



Figure S5 RT-qPCR to show aberrant RNA production. RT-qPCR to show RNA production from *sly1-1* at different time points in two crosses. (A) Schematic diagram of *sly1-1* and the positions of two probes located in the intergenic region (P1) and the penultimate *sly1-1* intron (P2), respectively. (B) Results of qPCR. Samples from left to right were obtained from tissues during vegetative growth, from protoperithecia of FGSC 2489, from perithecia 2 days, 4 days and 6 days post fertilization in the cross between FGSC 2489 and FGSC 8820, and from perithecia 2 days, 4 days and 6 days post fertilization in the cross between FGSC 2489 and *Sad-1*^Δ n = 3; error bars represent standard deviation. The *N. crassa* β -tubulin gene (NCU04054) was used as an internal control for qRT-PCR.