

Table S1. Organization of the complete mitochondrial genome of *A. hypoleucos*.

Gene	Strand	Position	Overlap/spacer	Size (bp)	Anticodon
<i>tRNA<sup>Phe</sup></i>	H	1-71		71	GAA
<i>s-rRNA</i>	H	72-1044		973	
<i>tRNA<sup>Val</sup></i>	H	1045-1116		72	TAC
<i>l-rRNA</i>	H	1117-2706	1	1590	
<i>tRNA<sup>Leu</sup>(UUR)</i>	H	2708-2781	13	74	TAA
<i>ND1</i>	H	2795-3772		978	
<i>tRNA<sup>Ile</sup></i>	H	3773-3842	9	70	GAT
<i>tRNA<sup>Gln</sup></i>	L	3852-3922	-1	71	TTG
<i>tRNA<sup>Met</sup></i>	H	3922-3990		69	CAT
<i>ND2</i>	H	3991-5029		1039	
<i>tRNA<sup>Trp</sup></i>	H	5030-5098	1	69	TCA
<i>tRNA<sup>Ala</sup></i>	L	5100-5168	3	69	TGC
<i>tRNA<sup>Asn</sup></i>	L	5172-5244	2	73	GTT
<i>tRNA<sup>Cys</sup></i>	L	5247-5313	-1	67	GCA
<i>tRNA<sup>Tyr</sup></i>	L	5313-5383	1	71	GTA
<i>COX1</i>	H	5385-6935	-15	1551	
<i>tRNA<sup>Ser</sup>(UCN)</i>	L	6921-7000	2	80	TGA
<i>tRNA<sup>Asp</sup></i>	H	7003-7071	1	69	GTC
<i>COX2</i>	H	7073-7756	1	684	
<i>tRNA<sup>Lys</sup></i>	H	7758-7828	1	71	TTT
<i>ATP8</i>	H	7830-7997	-10	168	
<i>ATP6</i>	H	7988-8671	-1	684	
<i>COX3</i>	H	8671-9454		784	
<i>tRNA<sup>Gly</sup></i>	H	9455-9523		69	TCC
<i>ND3</i>	H	9524-9875	4	352	
<i>tRNA<sup>Arg</sup></i>	H	9880-9949		70	TCG
<i>ND4L</i>	H	9950-10,246	-7	297	
<i>ND4</i>	H	10,240-11,617		1378	
<i>tRNA<sup>His</sup></i>	H	11,618-11,686	1	69	GTG
<i>tRNA<sup>Ser</sup>(AGN)</i>	H	11,688-11,751		64	GCT
<i>tRNA<sup>Leu</sup>(CUN)</i>	H	11,752-11,822		71	TAG
<i>ND5</i>	H	11,823-13,637	12	1815	
<i>CYTB</i>	H	13,650-14,792	2	1143	
<i>tRNA<sup>Thr</sup></i>	H	14,795-14,870	7	76	TGT
<i>tRNA<sup>Pro</sup></i>	L	14,878-14,947	12	70	TGG
<i>ND6</i>	L	14,960-15,481	3	522	
<i>tRNA<sup>Glu</sup></i>	L	15,485-15,558		74	TTC
<i>D-loop</i>	H	15,559-16,732		1174	

Table S2. Organization of the partial mitochondrial genome of *L. semipalmatus*.

Gene	Strand	Position	Overlap/spacer	Size (bp)	Anticodon
<i>tRNA<sup>Phe</sup></i>	H	1-73		73	GAA
<i>s-rRNA</i>	H	74-1046		973	

<i>tRNA<sup>Val</sup></i>	H	1047-1118		72	TAC
<i>l-rRNA</i>	H	1119-2716		1598	
<i>tRNA<sup>Leu(UUR)</sup></i>	H	2717-2790	16	74	TAA
<i>ND1</i>	H	2807-3784		978	
<i>tRNA<sup>Ile</sup></i>	H	3785-3854	11	70	GAT
<i>tRNA<sup>Gln</sup></i>	L	3866-3936	-1	71	TTG
<i>tRNA<sup>Met</sup></i>	H	3936-4004		69	CAT
<i>ND2</i>	H	4005-5043		1039	
<i>tRNA<sup>Trp</sup></i>	H	5044-5113	1	70	TCA
<i>tRNA<sup>Ala</sup></i>	L	5115-5183	2	69	TGC
<i>tRNA<sup>Asn</sup></i>	L	5186-5258	2	73	GTT
<i>tRNA<sup>Cys</sup></i>	L	5261-5327	-1	67	GCA
<i>tRNA<sup>Tyr</sup></i>	L	5327-5397	1	71	GTA
<i>COX1</i>	H	5399-6949	-9	1551	
<i>tRNA<sup>Ser(UCN)</sup></i>	L	6941-7014	2	74	TGA
<i>tRNA<sup>Asp</sup></i>	H	7017-7085	1	69	GTC
<i>COX2</i>	H	7087-7770	1	684	
<i>tRNA<sup>Lys</sup></i>	H	7772-7842	1	71	TTT
<i>ATP8</i>	H	7844-8011	-10	168	
<i>ATP6</i>	H	8002-8685	-1	684	
<i>COX3</i>	H	8685-9468		784	
<i>tRNA<sup>Gly</sup></i>	H	9469-9537		69	TCC
<i>ND3</i>	H	9538-9889	4	352	
<i>tRNA<sup>Arg</sup></i>	H	9894-9962	1	69	TCG
<i>ND4L</i>	H	9964-10,260	-7	297	
<i>ND4</i>	H	10,254-11,631		1378	
<i>tRNA<sup>His</sup></i>	H	11,632-11,700	1	69	GTG
<i>tRNA<sup>Ser(AGN)</sup></i>	H	11,702-11,765	1	64	GCT
<i>tRNA<sup>Leu(CUN)</sup></i>	H	11,767-11,837		71	TAG
<i>ND5</i>	H	11,838-13,652	9	1815	
<i>CYTB</i>	H	13,662-14,804	2	1143	
<i>tRNA<sup>Thr</sup></i>	H	14,807-14,882	15	76	TGT
<i>tRNA<sup>Pro</sup></i>	L	14,898-14,967	19	70	TGG
<i>ND6</i>	L	14,987-15,508	3	522	
<i>tRNA<sup>Glu</sup></i>	L	15,512-15,584		73	TTC
<i>D-loop</i>	H	15,585-15,739			

