

Pathogenicity genes of *Phytophthora cinnamomi* identified via RNA-Seq analysis of germinating cysts

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Supplementary Table S1. Putative secreted proteins identified from *Phytophthora cinnamomi* CNVDB29 cysts and germinating cysts with their best hit from the genomes of *Phytophthora infestans* and *Phytoththora cinnamomi* CBS144.22 through blastx analysis (E-value >1x10⁻⁵).

<i>Phytophthora cinnamomi</i> CBS144.22 proteins				<i>Phytophthora infestans</i> proteins				Sprob	SP (Y/N)	TMH
Query	Hit ID	Score (bit)	E-value	Hit ID	Score (Bit)	E-value	Putative annotation			
U9120*	Phyci1-319370	705.671	0	PITG_15900	631	0	ATP-binding Cassette (ABC) Superfamily (1291 aa)	0.968 Y		0
U3880	Phyci1-6331	388.652	7.41E-133	PITG_02623	718	0	aspartyl protease family A01B, putative (682 aa)	0.996 Y		0
U21374	Phyci1-209819	519.62	8.90E-167	PITG_10452	505	2.00E-143	CAD protein (1496 aa) dicarboxylate/Amino Acid:Cation (Na or H) Symporter (DAACS) family	0.809 Y		0
U15158	Phyci1-10058	462.996	4.70E-161	PITG_17951	418	1.00E-117	(571 aa)	0.964 Y		0
U12960	Phyci1-244533	405.216	1.71E-143	PITG_19184	388	1.00E-108	ER lumen protein retaining receptor (218 aa)	0.991 Y		0
U1541	Phyci1-209819	263.462	3.02E-102	PITG_10452	258	1.00E-100	CAD protein (1496 aa)	0.768 Y		0
U14728	Phyci1-224889	396.741	2.80E-137	PITG_08206	359	4.00E-100	signal peptidase complex subunit 3, putative (450 aa)	0.872 Y		0
U20732	Phyci1-304698	365.155	7.05E-124	PITG_05621	348	1.00E-96	conserved hypothetical protein (560 aa)	0.99 Y		0
U19356	Phyci1-313498	342.043	4.66E-119	PITG_09383	329	5.00E-91	aquaporin, putative (275 aa)	0.973 Y		0
U2213	Phyci1-324317	481.485	2.50E-169	PITG_04071	320	7.00E-88	putative extracellular dioxygenase (377 aa)	0.998 Y		0
U6780	Phyci1-206169	342.428	2.33E-118	PITG_13614	314	2.00E-86	malate dehydrogenase, mitochondrial precursor (336 aa)	0.942 Y		0
U18029*	Phyci1-89496	340.502	6.76E-119	PITG_13560	269	6.00E-73	endoglucanase, putative (206 aa)	1 Y		0
U19170	Phyci1-13922	304.679	4.07E-104	PITG_09470	260	1.00E-70	arabinan endo-1,5-alpha-L-arabinosidase A precursor (314 aa)	1 Y		0
U10762	Phyci1-68655	232.261	2.34E-76	PITG_02233	236	6.00E-63	conserved hypothetical protein (157 aa)	0.71 Y		0
U65523	Phyci1-92589	248.825	1.44E-81	PITG_19159	233	2.00E-62	conserved hypothetical protein (406 aa)	0.918 Y		0
U1781	Phyci1-246251	263.077	6.53E-85	PITG_15194	225	9.00E-60	Solute:Sodium Symporter (SSS) Family (354 aa)	0.819 Y		0
U12816	Phyci1-246251	263.077	1.42E-84	PITG_15194	225	1.00E-59	Solute:Sodium Symporter (SSS) Family (354 aa)	0.819 Y		0
U12000	Phyci1-97084	240.35	7.38E-82	PITG_18440	215	5.00E-57	conserved hypothetical protein (141 aa)	0.881 Y		0
U20271	Phyci1-90242	238.424	7.54E-74	PITG_12940	199	2.00E-52	P-type ATPase (P-ATPase) Superfamily (1020 aa)	0.863 Y		0
U4377*	Phyci1-98537	203.756	7.08E-65	PITG_19023	183	2.00E-47	NADH-cytochrome b5 reductase, putative (297 aa)	0.982 Y		0
U38373*	Phyci1-212628	182.57	3.29E-58	PITG_09031	179	3.00E-46	NADH ubiquinone oxidoreductase, putative (206 aa)	0.799 Y		0
U17139	Phyci1-92978	213.386	3.95E-66	PITG_16464	175	3.00E-45	Sulfate Permease (SulP) Family (699 aa)	0.838 Y		0
U4727	Phyci1-103444	351.673	1.06E-123	PITG_10429	174	3.00E-44	SCP-like extracellular protein (137 aa)	1 Y		0
U33065	Phyci1-110224	160.999	3.78E-51	PITG_01943	159	3.00E-40	60S ribosomal protein L23 (142 aa)	0.837 Y		0
U33066	Phyci1-110224	153.68	2.65E-48	PITG_01943	152	2.00E-38	60S ribosomal protein L23 (142 aa)	0.837 Y		0
U40444	Phyci1-213489	151.754	1.23E-44	PITG_07241	147	6.00E-37	Monovalent Cation:Proton Antiporter-1 (CPA1) Family (555 aa)	0.722 Y		0
U5664	Phyci1-91325	176.022	6.85E-51	PITG_05079	142	3.00E-35	glycosyltransferase (2248 aa)	0.927 Y		0

