Table S1. Accumulation of fumigaclavine C in strains of *Neosartorya fumigata*

Strain/treatment	Fumigaclavine C[a]
N. fumigata FGSC 1141	2.1 ± 0.8
dmaW knockout	n.d.[b]
dmaW knockout + *P. camemberti dmaW*	1.5 ± 0.2
easE ko	n.d.
easE knockout + *P. camemberti easE*	1.2 ± 0.2
easC ko	n.d.
easC knockout + *P. camemberti easC*	n.d.

[a] μmol fumigaclavine C/cm^2 culture surface area; mean +/- standard deviation

[b] none detected; limit of detection 0.6 nmol/cm^2

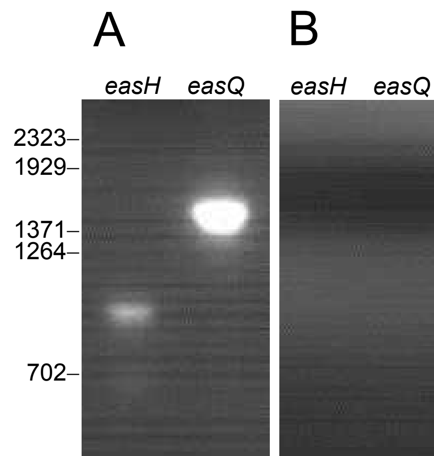

FIG S1 PCR products amplified from (A) cDNA of the *easH/easQ* transformed *N. fumigata easA* knockout and lack of PCR products from (B) non-transformed *N. fumigata easA* knockout genomic DNA primed with same primer pairs. Products in lanes labeled *easH* and *easQ* were amplified with primer combinations 19 and 18 (Table 1) respectively. Primers for *easQ* flanked an intron, and the size (and DNA sequence) of the PCR product demonstrate it was derived from processed mRNA. Relative migration of *Bst*EII-digested bacteriophage lambda fragments (sizes listed in bp) is provided as a length standard. Gels were run separately under similar conditions.

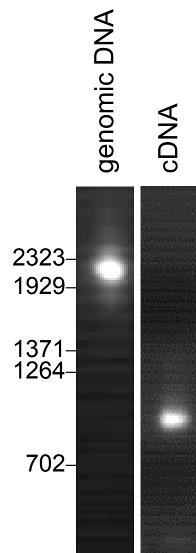

FIG S2 PCR products amplified from genomic DNA or cDNA of *easH* transformed *N. fumigata easA* knockout. Product in lane labeled genomic DNA was amplified with primer combination 6 (Table 1), and the product in the lane labeled cDNA was amplified with primer combination 19 (Table 1). Relative migration of *Bst*EII-digested bacteriophage lambda fragments (sizes listed in bp) is provided as a length standard. Gels were run separately under similar conditions.

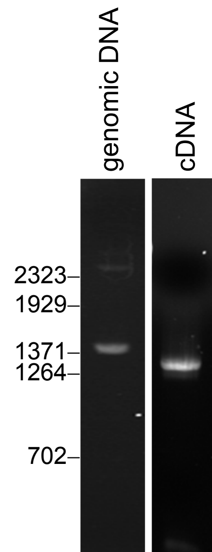

FIG S3 PCR products amplified from genomic DNA or cDNA of *P. camemberti easC* transformed *N. fumigata easC* knockout. Both products were amplified with primer combination 15 (Table 1) from the indicated templates. Relative migration of *Bst*EII-digested bacteriophage lambda fragments (sizes listed in bp) is provided as a length standard. Gels were run separately under similar conditions.

