Appendix

Terms from the Process Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
None			

Terms from the Function Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
NAD binding	2 out of 9 genes 22.2%	27 out of 6473 genes 0.4%	*C210070W_A, C503770C_A*
Oxidoreductase activity, acting on the CH-OH group of donors, NAD, or NADP as acceptor	2 out of 19 genes 26.3%	69 out of 6473 genes 1.1%	*C210070W_A, C503770C_A*
Oxidoreductase activity, acting on the CH-OH group of donors	2 out of 9 genes 22.2%	73 out of 6473 genes 1.1%	*C210070W_A, C503770C_A*

Terms from the Component Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
None			

Appendix Table S1. Results of gene ontology (GO) term enrichment analysis of differentially expressed genes between diploid and tetraploid cells on PRE-SPO medium at 3 h. Background frequency represents the total number of genes annotated to each GO term in the *C. albicans* genome divided by the total number of genes in the genome. All included terms are significantly enriched ($p < 0.05$).

Terms from the Process Ontology			
Gene Ontology term	**Cluster frequency**	**Background frequency**	**Genes annotated to the term**
Acetate catabolic process	2 out of 19 genes 10.5%	8 out of 6473 genes 0.1%	*CTN1, ICL1*
Regulation of flocculation	2 out of 19 genes 10.5%	9 out of 6473 genes 0.1%	*ALS1, PGA13*
Acetate metabolic process	2 out of 19 genes 10.5%	13 out of 6473 genes 0.1%	*CTN1, ICL1*

Terms from the Function Ontology			
Gene Ontology term	**Cluster frequency**	**Background frequency**	**Genes annotated to the term**
Structural constituent of ribosome	5 out of 19 genes 26.3%	162 out of 6473 genes 2.5%	*RDN18, RDN25, RDN5, RDN58, RRNS*
Structural molecule activity	5 out of 19 genes 26.3%	261 out of 6473 genes 4.0%	*RDN18, RDN25, RDN5, RDN58, RRNS*

Terms from the Component Ontology			
Gene Ontology term	**Cluster frequency**	**Background frequency**	**Genes annotated to the term**
Ribosomal subunit	5 out of 19 genes 26.3%	171 out of 6473 genes 2.6%	*RDN18, RDN25, RDN5, RDN58, RRNS*
Cytosolic ribosome	4 out of 19 genes 21.1%	101 out of 6473 genes 1.6%	*RDN18, RDN25, RDN5, RDN58*
Ribosome	5 out of 19 genes 26.3%	225 out of 6473 genes 3.5%	*RDN18, RDN25, RDN5, RDN58, RRNS*
Cytosolic large ribosomal subunit	3 out of 19 genes 15.8%	58 out of 6473 genes 0.9%	*RDN25, RDN5, RDN58*
Cytosolic part	4 out of 19 genes 21.1%	154 out of 6473 genes 2.4%	*RDN18, RDN25, RDN5, RDN58*
Cell wall	4 out of 19 genes 21.1%	163 out of 6473 genes 2.5%	*ALS1, HWP1, PGA13, PGA31*
Fungal-type cell wall	4 out of 19 genes 21.1%	163 out of 6473 genes 2.5%	*ALS1, HWP1, PGA13, PGA31*
External encapsulating structure	4 out of 19 genes 21.1%	164 out of 6473 genes 2.5%	*ALS1, HWP1, PGA13, PGA31*
Cell surface	4 out of 19 genes 21.1%	203 out of 6473 genes 3.1%	*ALS1, HWP1, PGA13, PGA31*

Appendix Table S2. Results of gene ontology (GO) term enrichment analysis of differentially expressed genes between diploid and tetraploid cells on PRE-SPO medium at 6 h. Background frequency represents the total number of genes annotated to each GO term in the *C. albicans*

genome divided by the total number of genes in the genome. All included terms are significantly

enriched (p<0.05).

