

SUPPLEMENTARY FILE S3.

(Sayari et al - *Ceratocystidaceae* Nonribosomal peptide synthetase gene clusters)

Blast hits for putative *Ceratocystidaceae* NRPS biosynthetic gene clusters predicted with antiSMASH. For confirmation of the antiSMASH results, we utilized SMURF (www.jcvi.org/smurf/; (Khaldi et al. 2010). For this purpose, genes that were 15Kb upstream and downstream of the identified NRPS genes, were retrieved and submitted to the BLASTp server at National Centre for Biotechnology Information (NCBI, <ftp://ftp.ncbi.nih.gov/blast/>) for identification.

A-1) <i>Ceratocystis adiposa</i> monomodular NRPS cluster Contig127 (LXGU00000127)							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ras_GTPase	208	10101-11196	<i>Grosmannia clavigera</i>	9e-142	96	98	XP_014176081
Peroxin 14/17	374	12451-13304	<i>Drechmeria coniospora</i>	1e-42	99	34	KYK54231
Hypothetical	799	17267-18477	<i>Metarhizium rileyi</i>	4e-45	40	41	OAA44328
Hypothetical	562	19710-23430	<i>Stachybotrys chartarum</i>	8e-31	50	31	KFA73722
NRPS	2092	29439-31379	<i>Colletotrichum gloeosporioides</i>	0	87	55	XP_007284335
CoA transferase	577	32137-38636	<i>Neonectria ditissima</i>	0	98	75	KPM45703
Siderophore transporter	586	44922-46799	<i>Trichoderma quizhouense</i>	0	96	55	OPB43222
Siderophore biosynthesis	452	48845-50814	<i>Purpureocillium lilacinum</i>	0	99	64	OAQ83990
Oxidoreductase	421	52470-53828	<i>Trichoderma quizhouense</i>	5e-156	98	53	OPB43223
ABC-multidrug transporter	1370	53943-55716	<i>Purpureocillium lilacinum</i>	0	97	57	OAQ83993
Transporter	832	65836-68393	<i>Colletotrichum incanum</i>	0	100	57	OHW98426
Geranylgeranyl transferase	322	70784-71997	<i>Colletotrichum salicis</i>	1e-80	97	43	KXH54021

A-2) <i>Ceratocystis adiposa</i> multi-modular NRPS cluster Contig 175 (LXGU00000175)							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Glutathione transferase	232	664-1427	<i>Umbilicaria pustulata</i>	3e-26	86	37	SLM39268
Transposase	333	6275-7575	<i>Fusarium oxysporum</i>	7e-133	88	70	ENH66637

Hydroxymate type ferrichrome siderophore peptide synthase	4810	8168-22785	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834
L-ornithine N-5 monooxygenase	523	32170-33814	<i>Fusarium avenaceum</i>	0	91	59	KIL93640
Endothiapepsin	415	35185-36432	<i>Nectria ditissima</i>	0	100	62	KPM38239
Mediator of RNA polymerase-II transcription subunit 7	297	39445-40399	<i>Fusarium poae</i>	3e-77	83	51	OBS21164
Hypothetical	323	40811-41782	<i>Fusarium langsethiae</i>	9e-28	82	41	KPA42345

B-1) *Ceratocystis albifundus* monomodular NRPS cluster Contig 1154 (JSSU000001154)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Glutamine synthase	684	470-3248	<i>Metarhizium brunneum</i>	0	99	69	XP_014545497
Geranylgeranyl transferase	316	3503-4522	<i>Tolypocladium ophioglossoides</i>	2e-97	98	47	KND94315
Transporter	795	5694-8351	<i>Colletotrichum tofieldiae</i>	0	98	72	KZL78304
ABC-transporter	1363	9455-13612	<i>Colletotrichum chlorophyti</i>	0	97	57	OLN95357
Oxidoreductase	420	15070-16498	<i>Trichoderma atroviride</i>	1e-162	96	55	XP_013943858
Siderophore biosynthesis	450	16684-18104	<i>Drechmeria coniospora</i>	0	99	62	ODA83897
Siderophore transporter	1151	18824-23219	<i>Trichoderma reesei</i>	0	47	75	XP_006968099
NRPS	2100	25279-31641	<i>Colletotrichum gloeosporioides</i>	0	88	53	EQB59356
Hypothetical	595	33229-35016	<i>Colletotrichum graminicola</i>	2e-82	75	40	XP_008096956

B-2) *Ceratocystis albifundus* multi-modular NRPS cluster-Contig1169 (JSSU000001169)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome	4919	2141-17203	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834

siderophore peptide synthase							
L-ornithine N-5 monooxygenase	530	23649-25327	<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Mediator of RNA polymerase-II transcription subunit 7	255	28185-29012	<i>Nectria haematococca</i>	1e-87	98	54	XP_003044025
Hypothetical	348	29567-30613	<i>Colletotrichum salicis</i>	3e-59	84	45	KXH53360

C-1) *Ceratocystis eucalypticola* monomodular NRPS cluster-Contig167 (LJOA00000167)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
MFS-type transporter	621	114070-116062	<i>Neonectria ditissima</i>	0	93	69	KPM45342
Glutamine synthase	1172	119620-124574	<i>Metarhizium brunneum</i>	0	99	69	XP_014545497
ABC multidrug transporter	2231	125712-133609	<i>Pochonia chlamydospora</i>	0	98	60	XP_018147652
Oxidoreductase	420	135058-136469	<i>Scedosporium apiospermum</i>	8e-155	98	56	XP_016644515
Siderophore biosynthesis	450	136660-138080	<i>Colletotrichum orchidophilum</i>	0	98	60	XP_022473331
Siderophore transporter	1155	138773-143113	<i>Trichoderma reesei</i>	0	48	75	XP_006968099
NRPS	2100	145186-151548	<i>Colletotrichum gloeosporioides</i>	0	88	53	EQB59356
Hypothetical	597	153090-154483	<i>Pochonia chlamydosporia</i>	1e-81	75	40	XP_018147657