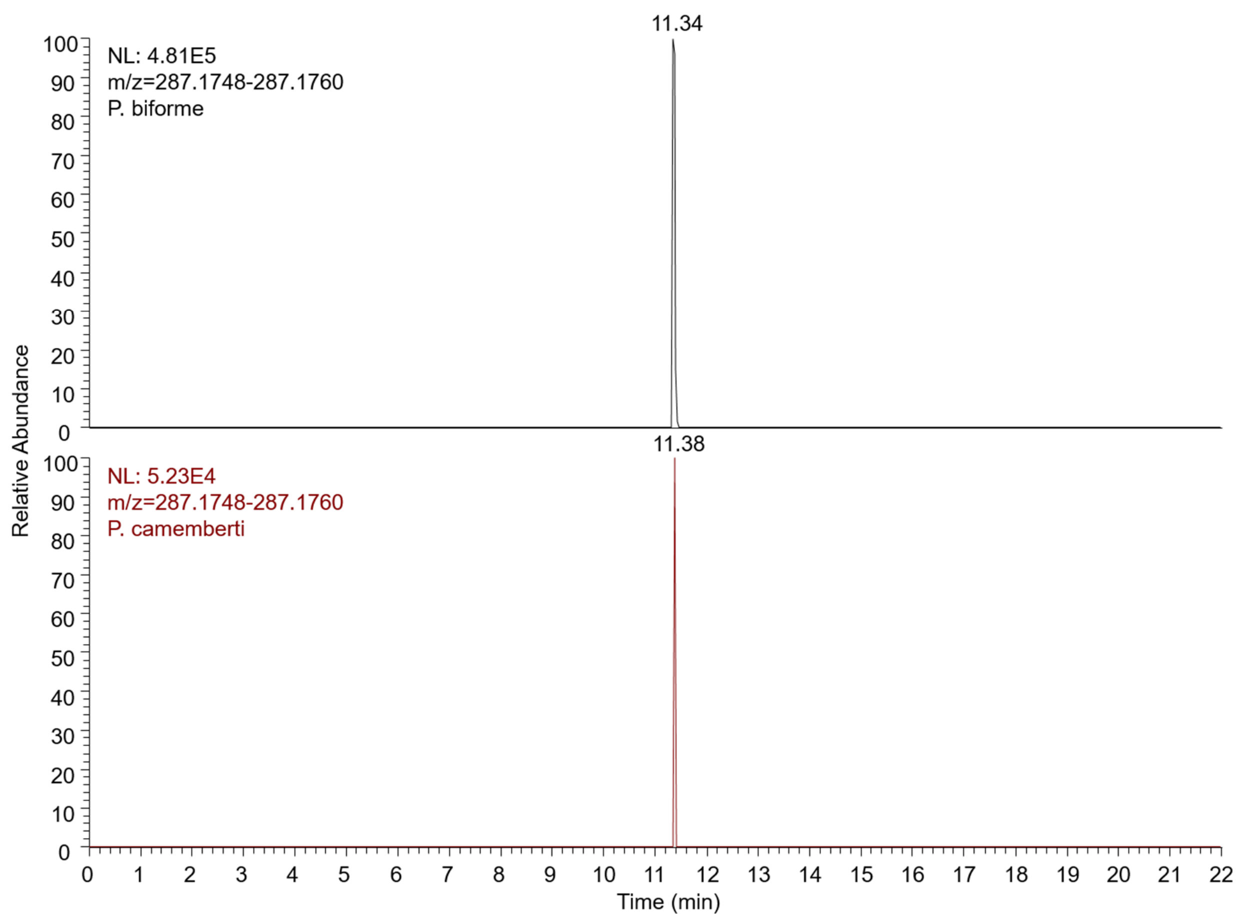

FIG S4 Extracted ion chromatogram showing presence of an analyte matching the mass of N-Me-DMAT (<2 ppm mass error) in *P. biforme* and *P. camemberti* cultured *in vitro*. These data were acquired on a Thermo Scientific Q Exactive mass spectrometer.

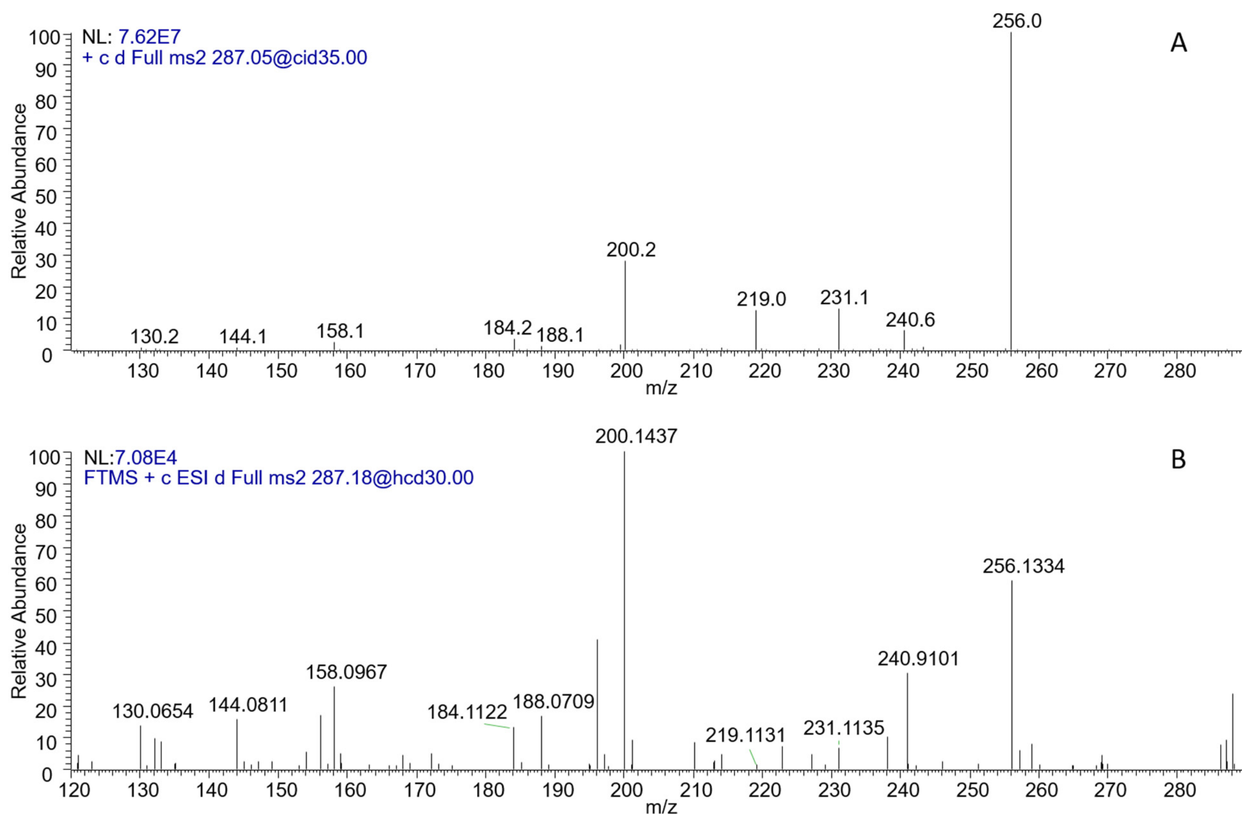

FIG S5 Previously acquired MS/MS spectrum from an N-Me-DMAT standard (A), resulting from fragmentation of the parent ion *m/z* 287.1. Data in panel A were acquired on a Thermo Scientific LCQ DecaXP mass spectrometer, using CID fragmentation. B) MS/MS spectrum acquired from the fragmentation of *m/z* 287.18 isolated from *P. biforme*. Data in panel B were acquired on a Thermo Scientific Q Exactive mass spectrometer, using HCD fragmentation.