

# **Supplemental Information for:**

## **Identification and confirmation of virulence factor production from *Fusarium avenaceum*, a casual agent of root rot in pulses**

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**Table S1.** Canadian Collection of Fungal Cultures (CCFC) accession number, strain name, isolation year and province of origin of all *Fusarium avenaceum* isolates profiled in this study.

CCFC Accession ID	Strain name	Year	Province of origin
DAOMC242072	FaLH01	2010	Saskatchewan
DAOMC242074	FaLH02	2010	Alberta
DAOMC242879	FaLH03	2011	New Brunswick
DAOMC242079	FaLH05	2010	Quebec
DAOMC242084	FaLH10	2011	Quebec
DAOMC242112	FaLH15	2011	New Brunswick
DAOMC242115	FaLH18	2011	New Brunswick
DAOMC242117	FaLH20	2011	New Brunswick
DAOMC242119	FaLH22	2011	Nova Scotia
DAOMC242121	FaLH24	2011	Nova Scotia
DAOMC242880	FaLH27	2011	Nova Scotia
DAOMC251794	FaLH29	2011	New Brunswick
DAOMC242379	FaLH32	2011	New Brunswick
DAOMC242381	FaLH36	2011	Ontario
DAOMC251795	FaLH37	2011	Ontario
DAOMC251796	FaLH38	2011	Ontario
DAOMC251797	FaLH39	2011	Ontario
NA	<i>FaLH27Δ<i>esy</i>n1_2</i>	NA	NA
NA	<i>FaLH27Δ<i>esy</i>n1_8</i>	NA	NA

