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Supporting Information

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***Candida glabrata* PHO4 Is Necessary and Sufficient for Pho2-Independent Transcription of Phosphate Starvation Genes**

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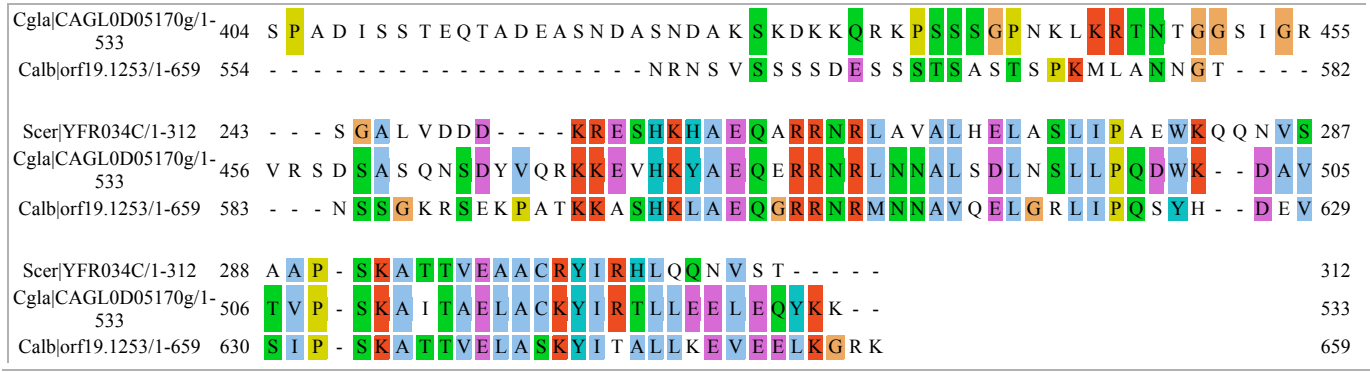


FIGURE S1.—Alignment of *ScPho4* with *CgPho4* and *CaPho4*. Utilizing a tree-assisted alignment of OG9983 which is the orthogroup of Pho4, we removed the other 16 species after CLUSTAL alignment, removed gaps common to all three proteins and colored residues according to the clustal option in Jalview. The most conserved portion of the proteins is in the C-terminal DNA binding domain. The known phosphorylation sites of *ScPho4* are surrounded by boxes.

