**Table S8.** Gene Ontology Term analysis for proteins present in increased abundance in *C. albicans ubc7*/*ubc7*mutants.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **GO Term** | **Corrected p value** | **FDR** | **Genes** |
| Process | small molecule metabolic process | 1.01E-05 | 0.00% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 GAD1 FAD3 ERG10 SER1 SPE3 IPP1 C2\_09970C ADE2 LYS9 SEC61 PEX5 PYC2 GDH3 ACH1 GRP2 HIS1 ERG5 C7\_04210C ATP3 ERG25 LAP3 URA2* |
| small molecule biosynthetic process | 8.02E-05 | 0.00% | *POR1 ERG3 PGA63 DPM1 SEC24 FAD3 ERG10 SER1 SPE3 IPP1 LYS9 SEC61 PEX5 PYC2 GDH3 HIS1 ERG5 C7\_04210C ERG25* |
| organic substance biosynthetic process | 0.00023 | 0.00% | *MVD ROT1 TIM21 POR1 ERG3 PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 FAD3 KAR2 ERG10 NDH51 SER1 SPE3 C2\_07680W IPP1 ADE2 C3\_05280C LYS9 SEC61 PEX5 PYC2 GDH3 TIF5 SUI1 C5\_04530W HIS1 C6\_00270W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 C7\_04210C ATP3 ERG25 URA2 CR\_10830C* |
| biosynthetic process | 0.00036 | 0.00% | *MVD ROT1 TIM21 POR1 ERG3 PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 FAD3 KAR2 ERG10 NDH51 SER1 SPE3 C2\_07680W IPP1 ADE2 C3\_05280C LYS9 SEC61 PEX5 PYC2 GDH3 TIF5 SUI1 C5\_04530W HIS1 C6\_00270W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 C7\_04210C ATP3 ERG25 URA2 CR\_10830C* |
| cellular biosynthetic process | 0.00052 | 0.00% | *MVD ROT1 TIM21 POR1 ERG3 PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 FAD3 KAR2 ERG10 NDH51 SER1 SPE3 C2\_07680W IPP1 ADE2 C3\_05280C LYS9 SEC61 PEX5 GDH3 TIF5 SUI1 C5\_04530W HIS1 C6\_00270W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 C7\_04210C ATP3 ERG25 URA2 CR\_10830C* |
| cellular process | 0.00057 | 0.00% | *MVD HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 GAD1 MRPS9 FAD3 DIM1 KAR2 C2\_02800W C2\_03450W DCK1 ERG10 NDH51 RPF2 SER1 SPE3 C2\_07680W IPP1 C2\_09970C HOS2 NCE103 ARF3 C3\_02620C ADE2 SFP1 C3\_05150W C3\_05280C LYS9 SEC61 PEX5 PYC2 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 GRP2 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C YHM1 C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 C7\_04210C ATP3 ERG25 RFG1 LAP3 HSP60 URA2 ACO1 CR\_10830C* |
| cellular amide metabolic process | 0.00076 | 0.00% | *MVD TIM21 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C PEX5 ACH1 TIF5 SUI1 C5\_04530W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| primary metabolic process | 0.00076 | 0.00% | *MVD ROT1 C1\_01160C TIM21 C1\_03830C POR1 ERG3 C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 GAD1 MRPS9 FAD3 DIM1 KAR2 C2\_03450W ERG10 NDH51 RPF2 SER1 SPE3 C2\_07680W IPP1 C2\_09970C HOS2 NCE103 ADE2 SFP1 C3\_05150W C3\_05280C LYS9 SEC61 PEX5 PYC2 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 PDI1 C7\_04210C ATP3 ERG25 LAP3 HSP60 URA2 ACO1 CR\_10830C* |
| organic substance metabolic process | 0.00103 | 0.00% | *MVD HMX1 ROT1 C1\_01160C TIM21 C1\_03830C POR1 ERG3 C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 GAD1 MRPS9 FAD3 DIM1 KAR2 C2\_03450W ERG10 NDH51 RPF2 SER1 SPE3 C2\_07680W IPP1 C2\_09970C HOS2 NCE103 ADE2 SFP1 C3\_05150W C3\_05280C LYS9 SEC61 PEX5 PYC2 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 GRP2 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 PDI1 C7\_04210C ATP3 ERG25 LAP3 HSP60 URA2 CR\_10830C* |
