

## SUPPLEMENTARY FILE S4.

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

The tables below show the putative Nonribosomal Peptide Synthetase (NRPS) gene clusters predicted by SMURF (Secondary Metabolite Unique Regions Finder) (Khaldi et al., 2010; Medema et al. 2011).

<i>Ceratocystis adiposa</i> multimodular NRPS cluster - Contig 175 (LXGU00000175)								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g26	g24	2	175	7	664-1427	1956	0	Glutathione transferase
g26	g23	3	175	6	6275-7575	293	0	Transposase
g26	g22	4	175	5	8168-22785	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
g26	g21	5	175	4	32170-33814	1442	1	L-ornithine N-5 monooxygenase
g26	g20	6	175	3	35185-36432	521	0	Endothiapepsin
g26	g25	10	175	8	39445-40399	196	0	Mediator of RNA polymerase-II transcription subunit 7
g26	g19	7	175	2	40811-41782	327		Hypothetical
g26	g20	8	175	1	664-1427	405		Glutathione transferase
g26	g18	9	175	9	6275-7575	1717		Transposase
<i>Ceratocystis albifundus</i> multimodular NRPS cluster - Contig1169 (JSSU000001169)								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g31	g33	-2	1169	7	470-3248	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
g31	g32	-1	1169	6	3503-4522	2611	1	L-ornithine N-5 monooxygenase
g31	g31	0	1169	5	5694-8351	3258	1	Mediator of RNA polymerase-II transcription subunit 7
g31	g27	6	1169	1	9455-13612	348	1	Hypothetical
<i>Ceratocystis eucalypticola</i> multimodular NRPS cluster - Contig 206 (LJOA00000206)								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g4	g11	-7	206	11	7544-8599	1446	1	Hypothetical
g4	g10	-6	206	10	9147-9974	1463	0	Mediator of RNA polymerase-II transcription subunit 7
g4	g9	-5	206	9	11685-12962	171	0	Aspergillopepsin

g4	g8	-4	206	8	14568-15786	610	0	L-ornithine N-5 monooxygenase
g4	g7	-3	206	7	21836-36887	607	0	Hydroxymate type ferrichrome siderophore peptide synthase
<b><i>Bretziella fagacearum</i> multimodular NRPS cluster - Contig 227 (MKGJ00000227)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
MJMS01000056_g6	MKGJ00000227_g9	-3	227	4	1-14960	0	0	Hydroxymate type ferrichrome siderophore peptide synthase
MJMS01000056_g6	MKGJ00000227_g8	-2	227	3	21912-23581	1834	0	L-ornithine N-5 monooxygenase
MJMS01000056_g6	MKGJ00000227_g7	-1	227	2	24912-26018	901	0	1,4 glucanase
MJMS01000056_g6	MKGJ00000227_g6	0	227	1	28750-31021	1757	0	Chitinase
MJMS01000056_g6	MKGJ00000227_g10 156	1	227	5	35659-37651	3335	1	Hypothetical
<b><i>Ceratocystis manginecans</i> multimodular NRPS cluster - Contig 189 (JJRZ000000189)</b>								
Gene positions	Chromosome-Contig	Gene_position	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
JMSH01000003_g25	JJRZ000000189_g31	-6	189	5	24617-39671	267	1	Hydroxymate type ferrichrome siderophore peptide synthase
JMSH01000003_g25	JJRZ000000189_g30	-5	189	4	46319-47994	1861	1	L-ornithine N-5 monooxygenase
JMSH01000003_g25	JJRZ000000189_g29	-4	189	3	48781-50058	274	0	Aspergillopepsin
JMSH01000003_g25	JJRZ000000189_g28	-3	189	2	51768-52595	1025	0	Mediator of RNA polymerase-II transcription subunit 7
JMSH01000003_g25	JJRZ000000189_g27	-2	189	1	53143-54198	285	0	Hypothetical
<b><i>Ceratocystis fimbriata</i> multimodular NRPS cluster - Contig 182 (APWK00000182)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
LXKZ01000105_g23	APWK00000182_g21	1	182	7	24617-39671	473	0	Hydroxymate type ferrichrome siderophore peptide synthase
LXKZ01000105_g23	APWK00000182_g20	2	182	6	46319-47994	699	1	L-ornithine N-5 monooxygenase
LXKZ01000105_g23	APWK00000182_g18	3	182	4	48781-50058	3613	0	Aspergillopepsin
LXKZ01000105_g23	APWK00000182_g17	4	182	3	51768-52595	130	1	Mediator of RNA polymerase-II transcription subunit 7
LXKZ01000105_g23	APWK00000182_g16	5	182	2	53143-54198	606	0	Hypothetical
<b><i>Ceratocystis harringtonii</i> multimodular NRPS cluster - Contig 378 (MKGM0000378)</b>								

Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
MKGM0000378_g24	MKGM0000378_g25	1	378	5	607-15650	0	0	Hydroxymate type ferrichrome siderophore peptide synthase
MKGM0000378_g24	MKGM0000378_g24	0	378	4	17900-21654	1541	1	L-ornithine N-5 monooxygenase
MKGM0000378_g24	MKGM0000378_g23	-1	378	3	24369-26700	1837	1	Aspergillopepsin
MKGM0000378_g24	MKGM0000378_g22	-2	378	2	27351-28215	18923	1	Mediator of RNA polymerase-II transcription subunit 7
MKGM0000378_g24	MKGM0000378_g21	-3	378	1	30100-31838	961	1	Hypothetical
<b><i>Ceratocystis platani</i> multimodular NRPS cluster - Contig 340 (LBBL00000340)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g17	g18	-1	340	7	21728-36752	131	1	Hydroxymate type ferrichrome siderophore peptide synthase
g17	g17	0	340	6	13709-15387	0	0	L-ornithine N-5 monooxygenase
g17	g14	3	340	3	11645-12922	3580	1	Aspergillopepsin
g17	g13	4	340	2	9105-9932	476	1	Mediator of RNA polymerase-II transcription subunit 7
g17	g16	8	340	5	7508-8557	2250	0	Hypothetical
<b><i>Ceratocystis smalleyi</i> multimodular NRPS cluster - Contig 288 (NETT01000228)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
NETT01000228_g19	NETT01000228_g20	-1	228	11	24617-39671	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
NETT01000228_g19	NETT01000228_g19	0	228	10	46319-47994	201	0	L-ornithine N-5 monooxygenase
NETT01000228_g19	NETT01000228_g17	2	228	8	48781-50058	429	0	Aspergillopepsin
NETT01000228_g19	NETT01000228_g16	3	228	7	51768-52595	303	0	Mediator of RNA polymerase-II transcription subunit 7
NETT01000228_g19	NETT01000228_g18	3	228	9	53143-54198	815	1	Hypothetical
<b><i>Huntia decipiens</i> multimodular NRPS cluster - Contig 307 (NETU00000307)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
NETU00000307_g13	NETU00000307_g13	0	307	5	52009-66674	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
NETU00000307_g13	NETU00000307_g11	2	307	3	42395-44050	2701	1	L-ornithine N-5 monooxygenase
NETU00000307_g13	NETU00000307_g10	3	307	2	40415-41656	914	1	Endothiaepsin

