

■ ASSOCIATED CONTENT

📄 Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: [10.1021/acs.jproteome.9b00299](https://doi.org/10.1021/acs.jproteome.9b00299).

Figure S1: Similar growth and viability profiles of *C. glabrata* wild-type (*wt*) and *Cgyps1-11Δ* strains at the time of secretome collection; **Figure S2:** *CgMSB2* gene is modestly upregulated in the *Cgyps1-11Δ* mutant;

Figure S3: *Cgyps1-11Δ* and *Cgyps7Δ* mutants show enhanced sensitivity to the cell wall stressor conogo red; **Figure S4:** comparative analysis of global secretomes of *wild-type*, *Cgyps1-11Δ*, *Cgyps7Δ*, and *Cgyps2ΔCΔ* strains (Figures S1–S4) (PDF)

Table S1: A list of mass spectrometry parameters used for global secretome analysis. **Table S2:** A list of mass spectrometry parameters used for quantitative secretome analysis. **Table S3:** A list of 119 proteins identified in the *wild-type* secretome in global secretome analysis. **Table S4:** A list of 548 proteins identified in the *Cgyps1-11Δ* secretome in global secretome analysis. **Table S5:** Functional classification of putative GPI-anchored proteins identified in the secretomes of *wild-type* and *Cgyps1-11Δ* strains. **Table S6:** DeepLoc 1.0 web server-based subcellular localization analysis of proteins identified in the *wild-type* secretome. **Table S7:** DeepLoc 1.0 web server-based subcellular localization analysis of proteins identified in the *Cgyps1-11Δ* secretome. **Table S8:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories for the *wild-type* secretome, as determined by the FungiFun tool. **Table S9:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories for the *Cgyps1-11Δ* secretome, as determined by the FungiFun tool. **Table S10:** Comparative analysis of identified and predicted secretome of *C. glabrata*. **Table S11:** A list of 29 proteins identified in the *wild-type* secretome, that were not predicted to be secretory. **Table S12:** Comparative analysis of identified secretory proteins in *C. glabrata*, *C. albicans*, and *S. cerevisiae*. **Table S13:** Analysis of secretory proteins that are unique to *C. glabrata*. **Table S14:** A list of 85 proteins identified in the *wild-type* secretome by label-free quantitative secretome profiling. **Table S15:** A list of 193 proteins identified in the *Cgyps1-11Δ* secretome by label-free quantitative secretome profiling. **Table S16:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories, as determined by the FungiFun tool, in the set of 114 proteins, that were unique to the *Cgyps1-11Δ* secretome in quantitative secretome analysis. **Table S17:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories, as determined by the FungiFun tool, in the set of 61 proteins, identified in *wt* secretome by both global and quantitative analysis. **Table S18:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories, as determined by the FungiFun tool, in the set of 155 proteins, identified in *Cgyps1-11Δ* secretome by both global and quantitative analysis. **Table S19:** A list of 53 common proteins in *wild-type* and *Cgyps1-11Δ* secretomes, that were identified by both global and quantitative secretome profiling. **Table S20:** A list of 79 proteins displaying differential abundance in the *Cgyps1-11Δ* secretome based on the peptide number ratio. **Table S21:** Relative abundance analysis, using spectral counting-based approach, of proteins identified in the global secretome. **Table S22:** Relative abundance analysis, using spectral counting-based approach, of proteins identified in the quantitative secretome. **Table S23:** A list of 59 proteins identified in

the *Cgyps7Δ* secretome in global secretome analysis. **Table S24:** A list of 52 proteins identified in the *Cgyps2ΔCΔ* secretome in global secretome analysis. **Table S25:** DeepLoc 1.0 web server-based subcellular localization analysis of proteins identified in the *Cgyps7Δ* secretome. **Table S26:** DeepLoc 1.0 web server-based subcellular localization analysis of proteins identified in the *Cgyps2ΔCΔ* secretome. **Table S27:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories for the *Cgyps7Δ* secretome, as determined by the FungiFun tool. **Table S28:** Enriched GO terms for biological process (BP), cellular component (CC), and molecular function (MF) categories for the *Cgyps2ΔCΔ* secretome, as determined by the FungiFun tool. (XLSX)