| intracellular protein transmembrane transport | 0.00114 | 0.00% | *TIM21 KAR2 C3\_02620C SEC61 PEX5 C4\_05820W TOM40 TOM70 HSP60 ACO1* |
| protein transmembrane transport | 0.00114 | 0.00% | *TIM21 KAR2 C3\_02620C SEC61 PEX5 C4\_05820W TOM40 TOM70 HSP60 ACO1* |
| organonitrogen compound biosynthetic process | 0.00153 | 0.00% | *ROT1 TIM21 DPM1 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 ADE2 C3\_05280C LYS9 PEX5 GDH3 TIF5 SUI1 C5\_04530W HIS1 C6\_00270W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 C7\_04210C ATP3 ERG25 URA2 CR\_10830C* |
| carboxylic acid metabolic process | 0.00177 | 0.00% | *ERG3 GAD1 FAD3 SER1 SPE3 LYS9 PEX5 PYC2 GDH3 ACH1 GRP2 HIS1 C7\_04210C ERG25 LAP3 URA2* |
| amide biosynthetic process | 0.00246 | 0.00% | *TIM21 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C PEX5 TIF5 SUI1 C5\_04530W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| oxoacid metabolic process | 0.00278 | 0.00% | *ERG3 GAD1 FAD3 SER1 SPE3 LYS9 PEX5 PYC2 GDH3 ACH1 GRP2 HIS1 C7\_04210C ERG25 LAP3 URA2* |
| sterol biosynthetic process | 0.00287 | 0.00% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| steroid biosynthetic process | 0.00287 | 0.00% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| organic acid metabolic process | 0.00345 | 0.00% | *ERG3 GAD1 FAD3 SER1 SPE3 LYS9 PEX5 PYC2 GDH3 ACH1 GRP2 HIS1 C7\_04210C ERG25 LAP3 URA2* |
| translation | 0.00372 | 0.00% | *TIM21 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C TIF5 SUI1 C5\_04530W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| peptide biosynthetic process | 0.00398 | 0.00% | *TIM21 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C TIF5 SUI1 C5\_04530W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| protein transmembrane import into intracellular organelle | 0.00411 | 0.00% | *TIM21 C3\_02620C SEC61 PEX5 C4\_05820W TOM40 TOM70 HSP60 ACO1* |
| cellular metabolic process | 0.00456 | 0.00% | *MVD HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 GAD1 MRPS9 FAD3 DIM1 KAR2 C2\_03450W DCK1 ERG10 NDH51 RPF2 SER1 SPE3 C2\_07680W IPP1 C2\_09970C NCE103 ADE2 SFP1 C3\_05150W C3\_05280C LYS9 SEC61 PEX5 PYC2 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 GRP2 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W YHM1 C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C ERG5 PDI1 C7\_04210C ATP3 ERG25 LAP3 URA2 ACO1 CR\_10830C* |
| sterol metabolic process | 0.00506 | 0.00% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| metabolic process | 0.00521 | 0.00% | *MVD HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 GAD1 MRPS9 FAD3 DIM1 KAR2 C2\_03450W DCK1 ERG10 NDH51 RPF2 SER1 SPE3 C2\_07680W IPP1 C2\_09970C HOS2 NCE103 ADE2 SFP1 C3\_05150W C3\_05280C LYS9 SEC61 PEX5 PYC2 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 GRP2 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C YHM1 C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C ERG5 PDI1 C7\_04210C ATP3 ERG25 LAP3 HSP60 URA2 ACO1 CR\_10830C* |