NETU00000307_g13	NETU00000307_g12	10	307	4	37016-37582	906	0	Hypothetical
NETU00000307_g13	NETU00000307_g10	5	307	1	31291-32148	1457	0	Hypothetical
NETU00000307_g13	NETU00000307_g12	7	307	8	30182-31007	1678	0	Mediator of RNA polymerase-II transcription subunit 7
NETU00000307_g13	NETU00000307_g12	6		7	26531-29451	1956	1	Membrane protein
<b>Huntiella bhutanensis multimodular NRPS cluster - Contig 83 (MJMS00000083)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g27	g24	3	83	1	111372-126028	24395	0	Hydroxymate type ferrichrome siderophore peptide synthase
g27	g25	2	83	2	101811-103465	17082	0	L-ornithine N-5 monooxygenase
g27	g26	1	83	3	99848-101089	5131	1	Endothiapepsin
g27	g27	0	83	4	96401-96964	0	0	Hypothetical
g27	g28	-1	83	5	90635-91486	13958	0	Hypothetical
g27	g29	-2	83	6	89531-90356	20223	0	Mediator of RNA polymerase-II transcription subunit 7
<b>Huntiella moniliformis multimodular NRPS cluster - Contig 10 (JMSH00000010)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
JMSH00000010_g19	JMSH00000010_g17	3	10	2	384688-400320	481	0	Hydroxymate type ferrichrome siderophore peptide synthase
JMSH00000010_g19	JMSH00000010_g16	2	10	1	374979-376635	1739	1	L-ornithine N-5 monooxygenase
JMSH00000010_g19	JMSH00000010_g20	1	10	5	373044-374285	133	0	Endothiapepsin
JMSH00000010_g19	JMSH00000010_g19	0	10	4	369599-370160	0	0	Hypothetical
JMSH00000010_g19	JMSH00000010_g18	-1	10	3	363872-364723	1373	0	Hypothetical
<b>Huntiella omanensis multimodular NRPS cluster - Contig 6485 (JSUI000006485)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
JSUI000006485_g5	JSUI000006485_g6	-1	6485	7	1-15106	131	1	Hydroxymate type ferrichrome siderophore peptide synthase
JSUI000006485_g5	JSUI000006485_g5	0	6485	6	23511-25392	0	0	L-ornithine N-5 monooxygenase
JSUI000006485_g5	JSUI000006485_g2	3	6485	3	26138-27379	3580	1	Endothiapepsin

JSUI000006485_g5	JSUI000006485_g1	4	6485	2	31312-32710	476	1	Hypothetical
JSUI000006485_g5	JSUI000006485_g4	8	6485	5	38419-38937	2250	0	Hypothetical
JSUI000006485_g5	JSUI000006485_g3	9	6485	4	39947-41054	785	0	Mediator of RNA polymerase-II transcription subunit 7
<b>Huntella savannae multimodular NRPS cluster - Contig 52 (LCZG00000052)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
LCZG00000052_g5	LCZG00000052_g11	-8	52	9	1-15106	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
LCZG00000052_g5	LCZG00000052_g10	-7	52	8	23511-25392	3089	1	L-ornithine N-5 monooxygenase
LCZG00000052_g5	LCZG00000052_g9	-6	52	7	26138-27379	265	0	Endothiapepsin
LCZG00000052_g5	LCZG00000052_g8	-5	52	6	31312-32710	27	0	Hypothetical
LCZG00000052_g5	LCZG00000052_g7	-4	52	5	38419-38937	52	1	Hypothetical
LCZG00000052_g5	LCZG00000052_g6	-3	52	4	39947-41054	421	0	Mediator of RNA polymerase-II transcription subunit 7
LCZG00000052_g5	LCZG00000052_g5	0	52	3	42379-47068	684	0	Membrane protein
<b>Thielaviopsis musarum multimodular NRPS cluster - Contig 131 (LKBB00000131)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
LKBB00000131_g44	LKBB00000131_g44	0	131	4	4928-14284	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
LKBB00000131_g44	LKBB00000131_g41	3	131	1	14427-14781	2611	1	No similarity
LKBB00000131_g44	LKBB00000131_g43	8	131	3	14895-19992	3258	1	No similarity
LKBB00000131_g44	LKBB00000131_g42	9	131	2	23912-25208	348	1	L-ornithine N-5 monooxygenase
LKBB00000131_g44	LKBB00000131_g4	5	131	5	25567-26826	1548	1	Endothiapepsin
<b>Thielaviopsis punctulata multimodular NRPS cluster - Contig 405 (LAEV00000405)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
LAEV00000405_g3	LAEV00000405_g5	-3	405	6	44375-58733	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
LAEV00000405_g3	LAEV00000405_g4	-2	405	5	38397-40068	4450	0	L-ornithine N-5 monooxygenase
LAEV00000405_g3	LAEV00000405_g3	-1	405	4	36850-38106	7008	0	Endothiapepsin

