

Table S1. Annotation of the mitochondrial genome of *M. stejnegeri*.

Gene	Nucleotide No.		Size(bp)	Codon		Spacer/ Overlap (-)	Strand
	From	To		Start	Stop		
D-loop	1	1071	1071				H
<i>trnF</i>	1072	1142	71			-1	H
<i>12S rRNA</i>	1142	2137	996			0	H
<i>trnV</i>	2138	2208	71			0	H
<i>16S rRNA</i>	2209	3810	1602			0	H
<i>trnL2</i>	3811	3884	74			6	H
<i>ND1</i>	3891	4868	978	ATG	AGG	-2	H
<i>trnI</i>	4867	4939	73			7	H
<i>trnQ</i>	4947	5017	71			-1	L
<i>trnM</i>	5017	5085	69			0	H
<i>ND2</i>	5086	6124	1039	ATG	T	0	H
<i>trnW</i>	6125	6200	76			3	H
<i>trnA</i>	6204	6272	69			1	L
<i>trnN</i>	6274	6346	73			0	L
<i>trnC</i>	6347	6412	66			0	L
<i>trnY</i>	6413	6482	70			1	L
<i>COX1</i>	6484	8034	1551	GTG	AGG	-9	H
<i>trnS2</i>	8026	8098	73			2	L
<i>trnD</i>	8101	8169	69			1	H
<i>COX2</i>	8171	8857	688	GTG	TAA	1	H
<i>trnK</i>	8859	8927	69			1	H
<i>ATP8</i>	8929	9096	168	ATG	TAA	-10	H
<i>ATP6</i>	9087	9770	684	ATG	TAA	-1	H
<i>COX3</i>	9770	10553	784	ATG	T	0	H
<i>trnG</i>	10554	10622	69			0	H
<i>ND3</i>	10623	10974	352	ATG	TAA	1	H
<i>trnR</i>	10976	11045	70			-1	H
<i>ND4L</i>	11046	11342	297	ATG	TAA	-7	H
<i>ND4</i>	11336	12713	1378	ATG	T	0	H
<i>trnH</i>	12714	12782	69			0	H
<i>trnS1</i>	12783	12848	66			-1	H
<i>trnL1</i>	12848	12918	71			-1	H
<i>ND5</i>	12919	14742	1824	GTG	TAA	-1	H
<i>CYTb</i>	14742	15884	1143	ATG	TAA	2	H
<i>trnT</i>	15887	15955	69			7	H
<i>trnP</i>	15963	16032	70			9	L
<i>ND6</i>	16042	16563	522	ATG	TAG	0	L
<i>trnE</i>	16564	16631	68				L

Table S2. Codon number and relative synonymous codon usage (RSCU) for the mitochondrial protein-coding genes (PCGs) of *M. stejnegeri*.

Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	42	0.38	UCU(S)	23	0.5	UAU(Y)	23	0.45	UGU(C)	3	0.21
UUC(F)	177	1.62	UCC(S)	94	2.06	UAC(Y)	79	1.55	UGC(C)	26	1.79
UUA(L)	37	0.33	UCA(S)	83	1.82	UAA(*)	7	2.8	UGA(W)	83	1.57
UUG(L)	14	0.13	UCG(S)	18	0.39	UAG(*)	1	0.4	UGG(W)	23	0.43
CUU(L)	42	0.38	CCU(P)	17	0.29	CAU(H)	11	0.2	CGU(R)	5	0.27
CUC(L)	181	1.62	CCC(P)	107	1.82	CAC(H)	101	1.8	CGC(R)	15	0.8
CUA(L)	285	2.55	CCA(P)	91	1.55	CAA(Q)	69	1.52	CGA(R)	37	1.97
CUG(L)	111	0.99	CCG(P)	20	0.34	CAG(Q)	22	0.48	CGG(R)	18	0.96
AUU(I)	48	0.35	ACU(T)	28	0.36	AAU(N)	8	0.13	AGU(S)	5	0.11
AUC(I)	223	1.65	ACC(T)	159	2.02	AAC(N)	112	1.87	AGC(S)	51	1.12
AUA(M)	104	1.22	ACA(T)	115	1.46	AAA(K)	74	1.66	AGA(*)	0	0
AUG(M)	67	0.78	ACG(T)	13	0.17	AAG(K)	15	0.34	AGG(*)	2	0.8
GUU(V)	32	0.65	GCU(A)	31	0.37	GAU(D)	7	0.22	GGU(G)	15	0.27
GUC(V)	66	1.33	GCC(A)	193	2.33	GAC(D)	57	1.78	GGC(G)	78	1.4
GUA(V)	71	1.43	GCA(A)	86	1.04	GAA(E)	72	1.52	GGA(G)	74	1.33
GUG(V)	29	0.59	GCG(A)	22	0.27	GAG(E)	23	0.48	GGG(G)	56	1