| steroid metabolic process | 0.00564 | 0.00% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| peptide metabolic process | 0.00753 | 0.00% | *TIM21 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C TIF5 SUI1 C5\_04530W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| carboxylic acid biosynthetic process | 0.01049 | 0.07% | *ERG3 FAD3 SER1 SPE3 LYS9 PEX5 GDH3 HIS1 C7\_04210C ERG25* |
| cellular macromolecule biosynthetic process | 0.01203 | 0.07% | *ROT1 TIM21 DPM1 MIR1 RPL2 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C3\_05280C TIF5 SUI1 C5\_04530W C6\_00270W YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 ATP3 ERG25 URA2 CR\_10830C* |
| phytosteroid biosynthetic process | 0.01539 | 0.07% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| secondary alcohol biosynthetic process | 0.01539 | 0.07% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| cellular alcohol biosynthetic process | 0.01539 | 0.06% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| ergosterol biosynthetic process | 0.01539 | 0.06% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| cellular lipid biosynthetic process | 0.01539 | 0.06% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| organic hydroxy compound biosynthetic process | 0.01542 | 0.06% | *MVD POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| organic acid biosynthetic process | 0.01711 | 0.06% | *ERG3 FAD3 SER1 SPE3 LYS9 PEX5 GDH3 HIS1 C7\_04210C ERG25* |
| phytosteroid metabolic process | 0.01802 | 0.11% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| cellular alcohol metabolic process | 0.01802 | 0.11% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| ergosterol metabolic process | 0.01802 | 0.11% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| secondary alcohol metabolic process | 0.02213 | 0.10% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| alcohol biosynthetic process | 0.052 | 0.25% | *POR1 ERG3 PGA63 DPM1 SEC24 ERG10 IPP1 SEC61 ERG5 ERG25* |
| protein targeting to mitochondrion | 0.05488 | 0.24% | *TIM21 C3\_02620C C4\_05820W C6\_00340C TOM40 TOM70 HSP60 ACO1* |
| protein import into mitochondrial matrix | 0.06458 | 0.29% | *TIM21 C3\_02620C C4\_05820W TOM40 TOM70 HSP60 ACO1* |
| organonitrogen compound metabolic process | 0.07465 | 0.47% | *MVD HMX1 ROT1 TIM21 DPM1 MIR1 RPL2 GAD1 MRPS9 KAR2 NDH51 SER1 SPE3 C2\_07680W IPP1 C2\_09970C HOS2 ADE2 C3\_05280C LYS9 SEC61 PEX5 C4\_05390W C4\_05820W GDH3 ACH1 TIF5 TRR1 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C YHM1 C6\_01980C C6\_02460C C7\_01350C TOM40 C7\_02120C ERG5 PDI1 C7\_04210C ATP3 ERG25 LAP3 HSP60 URA2 CR\_10830C* |
| protein localization to mitochondrion | 0.07741 | 0.45% | *TIM21 C3\_02620C C4\_05820W C6\_00340C TOM40 TOM70 HSP60 ACO1* |
| establishment of protein localization to mitochondrion | 0.07741 | 0.44% | *TIM21 C3\_02620C C4\_05820W C6\_00340C TOM40 TOM70 HSP60 ACO1* |
| Function | oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water | 0.00813 | 2.00% | *ERG3 FAD3 ERG5* |
| amide binding | 0.01649 | 1.00% | *SEC24 SEC61 PEX5 PYC2 TOM70* |
| sterol desaturase activity | 0.0195 | 1.33% | *ERG3 ERG5* |
| signal sequence binding | 0.02169 | 1.00% | *SEC24 SEC61 PEX5 TOM70* |
| oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 0.03237 | 1.20% | *HMX1 ERG3 FAD3 ERG5 ERG25* |
| peptide binding | 0.05491 | 2.33% | *SEC24 SEC61 PEX5 TOM70* |