Table S3. Organization of the partial mitochondrial genome of *N. arquata*.

Gene	Strand	Position	Overlap/spacer	Size (bp)	Anticodon
<i>tRNA<sup>Phe</sup></i>	H	1-72		72	GAA
<i>s-rRNA</i>	H	73-1045		973	
<i>tRNA<sup>Val</sup></i>	H	1046-1117		72	TAC
<i>l-rRNA</i>	H	1118-2710		1593	
<i>tRNA<sup>Leu(UUR)</sup></i>	H	2711-2784	12	74	TAA
<i>ND1</i>	H	2797-3774		978	
<i>tRNA<sup>Ile</sup></i>	H	3775-3844	12	70	GAT
<i>tRNA<sup>Gln</sup></i>	L	3857-3927	-2	71	TTG

<i>tRNA<sup>Met</sup></i>	H	3926-3995	1	70	CAT
<i>ND2</i>	H	3997-5037	6	1041	
<i>tRNA<sup>Trp</sup></i>	H	5044-5113	9	70	TCA
<i>tRNA<sup>Ala</sup></i>	L	5123-5191	2	69	TGC
<i>tRNA<sup>Asn</sup></i>	L	5194-5267	3	74	GTT
<i>tRNA<sup>Cys</sup></i>	L	5271-5337	-1	67	GCA
<i>tRNA<sup>Tyr</sup></i>	L	5337-5407	1	71	GTA
<i>COX1</i>	H	5409-6959	-9	1551	
<i>tRNA<sup>Ser(UCN)</sup></i>	L	6951-7024	2	74	TGA
<i>tRNA<sup>Asp</sup></i>	H	7027-7096	1	70	GTC
<i>COX2</i>	H	7098-7781	1	684	
<i>tRNA<sup>Lys</sup></i>	H	7783-7852	1	70	TTT
<i>ATP8</i>	H	7854-8021	-10	168	
<i>ATP6</i>	H	8012-8695	-1	684	
<i>COX3</i>	H	8695-9478		784	
<i>tRNA<sup>Gly</sup></i>	H	9479-9547		69	TCC
<i>ND3</i>	H	9548-9898	4	351	
<i>tRNA<sup>Arg</sup></i>	H	9903-9972		70	TCG
<i>ND4L</i>	H	9973-10,269	-7	297	
<i>ND4</i>	H	10,263-11,639	1	1377	
<i>tRNA<sup>His</sup></i>	H	11,641-11,709		69	GTG
<i>tRNA<sup>Ser(AGN)</sup></i>	H	11,711-11,774		64	GCT
<i>tRNA<sup>Leu(CUN)</sup></i>	H	11,775-11,845		71	TAG
<i>ND5</i>	H	11,846-13,660	10	1815	
<i>CYTB</i>	H	13,671-14,813	2	1143	
<i>tRNA<sup>Thr</sup></i>	H	14,816-14,887	21	72	TGT
<i>tRNA<sup>Pro</sup></i>	L	14,909-14,978		70	TGG
<i>ND6</i>	L				
<i>tRNA<sup>Glu</sup></i>	L				
<i>D-loop</i>	H				

Table S4. Organization of the partial mitochondrial genome of *L. limosa*.

Gene	Strand	Position	Overlap/spacer	Size (bp)	Anticodon
<i>tRNA<sup>Phe</sup></i>	H	1-71		71	GAA
<i>s-rRNA</i>	H	72-1043		972	
<i>tRNA<sup>Val</sup></i>	H	1044-1115		72	TAC
<i>l-rRNA</i>	H	1116-2707		1592	
<i>tRNA<sup>Leu(UUR)</sup></i>	H	2708-2781	13	74	TAA
<i>ND1</i>	H	2795-3772		978	
<i>tRNA<sup>Ile</sup></i>	H	3773-3842	9	70	GAT
<i>tRNA<sup>Gln</sup></i>	L	3852-3922	9	71	TTG
<i>tRNA<sup>Met</sup></i>	H	3932-4000		69	CAT
<i>ND2</i>	H	4001-5039		1039	
<i>tRNA<sup>Trp</sup></i>	H	5040-5110	1	71	TCA
<i>tRNA<sup>Ala</sup></i>	L	5112-5180	12	69	TGC
<i>tRNA<sup>Asn</sup></i>	L	5193-5265	2	73	GTT
<i>tRNA<sup>Cys</sup></i>	L	5268-5334	-1	67	GCA

