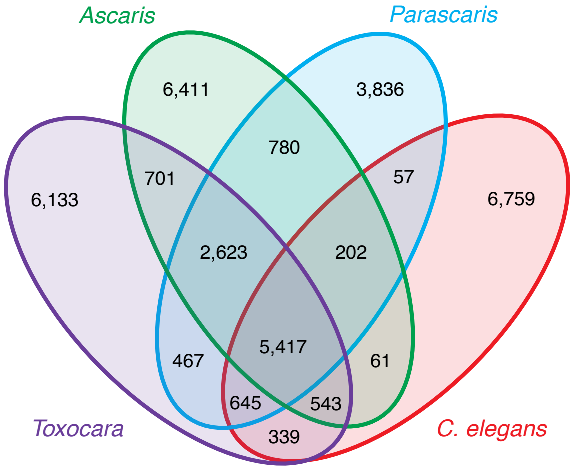
A



B

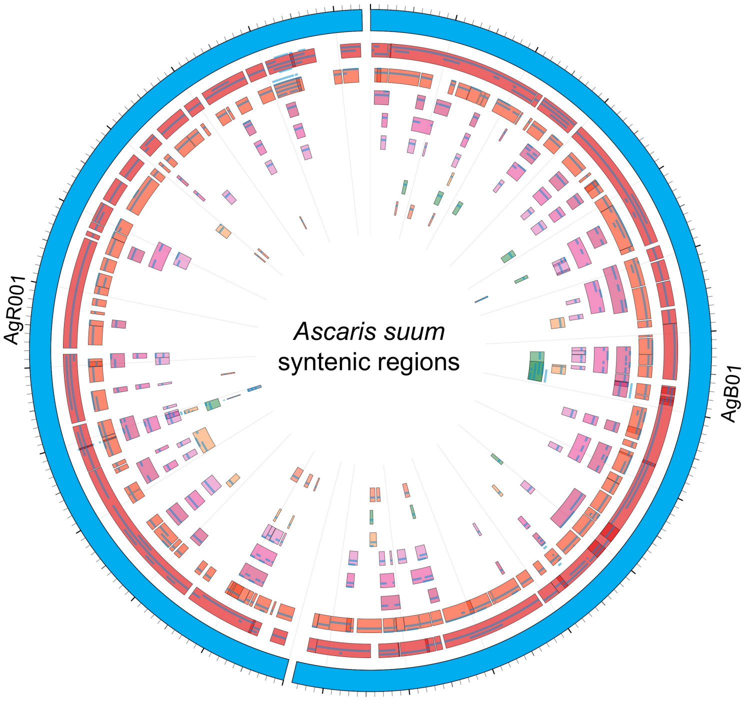


Figure S7. Comparative genomics in nematodes. A. Orthologous genes among ascarid nematodes and *C. elegans*. Predicted proteomes from three related ascarid nematodes (*Ascaris*, *Parascaris*, and *Toxocara*) were compared to the proteome of the free-living nematode *C. elegans*. Proteins were clustered into 34,974 orthologous groups (OrthoMCL) resulting in 13,659 groups and 21,315 singletons. Illustrated in the Venn diagram are the relationships of these proteins groups between species (including all singletons) (see Supplementary Methods). Note that most the species-specific genes are singletons. **B.** Synteny between *Ascaris* and 9 other nematodes. Illustrated are the two largest assembled scaffolds in *Ascaris* (AgB01, 13.4 Mb and AgR001, 11.4 Mb as the outer circle). Nematodes used for comparison are (from outer to inner circles): *Parascaris univalens, Toxocara canis, Brugia malayi, Onchocerca volvulus, Loa loa, Caenorhabditis elegans, Pristionchus pacificus, Strongyloides ratti,* and *Trichinella spiralis* (see Tables S7)(see also Ascaris genome browser, comparative genomics data track; https://genome.ucsc.edu/cgi-bin/hgHubConnect, using the ‘‘My Hubs’’ tab with the following link: http://amc-sandbox.ucdenver.edu/User14/genomes.txt). Synteny was identified using DAGchainer.