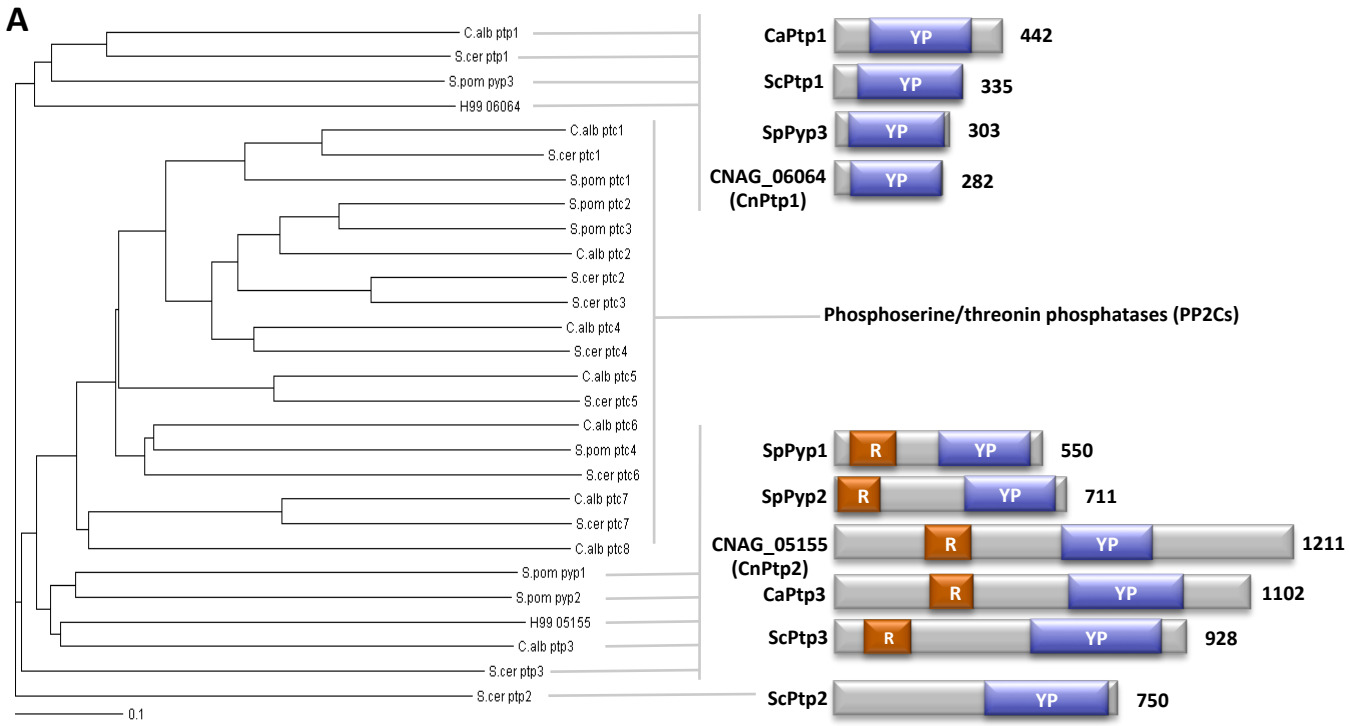
TABLE S1. Primers used in this study.

