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APPENDICES

APPENDIX A

REAGENTS PREPARATION

1) Luria-Bertani (LB) Medium

Bacto – tryptone	10	g
Bacto – Yeast extrct	5	g
NaCl	10	g
Adjust pH to 7.5 with 1M NaOH, add ddH_2O up to	1,000	ml

Shake until the solutes are dissolved. Sterilize by autoclaving for 20 min at 15 lbs on liquid cycle. To make an agar medium add 20 g of agar to the 1 L solution and sterile by autoclaving 121at °C at 15 lb/sq.in..min 15for

2) Sabouraud Dextrose Agar (SDA) pH 6.9

Dehydrated SDA agar (Difco)	65	g
Distilled water	1,000	ml

Mixed well thoroughly, and sterile by autoclaving.

3) Sabouraud Dextrose Broth (SDB) pH 6.9

Dehydrated SDB (Difco)	30	g
Distilled water	1,000	ml

Mixed well thoroughly, and sterile by autoclaving.

4) Zoospore induction medium

4.1) *Solution 1*

$K_2HPO_4.3H_2O$	11.4	g
KH_2PO_4	6.8	g
$NH_4H_2PO_4$	5.75	g
Distilled water up to	50	mL

4.2) *Solution 2*

$MgCl_2.6H_2O$	2.54	g
$CaCl_2.2H_2O$	1.84	g
Distilled water up to	25	mL

The medium is prepared by mixing 0.5 ml of solution 1 and 0.1 ml of solution 2. Adjust the volume of the medium to 1000 ml with distilled water.

5) Ampicillin (Amp 50)

Ampicillin	0.50	g
Sterile distilled water	10	mL

Mix by shaking until Ampicillin has dissolved. Filter and aliquot 1 mL. Store aliquots at -20°C.

6) X-gal

X-gal	0.2	g
DMF (DiMethyl Formamide)	10.0	mL
or 50% DMSO (DiMethyl-Sulfoxide)		

Mix by shaking until X-gal has dissolved. Aliquot 1.0 ml. Store aliquots at -20°C

7) Ethidium Bromide 5 mg/mL – in distilled water

8) 6X agarose-gel loading buffer

Bromophenol blue	0.025	g
Xylene cyanol FF	0.025	g
Glycerol	3.00	mL
Distilled water	6.95	mL

9) 10 X TBE buffer

Tris base	108	g.
Boric acid	55	g.
0.5 M EDTA (pH 8.0)	40	mL

add DW to final volume of 1 Liter.

10) 5.5 M Guanidinium thiocyanate

Guanidinium thiocyanate	65.0	g.
1M Sodium citrate,pH 7.0	2.5	mL
Sodium lauryl sarcosine	0.5	g.

add DW to final volume of 100 ml.

11) 1M MOPS (3-(N-morpholino)propan sulfonic acid)

MOPS	104.7	g.
DEPC H_2O	400	mL

Adjust pH to 7 with NaOH fill up to 500 ml with DEPC H_2O

12) 5X gel running buffer

1 M MOPS	25.0	mL
3 M NaAc	3.33	mL
0.35M EDTA, pH 8.0	2.5	mL

Adjust to 250 mL with DEPC H_2O. Filter-sterilize through a 0,2 µm. Store at 4°C, protect from light.

13) 1.5% Agarose gel

Agarose	1.5	g
1x TBE	35	mL

Dissolve by heating in microwave oven and occasional mix unit no granules of garose are visible.

14) 10X MOPS buffer

MOPS	83.6	g
NaOAC	8.2	g
Add DEPC – treated DW	800	mL
adjust pH to 7.0 with NaOH		
DEPC – treated 0.5 M EDTA (pH 8.0)	10	mL

Adjust the volume to 1 L with DEPC treat DW. Sterilize by filtration, store at RT, wrapped in foil to protect from light.

15) 0.5 M EDTA (pH 8.0)

$Na_2EDTA - 2H_20$	37.22	g
DW	160	mL
adjust pH to 8.0 with NaOH		
DEPC	0.2	mL

Stir overnight, and sterilize by autoclaving.

16) Loading buffer

Formamide	420	µL
10 x MOPS	100	µL
37 % Formaldehyde	135	µL
88% glycerol	50	µL
Bromphenol blue	1	µg

APPENDIX B

List of up-regulated transcripts in temperature response (27°C) in *P.insidiosum* strain PC7.

