

Supplementary information 2 for

The compact genome of a new *Caenorhabditis* species *Caenorhabditis niphades* n. sp., isolated from Niphades beetles

containing

Table S2 and S3

Figure S5-S9

Table S2. Repetitive element comparison. Repetitive element contents in *C. niphades* n. sp., *C. elegans*, *C. japonica*, *C. bovis*, *C. afra* and *C. sulstoni* were detected by combination of RepeatModeler2 (v 2.0.1) and transposonPSI.

	<i>C. niphades</i> n. sp.		<i>C. elegans</i>		<i>C. japonica</i>		<i>C. bovis</i>		<i>C. afra</i>		<i>C. sulstoni</i>	
	num element	% in bp	num element	% in bp	num element	% in bp	num element	% in bp	num element	% in bp	num element	% in bp
SINEs	126	0.04	190	0.03	842	0.07	79	0.02	227	0.06	557	0.13
LINEs	2155	0.70	14556	2.23	66781	6.37	986	0.68	2418	0.77	2368	0.75
LTR element	4575	1.82	14959	2.90	118007	11.22	3714	1.65	5065	1.98	5142	2.01
DNA element	9438	2.45	58525	9.68	121897	10.75	7016	3.05	13511	2.86	13317	2.61
Rolling- circles	331	0.09	3004	0.61	3606	0.37	247	0.07	1781	0.48	856	0.30
Unclassified	17230	6.25	11684	2.54	187813	16.63	19371	4.64	13485	4.51	15160	4.77
Total interspersed repeats		11.27		17.38		44.04		10.03		10.18		10.26
Small RNA	567	0.24	540	0.08	1540	0.32	307	0.07	718	0.14	627	0.13
Satellites	132	0.04	358	0.06	2952	0.60	88	0.02	111	0.04	254	0.10
Simple repeat	18348	1.15	20587	1.02	34767	0.85	17252	1.03	28794	1.63	28287	1.70
Low complexity	3311	0.27	5816	0.27	9377	0.26	3311	0.24	6670	0.49	6114	0.47
Total		13.06		19.41		46.45		11.46		12.95		12.96

Table S3. Chromosome size, gene number, and GPCR gene number on each chromosome of *C. niphades* and *C. elegans*.

	ChrI		ChrII		ChrIII		ChrIV		ChrV		ChrX	
	<i>C. elegans</i>	<i>C. niphades</i>	<i>C. elegans</i>	<i>C. niphades</i>	<i>C. elegans</i>	<i>C. niphades</i>	<i>C. elegans</i>	<i>C. niphades</i>	<i>C. elegans</i>	<i>C. niphades</i>	<i>C. elegans</i>	<i>C. niphades</i>
Chromosome size (bp)	15M	9M	15M	9M	14M	9M	17M	9M	21M	10M	18M	13M
gene number	2911	2690	3514	2929	2689	2592	3311	2728	4953	3194	2769	2775
GPCR gene number	34	17	171	61	36	17	153	55	899	225	36	7