**Table S2.** Assembly statistics.

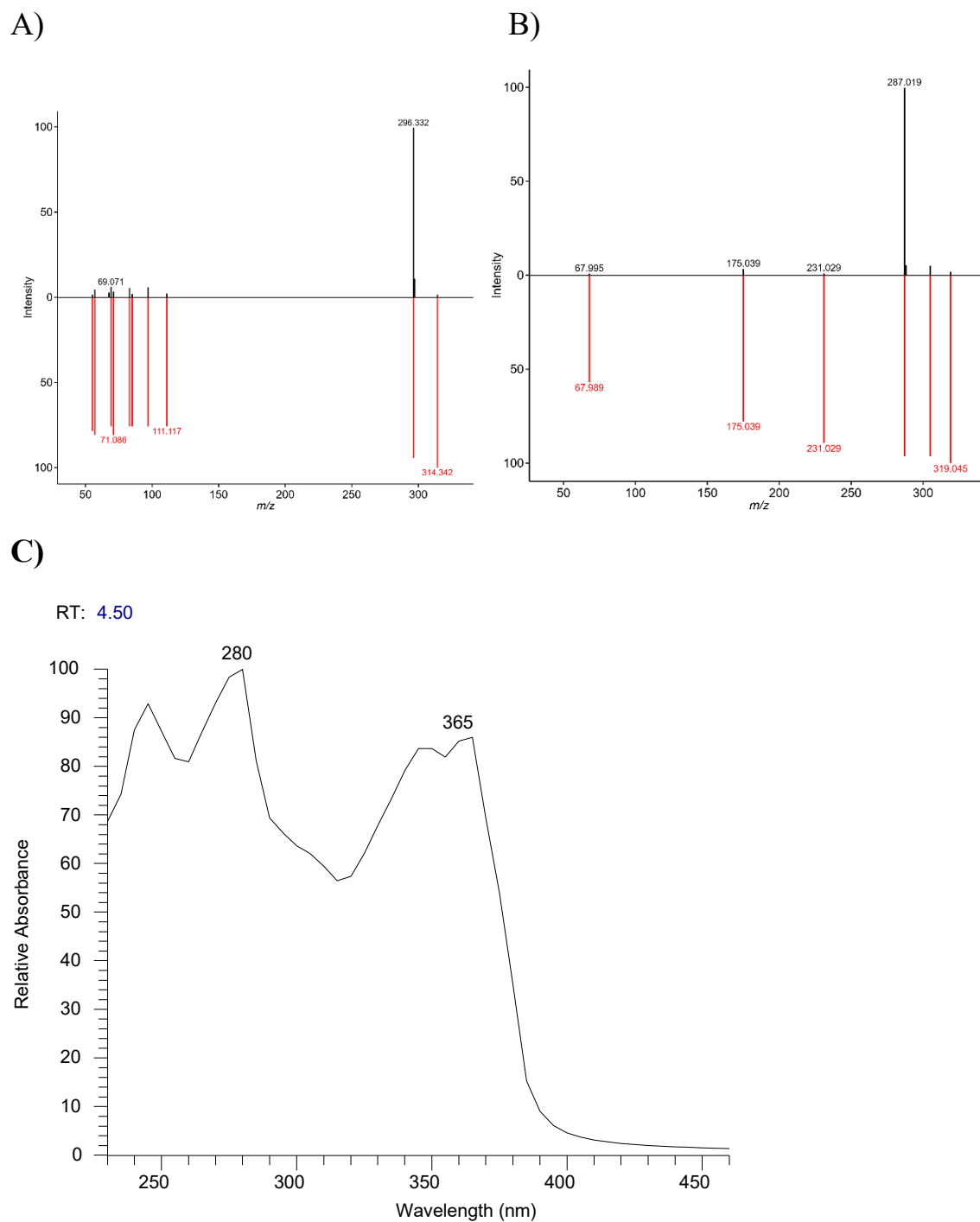
Assembly	FaLH01	FaLH05	FaLH10	FaLH15	FaLH18	FaLH20	FaLH22	FaLH24	FaLH29	FaLH32	FaLH36	FaLH37	FaLH38	FaLH39
Total length (Mb)	42.41	42.37	42.89	42.09	42.03	42.67	42.03	41.92	42.65	42.25	43.67	43.30	42.02	42.13
# scaffolds	51	76	61	66	119	75	102	58	108	105	189	55	61	72
GC (%)	47.9	47.9	47.9	47.9	48.1	47.9	48.0	48.0	48.0	48.1	47.9	47.9	48.0	48.0
N50 scaffold length (Mb)	1.52	1.22	1.68	1.84	1.56	1.38	1.43	1.69	1.22	1.21	0.93	1.78	1.51	1.13
N75 scaffold length (Mb)	1.04	0.69	1.25	0.84	0.86	0.85	1.09	1.12	0.76	0.77	0.41	0.92	0.93	0.78
L50 scaffold count	12	12	9	8	10	12	9	9	13	12	18	9	11	13
L75 scaffold count	20	24	16	17	20	22	18	17	24	22	36	17	20	24
# N's per 100 kbp	5.02	3.3	5.5	2.16	1.76	1.5	1.21	2.15	2.93	2.6	4.63	2.32	2.9	2.16
Average k-mer coverage *	63.5	15.7	83.1	30.24	23	25.4	36.4	22.7	15	13.6	10.7	21.2	20.4	21.8
BUSCO completeness (%)**	99.8	99.8	99.8	99.8	99.9	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.7	99.8

\* calculated at highest k-mer used by SPAdes during assembly (k=99).

