

**Supplementary Table S1.** Nucleotide codon usage for 12 protein-coding genes of the mitochondrial genome of *Spiruromorpha*

nematode species

Am Acid	Co don	Number and percentage																			
		<i>B. m.</i>		<i>W. b.</i>		<i>M. p.</i>		<i>C. m.</i>		<i>C. l.</i>		<i>S. d.</i>		<i>G. p.</i>		<i>H. l.</i>		<i>S. l.</i>		<i>M. m.</i>	
Ala	GC	4	0.1%	2	0.1%	3	0.1%	1	0.4%	3	0.1%	0	0.0%	5	0.2%	1	0.03	5	0.2%	9	0.3%
Ala	GC	7	0.2%	2	0.1%	1	0.03	6	0.2%	9	0.3%	0	0.0%	1	0.3%	1	0.3%	5	0.2%	5	0.1%
Ala	GC	5	1.7%	7	2.1%	6	1.9%	5	1.7%	5	1.6%	7	2.2%	6	2.0%	5	1.6%	6	2.0%	7	2.3%
Ala	GC	1	0.4%	3	0.1%	5	0.2%	7	0.2%	1	0.5%	0	0.0%	2	0.1%	9	0.3%	2	0.1%	2	0.1%
Cys	TG	9	2.8%	1	3.0%	9	2.7%	9	2.7%	9	2.8%	9	2.7%	8	2.5%	7	2.1%	8	2.4%	8	2.5%
Cys	TG	8	0.2%	3	0.1%	3	0.1%	4	0.1%	1	0.3%	2	0.1%	2	0.1%	3	0.1%	3	0.1%	4	0.1%
Asp	GA	8	2.4%	8	2.4%	8	2.5%	7	2.1%	7	2.1%	8	2.4%	7	2.2%	6	2.0%	7	2.0%	7	2.1%
Asp	GA	7	0.2%	4	0.1%	4	0.1%	7	0.2%	1	0.4%	2	0.1%	4	0.1%	3	0.1%	4	0.1%	1	0.03
Glu	GA	3	0.9%	4	1.2%	4	1.3%	3	1.1%	5	1.6%	3	1.1%	3	1.0%	2	0.8%	3	1.1%	4	1.2%
Glu	GA	2	0.8%	1	0.6%	2	0.6%	2	0.8%	1	0.3%	2	0.6%	3	1.0%	3	1.1%	3	1.0%	2	0.8%
Phe	TT	5	17.5	6	18.0	5	16.8	6	17.6	5	16.0	6	18.6	6	18.2	6	18.0	5	16.9	5	16.3
Phe	TT	1	0.4%	1	0.4%	1	0.5%	1	0.3%	9	0.3%	3	0.1%	7	0.2%	1	0.4%	7	0.2%	5	0.1%
Gly	GG	2	0.8%	2	0.7%	3	0.9%	5	1.5%	3	1.1%	1	0.5%	3	0.9%	2	0.8%	5	1.6%	4	1.3%
Gly	GG	2	0.8%	2	0.6%	2	0.9%	3	1.0%	1	0.4%	1	0.3%	3	1.0%	4	1.3%	2	0.7%	2	0.8%
Gly	GG	1	4.6%	1	5.2%	1	4.8%	1	3.9%	1	4.8%	2	5.9%	1	4.6%	1	3.7%	1	4.2%	1	4.8%
Gly	GG	2	0.7%	7	0.2%	1	0.3%	1	0.4%	3	1.0%	9	0.3%	2	0.1%	8	0.2%	1	0.3%	1	0.3%
His	CA	4	1.4%	4	1.4%	4	1.4%	5	1.6%	5	1.6%	5	1.5%	5	1.5%	5	1.5%	5	1.5%	5	1.6%
His	CA	3	0.1%	4	0.1%	4	0.1%	1	0.03	6	0.2%	1	0.03	4	0.1%	1	0.03	2	0.1%	0	0.0%
Ile	AT	7	2.2%	5	1.7%	7	2.3%	9	2.7%	8	2.5%	5	1.5%	8	2.5%	1	4.2%	5	1.5%	5	1.6%
Ile	AT	2	6.5%	1	5.6%	2	6.4%	2	6.8%	1	5.1%	1	5.6%	2	6.8%	3	8.8%	2	6.4%	2	6.3%
Ile	AT	1	0.3%	5	0.1%	5	0.2%	5	0.2%	5	0.2%	6	0.2%	6	0.2%	6	0.2%	8	0.2%	8	0.2%
