



Figure S9. Identification of chromosome Y contigs in the Dana.UMIGS assembly.

Male and female Illumina libraries were mapped to the Dana.UMIGS assembly, followed by filtering steps to remove duplicates and alignments with MAPQ < 10. A custom script adapted from Chang & Larracuente (2019) was used to calculate median female:male sequencing depth ratios for 10 kbp windows across the genome. Ratios are displayed for single contigs representing chromosomes XL and 3L in addition to 60 unordered contigs assigned as putative chromosome Y. Contigs assigned to chromosome Y had at least one 10 kbp window with a median female/male ratio of zero and $\geq 80\%$ of its windows with median female/male ratios below 0.05.