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C1-17/4	245	mitochondrion (*Phy. infestans*)	U17009	1.00E-66	88%	ND	-	-	-
C2-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C3-17/4	323	NM	-	-	-	protein enhancer of rudimentary [*Phy. infestans* T30-4]	EEY55861	2.00E-16	97%
C4-17/4	246	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-57	85%	cytochrome c oxidase subunit 3 [*Phy. ramorum*]	YP001165347	4.00E-22	66%
C5-17/4	537	mitochondrion (*Phy. infestans*)	AY898627	0	94%	ND	-	-	-
C6-17/4	749	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	5.00E-55	71%
C7-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	91%	ND	-	-	-
C8-17/4	419	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-135	90%	NADH dehydrogenase subunit 5 [*Phy. sojae*].	YP001165399	2.00E-66	96%
C9-17/4	286	Mitochondrion (*Phy. sojae*)	DQ832717	2.00E-60	84%	NADH dehydrogenase subunit 2 [*Phy. ramorum*]	YP001165351	3.00E-18	68%
C10-17/4	391	NM	-	-	-	ribosomal protein L2 [*Phy. sojae*]	YP001165413	4.00E-16	45%
C11-17/4	637	mitochondrion (*Phy. ramorum*)	EU427470	0	95%	conserved hypothetical protein [Onion yellows phytoplasma OY-M]	BAD04335	9.00E-26	78%
C12-17/4	611	mitochondrion (*Phy. ramorum*)	EU427470	0	96%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C13-17/4	306	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-104	91%	ND	-	-	-
C14-17/4	490	Uncultured bacterium partial 16S ribosomal RNA	FM956611	0	95%	predicted protein [*Populus trichocarpa*]	XP002337573	8.00E-05	60%
C15-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C16-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C17-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C18-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C19-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C20-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C21-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C22-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C23-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C24-17/4	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C25-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C26-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C27-17/4	561	Mitochondrion (*Phy. sojae*)	DQ832717	0	94%	ND	-	-	-
C28-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C29-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C30-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C31-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C32-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C33-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C34-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C35-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C37-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C40-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C41-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C44-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C67-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C68-17/4	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C70-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C72-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C77-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C78-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C79-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C80-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C81-17/4	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C82-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C83-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C87-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C88-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C89-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C90-17/4	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C92-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C93-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C97-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C98-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C99-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C100-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C101-17/4	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C102-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C105-17/4	245	mitochondrion (*Phy. infestans*)	U17009	1.00E-66	88%	ND	-	-	-
C107-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C108-17/4	245	mitochondrion (*Phy. infestans*)	U17009	1.00E-66	88%	ND	-	-	-
C109-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C1-3/6	427	Uncultured bacterium partial 16S ribosomal RNA	FM956611	5.00E-177	95%	ND	-	-	-

