## Supplementary Table 1: The major GO terms in three categories (Biological Process, Cellular

Components, Molecular Function)

Category	Terms (functionally grouped)	GO Terms	Group P-value
Biological Process	Regulation of transcription by RNA polymerase II	GO:0006357	0.00043363546137698
	Regulation of response to extracellular stimulus	GO:0032104	1.04959148927719E-07
	Fungal-type cell wall organization or biogenesis	GO:0071852	0.0000675916089676321
	Mitotic cell cycle	GO:0000278	0.117416225373745
	Biofilm formation	GO:0042710	0.0000209231147891842
	Adhesion of symbiont to host	GO:0044406	0.0231961607933044
	Regulation of filamentous growth	GO:0010570	0.000333892909111455
	Pathogenesis	GO:0009405	2.09260506058712E-15
	Regulation of transferase activity	GO:0051338	3.31670480591129E-06
	Regulation of kinase activity	GO:0043549	3.31670480591129E-06
Cellular Components	Plasma membrane	GO:0005886	0.021643377840519
	Intracellular organelle	GO:0043229	0.469022780656815
	Membrane-bounded organelle	GO:0043227	0.469022780656815
	Nucleus	GO:0005634	0.469022780656815
	Non-membrane-bounded organelle	GO:0043228	0.853274881839752
	Organelle lumen	GO:0043233	0.853274881839752
	Chromatin	GO:0000785	0.853274881839752
Molecular Function	Nucleic acid binding	GO:0003676	0.24788410961628
	Transcription factor binding	GO:0008134	0.419339299201965
	GTPase activity	GO:0003924	0.126110598444939
	Positive regulation of catalytic activity	GO:0043085	2.86398130810994E-06
	Regulation of transferase activity	GO:0051338	2.86398130810994E-06
	Regulation of kinase activity	GO:0043549	2.86398130810994E-06
	Nucleoside binding	GO:0001882	1
	Pyrophosphatase activity	GO:0016462	1
	ATP binding	GO:0005524	0.0217242781072855

**Supplementary Table 2**: The top enriched pathways by KEGG pathway enrichment analysis:

Terms	<b>KEGG Terms</b>	Group P-value
MAPK signaling pathway	KEGG:04011	3.23E-10
Hippo signaling pathway	KEGG:04392	0.00590951833873987
AGE-RAGE signaling pathway in diabetic		0.0610026250150204
complications	KEGG:04933	0.0019930230130204
Meiosis	KEGG:04113	0.0000845376707729883
Autophagy	KEGG:04138	0.0000845376707729883
Longevity regulating pathway	KEGG:04213	0.0000845376707729883

**Supplementary Table 3**: Comparative analysis of *Candida* core PPI network with random networks of the same node size.

Properties	Core <i>Candida</i> PPI Network	Degree preserving random network of <i>Candida</i>	Random Network (BA Algorithm)	Random Network (ER Algorithm)
Nodes	165	165	165	165
Edges	611	611	165	611
Clustering co-efficient	0.490	0.097	0.000	0.040
Network diameter	8	6	13	5
Network radius	4	4	7	3
Average Number of Neighbors	8.388	7.406	2.000	7.406
Characteristics path length	2.971	2.784	5.452	2.758
Network Density	0.061	0.045	0.012	0.045
Network Heterogeneity	0.780	0.869	1.143	0.337
Network Centralization	0.174	0.152	0.086	0.041
Connected Components	9	1	1	1

**Supplementary Figure 1**: PPIs network on pathogenic attributes (a): Overall PPIs network on pathogenic attributes of *C. albicans*, (b): Biofilm forming proteins, (c): Biofilm and Hyphae development proteins, (d): Biofilm and Thigmotrophism forming proteins, (e): Hyphae and Thigmotropism development proteins, (f): Biofilm, Hyphae and Thigmotropism development, (g): Hyphae forming proteins, (h): other function involving proteins.





Supplementary Figure 2: Individual interactions of top 5 Hub proteins with other proteins.

**Supplementary Figure 3**: The subnetwork clusters were intricately linked in the PPI network. Each cluster were designated with a particular colour and the variations in the size of the nodes represent node degree distribution.





**Supplementary Figure 4**: Node degree distribution of real core *Candida* PPI network (a) and the degree distribution of randomized networks of comparable node size (b–d)

**Supplementary Figure 5**: The behaviours of Neighborhood connectivity, Betweenness Centrality, Closeness Centrality, Clustering Co-efficient, Average shortest path length and Topological co-efficient measurements against the function Degree for Real core *Candida* PPI network, randomized *Candida* networks by Preserving the Degree, Barabasi-Albert (BA) and Erdős-Rényi (ER) algorithm.



Supplementary Equation S1: Calculation of average degree ( $K_{mean}$ ).

$$K_{\text{mean}} = \frac{\frac{2E}{N}}{N} = \frac{2 \times 611}{165} = 7.4$$

E= Total Number of Edges, N= Total number of nodes.

Supplementary Equation S2: Calculation of P-value.

The p-value =  
Number of permutations with metric 
$$\geq 0$$
 bserved metric  
Total number of permutations  
 $\frac{0 \geq 7.4}{00} = 0$ 

Remarks: 0 < 0.05, The Low p-value (< 0.05) in the observed network property is unlikely to be due to random chance, indicating a significant feature of the network structure.