

Supplementary material

Supplementary Table 1. Complete annelid mitochondrial genomes. Data obtained from GenBank. Gene order of protein coding and ribosomal genes are either referred to as “Pleisto” for the ground pattern of Pleistoannelida, or “other” for different gene orders.

Taxon	higher Taxon	Authors	Gene order	Length	AT
<i>Eurythoe complanata</i>	Amphinomida	Weigert et al. (2016)	other	15829	58.2
<i>Phyllochaetopterus</i> sp.	Chaetopteridae	Weigert et al. (2016)	other	16087	58.1
<i>Chaetopterus variopedatus</i>	Chaetopteridae	Weigert et al. (2016)	other	16143	64.4
<i>Erpobdella octoculata</i>	Clitellata	Xu and Nie (2016)	Pleisto	14407	71.6
<i>Whitmania acranulata</i>	Clitellata	NC_023928	Pleisto	14462	71.6
<i>Whitmania laevis</i>	Clitellata	Ye et al. (2015)	Pleisto	14442	73.0
<i>Whitmania laevis</i>	Clitellata	NC_023926	Pleisto	14433	71.9
<i>Whitmania pigra</i>	Clitellata	Shen et al. (2011)	Pleisto	14426	72.2
<i>Amyntas corticis</i>	Clitellata	Zhang et al. (2015)	Pleisto	15126	66.3
<i>Amyntas longisiphonis</i>	Clitellata	Zhang et al. (2015)	Pleisto	15176	66.2
<i>Amyntas gracilis</i>	Clitellata	Zhang et al. (2015)	Pleisto	15161	65.9
<i>Amyntas aspergillus</i>	Clitellata	NC_025292	Pleisto	15115	63.0
<i>Amyntas jiriensis</i>	Clitellata	Hong et al. (2015)	Pleisto	15151	?
<i>Amyntas carnosus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15160	62.6
<i>Amyntas hupeiensis</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15069	65.9
<i>Amyntas pectiniferus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15188	66.2
<i>Amyntas morrissi</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15026	65.4
<i>Amyntas robustus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15013	64.9
<i>Amyntas triastriatus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15160	65.3
<i>Amyntas instabilis</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15159	64.9
<i>Amyntas cucullatus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15122	64.8
<i>Amyntas redactus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15131	67.6
<i>Amyntas moniliatus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15133	66.7
<i>Amyntas spatiosus</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15152	66.2
<i>Amyntas rongshuiensis</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15086	67.2