C-2) *Ceratocystis eucalypticola* multi-modular NRPS cluster-Contig 206 (LJOA00000206)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	351	7544-8599	<i>Colletotrichum salicis</i>	4e-61	85	45	KXH53360
Mediator of RNA polymerase-II transcription subunit 7	255	9147-9974	<i>Nectria haematococca</i>	2e-85	98	53	XP_003044025
Aspergillopepsin	425	11685-12962	<i>Ceratocystis fimbriata</i>	0	100	97	PHH49949

L-ornithine N-5 monooxygenase	530		<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Hydroxymate type ferrichrome siderophore peptide synthase	4918	21836-36887	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834

D-1) *Bretziella fagacearum* monomodular NRPS cluster Contig 3 (MKGJ00000003)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Geranylgeranyl transferase	330	13506-14685	<i>Magnaporthe poae</i>	7e-110	79	61	KLU91995
Transporter	932	16580-19884	<i>Colletotrichum gloeosporioides</i>	0	96	69	XP_007273195
ABC-transporter	1374	20758-24989	<i>Metarhizium acridum</i>	0	99	55	XP_007808197
Oxidoreductase	420	28003-29707	<i>Metarhizium rileyi</i>	4e-145	96	56	OAA44322
Siderophore biosynthesis	452	29922-31280	<i>Purpureocillium lilacinum</i>	0	99	65	OAA44322
Siderophore transporter	555	33090-34757	<i>Trichoderma quizhouense</i>	0	100	56	OPB43222
Acyl-CoA synthetase	577	36234-38121	<i>Nectria ditissima</i>	0	98	75	KPM45703
NRPS	1960	41315-47342	<i>Colletotrichum gloeosporioides</i>	0	96	54	EQB59356
Hypothetical	595	47969-50689	<i>Thielavia terrestris</i>	2e-65	67	37	XP_003657661

D-2) *Bretziella fagacearum* multi-modular NRPS cluster-Contig 227 (MKGJ00000227)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4766	1-14960	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	527	21912-23581	<i>Purpureocillium lilacinum</i>	0	89	60	XP_018181246

1,4 glucanase	41	24912-26018	<i>Neonectria ditissima</i>	2e-130	99	55	KPM42114
Chitinase	714	28750-31021	<i>Valsa mali</i>	6e-23	42	43	KUI56008
Hypothetical	618	35659-37651	<i>Thielavia terrestris</i>	2e-65	67	37	XP_003657661

E-1) *Ceratocystis manginecans* monomodular NRPS cluster-Contig 3 (JJRZ000000003)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	597	1888-3681	<i>Pochonia chlamydosporia</i>	1e-81	75	40	XP_018147657
NRPS	2100	5223-11585	<i>Colletotrichum gloeosporioides</i>	0	86	53	XP_007284335
Siderophore transporter	1158	13658-17997	<i>Trichoderma reesei</i>	0	48	75	XP_006968099
Siderophore biosynthesis	450	18684-20104	<i>Colletotrichum orchidophilum</i>	0	98	60	XP_022473331
Oxidoreductase	420	20295-21706	<i>Scedosporium apiospermum</i>	5e-155	97	56	XP_016644515
ABC-multidrug transporter	2231	23155-31053	<i>Pochonia chlamydosporia</i>	0	98	60	XP_018147652
Glutamine synthase	1147	32191-37148	<i>Metarhizium brunneum</i>	0	61	71	XP_014545497

E-2) *Ceratocystis manginecans* multi-modular NRPS cluster-Contig 189 (JJRZ000000189)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4919	24617-39671	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	530	46319-47994	<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Aspergillopepsin	425	48781-50058	<i>Ceratocystis fimbriata</i>	0	100	97	PHH49949
Mediator of RNA polymerase-II transcription subunit 7	255	51768-52595	<i>Nectria haematococca</i>	4e-86	98	54	XP_003044025
Hypothetical	351	53143-54198	<i>Colletotrichum salicis</i>	4e-61	85	45	KXH53360

F-1) *Ceratocystis fimbriata* monomodular NRPS cluster-Contig 521 (APWK0000521)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NRPS	2100	848-7210	<i>Colletotrichum gloeosporioides</i>	0	88	53	XP_007284335
Hypothetical	597	8963-10756	<i>Pochonia chlamyosporia</i>	1e-81	75	40	XP_018147657
Siderophore transporter	1158	16157-17422	<i>Trichoderma reesei</i>	0	48	75	XP_006968099
Siderophore biosynthesis	451	22831-24020	<i>Colletotrichum orchidophilum</i>	0	97	59	XP_022473331
Oxidoreductase	420	25221-26372	<i>Scedosporium apiospermum</i>	5e-1152	96	55	XP_016644515
ABC-multidrug transporter	2230	27634-30122	<i>Pochonia chlamyosporia</i>	0	98	60	XP_018147652
Glutamine synthase	1145	31054-32961	<i>Metarhizium brunneum</i>	0	60	70	XP_014545497

F-2) *Ceratocystis fimbriata* multi-modular NRPS cluster-Contig 182 (APWK0000182)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4919	24617-39671	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	530	46319-47994	<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Aspergillopepsin	425	48781-50058	<i>Ceratocystis fimbriata</i>	0	100	97	PHH49949
Mediator of RNA polymerase-II transcription subunit 7	255	51768-52595	<i>Nectria haematococca</i>	4e-86	98	54	XP_003044025
Hypothetical	351	53143-54198	<i>Colletotrichum salicis</i>	4e-61	85	45	KXH53360

G-1) *Ceratocystis harringtonii* monomodular NRPS cluster-Contig 60 (MKGM000060)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	597	75458-77251	<i>Pochonia chlamyosporia</i>	4e-82	75	40	XP_018147657
NRPS	2100	78788-85150	<i>Colletotrichum gloeosporioides</i>	0	87	53	XP_007284335
Siderophore transporter	1116	87218-93614	<i>Trichoderma reesei</i>	0	35	74	XP_006968099
Siderophore biosynthesis	450	93808-95231	<i>Colletotrichum orchidophilum</i>	0	98	60	XP_022473331