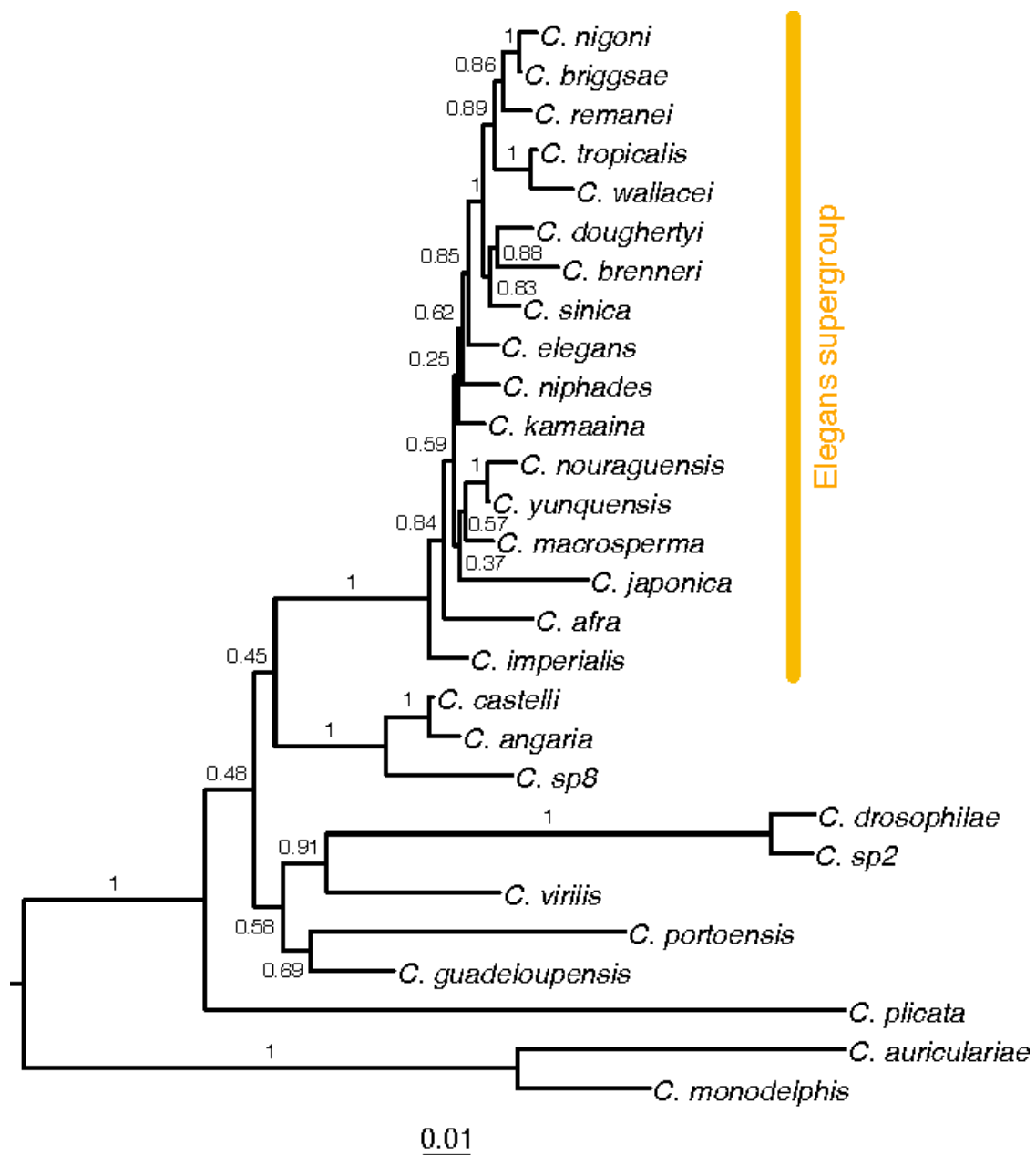


Figure S5. Phylogenetic relationships of *C. niphades* n. sp. and the other 26 *Caenorhabditis* species inferred by near-full-length 18S and D2/D3 region of 28S ribosomal RNA genes. Nucleotide sequences were aligned before concatenation, and maximum-likelihood trees were generated with RAxML v7.2.8 using the best-fitting empirical model with 1,000 bootstrap resampling replicates with the support percentage shown on the nodes. The scale bar shows nucleotide substitutions per site.