Taxon	higher Taxon	Authors	Gene order	Length	AT
<i>Hirudo medicinalis</i>	Clitellata	Nikitina et al. (2016)	Pleisto	14729	tba
<i>Hirudo nipponia</i>	Clitellata	Xu et al. (2016)	Pleisto	14414	72.6
<i>Hirudo verbana</i>	Clitellata	Nikitina et al. (2016)	Pleisto	14604	tba
<i>Metaphire californica</i>	Clitellata	Zhang et al. (2015)	Pleisto	15147	64.1
<i>Metaphire guillelmi</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15174	65.3
<i>Metaphire schmardae</i>	Clitellata	Zhang et al. (2016b)	Pleisto	15156	66.7
<i>Metaphire vulgaris</i>	Clitellata	Zhang et al. (2016a)	Pleisto	15061	64.6
<i>Tonoscolex birmanicus</i>	Clitellata	Wang et al. (2015)	Pleisto	15170	63.3
<i>Drawida japonica</i>	Clitellata	Zhang et al. (2016b)	Pleisto	14648	69.7
<i>Perionyx excavatus</i>	Clitellata	NC_009631	Pleisto	15083	64.5
<i>Lumbricus terrestris</i>	Clitellata	Boore and Brown (1995)	Pleisto	14998	61.6
<i>Poecilobdella manillensis</i>	Clitellata	NC_023925	Pleisto	14470	71.2
<i>Urechis caupo</i>	Echiura	Boore (2004)	other	15113	62.0
<i>Urechis unicinctus</i>	Echiura	Wu et al. (2009)	other	15761	61.9
<i>Marphysa sanguinea</i>	Eunicidae	Li et al. (2016)	Pleisto	15159	61.0
<i>Glycera oxycephala</i>	Glyceridae	Richter et al. (2015)	Pleisto	15852	66.4
<i>Glycera fallax</i>	Glyceridae	Richter et al. (2015)	Pleisto	20896	64.2
<i>Glycera americana FS10</i>	Glyceridae	Richter et al. (2015)	Pleisto	15271	66.6
<i>Glycera americana FS12</i>	Glyceridae	Richter et al. (2015)	Pleisto	15571	66.7
<i>Glycera tridactyla</i>	Glyceridae	Richter et al. (2015)	Pleisto	15361	66.7
<i>Glycera</i> cf. <i>tridactyla</i> FS19	Glyceridae	Richter et al. (2015)	Pleisto	15373	66.7
<i>Glycera</i> cf. <i>tridactyla</i> FS20	Glyceridae	Richter et al. (2015)	Pleisto	15510	66.1
<i>Glycera tessellata</i>	Glyceridae	Richter et al. (2015)	Pleisto	15591	68.6
<i>Glycera capitata FS10</i>	Glyceridae	Richter et al. (2015)	Pleisto	15182	66.6
<i>Glycera capitata FS11</i>	Glyceridae	Richter et al. (2015)	Pleisto	15178	66.6
<i>Glycera dibranchiata</i>	Glyceridae	Richter et al. (2015)	Pleisto	16085	66.5
<i>Glycera unicornis</i>	Glyceridae	Richter et al. (2015)	Pleisto	20366	62.0
<i>Hemipodia simplex</i>	Glyceridae	Richter et al. (2015)	Pleisto	15401	63.7
<i>Glycinde armigera</i>	Glyceridae	Richter et al. (2015)	Pleisto	15077	68.5
<i>Goniada japonica</i>	Goniadidae	Chen et al. (2015a)	Pleisto	15327	68.7

Taxon	higher Taxon	Authors	Gene order	Length	AT
<i>Magelona mirabilis</i>	Magelonidae	Weigert et al. (2016)	other	15239	63.5
<i>Clymenella torquata</i>	Maldanidae	Jennings and Halanych (2005)	Pleisto	15538	67.2
<i>Nephtys</i> sp.	Nephtyidae	Vallès et al. (2008)	Pleisto	17217	63.4
<i>Platynereis dumerilii</i>	Nereididae	Boore and Brown (2000)	Pleisto	15619	64.1
<i>Perinereis aibuhitensis</i>	Nereididae	Kim et al. (2015)	Pleisto	15852	64.6
<i>Perinereis nuntia</i>	Nereididae	Won et al. (2013)	Pleisto	15824	65.1
<i>Tylorrhynchus heterochaetus</i>	Nereididae	Chen et al. (2015b)	Pleisto	16106	65.0
<i>Orbinia latreillii</i>	Orbiniidae	Bleidorn et al. (2006)	Pleisto	15558	61.1
<i>Owenia fusiformis</i>	Oweniidae	Weigert et al. (2016)	other	16204	69.6
<i>Ridgeia piscesae</i>	Siboglinidae	Jun et al. (2016)	Pleisto	15002	63.2
<i>Siboglinum fiordicum</i>	Siboglinidae	Li et al. (2015)	Pleisto	19502	74.5
<i>Sclerolinum brattstromi</i>	Siboglinidae	Li et al. (2015)	Pleisto	15383	64.9
<i>Escarpia spicata</i>	Siboglinidae	Li et al. (2015)	Pleisto	15445	66.1
<i>Galathealinum brachiosum</i>	Siboglinidae	Li et al. (2015)	Pleisto	14779	77.9
<i>Lamellibrachia luymesii</i>	Siboglinidae	Li et al. (2015)	Pleisto	14991	64.6
<i>Lamellibrachia satsuma</i>	Siboglinidae	Patra et al. (2016)	Pleisto	15037	65.6
<i>Oasisia alvinae</i>	Siboglinidae	Li et al. (2015)	Pleisto	14849	64.9
<i>Riftia pachyptila</i>	Siboglinidae	Li et al. (2015)	Pleisto	14987	66.8
<i>Seepiophila jonesi</i>	Siboglinidae	Li et al. (2015)	Pleisto	15092	64.8
<i>Tevnia jerichonana</i>	Siboglinidae	Li et al. (2015)	Pleisto	14891	64.5
<i>Escarpia spicata</i>	Siboglinidae	Li et al. (2015)	Pleisto	15445	66.1
<i>Spirobrachia</i> sp.	Siboglinidae	Li et al. (2015)	Pleisto	15581	74.6
<i>Sipunculus nudus</i>	Sipuncula	Song et al. (2016)	other	15376	58.0
<i>Sipunculus nudus</i>	Sipuncula	Mwinyi et al. (2009)	other	15502	54.2
<i>Phascolosma esculenta</i>	Sipuncula	Shen et al. (2009)	other	15494	65.5
<i>Ramisyllis multicaudata</i>	Syllidae	Aguado et al. (2015)	other	15748	66.6
<i>Trypanobia cryptica</i>	Syllidae	Aguado et al. (2015)	other	16630	68.9
<i>Streptosyllis</i> sp.	Syllidae	this study	other	14983	74.4
<i>Eusyllis blomstrandii</i>	Syllidae	this study	Pleisto	14712	71.1