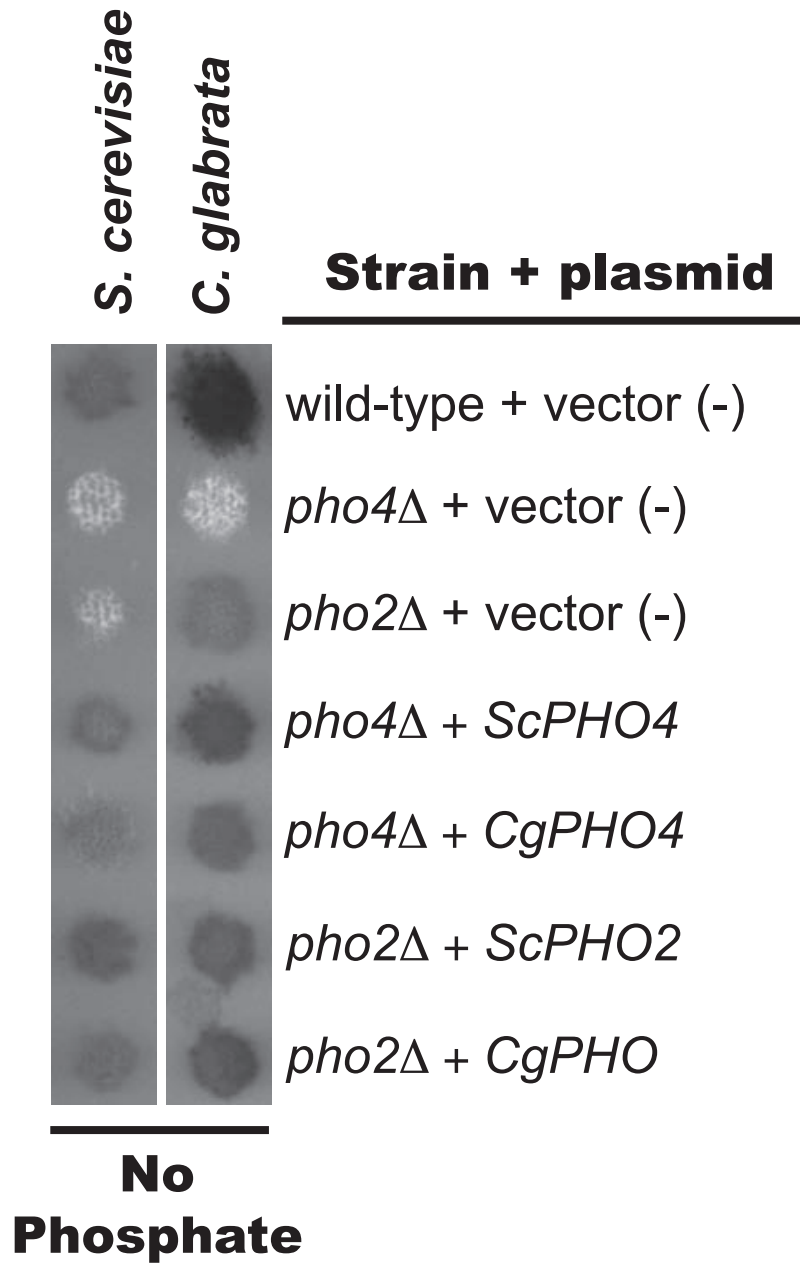


FIGURE S2.—Semi-quantitative phosphatase assay demonstrating that *PHO4* and *PHO2* plasmids are functional. *S. cerevisiae* and *C. glabrata* mutants lacking the Pho4 transcription factor (*pho4*Δ) contain either empty vector (pRS313), *ScPHO4*, or *CgPHO4* plasmids. *S. cerevisiae* and *C. glabrata* mutants lacking the Pho2 transcription factor (*pho2*Δ) contain either empty vector (pRS313), *ScPHO2*, or *CgPHO2* plasmids. These strains were grown on solid media lacking phosphate and overlaid with phosphatase substrate.

TABLE S1**Primers used in this study**

| Primer | Sequence | Purpose |
|--------|---|---|
| OD16 | tgactgggattccgtgagacggac | Delete <i>C. glabrata</i> <i>PHO4</i> with <i>KANMX6</i> |
| OD17 | ttaattaacccgggatccgacctgttcacccatcactaacag | |
| OD18 | ctgttagtgatgggtgaacaggtcggatccccgggtaattaa | |
| OD19 | gtttaaacgagctcgaattctacagatactcaagacaaaac | |
| OD20 | gtttgtcttgagatctctgagaattcgagctcgtttaaac | |
| OD21 | atcttgtccctccaaacagaactg | |
| OD25 | gctcgctctccattgcctattgtag | Delete <i>C. glabrata</i> <i>PHO2</i> with <i>KANMX6</i> |
| OD26 | ttaattaacccgggatccgccatccatttaactacaaagtggc | |
| OD27 | gccaaactttagttaaatggatggcggatccccgggtaattaa | |
| OD28 | gtttaaacgagctcgaattcgctacgaatattcatgtacat | |
| OD29 | atgtacatgaatattcgtagcgaattcgagctcgtttaaac | |
| OD30 | tccatccaatcttatccgggtgc | |
| O1 | gacagtcaaagtgtaaaggg | Delete <i>C. glabrata</i> <i>PHO31</i> with <i>KANMX6</i> |
| O2 | ttaattaacccgggatccgcagatattaccaaactcat | |
| O3 | atgaagttggtaaatatctcggatccccgggtaattaa | |
| O4 | GTTTAAACGAGCTCGAATTCgacgataaaaacctgatgctt | |
| O5 | aagcatcaggtttttatcgtcGAATTCGAGCTCGTTTTAAAC | |
| O6 | taatctagatcttcaaacgtc | |
| O7 | ctgcctggcttgggtggc | |
| O15 | caccagacatccttagtgat | Delete <i>C. glabrata</i> <i>PHO30</i> with <i>NATMX6</i> |
| O16 | ttaattaacccgggatccgctgagcatcttggggagtc | |