<i>tRNA<sup>Tyr</sup></i>	L	5334-5404	13	71	GTA
<i>COX1</i>	H	5418-6968	-15	1551	
<i>tRNA<sup>Ser(UCN)</sup></i>	L	6954-7033	2	80	TGA
<i>tRNA<sup>Asp</sup></i>	H	7036-7104	1	69	GTC
<i>COX2</i>	H	7106-7789	1	684	
<i>tRNA<sup>Lys</sup></i>	H	7791-7860	1	70	TTT
<i>ATP8</i>	H	7862-8029	-10	168	
<i>ATP6</i>	H	8020-8703	-1	684	
<i>COX3</i>	H	8703-9486		784	
<i>tRNA<sup>Gly</sup></i>	H	9487-9555		69	TCC
<i>ND3</i>	H	9556-9907	4	352	
<i>tRNA<sup>Arg</sup></i>	H	9912-9980	1	69	TCG
<i>ND4L</i>	H	9982-10,278	-7	297	
<i>ND4</i>	H	10,272-11,649		1378	
<i>tRNA<sup>His</sup></i>	H	11,650-11,718		69	GTG
<i>tRNA<sup>Ser(AGN)</sup></i>	H	11,720-11,783		64	GCT
<i>tRNA<sup>Leu(CUN)</sup></i>	H	11,784-11,854		71	TAG
<i>ND5</i>	H	11,855-13,669	11	1814	
<i>CYTB</i>	H	13,681-14,823	1	1143	
<i>tRNA<sup>Thr</sup></i>	H	14,825-14,898	2	74	TGT
<i>tRNA<sup>Pro</sup></i>	L	14,901-14,974	14	74	TGG
<i>ND6</i>	L	14,989-15,510	3	522	
<i>tRNA<sup>Glu</sup></i>	L	15,514-15,587		74	TTC
<i>D-loop</i>	H				

Table S5. The base composition and skew rate of the family Scolopacidae.

Scientific name	Accession	Size (bp)	Proportion of nucleotides (%)					AT skew	GC skew
			T	C	A	G	A+T		
<b><i>A. hypoleucos</i></b>	KM434134	<b>16,732</b>	<b>25.99</b>	<b>29.21</b>	<b>31.37</b>	<b>13.43</b>	<b>57.36</b>	<b>0.09</b>	<b>-0.37</b>
<i>A. interpres</i>	AY074885	16,984	24.71	30.72	30.64	13.94	55.34	0.11	-0.38
<i>C. alba</i>	KP742478	16,725	25.09	29.86	31.45	13.60	56.54	0.11	-0.37
<i>C. alpina</i>	KY056596	16,707	25.20	29.83	31.22	13.76	56.41	0.11	-0.37
<i>C. pugnax</i>	KP308149	16,899	26.14	28.77	32.21	12.88	58.35	0.10	-0.38
<i>C. pygmaea</i>	OK552672	17,091	25.40	29.83	30.95	13.83	56.35	0.10	-0.37
<i>C. ruficollis</i>	KY230384	17,047	24.78	29.85	31.88	13.49	56.66	0.13	-0.38
<i>C. subminuta</i>	KX644890	17,668	24.44	30.54	31.61	13.41	56.05	0.13	-0.39
<i>C. tenuirostris</i>	KX230491	16,817	24.91	30.12	31.08	13.90	55.98	0.11	-0.37
<i>C. tenuirostris</i>	KX668223	16,683	24.98	30.01	31.60	13.41	56.58	0.12	-0.38
<i>C. tenuirostris</i>	MF036175	16,906	25.53	29.47	31.62	13.39	57.15	0.11	-0.38
<i>E. pygmeus</i>	KX371106	16,603	24.85	30.02	31.29	13.84	56.14	0.11	-0.37
<i>G.gallinago</i>	KY765409	16,732	25.63	29.65	30.67	14.04	56.31	0.09	-0.36
<i>G. gallinago</i>	MG736926	16,714	25.74	29.44	31.05	13.77	56.78	0.09	-0.36
<i>G. stenura</i>	MW168383	16,860	26.14	28.77	32.21	12.88	58.35	0.10	-0.38
<i>G. stenura</i>	MW168385	16,791	26.33	28.70	32.13	12.83	58.47	0.10	-0.38
<i>L. falcinellus</i>	MK992912	16,765	24.81	30.11	31.50	13.58	56.31	0.12	-0.38
<i>L. lapponica</i>	MW168384	16,642	25.63	29.65	30.67	14.04	56.31	0.09	-0.36
<i>L. lapponica</i>	MW160420	15,555	24.81	30.11	31.50	13.58	56.31	0.12	-0.38

