

SUPPLEMENTAL MATERIAL

“Global Translational Landscape of the *Candida albicans* Morphological Transition”

Table S1. Biotinylated subtraction oligonucleotides used for *C. albicans* ribosome profiling experiments.

Table S2. Number of genes showing significantly altered translational efficiency and RNA differential expression (DE) during the *C. albicans* yeast-filament transition.

Figure S1. Ribo-seq and RNA-seq biological replicates show strong consistency.

Figure S2. Gene ontology (GO) and network analysis of genes showing differential expression (DE) at the transcript level.

Figure S3. Volcano plot of genes showing differential expression (DE) at the transcript level during the *C. albicans* morphological transition.

Dataset S1. Translational efficiency (TE) and RNA differential gene expression (DE) data for annotated genes as well as potential novel genes and uORFs in *C. albicans* cells undergoing the yeast-filament transition. Gene names and descriptions are based on *Candida* Genome Database annotations (<http://www.candidagenome.org>).

Dataset S2. Gene Ontology (GO) data for genes showing alterations in translational efficiency (TE) and RNA differential gene expression (DE) during the *C. albicans* morphological transition as well as *C. albicans* genes possessing potential uORFs and ribosome pausing sites.

Dataset S3. Re-annotated *C. albicans* GTF file.

Dataset S4. GTF file for potential novel *C. albicans* ORFs only.

Dataset S5. *C. albicans* potential uORFs identified in this study. Please note that potential uORFs identified for both alleles are shown.

Dataset S6. Potential novel *C. albicans* ORFs identified in this study.

Dataset S7. *C. albicans* ribosome pausing sites identified in this study.

Table S1. Biotinylated subtraction oligonucleotides used for *C. albicans* ribosome profiling experiments.

