Figure S1  Sequence coverage improves across the *W. pipiens* genome due to selective whole genome amplification (SWGA). In all three *D. melanogaster-W. pipiens* samples tested, SWGA resulted in nearly 10 fold elevation in sequence coverage across the *W. pipiens* genomes. For example, while none of the sites in the Fly 1 genome had greater than 10X coverage when sequenced directly from the fly (dark bars), the majority of sites from the same fly extract had greater than 10X coverage after SWG amplification. The sequence coverage estimates for each sample were standardized to the equivalent of 1/96th of an Illumina HiSeq lane (200 million 50 bp SE reads).