Taxon	higher Taxon	Authors	Gene order	Length	AT
<i>Myrianida brachycephala</i>	Syllidae	this study	Pleisto	15032	69.5
<i>Typosyllis antoni</i>	Syllidae	this study	other	16902	70.7
<i>Typosyllis</i> sp.	Syllidae	this study	other	16241	67.1
<i>Pista cristata</i>	Terebellidae	Zhong et al. (2008)	Pleisto	15894	68.1
<i>Terebellides stroemii</i>	Trichobranchidae	Zhong et al. (2008)	Pleisto	15755	67.2

Supplementary Table 2. Gene content of the mitochondrial genome of *Streptosyllis* sp.

Name	Start	Stop	Strand	Start codon	Stop codon
nad1	85	1011	+	ATG	TAA
cox1	1013	2548	+	ATG	TAA
cox2	2606	3313	+	ATA	TAA
trnD	3288	3348	+		
atp6	3351	4034	+	ATG	TAA
trnH	4039	4096	+		
nad5	4124	5759	+	AGA	T
trnE	5796	5854	+		
nad4L	5993	6294	+	AAG	TA
nad4	6325	7641	+	ATA	TAA
trnN	7613	7673	+		
trnS2	7674	7726	+		
trnL2	7731	7783	+		
trnA	7784	7842	+		
atp8	7843	7998	+	ATG	TAA
cox3	8007	8789	+	ATG	TAA
trnQ	8785	8844	+		
nad6	8854	9318	+	ATT	TAA
cob	9311	10444	+	ATG	TAA
trnW	10443	10502	+		
trnF	10631	10690	+		
trnP	10696	10756	+		
trnC	10762	10822	+		
trnM	10825	10885	+		
rrnS	11005	11537	+		
rrnL	11982	12569	+		
trnL1	12621	12680	+		
nad3	12837	13199	+	ATA	TAG
nad2	13300	14253	+	ATG	TAG
trnI	14260	14320	+		

trnK	14320	14381	+		
trnY	14382	14443	+		
trnG	14444	14502	+		
trnR	14503	14556	+		
trnV	14562	14621	+		
trnT	14624	14684	+		
trnS1	14690	14739	+		

Supplementary Table 3. Gene content of the mitochondrial genome of *Eusyllis blomstrandii*

Name	Start	Stop	Strand	Start codon	Stop codon
nad1	128	1051	+	ATG	TAA
trnI	1050	1111	+		
trnK	1112	1175	+		
nad3	1176	1529	+	ATG	TAG
trnS1	1528	1593	+		
nad2	1594	2592	+	ATG	TAA
cox1	2596	4152	+	ATG	TAG
cox2	4160	4843	+	ATG	TAA
trnD	4842	4904	+		
atp8	4905	5066	+	ATG	TAA
trnY	5062	5122	+		
cox3	5123	5905	+	ATG	TAA
trnQ	5901	5963	+		
nad6	5964	6467	+	ATG	TAA
cob	6430	7560	+	ATG	TAA
trnW	7559	7618	+		
atp6	7619	8317	+	ATG	TAA
trnR	8316	8365	+		
trnH	8366	8428	+		
nad5	8429	10168	+	ATG	TAA
trnF	10168	10227	+		
trnE	10231	10286	+		