Oligonucleotide	Sequence	Concentration in cocktail (μM)
oDM011	/5Biosg/GGCCATGCGATTCGAAAAGTTATTATGAATCATCAAAGA	10
oDM012	/5Biosg/AAACGACGCTCAAACAGGCATGCCCTCCGGAATA	10
oDM013	/5Biosg/TACCTTCTTCAAATTACAACCTCGGACGCCAAAAA	5
oDM014	/5Biosg/ACCTCCAGCTCCGCTTCATTGAATAAGTAAAAAACTA	5
oDM015	/5Biosg/ACATCAGGATCGGTTCGATGGTGCACCCATAA	5
oDM016	/5Biosg/ACTTTCGTTCTTGATTAATGAAAACGTCCTTGGTAAA	5
oDM017	/5Biosg/AACCAATCCGGAGGCCTCACTAAGCCATTCAAA	5
oDM018	/5Biosg/CCAGAGGGCGCAATGTGCGTTCAAAGATTCGATGATT	10
oDM019	/5Biosg/AACGACGCTCAAACAGGCATGCCCTCCGGAATAC	10
oDM020	/5Biosg/ATTCTATTATTCATGCTAATATATTCGAGCAAAGG	10
VMO 171	/5Biosg/AGCTCTAGAATTACCACGGTTATCCAAG	5
VMO 172	/5Biosg/ATACCCCGACCGTCCCTATTAATCA	5
VMO 173	/5Biosg/CCCAGCACGACGGAGTTTCACAAGAT	5
VMO 174	/5Biosg/TCGGTCTAGGCTGGCAGTATCGTCAGAGGC	10
VMO 175	/5Biosg/ACCATCTTTCGGGTCCCAACAGCTATGCTC	5
VMO 176	/5Biosg/GTCAGAACCGCTACGAGCCTCCACCAGAG	5
VMO 177	/5Biosg/GCAATCACGGTGAAGTATAAGTAGCACGCT	5
VMO178	/5Biosg/GGACCGTCGTAAGCGCACCCGGACGCGGCA	5
VMO 179	/5Biosg/AGGGCTTAATGCTAGAACGTGGAG	5
VMO 180	/5Biosg/TAAACCCAGCTCACGTTCCCTATTAGTGG	5
VMO 181	/5Biosg/CCCAGGGCTCACGCCGACGTCTCCACAT	5
VMO 182	/5Biosg/GACTTTGATTTCTCGTAAGGTGCCGATTGCGTC	5
VMO 183	/5Biosg/AATGACCAAGTTTGACCAGCTTCTCGG	10
VMO 184	/5Biosg/TCTCCACATTCAGTTACGTTGCCGT	5
VMO 235	/5Biosg/TGTAACTTGTTTCAGATATTAGATACA	5
VMO 236	/5Biosg/TTCACAGGGATTATCTCATACCCATT	5
VMO 237	/5Biosg/ATGCTAGCAGCACTATTTAGTAGGTTAAGG	5
VMO 238	/5Biosg/CCCTCTAAGAAGTGACTATAACCAGCA	5
VMO 239	/5Biosg/TATCCTGCCGCTCCAAACCGATGCTGGCCC	5
VMO 240	/5Biosg/ATGGCCCACTAAAAGCTCTTCATTCAA	5
VMO 241	/5Biosg/TTCAGCGGGTAGTCCTACCTGATTTGAGGTC	5
VMO 242	/5Biosg/GCCGACATCGAAGAATCAAAAAGCAATGTTCGC	5
VMO 245	/5Biosg/AGATTGCAGCACAAATAGTTTCGCGTATGG	10
VMO 246	/5Biosg/GTCAAATTAAGCCGAGGCTCCACTCCTGG	5
VMO 247	/5Biosg/AAACCGCAGTCCTCGGTCTAGGCTGGCAGTA	5