Terms from the Process Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
None			

Terms from the Function Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
None			

Terms from the Component Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
Chromosomal part	7 out of 27 genes 25.9%	384 out of 6473 genes 5.9%	*CDC6, HCM1, HHT2, MCD1, OGG1, PRI2 TOS4*
Chromosome	7 out of 27 genes 25.9%	404 out of 6473 genes 6.2%	*CDC6, HCM1, HHT2, MCD1, OGG1, PRI2 TOS4*
Nuclear chromosome part	6 out of 27 genes 22.2%	311 out of 6473 genes 4.8%	*CDC6, HCM1, HHT2, MCD1, PRI2, TOS4*
Protein-DNA complex	3 out of 27 genes 11.1%	56 out of 6473 genes 0.9%	*CDC6, HHT2, PRI2*

Appendix Table S3. Results of gene ontology (GO) term enrichment analysis of differentially expressed genes between diploid and tetraploid cells on PRE-SPO medium at 12 h. Background frequency represents the total number of genes annotated to each GO term in the *C. albicans* genome divided by the total number of genes in the genome. All included terms are significantly enriched (p<0.05).

Terms from the Process Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
Negative regulation of hydrolase activity	6 out of 1173 genes 3.5%	19 out of 6473 genes 0.3%	*C1_14190C_A, CDC46, CDC54, HSP30, MCM2, MCM3*
Negative regulation of helicase activity	4 out of 173 genes 2.3%	6 out of 6473 genes 0.1%	*CDC46, CDC54, MCM2, MCM3*
Regulation of helicase activity	4 out of 173 genes 2.3%	8 out of 6473 genes 0.1%	*CDC46, CDC54, MCM2, MCM3*
DNA replication	12 out of 19 genes 6.9%	115 out of 6473 genes 1.8%	*C1_01130W_A, C1_07490C_A, CDC46, CDC54, DUN1, DUT1, MCM2, MCM3, PRI2, RFA1, RNR1, YBL053*

Terms from the Function Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
Single-stranded DNA-dependent ATP-dependent DNA helicase activity	4 out of 173 genes 2.3%	7 out of 6473 genes 0.1%	*CDC46, CDC54, MCM2, MCM3*
Single-stranded DNA-dependent ATPase activity	4 out of 173 genes 2.3%	11 out of 6473 genes 0.2%	*CDC46, CDC54, MCM2, MCM3*
Double-stranded DNA binding	13 out of 173 genes 7.5%	157 out of 6473 genes 2.4%	*CDC46, CDC54, CR_02510W_A, CSR1, MCM2, MCM3, NRG1, RFA2, RME1, STP2, UGA3, WOR4, YBL053*
Sequence-specific DNA binding	14 out of 173 genes 8.1%	184 out of 6473 genes 2.8%	*AHR1, CDC46, CDC54, CR02510W_A, CSR1, CUP9, MCM2, MCM3, NRG1, RFA2, RME1, STP2, UGA3, WOR4*
Sequence-specific double-stranded DNA binding	10 out of 173 genes 5.8%	110 out of 6473 genes 1.7%	*CDC46, CDC54, CR02510W_A, CSR1, MCM2, MCM3, RME1, STP2, UGA3, WOR4*

Terms from the Component Ontology			
Gene Ontology term	Cluster frequency	Background frequency	Genes annotated to the term
MCM complex	4 out of 173 genes 2.3%	6 out of 6473 genes 0.1%	*CDC46, CDC54, MCM2, MCM3*
Nuclear replication fork	8 out of 173 genes 4.6%	42 out of 6473 genes 0.6%	*C1_07490C_A, CDC46, CDC54, MCM2, MCM3, PRI2, RFA2, YBL053*
Replication fork	8 out of 173 genes 4.6%	52 out of 6473 genes 0.8%	*C1_07490C_A, CDC46, CDC54, MCM2, MCM3, PRI2, RFA2, YBL053*
CMG complex	4 out of 173 genes 2.3%	11 out of 6473 genes 0.2%	*CDC46, CDC54, MCM2, MCM3*
Replication fork protection complex	5 out of 173 genes 2.9%	24 out of 6473 genes 0.4%	*CDC46, CDC54, MCM2, MCM3, YBL053*
Protein-DNA complex	7 out of 173 genes 4.0%	56 out of 6473 genes 0.9%	*C1_07490C_A, CDC46, CDC54, MCM2, MCM3, PRI2, RFA2*

