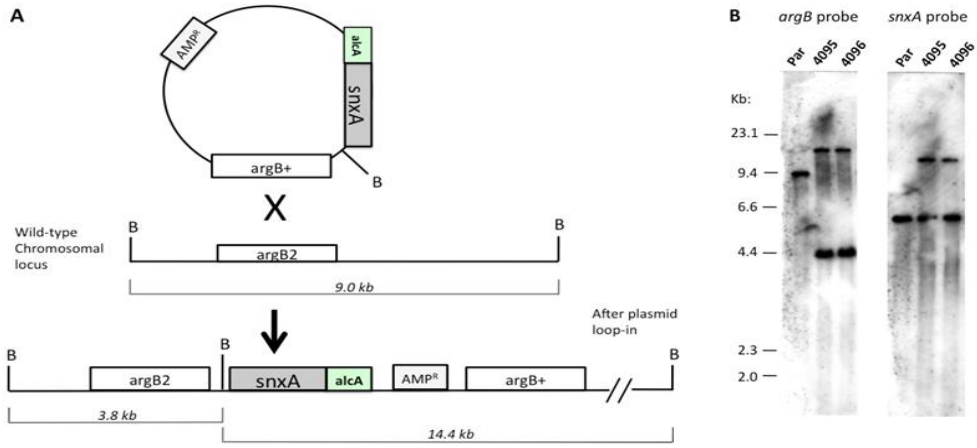

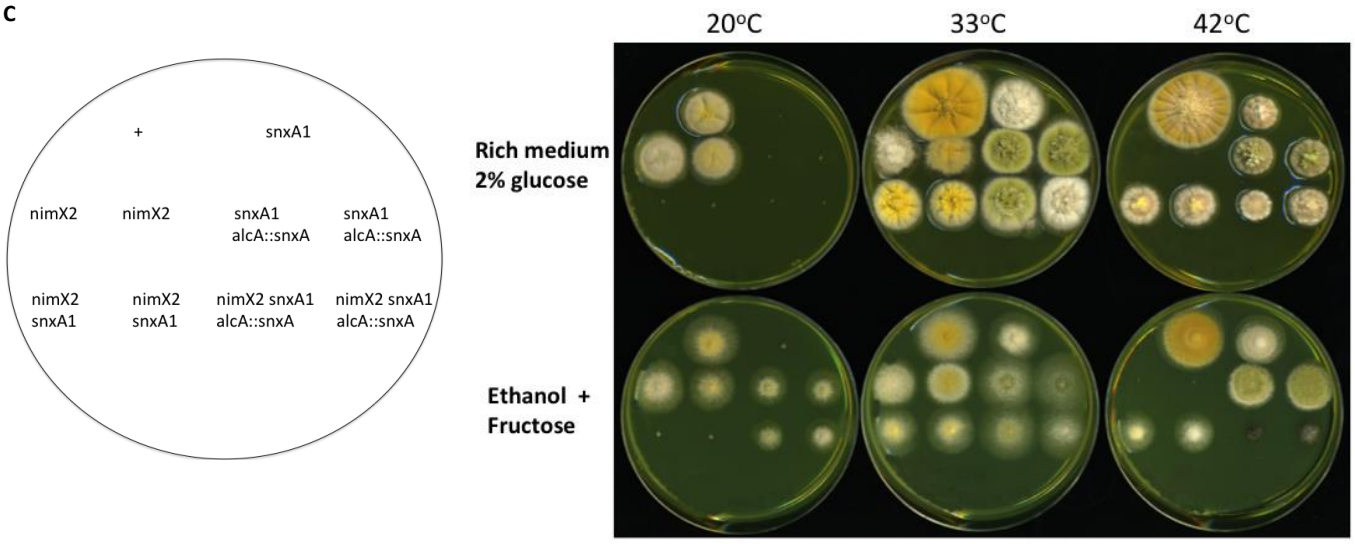

Figure S4 *alcA::snxA* construct. A *snxA*$^{+}$ wild-type 9-exon genomic clone was fused with the *alcA* alcohol dehydrogenase gene promoter as described in Materials & Methods. An *alcA::snxA*-containing plasmid was transformed into a *snxA*1 strain (SWJ 3676: *riboA*1; *snxA*1; *argB*2; *pyroA*4; *chaA*1), and *argB*$^{+}$ transformants were recovered and purified. Total genomic DNAs were digested with *BamH*I and subjected to Southern blotting. (A) Southern blot strategy for plasmid integration at the *argB* locus. B, *BamH*I. (B) Southern blots were analyzed using probes corresponding to the coding regions of *Aspergillus nidulans argB* and *snxA*. When probed with *argB*, single-copy integration at the *argB* locus should replace the 9.0 kb wild-type *BamH*I band with two bands of 3.8 and 14.4 kb, respectively. Probing the same blot with *snxA* should produce a 6 kb band corresponding to the wild-type *snxA* locus, and a 14.4 kb band corresponding to integration at *argB*. Par, parental strain; 4095 & 4096, tSWJ 4095 and tSWJ 4096 (cf. Table S1). (C) *snxA*$^{+}$ overexpression rescues pleiotropic *snxA*1 phenotypes. An *alcA*-driven copy of wild-type

snxA (*alcA::snxA*$^{+}$) was integrated at the *argB* locus, and then combined in strains bearing *snxA*1 or *snxA*1 + *nimX*2 mutations. Complementation of *snxA*1 cold-sensitive and suppressor phenotypes was assessed by comparing growth at three temperatures during *alcA* repression (rich media containing 2% glucose) or *alcA* induction (minimal media containing 200mM ethanol + 0.04% fructose). Strains were point-inoculated using conidia from fresh streaks. Two representative strains of each genotype are shown. Plates were incubated for the following times: 20°C, 10 days; 33°C and 42°C, 3 days.