

Table S2. Quality of the genome sequences used in this study. The genomes of *C. elegans* and *C. briggsae* have been assembled into chromosomes, while the qualities of the other four genomes are shown here. The sources of the quality information are <http://genome.wustl.edu/pub/organism/Invertebrates/> and ftp://ftp.tigr.org/private/euk/b_malayi_fh574.

	<i>C. brenneri</i>	<i>C. remanei</i>	<i>P. pacificus</i>	<i>B. malayi</i>
Sequence redundancy	9.5X	9.2X	8.92X	8.56X
Supercontig number	10,292	3,670	5,106	8,180
Supercontig N50 length	88,950	461,060	737,446	93,771