LAEV00000405_g3	LAEV00000405_g3	0	405	3	30987-32033	225	0	Hypothetical
LAEV00000405_g3	LAEV00000405_g1	1	405	2	29339-30675	24752	1	F-box domain
LAEV00000405_g3	LAEV00000405_g8	2	405	1	44375-58733	27509	0	Hydroxymate type ferrichrome siderophore peptide synthase
<b><i>Endoconidiophora laricicola</i> multimodular NRPS cluster - Contig 376 (LXGT00000376)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
LXGT00000376_g25	LXGT00000376_g25	0	376	4	664-1427	3258	1	Glutathione transferase
LXGT00000376_g25	LXGT00000376_g26	3	376	1	6275-7575	2611	1	Transposase
LXGT00000376_g25	LXGT00000376_g27	8	376	3	8168-22785	0	1	Hydroxymate type ferrichrome siderophore peptide synthase
LXGT00000376_g25	LXGT00000376_g28	9	376	2	32170-33814	348	1	L-ornithine N-5 monooxygenase
LXGT00000376_g25	LXGT00000376_g23	7	376	6	35185-36432	568	0	Endothiapepsin
LXGT00000376_g25	LXGT00000376_g24	6	376	7	39445-40399	456	0	Mediator of RNA polymerase-II transcription subunit 7
<b><i>Endoconidiophora polonica</i> multimodular NRPS cluster - Contig 625 (LXKZ00000625)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g19	g18	-1	625	7	1-15495	131	1	Hydroxymate type ferrichrome siderophore peptide synthase
g19	g17	0	625	6	28287-29935	0	0	L-ornithine N-5 monooxygenase
g19	g14	3	625	3	30734-31996	3580	1	Endothiapepsin
g19	g13	4	625	2	36085-36931	476	1	Mediator of RNA polymerase-II transcription subunit 7
g19	g16	8	625	5	37350-38432	2250	0	Hypothetical
<b><i>Davidsoniella virescens</i> multimodular NRPS cluster - Contig 225 (LJZU00000225)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g24	g24	3	225	1	68003-68824	24395	0	F-box domain
g24	g25	2	225	2	69398-70459	17082	0	Hypothetical
g24	g26	1	225	3	70871-71731	5131	1	Transcription subunit 7
g24	g27	0	225	4	75705-76976	0	0	Peptidase A1
g24	g28	-1	225	5	77871-79530	13958	0	L-ornithine N-5-monooxygenase

g24	g29	-2	225	6	90563-105723	20223	0	NRPS
<b>Ambrosiella xylebori multi modular NRPS Contig 4 (PCDO01000004)</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
PCDO01000004_g12	PCDO01000004_g13	0	4	5	27849-31063	0	1	HIR 1
PCDO01000004_g12	PCDO01000004_g11	2	4	3	33739-35426	2701	1	UDP-galactose transporter
PCDO01000004_g12	PCDO01000004_g10	3	4	2	35787-37176	914	1	Mannose-1-phosphate guanylyltransferase
PCDO01000004_g12	PCDO01000004_g12	10	4	4	49879-64319	906	0	NRPS
PCDO01000004_g12	PCDO01000004_g10	5	4	1	73111-74807	1457	0	L-ornithine 5-monooxygenase
<b>Davidsoniella australis multi modular NRPS contig 143</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g15	g21	1	143	6	6309-7485	473	0	Ergosterol biosynthetic protein 28
g15	g20	2	143	5	7946-8525	699	1	Galactose-1-phosphate uridylyltransferase
g15	g18	3	143	4	8616-10034	3613	0	Transcriptional adapter 2
g15	g17	4	143	3	10992-12653	130	1	Hypothetical
g15	g16	5	143	2	14724-15219	606	0	HD Domain
g15	g15	6	143	1	18529-33759	0	1	NRPS
<b>Berkeleyomyces basicola multimodular NRPS cluster - Contig 12</b>								
Backbone_gene_id	Gene_id	Gene positions	Contig	Gene order	5'-3' end	Gene distance	Domain score	Annotated gene function
g24	g25	1	12	5	1-1493	0	0	Hypothetical
g24	g24	0	12	4	6645-21513	1541	1	NRPS
g24	g23	-1	12	3	27720-29384	1837	1	L-ornithine 5-monooxygenase
g24	g22	-2	12	2	31358-32199	18923	1	RNA polymerase II subunit 7
g24	g21	-3	12	1	43568-44221	961	1	Hypothetical