Table S3. Base composition of ribosomal and transfer RNA genes of *M. stejnegeri*.

	T%	C%	A%	G%	Size(bp)	A+T%	G+C%
<i>12S rRNA</i>	18.67	29.22	31.53	20.58	996	50.20	49.80
<i>16S rRNA</i>	19.79	25.66	34.33	20.22	1602	54.12	45.88
Avg	19.36	27.02	33.26	20.36	1299.00	52.62	47.38
<i>trnF</i>	12.68	30.99	33.80	22.54	71	46.48	53.52
<i>trnV</i>	21.13	28.17	29.58	21.13	71	50.70	49.30
<i>trnL2</i>	21.62	28.38	27.03	22.97	74	48.65	51.35
<i>trnI</i>	21.92	24.66	32.88	20.55	73	54.79	45.21
<i>trnQ</i>	39.44	9.86	29.58	21.13	71	69.01	30.99
<i>trnM</i>	20.29	33.33	27.54	18.84	69	47.83	52.17
<i>trnW</i>	25.00	25.00	34.21	15.79	76	59.21	40.79
<i>trnA</i>	36.23	14.49	28.99	20.29	69	65.22	34.78
<i>trnN</i>	28.77	17.81	27.40	26.03	73	56.16	43.84
<i>trnC</i>	24.24	22.73	16.67	36.36	66	40.91	59.09
<i>trnY</i>	37.14	17.14	20.00	25.71	70	57.14	42.86
<i>trnS2</i>	30.14	16.44	23.29	30.14	73	53.42	46.58
<i>trnD</i>	23.19	23.19	33.33	20.29	69	56.52	43.48
<i>trnK</i>	23.19	27.54	31.88	17.39	69	55.07	44.93
<i>trnG</i>	27.54	23.19	33.33	15.94	69	60.87	39.13
<i>trnR</i>	22.86	27.14	30.00	20.00	70	52.86	47.14
<i>trnH</i>	26.09	23.19	34.78	15.94	69	60.87	39.13
<i>trnS1</i>	22.73	27.27	25.76	24.24	66	48.48	51.52
<i>trnL1</i>	25.35	22.54	32.39	19.72	71	57.75	42.25
<i>trnT</i>	28.99	18.84	34.78	17.39	69	63.77	36.23
<i>trnP</i>	35.71	11.43	27.14	25.71	70	62.86	37.14
<i>trnE</i>	26.47	17.65	25.00	30.88	68	51.47	48.53
Avg	26.39	22.32	29.11	22.19	70.27	55.50	44.50

Table S4. Accession numbers of 76 Anseriformes species and one outgroup.

