<i>cox2</i>	3059–3746	688	Forward	3	ATG/T-	57.21
<i>trnLys</i> (K)	3747–3816	70	Forward	0	CAT	64.29
<i>trnAsp</i> (D)	3817–3883	67	Forward	0	AAA	76.12
<i>atp8</i>	3884–4045	162	Forward	0	ATG/TAA	66.67
<i>atp6</i>	4039–4716	678	Forward	–7	ATG/TAA	58.96
<i>cox3</i>	4716–5504	789	Forward	–1	ATG/TAA	55.73
<i>trnGly</i> (G)	5506–5574	69	Forward	1	ATT	71.01
<i>nad3</i>	5584–5928	345	Forward	9	ATA/TAA	58.19
<i>trnAla</i> (A)	5933–5999	67	Forward	4	GGG	68.66
<i>trnArg</i> (R)	6004–6068	65	Forward	4	AAG	66.16
<i>trnAsn</i> (N)	6068–6132	65	Forward	–1	TTA	63.07
<i>trnSer1</i> (AGN)	6133–6199	67	Forward	0	GAA	64.18
<i>trnGlu</i> (E)	6202–6266	65	Forward	2	ATT	83.08
<i>trnPhe</i> (F)	6267–6336	70	Reverse	0	GTT	62.86
<i>nad5</i>	6337–8071	1735	Reverse	0	GTG/T-	62.57
<i>trnHis</i> (H)	8072–8145	74	Reverse	0	ACT	67.57
<i>nad4</i>	8145–9485	1341	Reverse	–1	GTG/TAA	62.7
<i>nad4l</i>	9479–9775	297	Reverse	–7	ATG/TAA	68.37
<i>trnThr</i> (T)	9778–9844	67	Forward	2	GTT	76.12
<i>trnPro</i> (P)	9846–9911	66	Reverse	1	CAG	66.67
<i>nad6</i>	9925–10437	513	Forward	13	ATT/TAA	59.88
<i>Cytb</i>	10437–11573	1137	Forward	–1	ATG/TAG	55.38
<i>trnSer2</i> (UCN)	11572–11641	70	Forward	–2	AGT	75.71
<i>nad1</i>	11658–12581	924	Reverse	16	GTG/TAG	64.17
<i>trnLeu1</i> (CUN)	12610–12676	67	Reverse	28	TCT	62.69
<i>rrnL</i>	12637–14001	1365	Reverse	–40		65.27
<i>trnVal</i> (V)	14034–14105	72	Reverse	32	CGA	61.11
<i>rrnS</i>	14107–14942	836	Reverse	1		62.32
CR	14943–15774	832		0		71.51

**Table S2.** Organization of the *Claassenia* sp. 2 mitogenome.

Gene	Position (bp)	Size (bp)	Direction	Intergenic Nucleotides (IGN)	Anti- or Start/Stop Codons	A+T %
<i>trnIle</i> (I)	1–66	66	Forward	0	AAT	68.18