Name	Sequence	Description
B79	TGTGGATGCTGGCGGAGGATA	Common screening primer on the *NAT* or *NEO* cassette
B1026	GTAAAACGACGGCCAGTGAGC	M13F
B1027	CAGGAAACAGCTATGACCATG	M13R
B1454	AAGGTGTTCCCCGACGACGAATCG	NAT split marker primer 1
B1455	AACTCCGTCGCGAGCCCCATCAAC	NAT split marker primer 2
B1886	TGGAAGAGATGGATGTGC	NEO split marker primer 1
B1887	ATTGTCTGTTGTGCCCAG	NEO split marker primer 2
B4017	GCATGCAGGATTCGAGTG	Primer 1 for overexpression promoter with NEO marker
B4018	GTGATAGATGTGTTGTGGTG	Primer 2 for overexpression promoter with NEO marker
B354	GCATGCAGGATTCGAGTG	Primer 1 for *GFP* gene amplification
B5665	GGTGGCGGTGGCTCTGTGAGC	Primer 2 for *GFP* gene amplification
B3656	TTTGGAGGTTCAGGAGTGGC	Primer L1 for the left flanking region of *PTP1*
B3657	TCACTGGCCGTCGTTTTACTTGTGAAGCAGCGAATACTC	Primer L2 for the left flanking region of *PTP1*
B3658	CATGGTCATAGCTGTTTCCTGTGCGTTCCTGAAAGTGTCCC	Primer R1 for the right flanking region of *PTP1*
B3659	GTGATGATTTGCTCGTCG	Primer R2 for the left flanking region of *PTP1*
B3655	TTGACAGGTGACTGGAAGG	Screening primer to detect *PTP1* deletion, pairing with B79
B3660	TCCATCTGTTACCACATTGG	PTP1 probe primer 1 for Southern blot
J13644	TTTCCTTGCCTGGGTTTG	Primer L1 for the left flanking region of *PTP2*
J13645	CTGGCCGTCGTTTTACCTTTTCTATTCCAGCCCG	Primer L2 for the left flanking region of *PTP2*
J13646	GTCATAGCTGTTTCCTGCATAACAGTCATCATCCCCTAC	Primer R1 for the right flanking region of *PTP2*
J13647	TAGTTTCTGCCCCTTCACGG	Primer R2 for the left flanking region of *PTP2*
J13648	CATTCAAACTCGGCGTAG	Screening primer to detect *PTP2* deletion, pairing with B79
J13649	ATAGGCAGTCCTTTTCGC	*PTP2* probe primer 1 for Southern blot
J13650	GAGGACGAAATCTACGGTTC	*PTP2* probe primer 2 for Southern blot
B3656	TTTGGAGGTTCAGGAGTGGC	*PTP1* left flanking primer for complementation
B3659	GTGATGATTTGCTCGTCG	*PTP1* right flanking primer for complementation
B3756	GCTTCCATCGCAAACATAG	*PTP1* probe primer 1 for Northern blot
B3757	CGAATGGTGTCTACAGTCTTG	*PTP1* probe primer 2 for Northern blot
B2895	CGCAAGCTTGATACGCCATAGTCCGAACGA	*PTP2* left flanking primer for complementation
B2896	CGCAAGCTTCTAGCGGCTCTTGATCGGCC	*PTP2* right flanking primer for complementation
B2897	GTGGAACCAGGGTGTTTAC	Sequencing primer 1 for *PTP2*
B2898	ATCGTCTGGCTTCTCCTTG	Sequencing primer 2 for *PTP2*
B2899	TTCCCTCTACTCTGCTTCG	Sequencing primer 3 for *PTP2*
B2900	CCTATGACTACTGCTGTTACCG	Sequencing primer 4 for *PTP2*
B2901	CGATTACATCAACGCATCC	Sequencing primer 5 for *PTP2*
B2902	AGCATTCAACCTCTCCTGG	Sequencing primer 6 for *PTP2*
B2903	ATGTTCTTTCTGTGGGCTC	Sequencing primer 7 for *PTP2*