Clone	**Size (bp.)**	**Search result by BLASTN Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**	**Search result by BLASTx Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**
C2-3/6	519	28S ribosomal RNA (*P.megasperma*)	X75631	0	98%	similar to predicted protein, partial [*Hydra magnipapillata*]	XP002168570	9.00E-33	78%
C3-3/6	245	mitochondrion (*Phy. infestans*)	U17009	3.00E-63	87%	ND	-	-	-
C4-3/6	366	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	100%	ND	-	-	-
C5-3/6	270	Uncultured bacterium clone GASP-MA1W3_F02 16S ribosomal RNA gene	EF662800	8.00E-114	99%	ND	-	-	-
C6-3/6	699	NM	-	-	-	NM	-	-	-
C7-3/6	763	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	unknown [*Medicago truncatula*]	ACJ85262	93-38	72%
C8-3/6	712	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	hypothetical protein [*Arabidopsis thaliana*]	BAF01964	1.00E-55	77%
C9-3/6	245	mitochondrion (*Phy. infestans*)	U17009	1.00E-66	88%	ND	-	-	-
C10-3/6	419	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-134	89%	NADH dehydrogenase subunit 5 [*Phy. sojae*].	YP001165399	3.00E-22	51%
C11-3/6	322	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C12-3/6	417	ND	-	-	-	ribosomal protein L2 [*Phy. sojae*]	YP001165413	2.00E-49	92%
C13-3/6	324	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	91%	ND	-	-	-
C14-3/6	389	Uncultured bacterium partial 16S ribosomal RNA	EF663023	5.00E-167	97%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C15-3/6	330	28S ribosomal RNA (*P.megasperma*)	X75631	8.00E-100	90%	ND	-	-	-
C16-3/6	324	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C17-3/6	269	mitochondrion (*Phy. ramorum*)	EU427470	6.00E-60	85%	cytochrome c oxidase subunit 3 [*Phy. ramorum*]	YP001165347	4.00E-23	67%
C18-3/6	257	NM	-	-	-	NM	-	-	-
C20-3/6	366	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	100%	ND	-	-	-
C21-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-142	95%	ND	-	-	-
C22-3/6	527	*Phy. infestans* isolate 16/99 tRNA-Pro (trnP(ugg)) and tRNA-Met (trnM(cau)) genes	EF366732	2.00E-87	86%	ribosomal protein L14 [*Phy. ramorum*]	YP001165335	5.00E-21	71%
C23-3/6	427	Uncultured bacterium partial 16S ribosomal RNA	FM956511	3.00E-175	95%	ND	-	-	-
C24-3/6	436	Uncultured bacterium partial 16S ribosomal RNA	FM956511	2.00E-177	95%	ND	-	-	-
C26-3/6	358	mitochondrion (*Phy. infestans*)	U17009	1.00E-147	96%	ND	-	-	-
C27-3/6	595	*P. insidiosum* 18S ribosomal RNA gene	AF442497	0	99%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C28-3/6	442	Uncultured bacterium partial 16S ribosomal RNA	FM956511	0	96%	ND	-	-	-
C29-3/6	196	NM	-	-	-	NM	-	-	-
C30-3/6	367	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-142	95%	ND	-	-	-
C31-3/6	255	NM	-	-	-	NM	-	-	-
C32-3/6	192	NM	-	-	-	ND	-	-	-
C33-3/6	364	NM	-	-	-	ND	-	-	-
C34-3/6	324	NM	-	-	-	ND	-	-	-
C35-3/6	367	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	100%	ND	-	-	-
C36-3/6	428	*Phy. lateralis* strain PL33 NADH dehydrogenase subunit 5	AY423337	1.00E-74	88%	NADH dehydrogenase subunit 5 [*Phy. sojae*].	YP001165399	8.00E-56	86%
C37-3/6	335	Uncultured bacterium gene for 16S rRNA	AB075125	1.00E-128	95%	ND	-	-	-
C38-3/6	332	Uncultured bacterium gene for 16S rRNA	AB075125	9.00E-129	95%	ND	-	-	-
C39-3/6	326	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C40-3/6	326	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C41-3/6	256	NM	-	-	-	ND	-	-	-
C43-3/6	520	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	similar to predicted protein, partial [*Hydra magnipapillata*]	XP002168570	6.00E-34	78%

Clone	**Size (bp.)**	**Search result by BLASTN Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**	**Search result by BLASTx Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**
C44-3/6	405	Uncultured bacterium clone GASP-MA1W3_F02 16S ribosomal RNA gene	EF662800	9.00E-120	100%	ND	-	-	-
C46-3/6	255	NM	-	-	-	NM	-	-	-
C47-3/6	367	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	100%	ND	-	-	-
C48-3/6	595	*P. insidiosum* 18S ribosomal RNA gene	AF442497	0	99%	ND	-	-	-
C50-3/6	366	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	100%	ND	-	-	-
C52-3/6	321	NM	-	-	-	protein enhancer of rudimentary [*Phy. infestans* T30-4]	EEY55861	2.00E-16	97%
C53-3/6	335	Uncultured bacterium gene for 16S rRNA	AB075125	1.00E-128	95%	ND	-	-	-
C55-3/6	332	Uncultured bacterium gene for 16S rRNA	AB075125	9.00E-129	95%	ND	-	-	-
C61-3/6	326	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C62-3/6	326	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C63-3/6	389	Uncultured proteobacterium clone GASP-MA2S3_B04 16S ribosomal RNA	EF663023	5.00E-167	97%	ND	-	-	-
C66-3/6	330	28S ribosomal RNA (*P.megasperma*)	X75631	8.00E-100	90%	ND	-	-	-
C67-3/6	324	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C68-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTN Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C70-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C71-3/6	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C72-3/6	427	Uncultured proteobacterium clone GASP-MA2S3_B04 16S ribosomal RNA	EF663023	3.00E-175	95%	ND	-	-	-
C76-3/6	324	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-104	91%	ND	-	-	-
C77-3/6	389	Uncultured proteobacterium clone GASP-MA2S3_B04 16S ribosomal RNA	EF663023	5.00E-167	97%	ND	-	-	-
C78-3/6	330	28S ribosomal RNA (*P.megasperma*)	X75631	8.00E-100	90%	ND	-	-	-
C79-3/6	324	28S ribosomal RNA (*P.megasperma*)	X75631	6.00E-101	90%	ND	-	-	-
C80-3/6	330	28S ribosomal RNA (*P.megasperma*)	X75631	8.00E-100	90%	ND	-	-	-
C81-3/6	367	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-72	84%	ND	-	-	-
C83-3/6	130	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-37	98%	ND	-	-	-
C84-3/6	742	NM	-	-	-	ND	-	-	-
C85-3/6	130	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-37	98%	ND	-	-	-
C86-3/6	527	mitochondrion (*Phy. ramorum*)	EU427470	0	96%	ND	-	-	-
C87-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C88-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C89-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C90-3/6	130	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-37	98%	ND	-	-	-