Family	Genus	Species name	Data sources	Accession number	Mitogenome	Genome
Anatidae	<i>Aix</i>	<i>Aix galericulata</i>	Mitogenome	NC_023969, GCA_024635365.1	✓	✓
		<i>A. sponsa</i>	Genome, nucleotides	GCA_032270905, EU585668.1, AF173741.1	NA	✓
	<i>Anas</i>	<i>Anas acuta</i>	Mitogenome	NC_024631, GCA_963932015.1	✓	✓
		<i>A. bernieri</i>	Genome, nucleotides	GCA_032165215, AF059121.1	NA	✓
		<i>A. capensis</i>	Genome	GCA_032357685	NA	✓
		<i>A. chathamica</i>	Mitogenome	KF562761	✓	NA
		<i>A. crecca</i>	Mitogenome	KF203133, GCA_036873605.1	✓	✓
		<i>A. georgica</i>	Genome	GCA_032275265	NA	✓
		<i>A. platyrhynchos</i>	Mitogenome	MW354666, GCA_015476345.1	✓	✓
		<i>A. poecilorhyncha</i>	Mitogenome	KF156760, GCA_040966495.1	✓	✓
		<i>A. zonorhyncha</i>	Mitogenome	MZ593724, GCA_002224875.1	✓	✓
	<i>Anser</i>	<i>Anser albifrons</i>	Mitogenome	NC_004539	✓	NA
		<i>A. anser</i>	Mitogenome	NC_011196, GCA_964211835.1	✓	✓
		<i>A. brachyrhynchus</i>	Mitogenome	OZ035927.1, GCA_002592135.1	✓	✓
		<i>A. cygnoides</i>	Mitogenome	NC_023832, GCA_040182565.1	✓	✓
		<i>A. fabalis</i>	Mitogenome	HQ890328	✓	NA
		<i>A. indicus</i>	Mitogenome	NC_025654, GCA_025583725.1	✓	✓
	<i>Asarcornis</i>	<i>Asarcornis scutulata</i>	Mitogenome	NC_052827, GCA_013398475.1	✓	✓
	<i>Aythya</i>	<i>Aythya americana</i>	Mitogenome	NC_000877	✓	NA
		<i>A. baeri</i>	Mitogenome	NC_057048, GCA_026413565.1	✓	✓
		<i>A. ferina</i>	Mitogenome	NC_024602, GCA_964211825.1	✓	✓
		<i>A. fuligula</i>	Mitogenome	OQ979258, GCA_009819795.1	✓	✓
		<i>A. marila</i>	Mitogenome	NC_068663, GCA_029042245.1	✓	✓
		<i>A. nyroca</i>	Mitogenome	NC_059801	✓	NA
		<i>Bucephala albeola</i>	Mitogenome	MW849286	✓	NA
	<i>Bucephala</i>	<i>B. clangula</i>	Mitogenome	MW849283, GCA_964059595.1	✓	✓
		<i>B. islandica</i>	Mitogenome	MW849281	✓	NA
		<i>Branta bernicla</i>	Mitogenome	KJ680301	✓	NA
	<i>Branta</i>	<i>B. canadensis</i>	Mitogenome	NC_007011, GCA_006130075.1	✓	✓
		<i>B. hutchinsii</i>	Genome, nucleotides	GCA_032270845, FJ582576.1	NA	✓
	<i>Cairina</i>	<i>Cairina moschata</i>	Mitogenome	NC_010965, GCA_018104995.1	✓	✓
	<i>Clangula</i>	<i>Clangula hyemalis</i>	Mitogenome	MW077850, GCA_963989345.1	✓	✓
	<i>Cygnus</i>	<i>Cygnus atratus</i>	Mitogenome	NC_012843, GCA_013377495.2	✓	✓

