

DataFile 1

Detailed information concerning the raw data files (FASTQ) used to create 3D models of the *Podospora anserina* genome using 3DGB software (1) (**Table S1.1**, **Figure S1.1** and **Table S1.2**), and output statistics from the Hi-Pro software (2) regarding the analysis of FASTAQ files with 3DGB (1) (**Figure S1.2** and **Figure S1.3**).

File name	Number of reads	Initial read length	% duplicated reads	% GC
WT1_R1.fastq	71.3 millions	150 bp	48.3	51
WT1_R2.fastq	71.3 millions	150 bp	41.0	52
WT2_R1.fastq	51.7 millions	150 bp	42.6	51
WT2_R2.fastq	51.7 millions	150 bp	35.9	52

Table S1.1 : General statistics of the FASTQ files obtained from the MultiQC program (3).

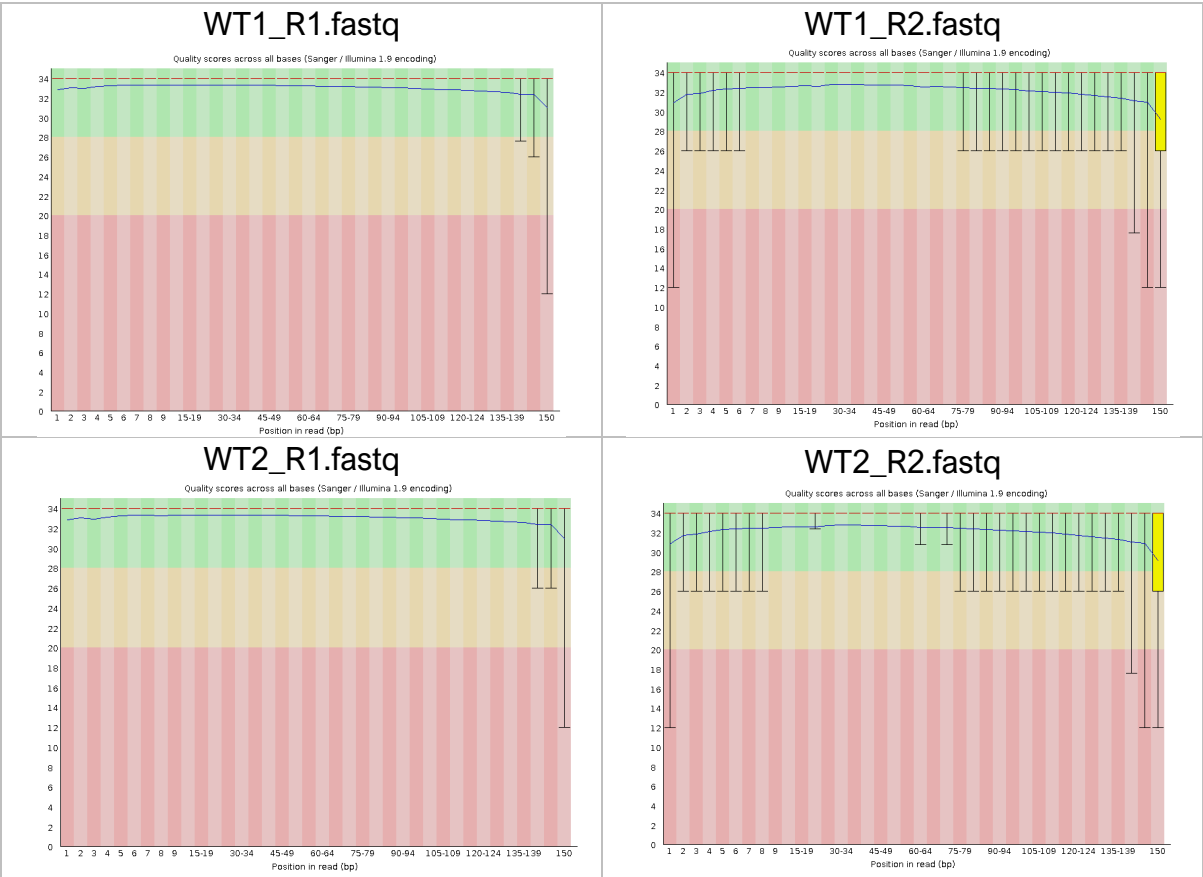
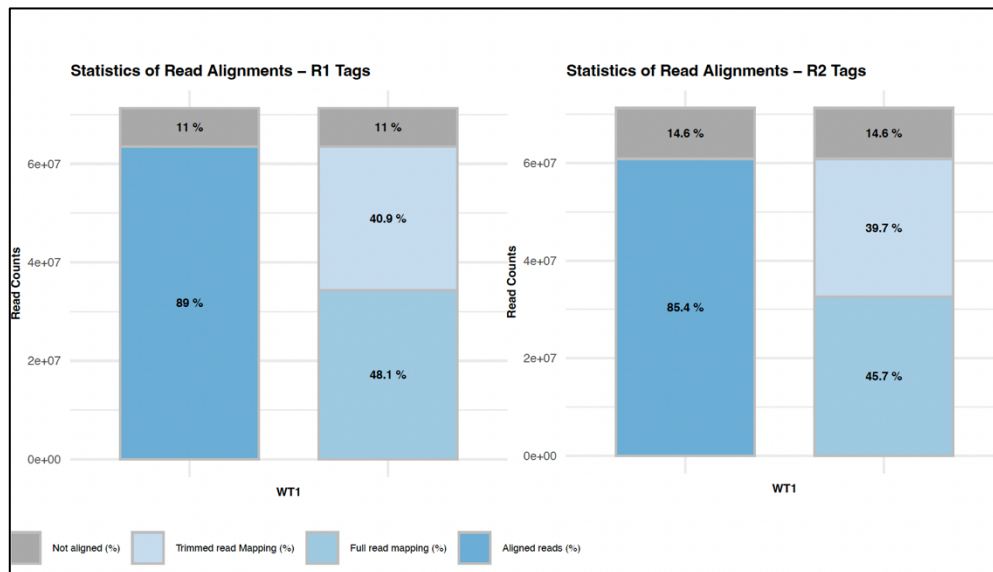