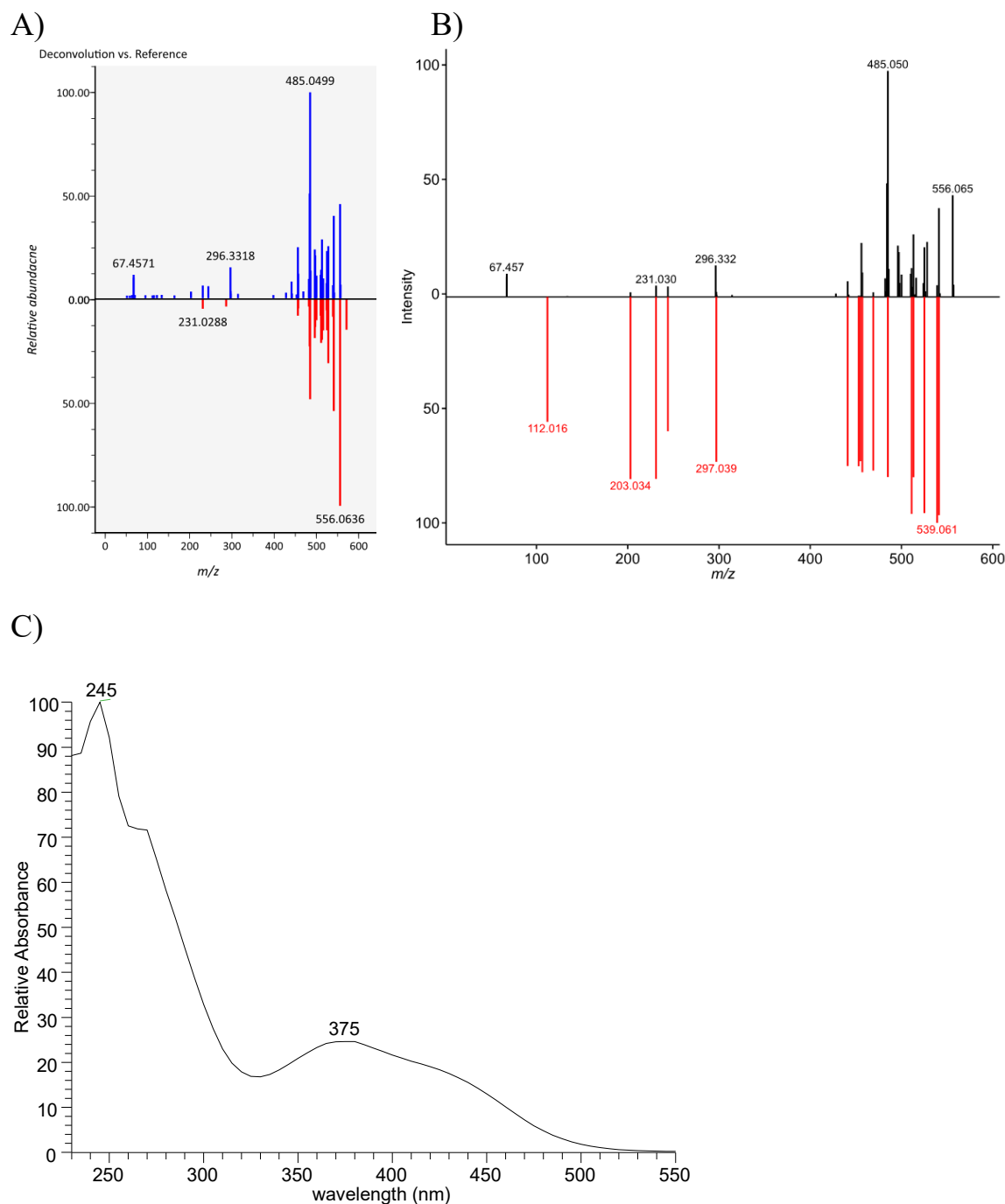
\*\* database = Hypocreales\_ODB10

**Table S3.** Mass features annotations, predicted chemical formulas, chromatographic retention times (RT), observed protonated ( $[M+H]^+$ ) mass to charge ratio ( $m/z$ ) and mass accuracy compared to calculated exact masses of annotated molecules. Annotation levels refer to methods, where 1 =  $m/z$  match (<5 ppm), 2 = top MS-FINDER filtered match to reference structure library, 3 = MS-DIAL match of mass feature  $MS^2$  to MassBank  $MS^2$  reference library, 4 = match to chemical standard.