trnP	10287	10348	+		
trnT	10349	10409	+		
nad4L	10392	10706	+	ATG	TAA
nad4	10700	12034	+	ATG	TAG
trnS2	12033	12099	+		
trnL2	12101	12161	+		
trnG	12164	12220	+		
trnM	12223	12283	+		
rrnS	12282	13024	+		
trnV	13017	13077	+		
rrnL	13213	14213	+		
trnL1	14240	14299	+		
trnN	14300	14360	+		
trnC	14361	14422	+		
trnA	14423	14484	+		

Supplementary Table 4. Gene content of the mitochondrial genome of *Myrianida brachycephala*

Name	Start	Stop	Strand	Start codon	Stop codon
nad1	620	1540	+	ATG	TAA
trnI	1539	1601	+		
nad3	1602	1943	+	ATG	TAA
trnS1	1942	2009	+		
nad2	2010	2993	+	ATG	TAA
cox1	2995	4530	+	ATG	TAA
cox2	4541	5227	+	ATG	TAG
trnD	5227	5290	+		
atp8	5291	5452	+	ATG	TAA
trnY	5457	5516	+		
cox3	5518	6297	+	ATG	TAA
trnQ	6301	6361	+		
nad6	6362	6859	+	ATG	TAA
cob	6822	7961	+	ATG	TAA

trnW	7960	8021	+		
atp6	8022	8717	+	ATG	TAA
trnR	8717	8770	+		
trnH	8769	8831	+		
nad5	8832	10553	+	ATG	TAA
trnF	10553	10615	+		
trnT	10616	10676	+		
nad4L	10677	10967	+	ATG	TAA
nad4	10961	12301	+	ATG	TAA
trnS2	12300	12365	+		
trnL2	12366	12428	+		
trnK	12430	12486	+		
trnG	12487	12548	+		
trnM	12559	12622	+		
rrnS	12621	13377	+		
trnV	13370	13432	+		
rrnL	13567	14578	+		
trnL1	14609	14669	+		
trnC	14670	14731	+		
trnE	14732	14794	+		
trnP	14795	14858	+		
trnN	14861	14924	+		
trnA	14923	14984	+		

Supplementary Table 5. Gene content of the mitochondrial genome of *Typosyllis antoni*

Name	Start	Stop	Strand	Start codon	Stop codon
cox3	986	1783	+	ATA	TAA
nad6	1948	2415	+	ATA	TAA
trnF	2414	2475	+		
trnD	2478	2533	+		
trnT	2534	2596	+		
trnS2	2597	2654	+		

trnK	2654	2714	+		
trnY	2715	2776	+		
rrnL	2927	3927	+		
nad2	3951	4958	+	ATG	TAG
trnR	4942	4998	+		
trnS1	4997	5064	+		
trnE	5062	5124	+		
trnV	5126	5185	+		
trnI	5187	5249	+		
atp8	5250	5417	+	ATG	TAA
cob	5596	6729	+	ATG	TAA
nad3	6731	7126	+	ATG	TAA
trnN	7092	7152	+		
trnM	7153	7212	+		
trnM	7221	7281	+		
nad5	7339	9314	+	ATG	TA
nad1	9293	10225	+	ATG	TAA
cox2	10233	10916	+	ATA	TAA
trnA	10919	10980	+		
nad4	10981	12309	+	ATG	TAA
nad4L	12381	12647	+	ATA	TAG
trnL1	12649	12711	+		
rrnS	12715	13592	+		
trnW	13597	13659	+		
trnH	13664	13725	+		
trnG	13797	13860	+		
trnC	14002	14052	+		
atp6	14090	14785	+	TTG	TAG
trnL2	14806	14867	+		
cox1	14914	16503	+	ATA	TAA
trnQ	16610	16671	+		
trnP	16795	16858	+		

Supplementary Table 6. Gene content of the mitochondrial genome of *Typosyllis* sp.

