

780 **Supplementary Files:**

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782 **Supplementary File 1:** Excel file containing the transcriptional profiling data.

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784 **Supplementary File 2:** Archived .zip folder containing the .gmx .gmt and .chip files

785 necessary for the execution of GSEA from *C. albicans* genome data. See

786 [http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data\\_formats](http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data_formats) for

787 details on these file formats. Because of issues with the Enrichment Map plug-in

788 systematic gene numbers do not contain the “orf19.” prefix.

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790 **Supplementary File 3:** Archived .zip folder containing Cytoscape Session Files (.cys)

791 for Supplementary Figure 1, Figure 7 and Supplementary Figure 6.

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793 **Supplementary File 4:** Excel file containing significantly-modulated transcripts at each

794 time point during hypoxia adaptation

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796 **Supplementary File 5:** Excel file whose worksheets contain the input files used in the

797 Network Components Analysis as well as the resulting output files.

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799 **Supplementary File 6:** Quicktime .mov file illustrating the temporal changes in

800 transcript abundance, in the context of a simplified transcription factor network, during

801 the 1st hour of hypoxia in wild type cells.

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803 **Supplementary File 7:** Quicktime .mov file illustrating the temporal changes in

804 transcript rate changes, in the context of a simplified transcription factor network, during  
805 the 1st hour of hypoxia in wild type cells.

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