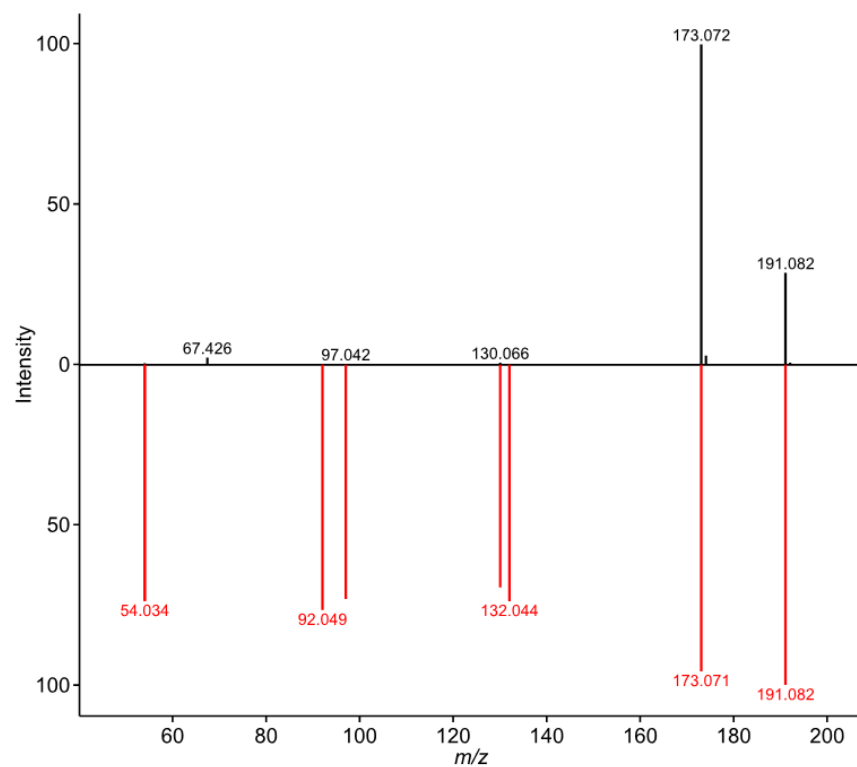
Compound name	Chemical formula	RT	Precursor $m/z$ $[M+H]^+$	accuracy (ppm)	Annotation level
AOD	C20H43NO	6.03	314.34134	1.28	2
Acuminatopyrone	C11H11NO3	2.5	206.08154	1.65	1
Antibiotic Y	C15H10O8	4.48	319.04474	0.33	2
Aurofusarin	C30H18O12	4.95	571.08704	0.11	3
Chlamydosporiol	C11H16O5	3.06	229.10764	0.17	1
Chlamydosporols	C11H14O5	3.32, 3.41	227.09192	2.29	4
Chrysogine	C10H10N2O2	3.09	191.08173	0.226	1
Enniatin A	C36H63N3O9	6.61	682.46484	1.67	4
Enniatin A1	C35H61N3O9	6.39	668.45044	2.75	4
Enniatin B	C33H57N3O9	5.99	640.41949	3.45	4
Enniatin B1	C34H59N3O9	6.17	654.43494	3.12	4
FDDP-shunt	C28H42O4	5.93	443.3164	1.93	1
FDDP-D	C29H42O7	5.71	503.30157	2.46	4
FDDP-E	C29H42O6	6.15	487.30649	2.21	4
Fusahexin	C30H50N6O7	4.71	607.3811	0.45	1
Fusahexins (hydrolyzed)	C30H52N6O8	4.26, 4.43	625.39368	2.78	1
Fusaoctaxin A	C36H68N8O10	3.95	773.51324	0.16	1
Fusaoctaxin analog 2	C36H68N8O9	3.93	757.51762	1.13	1
Fusaoctaxin analog 3	C35H67N10O9	3.93	771.5085	1.1	1
Fusaoctaxin analog 4	C36H69N10O10	3.98	801.51561	3.57	1
Fusapentaxin A	C21H39N5O7	3.32	474.29016	2.07	1
Fusarin A	C23H29NO6	4.96	416.206545	0.54	2
Fusarin C	C23H29NO7	4.61	432.20166	0.043	2
Fusarin PM	C22H27NO7	4.02	418.18588	0.36	2
Fusaristatin A	C36H58N4O7	5.78	659.43787	0.066	2
Fusatrixin A	C15H31N3O4	3.57	318.23821	0.86	1
Fuscofusarin	C30H20O11	5.38	557.10803	0.35	2
JM-47	C21H36N4O6	3.5	439.25485	0.596	2
N-desmethyl sambutoxin	C27H7NO4	5.88	440.27936	0.4	2
Rubrofusarin	C15H12O5	5.33	273.07544	1.14	3
Sambutoxin	C28H39NO4	6.12	454.29507	0.25	2



