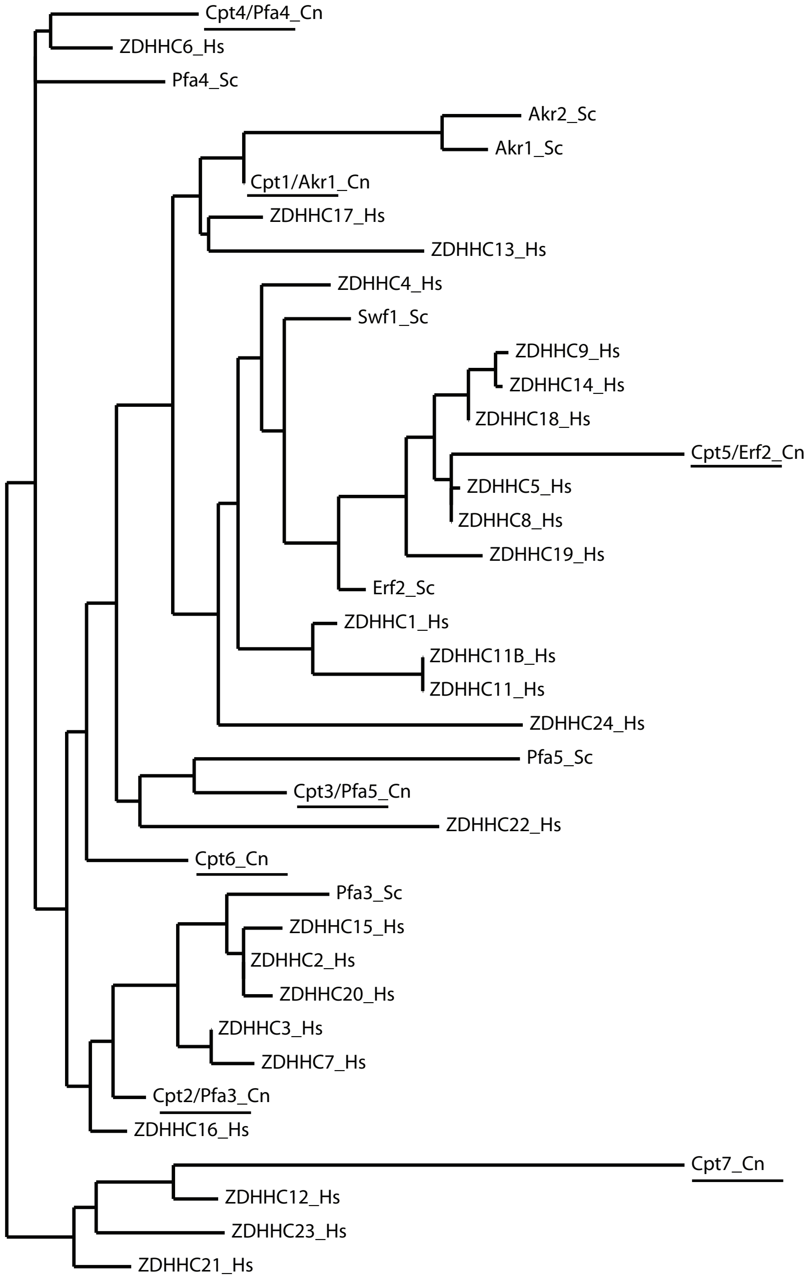
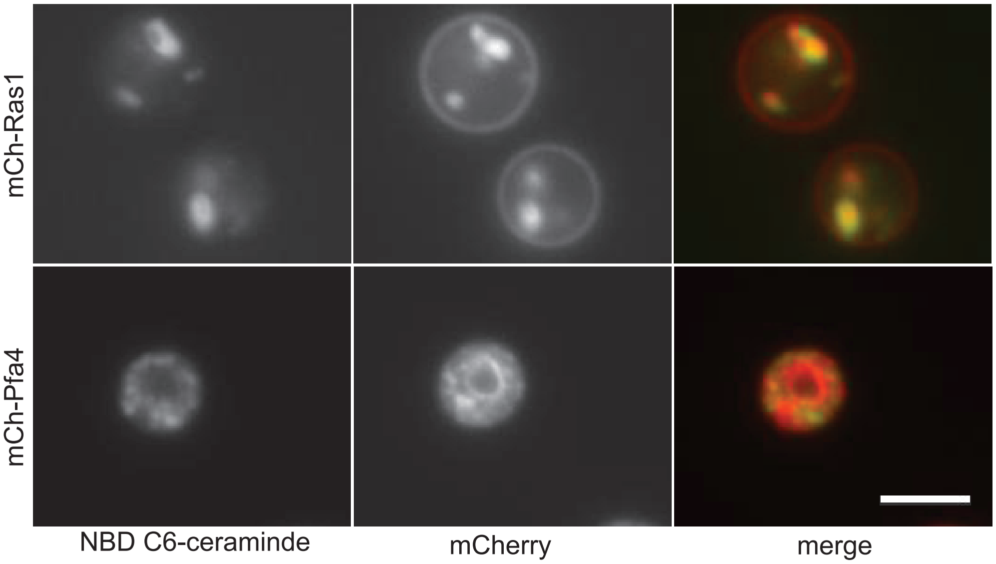
A