Clone	**Size (bp.)**	**Search result by BLASTN Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**	**Search result by BLASTx Annotation (species)**	**GeneBank Accession**	**E - value**	**Identity**
C91-3/6	428	Uncultured bacterium partial 16S ribosomal RNA	FM956511	2.00E-167	94%	ND	-	-	-
C92-3/6	361	28S ribosomal RNA (*P.megasperma*)	X75631	5.00E-122	91%	ND	-	-	-
C93-3/6	337	mitochondrion (*Phy. infestans*)	U17009	2.10E-134	96%	ND	-	-	-
C94-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	3.00E-139	94%	ND	-	-	-
C95-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C97-3/6	559	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C98-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C99-3/6	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C101-3/6	130	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-37	98%	ND	-	-	-
C102-3/6	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-140	95%	ND	-	-	-
C103-3/6	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	ND	-	-	-
C104-3/6	130	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-37	98%	ND	-	-	-
C105-3/6	527	mitochondrion (*Phy. ramorum*)	EU427470	0	96%	ND	-	-	-

APPENDIX C

List of up-regulated transcripts in temperature response (37°C) in *P.insidiosum* strain PC7.

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C2-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C3-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C4-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C6-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C8-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C12-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C13-6/1	456	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C14-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C17-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C20-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C21-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C22-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C25-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C26-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C30-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C31-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C32-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C33-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C35-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C35-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C38-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C39-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C45-6/1	457	Mitochondrion (*Phy. sojae*)	DQ832717	3.00E-179	95%	ND	-	-	-
C2-14/2	464	Mitochondrion (*Phy. sojae*)	DQ832717	4.00E-133	89%	ND	-	-	-
C40-14/2	471	Mitochondrion (*Phy. sojae*)	DQ832717	6.00E-171	95%	ND	-	-	-
C40-14/2	471	Mitochondrion (*Phy. sojae*)	DQ832717	6.00E-171	95%	ND	-	-	-
C20-17/4	589	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C31-17/4	590	Mitochondrion (*Phy. sojae*)	DQ832717	0	96%	ND	-	-	-
C33-17/4	591	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C34-17/4	586	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C215-17/4	520	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C250-17/4	750	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C253-17/4	590	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C260-17/4	387	Mitochondrion (*Phy. sojae*)	DQ832717	0	86%	ND	-	-	-
C267-17/4	767	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C268-17/4	588	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C270-17/4	590	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C281-17/4	590	Mitochondrion (*Phy. sojae*)	DQ832717	0	96%	ND	-	-	-
C285-17/4	589	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C311-17/4	590	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C318-17/4	537	Mitochondrion (*Phy. sojae*)	DQ832717	0	95%	ND	-	-	-
C320-17/4	580	Mitochondrion (*Phy. sojae*)	DQ832717	0	96%	ND	-	-	-
C6-14/2	369	mRNA (*Phy. caposi*)	BT032625	1.00E-92	86%	phosphate carrier protein (*Phy.infestan*)	EEY66591	6.00E-46	80%
C52-14/2	556	myo-inositol-phosphate synthase (*Anopheles gambiae*)	XM320685	6.00E-88	81%	inositol-3-phosphate synthase (*Phy.infestan*)	EEY61403	7.00E-55	94%
C1-17/4	159	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C10-17/4	296	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C12-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C13-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C18-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C19-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C21-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C22-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C25-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C27-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C28-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C29-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C30-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C35-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C67-17/4	239	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	2.00E-98	82%	ND	-	-	-
C240-17/4	270	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	6.00E-104	98%	ND	-	-	-
C249-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C255-17/4	288	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C258-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C261-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C262-17/4	264	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	3.00E-109	99%	ND	-	-	-
C263-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P. insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C264-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C265-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C269-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C271-17/4	296	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C273-17/4	296	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C275-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C282-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C290-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C298-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C299-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C300-17/4	296	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C301-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C302-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C303-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C304-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C305-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C314-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C315-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C317-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C321-17/4	297	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C322-17/4	296	internal transcribed spacer 1, 5.8S ribosomal RNA (*P.insidiosum*)	AY598637	8.00E-56	100%	ND	-	-	-
C2-17/4	488	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	ND	-	-	-
C5-17/3	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C16-17/3	383	28S ribosomal RNA (*P.megasperma*)	X75631	4.00E-132	91%	ND	-	-	-
