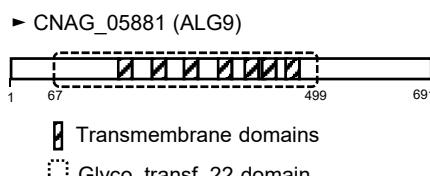


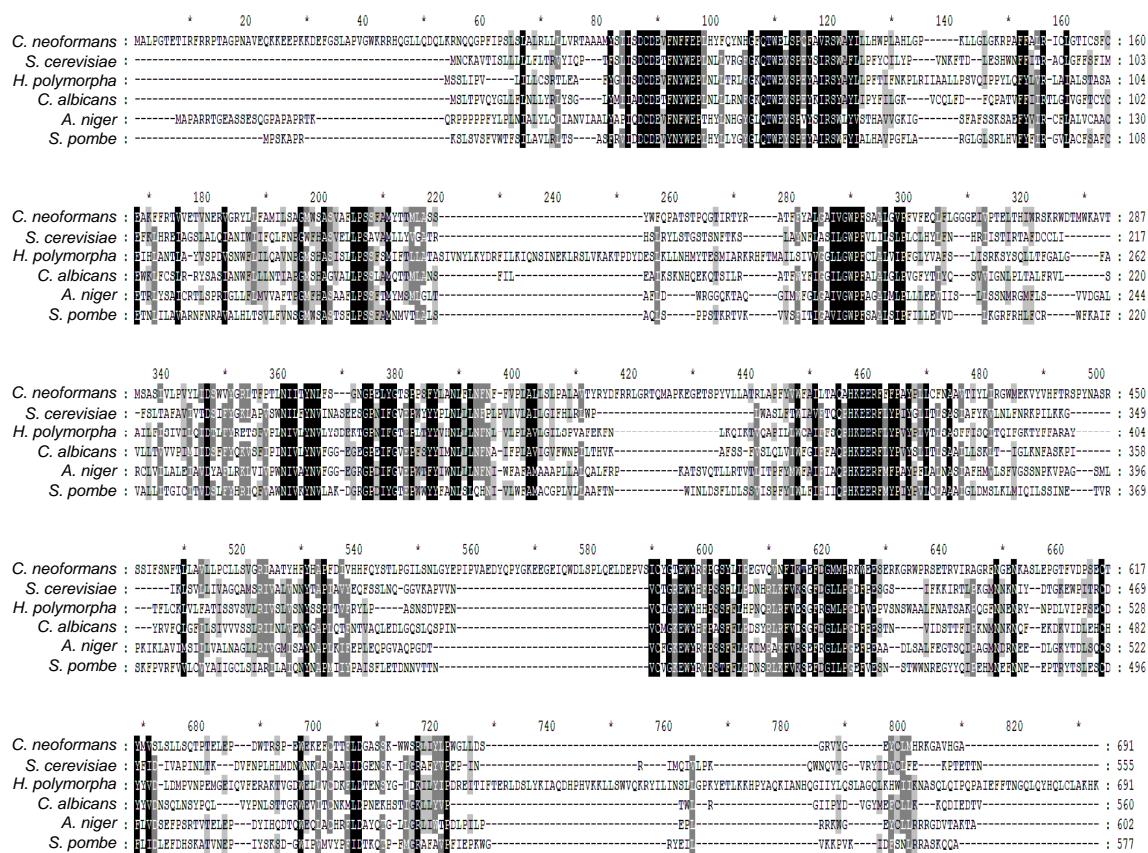
Supplementary Fig. 4

A.



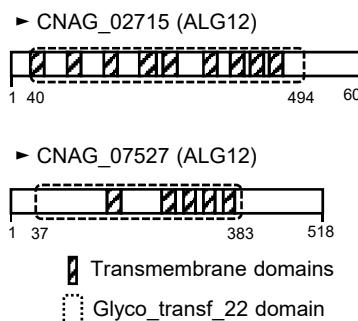
Percent Identity (%)

	CnAlg9p	ScAlg9p	HpAlg9p	CaAlg9p	AnAlg9p	SpAlg9p
CnAlg9p		28.4	27.4	31.0	32.0	31.0
ScAlg9p	170.8		38.0	38.4	34.7	33.1
HpAlg9p	178.0	119.3		44.8	33.4	31.9
CaAlg9p	154.1	117.6	95.0		35.3	32.6
AnAlg9p	148.1	134.1	140.6	131.2		39.9
SpAlg9p	153.6	141.9	148.9	144.9	111.7	



Supplementary Fig. 4

B.



