



Table S1. The SRA numbers of sequencing reads (FASTQ), sequencing dates, base-call model used, and number of bases of all samples used in this study

Species	Sample number	SRA number	Sequencing Date	Caller Used	Model	Number of Bases	Reference
<i>C. albicans</i>	Sample 1	SRR19900988	29-06-2022	Guppy (v6.0.1)		39.6M	[48]
	Sample 2	SRR19901033	29-06-2022	Guppy (v6.0.1)		74.8M	[48]
	Sample 3	SRR7874309	18-09-2018	Guppy (v6.0.1)		1.1G	[49]
	Sample 4	SRR21528967	19-12-2022	GridION	X5 platform set to super accurate base calling	709.6M	[50]
	Sample 5	SRR17110952	08-12-2021	GridION		1.5G	N/A
	Sample 6	SRR17110953	08-12-2021	GridION		2.3G	N/A
<i>C. gattii</i>	Sample 1	SRR23862319	17-03-2023	N/A		77.9M	[51]
	Sample 2	SRR23862320	17-03-2023	N/A		244M	[51]
	Sample 3	SRR23862321	17-03-2023	N/A		221.5M	[51]
	Sample 4	SRR23862337	17-03-2023	N/A		308.3M	[51]
	Sample 5	SRR8435355	31-10-2019	Albacore (v2.3.1)		319.1M	[52]
	Sample 6	SRR8435356	31-10-2019	Albacore (v2.3.1)		604.9M	[52]
<i>S. cerevisiae</i>	Sample 1	ERR8609718	27-11-2022	Metrichor		1.4G	[53]
	Sample 2	ERR8562481	27-11-2022	Metrichor		1.6G	[53]
	Sample 3	ERR8562480	27-11-2022	Metrichor		1.3G	[53]
	Sample 4	ERR8562473	27-11-2022	Metrichor		593.7M	[53]
	Sample 5	ERR8562469	27-11-2022	Metrichor		811.9M	[53]
	Sample 6	ERR8562397	27-11-2022	Metrichor		857.5M	[53]
<i>P. falciparum</i>	Sample 1	ERR10160144	02-10-2022	MinIT (v18.09.1)		2.9G	[54]
	Sample 2	ERR10160143	02-10-2022	MinIT (v18.09.1)		1.2G	[54]
	Sample 3	ERR10160142	02-10-2022	MinIT (v18.09.1)		1.1G	[54]

Sample 4	ERR10160141	02-10-2022	MinIT (v18.09.1)	902.7M	[54]
Sample 5	ERR10502702	01-12-2022	Guppy (v6.0.7)	195.9M	[55]
Sample 6	ERR10502698	01-12-2022	Guppy (v6.0.7)	135.1M	[55]

N/A: not applicable.

Table S2. NCBI references used for the four eukaryotic species, *C. albicans*, *C. gattii*, *S. cerevisiae*, and *P. falciparum*.

Species	Reference
<i>C. albicans</i>	CP017623.1 <i>Candida albicans</i> SC5314
<i>C. gattii</i>	CP000286.1 <i>Cryptococcus gattii</i> WM276
<i>S. cerevisiae</i>	BK006935.2 TPA_inf: <i>Saccharomyces cerevisiae</i> S288C
<i>P. falciparum</i>	AL844501.2 <i>Plasmodium falciparum</i> 3D7

Table S3. Mapped reads percentage against the appropriate reference genome as detected by qualimap.

Species	Sample number	Coverage %
<i>C. albicans</i>	Sample 1	99.25
	Sample 2	88.57
	Sample 3	99.29
	Sample 4	99.59
	Sample 5	97.39
	Sample 6	99.23
<i>C. gattii</i>	Sample 1	98.53
	Sample 2	98.57
	Sample 3	91.7
	Sample 4	98.54
	Sample 5	93.93
	Sample 6	95.71
<i>S. cerevisiae</i>	Sample 1	99.45
	Sample 2	99.7
	Sample 3	97.53
	Sample 4	96.53
	Sample 5	96.53
	Sample 6	86.44
<i>P. falciparum</i>	Sample 1	99.77
	Sample 2	99.96
	Sample 3	99.94
	Sample 4	99.98
	Sample 5	100
	Sample 6	100