| Component | cytoplasm | 2.60E-10 | 0.00% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 KAR2 C2\_02800W DCK1 ERG10 NDH51 C2\_07680W IPP1 HOS2 NCE103 C3\_02620C SFP1 RPL18 C3\_05150W SEC61 PEX5 PYC2 C4\_05820W GDH3 ACH1 TIF5 TRR1 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 LAP3 HSP60 URA2 ACO1 CR\_10830C* |
| mitochondrion | 8.98E-06 | 0.00% | *TIM21 POR1 C1\_05490C MIR1 MRPS9 DCK1 NDH51 C2\_07680W NCE103 C3\_02620C C4\_05820W ACH1 TRR1 C5\_04530W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ATP3 HSP60 ACO1 CR\_10830C* |
| mitochondrial protein-containing complex | 0.00015 | 0.00% | *TIM21 C1\_05490C MRPS9 NDH51 C2\_07680W C5\_04530W C6\_01980C C6\_02460C TOM40 C7\_02120C TOM70 ATP3 CR\_10830C* |
| intracellular anatomical structure | 0.00019 | 0.00% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 KAR2 C2\_02800W DCK1 ERG10 NDH51 RPF2 C2\_07680W IPP1 C2\_09970C HOS2 NCE103 ARF3 C3\_02620C SFP1 RPL18 C3\_05150W SEC61 PEX5 PYC2 C4\_05820W GDH3 ACH1 TIF5 TRR1 SUI1 C5\_04530W TIP20 HIS1 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 LAP3 HSP60 URA2 ACO1 CR\_10830C* |
| organelle membrane | 0.00154 | 0.00% | *HMX1 ROT1 TIM21 POR1 C1\_05490C PGA63 SEC24 MIR1 KAR2 C2\_02800W NDH51 C3\_02620C SEC61 PEX5 C4\_05820W C6\_00270W C6\_02460C TOM40 TOM70 ATP3 ERG25 HSP60* |
| mitochondrial envelope | 0.0016 | 0.00% | *TIM21 POR1 C1\_05490C MIR1 NDH51 NCE103 C3\_02620C C4\_05820W TRR1 C6\_02460C TOM40 TOM70 ATP3 HSP60* |
| membrane-bounded organelle | 0.00221 | 0.00% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 MRPS9 KAR2 C2\_02800W DCK1 NDH51 RPF2 C2\_07680W C2\_09970C HOS2 NCE103 ARF3 C3\_02620C SFP1 C3\_05150W SEC61 PEX5 C4\_05820W GDH3 ACH1 TRR1 C5\_04530W TIP20 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 HSP60 ACO1 CR\_10830C* |
| organelle envelope | 0.00306 | 0.00% | *HMX1 TIM21 POR1 C1\_05490C MIR1 KAR2 NDH51 NCE103 C3\_02620C C4\_05820W TRR1 C6\_02460C TOM40 TOM70 ATP3 HSP60* |
| intracellular membrane-bounded organelle | 0.00316 | 0.00% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 MRPS9 KAR2 C2\_02800W DCK1 NDH51 RPF2 C2\_07680W C2\_09970C HOS2 NCE103 C3\_02620C SFP1 C3\_05150W SEC61 PEX5 C4\_05820W GDH3 ACH1 TRR1 C5\_04530W TIP20 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 HSP60 ACO1 CR\_10830C* |
| envelope | 0.00325 | 0.00% | *HMX1 TIM21 POR1 C1\_05490C MIR1 KAR2 NDH51 NCE103 C3\_02620C C4\_05820W TRR1 C6\_02460C TOM40 TOM70 ATP3 HSP60* |
| integral component of mitochondrial membrane | 0.00402 | 0.00% | *POR1 C1\_05490C MIR1 C3\_02620C C6\_02460C TOM70* |
| intrinsic component of mitochondrial membrane | 0.00505 | 0.00% | *POR1 C1\_05490C MIR1 C3\_02620C C6\_02460C TOM70* |
| mitochondrial membrane | 0.00528 | 0.00% | *TIM21 POR1 C1\_05490C MIR1 NDH51 C3\_02620C C4\_05820W C6\_02460C TOM40 TOM70 ATP3 HSP60* |
| mitochondrial matrix | 0.00686 | 0.00% | *MRPS9 C2\_07680W C4\_05820W C5\_04530W C6\_00340C C6\_01980C C6\_02460C C7\_02120C HSP60 ACO1 CR\_10830C* |
| integral component of organelle membrane | 0.0088 | 0.00% | *POR1 C1\_05490C MIR1 C2\_02800W C3\_02620C SEC61 C6\_00270W C6\_02460C TOM70* |
| endoplasmic reticulum | 0.00905 | 0.00% | *HMX1 ROT1 ERG3 DPM1 SEC24 KAR2 C2\_02800W SEC61 TIP20 C6\_00270W ERG5 PDI1 ERG25* |
| organellar ribosome | 0.00959 | 0.00% | *MRPS9 C2\_07680W C5\_04530W C6\_01980C C6\_02460C C7\_02120C CR\_10830C* |