<i>trnGln</i> (Q)	64–132	69	Reverse	–3	TAT	71.01
<i>trnMet</i> (M)	143–210	68	Forward	10	AGA	60.29
<i>nad2</i>	214–1245	1032	Forward	3	ATC/TAA	65.89
<i>trnTrp</i> (W)	1244–1310	67	Forward	–2	AAG	73.14
<i>trnCys</i> (C)	1303–1370	68	Reverse	–8	AGC	63.23
<i>trnTyr</i> (Y)	1371–1437	67	Reverse	0	GGT	59.71
<i>cox1</i>	1430–2974	1545	Forward	–8	ATT/TAA	60.51
<i>trnLeu2</i> (UUR)	2970–3033	64	Forward	–5	TCT	64.06
<i>cox2</i>	3038–3725	688	Forward	4	ATG/T-	60.41
<i>trnLys</i> (K)	3726–3795	70	Forward	0	CAT	65.72
<i>trnAsp</i> (D)	3796–3864	69	Forward	0	AAA	78.26
<i>atp8</i>	3865–4026	162	Forward	0	ATC/TAA	66.04
<i>atp6</i>	4020–4697	678	Forward	–7	ATG/TAA	61.78
<i>cox3</i>	4697–5485	789	Forward	–1	ATG/TAA	59.16
<i>trnGly</i> (G)	5485–5551	67	Forward	–1	ATC	74.63
<i>nad3</i>	5552–5905	354	Forward	0	ATG/TAA	61.54
<i>trnAla</i> (A)	5910–5976	67	Forward	4	GGG	73.14
<i>trnArg</i> (R)	5981–6046	66	Forward	4	AAG	65.15
<i>trnAsn</i> (N)	6046–6111	66	Forward	–1	TTA	65.15
<i>trnSer1</i> (AGN)	6112–6178	67	Forward	0	GAA	64.18
<i>trnGlu</i> (E)	6181–6245	65	Forward	2	ATT	87.7
<i>trnPhe</i> (F)	6245–6316	72	Reverse	–1	ACT	68.05
<i>nad5</i>	6317–8051	1735	Reverse	0	GTG/T-	67.64
<i>trnHis</i> (H)	8052–8123	72	Reverse	0	ACT	69.45
<i>nad4</i>	8124–9462	1339	Reverse	0	ATG/T-	67.34
<i>nad4l</i>	9456–9752	297	Reverse	–7	ATG/TAA	72.11
<i>trnThr</i> (T)	9755–9821	67	Forward	2	GTT	77.61
<i>trnPro</i> (P)	9823–9887	65	Reverse	1	CAG	66.15
<i>nad6</i>	9889–10413	525	Forward	1	ATT/TAA	63.41
<i>Cytb</i>	10413–11549	1137	Forward	–1	ATG/TAG	61.02
<i>trnSer2</i> (UCN)	11548–11618	71	Forward	–2	AGT	74.65
<i>nad1</i>	11636–12586	951	Reverse	17	TTG	66.77
<i>trnLeu1</i> (CUN)	12588–12654	67	Reverse	1	TCT	67.17
<i>rrnL</i>	12613–14004	1392	Reverse	–42		69.68
<i>trnVal</i> (V)	14006–14077	72	Reverse	1	CAA	55.55
<i>rrnS</i>	14079–14908	830	Reverse	1		67.95
CR	14909–15777	869		0		74.45

**Table S3.** Organization of the *C. xucheni* mitogenome.

Gene	Position (bp)	Size (bp)	Direction	Intergenic Nucleotides (IGN)	Anti- or Start/Stop Codons	A+T %
<i>trnIle</i> (I)	1–66	66	Forward	0	AAT	60.6
<i>trnGln</i> (Q)	64–132	69	Reverse	–3	TAT	69.56
<i>trnMet</i> (M)	144–213	70	Forward	11	AGA	61.43
<i>nad2</i>	217–1248	1032	Forward	3	ATC/TAA	60.35
<i>trnTrp</i> (W)	1247–1313	67	Forward	–2	AAG	73.14
<i>trnCys</i> (C)	1306–1373	68	Reverse	–8	AGC	60.29
<i>trnTyr</i> (Y)	1374–1438	65	Reverse	0	GGT	63.08
<i>cox1</i>	1431–2975	1545	Forward	–8	ATT/TAA	56.49
<i>trnLeu2</i> (UUR)	2971–3034	64	Forward	–5	TCT	64.06
<i>cox2</i>	3039–3726	688	Forward	4	ATG/T-	56.63