Name	Start	Stop	Strand	Start codon	Stop codon
cox3	664	1473	+	ATA	TAA
trnC	1486	1536	+		
nad6	1537	2007	+	ATG	TAG
trnF	2011	2071	+		
trnD	2072	2128	+		
trnQ	2181	2239	+		
trnT	2541	2601	+		
trnS2	2602	2657	+		
trnK	2658	2718	+		
trnY	2721	2780	+		
rrnL	2926	3927	+		
nad2	3943	4927	+	ATG	T
trnR	4935	4988	+		
trnS1	4998	5056	+		
trnE	5054	5117	+		
trnV	5120	5179	+		
trnI	5181	5244	+		
atp8	5239	5396	+	ATA	TA
cob	5396	6556	+	ATG	TAA
nad3	6560	6922	+	ATG	TAA
trnN	6924	6987	+		
trnM	6988	7047	+		
trnM	7049	7108	+		
nad5	7172	9119	+	ATA	T
nad1	9120	10052	+	ATG	TAA
cox2	10137	10818	+	ATA	T
trnA	10821	10882	+		
nad4	10883	12211	+	GTG	TAA
nad4L	12240	12515	+	ATG	TAA
trnL1	12511	12573	+		

rrnS	12577	13481	+		
trnW	13476	13539	+		
trnP	13541	13603	+		
trnG	13615	13675	+		
trnL2	13677	13738	+		
atp6	13773	14480	+	GTG	TAA
trnH	14497	14560	+		
cox1	14621	16143	+	ATG	TAA

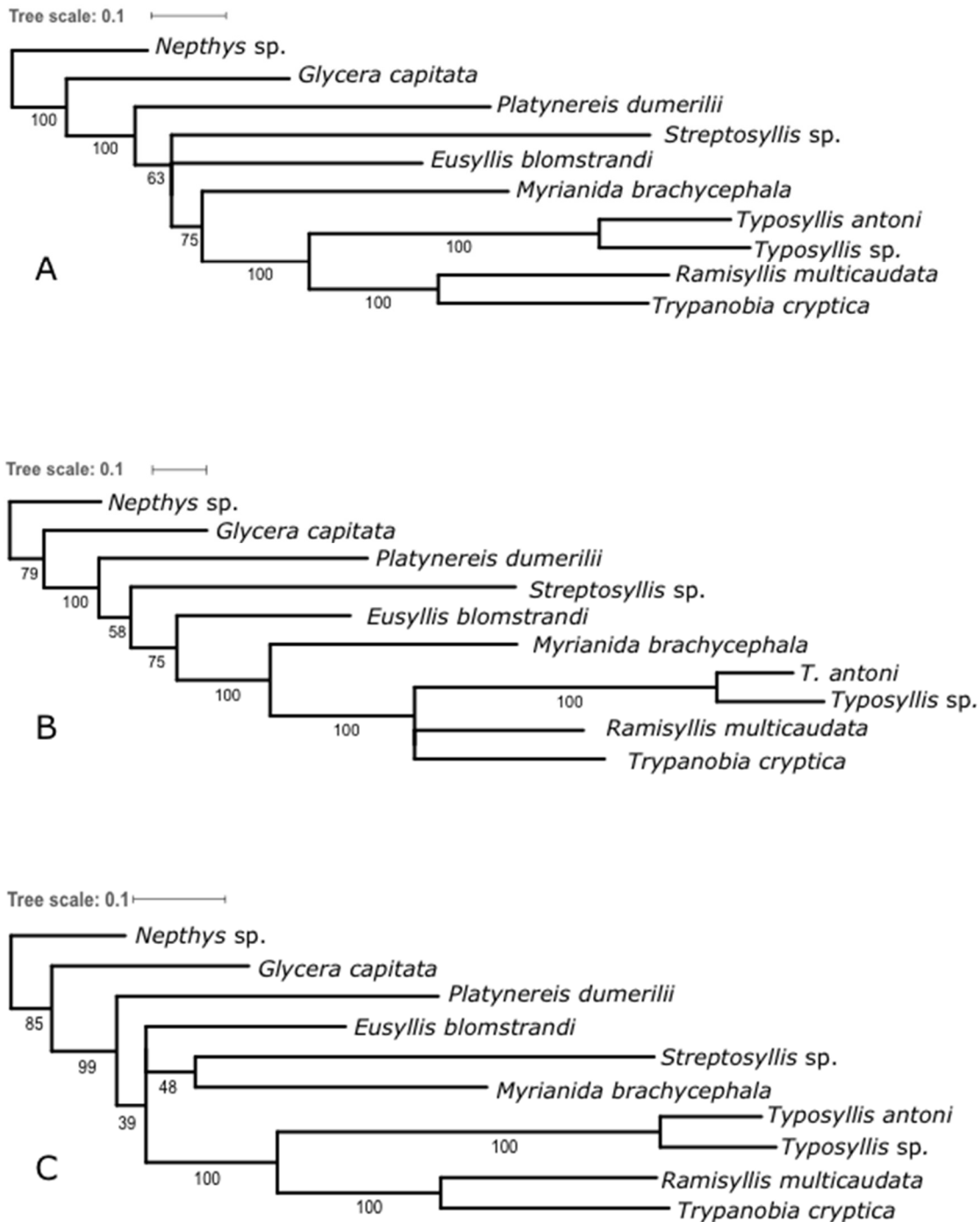
Supp. Table 7. Codon usage. The relative synonymous codon usage (RSCU) is the number of times a codon appears in a gene divided by the number of expected occurrences under equal codon usage. If the synonymous codons of an amino acid are used with equal frequencies, their RSCU values will equal 1.