C23-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C37-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C38-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C39-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C40-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C42-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C43-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C44-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C45-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C46-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C47-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C48-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C49-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C50-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C51-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C52-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C53-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C54-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C55-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C56-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C57-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C58-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C59-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C60-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C61-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C62-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C63-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C64-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C66-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C68-17/4	379	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-131	99%	ND	-	-	-
C69-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C70-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C71-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C72-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C74-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C75-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C77-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C79-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C81-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C83-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C84-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C85-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C86-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C87-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C88-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C89-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C90-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C91-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C92-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C95-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C96-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C97-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C98-17/4	379	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-131	92%	ND	-	-	-
C100-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C102-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C103-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C104-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C107-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C110-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C111-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C114-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C115-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C116-17/4	313	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C117-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C119-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C120-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C121-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C123-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C125-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C126-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C127-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C129-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C130-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C132-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C134-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C136-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C137-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C138-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C139-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C140-17/4	328	28S ribosomal RNA (*P.megasperma*)	X75631	5.00E-101	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C141-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C142-17/4	328	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-97	89%	ND	-	-	-
C143-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C144-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C145-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C146-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C147-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C148-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C149-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C150-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C151-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C152-17/4	305	28S ribosomal RNA (*P.megasperma*)	X75631	3.00E-87	87%	ND	-	-	-
C153-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C155-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C156-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C157-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C159-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C160-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C161-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C162-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C163-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C164-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C165-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C166-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C167-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C168-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C169-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C170-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C171-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C172-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C173-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C174-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C175-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C177-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C178-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C179-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C180-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C181-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C182-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C183-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C184-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C186-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C187-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C188-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C190-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C191-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C192-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C195-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C196-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C198-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C200-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C201-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C202-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C203-17/4	270	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-64	89%	ND	-	-	-