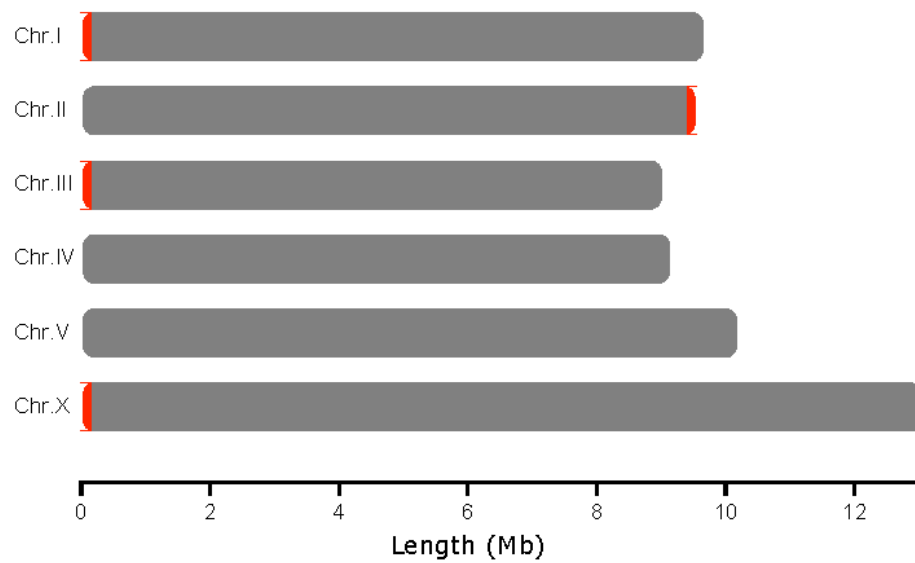


Figure S6. Schematic overview of six big contigs of the *C. niphades* n. sp. genome. Red color indicates positions where telomeric repeats (>20 TTAGGC unit) were detected.

