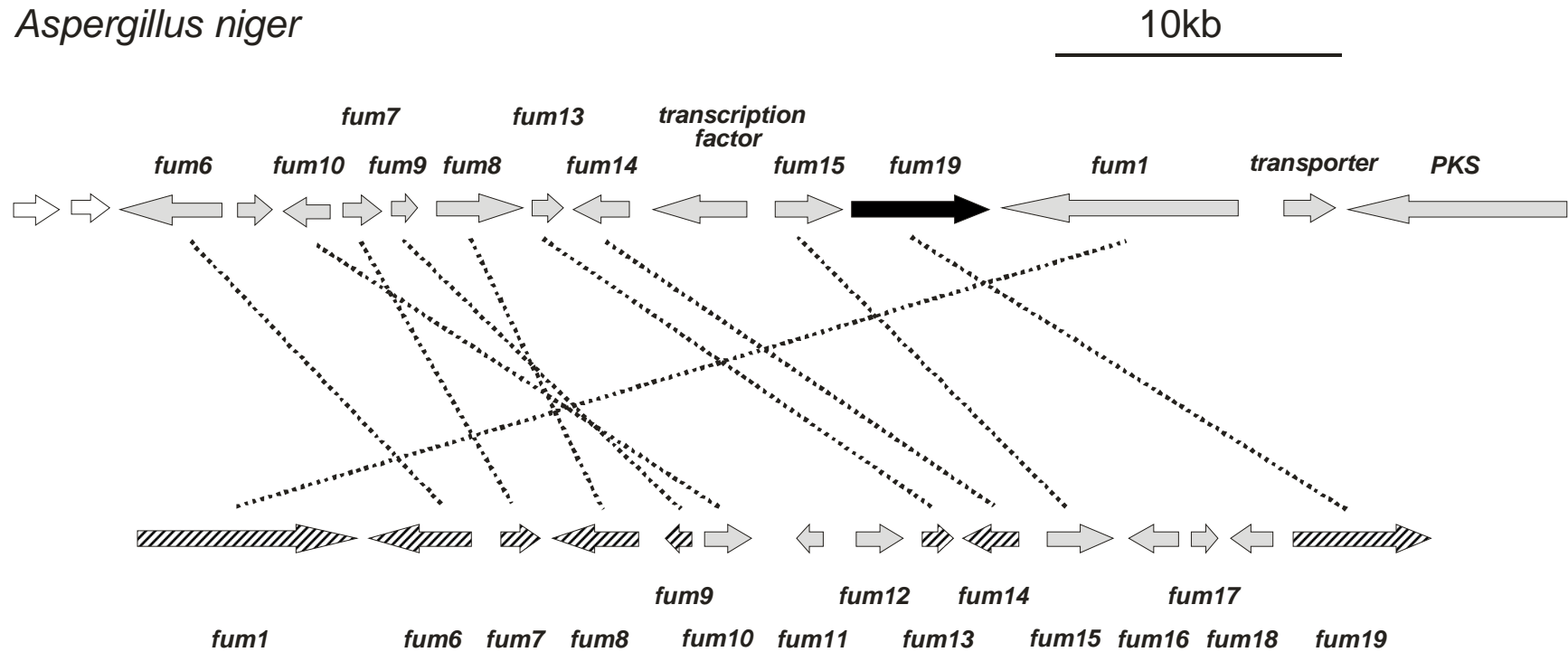


Aspergillus niger



Gibberella moniliformis

Supplementary Figure 7 Putative *A. niger* fumonisin cluster Orthologs of the *Gibberella moniliformis* fumonisin gene cluster are connected to the gene cluster region of *A. niger*. Genes at the left and right hand borders of the *A. niger* cluster region do not appear to be secondary metabolism genes. *G. moniliformis* genes which have been shown by deletion and/or over-expression to be involved in fumonisin biosynthesis are highlighted by cross-hatching. Deletion of *fum19* (ABC transporter) had a slight effect, and the *fum19* ortholog in *A. niger* is the only gene for which significant transcription could be detected under standard fermentation conditions (highlighted in black). Orthologs of *Gibberella fum11* (tricarboxylate transporter), *fum12* (P450 hydroxylase) and *fum16* (fatty acyl-CoA synthetase) were not identified in the *A. niger* genome. Predicted gene functions are: *fum1* polyketide synthase, *fum6* cytochrome P450 monooxygenase, *fum7* dehydrogenase, *fum8* aminotransferase, *fum9* dioxygenase, *fum10* fatty acyl-CoA synthetase, *fum11* tricarboxylate transporter, *fum12* cytochrome P450 monooxygenase, *fum13* short chain dehydrogenase, *fum14* NRPS-like condensation domain, *fum15* cytochrome P450 monooxygenase, *fum16* fatty acyl-CoA synthetase, *fum17* longevity assurance factor, *fum18* longevity assurance factor, *fum19* ABC transporter.