	<i>C. buccinator</i>	Genome, nucleotides	GCA_019232035, AY666404.1, AY509690.1, EF165358.1	NA	✓
	<i>C. columbianus bewickii</i>	Mitogenome	NC_017604	✓	NA
	<i>C. cygnus</i>	Mitogenome	KP981363, GCA_014362685.1	✓	✓
	<i>C. olor</i>	Mitogenome	NC_027096, GCA_009769625.2	✓	✓
<i>Dendrocygna</i>	<i>Dendrocygna javanica</i>	Mitogenome	NC_012844	✓	NA
<i>Heteronetta</i>	<i>Heteronetta atricapilla</i>	Genome	GCA_011075105	NA	✓
<i>Histrionicus</i>	<i>Histrionicus histrionicus</i>	Mitogenome	MW849288	✓	NA
<i>Lophodytes</i>	<i>Lophodytes cucullatus</i>	Mitogenome	MW849287	✓	NA
<i>Lophonetta</i>	<i>Lophonetta specularioides</i>	Genome	GCA_032165235	NA	✓
<i>Mareca</i>	<i>Mareca americana</i>	Mitogenome	NC_088449.1, GCA_035588595.1	✓	✓
	<i>M. falcata</i>	Mitogenome	MW020580, GCA_038382085.1	✓	✓
	<i>M. penelope</i>	Mitogenome	MW020582, GCA_036026335.1	✓	✓
	<i>M. sibilatrix</i>	Genome, nucleotides	GCA_034783215, FJ027105.1, EU914149.1, AF059168.1	NA	✓
	<i>M. strepera</i>	Mitogenome	NC_045373, GCA_035583915.1	✓	✓
<i>Melanitta</i>	<i>Melanitta americana</i>	Mitogenome	MW849282	✓	NA
	<i>M. deglandi</i>	Mitogenome	MW849279	✓	NA
	<i>M. fusca</i>	Genome	GCA_029620185	NA	✓
	<i>M. perspicillata</i>	Mitogenome	MW849280	✓	NA
	<i>M. stejnegeri</i>	Mitogenome	PP990569	✓	NA
<i>Mergus</i>	<i>Mergus merganser</i>	Mitogenome	NC_040986	✓	NA
	<i>M. serrator</i>	Mitogenome	MZ365040	✓	NA
	<i>M. squamatus</i>	Mitogenome	NC_016723	✓	NA
<i>Netta</i>	<i>Netta rufina</i>	Mitogenome	NC_024922, GCA_964035555.1	✓	✓
<i>Nettapus</i>	<i>Nettapus auritus</i>	Genome	GCA_011076525	NA	✓
<i>Oxyura</i>	<i>Oxyura jamaicensis</i>	Mitogenome	MW574354, GCA_011077185.1	✓	✓
<i>Polysticta</i>	<i>Polysticta stelleri</i>	Mitogenome	MW849289	✓	NA
<i>Sibirionetta</i>	<i>Sibirionetta formosa</i>	Mitogenome	NC_015482, GCA_038406215.1	✓	✓
<i>Somateria</i>	<i>Somateria fischeri</i>	Mitogenome	MW849290	✓	NA
	<i>S. mollissima</i>	Mitogenome	MW849292, GCA_951411735.1	✓	✓
	<i>S. spectabilis</i>	Mitogenome	MW849291	✓	NA
<i>Spatula</i>	<i>Spatula clypeata</i>	Mitogenome	KT345702, GCA_038406095.1	✓	✓
	<i>S. discors</i>	Genome	GCA_032165275	NA	✓
	<i>S. querquedula</i>	Genome, nucleotides	GCA_032191525, AF059146.1	NA	✓
	<i>S. rhynchotis</i>	Genome	GCA_034783165	NA	✓
	<i>S. smithii</i>	Genome	GCA_035221675	NA	✓

	<i>Speculanas</i>	<i>Speculanas specularis</i>	Genome, nucleotides	GCA_032165255, AF059150.1	NA	√
	<i>Stictonetta</i>	<i>Stictonetta naevosa</i>	Genome	GCA_011074415	NA	√
	<i>Tachyeres</i>	<i>Tachyeres brachypterus</i>	Genome	GCA_032357605	NA	√
		<i>T. leucocephalus</i>	Genome	GCA_034780855	NA	√
	<i>Tadorna</i>	<i>Tadorna ferruginea</i>	Mitogenome	NC_024640	√	NA
		<i>T. tadorna</i>	Mitogenome	KU140668	√	NA
Anseranatidae	<i>Anseranas</i>	<i>Anseranas semipalmata</i>	Mitogenome	MN356217, GCA_013399115.1	√	√
Anhimidae	<i>Chauna</i>	<i>Chauna torquata</i>	Mitogenome	NC_052807, GCA_013399475.1	√	√
Phasianidae	<i>Gallus</i>	<i>Gallus gallus</i>	Mitogenome	MH732978.1, GCA_018104995.1	√	√