| mitochondrial ribosome | 0.00959 | 0.00% | *MRPS9 C2\_07680W C5\_04530W C6\_01980C C6\_02460C C7\_02120C CR\_10830C* |
| intrinsic component of organelle membrane | 0.01337 | 0.00% | *POR1 C1\_05490C MIR1 C2\_02800W C3\_02620C SEC61 C6\_00270W C6\_02460C TOM70* |
| organelle | 0.01379 | 0.00% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 KAR2 C2\_02800W DCK1 NDH51 RPF2 C2\_07680W C2\_09970C HOS2 NCE103 ARF3 C3\_02620C SFP1 RPL18 C3\_05150W SEC61 PEX5 C4\_05820W GDH3 ACH1 TRR1 C5\_04530W TIP20 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 HSP60 ACO1 CR\_10830C* |
| intracellular organelle | 0.01862 | 0.10% | *HMX1 ROT1 C1\_01160C TIM21 AGE1 C1\_03830C POR1 ERG3 C1\_05490C C1\_06540C PGA63 TAF145 DPM1 SEC24 MIR1 RPL2 MRPS9 KAR2 C2\_02800W DCK1 NDH51 RPF2 C2\_07680W C2\_09970C HOS2 NCE103 C3\_02620C SFP1 RPL18 C3\_05150W SEC61 PEX5 C4\_05820W GDH3 ACH1 TRR1 C5\_04530W TIP20 C6\_00270W C6\_00340C C6\_01980C C6\_02460C SOD3 C7\_01350C TOM40 C7\_02120C TOM70 ERG5 PDI1 ATP3 ERG25 HSP60 ACO1 CR\_10830C* |
| extracellular region | 0.01979 | 0.09% | *POR1 MIR1 KAR2 SPE3 IPP1 ARF3 SEC61 GDH3 GRP2 PDI1* |
| plasma membrane | 0.02334 | 0.09% | *HMX1 TIM21 AGE1 POR1 ERG3 DPM1 MIR1 DCK1 NDH51 SEC61 YHM1 TOM40 TOM70 ERG5 ATP3 ERG25* |
| endoplasmic reticulum lumen | 0.03455 | 0.08% | *ERG3 KAR2 PDI1* |
| nuclear exosome (RNase complex) | 0.04565 | 0.08% | *C1\_01160C C1\_03830C C1\_06540C* |
| cytoplasmic exosome (RNase complex) | 0.04565 | 0.08% | *C1\_01160C C1\_03830C C1\_06540C* |
| membrane | 0.05042 | 0.07% | *HMX1 ROT1 TIM21 AGE1 POR1 ERG3 C1\_05490C PGA63 DPM1 SEC24 MIR1 KAR2 C2\_02800W DCK1 NDH51 C3\_02620C C3\_05280C SEC61 PEX5 C4\_05820W C6\_00270W YHM1 C6\_02460C TOM40 TOM70 ERG5 ATP3 ERG25 HSP60 URA2* |
| exosome (RNase complex) | 0.07417 | 0.36% | *C1\_01160C C1\_03830C C1\_06540C* |
| membrane-enclosed lumen | 0.07845 | 0.34% | *C1\_01160C C1\_03830C ERG3 C1\_06540C TAF145 MRPS9 KAR2 RPF2 C2\_07680W HOS2 NCE103 C4\_05820W TRR1 C5\_04530W C6\_00340C C6\_01980C C6\_02460C C7\_02120C PDI1 HSP60 ACO1 CR\_10830C* |
| organelle lumen | 0.07845 | 0.33% | *C1\_01160C C1\_03830C ERG3 C1\_06540C TAF145 MRPS9 KAR2 RPF2 C2\_07680W HOS2 NCE103 C4\_05820W TRR1 C5\_04530W C6\_00340C C6\_01980C C6\_02460C C7\_02120C PDI1 HSP60 ACO1 CR\_10830C* |
| intracellular organelle lumen | 0.07845 | 0.32% | *C1\_01160C C1\_03830C ERG3 C1\_06540C TAF145 MRPS9 KAR2 RPF2 C2\_07680W HOS2 NCE103 C4\_05820W TRR1 C5\_04530W C6\_00340C C6\_01980C C6\_02460C C7\_02120C PDI1 HSP60 ACO1 CR\_10830C* |
| ribosome | 0.07939 | 0.31% | *RPL2 MRPS9 C2\_07680W RPL18 C5\_04530W C6\_01980C C6\_02460C C7\_02120C CR\_10830C* |
| cell periphery | 0.08965 | 0.42% | *HMX1 TIM21 AGE1 POR1 ERG3 DPM1 MIR1 KAR2 DCK1 NDH51 IPP1 SEC61 TRR1 GRP2 YHM1 TOM40 TOM70 ERG5 ATP3 ERG25 ACO1* |
| exoribonuclease complex | 0.09186 | 0.47% | *C1\_01160C C1\_03830C C1\_06540C* |

Genes encoding proteins with altered abundance in *ubc7*/*ubc7 C. albicans* mutants were analyzed using the Gene Ontology Term Finder at the Candida Genome Database (<http://www.candidagenome.org/cgi-bin/GO/goTermFinder>). No significant Process, Function, or Component GO Terms were found for proteins present in decreased abundance in *ubc7*/*ubc7* mutants.