Oxidoreductase	429	96635-98124	<i>Scedosporium apiospermum</i>	1e-164	97	56	XP_016644515
ABC-multidrug transporter	2231	100363-107756	<i>Pochonia chlamydosporia</i>	0	98	60	XP_018147652
Glutamine synthase	1147	108239-110589	<i>Metarhizium brunneum</i>	0	61	71	XP_014545497

G-2) *Ceratocystis harringtonii* multi-modular NRPS cluster-Contig 378 (MKGM0000378)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4919	607-15650	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	530	17900-21654	<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Aspergillopepsin	425	24369-26700	<i>Ceratocystis fimbriata</i>	0	100	97	PHH49949
Mediator of RNA polymerase-II transcription subunit 7	255	27351-28215	<i>Nectria haematococca</i>	4e-86	98	54	XP_003044025
Hypothetical	351	30100-31838	<i>Colletotrichum salicis</i>	4e-61	85	45	KXH53360

H-1) *Ceratocystis platani* monomodular NRPS cluster-Contig 109 (LBBL00000109)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transposable element	403	1-1320	<i>Fusarium oxysporum</i>	2e-129	93	68	ENH65995
Hypothetical	204	7955-8569	<i>Pochonia chlamydosporia</i>	1e-81	75	40	XP_018147657
Glutamine synthase	1370	14397-19936	<i>Metarhizium brunneum</i>	0	51	71	XP_014545497
ABC-multidrug transporter	2233	21080-28988	<i>Pochonia chlamydosporia</i>	0	98	60	XP_018147652
Oxidoreductase	420	30437-31848	<i>Scedosporium apiospermum</i>	4e-155	97	56	XP_016644515
Siderophore	450	32039-38464	<i>Colletotrichum orchidophilum</i>	0	98	60	XP_022473331

biosynthesis							
Siderophore transporter	1618	40639-47001	<i>Trichoderma reesei</i>	0	34	76	XP_006968099
NRPS	2100	48540-50333	<i>Colletotrichum gloeosporioides</i>	0	88	53	XP_007284335
Hypothetical	597	53928-55020	<i>Pochonia chlamyosporia</i>	1e-81	75	40	XP_018147657
Hypothetical	306	55777-57041	<i>Stachybotrys chlorohalonata</i>	6e-48	99	48	KFA61745

H-2) *Ceratocystis platani* multi-modular NRPS cluster-Contig 340 (LBBL00000340)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4909	21728-36752	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	530	13709-15387	<i>Fusarium graminearum</i>	0	99	55	XP_011323895
Aspergillopepsin	425	11645-12922	<i>Ceratocystis fimbriata</i>	0	100	96	PHH49949
Mediator of RNA polymerase-II transcription subunit 7	255	9105-9932	<i>Nectria haematococca</i>	2e-87	98	54	XP_003044025
Hypothetical	349	7508-8557	<i>Colletotrichum salicis</i>	1e-60	85	45	KXH53360

I-1) *Ceratocystis smalleyi* monomodular NRPS cluster-Contig 330 (NETT01000330)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	349	20919-22712	<i>Pochonia chlamyosporia</i>	9e-81	75	40	XP_018147657
NRPS	2100	13000-19362	<i>Colletotrichum gloeosporioides</i>	0	87	53	XP_007284335
Siderophore transporter	1155	6583-10915	<i>Trichoderma reesei</i>	0	48	75	XP_006968099
Siderophore biosynthesis	85	6200-6485	<i>Colletotrichum orchidophilum</i>	0	98	60	XP_022473331
Oxidoreductase	420	5100-6123	<i>Scedosporium apiospermum</i>	5e-155	97	56	XP_016644515
ABC-multidrug	1231	1-4863	<i>Pochonia chlamyosporia</i>	0	98	60	XP_018147652

transporter							
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I-2) *Ceratocystis smallei* multi-modular NRPS cluster-Contig 288 (NETT01000228)

Gene name	Size	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4920	24617-39671	<i>Scedosporium apiospermum</i>	0	99	42	XP_016639834
L-ornithine N-5 monooxygenase	530	46319-47994	<i>Fusarium graminearum</i>	0	88	60	XP_011323895
Aspergillopepsin	164	48781-50058	<i>Ceratocystis fimbriata</i>	2e-57	100	97	PHH49949
Mediator of RNA polymerase-II transcription subunit 7	255	51768-52595	<i>Nectria haematococca</i>	5e-87	98	54	XP_0030444025
Hypothetical	354	53143-54198	<i>Colletotrichum salicis</i>	2e-58	83	45	KXH53360

J-1) *Huntia decipiens* monomodular NRPS cluster Contig 65 (NETU0000065)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	662	153578-156583	<i>Colletotrichum nymphaeae</i>	8e-62	65	35	KXH42342
NRPS	2077	156800-163089	<i>Colletotrichum gloeosporioides</i>	0	90	54	XP_007284335
CoA transferase	577	166514-168357	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	585	169239-170996	<i>Trichoderma quizhouense</i>	0	94	54	OPB43222
Siderophore biosynthesis	451	171835-173190	<i>Purpureocillium lilacinum</i>	0	99	62	OAQ83990
Oxidoreductase	430	173298-174886	<i>Trichoderma quizhouense</i>	3e-144	97	51	OPB43223
ABC-multidrug transporter	1363	178036-182188	<i>Purpureocillium lilacinum</i>	0	96	58	OAQ83993
Transporter	971	182594-185767	<i>Colletotrichum gloeosporioides</i>	0	94	67	XP_007273195
Geranylgeranyl transferase	322	186098-187816	<i>Colletotrichum salicis</i>	1e-80	97	43	KXH54021