C204-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C205-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C206-17/4	270	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-64	89%	ND	-	-	-
C207-17/4	270	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-64	89%	ND	-	-	-
C208-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C209-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C210-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C211-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C213-17/4	270	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-64	89%	ND	-	-	-
C219-17/4	240	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-64	89%	ND	-	-	-
C220-17/4	270	28S ribosomal RNA (*P.megasperma*)	X75631	2.00E-64	89%	ND	-	-	-
C221-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C222-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C224-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C226-17/4	324	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C227-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C228-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C229-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C230-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C231-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C232-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C233-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C235-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C237-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C238-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C241-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C242-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C243-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C244-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C245-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C246-17/4	325	28S ribosomal RNA (*P.megasperma*)	X75631	1.00E-102	90%	ND	-	-	-
C251-17/4	437	28S ribosomal RNA (*P.megasperma*)	X75631	4.00E-123	87%	ND	-	-	-
C36-17/4	461	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	2.00E-26	80%
C78-17/4	485	28S ribosomal RNA (*P.megasperma*)	X75631	0	98%	predicted protein (*Hydra magnipapillata*)	XP002168570	3.00E-34	78%
C94-17/4	485	28S ribosomal RNA (*P.megasperma*)	X75631	0	98%	predicted protein (*Hydra magnipapillata*)	XP002168570	3.00E-34	78%
C128-17/4	485	28S ribosomal RNA (*P.megasperma*)	X75631	0	98%	predicted protein (*Hydra magnipapillata*)	XP002168570	3.00E-34	78%
C252-17/4	461	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	2.00E-26	80%
C266-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	5.00E-31	82%
C276-17/4	461	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	2.00E-26	80%
C277-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	5.00E-31	82%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C280-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	5.00E-31	82%
C291-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	5.00E-31	82%
C312-17/4	461	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	2.00E-26	80%
C316-17/4	463	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	predicted protein (*Hydra magnipapillata*)	XP002168570	5.00E-31	82%
C323-17/4	461	28S ribosomal RNA (*P.megasperma*)	X75631	0	98%	predicted protein (*Hydra magnipapillata*)	XP002168570	2.00E-26	80%
C41-17/4	597	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	1.00E-52	70%
C65-17/4	593	28S ribosomal RNA (*P.megasperma*)	X75631	0	99%	senescence-associated protein (*Picea abies*)	ACA04850	1.00E-52	70%
C76-17/4	597	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	1.00E-52	70%
C80-17/4	592	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	7.00E-52	70%
C93-17/4	596	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	1.00E-52	70%
C109-17/4	593	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	1.00E-52	70%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C124-17/4	594	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	7.00E-52	70%
C135-17/4	568	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	2.00E-48	69%
C158-17/4	601	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	3.00E-54	71%
C176-17/4	513	28S ribosomal RNA (*P.megasperma*)	X75631	0	95%	senescence-associated protein (*Picea abies*)	ACA04850	2.00E-36	66%
C236-17/4	576	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	5.00E-50	70%
C234-17/4	587	28S ribosomal RNA (*P.megasperma*)	X75631	0	96%	senescence-associated protein (*Picea abies*)	ACA04850	2.00E-51	70%
C3-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C17-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C223-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C232-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C272-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C278-17/4	436	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C279-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C284-17/4	436	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C287-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C292-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C292-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C295-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C296-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C307-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C310-17/4	436	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C354-17/4	437	mitochondrion (*Phy. ramorum*)	EU427470	5.00E-123	87%	NADH dehydrogenase subunit 7 [*Heterosigma akashiwo*]	BAI70606	7.00E-07	89%
C14-17/4	416	mitochondrion (*Phy. ramorum*)	EU427470	9.00E-165	95%	hypothetical protein (*Providencia stuartii*)	ZP02997467	9.00E-18	61%
C297-17/4	418	mitochondrion (*Phy. ramorum*)	EU427470	4.00E-123	93%	NM	-	-	-
C26-17/4	365	mitochondrion (*Phy. ramorum*)	EU427470	2.00E-104	95%	ND	-	-	-
C194-17/4	328	28S rRNA (*Pythium* sp.)	AB254193	8.00E-74	93%	ND	-	-	-
C9-6/1	650	NM	-	-	-	serine carboxypeptidase (*Phy. infestan*)	EEY53505	1.00E-21	40%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C15-6/1	650	NM	-	-	-	serine carboxypeptidase (*Phy.infestan*)	EEY53505	1.00E-21	40%
C16-6/1	650	NM	-	-	-	serine carboxypeptidase (*Phy.infestan*)	EEY53505	1.00E-21	40%
C18-6/1	329	NM	-	-	-	60S ribosomal protein L6 (*Phy.infestan*)	EEY65770	2.00E-19	86%
C43-14/2	358	NM	-	-	-	60S ribosomal protein L6 (*Phy.infestan*)	EEY65770	4.00E-20	81%
C47-14/2	411	NM	-	-	-	60S ribosomal protein L6 (*Phy.infestan*)	EEY65770	2.00E-23	65%
C52-6/1	645	NM	-	-	-	hypothetical protein (*Ajellomyces capsulatus NAm1*)	XP001536497	1.00E-15	34%
C29-14/2	718	NM	-	-	-	hypothetical protein (*Ajellomyces capsulatus NAm1*)	XP001535830	9.00E-40	38%
C4-14/2	590	NM	-	-	-	hypothetical protein (*Dunaliella viridis*)	ABG38270	5.00E-18	34%
C8-14/2	589	NM	-	-	-	hypothetical protein (*Dunaliella viridis*)	ABG38270	5.00E-18	34%
C57-14/2	816	NM	-	-	-	hypothetical protein (*Dunaliella viridis*)	ABG38270	3.00E-18	34%
C66-14/2	692	NM	-	-	-	reverse transcriptase (*Phy.ramorum*)	ABG66535	2.00E-32	38%
C24-14/2	411	NM	-	-	-	retrotransposon nucleocapsid protein (*C.neoformans*)	XP571377	3.00E-11	36%
C6-17/4	587	NM	-	-	-	pol protein (*Phy.infestan*)	EU427470	3.00E-15	42%