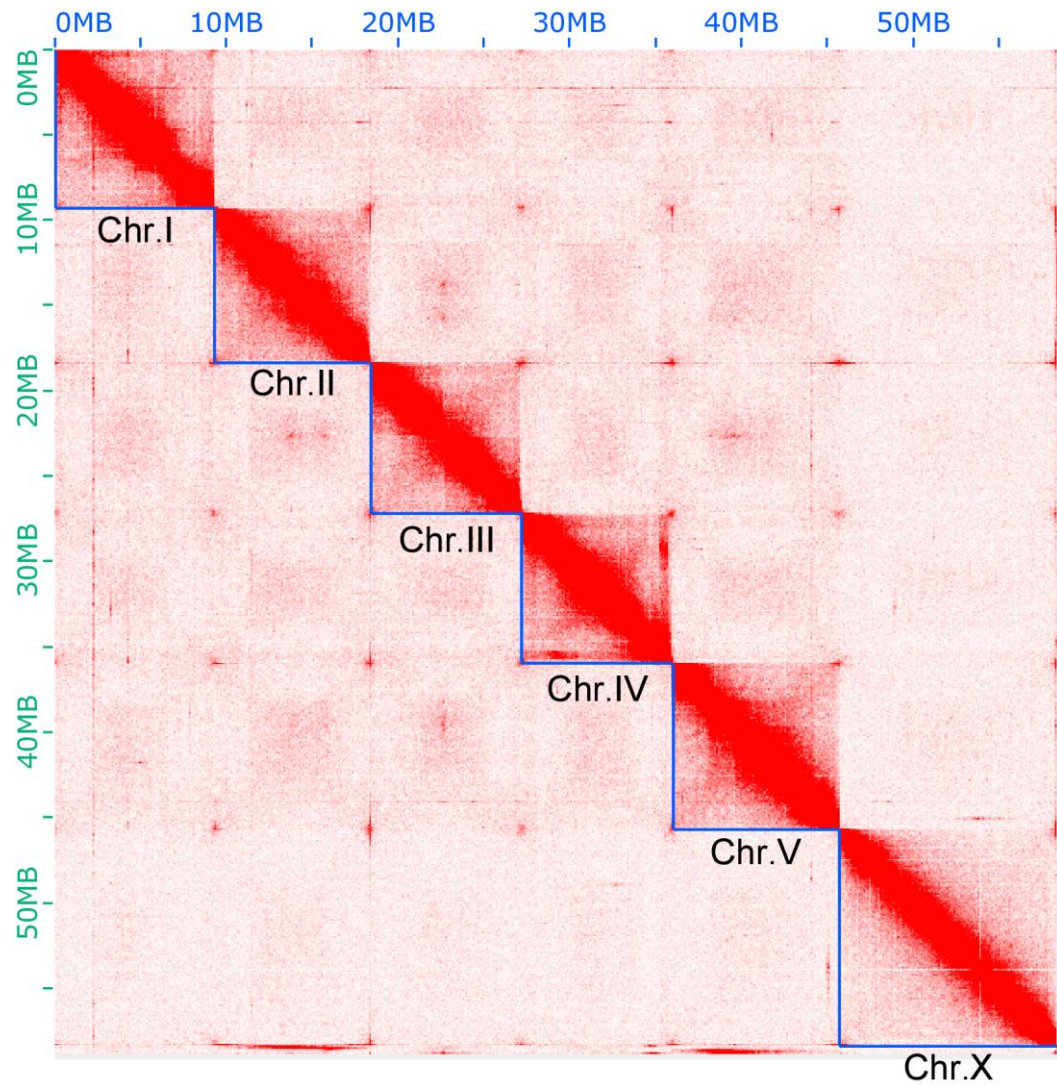


Figure S7. Hi-C contact map of the assembled chromosome-length scaffolds for *C. niphades* n. sp. The six scaffolds are indicated by blue lines, corresponding to the six chromosomes in *C. niphades* n. sp. genome.

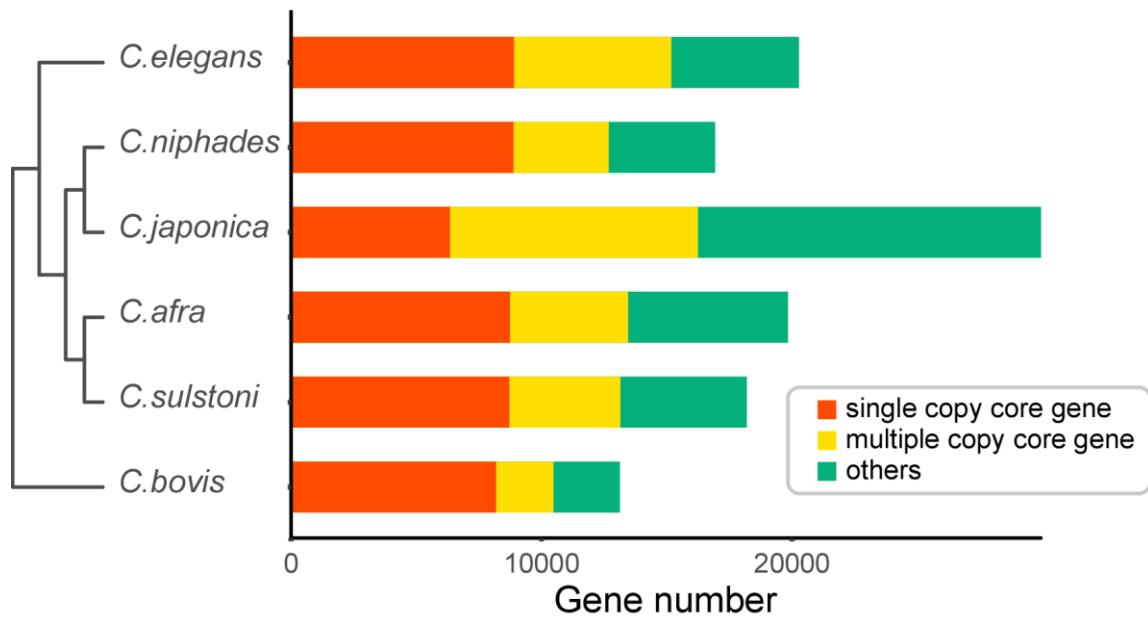


Figure S8. Species-specific genes and Orthologues between various *Caenorhabditis* species. Core genes were defined as those present in the core orthogroup (identified by Othofinder version 2.2.6), in which orthologues of *C. elegans*, *C. inopinata*, *C. nigoni*, and *C. briggsae* must be detected.