N. <i>madagascariensis</i>	KY128485	16,804	25.89	29.36	30.94	13.80	56.84	0.09	-0.36
N. <i>madagascariensis</i>	MK460251	16,682	24.93	29.82	31.81	13.44	56.74	0.12	-0.38
<i>N. minutus</i>	MN956840	16,902	25.36	29.69	31.31	13.64	56.67	0.11	-0.37
<i>N. phaeopus</i>	KY434065	16,709	25.40	29.83	30.95	13.83	56.35	0.10	-0.37
<i>N. tenuirostris</i>	MK341548	16,732	24.64	30.51	30.92	13.93	55.57	0.11	-0.37
<i>P. lobatus</i>	MW160419	16,678	25.74	29.44	31.05	13.77	56.78	0.09	-0.36
<i>P. parvirostris</i>	MZ157405	16,919	26.17	28.59	32.53	12.71	58.70	0.11	-0.38
<i>S. rusticola</i>	MW865755	16,814	25.02	29.85	31.79	13.34	56.81	0.12	-0.38
<i>T. erythropus</i>	KY888681	18,153	24.98	30.01	31.60	13.41	56.58	0.12	-0.38
<i>T. glareola</i>	MT188757	16,695	25.65	29.26	31.67	13.41	57.33	0.10	-0.37
<i>T. guttifer</i>	MK341549	16,773	25.52	29.71	30.79	13.99	56.30	0.09	-0.36
<i>T. nebularia</i>	MW930394	17,117	24.93	29.82	31.81	13.44	56.74	0.12	-0.38
<i>T. nebularia</i>	MK108195	16,705	25.40	29.72	30.87	14.02	56.26	0.10	-0.36
<i>T. ochropus</i>	MT880247	15,590	25.53	29.47	31.62	13.39	57.15	0.11	-0.38
<i>T. semipalmata</i> <i>inornata</i>	MK905885	16,835	25.24	29.89	31.24	13.64	56.47	0.11	-0.37
<i>T. stagnatilis</i>	MG883743	16,689	25.15	29.92	31.59	13.34	56.74	0.11	-0.38
<i>T. totanus</i>	MT572847	16,799	25.46	29.52	31.52	13.50	56.98	0.11	-0.37
<i>X. cinereus</i>	MK922124	16,818	24.86	30.17	30.71	14.27	55.56	0.11	-0.36
Average		16,793	25.32	29.71	31.39	13.58	56.71	0.11	-0.37

Table S6. The base composition and skew rate of PCGs.

Species	Gene	Size(bp)	Proportion of nucleotides (%)					AT skew	GC skew
			T	C	A	G	A+T		
<i>A. hypoleucos</i>	ND1	978	31.08	28.53	28.32	12.07	59.41	-0.05	-0.41
	ND2	1041	27.33	30.13	32.72	9.82	60.06	0.09	-0.50
	COX1	1551	28.63	28.11	27.21	16.05	55.83	-0.03	-0.27
	COX2	684	26.75	28.36	30.70	14.18	57.46	0.07	-0.33
	ATP8	168	22.62	36.90	35.71	4.76	58.33	0.22	-0.77
	ATP6	684	27.34	34.06	28.51	10.09	55.85	0.02	-0.54
	COX3	784	27.55	28.32	28.70	15.43	56.25	0.02	-0.29
	ND3	352	29.34	29.34	29.63	11.68	58.97	0.00	-0.43
	ND4L	297	26.94	30.98	29.63	12.46	56.57	0.05	-0.43
	ND4	1378	25.54	33.09	32.15	9.22	57.69	0.11	-0.56
	ND5	1815	24.46	31.79	32.89	10.85	57.36	0.15	-0.49
	CYTB	1143	27.38	31.93	29.05	11.64	56.43	0.03	-0.47
	ND6	522	42.72	9.39	12.64	35.25	55.36	-0.54	0.58
	ND1	978	28.32	32.00	26.99	12.68	55.32	-0.02	-0.43
<i>L. semipalmatus</i>	ND2	1041	24.16	33.97	31.95	9.91	56.11	0.14	-0.50
	COX1	1551	27.60	28.82	27.92	15.67	55.51	0.01	-0.30
	COX2	684	25.73	28.95	31.43	13.89	57.16	0.10	-0.35
	ATP8	168	25.00	35.12	34.52	5.36	59.52	0.16	-0.74
	ATP6	684	23.83	37.43	28.36	10.38	52.19	0.09	-0.57
	COX3	784	26.66	29.72	27.55	16.07	54.21	0.02	-0.30
	ND3	352	27.35	31.34	28.77	12.54	56.13	0.03	-0.43
	ND4L	297	25.59	32.66	27.95	13.80	53.54	0.04	-0.41

