

Additional file 4. Consensus sequence alignments for the annotated Nematode-Specific Peptide family, group D (NSPD) orthologs in 11 *Caenorhabditis* species. Each species is represented by the consensus sequences for the 3-10 paralogs (90% identity threshold). Ambiguous amino acids are marked with an “X”. *C. briggsae*, *C. sinica*, and *C. remanei* each had one gene with additional sequence on the N-terminus, which was excluded from the consensus. The region of species-specific repeats is between residues 39 and 51.

	1	20	40	60	77
<i>C. briggsae</i>					
	MADKSAYMSAGGYXSGYMGSNASSSGYAXEDYASGGSGG----	XXXNNNQGGSGGXXNPGXQVFKARTDQSCYLGP-			
<i>C. nigoni</i>	MADKSAYMXAGGYSSGYMGXNASSSGYAREDYAXGGXGX----	XXXNNXXGSGGXXNPGXQVFKARTDQSCYLGP-			
<i>C. sinica</i>	MADKSAYMXAGGYSSGYMGXNASSSGYAREXYAXGGXGXXASGGXNNNNXXGSGGXTNPGXQVFKARTDQSCYLGP-				
<i>C. latens</i>	MADKSAYMSAGGXSSGYMGSNASSSGYAREDYASGGSGG----	XXXNNQXQSGGNTNPGXQVFKARTDQSCYLGP-			
<i>C. remanei</i>	MADKSAYMSXGXYSSGYMGSNASSSGYAREDYASGGXGG----	GXXNNXXQGGXGGNTNXGXQVFKARTDQSCYLGP-			
<i>C. sp33</i>	MADKSAYMSAGGYXSGYMGSNASSSGYAREXYASGGSGG----	XXXXNNXXXGXGGNXXNPGXQVFKARTDQSCYLGP-			
<i>C. wallacei</i>	MADKSAYMSAGGYSSGYMGSNASSSGYAREDYASGGSGG----	GXXNNNNQSGGXXNPGXQVFKARTDQSCYLGP-			
<i>C. tropicalis</i>	MXDKXAYMSAGGYSSGYMGSNASSSGYXREDYASXGSGX----	XXXNNXNQSGGXNXXNPGXQVFKARTDQXCYLGP-			
<i>C. doughterti</i>	MADKSAYMXAGGYXSGYMGSNASSSGYAREDYAXGGSGXX--	XXXXNNXQGGXGGNTNPGXQVFKARTDQSCYLGP-			
<i>C. sp34</i>	MADKSAYMXXGGYXSGYMGSNASSSGYAREXXAXGGXGX-----	GNQSGGXXXXGXQVFKARTDQSXYLGX-			
<i>C. elegans</i>	MADKSAYMGAGGYGSGYMGSNASSSGYAREDYAQGGGX--	GGXXXXXXXXXGSGGNTNPGGQVFKARTDQSCYLGP-			
<i>C. kamaaina</i>	MADKSAYMSAGGYSSGYMGSNASSSGYAREXYASGGSGX-----	SGGXQSGGAVSNPGGQVFKARTDQSAYLGPS			