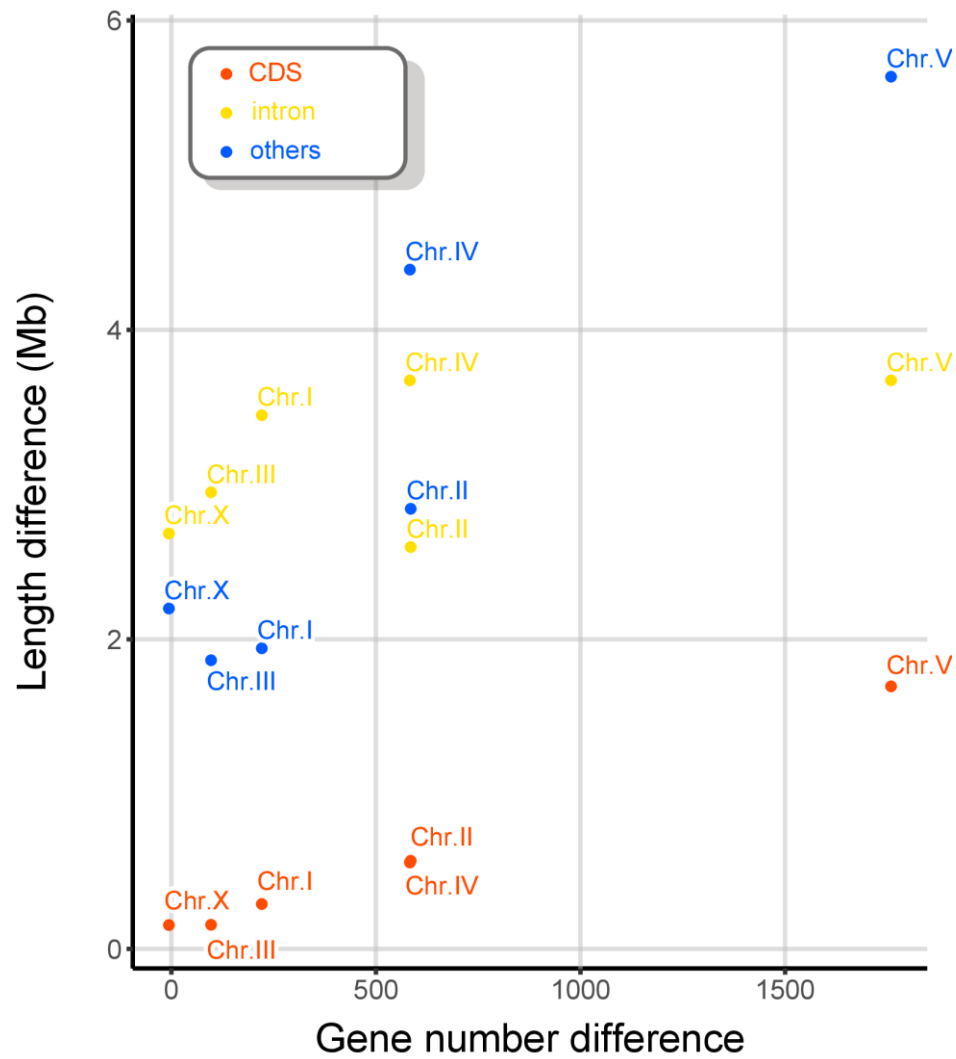


Figure S9. Relationship between gene number and genomic feature size in *C. niphades* n. sp. and *C. elegans*.