Percent Identity (%)

	CNAG_02715 (CnAlg12p)	CNAG_07527 (CnAlg12p)	ScAlg12p	HpAlg12p	CaAlg12p	AnAlg12p	SpAlg12p
CNAG_02715 (CnAlg12p)		35.6	24.5	24.9	25.0	23.6	24.8
CNAG_07527 (CnAlg12p)	130.0		25.3	23.7	24.7	24.8	22.6
ScAlg12p	200.0	195.5		29.9	35.8	29.0	28.9
HpAlg12p	195.0	206.0	160.8		32.7	27.0	24.8
CaAlg12p	195.0	198.0	129.1	144.1		28.0	26.8
AnAlg12p	208.0	197.0	166.4	181.5	173.6		25.7
SpAlg12p	196.0	216.0	166.9	196.0	182.9	192.4	

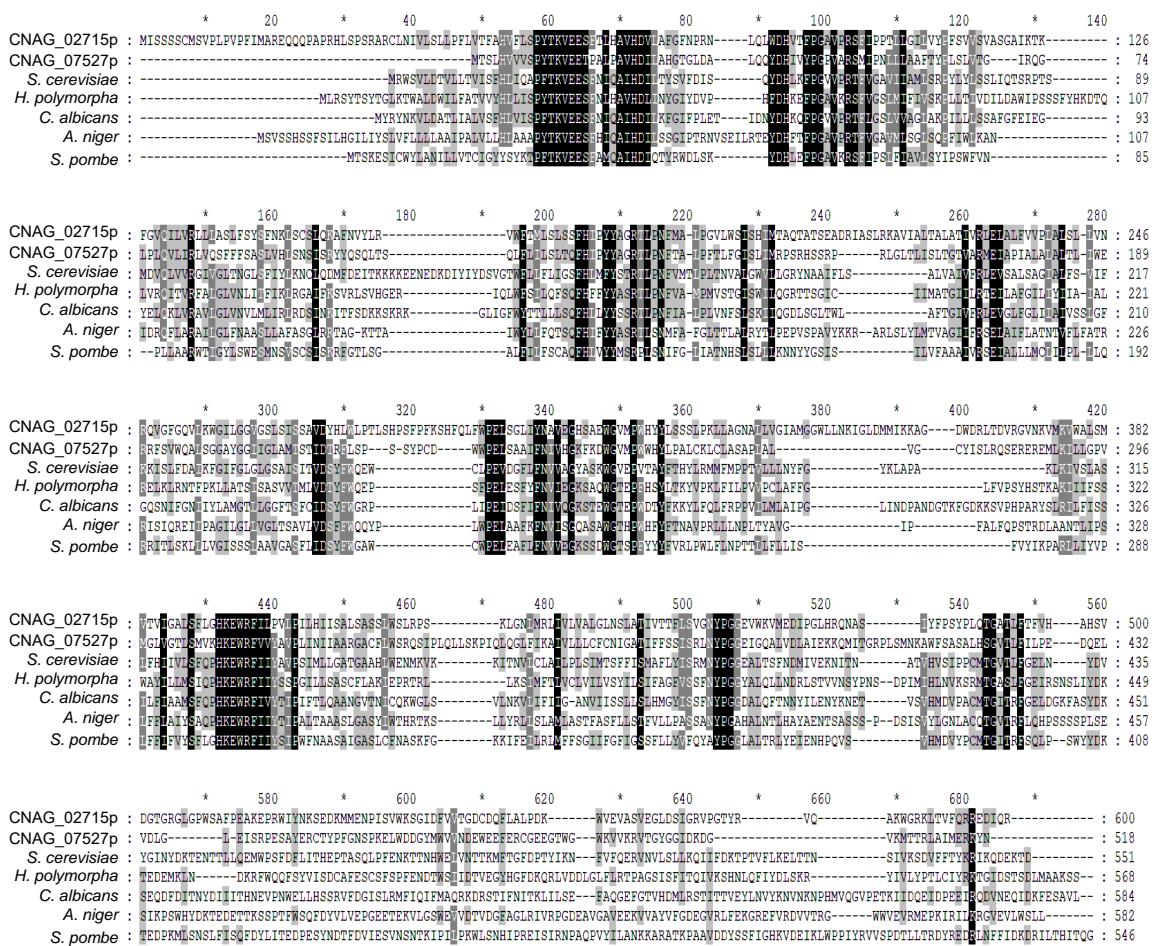


FIG S4 Bioinformatics analysis of Alg9 and Alg12. (A, B) Predicted transmembrane and Glyco_transf_22 (glycosyltransferase 22 family) domains of Alg proteins are indicated by slashes and dotted boxes, respectively. Sequence identities and similarities between Alg9 and Alg12 homologs of *S. cerevisiae*, *H. polymorpha*, *C. albicans*, *A. niger*, and *S. pombe*. Multiple sequence alignment of Alg9 and Alg12 homologs generated using ClustalW 1.8. Identical residues and conservative amino acid substitutions are indicated by black and gray shading, respectively.