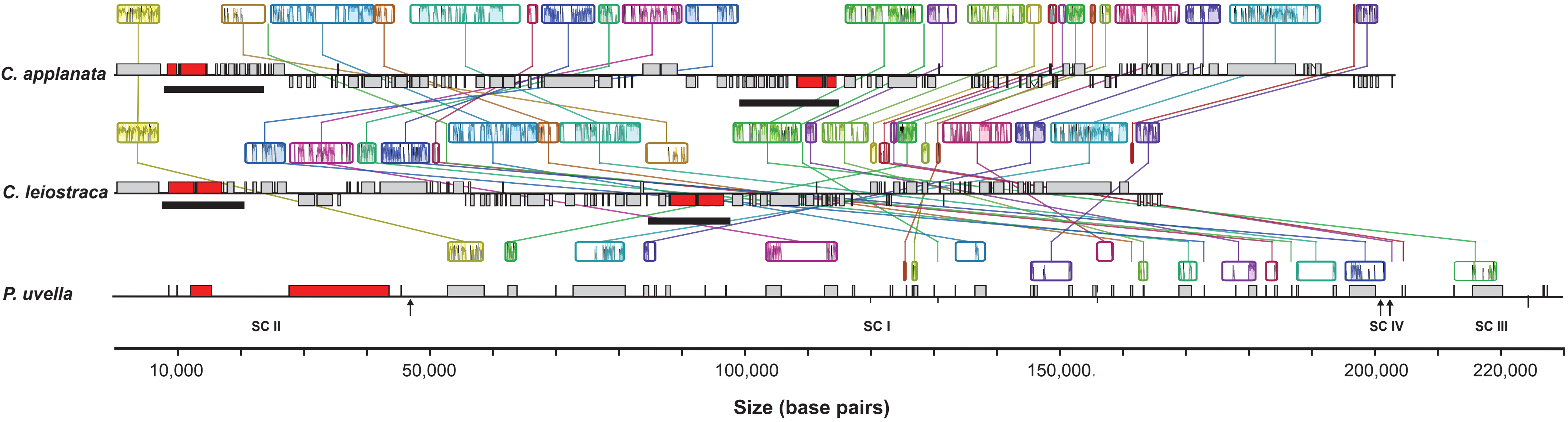
Figure S1



Supplemental Figure S1. Alignment of plastid genomes of *Chlamydomonas applanata* (partial sequence, 203 kb), *Chlamydomonas leiostraca* (167 kb) and *Polytoma uvella* (partial sequence, ~230 kb). Linearized genomic sequences were aligned using Mauve 2.3.1 (progressive algorithm, computing local collinear blocks and with automatic calculation of seed weight). Coloured boxes represent conserved blocks and the internal bars the similarity profiles (average level of sequence conservation) per block. Putative rearrangements are highlighted with colour lines. Red and white rectangles represent ribosomal RNA and protein-coding genes, respectively. Inverted repeat regions, when present, are indicated with black rectangles. Arrowheads in the *P.uvella* genomic map highlight the separation between the four assembled scaffolds (SC) ordered arbitrarily for this analysis.