

view of OMcontig_6, locating the large gap within the grayed restriction fragments. FPC gap sizes are calculated as: pseudomolecule. Dashed lines show alignments of ct280 and ctg281 against OMcontig_6 (gold track) and a large gap. (C) Restriction map contigs ct280 and ctg281 to Chr6 pseudomolecule. A gap of unknown size is illustrated, with green lines showing alignment to the fragment) of FPC contigs aligned to the AGP Chr 6 pseudomolecule; the gap is highlighted. (B) Cartoon showing the alignments of FPC Gap (kb) = [[(right optical coordinate) – (left optical coordinate)] - [(right sequence coordinate) – (left sequence coordinate)]/1000 Figure S1. Using optical contigs to estimate sizes of gaps between adjacent FPC contigs. (A) Restriction map view (box = restriction