Figure S1: Graphical representations of the quality scores across all bases in each FASTQ file, obtained from the FASTQC program
<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.

	Aligned reads (R1)	Aligned reads (R2)	Reported pairs
WT1 replicate	89%	85.4%	68.7% (~50 millions)
WT2 replicate	88.7%	85.1%	68.4% (~35 millions)

Table S1.2: General statistics of the FASTQ file analyses, performed with HiC-Pro (2).

- WT1 replicate



- WT2 replicate

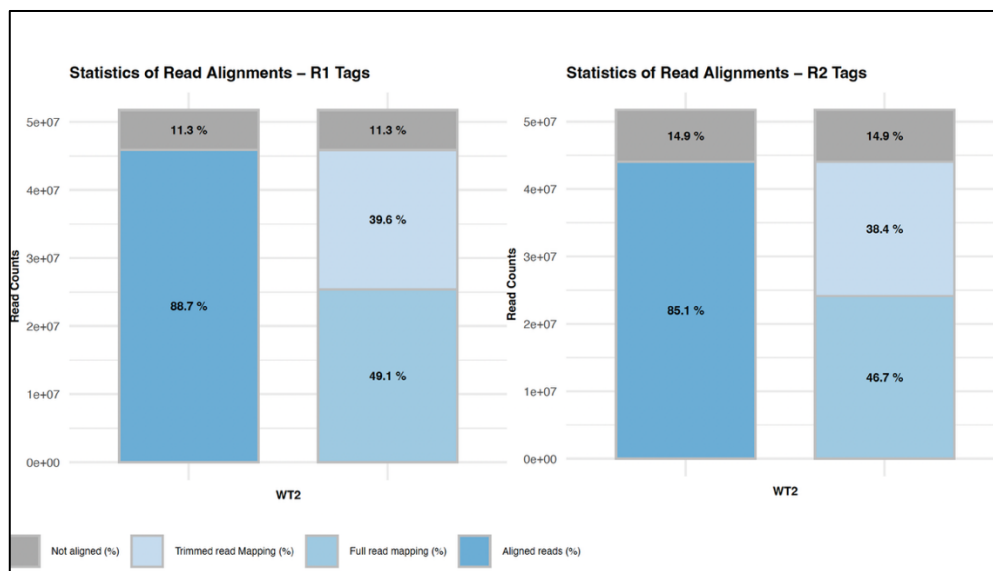
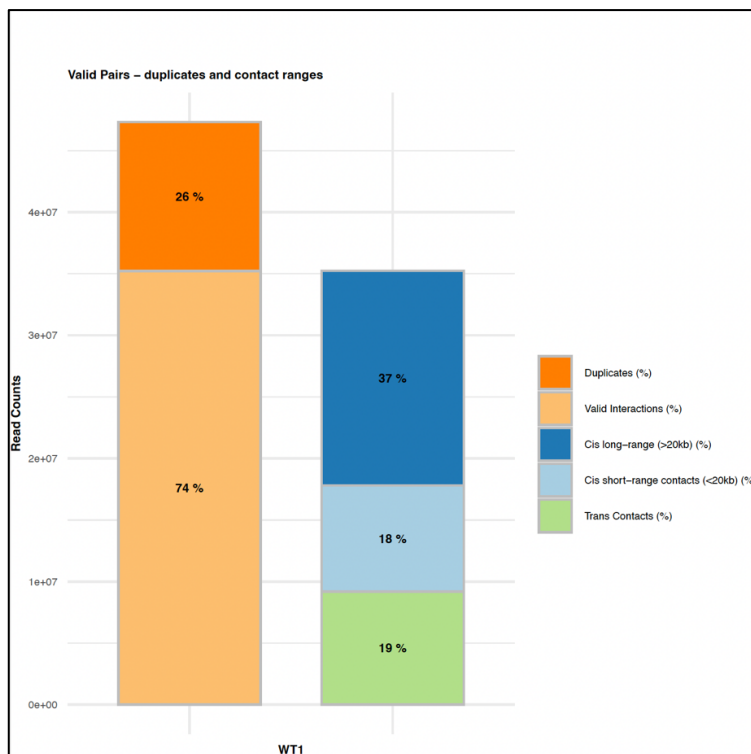