<i>N. arquata</i>	ND4	1378	25.11	33.74	31.13	10.01	56.24	0.11	-0.54
	ND5	1815	24.63	31.40	32.95	11.02	57.58	0.14	-0.48
	CYTB	1143	26.77	32.46	29.05	11.72	55.82	0.04	-0.47
	ND6	522	42.53	8.43	12.84	36.21	55.36	-0.54	0.62
	ND1	978	28.94	30.78	27.40	12.88	56.34	-0.03	-0.41
	ND2	1039	25.36	32.47	32.76	9.41	58.12	0.13	-0.55
	COX1	1551	25.98	30.63	26.95	16.44	52.93	0.02	-0.30
	COX2	684	25.44	29.39	30.12	15.06	55.56	0.08	-0.32
	ATP8	168	27.98	32.74	33.93	5.36	61.90	0.10	-0.72
	ATP6	684	26.02	35.23	28.22	10.53	54.24	0.04	-0.54
	COX3	784	27.93	28.32	27.93	15.82	55.87	0.00	-0.28
	ND3	351	27.07	31.91	28.49	12.54	55.56	0.03	-0.44
	ND4L	297	28.28	28.96	27.61	15.15	55.89	-0.01	-0.31
	ND4	1377	25.13	33.70	30.36	10.82	55.48	0.09	-0.51
	ND5	1815	25.40	31.40	32.34	10.85	57.74	0.12	-0.49
	CYTB	1143	26.33	32.55	28.78	12.34	55.12	0.04	-0.45
	ND1	978	27.81	31.60	26.89	13.70	54.70	-0.02	-0.40
	ND2	1041	25.99	32.05	31.67	10.30	57.65	0.10	-0.51
	COX1	1551	27.21	29.34	27.40	16.05	54.61	0.00	-0.29
	COX2	684	25.73	29.97	29.53	14.77	55.26	0.07	-0.34
	ATP8	168	23.81	36.90	35.71	3.57	59.52	0.20	-0.82
	ATP6	684	25.88	35.67	27.78	10.67	53.65	0.04	-0.54
	COX3	784	27.81	28.06	29.08	15.05	56.89	0.02	-0.30
	ND3	352	25.64	33.05	29.91	11.40	55.56	0.08	-0.49
	ND4L	297	26.94	30.64	26.94	15.49	53.87	0.00	-0.33
	ND4	1378	25.25	33.89	30.48	10.38	55.73	0.09	-0.53
	ND5	1814	23.86	32.34	32.51	11.29	56.36	0.15	-0.48
	CYTB	1143	25.13	34.15	28.28	12.43	53.42	0.06	-0.47
	ND6	522	41.38	10.54	13.79	34.29	55.17	-0.50	0.53
<i>L. limosa</i>	ND1	978	27.81	31.60	26.89	13.70	54.70	-0.02	-0.40
	ND2	1041	25.99	32.05	31.67	10.30	57.65	0.10	-0.51
	COX1	1551	27.21	29.34	27.40	16.05	54.61	0.00	-0.29
	COX2	684	25.73	29.97	29.53	14.77	55.26	0.07	-0.34
	ATP8	168	23.81	36.90	35.71	3.57	59.52	0.20	-0.82
	ATP6	684	25.88	35.67	27.78	10.67	53.65	0.04	-0.54
	COX3	784	27.81	28.06	29.08	15.05	56.89	0.02	-0.30
	ND3	352	25.64	33.05	29.91	11.40	55.56	0.08	-0.49
	ND4L	297	26.94	30.64	26.94	15.49	53.87	0.00	-0.33
	ND4	1378	25.25	33.89	30.48	10.38	55.73	0.09	-0.53
	ND5	1814	23.86	32.34	32.51	11.29	56.36	0.15	-0.48
	CYTB	1143	25.13	34.15	28.28	12.43	53.42	0.06	-0.47

