

## Supplemental Table S1: *C. gattii* genome statistics

### a. Overview of the WM276 Sequencing Project

Shotgun sequencing overview				
Clones	Total reads	Unique reads	Q20 Bases sequenced (coverage)	Size
89,185	182,363	172,960	118,625,630 (6.48X)	18.38 Mb
Sequencing libraries				
Library	Insert size	Reads	Unique reads	Clones
CN022 Plasmid	2.2 kb	67,392	67,392	35,328
CN23E Plasmid	2.3 kb	47,136	47,136	24,096
CN13E Plasmid	13 kb	38,014	38,014	19,199
CF001 Fosmid	40 kb	11,520	11,520	5,760
CNWM1 BAC	100 kb	12,864	6,144	3,072
CZ000 Finishing	Variable	5,437	2,754	1,730

### b. Summary of the sequence assembly for the genome of the *C. gattii* strain WM276

Chromosome	Length (Mb)	Total gaps	Non-centromere gaps	Telomeric sequences	Error rate per 10kb
1	1.98	0	0	1	0.002
2	2.19	2	0	1	0.384
3	1.96	1	1	1	0.018
4	2.22	1	0	0	0.116
5	1.33	1	1	2	0.267
6	1.33	0	0	0	0.378
7	1.32	0	0	2	0.003
8	1.27	0	0	1	0.036
9	0.99	0	0	2	0.09
10	0.52	1	1	2	0.675
11	1.04	0	0	2	0.002
12	0.82	0	0	2	0.34
13	0.7	1	0	2	0.494
14	0.68	1	0	2	0.01
mtDNA	0.03	0	0	-	0.0005
<b>TOTAL</b>	<b>18.38</b>	<b>8</b>	<b>4</b>	<b>20</b>	<b>0.170</b>

### c. *C. gattii* R265 sequencing statistics

Genomic Libraries	Insert size $\pm$ STD	Reads	Coverage
pOT	4,233 $\pm$ 131	114,345	4.52x
pJAN	9,197 $\pm$ 303	47,322	1.94x
<b>TOTAL</b>	-	<b>161,667</b>	<b>6.46x</b>