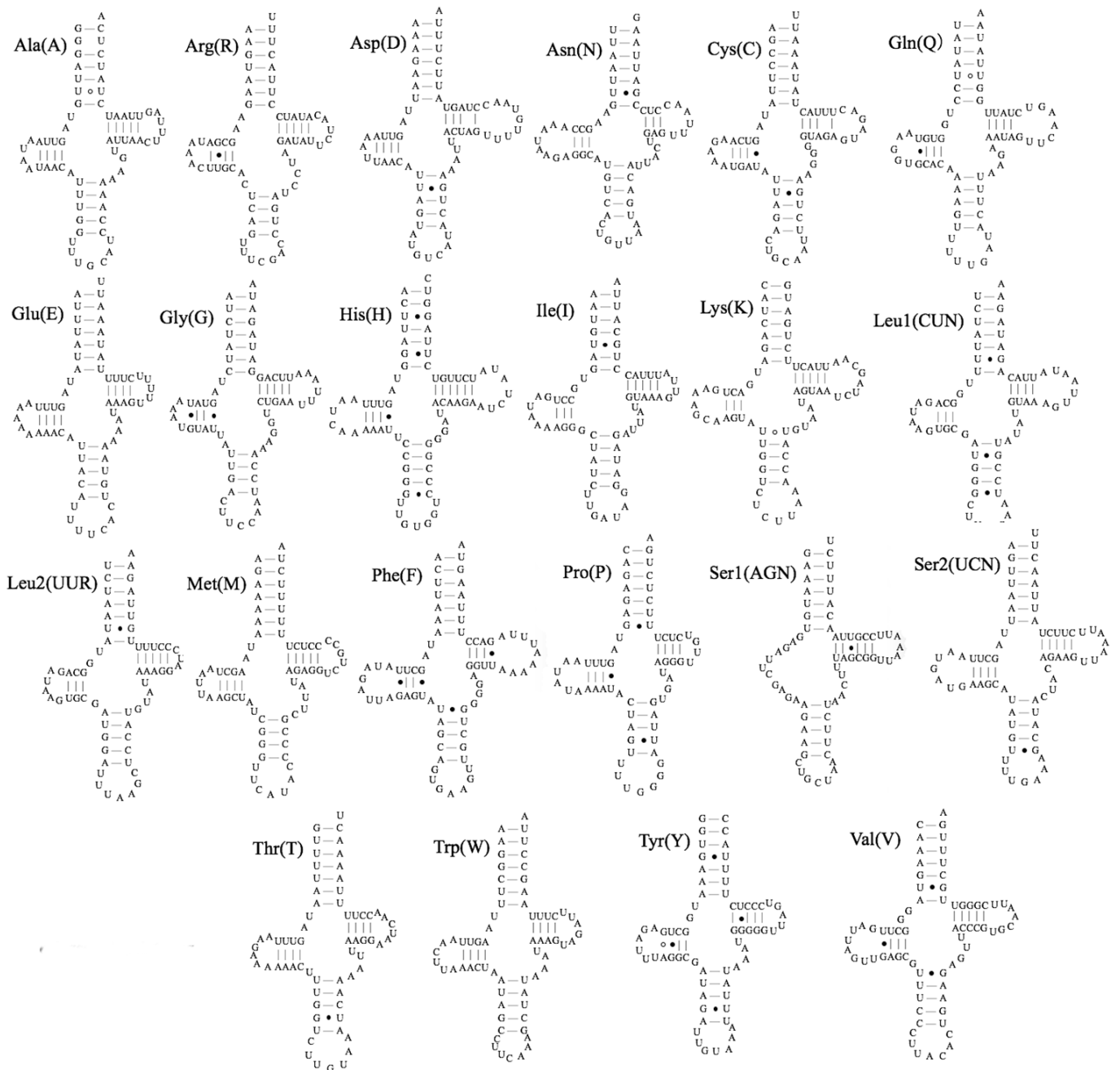
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<i>trnLys</i> (K)	3727–3796	70	Forward	0	CAT	65.72
<i>trnAsp</i> (D)	3797–3864	68	Forward	0	AAA	75
<i>atp8</i>	3865–4026	162	Forward	0	ATT/TAA	64.78
<i>atp6</i>	4020–4697	678	Forward	−7	ATG/TAA	59.26
<i>cox3</i>	4697–5485	789	Forward	−1	ATG/TAA	55.09
<i>trnGly</i> (G)	5485–5551	67	Forward	−1	ACC	68.66
<i>nad3</i>	5555–5905	351	Forward	3	ATA/TAA	62.07
<i>trnAla</i> (A)	5910–5976	67	Forward	4	GGG	70.15
<i>trnArg</i> (R)	5982–6048	67	Forward	5	AAG	64.18
<i>trnAsn</i> (N)	6048–6113	66	Forward	−1	TTA	65.15
<i>trnSer1</i> (AGN)	6114–6180	67	Forward	0	GAA	64.18
<i>trnGlu</i> (E)	6185–6250	66	Forward	4	ATT	83.33
<i>trnPhe</i> (F)	6250–6321	72	Reverse	−1	ACT	65.27
<i>nad5</i>	6322–8020	1699	Reverse	0	ATT/T-	64.07
<i>trnHis</i> (H)	8057–8127	71	Reverse	36	ACT	70.43
<i>nad4</i>	8128–9466	1339	Reverse	0	ATG/T-	65.85
<i>nad4l</i>	9460–9756	297	Reverse	−7	ATG/TAA	68.71
<i>trnThr</i> (T)	9759–9823	65	Forward	2	GTT	78.46
<i>trnPro</i> (P)	9825–9890	66	Reverse	1	CAG	68.18
<i>nad6</i>	9904–10416	513	Forward	13	ATC/TAA	57.65
<i>Cytb</i>	10428–11552	1125	Forward	11	ATA/TAG	57.21
<i>trnSer2</i> (UCN)	11551–11621	71	Forward	−2	AGT	73.24
<i>nad1</i>	11640–12560	921	Reverse	18	GTG/TAG	63.29
<i>trnLeu1</i> (CUN)	12592–12658	67	Reverse	31	TCT	62.69
<i>rrnL</i>	12636–14006	1371	Reverse	−23		67.98
<i>trnVal</i> (V)	14008–14079	72	Reverse	1	CAA	56.94
<i>rrnS</i>	14081–14913	833	Reverse	1		65.54
CR	14914–15746	832		0		73.95