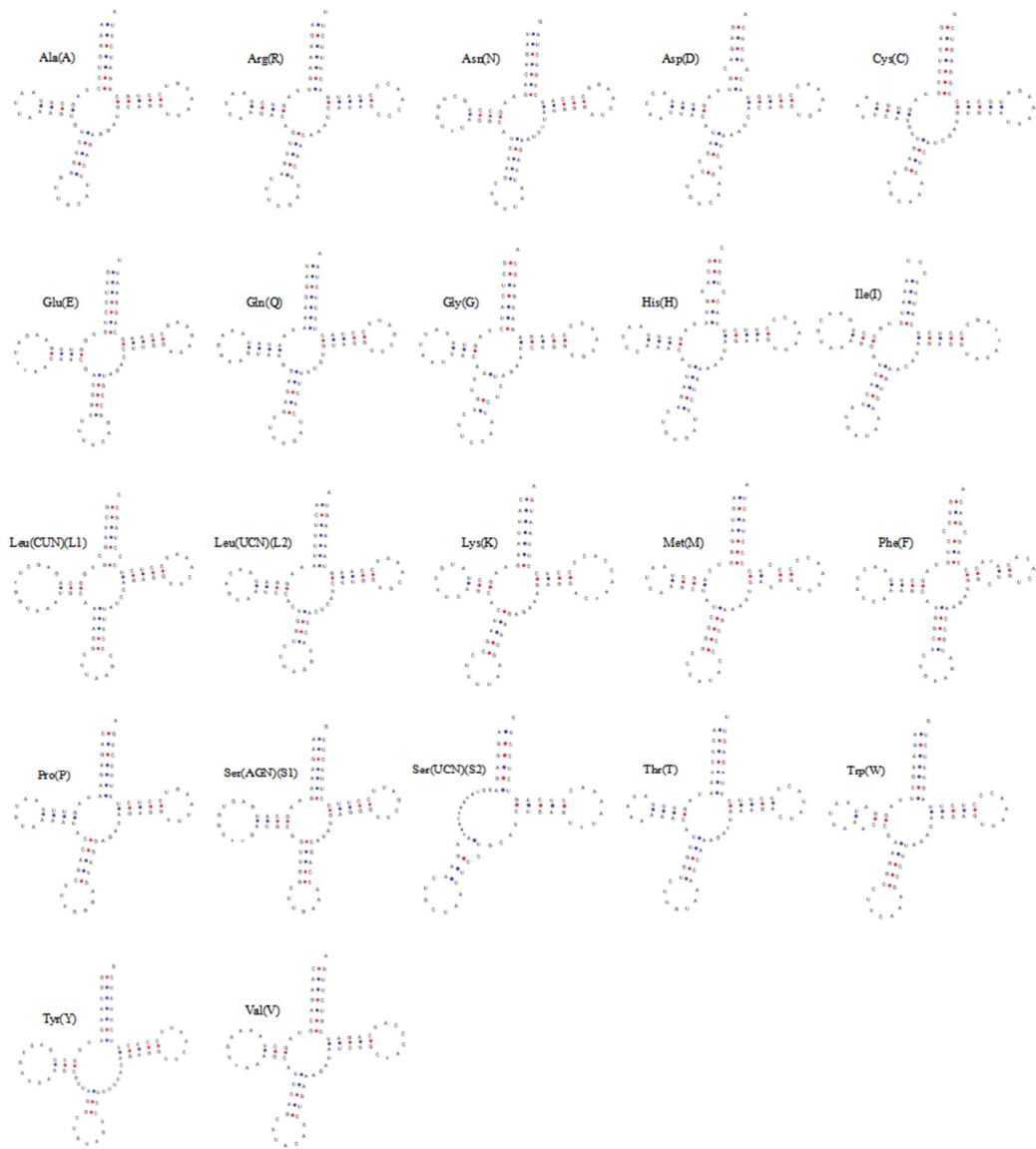


Figure S1. Secondary structures of the 22 tRNA genes of *A. hypoleucos*.

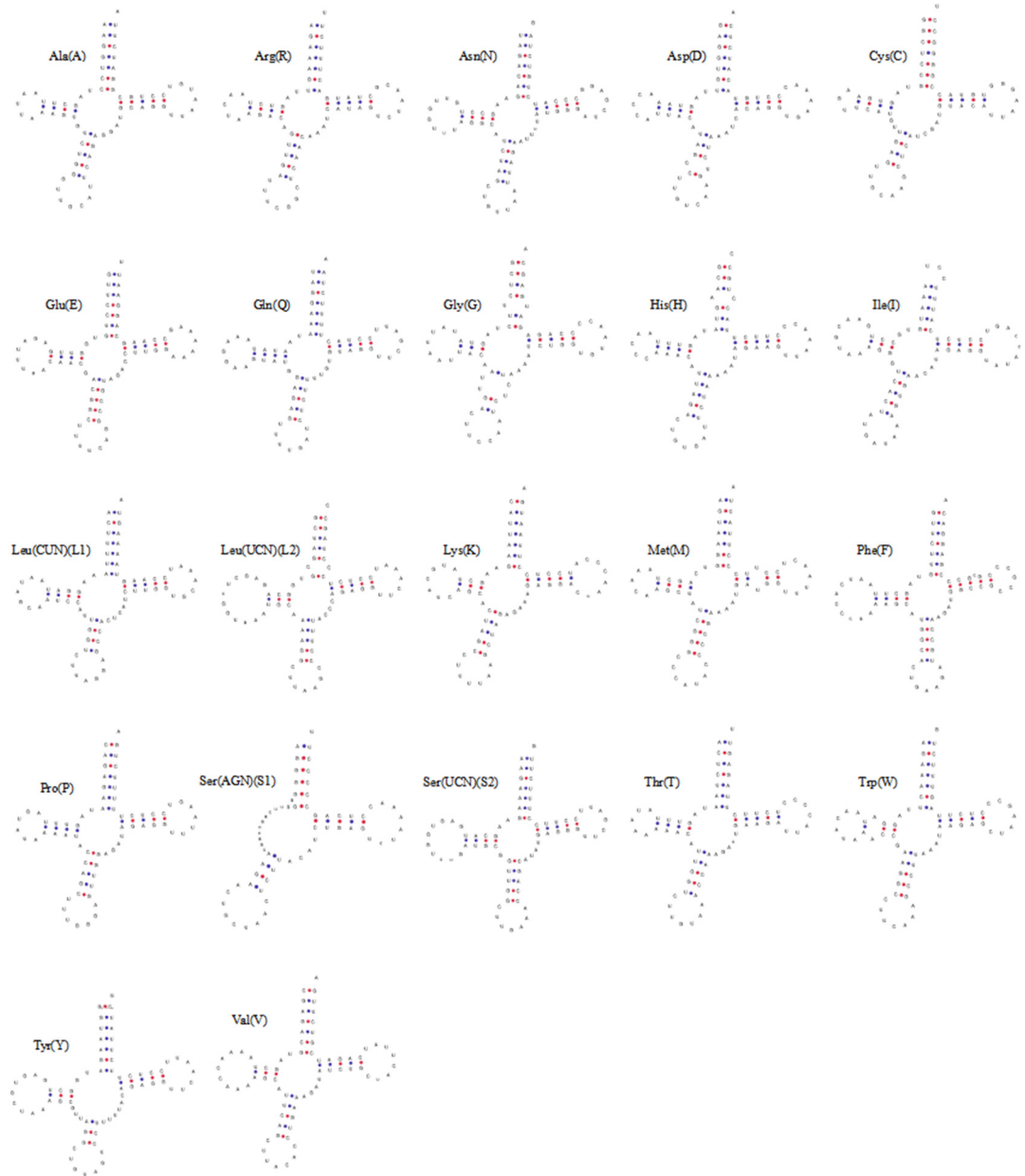


Figure S2. Secondary structures of the 22 tRNA genes of *L. semipalmatus*.



