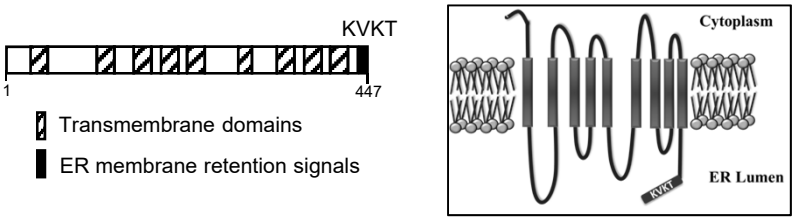
Supplementary Fig. 1

A.



B.

Percent Identity (%)

Divergence	CnAlg3p	ScAlg3p	HpAlg3p	CaAlg3p	AnAlg3p	SpAlg3p
CnAlg3p		38.3	38.6	25.1	45.5	44.5
ScAlg3p	145.5		43.1	33.0	40.8	39.8
HpAlg3p	134.1	121.8		39.0	40.5	41.4
CaAlg3p	156.9	121.9	106.7		26.9	27.1
AnAlg3p	121.1	131.0	130.2	148.1		52.6
SpAlg3p	130.0	144.0	129.0	152.9	114.2	

C.

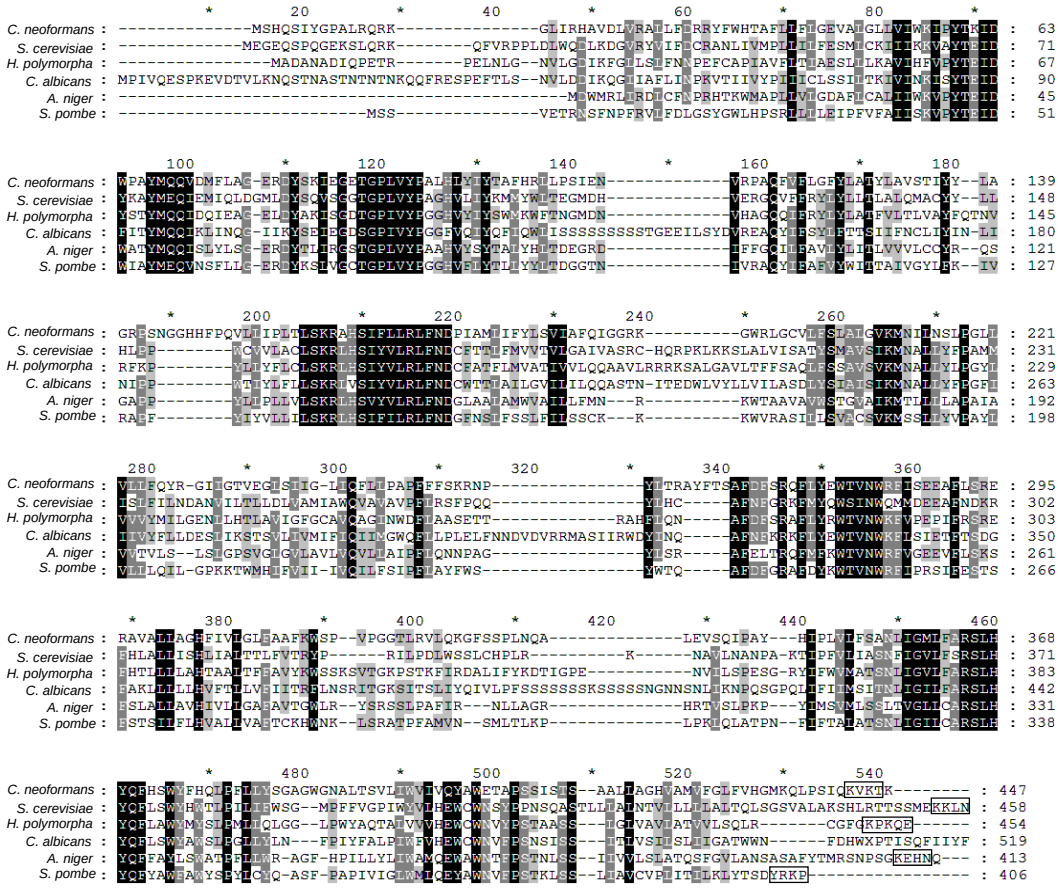


FIG S1 Bioinformatics analysis of Alg3 protein. (A) Domain structure of *C. neoformans* Alg3. Predicted transmembrane domains and ER retention signal of Alg3 are indicated by slashes and a box, respectively. (B) Sequence identities and similarities between Alg3 homologs of *S. cerevisiae* (ScAlg3: NP_009471), *H. polymorpha* (HpAlg3: ABB04524), *C. albicans* (CaAlg3: XP_712105), *A. niger* (AnAlg3: XP_001398696), and *S. pombe* (SpAlg3: NP_593853). (C) Multiple sequence alignment of Alg3 homologs generated using ClustalW 1.8. Identical residues and conservative amino acid substitutions are indicated by black and gray shading, respectively. The ER retention signal, KKXX-like (X = any amino acid) motif, is boxed.