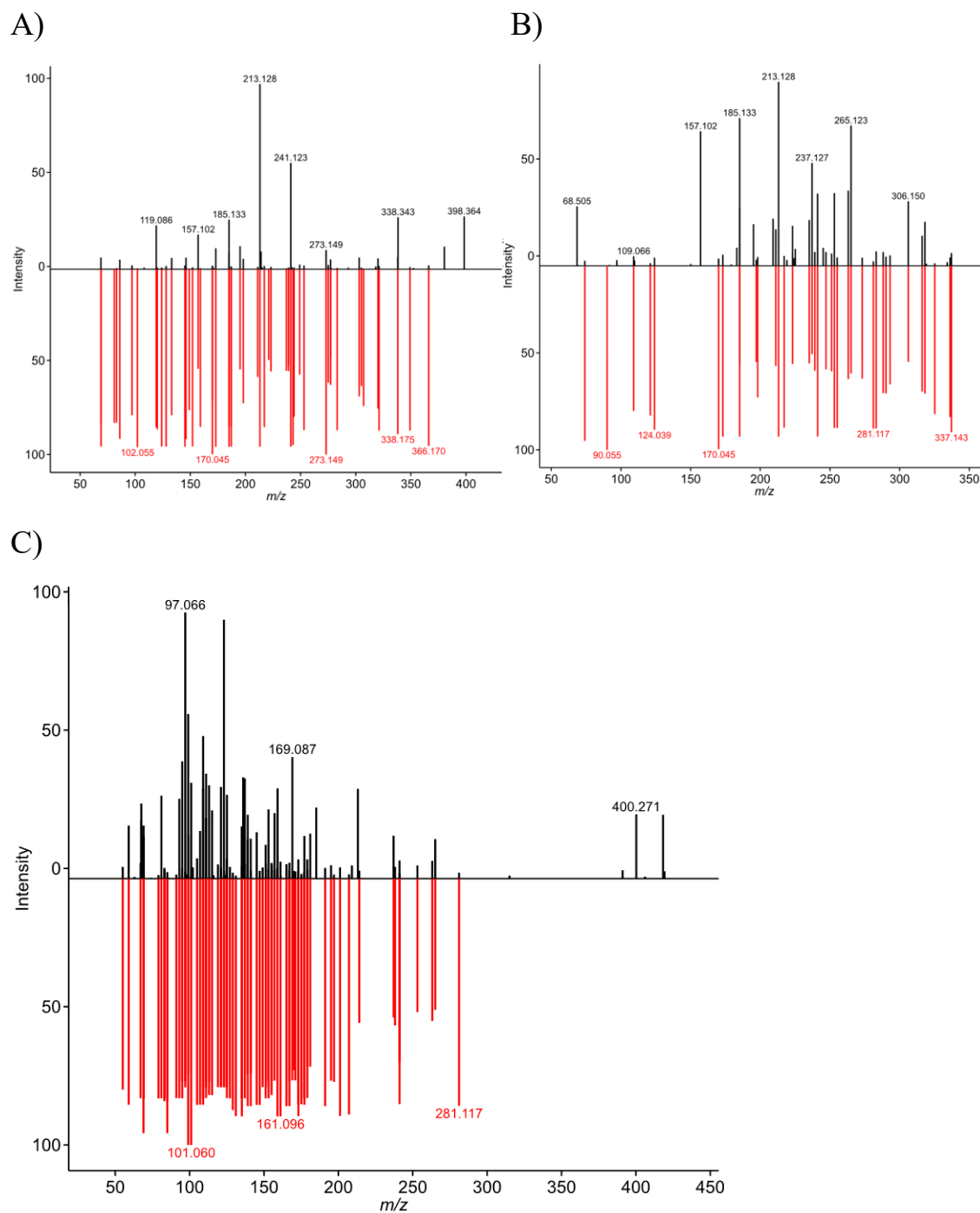
**Figure S1.** Mirror plots and UV absorbance spectrum supporting AOD and antibiotic Y mass feature annotations. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red. **A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT6.03\_314.34134, annotated as 2-AOD-3-ol. **B)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT4.48\_319.04474, annotated as antibiotic Y. **C)** UV absorbance spectrum of associated with mass feature RT4.48\_319.04474, annotated as antibiotic Y



**Figure S2.** Mirror plots and UV absorbance spectrum supporting aurofusarin mass feature annotation. **A)** MS-DIAL mirror plot comparing aurofusarin-associated MS<sup>2</sup> spectrum from MassBank to MS<sup>2</sup> spectrum from mass feature RT4.95\_571.08704, annotated as aurofusarin. Experimentally obtained spectrum is in blue (top plot), database matched MS<sup>2</sup> spectrum is in red (bottom plot). **B)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT4.95\_571.08704, annotated as aurofusarin. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red. **C)** UV absorbance spectrum of associated with mass feature RT4.95\_571.08704, annotated as aurofusarin.

