



Figure S4: The median female-to-male coverage ratio of Illumina reads across different chromosomes based on the R6 annotation. We mapped the male and female Illumina reads to our new genome using bwa, and called median of female-to-male coverage ratio using samtools and custom scripts for each 10-kb region. The median female-to-male mapping ratio was normalized by total mapped reads. Contig location was determined by known gene content. Regions from contigs with Y-linked genes have a median female-to-male coverage ratio of 0.