

Figure S3

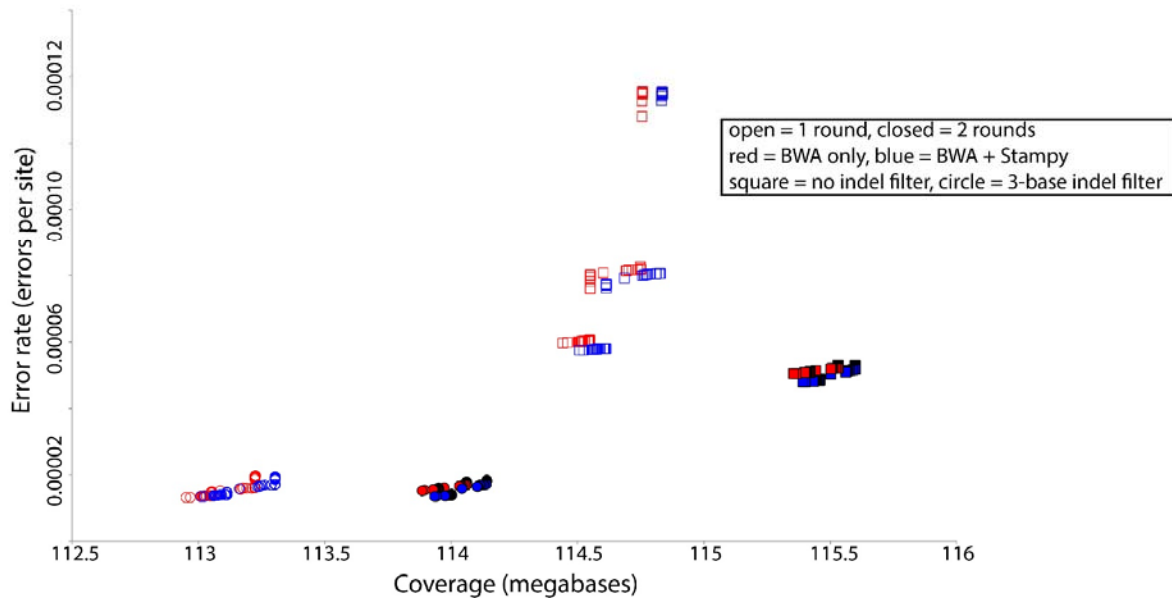


Figure S3 Comparison of genomic coverage and error rate for various genome assembly pipeline variations, based on resequencing of the *D. melanogaster* reference strain (Pool *et al.* 2012). All quality values from Q10 to Q100 are shown; many gave very similar results. Open symbols indicate a single round of mapping, while closed symbols indicate two rounds of mapping. Red symbols indicate only BWA was used to map, while blue symbols indicate BWA and Stampy were both used. Square symbols indicate no indel filter was applied, while circular symbols indicate a 3-base filter was applied.