Codon	AA	<i>Streptosyllis</i> sp.		<i>Eusyllis blomstrandii</i>		<i>Myrianida brachycephala</i>		<i>Typosyllis antoni</i>		<i>Typosyllis</i> sp.	
		Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU
UAG	*	56	0,554	39	0,619	76	0,623	40	0,65	47	0,623
UAA	*	146	1,446	87	1,381	168	1,377	83	1,35	104	1,377
GCU	A	29	2	39	1,545	30	1,481	49	1,289	18	0,935
GCG	A	8	0,552	9	0,356	6	0,296	7	0,184	5	0,26
GCC	A	10	0,69	24	0,95	16	0,79	36	0,947	31	1,61
GCA	A	11	0,759	29	1,149	29	1,432	60	1,579	23	1,195
UGU	C	71	1,315	37	0,804	31	1,265	28	0,933	33	0,835
UGC	C	37	0,685	55	1,196	18	0,735	32	1,067	46	1,165
GAU	D	43	1,593	38	1,462	41	1,281	48	1,352	34	1,333
GAC	D	11	0,407	14	0,538	23	0,719	23	0,648	17	0,667
GAG	E	28	0,875	17	0,944	21	0,627	18	0,621	26	0,912
GAA	E	36	1,125	19	1,056	46	1,373	40	1,379	31	1,088
UUU	F	430	1,575	287	1,688	193	1,282	215	1,514	166	1,419
UUC	F	116	0,425	53	0,312	108	0,718	69	0,486	68	0,581
GGU	G	50	1,613	37	0,98	26	0,765	20	0,576	11	0,571
GGG	G	26	0,839	56	1,483	42	1,235	29	0,835	29	1,506
GGC	G	21	0,677	24	0,636	22	0,647	24	0,691	19	0,987
GGA	G	27	0,871	34	0,901	46	1,353	66	1,899	18	0,935
CAC	H	15	0,588	34	0,819	37	0,529	46	0,807	64	0,715
CAU	H	36	1,412	49	1,181	103	1,471	68	1,193	115	1,285
AUU	I	227	1,627	281	1,523	175	1,362	253	1,454	202	1,418
AUC	I	52	0,373	88	0,477	82	0,638	95	0,546	83	0,582
AAA	K	96	1,255	111	1,396	75	1,389	135	1,543	126	1,44
AAG	K	57	0,745	48	0,604	33	0,611	40	0,457	49	0,56
CUA	L	32	0,719	45	0,905	113	1,507	83	1,372	68	1,092
CUC	L	34	0,764	55	1,106	55	0,733	44	0,727	69	1,108
CUG	L	20	0,449	14	0,281	30	0,4	15	0,248	16	0,257