Note: Oligonucleotides oDMO11-oDMO20 were initially reported by Muzzey, *et al.*, *Genome Res.* 24:963-973 (2014).

Table S2. Number of genes showing significantly altered translational efficiency and RNA differential expression during the *C. albicans* yeast-filament transition.

	≥ 2-fold	≥ 4-fold	≥ 8-fold
# of genes showing increased TE*	176	73	20
# of genes showing reduced TE*	111	43	6
# of genes showing increased RNA DE†	499	166	63
# of genes showing reduced RNA DE†	387	84	15

* Fold changes are based on mean translational efficiency (TE) values in cells grown in YEPD + 10% serum at 37°C vs. YEPD at 30°C at the 1-hour time point, from three independent experiments (n=3, TPM >1 in at least 2 replicates, $p \leq 0.05$).

† Fold changes are based on mean RNA differential expression (DE) values in cells grown in YEPD + 10% serum at 37°C vs. YEPD at 30°C at the 1-hour time point, from three independent experiments (n=3, TPM >1 in at least 2 replicates, $p_{\text{adj}} \leq 0.05$).

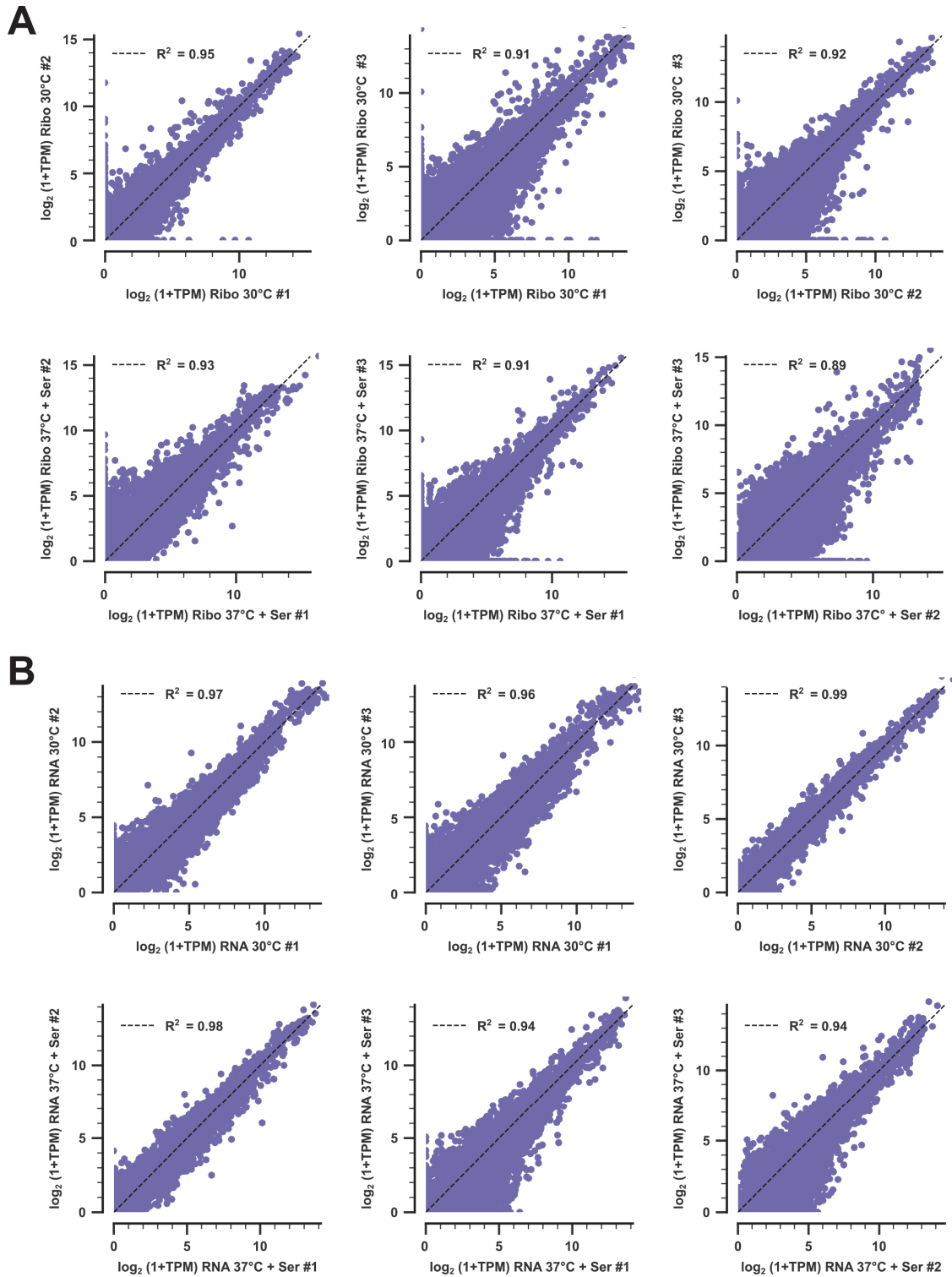


Figure S1. Ribo-seq and RNA-seq biological replicates show strong consistency. (A) Scatter plots indicating a strong correlation in gene Ribo-seq data TPM counts among all three biological replicates for each growth condition. (B) Scatter plots indicating a strong correlation in gene RNA-seq data TPM counts among all three biological replicates for each growth condition.