J-2) *Huntia decipiens* multi-modular NRPS cluster Contig 307 (NETU00000307)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4782	52009-66674	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834
L-ornithine N-5 monooxygenase	528	42395-44050	<i>Fusarium oxysporum</i>	0	99	55	PCD43854
Endothiapepsin	413	40415-41656	<i>Nectria ditissima</i>	0	100	58	KPM38239
Hypothetical	153	37016-37582	<i>Scedosporium apiospermum</i>		89	36	XP_016639846
Hypothetical	285	31291-32148	<i>Fusarium avenaceum</i>		96	35	KIL93607
Mediator of RNA polymerase-II transcription subunit 7	297	30182-31007	<i>Nectria haematococca</i>	4e-85	95	45	XP_003044025
Membrane protein	323	26531-29451	<i>Colletotrichum graminicola</i>	0	89	53	XP_008095397

K-1) *Huntia bhutanensis* monomodular NRPS cluster Contig 96 (MJMS00000096)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	649	28120-30368	<i>Verticillium longisporum</i>	7e-64	67	40	CRK10802
NRPS	2081	30585-36886	<i>Colletotrichum gloeosporioides</i>	0	90	54	XP_007284335
CoA transferase	577	40294-42137	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	585	43020-44777	<i>Trichoderma quizhouense</i>	0	94	53	OPB43222
Siderophore biosynthesis	451	45614-46969	<i>Purpureocillium lilacinum</i>	0	99	62	OAQ83990
Oxidoreductase	430	47077-48665	<i>Trichoderma quizhouense</i>	9e-149	97	51	OPB43223
ABC-multidrug transporter	1363	51817-55969	<i>Purpureocillium lilacinum</i>	0	98	57	OAQ83993
Transporter	1379	56375-61590	<i>Scedosporium apiospermum</i>	0	93	56	XP_016644513
Oxidoreductase	432	61637-62985	<i>Colletotrichum gloeosporioides</i>	7e-98	96	42	KXH54021
N-Acyltransferase	257	63280-64165	<i>Aschersonia aleyrodis</i>	8e-62	86	44	KZZ98783
Glutamine synthase	722	65142-67536	<i>Colletotrichum salicis</i>	0	98	72	KXH63435

K-2) *Huntia bhutanensis* multi-modular NRPS cluster Contig 83 (MJMS00000083)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate	4782	111372-126028	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834

type ferrichrome siderophore peptide synthase							
L-ornithine N-5 monooxygenase	528	101811-103465	<i>Fusarium oxysporum</i>	0	99	55	PCD43854
Endothiapepsin	413	99848-101089	<i>Nectria ditissima</i>	2e-167	100	58	KPM38239
Hypothetical	152	96401-96964	<i>Scedosporium apiospermum</i>	8e-17	77	39	XP_016639846
Hypothetical	283	90635-91486	<i>Fusarium avenaceum</i>		96	35	KIL93607
Mediator of RNA polymerase-II transcription subunit 7	256	89531-90356	<i>Nectria haematococca</i>	1e-82	95	52	XP_003044025
Membrane protein	954	85883-88797	<i>Colletotrichum tofieldiae</i>	0	89	52	KZL73724
Hydrolase	227	84610-85545	<i>Trichoderma harzianum</i>	0	97	60	KKP04280

L-1) *Huntiaella moniliformis* monomodular NRPS cluster Contig 76 (JMSH00000076)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	649	65356-67601	<i>Verticillium longisporum</i>	2e-60	67	39	CRK10802
NRPS	2081	67818-74119	<i>Colletotrichum gloeosporioides</i>	0	90	54	XP_007284335
CoA transferase	577	77591-79435	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	585	80316-82073	<i>Trichoderma quizhouense</i>	0	94	52	OPB43222
Siderophore biosynthesis	451	82913-84268	<i>Purpureocillium lilacinum</i>	0	99	62	OAQ83990
Oxidoreductase	421	84374-85964	<i>Trichoderma quizhouense</i>	5e-148	97	52	OPB43223
ABC-multidrug transporter	1363	89140-93292	<i>Purpureocillium lilacinum</i>	0	98	57	OAQ83993
Transporter	1243	94260-98918	<i>Scedosporium apiospermum</i>	0	99	58	XP_016644513
Oxidoreductase	432	98965-101492	<i>Colletotrichum gloeosporioides</i>	1e-100	96	43	KXH54021
Glutamine synthase	722	102448-104841	<i>Colletotrichum salicis</i>	0	98	72	KXH63435

L-2) *Huntiaella moniliformis* multi-modular NRPS cluster Contig 10 (JMSH00000010)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4958	384688-400320	<i>Scedosporium apiospermum</i>	0	96	40	XP_016639834

L-ornithine N-5 monooxygenase	528	374979-376635	<i>Fusarium oxysporum</i>	0	99	54	PCD43854
Endothiapepsin	413	373044-374285	<i>Nectria ditissima</i>	1e-163	100	57	KPM38239
Hypothetical	152	369599-370160	<i>Scedosporium apiospermum</i>	1e-17	88	36	XP_016639846
Hypothetical	283	363872-364723	<i>Pseudogymnoascus</i> sp	4e-17	94	33	OBT55546
Mediator of RNA polymerase-II transcription subunit 7	256	362779-363604	<i>Nectria haematococca</i>	2e-82	95	52	XP_003044025
Membrane protein	1002	359094-362638	<i>Colletotrichum tofieldiae</i>	0	75	56	KZL73724
Hydrolase	250	357903-358753	<i>Fusarium avenaceum</i>	5e-98	100	55	KIL90716

M-1) *Huntia omanensis* monomodular NRPS cluster Contig 6521 (JSUI000006521)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	649	34581-36919	<i>Verticillium longisporum</i>	1e-62	67	39	CRK10802
NRPS	2081	37136-43437	<i>Colletotrichum gloeosporioides</i>	0	90	54	XP_007284335
CoA transferase	577	46865-48708	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	585	49586-51343	<i>Trichoderma quizhouense</i>	0	94	53	OPB43222
Siderophore biosynthesis	451	52183-53538	<i>Purpureocillium lilacinum</i>	0	99	62	OAQ83990
Oxidoreductase	498	53646-55494	<i>Colletotrichum simmondsii</i>	3e-84	97	41	KXH33196
ABC-multidrug transporter	1363	58885-63037	<i>Purpureocillium lilacinum</i>	0	98	57	OAQ83993
Transporter	1243	63443-68668	<i>Scedosporium apiospermum</i>	0	92	56	XP_016644513
Oxidoreductase	685	68715-71241	<i>Colletotrichum gloeosporioides</i>	1e-95	61	43	KXH54021
Glutamine synthase	722	72220-80817	<i>Colletotrichum salicis</i>	0	98	72	KXH63435