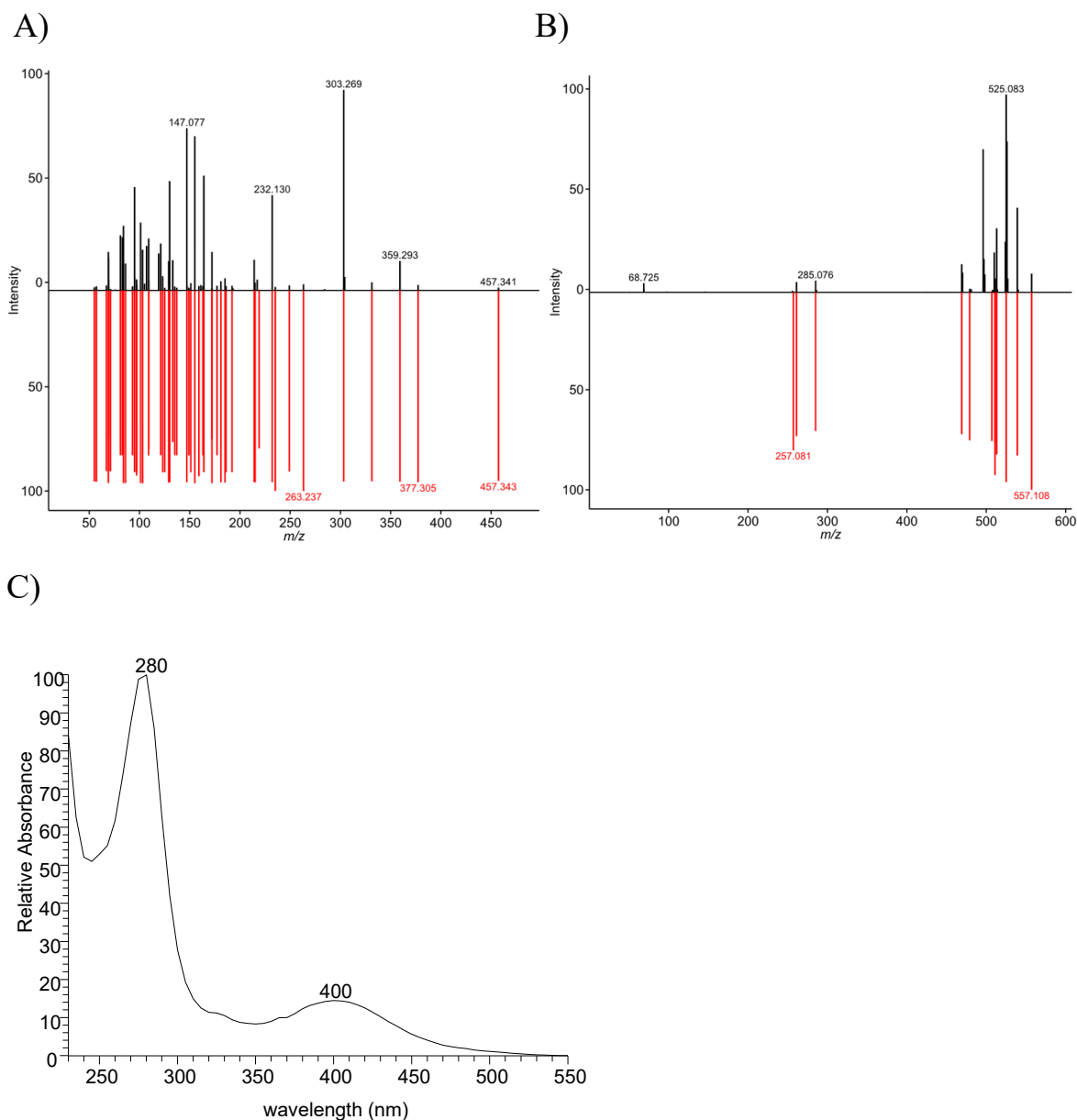


**Figure S3.** Mirror plots supporting chrysogine mass feature annotation. **A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT3.09\_191.08173, annotated as chrysogine. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red.