| | | |
|-------|--|---|
| O17 | atgactccccaagatgctcagcggatccccgggtaattaa | |
| O18 | GTTTAAACGAGCTCGAATTCagcatatccttcatctata | |
| O19 | tatagatgaaggatatatctGAATTCGAGCTCGTTTAAAC | |
| O20 | cggtgaaatacacacctctg | |
| O21 | cggtcaaaaactgattccag | |
| O29 | ggcacttaagttaatatattc | Delete <i>C. glabrata</i> <i>MSN5</i> with <i>NATMX6</i> |
| O30 | ttaattaaccggggatccgactggccaactctccttta | |
| O31 | taaaggagaagttggccagtcggatccccgggtaattaa | |
| O32 | GTTTAAACGAGCTCGAATTCctgatagcggctggcttc | |
| O33 | gaaccagccatcgctatcagGAATTCGAGCTCGTTTAAAC | |
| O34 | acacgagcaccataaatcca | |
| O35 | atgaatgctggggctaatcaag | |
| OD18 | ctgttagtgatgggtgaacaggtcggatccccgggtaattaa | Delete <i>C. glabrata</i> <i>PHO4</i> with <i>NATMX6</i> in DG3 |
| OD20 | gtttgtcttgagtatctgtagaattcgactcgtttaaac | |
| DWO1 | CGATCGGCGGCCGCTGCATTATTTAGATCGGAAAAAGTC | Amplify <i>S. cerevisiae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites |
| DWO2 | CGACACTTAATTAACGTGCTCACGTTCTGCTGTAGGTG | for cloning into pRS313-13myc |
| DWO7 | CGATCGGCGGCCGCGATGAGCTCTTTTCATCACTTCTCG | Amplify <i>S. cerevisiae</i> <i>PHO2</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites |
| DWO8 | CGACACTTAATTAATATCCATCTATGCTCGTCAGTTAG | for cloning into pRS313-13myc |
| DWO5 | CGATCGGCGGCCGCGTATGCATTACCTTCTCAATTAGG | Amplify <i>C. glabrata</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites |
| DWO6 | CGACACTTAATTAATTTCTTGTACTGCTCAAGCTCTTCG | for cloning into pRS313-13myc |
| DWO11 | CGATCGGCGGCCGCGCAGCAACCACCTTGGCGTCTGCGC | Amplify <i>C. glabrata</i> <i>PHO2</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites |
| DWO12 | CGACACTTAATTAATATCCAACGGTTGTCTTCGTTTAC | for cloning into pRS313-13myc |

| | | |
|------|--|--|
| O163 | CGATCGGCGGCCGCtgcattatttagatcgaaaaagtc | Amplify <i>S. cerevisiae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon |
| O164 | CGACACTTAATTAAtcacgtgctcagttctgctgtaggtg | |
| O128 | CGATCGGCGGCCGCtagtgaagccagtccttcacgcca | Amplify <i>S. mikatae</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon |
| O161 | CGACACTTAATTAAtcacgtgctccattccgtttagatga | |
| O174 | CGATCGGCGGCCGCaggtagaggaggaggcagag | Amplify <i>S. castellii</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon |
| O175 | CGACACTTAATTAAggaatttgcttagattcctaactg | |
| O167 | CGATCGGCGGCCGCgtatgcattaccttctcaattagg | Amplify <i>C. glabrata</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon |
| O168 | CGACACTTAATTAAtcatttctgtactgctcaagctcttg | |
| O157 | CGATCGGCGGCCGCcagccatgtactcatgatactg | Amplify <i>C. albicans</i> <i>PHO4</i> with 5' <i>NotI</i> and 3' <i>PacI</i> restriction sites for cloning into pRS313-13myc, with stop codon |
| O158 | CGACACTTAATTAAAttacttctctcttcaactctcaac | |
| O155 | TCCTACGAACTTCCAGATGGT | Quantify <i>S. cerevisiae</i> <i>ACT1</i> with quantitative reverse-transcription PCR |
| O156 | GGCAGATTCCAAAACCCAAAA | |
| O153 | GCCGGTTCCAAAACGTTTA | Quantify <i>S. cerevisiae</i> <i>PHO84</i> with quantitative reverse-transcription PCR |
| O154 | GACAGTGAAGACGGATACCCA | |
| O151 | TGCTTGTAACATCATGTCCTGC | Quantify <i>S. cerevisiae</i> <i>PHO5</i> with quantitative reverse-transcription PCR |
| O152 | TTGAGGTCAAGTTCAAACCCT | |
| O75 | gaccaaactacttacaactcc | Quantify <i>C. glabrata</i> <i>ACT1</i> with quantitative reverse-transcription PCR |
| O76 | ccactttcgctgattcttgcttg | |
| O78 | gccttgggtactctgatcgacc | Quantify <i>C. glabrata</i> <i>PHO84</i> with quantitative reverse-transcription PCR |
| O79a | gtgctgctcggcgacagtaac | |
| O81 | ggttaacgccacaccagtaagagc | Quantify <i>C. glabrata</i> <i>GIT1</i> with quantitative reverse-transcription PCR |
| O82 | gatagtgacaattcactctctc | |