M-2) *Huntia omanensis* multi-modular NRPS cluster Contig 6485 (JSUI000006485)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4800	1-15106	<i>Pestalotiopsis fici</i>	0	98	39	XP_007837428
L-ornithine N-5 monooxygenase	568	23511-25392	<i>Fusarium oxysporum</i>	0	92	58	PCD43854
Endothiapepsin	413	26138-27379	<i>Nectria ditissima</i>	5e-165	100	57	KPM38239

Hypothetical	230	31312-32710	<i>Scedosporium apiospermum</i>	2e-16	83	32	XP_016639846
Hypothetical	172	38419-38937	<i>Pseudogymnoascus</i> sp	3e-07	98	40	OBT55546
Mediator of RNA polymerase-II transcription subunit 7	323	39947-41054	<i>Fusarium langsethiae</i>	1e-40	94	43	KPA42344
Membrane protein	1489	42379-47068	<i>Drechmeria coniospora</i>	0	66	57	KYK61075
Hydrolase	250	47570-48420	<i>Fusarium avenaceum</i>	5e-98	100	55	KIL90716

N-1) *Huntia savannae* monomodular NRPS cluster Contig 3 (LCZG0000003)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	649	34581-36919	<i>Verticillium longisporum</i>	1e-62	67	39	CRK10802
NRPS	2081	37136-43437	<i>Colletotrichum gloeosporioides</i>	0	90	54	XP_007284335
CoA transferase	577	46865-48708	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	585	49586-51343	<i>Trichoderma quizhouense</i>	0	94	53	OPB43222
Siderophore biosynthesis	451	52183-53538	<i>Purpureocillium lilacinum</i>	0	99	62	OAQ83990
Oxidoreductase	498	53646-55494	<i>Colletotrichum simmondsii</i>	3e-84	97	41	KXH33196
ABC-multidrug transporter	1363	58885-63037	<i>Purpureocillium lilacinum</i>	0	98	57	OAQ83993
Transporter	1243	63443-68668	<i>Scedosporium apiospermum</i>	0	92	56	XP_016644513
Oxidoreductase	685	68715-71241	<i>Colletotrichum gloeosporioides</i>	1e-95	61	43	KXH54021
Glutamine synthase	722	72220-80817	<i>Colletotrichum salicis</i>	0	98	72	KXH63435

N-2) *Huntia savannae* multi-modular NRPS cluster Contig 52 (LCZG0000052)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxamate type ferrichrome siderophore peptide synthase	4800	1-15106	<i>Pestalotiopsis fici</i>	0	98	39	XP_007837428
L-ornithine N-5 monooxygenase	568	23511-25392	<i>Fusarium oxysporum</i>	0	92	58	PCD43854
Endothiapepsin	413	26138-27379	<i>Nectria ditissima</i>	4e-135	100	57	KPM38239
Hypothetical	230	31312-32710	<i>Scedosporium apiospermum</i>	2e-117	83	32	XP_016639846
Hypothetical	172	38419-38937	<i>Pseudogymnoascus</i> sp	3e-16	98	40	OBT55546
Mediator of RNA	323	39947-41054	<i>Fusarium langsethiae</i>	1e-40	94	43	KPA42344

polymerase-II transcription subunit 7							
Membrane protein	1489	42379-47068	<i>Drechmeria coniospora</i>	0	66	57	KYK61075
Hydrolase	250	47570-48420	<i>Fusarium avenaceum</i>	5e-98	100	55	KIL90716

O-1) *Thielaviopsis musarum* monomodular NRPS cluster Contig 4 (LKBB00000004)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ras GTPase	208	140618-141708	<i>Grosmannia clavigera</i>	8e-147	100	97	XP_014176081
No similarity	1357	142931-147060	-	-	-	-	-
Hypothetical	378	147258-148473	<i>Beauveria bassiana</i>	3e-46	97	35	PMB66460
Hypothetical	367	149631-150925	<i>Trichoderma virens</i>	7e-58	99	40	XP_013952880
No similarity	448	158157-159503	-	-	-	-	-
NRPS	2073	160222-166562	<i>Colletotrichum gloeosporioides</i>	0	92	54	XP_007284335
CoA transferase	577	170543-172382	<i>Pochinia chlamydosporia</i>	0	98	76	XP_018147655
Siderophore transporter	616	172932-174833	<i>Trichoderma citrinoviride</i>	0	95	55	XP_024745106
Siderophore biosynthesis	451	175670-177084	<i>Stachybotrys chartarum</i>	0	96	67	KEY64463
Oxidoreductase	419	177211-178571	<i>Colletotrichum incanum</i>	3e-148	96	55	OHW97157
ABC-multidrug transporter	1352	180747-184872	<i>Scedosporium apiospermum</i>	0	98	58	XP_016644514
Transporter	839	186014-188661	<i>Colletotrichum tofieldiae</i>	0	100	74	KZL78304
Geranylgeranyl transferase	322	189812-190917	<i>Colletotrichum incanum</i>	3e-103	79	57	KZL75621

O-2) *Thielaviopsis musarum* multi-modular NRPS cluster Contig 131 (LKBB00000131)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4810	4928-14284	<i>Fusarium oxysporum</i>	0	99	39	EWZ42025
No similarity	103	14427-14781	-	-	-	-	-
No similarity	1604	14895-19992	-	-	-	-	-