B3660	TCCATCTGTTACCACATTGG	5’ RACE primer 1 for *PTP1*
B3661	GCATTGAGGGAGTTAGTAAAGG	3’ RACE primer 1 for *PTP1*
B3095	AGTATGCGAGTCCAGCGTATGTC	5’ RACE primer 1 for *PTP2*
B3096	GACCCAATCCCTCTCCTTTACAG	5’ RACE primer 2 for *PTP2*
B3365	GCGTGACCCAGTGTCGTGTGTTCTTG	3’ RACE primer 1 for *PTP2*
B3366	GCGATTGGGTCACTCGGGTCATTAGG	3’ RACE primer 2 for *PTP2*
B3758	TTTTCGTTCCCCAAGCCGTC	*PTP2* probe primer 1 for Northern blot
B3759	AAACCTTTCTGAGCACCCGC	*PTP2* probe primer 2 for Northern blot
B3655	TTGACAGGTGACTGGAAGG	Left flanking primer 1 for overexpression of *PTP1*
B5059	cactcgaatcctgcatgcTAGATTCACAGTGCCGCCTC	Left flanking primer 2 for overexpression of *PTP1*
B5060	accacaacacatctatcacATGGCTTCCATCGCAAACATAG	Right flanking primer 1 for overexpression of *PTP1*
B3764	CAATGAAAGTTCCAGTGCG	Right flanking primer 2 for overexpression of *PTP1*
B5685	AAGTTGCTGATTGGACCC	Screening primer to detect H3 promoter insersion, pairing with B79
B3656	TTTGGAGGTTCAGGAGTGGC	*PTP1* overexpression probe primer 1 for Southern blot
B3660	TCCATCTGTTACCACATTGG	*PTP1* overexpression probe primer 2 for Southern blot
B4470	GACGACGAAACGAATGACGG	Left flanking primer 1 for overexpression of *PTP2*
B5061	cactcgaatcctgcatgcTCGTGATTAGCAAGCCGTG	Left flanking primer 2 for overexpression of *PTP2*
B5062	accacaacacatctatcacATGGGTCGACAAGCTCCCCCGA	Right flanking primer 1 for overexpression of *PTP2*
B3759	AAACCTTTCTGAGCACCCGC	Right flanking primer 2 for overexpression of *PTP2*
J13644	TTTCCTTGCCTGGGTTTG	Screening primer to detect H3 promoter insersion, pairing with B79
B3758	TTTTCGTTCCCCAAGCCGTC	*PTP2* overexpression probe primer 1 for Southern blot
B3759	AAACCTTTCTGAGCACCCGC	*PTP2* overexpression probe primer 2 for Southern blot
B5671	GCGGCCGCTTTGGAGGTTCAGGAGTGGC	Left flanking primer 1 for *PTP1:GFP* strain
B5672	GCGGCCGCTTGCATTCGGTACAGAAGCT	Right flanking primer 1 for *PTP1:GFP* strain
B2902	AGCATTCAACCTCTCCTGG	Left flanking primer 1 for *PTP2:GFP* strain
B5924	GCTCACAGAGCCACCGCCACCGTTCTTTAATTCCTCCGCTAC	Left flanking primer 1 for *PTP2:GFP* strain
B5925	GCCACTCGAATCCTGCATGCAAAAGGAATTGACCGTCCTAG	Right flanking primer 1 for *PTP2:GFP* strain
J13647	TAGTTTCTGCCCCTTCACGG	Right flanking primer 1 for *PTP2:GFP* strain
B2903	ATGTTCTTTCTGTGGGCTC	*PTP2* probe primer 1 for *PTP2:GFP* strain Southern blot
B678	TTCAGGGAACTTGGGAACAGC	*ERG11* probe primer 1 for Northern blot
B1598	CAGGAGCAGAAACAAAAGC	*ERG11* probe primer 2 for Northern blot
B1894	TTTTACGCTTTTTGCAGATTCCGCCAAA	Mating pheromone probe primer 1 for Northern blot
B1895	GACCACTGTTT CTTTCGTTCT	Mating pheromone probe primer 2 for Northern blot