Figure S1.2: Graphical representations of statistics from the Hi-C Pro software, associated with the mapping step. Detailed graphic explanations can be found here: <https://inservant.github.io/HiC-Pro/RESULTS.html#mapping-results>.

- WT1 replicate



- WT2 replicate

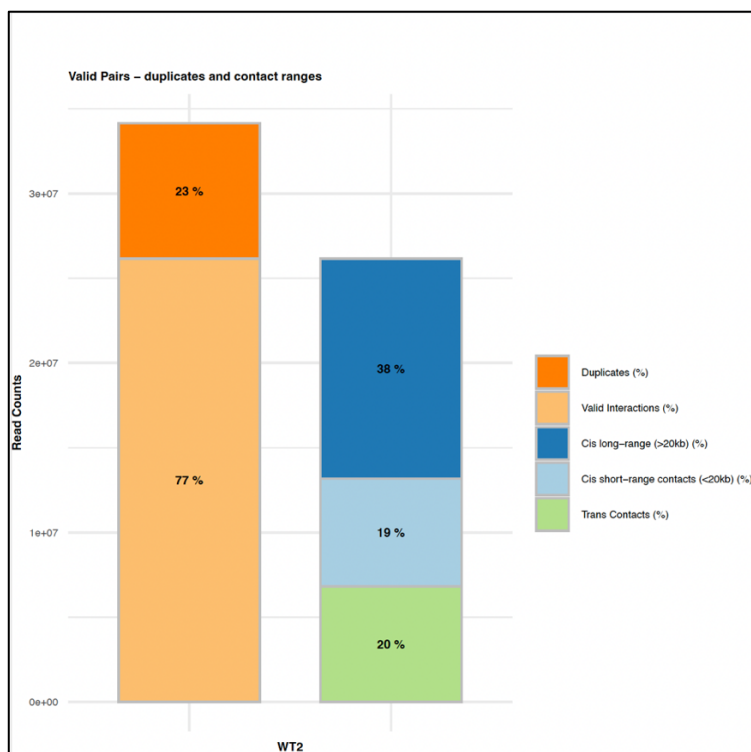


Figure S1.3: Intra- and inter-chromosomal contact maps identified using Hi-C Pro. Detailed graphic explanations can be found here: <https://nservant.github.io/HiC-Pro/RESULTS.html#intra-and-inter-chromosomal-contact-maps>.

References

1. Poinsignon,T., Gallopin,M., Grognet,P., Malagnac,F., Lelandais,G. and Poulain,P. (2023) 3D models of fungal chromosomes to enhance visual integration of omics data. *NAR Genomics and Bioinformatics*, **5**, lqad104.
2. Servant,N., Varoquaux,N., Lajoie,B.R., Viara,E., Chen,C.-J., Vert,J.-P., Heard,E., Dekker,J. and Barillot,E. (2015) HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. *Genome Biol*, **16**, 259.
3. Ewels,P., Magnusson,M., Lundin,S. and Käller,M. (2016) MultiQC: summarize analysis results for multiple tools and samples in a single report. *Bioinformatics*, **32**, 3047–3048.