

## Supplementary information

### **Assembly of *Schizosaccharomyces cryophilus* chromosomes and their comparative genomic analyses revealed principles of genome evolution of the haploid fission yeasts**

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**General description:** Here we provided the sequences of the concerning supercontig (Sc) ends and the confirmation of their overlaps and adjacency by Sanger sequencing. We highlighted the sequences as follows: light blue and grey represent sequences of the Scs. Green highlight show the positions of the primers used for the PCR and for the sequencing. Primers were designed to hybridize to the corresponding contig ends of the concerning Scs (see methods in the main text). Yellow highlight indicate results of the sequencing, which were in good agreement with the lengths of the PCR products in the case of Sc9-Sc1 and Sc5-Sc8. In the case of Sc8-Sc6 we did not sequence the entirety of the amplified product, we just validated the togetherness of these Scs. “+” and “-“ symbols in the brackets correspond to the original orientation of the Scs available in the corresponding databases. Results of the sequencing are available in Genbank under the accession numbers: MH605091- MH605096.

## Sc9 and Sc1 overlapping contig ends and sequencing

>Sc9\_end (-) & Sc1\_end (-)

```
atatgtgaattaagaagaagttatgggaagatgataagttgctgcataactggcaacctagtcattctcattgatagaagtaaaagacgtaac
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## Sc5 and Sc8 overlapping contig ends and sequencing

>Sc5\_end (-) & Sc8\_end (-)

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