



Figure S2. Sex chromosome identification. Raw sequencing read coverage enables sex chromosome identification based on 2X read coverage of the diploid female sex chromosomes (XXs) compared to the haploid male chromosomes (Xs). We generated genomic reads for the intestine of a single female and a male *Ascaris*. Illustrated in Fig. S2A is the genomic read coverage for *Ascaris* scaffolds. Whereas the read coverage observed is the same for the autosomes, the read coverage for females is 2-fold the coverage observed in the male. Illustrated in Fig. S2B are genomic read coverages for male *Parascaris* scaffolds. Note that the drop in read coverage for a set of chromosomes which are the sex chromosomes (1X vs. 2X autosomes). All scaffolds for the autosomes and sex chromosomes are sorted based on their length (from large to small on the x axis).