



**Figure S1** Heatmap showing count of *Megaselia* 15-mers by  $\log_{10}(\text{Contig Size})$  and percent of single copy 15-mers that were unmatched (USC) by female short read data. Note peaks at 0% USC and 100% USC 15-mers. These are inferred to be caused by autosomal vs. male-specific contigs, respectively.