Figure S1 (Lee et al. 2014)



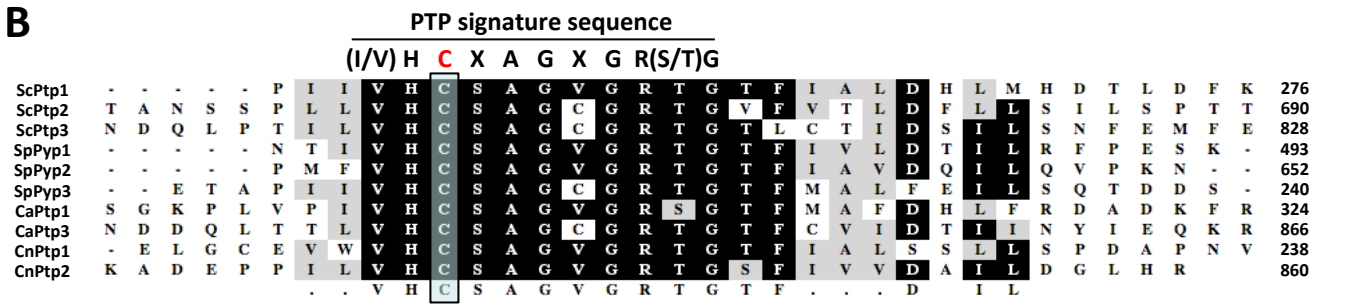


Fig S1: Protein tyrosine phosphatases, Ptp1 and Ptp2, in *C. neoformans*. (A) Phylogenetic tree of protein Tyr phosphatases (PTPs) and protein Ser/Thr phosphatases (PP2Cs) in *C. neoformans* and other fungi. The phylogenetic tree was generated by the philodendron phylogenetic tree printer (http://iubio.bio.indiana.edu/treeapp/treeprint-form.html). The scale bar line represents an evolutionary distance of 0.1. Protein sequences were retrieved from the following database: *C. neoformans* Ptp1: CNAG_06064, Ptp2: CNAG_05155 from the *C. neoformans* var. *grubii* H99 database of the Broad Institute http://www.broadinstitute.org), *S. cerevisiae* Ptp1: YDL230W, Ptp2: YOR208W, Ptp3: YER075C, Ptc2: YER089C, Ptc3: YBL056W, Ptc4: YBR125C, Ptc5: YOR090C, Ptc6: YCR079W, Ptc7: YHR076W from the *Saccharomyces* genome database (http://www.yeastgenome.org/), *C. albicans* Ptp1: orf19.6365, Ptp3: orf19.7610, Ptc1: orf19.4785, Ptc2: orf19.2538, Ptc4: orf19.6638, Ptc5: orf19.6376, Ptc6: orf19.3705, Ptc7: orf19.5661, Ptc8: orf19.4698 from the *Candida* genome database (http://www.candidagenome.org/), *S. pombe* Pyp1: SPAC26F1. 10c, Pyp2: SPAC19D5.01, Pyp3: SPAC11E3.09, Ptc1: SPCC4F11.02, Ptc2: SPCC1223.11, Ptc3: SPAC2G11.07c, Ptc4: SPAC4A8.03c, from the *S. pombe* genome database (http://www.pombase.org/). The protein domains in PTPs predicted by Pfam (pfam.sanger.ac.uk) were illustrated on the right side of the phylogenetic tree. The R box represents a Rhodanese-like domain (PF00581) and the YP box represents a protein-tyrosine phosphatase domain (PF00102). (B) Comparison of PTP signature sequences. Multiple sequence alignment of yeast PTP signature sequences was depicted by Clustal W alignment from MacVector software (version 12.5.1, Accelrys).

Figure S2 (Lee et al. 2014)