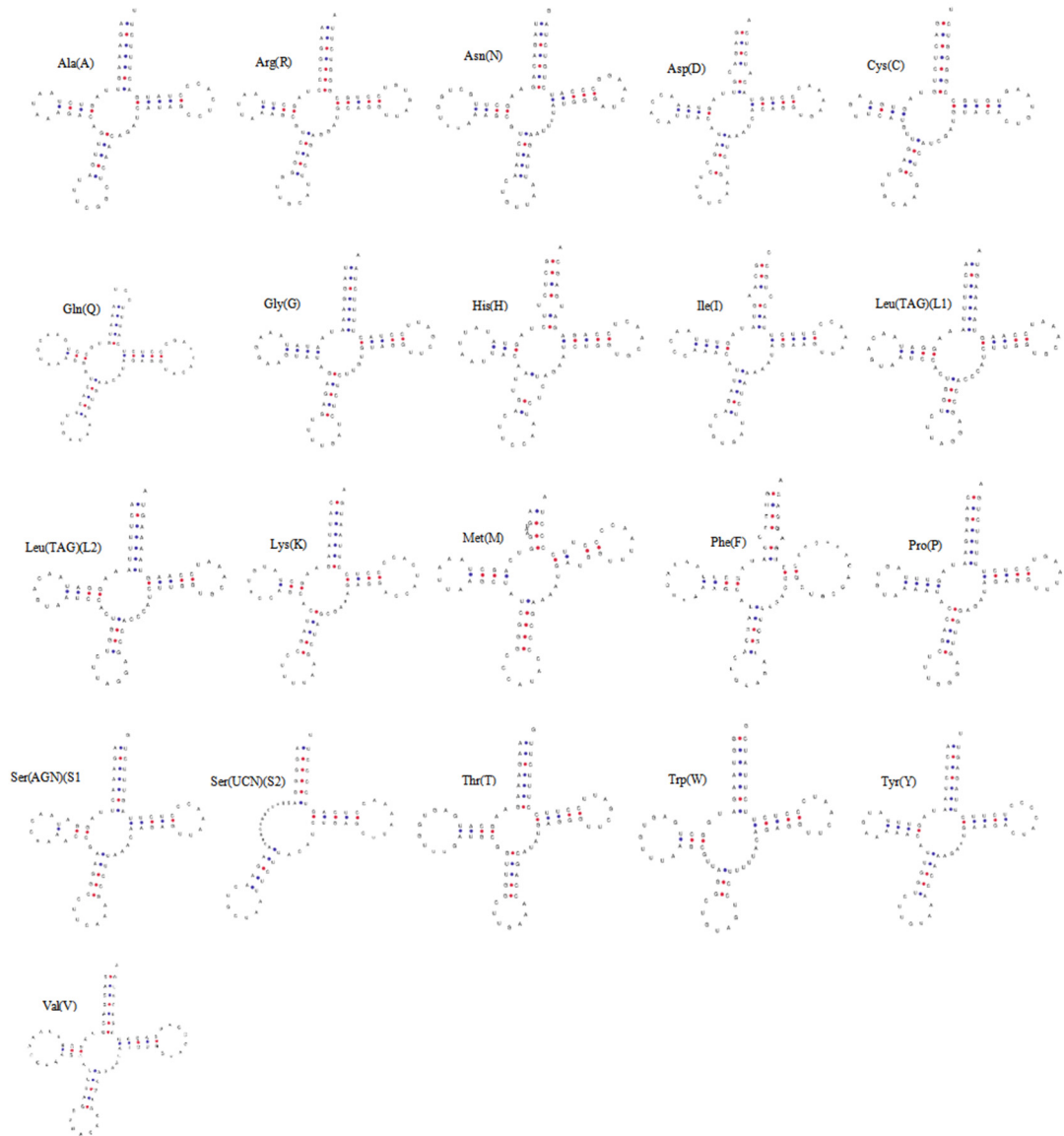


Figure S3. Secondary structures of the 21 tRNA genes of *N. arquata*.