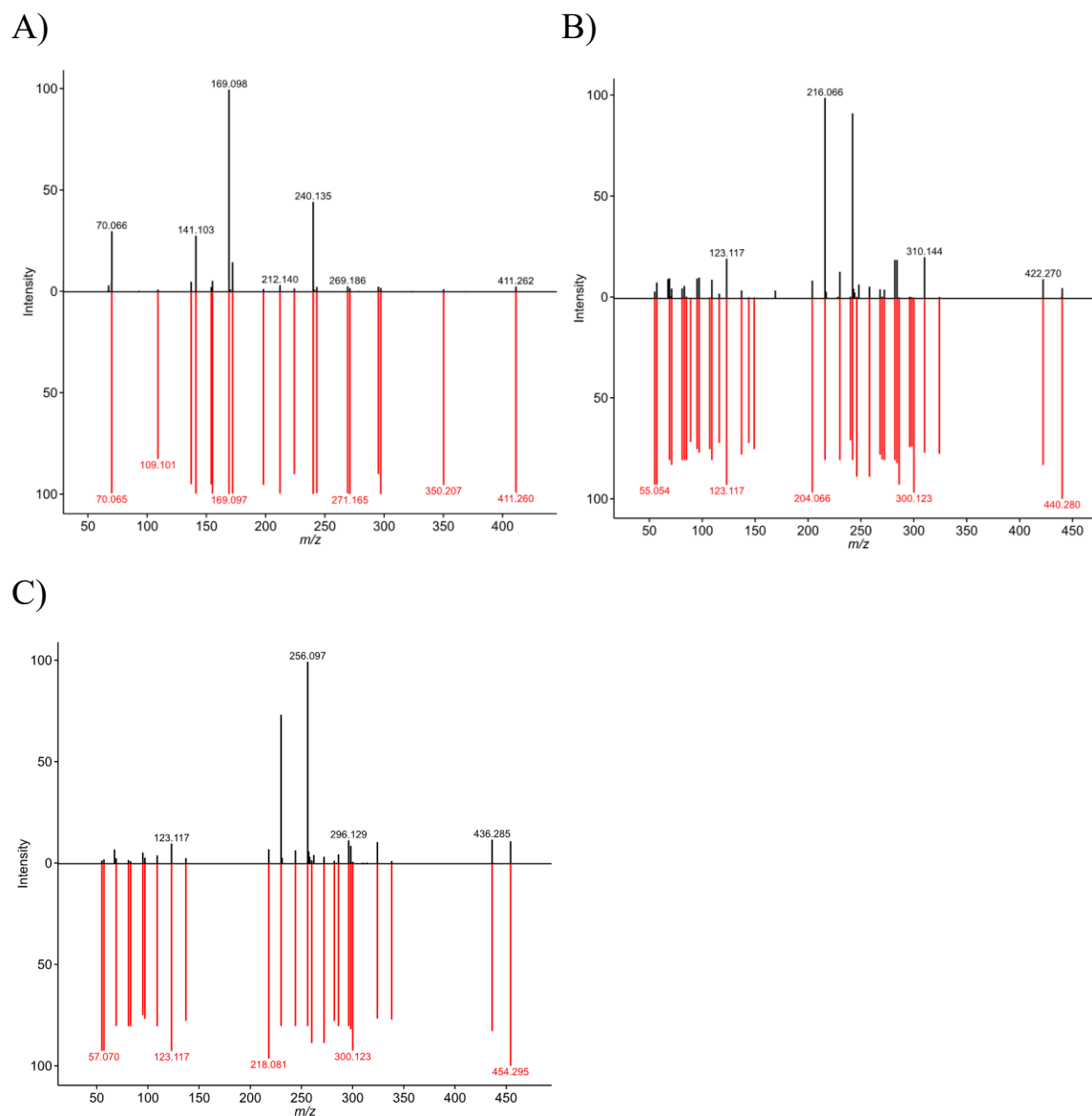


**Figure S4.** Mirror plots supporting fusarin mass feature annotations. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red. **A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT4.96\_416.206545, annotated as fusarin A. **B)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT4.61\_432.20166, annotated as fusarin C. **C)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT4.02\_418.18588, annotated as fusarin PM.