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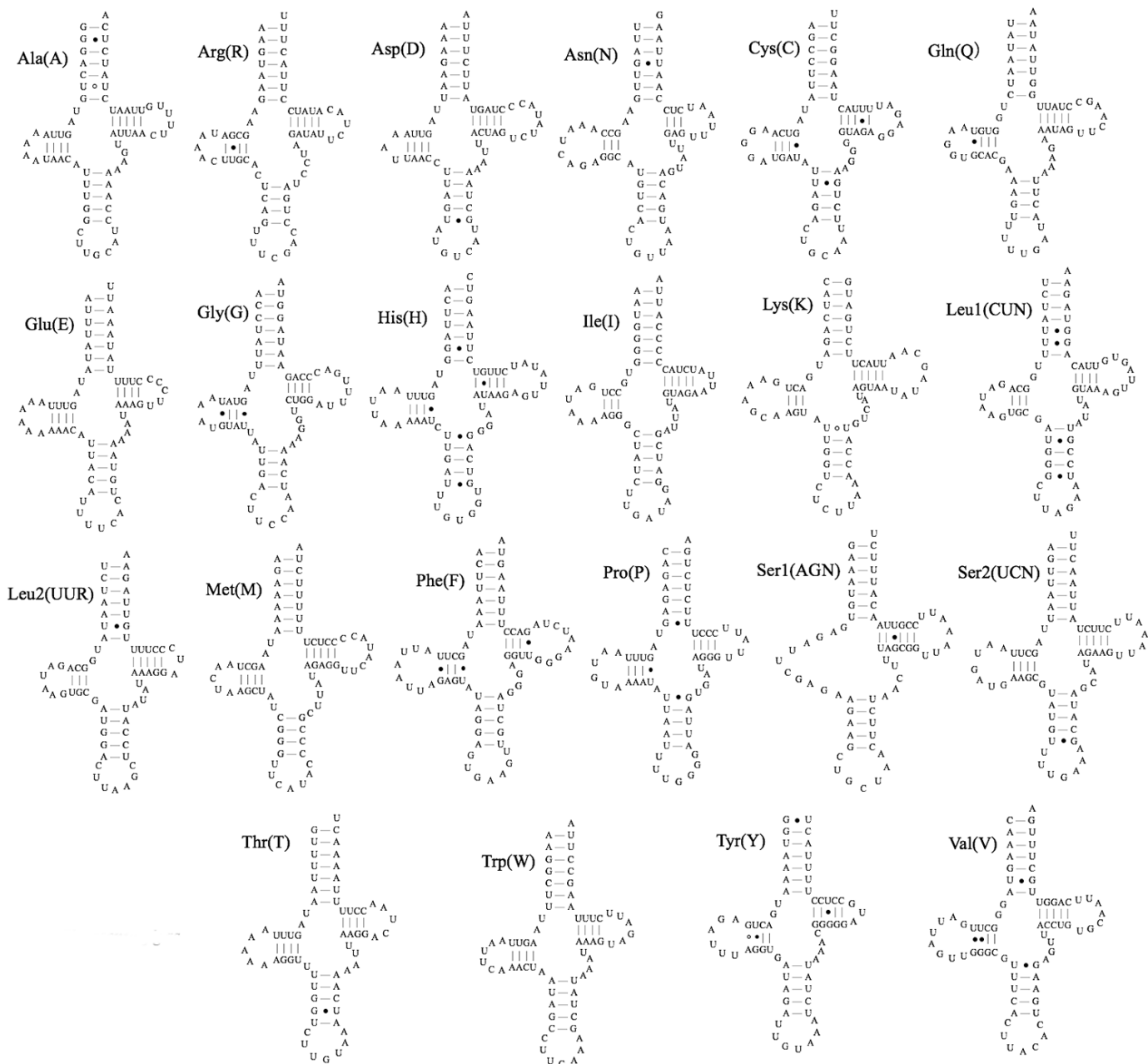






### *Claassenia* sp.2

**Figure S3.** Predicted secondary structures of tRNAs in *claassenia* sp.2. The tRNAs are labelled with abbreviations of their corresponding amino acids.



### *Claassenia xucheni*

**Figure S4.** Predicted secondary structures of tRNAs in in *C. xucheni*. The tRNAs are labelled with abbreviations of their corresponding amino acids.