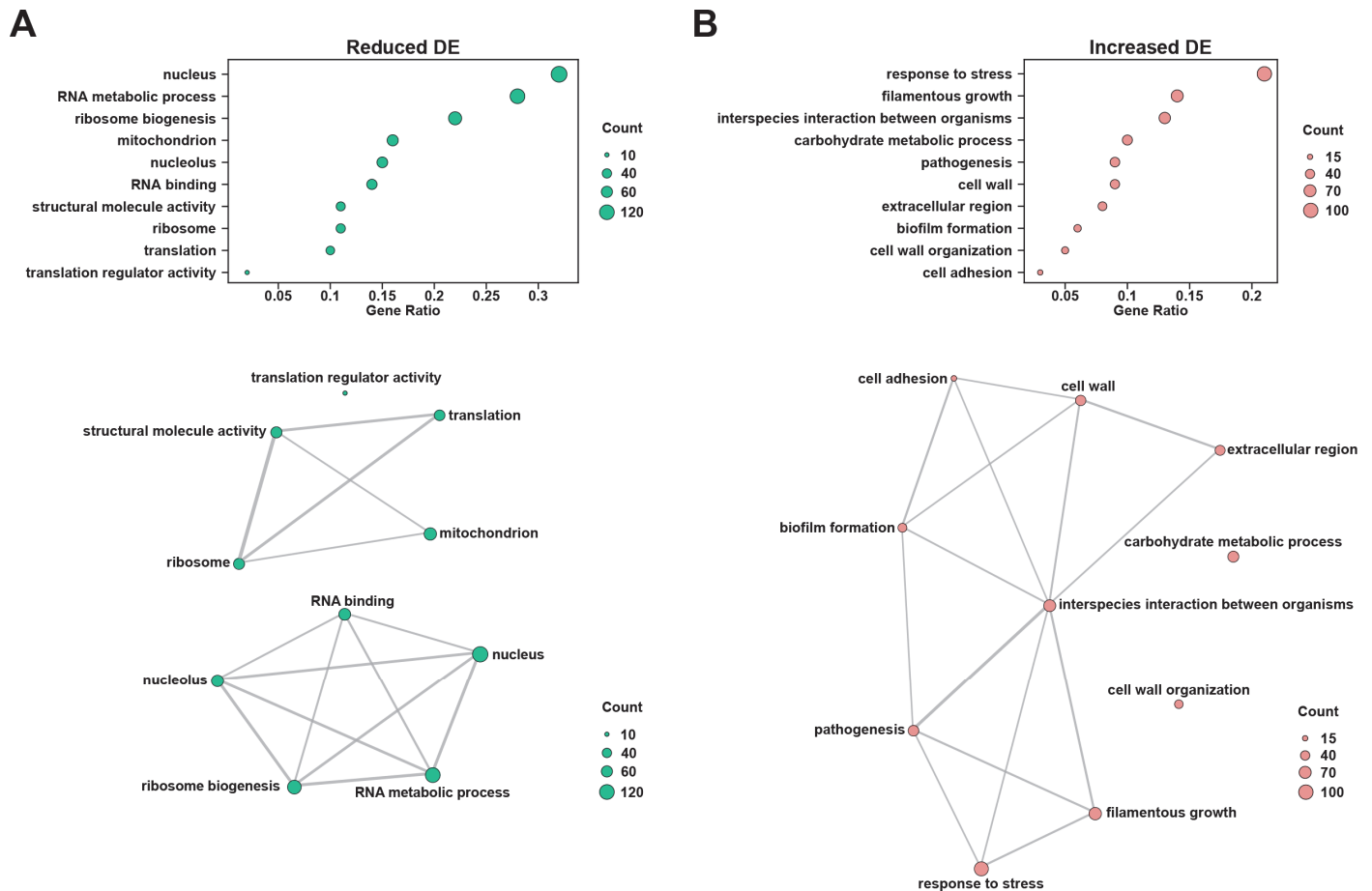


Figure S2. Gene ontology (GO) and network analysis of genes showing differential expression (DE) at the transcript level. (A) Genes showing significantly reduced DE as defined in Table S1 were classified by GO terms using the *C. albicans* GO Slim ontology (*Candida* Genome database, <http://www.candidagenome.org/>) (upper panel). Overlap among genes associated with specific GO terms is denoted by line thickness in a network analysis (lower panel). (B) Genes showing significantly increased DE as defined in Table S1 were classified by GO terms (upper panel) and were used for network analysis (lower panel) as described in part (A). Only GO terms with gene ratios ≥ 0.02 and $p_{adj} \leq 0.05$ are shown. Count = number of genes within each GO term.