Lys	AA	4	1.3%	5	1.5%	6	1.8%	4	1.4%	4	1.4%	6	1.9%	3	1.0%	2	0.6%	6	1.8%	7	2.0%
Leu	TT	1	5.5%	2	7.2%	2	6.3%	1	5.8%	2	7.6%	2	7.7%	2	6.8%	1	3.4%	2	7.0%	2	8.5%
Leu	TT	2	6.3%	1	5.0%	1	4.9%	2	6.5%	1	4.7%	1	4.2%	1	5.7%	3	9.4%	2	5.9%	1	4.6%
Leu	CT	1	0.4%	2	0.1%	7	0.2%	6	0.2%	7	0.2%	1	0.03	0	0.0%	2	0.1%	4	0.1%	7	0.2%
Leu	CT	1	0.4%	7	0.2%	1	0.3%	1	0.4%	1	0.4%	1	0.03	8	0.2%	1	0.3%	5	0.2%	5	0.1%
Leu	CT	2	0.7%	3	0.9%	4	1.4%	2	0.7%	3	1.0%	3	0.9%	2	0.6%	1	0.5%	2	0.8%	2	0.8%
Leu	CT	2	0.1%	0	0.0%	1	0.03	2	0.1%	0	0.0%	4	0.1%	1	0.03	0	0.0%	0	0.0%	1	0.03
Met	AT	7	2.1%	9	2.6%	8	2.5%	7	2.1%	8	2.5%	9	2.6%	8	2.5%	3	1.0%	9	2.9%	9	2.7%
Asn	AA	2	0.8%	1	0.6%	1	0.3%	2	0.7%	1	0.5%	7	0.2%	4	1.3%	5	1.7%	2	0.7%	1	0.4%
Asn	AA	9	2.8%	9	2.8%	9	2.7%	9	2.9%	8	2.3%	9	2.8%	1	3.0%	1	3.6%	9	2.8%	9	2.6%
Asn	AA	5	0.2%	7	0.2%	3	0.1%	5	0.2%	2	0.1%	4	0.1%	4	0.1%	1	0.03	4	0.1%	6	0.2%
Pro	CC	2	0.1%	2	0.1%	3	0.1%	9	0.3%	7	0.2%	2	0.1%	1	0.03	4	0.1%	9	0.3%	4	0.1%
Pro	CC	1	0.3%	7	0.2%	7	0.2%	8	0.2%	6	0.2%	1	0.03	0	0.0%	1	0.4%	3	0.1%	2	0.1%
Pro	CC	5	1.7%	6	1.9%	6	1.9%	5	1.7%	5	1.7%	7	2.2%	7	2.2%	6	1.9%	6	1.9%	6	1.9%
Pro	CC	4	0.1%	1	0.03	1	0.03	4	0.1%	3	0.1%	1	0.03	2	0.1%	5	0.2%	2	0.1%	2	0.1%
Gln	CA	2	0.8%	3	1.0%	2	0.8%	2	0.8%	2	0.7%	3	1.1%	1	0.6%	1	0.5%	3	1.0%	3	1.1%
Gln	CA	2	0.7%	1	0.6%	1	0.5%	1	0.5%	7	0.2%	1	0.5%	3	0.9%	2	0.8%	1	0.6%	1	0.4%
Arg	CG	7	0.2%	6	0.2%	7	0.2%	4	0.1%	4	0.1%	0	0.0%	6	0.2%	5	0.2%	4	0.1%	9	0.3%
Arg	CG	3	0.1%	2	0.1%	3	0.1%	5	0.2%	2	0.1%	3	0.1%	1	0.4%	5	0.2%	4	0.1%	5	0.1%
Arg	CG	4	1.2%	4	1.4%	4	1.4%	4	1.2%	3	0.9%	5	1.5%	3	1.1%	4	1.2%	4	1.4%	4	1.2%
Arg	CG	2	0.1%	1	0.03	0	0.0%	4	0.1%	2	0.1%	1	0.03	2	0.1%	2	0.1%	0	0.0%	0	0.0%
Ser	AG	1	0.4%	1	0.5%	3	0.9%	2	0.7%	3	0.9%	5	0.1%	2	0.9%	1	0.4%	2	0.7%	2	0.6%
Ser	AG	2	0.7%	1	0.5%	3	1.0%	3	1.1%	3	0.9%	6	0.2%	3	0.9%	5	1.5%	1	0.5%	2	0.8%
Ser	AG	1	3.3%	1	3.4%	9	2.7%	9	2.8%	1	3.7%	1	4.1%	9	2.6%	1	2.9%	1	3.0%	1	3.1%
Ser	AG	9	0.3%	1	0.03	5	0.2%	5	0.2%	1	0.4%	2	0.1%	2	0.1%	1	0.03	5	0.2%	5	0.1%