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C8-17/4	650	NM	-	-	-	pol protein (*Phy.infestan*)	AAV92918	1.00E-27	56%
C225-17/4	360	NM	-	-	-	reverse transcriptase (*Phy.ramorum*)	ABG66535	1.00E-09	35%
C248-17/4	475	NM	-	-	-	reverse transcriptase (*Phy.ramorum*)	ABG66535	7.00E-07	29%
C1-6/1	600	NM	-	-	-	NM	-	-	-
C5-6/1	712	NM	-	-	-	NM	-	-	-
C7-6/1	629	NM	-	-	-	NM	-	-	-
C10-6/1	711	NM	-	-	-	NM	-	-	-
C11-6/1	629	NM	-	-	-	NM	-	-	-
C23-6/1	711	NM	-	-	-	NM	-	-	-
C24-6/1	251	NM	-	-	-	NM	-	-	-
C28-6/1	250	NM	-	-	-	NM	-	-	-
C29-6/1	629	NM	-	-	-	NM	-	-	-
C34-6/1	629	NM	-	-	-	NM	-	-	-
C36-6/1	251	NM	-	-	-	NM	-	-	-
C37-6/1	629	NM	-	-	-	NM	-	-	-
C40-6/1	628	NM	-	-	-	NM	-	-	-
C41-6/1	251	NM	-	-	-	NM	-	-	-
C42-6/1	251	NM	-	-	-	NM	-	-	-
C43-6/1	628	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C47-6/1	450	NM	-	-	-	NM	-	-	-
C49-6/1	659	NM	-	-	-	NM	-	-	-
C50-6/1	609	NM	-	-	-	NM	-	-	-
C51-6/1	358	NM	-	-	-	NM	-	-	-
C53-6/1	548	NM	-	-	-	NM	-	-	-
C55-6/1	230	NM	-	-	-	NM	-	-	-
C57-6/1	711	NM	-	-	-	NM	-	-	-
C58-6/1	629	NM	-	-	-	NM	-	-	-
C60-6/1	711	NM	-	-	-	NM	-	-	-
C64-6/1	251	NM	-	-	-	NM	-	-	-
C72-6/1	251	NM	-	-	-	NM	-	-	-
C73-6/1	628	NM	-	-	-	NM	-	-	-
C74-6/1	450	NM	-	-	-	NM	-	-	-
C79-6/1	659	NM	-	-	-	NM	-	-	-
C80-6/1	609	NM	-	-	-	NM	-	-	-
C81-6/1	358	NM	-	-	-	NM	-	-	-
C82-6/1	600	NM	-	-	-	NM	-	-	-
C85-6/1	712	NM	-	-	-	NM	-	-	-
C87-6/1	629	NM	-	-	-	NM	-	-	-
C88-6/1	250	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C90-6/1	711	NM	-	-	-	NM	-	-	-
C91-6/1	629	NM	-	-	-	NM	-	-	-
C93-6/1	711	NM	-	-	-	NM	-	-	-
C94-6/1	251	NM	-	-	-	NM	-	-	-
C95-6/1	251	NM	-	-	-	NM	-	-	-
C99-6/1	629	NM	-	-	-	NM	-	-	-
C100-6/1	711	NM	-	-	-	NM	-	-	-
C103-6/1	628	NM	-	-	-	NM	-	-	-
C104-6/1	629	NM	-	-	-	NM	-	-	-
C106-6/1	251	NM	-	-	-	NM	-	-	-
C107-6/1	251	NM	-	-	-	NM	-	-	-
C109-6/1	659	NM	-	-	-	NM	-	-	-
C110-6/1	712	NM	-	-	-	NM	-	-	-
C1-14/2	426	NM	-	-	-	NM	-	-	-
C3-14/2	113	NM	-	-	-	NM	-	-	-
C5-14/2	400	NM	-	-	-	NM	-	-	-
C7-14/2	588	NM	-	-	-	NM	-	-	-
C9-14/2	659	NM	-	-	-	NM	-	-	-
C10-14/2	547	NM	-	-	-	NM	-	-	-
C11-14/2	550	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C12-14/2	545	NM	-	-	-	NM	-	-	-
C14-14/2	573	NM	-	-	-	NM	-	-	-
C15-14/2	687	NM	-	-	-	NM	-	-	-
C16-14/2	619	NM	-	-	-	NM	-	-	-
C17-14/2	670	NM	-	-	-	NM	-	-	-
C18-14/2	683	NM	-	-	-	NM	-	-	-
C19-14/2	710	NM	-	-	-	NM	-	-	-
C20-14/2	692	NM	-	-	-	NM	-	-	-
C21-14/2	409	NM	-	-	-	NM	-	-	-
C23-14/2	476	NM	-	-	-	NM	-	-	-
C25-14/2	492	NM	-	-	-	NM	-	-	-
C26-14/2	451	NM	-	-	-	NM	-	-	-
C30-14/2	593	NM	-	-	-	NM	-	-	-
C32-14/2	591	NM	-	-	-	NM	-	-	-
C33-14/2	626	NM	-	-	-	NM	-	-	-
C34-14/2	113	NM	-	-	-	NM	-	-	-
C35-14/2	683	NM	-	-	-	NM	-	-	-
C36-14/2	426	NM	-	-	-	NM	-	-	-
C37-14/2	537	NM	-	-	-	NM	-	-	-
C38-14/2	261	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C39-14/2	543	NM	-	-	-	NM	-	-	-
C41-14/2	411	NM	-	-	-	NM	-	-	-
C42-14/2	661	NM	-	-	-	NM	-	-	-
C44-14/2	635	NM	-	-	-	NM	-	-	-
C45-14/2	236	NM	-	-	-	NM	-	-	-
