

1. Structure of the *Pichia sorbitophila* nuclear genome

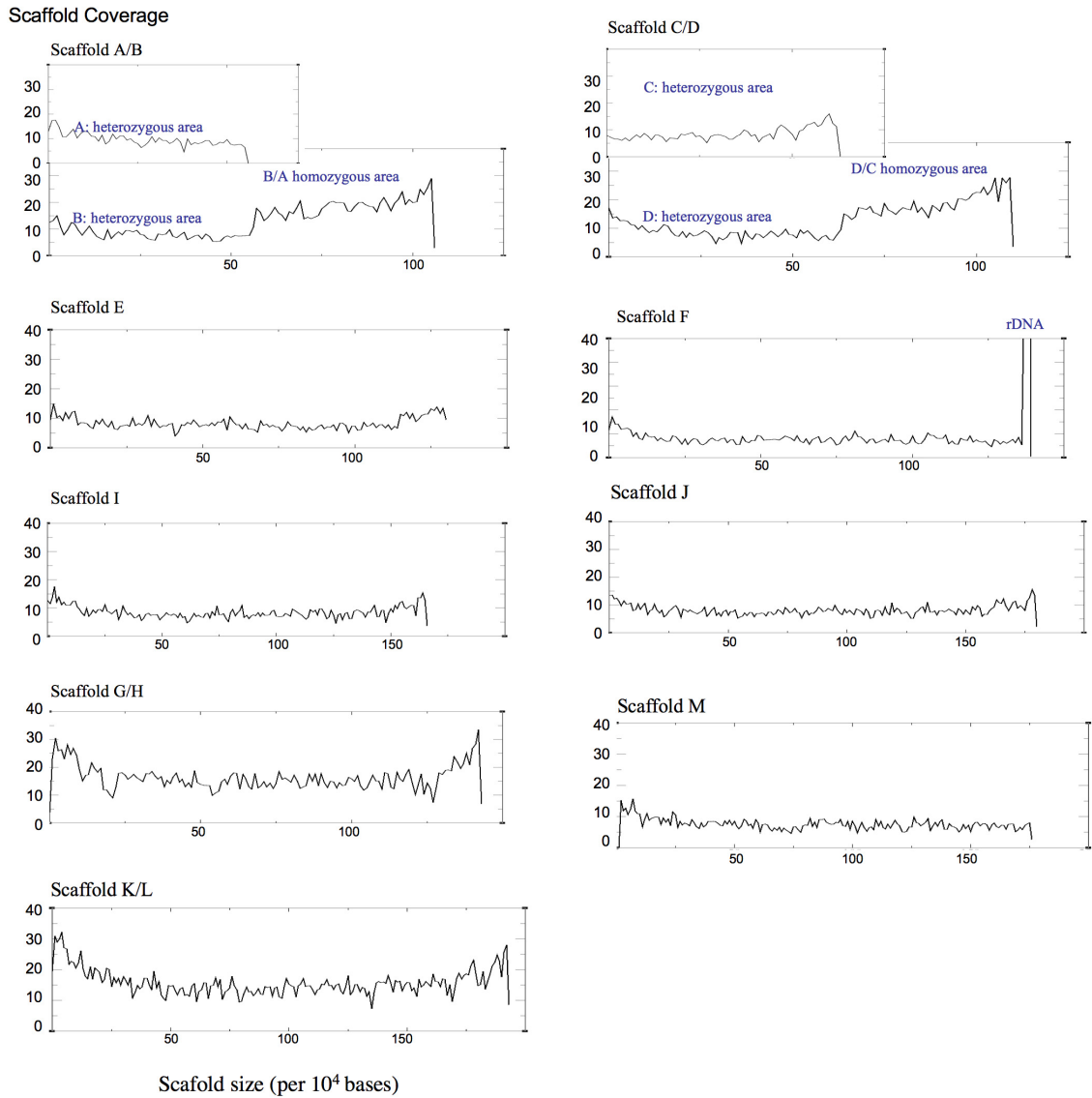


Figure S1 Sequencing coverage (X) along scaffolds. Sequencing depth (Y-axis) was calculated along finished scaffolds (X-axis) by mapping initial Sanger reads on scaffolds. The 11 contigs (7.5X covered) obtained before finishing (see Methods) correspond to the heterozygous regions in A, B, C, D, and to the heterozygous chromosomes E, F, I, J, M, and N (2 contigs), respectively. The six 14X covered contigs correspond to the homozygous parts in A/B, and C/D and to the homozygous chromosomes G/H (2 contigs) and K/L (2 contigs).