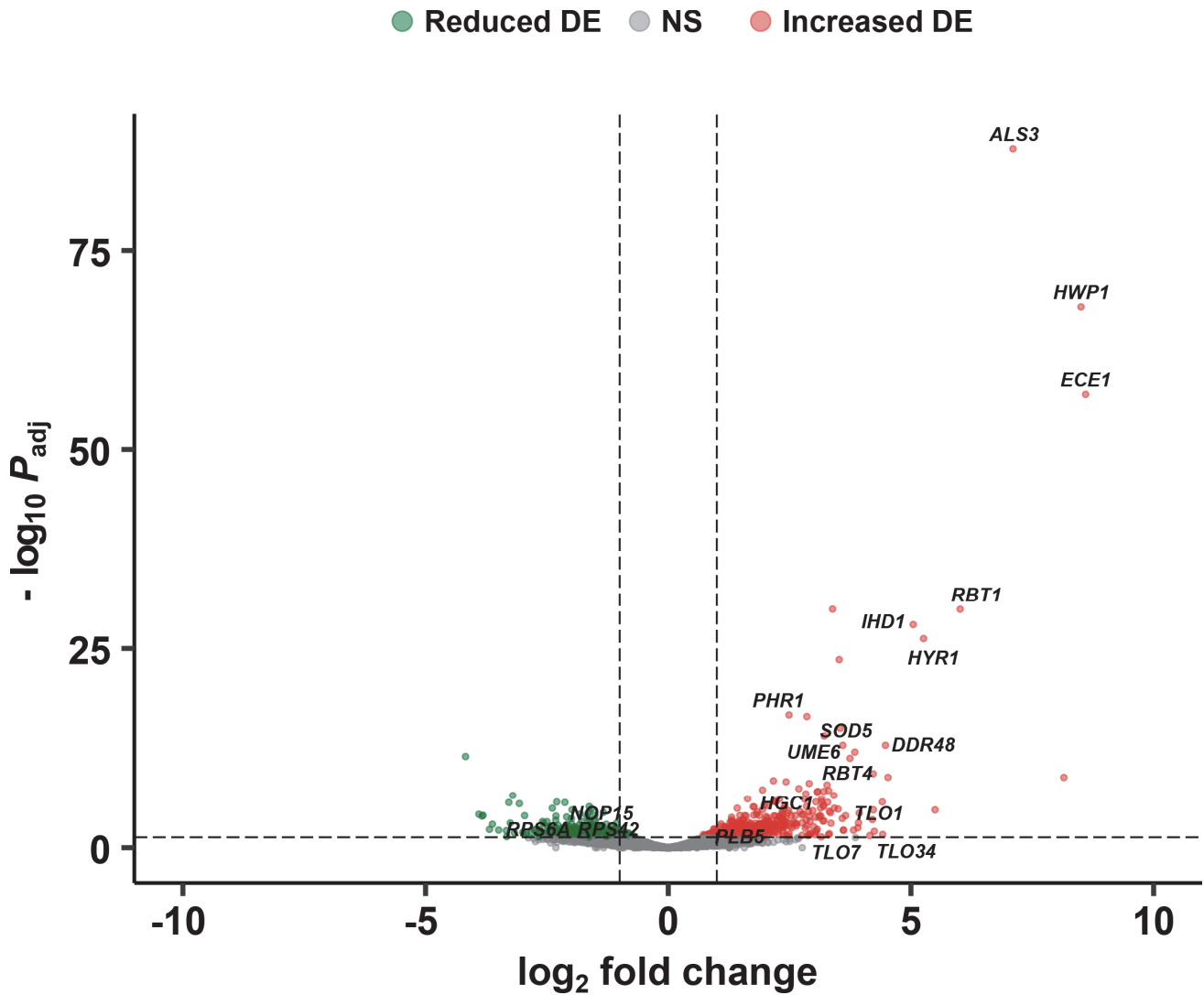


Figure S3. Genes showing differential expression (DE) at the transcript level during the *C. albicans* morphological transition. Volcano plot of *C. albicans* genes showing altered DE in the presence (37°C + serum) vs. absence (30°C) of filament-inducing conditions. Vertical dotted lines indicate 2-fold change cutoff in DE. Horizontal dotted line indicates $p_{adj} = 0.05$ cutoff. Genes of interest are shown in black. NS = non-significant.