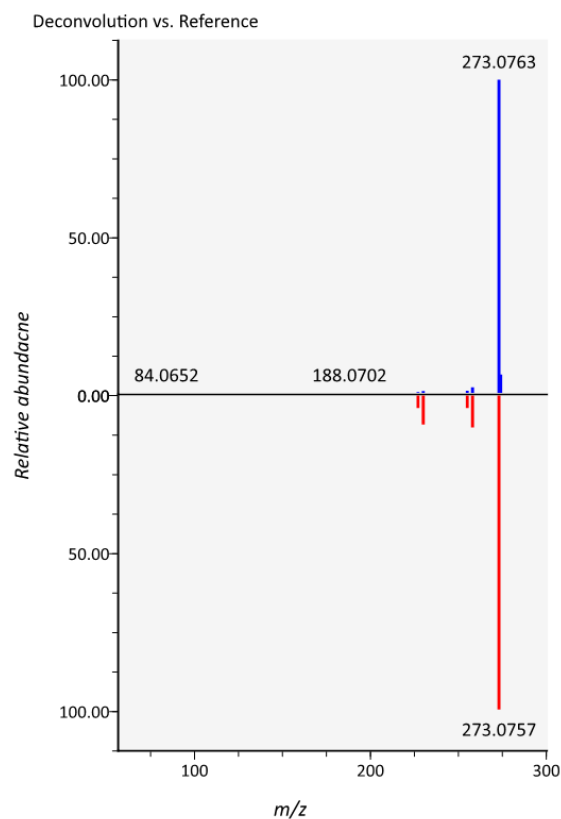


**Figure S5.** Mirror plot and UV absorbance spectrum supporting fusaristatin A and fuscofusarin mass feature annotations. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red. **A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT5.78\_659.4387, annotated as fusaristatin A. **B)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT5.38\_557.10803, annotated as fuscofusarin. **C)** UV absorbance spectrum of associated with mass feature RT5.38\_557.10803, annotated as fuscofusarin

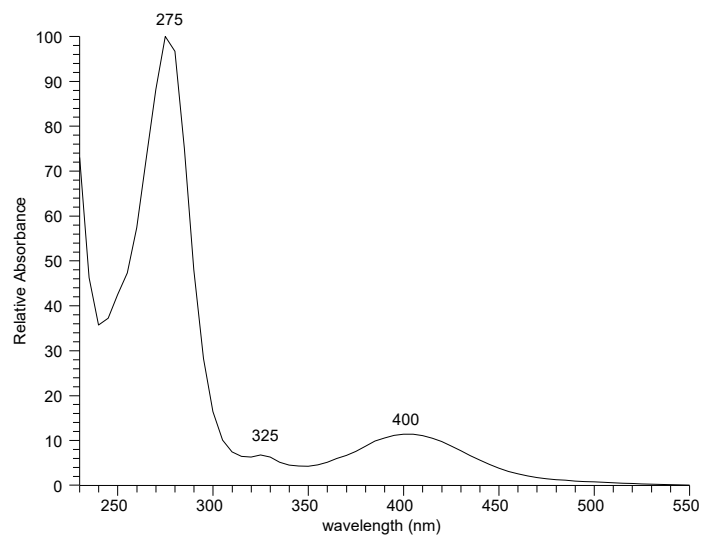


**Figure S6.** Mirror plots supporting JM-47 and sambutoxin mass feature annotations. Experimentally obtained spectrum is in black while *in silico* predicted spectral scores are in red. **A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT3.50\_439.25485, annotated as JM-47. **B)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT5.88\_440.27936, annotated as N-desmethyl-sambutoxin. **C)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT6.12\_454.29507, annotated as sambutoxin.

A)



B)



**Figure S7.** Mirror plot and UV absorbance spectrum supporting rubrofusarin mass feature annotation.

**A)** MS-FINDER MS<sup>2</sup> analysis of mass feature RT5.33\_273.07544, annotated as rubrofusarin.

Experimentally obtained spectrum is in blue (top plot), database matched MS<sup>2</sup> spectrum is in red (bottom plot). **B)** UV absorbance spectrum of associated with mass feature RT5.33\_273.07544, annotated as rubrofusarin.