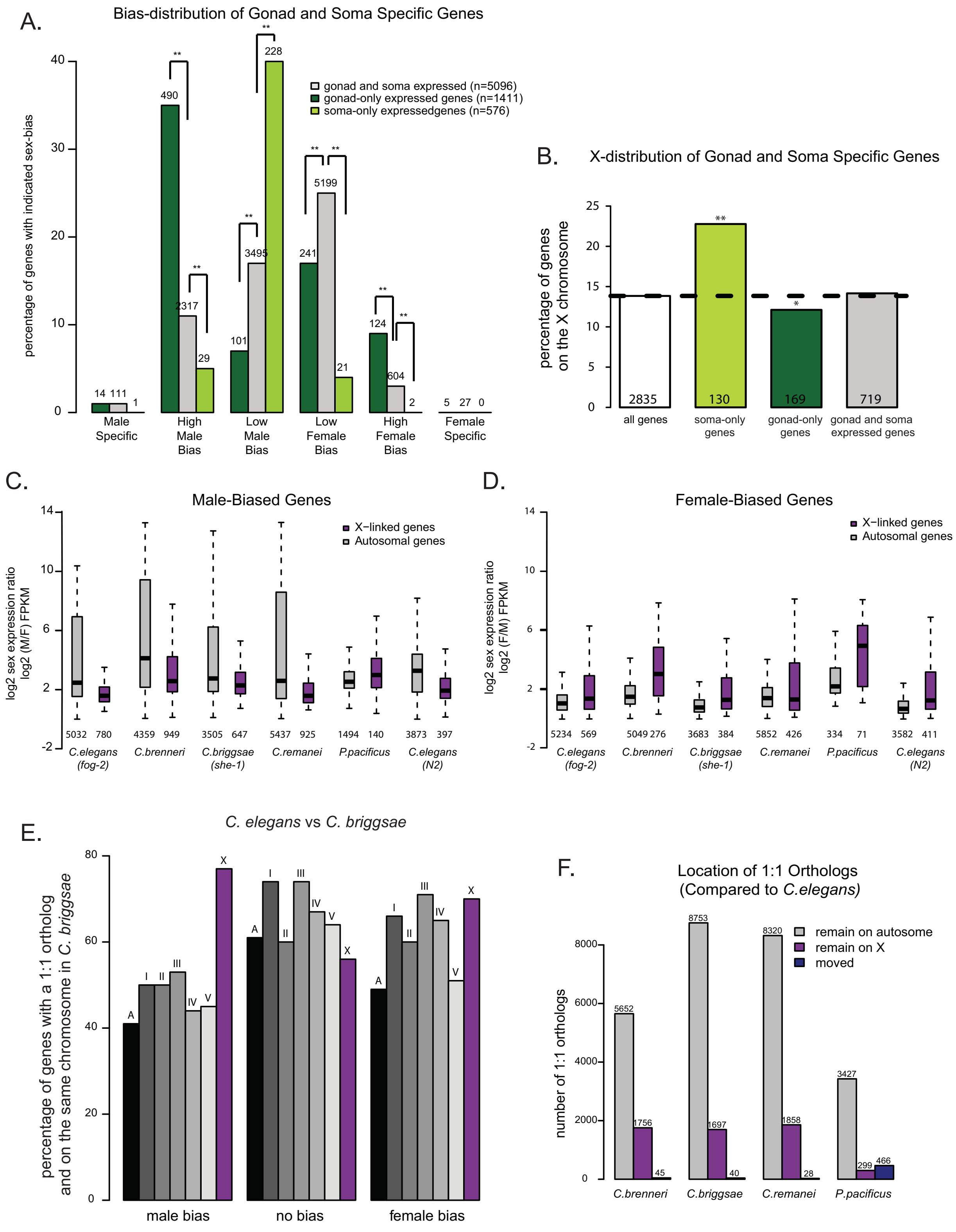

Figure S4 **A)** *C. elegans* genes were grouped into genes expressed in gonad and soma (gray), soma-only (light green), and gonad-only (dark green). For each category, the percentage of genes that fall into the indicated sex-bias category is plotted. Significance by Fisher test: (**) indicates p value less than 0.001. **B)** For each expression category the percentage of genes located on the X chromosome was plotted. Significance of enrichment or depletion was calculated using Fisher test: (*) indicates p value less than 0.05; (**) indicates p value less than 0.001. Number of X-linked genes is indicated at the bottom of each bar. **C)** As in Figure 4C, magnitude of male-biased expression (log2 male over female expression) was calculated for each male-biased gene. Here, bias magnitude of male-biased genes is plotted. Number of genes analyzed is indicated below each box. **D)** Same as **C,** but for all female-biased genes. **E)** In Figure 6A we used a defined set of 1:1:1:1 orthologs to determine locational conservation of biased and unbiased genes. Here we define a set of 1:1 orthologs between *C. elegans* and *C. briggsae*. This less stringent definition of orthology gave a larger list of genes, and all chromosomes could be evaluated individually. The number of 1:1 orthologs located on the same chromosome was calculated. For each chromosome, the conservation is plotted as the percentage of *C. elegans* genes that have a 1:1 ortholog in *C. briggsae* located on the same chromosome. **F)** Macrosynteny is high amongst the *Caenorhabditis* species. Between *C. elegans* and each of the other four species, the number of 1:1 orthologs that remain autosomal (grey), remain X-linked (purple) or move between X and autosomes (dark blue) in the two species are plotted.