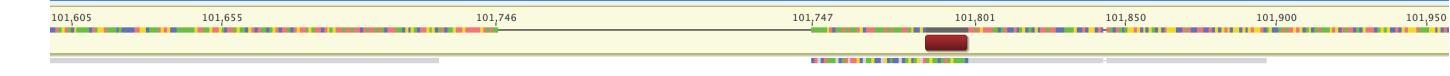
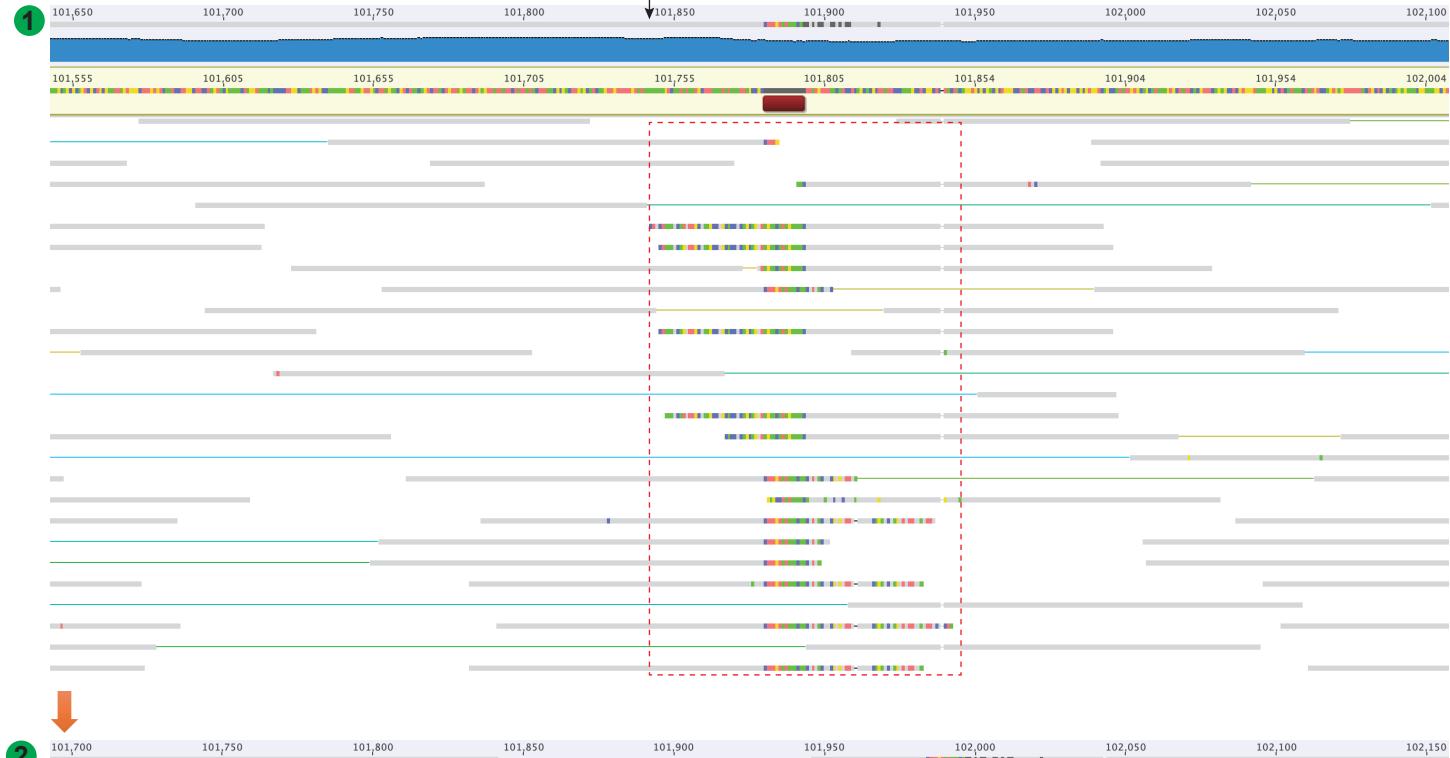


insert a gap in the "Consensus"



move the reads to the left (or right), and delete gaps in the sequences.



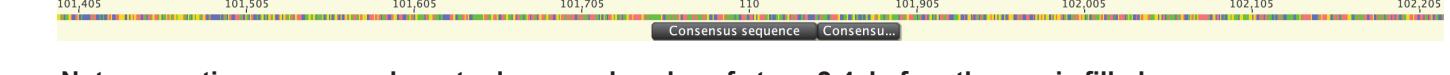
fill the consensus sequence based on the aligned reads



Map the unplaced paired reads to the scaffold



Once the gap is filled, remove empty columns



Note: sometimes you may have to do several cycles of steps 2-4, before the gap is filled.

Supplemental Fig S3. Diagrams showing the procedure used to fix a local assembly error using unplaced paired-end reads mapped to the problem region after opening a gap.