

Table S1. Summary statistics of RNA sequencing reads and mapping to <i>S. cere</i>					
Sample	Replicate	Treatment	Number Raw Reads	Q20 %	Total read count
WA	2	Control	16831498	97.17	14161892
WA	3	Control	18613634	97.23	15546563
WA	4	Control	19217926	96.81	16036387
WE	3	Control	18302888	97.26	15620111
WE	4	Control	21871922	97.23	18515199
WA	1	Patulin	22181400	97.1	18373123
WA	3	Patulin	16877538	97.18	14084672
WA	4	Patulin	19104102	97.27	16208961
WE	2	Patulin	20767430	97.1	17594079
WE	3	Patulin	19596870	97.09	16725189
WE	4	Patulin	17801742	97.27	14983188

visiae genome	
Mapping percentage	
	83.70%
	83.80%
	83.60%
	83.90%
	84.10%
	84.00%
	83.60%
	83.90%
	84.30%
	84.10%
	83.30%