L-ornithine N-5 monooxygenase	509	23912-25208	<i>Fusarium poae</i>	0	92	61	OBS21156
Endothiapepsin	419	25567-26826	<i>Nectria ditissima</i>	1e-178	99	61	KPM38239
Mediator of RNA polymerase-II transcription subunit 7	255	3119-31936	<i>Fusarium fujikuroi</i>	2e-82	97	54	SCO37772.
Hypothetical	337	32402-33415	<i>Colletotrichum nymphaeae</i>	4e-60	92	45	KXH63278

P-1) *Thielaviopsis punctulata* monomodular NRPS cluster Contig 782 (LAEV00000782)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ras GTPase	208	77436-78556	<i>Grosmannia clavigera</i>	8e-147	100	97	XP_014176081
No similarity	1342	72076-76315	-	-	-	-	-
Hypothetical	388	70614-71872	<i>Beauveria bassiana</i>	3e-46	97	35	PMB66460
Hypothetical	367	68126-69353	<i>Trichoderma virens</i>	6e-59	98	40	XP_013952880
No similarity	243	66653-67585	-	-	-	-	-
No similarity	612	59372-61333	-	-	-	-	-
NRPS	2066	52495-58885	<i>Colletotrichum gloeosporioides</i>	0	86	57	XP_007284335
CoA transferase	574	46729-48552	<i>Pochinia chlamydozporia</i>	0	98	76	XP_018147655
Siderophore transporter	558	44480-46156	<i>Trichoderma citrinoviride</i>	0	91	58	XP_024745106
Siderophore biosynthesis	451	42077-43486	<i>Purpureocillium lilacinum</i>	0	99	64	OAQ83990
Oxidoreductase	419	40667-41977	<i>Colletotrichum incanum</i>	1e-150	96	56	OHW97157
ABC-multidrug transporter	1374	34218-38342	<i>Scedosporium apiospermum</i>	0	96	58	XP_016644514
Transporter	1233	28225-33041	<i>Colletotrichum higginsianum</i>	0	67	73	XP_018152026

P-2) *Thielaviopsis punctulata* multi-modular NRPS cluster Contig 405 (LAEV00000405)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4697	44375-58733	<i>Scedosporium apiospermum</i>	0	99	41	XP_016639834

L-ornithine N-5 monooxygenase	516	38397-40068	<i>Fusarium avenaceum</i>	0	92	60	KIL93640
Endothiapepsin	418	36850-38106	<i>Nectria ditissima</i>	8e-175	99	60	KPM38239
Hypothetical	348	30987-32033	<i>Fusarium venenatum</i>	7e-54	99	43	CEI68809
F-box domain	339	29339-30675	<i>Ophiocordyceps unilateralis</i>				PFH60124

Q-1) *Endoconidiophora laricicola* monomodular NRPS cluster Contig 63 (LXGT0000063)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Transporter	843	55938-58665	<i>Colletotrichum incanum</i>	0	100	73	OHW98426
Leptomycin B resistance protein	1368	60436-64603	<i>Purpureocillium lilacinum</i>	0	97	58	OAQ83393
Oxoreductase	418	69286-70828	<i>Trichoderma gamsii</i>	1e-155	97	53	PNP37940
Siderophore biosynthesis protein	452	71094-72532	<i>Prechmeria coniospora</i>	0	99	63	KYK58456
Acyl-CoA synthetase	576	75486-77380	<i>Neonectria ditissima</i>	0	98	75	KPM45703
NRPS	2075	82078-88480	<i>Theilaviopsis punctulata</i>	0	100	76	KKA29546
Hypothetical	658	90388-92589	<i>Lomentospora prolificans</i>	2e-81	67	36	PKS12262
Hypothetical	364	102529-103761	<i>Trichoderma hazianum</i>	99	0	64	OAQ83990

Q-2) *Endoconidiophora laricicola* multi-modular NRPS cluster Contig 376 (LXGT00000376)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Glutathione transferase	232	664-1427	<i>Umbilicaria pustulata</i>	3e-26	86	37	SLM39268
Transposase	333	6275-7575	<i>Fusarium oxysporum</i>	7e-133	88	70	ENH66637
Hydroxymate type ferrichrome siderophore peptide synthase	4810	8168-22785	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834
L-ornithine N-5 monooxygenase	523	32170-33814	<i>Fusarium avenaceum</i>	0	91	59	KIL93640
Endothiapepsin	415	35185-36432	<i>Nectria ditissima</i>	0	100	62	KPM38239
Mediator of RNA polymerase-II	297	39445-40399	<i>Fusarium poae</i>	3e-77	83	51	OBS21164

transcription subunit 7							
Hypothetical	323	40811-41782	<i>Fusarium langsethiae</i>	9e-28	82	41	KPA42345

R-1) *Endoconidiophora polonica* monomodular NRPS cluster Contig 369 (LXKZ00000369)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Ras GTPase	229	65181-66538	<i>Grosmannia clavigera</i>	6e-141	100	89	XP_014176081
Hypothetical	357	54635-55845	<i>Stachybotrys chlorohalonata</i>	7e-56	92	41	KFA61745
Hypothetical	658	42479-45109	<i>Diaporthe ampelina</i>	8e-31	50	31	PKS12262
NRPS	2074	34176-40574	<i>Colletotrichum gloeosporioides</i>	0	86	56	XP_007284335
CoA transferase	584	27375-29267	<i>Neotectria ditissima</i>	0	98	74	KPM45703
Siderophore biosynthesis	452	23021-24452	<i>Purpureocillium lilacinum</i>	0	98	64	OAQ83990
Oxidoreductase	418	21209-22750	<i>Trichoderma gamsii</i>	5e-156	98	53	PNP37940
ABC-multidrug transporter	1353	12586-16753	<i>Purpureocillium lilacinum</i>	0	97	57	OAQ83993
Transporter	843	8222-10949	<i>Colletotrichum incanum</i>	0	100	74	OHW98426
PH domain	1498	3239-7791	<i>Colletotrichum chlorophyti</i>	0	96	48	KXH54021