C48-14/2	676	NM	-	-	-	NM	-	-	-
C50-14/2	695	NM	-	-	-	NM	-	-	-
C51-14/2	565	NM	-	-	-	NM	-	-	-
C53-14/2	592	NM	-	-	-	NM	-	-	-
C54-14/2	541	NM	-	-	-	NM	-	-	-
C55-14/2	277	NM	-	-	-	NM	-	-	-
C56-14/2	377	NM	-	-	-	NM	-	-	-
C58-14/2	386	NM	-	-	-	NM	-	-	-
C60-14/2	628	NM	-	-	-	NM	-	-	-
C62-14/2	604	NM	-	-	-	NM	-	-	-
C63-14/2	511	NM	-	-	-	NM	-	-	-
C64-14/2	626	NM	-	-	-	NM	-	-	-
C65-14/2	696	NM	-	-	-	NM	-	-	-
C67-14/2	563	NM	-	-	-	NM	-	-	-
C68-14/2	653	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C69-14/2	694	NM	-	-	-	NM	-	-	-
C70-14/2	668	NM	-	-	-	NM	-	-	-
C71-14/2	550	NM	-	-	-	NM	-	-	-
C75-14/2	683	NM	-	-	-	NM	-	-	-
C76-14/2	426	NM	-	-	-	NM	-	-	-
C77-14/2	537	NM	-	-	-	NM	-	-	-
C80-14/2	695	NM	-	-	-	NM	-	-	-
C81-14/2	565	NM	-	-	-	NM	-	-	-
C83-14/2	592	NM	-	-	-	NM	-	-	-
C84-14/2	541	NM	-	-	-	NM	-	-	-
C85-14/2	277	NM	-	-	-	NM	-	-	-
C86-14/2	377	NM	-	-	-	NM	-	-	-
C94-14/2	573	NM	-	-	-	NM	-	-	-
C95-14/2	687	NM	-	-	-	NM	-	-	-
C96-14/2	619	NM	-	-	-	NM	-	-	-
C97-14/2	670	NM	-	-	-	NM	-	-	-
C7-17/4	284	NM	-	-	-	NM	-	-	-
C11-17/4	284	NM	-	-	-	NM	-	-	-
C24-17/4	284	NM	-	-	-	NM	-	-	-
C82-17/4	282	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn Annotation (species)	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C99-17/4	284	NM	-	-	-	NM	-	-	-
C101-17/4	284	NM	-	-	-	NM	-	-	-
C105-17/4	286	NM	-	-	-	NM	-	-	-
C108-17/4	284	NM	-	-	-	NM	-	-	-
C122-17/4	285	NM	-	-	-	NM	-	-	-
C154-17/4	284	NM	-	-	-	NM	-	-	-
C185-17/4	284	NM	-	-	-	NM	-	-	-
C199-17/4	284	NM	-	-	-	NM	-	-	-
C214-17/4	284	NM	-	-	-	NM	-	-	-
C217-17/4	283	NM	-	-	-	NM	-	-	-
C257-17/4	286	NM	-	-	-	NM	-	-	-
C286-17/4	284	NM	-	-	-	NM	-	-	-
C289-17/4	284	NM	-	-	-	NM	-	-	-
C293-17/4	284	NM	-	-	-	NM	-	-	-
C319-17/4	284	NM	-	-	-	NM	-	-	-
C325-17/4	283	NM	-	-	-	NM	-	-	-
C329-17/4	284	NM	-	-	-	NM	-	-	-
C331-17/4	284	NM	-	-	-	NM	-	-	-
C333-17/4	284	NM	-	-	-	NM	-	-	-
C334-17/4	284	NM	-	-	-	NM	-	-	-

Clone	Size (bp.)	Search result by BLASTn	GeneBank Accession	E - value	Identity	Search result by BLASTx Annotation (species)	GeneBank Accession	E - value	Identity
C337-17/4	283	NM	-	-	-	NM	-	-	-
C340-17/4	284	NM	-	-	-	NM	-	-	-
C350-17/4	284	NM	-	-	-	NM	-	-	-

VITAE

Name	Miss Patcharee Kammarnjassadakul
Date of Birth	March 2, 1977
Place of Birth	Bangkok, Thailand
Address	49/3 M.10 T. Bangyor A. Phapradang, Samutprakarn. 10130
Education	
1997	Bachelor of Science (Medical Technology) Chulalongkorn University, Bangkok, Thailand.
2001	Master of Science (Medical Microbiology) Interdisciplinary Program, Graduate School, Chulalongkorn University, Bangkok, Thailand.
Career:	
2001	Lecturer at Department of Microbiology, Faculty of Medical Technology, Huacheiw Chalermprakiat University.
Presentation	Phylogenetic relationships of *Pythium insidiosum* isolate using cytochrome oxidase II sequences Medical Mycology in the 21^{st} Century: Scientific Base and Anticipated Challenges May 25-29, 2009. Tokyo, Japan.