



Figure S7. *D. ananassae* k-mer assembly spectra copy number plots.

K-mers from assembled *D. ananassae* genomes were compared to k-mers present in the paired end Illumina library using KAT. The spectra copy number plot displays how k-mers in the short reads are represented in the assembly, with optimal reconstruction of a homozygous genome shown as a single peak with 1X coverage. The black arrows at the peaks of Canu plots highlight the presence of k-mer content above the expected 1X and are indicative of uncollapsed content in genome assemblies. The white arrows in ONT and Flye plots highlight the absence of k-mer content and are indicative of overly collapsed or missing content in genome assemblies.