R-2) *Endoconidiophora polonica* multi-modular NRPS cluster Contig 625 (LXKZ00000625)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hydroxymate type ferrichrome siderophore peptide synthase	4939	1-15495	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834
L-ornithine N-5 monooxygenase	520	28287-29935	<i>Fusarium longsethiae</i>	0	99	57	KPA42335
Endothiapepsin	420	30734-31996	<i>Nectria ditissima</i>	8e-161	99	57	KPM38239
Mediator of RNA polymerase-II transcription subunit 7	253	36085--36931	<i>Fusarium graminearum</i>	3e-89	96	56	XP_011323885
Hypothetical	360	37350-38432	<i>Fusarium langsethiae</i>	9e-28	82	41	KPA42345

S-1) <i>Davidsoniella virescens</i> monomodular NRPS cluster Contig 219 (LJZU000000219)							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NRPS	2058	6581-12991	<i>Thelaviopsis punctulata</i>	0	100	79	KKA29546
Acyl-CoA Synthetase	589	20537-22468	<i>Neonectria ditissima</i>	0	98	73	KPM45703
Siderophore biosynthetic protein	452	27550-28992	<i>Colletotrichium hymphaeae</i>	0	96	64	KXH42363
Oxidoreductase	427	29213-30785	<i>Nectria haematococca</i>	2e-151	96	56	XP_003048494
Leptomycin B resistance protein	1367	35507-39671	<i>Purpureocillium lilacinum</i>	0	98	58	OAQ83993
SPX domain	1030	40078-43976	<i>Colletotrichium gloesporioides</i>	0	85	73	ELA37746
PH domain	1497	44403-48952	<i>Colletotrichium chlorophyti</i>	0	96	47	OLN81630

S-2) <i>Davidsoniella virescens</i> multi-modular NRPS cluster Contig 225 (LJZU000000225)							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
F-box domain	194	68003-68824	<i>Colletotrichium graminicila</i>	2e-77	97	61	XP_008095400
Hypothetical	353	69398-70459	<i>Fusarium guenaceum</i>	2e-54	98	40	KIL93607
Transcription subunit 7	254	70871-71731	<i>Colletotrichum salicis</i>	2e-85	97	53	KXH53359
Peptidase A1	423	75705-76976	<i>Neonectria ditissima</i>	6e-160	100	57	KPM38239
L-ornithine N-5-monooxygenase	528	77871-79530	<i>Fusarium pseudograminearum</i>	0	94	58	XP_009260674
NRPS	4968	90563-105723	<i>Scedosporium apiospermum</i>	0	99	40	XP_016639834
HD Domain	251	106520-107548	<i>Colletotrichum chlorophyti</i>	5e-89	92	57	OLN87347
Hypothetical	143	109001-109486	<i>Scedosporum apiospermum</i>	3e-57	97	57	XP_016640357
Transcriptional adapter 2	538	111648-113348	<i>Colletotrichum sublineola</i>	0	100	74	KDN70890
Galactose-1-phosphate uridylyltransferase	386	114287-115699	<i>Lomentospora prolificans</i>	0	98	68	PKS07387

V-1) <i>Ambrosiella xylebori</i> multi modular NRPS Contig 4 (PCDO01000004)							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
HIR 1	232	27849-31063	<i>Trichoderma patareesei</i>	0	99	70	OTA00320
UDP-galactose transporter	333	33739-35426	<i>Pseudomassariella vexata</i>	0	95	61	ORY61530
Mannose-1-phosphate guanylyltransferase	523	35787-37176	<i>Fusarium avenaceum</i>	0	100	80	KIL93620

NRPS	4810	49879-64319	<i>Ceratocystis fimbriata</i>	0	99	39	PHH49945
L-ornithine 5-monooxygenase	415	73111-74807	<i>Fusarium oxysporum</i>	0	99	56	PCD43854
Peptidase A1	297	76066-77298	<i>Neonectria ditissima</i>	6e-178	99	61	KPM38239
Hypothetical	323	88612-91585	<i>Neonectria ditissima</i>	0	80	54	KPM43303

V-2) *Ambrosiella xylebori* mono modular NRPS Contig 1 (PCDO01000001)

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NRPS	2110	158842-165401	<i>Colletotrichum orbiculare</i>	0	86	55	ENH80243
CoA transferase	577	171906-173804	<i>Neonectria ditissima</i>	0	98	74	KPM45703
Siderophore transporter	560	175045-176727	<i>Trichoderma citrinoviride</i>	0	95	54	XP_024745106
Siderophore biosynthesis	452	182043-183401	<i>Purpureocillium lilacinum</i>	0	99	65	OAQ83990
Oxidoreductase	419	183672-185280	<i>Cordyceps militaris</i>	1e-146	96	55	XP_006671902
ABC-multidrug transporter	1371	189996-194333	<i>Metarhizium acridum</i>	0	98	57	XP_007808197
Transporter	845	195825-198390	<i>Colletotrichum incanum</i>	0	100	74	OHW98426

W-1-A) *Davidsoniella australis* mono modular NRPS contig 1

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Siderophore iron transporter	208	845-2545	<i>Chaetomium globosum</i>	0	97	54	XP_001227831
Acyl-CoA Synthetase	374	3702-5633	<i>Neonectria ditissima</i>	0	98	75	KPM45703
NRPS	799	13876-20305	<i>Thielaviopsis punctulata</i>	0	100	80	KKA29546
Hypothetical	562	38791-40007	<i>Trichoderma hazianum</i>	2e-57	97	41	PNP45214
RAS GTPase	2092	49485-50850	<i>Grosmannia clavigera</i>	1e-140	90	96	XP_014176081

W-1-B) *Davidsoniella australis* mono modular NRPS contig 393

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
ABC-multidrug transporter	1267	9102-11586	<i>Purpureocillium lilacinum</i>	0	97	57	OAQ83993
Transporter	848	13425-16894	<i>Purpureocillium lilacinum</i>	0	96	59	OAQ83993
Oxidoreductase	421	22105-23676	<i>Nectria haematococca</i>	2e-26	97	58	XP_003048494
Siderophore biosynthesis	455	23895-24712	<i>Colletotrichum hymphaeae</i>	0	97	66	KXH42363