Ser	TC	1	0.03	2	0.1%	8	0.2%	8	0.2%	5	0.2%	1	0.03	4	0.1%	1	0.03	5	0.2%	6	0.2%
Ser	TC	4	0.1%	8	0.2%	1	0.4%	1	0.3%	2	0.6%	3	0.1%	5	0.2%	1	0.5%	6	0.2%	8	0.2%
Ser	TC	1	4.7%	1	4.4%	1	4.4%	1	4.3%	1	3.8%	1	5.0%	1	4.4%	1	3.7%	1	4.4%	1	4.3%
Ser	TC	3	0.1%	9	0.3%	1	0.03	5	0.2%	4	0.1%	3	0.1%	4	0.1%	1	0.3%	2	0.1%	1	0.03
Thr	AC	0	0.0%	0	0.0%	3	0.1%	3	0.1%	4	0.1%	2	0.1%	5	0.2%	1	0.03	6	0.2%	4	0.1%
Thr	AC	4	0.1%	1	0.03	4	0.1%	7	0.2%	1	0.3%	0	0.0%	1	0.3%	6	0.2%	1	0.03	2	0.1%
Thr	AC	8	2.5%	8	2.4%	7	2.3%	7	2.1%	6	1.8%	8	2.3%	6	2.0%	7	2.2%	7	2.3%	9	2.7%
Thr	AC	3	0.1%	4	0.12	1	0.03	6	0.2%	7	0.2%	0	0.0%	0	0.0%	9	0.3%	2	0.1%	1	0.03
Val	GT	1	0.6%	2	0.6%	3	1.1%	4	1.4%	7	2.1%	2	0.6%	4	1.3%	1	0.4%	3	1.0%	4	1.4%
Val	GT	2	0.7%	2	0.8%	3	0.9%	3	1.0%	7	2.2%	1	0.4%	2	0.7%	4	1.2%	3	1.0%	2	0.8%
Val	GT	2	6.4%	2	7.8%	2	6.6%	1	5.3%	2	6.5%	2	7.9%	2	5.9%	1	4.0%	2	7.1%	2	6.7%
Val	GT	1	0.5%	7	0.2%	9	0.3%	5	0.2%	1	0.4%	3	0.1%	1	0.03	5	0.2%	3	0.1%	2	0.1%
Trp	TG	3	1.0%	4	1.2%	4	1.3%	3	1.0%	4	1.4%	4	1.4%	3	1.0%	4	1.2%	4	1.4%	4	1.2%
Trp	TG	3	1.1%	3	0.9%	3	0.9%	3	1.1%	2	0.9%	2	0.8%	4	1.3%	4	1.4%	3	1.1%	3	1.1%
Tyr	TA	5	0.2%	2	0.1%	4	0.1%	6	0.2%	3	0.1%	4	0.1%	6	0.2%	7	0.2%	6	0.2%	6	0.2%
Tyr	TA	2	6.2%	2	6.2%	2	6.4%	2	6.4%	1	5.1%	2	7.0%	2	6.0%	2	6.0%	2	6.2%	1	5.6%
Tyr	TA	1	0.4%	1	0.4%	1	0.4%	7	0.2%	1	0.4%	0	0.0%	5	0.2%	9	0.3%	6	0.2%	4	0.1%

Total number of codons is 3408 (*B. m.*), 3452 (*W. b.*), 3401 (*M. p.*), 3440 (*C. m.*), 3422 (*C. l.*), 3461 (*S. d.*), 3416 (*G. p.*), 3418 (*H. l.*), 3431 (*S. l.*), 3457 (*M. m.*); Results obtained from GenBank accessions.

*B. m.*, *Brugia malayi* (MT149211.1); *W. b.*, *Wuchereria bancrofti* (JN367461.1); *M. p.*, *Mansonella perstans* (MT361687.1); *C. m.*, *Crassicauda magna* (OQ834322.1); *C. l.*, *Camallanus lacustris* (NC\_070137.1); *S. d.*, *Setaria digitata* (NC\_014282.1); *G. p.*, *Gongylonema pulchrum* (NC\_026687.1); *H. l.*, *Heliconema longissimum*; *S. l.*, *Spirocerca lupi* (MK922357.1); *M. m.*, *Mastophorus muris* (NC\_085209.1).