## **Supplementary Material**

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A comprehensive analysis of *Candida albicans* phosphoproteome reveals dynamic changes in phosphoprotein abundance during hyphal morphogenesis Priyanka Ghorai<sup>1,2</sup>, Mohammad Irfan<sup>1</sup>, Alka Narula<sup>2</sup>, Asis Datta<sup>1\*</sup> <sup>1</sup>National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi – 110067, India <sup>2</sup>Department of Biotechnology, Faculty of Science, Jamia Hamdard, Hamdard Nagar, New Delhi – 110062, India

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Supplementary Figure S1. Functional annotation of unique phosphoproteins identified in response to (A) temperature, (B) serum and (C) GlcNAc treatment conditions.
Biological function, molecular process and cellular component of each set has been shown. The number of proteins falling in each GO category is directly proportional to the node size. The nodes are colour shaded according to the significance level (corrected *P*-value).
Supplementary Figure S2. Venn diagram showing the comparative analysis of proteins specifically phosphorylated in temperature, serum and GlcNAc treated conditions.
Supplementary Table S1. Catalog of differentially phosphorylated proteins in different hypha-inducing conditions.
Supplementary Table S2. Catalog of protein kinases identified in *C. albicans*.
Supplementary Table S3. Summary of orthologous protein kinase-encoding genes between *C. albicans* and *C. glabrata*.



















**Supplementary Figure S2.** Venn diagram showing the comparative analysis of proteins specifically phosphorylated in temperature, serum and GlcNAc treated conditions.

