Table S2 Summary of sequence reads generated with RNA-seq analysis in this study

Condition	Sample	No. of reads	No. of reads mapped to reference genome	% of reads mapped to reference genome
wild type sexual mycelium	SM10	43,457,800	40,739,279	93.7
Δnox1 sexual mycelium	SM12	48,567,244	46,076,199	95.1
	SM15	58,330,616	55,736,653	95.6
Δnox1 protoperithecia	SM16	71,689,682	65,226,730	91.0
	SM17	65,178,132	60,057,518	92.1