Codon	AA	<i>Streptosyllis</i> sp.		<i>Eusyllis blomstrandii</i>		<i>Myrianida brachycephala</i>		<i>Typosyllis antoni</i>		<i>Typosyllis</i> sp.	
		Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU
CUU	L	92	2,067	85	1,709	102	1,36	100	1,653	96	1,542
UUA	L	138	1,302	191	1,547	198	1,565	242	1,786	128	1,488
UUG	L	74	0,698	56	0,453	55	0,435	29	0,214	44	0,512
AUG	M	39	0,765	41	0,503	47	0,614	41	0,352	74	0,855
AUA	M	63	1,235	122	1,497	106	1,386	192	1,648	99	1,145
AAC	N	54	0,427	80	0,582	42	0,494	77	0,716	96	0,711
AAU	N	199	1,573	195	1,418	128	1,506	138	1,284	174	1,289
CCU	P	25	1,449	60	1,569	79	1,646	53	1,254	62	1,285
CCG	P	9	0,522	11	0,288	6	0,125	9	0,213	13	0,269
CCC	P	20	1,159	45	1,176	67	1,396	45	1,065	62	1,285
CCA	P	15	0,87	37	0,967	40	0,833	62	1,467	56	1,161
CAG	Q	8	0,4	8	0,356	13	0,394	15	0,337	30	0,561
CAA	Q	32	1,6	37	1,644	53	1,606	74	1,663	77	1,439
CGA	R	6	1,043	21	1,867	18	1,532	32	2,246	15	0,769
CGC	R	5	0,87	12	1,067	11	0,936	11	0,772	29	1,487
CGG	R	3	0,522	2	0,178	7	0,596	2	0,14	10	0,513
CGU	R	9	1,565	10	0,889	11	0,936	12	0,842	24	1,231
AGC	S	38	0,762	55	1,125	34	0,723	28	0,626	70	1,092
AGA	S	44	0,882	49	1,003	34	0,723	58	1,296	50	0,78
UCA	S	68	1,363	75	1,535	53	1,128	91	2,034	96	1,497
UCC	S	46	0,922	38	0,777	68	1,447	43	0,961	56	0,873
UCG	S	16	0,321	13	0,266	16	0,34	16	0,358	16	0,25
UCU	S	76	1,524	64	1,309	118	2,511	74	1,654	93	1,45
AGG	S	57	1,143	41	0,839	25	0,532	21	0,469	67	1,045
AGU	S	54	1,083	56	1,146	28	0,596	27	0,603	65	1,014
ACA	T	27	0,908	57	1,382	42	0,875	99	1,65	57	0,942
ACC	T	35	1,176	30	0,727	57	1,188	49	0,817	64	1,058
ACG	T	12	0,403	15	0,364	20	0,417	17	0,283	29	0,479
ACU	T	45	1,513	63	1,527	73	1,521	75	1,25	92	1,521

Codon	AA	<i>Streptosyllis</i> sp.		<i>Eusyllis blomstrandii</i>		<i>Myrianida brachycephala</i>		<i>Typosyllis antoni</i>		<i>Typosyllis</i> sp.	
		Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU	Obs Freq	RSCU
GUC	V	15	0,451	16	0,485	14	0,528	14	0,509	22	1,1
GUG	V	18	0,541	22	0,667	9	0,34	12	0,436	16	0,8
GUU	V	84	2,526	60	1,818	46	1,736	34	1,236	20	1
GUA	V	16	0,481	34	1,03	37	1,396	50	1,818	22	1,1
UGA	W	63	0,992	62	1,148	43	1,194	68	1,6	48	1,055
UGG	W	64	1,008	46	0,852	29	0,806	17	0,4	43	0,945
UAC	Y	53	0,398	63	0,439	82	0,521	64	0,598	83	0,648
UAU	Y	213	1,602	224	1,561	233	1,479	150	1,402	173	1,352

Supplementary Figure 1. A. Maximum likelihood tree obtained when analyzing nucleotides from protein coding genes and *rrnL* and *rrnS*, ambiguous regions not excluded; B. Maximum likelihood tree obtained when analyzing amino acids partition data sets from protein coding genes, ambiguous regions not excluded; C. Maximum likelihood tree obtained when analyzing amino acids partition data sets from protein coding genes, ambiguous regions excluded. Bootstrap support values below nodes.



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