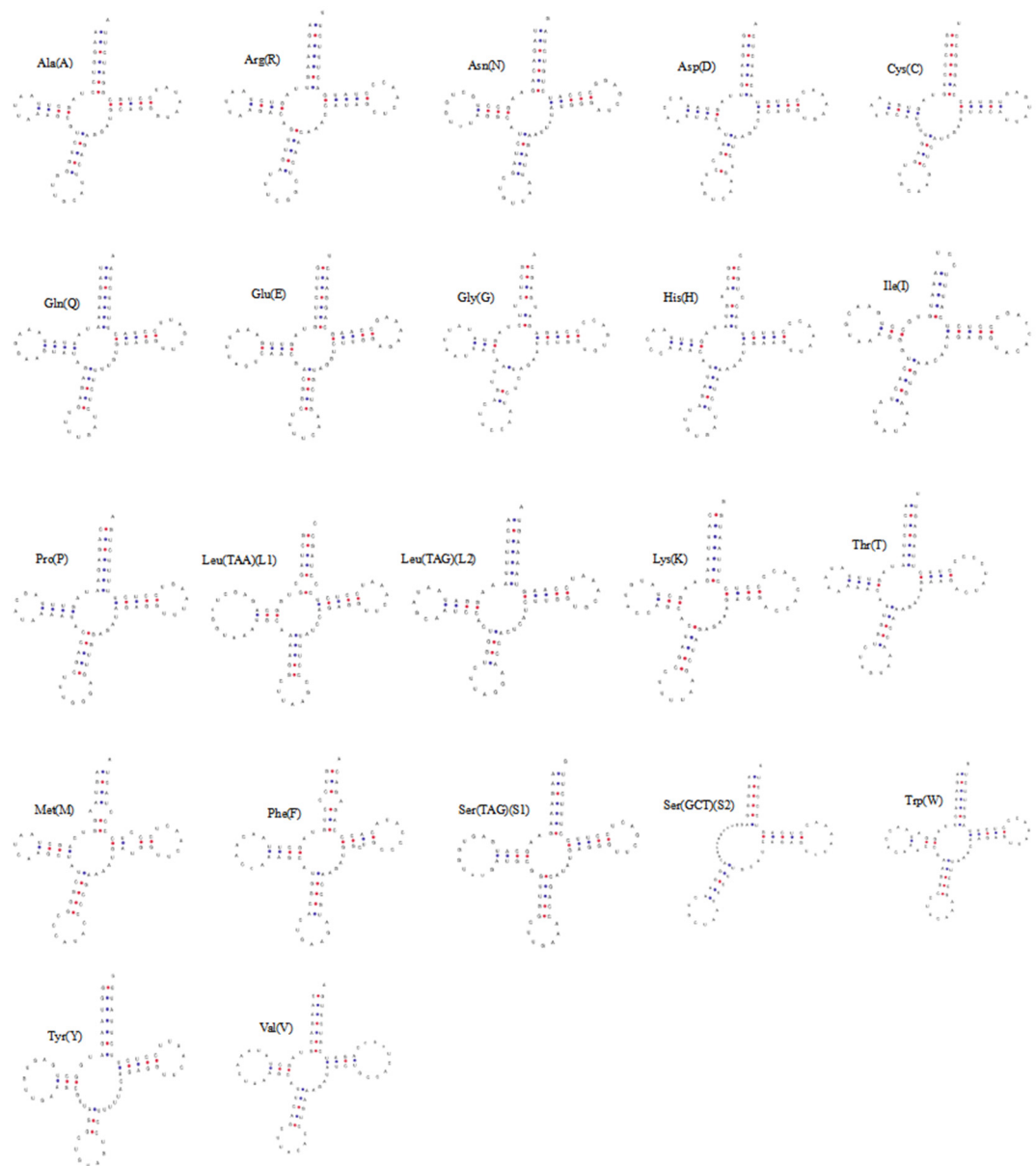


Figure S4. Secondary structures of the 22 tRNA genes of *L. limosa*.

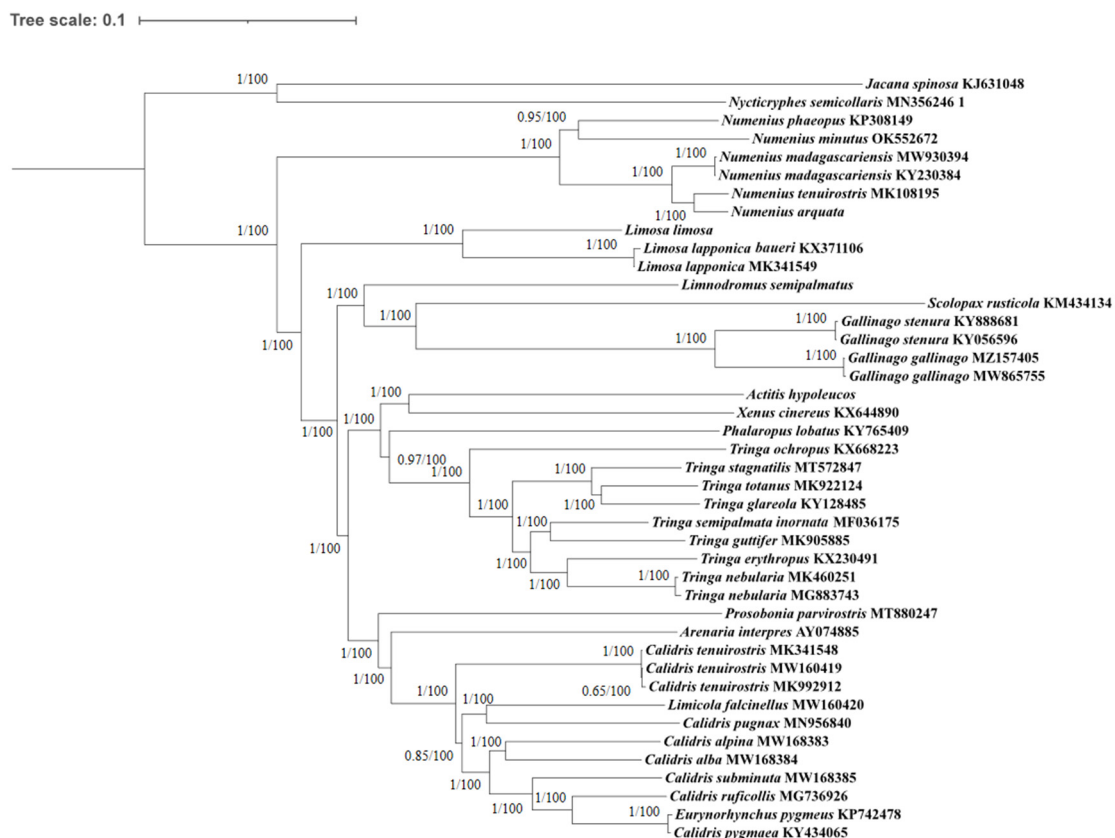


Figure S5. Phylogenetic relationships among Scolopacidae species based on mitochondrial genes (concatenated 12 protein-coding genes, 12S and 16S rRNA), using Bayesian inference (BI) and Maximum likelihood (ML). Numbers at nodes represent the Bayesian percent posterior probabilities and Maximum likelihood bootstrap values, separated by ‘/’.