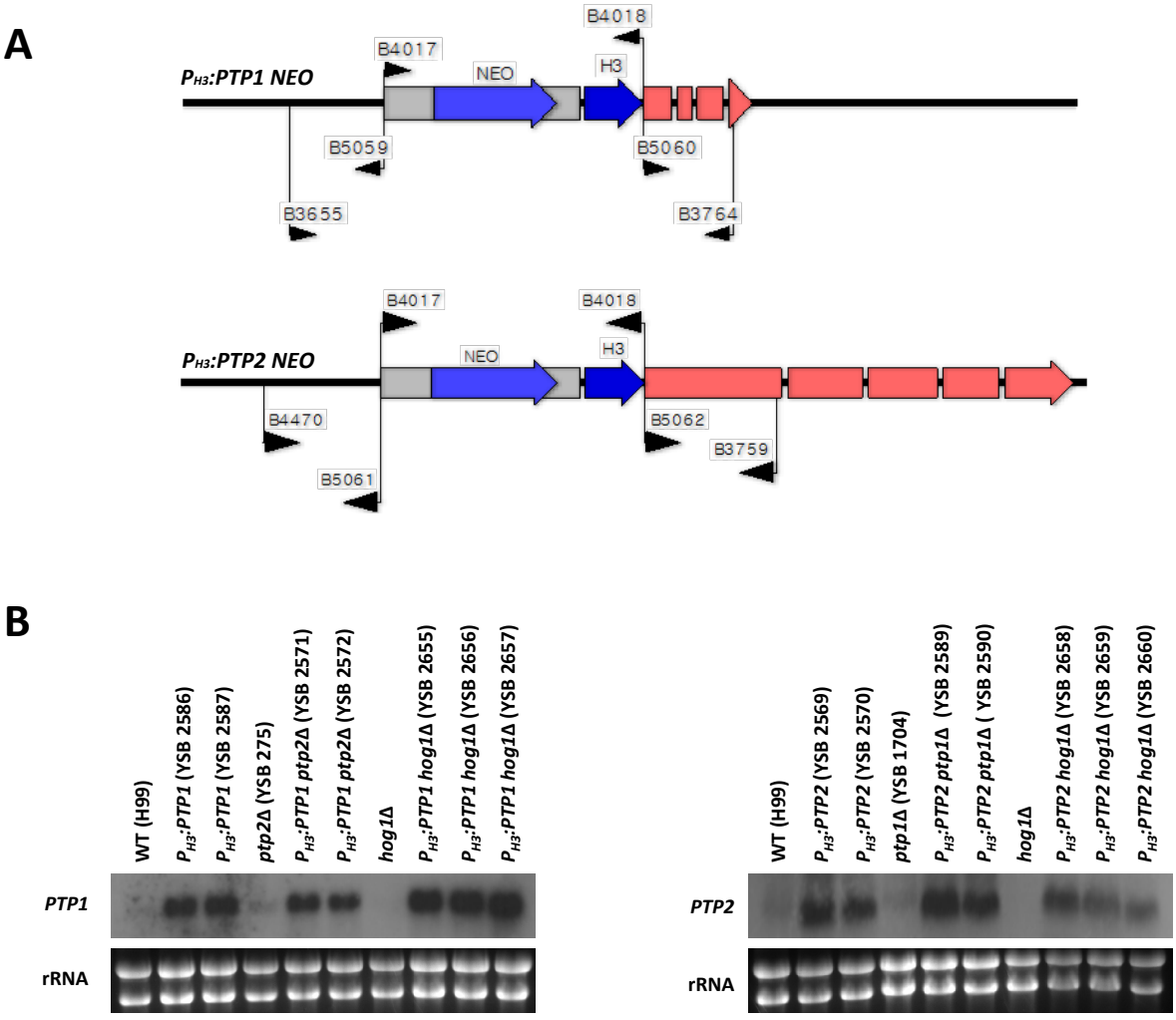


Fig S2: Construction of the constitutive *PTP1* or *PTP2* overexpression strains in *C. neoformans*. (A) The strategy for the construction of the *PTP1* or *PTP2* overexpression strains by using the constitutively active H3 promoter. (B) Northern blot analyses for measuring *PTP1* or *PTP2* expression in P_{H3}:*PTP1* or P_{H3}:*PTP2* strains, respectively. Ethidium bromide staining results of rRNA were used as loading controls.

Figure S3 (Lee et al. 2014)

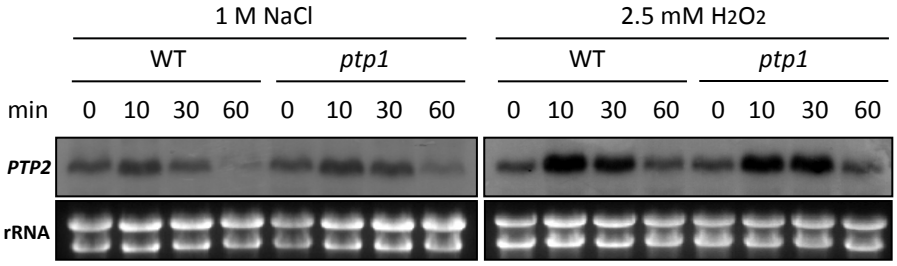


Fig S3: Ptp1 was not involved in expression levels of *PTP2*. Northern blot analysis using the total RNA isolated from each strain [WT (H99) and *ptp1* (YSB275)] grown to mid-logarithmic phase at 30°C in YPD medium and exposed to 1 M NaCl or 2.5 mM H_2O_2. Each membrane was hybridized with *PTP2* specific probes washed and developed. Ethidium bromide staining results of rRNA were used as loading controls.