W-2) *Davidsoniella australis* multi modular NRPS contig 143

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
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Nucleoporin	232	664-1427	<i>Colletotrichium simmondsii</i>	0	99	66	KXH44332
3-ketoacyl-CoA reductase	333	800-5192	<i>Colletotrichium higginsianum</i>	2e-171	97	70	XP_018151184
Ergosterol biosynthetic protein 28	4810	6309-7485	<i>Colletotrichum gloesporioides</i>	3e-69	97	72	EQB54482
Galactose-1-phosphate uridylyltransferase	523	7946-8525	<i>Lomentospora prolificans</i>	0	98	68	PKS07387
Transcriptional adapter 2	415	8616-10034	<i>Colletotrichum sublineola</i>	0	95	73	KDN70890
Hypothetical	297	10992-12653	<i>Scedosporium apiospermum</i>	5e-59	97	58	XP_016640357
HD Domain	323	14724-15219	<i>Hypoxylon</i> Spp	6e-99	95	64	OTB00397
NRPS	4750	18529-33759	<i>Scedosporium apiospermum</i>	0	100	39	XP_016639834

X-1) *Davidsoniella neocaledoniae* multi modular NRPS Contig 6

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
NRPS	208	10101-11196	<i>Ceratocystis fimbriata</i>	0	99	48	PHH49945
HD Domain	374	12451-13304	<i>Hypoxylon</i>	1e-98	85	64	OTB00397
Hypothetical	799	17267-18477	<i>Scedosporium apiospermum</i>	2e-58	97	58	XP_016640357
Transcriptional activator	562	19710-23430	<i>Colletotrichum sublineola</i>	0	100	74	KDN70890
Galactose-1-phosphate uridylyltransferase	2092	29439-31379	<i>Colletotrichum graminicola</i>	5e-123	96	64	XP_008100599
Ergosterol biosynthetic protein 28	577	32137-38636	<i>Escovopsis chlorophyte</i>	3e-70	88	63	OLN97423
3-ketoacyl-CoA Reductase	586	44922-46799	<i>Colletotrichum higginsianum</i>	3e-172	97	71	XP_018151184
Nucleoporin	452	48845-50814	<i>Colletotrichum simmondsii</i>	0	99	66	KXH44332
Sugar transporter STL1	421	52470-53828	<i>Verticillium dahliae</i>	0	76	71	PNH43205

X-2-A) *Davidsoniella neocaledoniae* Mono modular NRPS Contig 1989

Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Siderophore iron transporter	208	845-2545	<i>Chaetomium globosum</i>	0	97	54	XP_001227831
Acyl-CoA Synthetase	374	3702-5633	<i>Neonectria ditissima</i>	0	98	75	KPM45703
NRPS	799	13876-20305	<i>Thielaviopsis punctulata</i>	0	100	80	KKA29546

Hypothetical	562	38791-40007	<i>Trichoderma hazianum</i>	2e-57	97	41	PNP45214
RAS GTPase	2092	49485-50850	<i>Grosmannia clavigera</i>	1e-140	90	96	XP_014176081
X-2-B) <i>Davidsoniella neocaledoniae</i> Mono modular NRPS Contig 280							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
ABC-multidrug transporter	1264	3235-7431	<i>Purpureocillium lilacinum</i>	0	98	57	OAQ83993
Transporter	845	8475-11637	<i>Purpureocillium lilacinum</i>	0	96	59	OAQ83993
X-2-C) <i>Davidsoniella neocaledoniae</i> Mono modular NRPS Contig 3038							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Oxidoreductase	397	1-1112	<i>Nectria haematococca</i>	1e-154	98	59	XP_003048494
Siderophore biosynthesis	456	1135-2589	<i>Colletotrichium hymphaeae</i>	0	96	66	KXH42363

W-1) <i>Berkeleyomyces basicola</i> monomodular NRPS cluster Contig8							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
GTPase	575	1671203-1674202	<i>Grosmannia clavigera</i>	4e-139	35	97	XP_014176081
Hypothetical (PAPA)	319	1674702-1675822	<i>Metarhizium rileyi</i>	2e-60	98	45	OAA44328
Hypothetical	666	1680570-1682570	<i>Colletotrichium gloeosporioides</i>	2e-74	67	39	EQB54599
NRPS	2098	1683637-1675822	<i>Colletotrichium gloeosporioides</i>	0	86	54	EQB69356
Acyl-CoA Synthetase	579	1692143-1694003	<i>Trichoderma citrinoviridae</i>	0	97	76	XP_024745104
Siderophore iron transposase	570	1694626-1696507	<i>Thermothelomyces thermophile</i>	0	89	57	XP_003665004
Siderophore biosynthesis protein	448	1697003-1698433	<i>Metarhizium brunneum</i>	0	98	64	XP_014549676
ABC transporter	2302	1701212-1709524	<i>Pochonia chlamytoporia</i>	0	98	60	XP_018147652

W-2) <i>Berkeleyomyces basicola</i> multi-modular NRPS cluster Contig 12							
Gene name	Size (aa)	Location on the contig	Species	E value	% Coverage	% identity	Accession number of top blast hit
Hypothetical	371	1-1493	<i>Fusarium oxysporum</i>	0	100	69	EXL64588

NRPS	4885	6645-21513					
L-ornithine 5-monooxygenase	531	27720-29384	<i>Fusarium oxysporum</i>	0	99	56	PCD43854
RNA polymerase II subunit 7	259	31358-32199	<i>Colletotrichum simmondsii</i>	5e-87	97	53	KXH42963
Hypothetical	165	43568-44221	<i>Colletotrichum incanum</i>	4e-42	99	52	OHW92273
Membrane protein	1056	45197-48475	<i>Colletotrichum incanum</i>	0	82	57	KZL86520
Transcription factor	790	49391-51907	<i>Lomentospora prolificans</i>	0	99	47	PKS11306