B

		DPG	DHHC-CRD	TTxE
CNAG_00436	Cpt1	TDPGF	NFCIVCMARKPLRSKHCRTCNRCVARFDHHCPWIWNCVGAKNHRSFLLFV	MTTFEV
CNAG_02481	Cpt2	VPPGF	RRCRKCDGPKPERTHHCSICKRCVLMMDHHCPWINNCVGLHNQRHFVLFM	ETSIES
CNAG_04849	Cpt3	PDPAN	RWCRFCEIVKPDRTHHCRHCGTCVMQFDHHCLWIGQCVGWANHKFFIIFN	RTTVES
CNAG_03891	Cpt4	TSPGT	RYCKNCAHYKPPRAHHCRQCKTCWLKLDHHCPWIGNCVGFYNQGHFIRFL	STTIEG
CNAG_00274	Cpt5	PDPPM	KYCETCETYRPPRCSHCRLCGNCVDGIDHHCSYLHTCVGKRNYFSFIVLL	ITTLEQ
CNAG_06862	Cpt6	RSPGS	RWCKQCNAWKPDRTHHCRHCHRCVLKMDHHCPWVGTCVGYRNYKPFLLFI	MTTLES
CNAG_04167	Cpt7	YDPPL	YKGRCGGRWKPARTRHCTQCGVCRAGFDHHCPFFANCLTAPYIPTFLAVL	


Cpt4/Pfa4_Cn
ZDHHC6_Hs
Pfa4_Sc
Akr2_Sc
Akr1_Sc
Cpt1/Akr1_Cn
ZDHHC17_Hs
ZDHHC13_Hs
ZDHHC4_Hs
Swf1_Sc
ZDHHC9_Hs
ZDHHC14_Hs
ZDHHC18_Hs
Cpt5/Erf2_Cn
ZDHHC5_Hs
ZDHHC8_Hs
ZDHHC19_Hs
Erf2_Sc
ZDHHC1_Hs
ZDHHC11B_Hs
ZDHHC11_Hs
ZDHHC24_Hs
Pfa5_Sc
Cpt3/Pfa5_Cn
ZDHHC22_Hs
Cpt6_Cn
Pfa3_Sc
ZDHHC15_Hs
ZDHHC2_Hs
ZDHHC20_Hs
ZDHHC3_Hs
ZDHHC7_Hs
Cpt2/Pfa3_Cn
ZDHHC16_Hs
Cpt7_Cn
ZDHHC12_Hs
ZDHHC23_Hs
ZDHHC21_Hs


mCh-Ras1
mCh-Pfa4
NBD C6-ceraminde
mCherry
merge

Supplementary Figure 1. Conserved domains in *C. neoformans* putative PAT genes. (A). Diagram of conserved PAT domains. The DHHC-CRD domain is flanked by TM (transmembrane) domains, a DPG domain, and a TTxE domain. (B). Alignment of *C. neoformans* conserved PAT domains.

Supplementary Figure 2. Phylology tree of *C. neoformans*, *S. cerevisiae*, and *H. sapiens* PATs. Protein sequence alignment (MUSCLE) and tree phylogeny (PhyML) was constructed using Phylogeny.fr. Tree was drawn using TreeDyn.

Supplementary Figure 3. Golgi localization of *C. neoformans* mCh-Ras1 and mCh-Pfa4. Wild type cells expressing mCh-Ras1 (CBN116) and mCh-Pfa4 (CBN451) were fixed in 3.7% formaldehyde then incubated with the green-emission fluorescent Golgi marker NBD C6-Ceramide to compare Golgi localization to mCh-Ras1 (top panels) and mCh-Pfa4 (bottom panels). Images (x100) were taken at the using the appropriate filter and merged. Bar, 5 μm.