Appendix Table S4. Results of gene ontology (GO) term enrichment analysis of differentially expressed genes between diploid and tetraploid cells on PRE-SPO medium at 24 h. Background frequency represents the total number of genes annotated to each GO term in the *C. albicans*

genome divided by the total number of genes in the genome. All included terms are significantly

enriched (p<0.05).

Oligo Number	Oligo Name	Oligo Sequence
4564	Cap1-Neon long oligo for	GCTAAATGTTCTGAAAAGGGAGTAGTGATA AATACTGCTGATGTGAATCAATTACTAGAGC GAAGTATAAAACATGGTGGTAGTGGTATGG TTTCTAAAG
4565	Cap1-Neon long oligo rev	CCAAATATAAATATAAATACAAAAAAATAAA GCCAAATAGATGTCAATTGAAATACCGTAAA ATAAATTAAACCCCCGCTCTAGAACTAGTGGAT
5547	SOD1_TetOff_For	TTAGTACACGACCTTAATTTGTCACATACATG CTTTACTTTCTCCGATCCAACGGGGATTCATT ATTATTATTTGCTTATGggaaacagctatgaccatg
5548	SOD1_TetOff_Rev	AGATTATAATTGTTTCTTTTTCTATTATTTTGC AACCATTAAGATACAATTGCATTGAATTACAT ACCAGCTTTAACCATcgactatttatatttgtatg
4823	SOD2_TetOff_For	GATAGCGCTACATATAGATTAATCACCAGTTT ATGATAGTAAACACATGAAAAAGTTACACAT AATAATTGCTTACAAATGggaaacagctatgaccatg
4824	SOD2_TetOff_Rev	GCAGCGGCGTTCAAAGTAGCACGGGTAGTTG CGGAAGAAGCCTTTAATAAAACACGAGATGA TGATCTGATAGAAACATcgactatttatatttgtatg
4702	SOD3_TetOff_For	ATTCAATCACACATTTCCAGTATGCATTTCCCA GAGGAAAAAGCGTTCAAGTCGCTTGCTATAAT GAGTTGCGGAAATGggaaacagctatgaccatg
4703	SOD3_TetOff_Rev	GCTTTTATACCCAGAGAGTGCTGTGAGGTTAT GTATACTCCCTACGCAAAATTAAACTTTGTACT ATTGTGGTTATCCATcgactatttatatttgtatg
4813	TRX1_TetOff_For	AAAAGATAAGCAAGATAATTGATGATGATGA ATAATAAATGTTGATTTCTCAGCAACGATCTA CTGCCGCGGCGGCCAATGggaaacagctatgaccatg
4814	TRX1_TetOff_Rev	GCAAAAAAGTCAACAATAACTAAGTTGTTTTC CTTTAAAAGGGTTTGGAATTCGTTAACTTCAG TGACAACGTGAACCATcgactatttatatttgtatg
4817	GCS1_TetOff_For	GTTCAATTCGATTTAATTCAACTCACAACCAAA CGTATGTATACTTGTTGATTGAGTTGTGACAA AACTATTTGGCAGATGggaaacagctatgaccatg
4818	GCS1_TetOff_Rev	ATCCCATTGGTTCTAACATGATTATTATACTTTT TCGATTCATCCCAACTTAAAGGTGTACCAATA GATAAAAGACCCATcgactatttatatttgtatg

Appendix Table S5. Oligonucleotides used in this study.