U32501	Phyci1-93612	171.014	5.55E-52	PITG_05311	132	4.00E-32	kinetochore protein NUF2-like protein (429 aa)	0.87 Y	0
U26137	Phyci1-93800	143.28	6.15E-43	PITG_17393	128	1.00E-30	conserved hypothetical protein (141 aa)	0.964 Y	0
U67457	Phyci1-92208	143.28	1.56E-41	PITG_11838	120	1.00E-28	Major facilitator Superfamily (412 aa)	0.923 Y	0
U2225	Phyci1-101986	130.568	2.60E-38	PITG_20795	119	8.00E-28	ribosomal protein (112 aa)	1 Y	0
U2222	Phyci1-101986	130.568	3.22E-38	PITG_20795	119	8.00E-28	ribosomal protein (112 aa)	1 Y	0
U2219	Phyci1-101986	130.568	1.62E-37	PITG_20795	119	1.00E-27	ribosomal protein (112 aa)	1 Y	0
U24469	Phyci1-105848	95.13	9.67E-24	PITG_06556	116	2.00E-27	transmembrane protein, putative (494 aa)	0.812 Y	0
U24542	Phyci1-95946	106.686	9.45E-30	PITG_15871	114	1.00E-26	nucleolar protein, putative (677 aa)	0.927 Y	0
U44861	Phyci1-316302	259.61	1.02E-81	PITG_13030	113	2.00E-26	P-type ATPase (P-ATPase) Superfamily (1299 aa)	0.752 Y	0
							3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial precursor (418		
U20274	Phyci1-8252	115.546	2.71E-29	PITG_00300	112	2.00E-25	aa)	0.875 Y	0
U12572*	Phyci1-234803	116.316	2.15E-26	PITG_05815	111	1.00E-24	ATP-binding Cassette (ABC) Superfamily (1823 aa)	0.967 Y	0
U63202*	Phyci1-8522	172.94	5.74E-53	PITG_12041	106	2.00E-24	cysteine protease family C01A, putative (377 aa)	1 Y	0
U6039	Phyci1-97941	107.842	1.98E-28	PITG_11792	107	2.00E-24	conserved hypothetical protein (363 aa)	0.956 Y	0
U20262	Phyci1-21078	109.383	1.60E-26	PITG_07216	108	2.00E-24	ATPase WRNIP1 (500 aa)	1 Y	0
U27102	Phyci1-95946	100.523	1.76E-27	PITG_15871	104	8.00E-24	nucleolar protein, putative (677 aa)	0.928 Y	0
U11342	Phyci1-278843	102.064	1.29E-24	PITG_09400	104	4.00E-23	pyruvate kinase (507 aa)	0.703 Y	0
U23493	Phyci1-92380	92.434	8.65E-23	PITG_02621	93.6	1.00E-20	CTP synthase, putative (603 aa)	0.763 Y	0
U8831	Phyci1-217253	92.434	4.12E-23	PITG_11619	95.5	2.00E-20	FKBP-type peptidyl-prolyl cis-trans isomerase, putative (109 aa)	0.994 Y	0
U15267*	Phyci1-474211		4.34E-23	PITG_18317	93.6	2.00E-20	phospholipid hydroperoxide glutathione peroxidase, putative (289 aa)	1 Y	0
U14879*	Phyci1-89305	69.322	8.25E-15	PITG_01172	94.7	3.00E-20	methionine-R-sulfoxide reductase (139 aa)	0.994 Y	0
U3478	Phyci1-212790	102.834	4.40E-23	PITG_17323	94	1.00E-19	multicopper oxidase, putative (561 aa)	0.988 Y	0
U34848*	Phyci1-197955	122.479	7.73E-36	PITG_08143	90.1	2.00E-19	elicitin-like protein (153 aa)	0.999 Y	0
							putative GPI-anchored serine-glycine rich elicitin INL3a-like protein (176		
U3845*	Phyci1-96865	134.806	1.69E-38	PITG_06370	91.3	3.00E-19	aa)	1 Y	0
U40728*	Phyci1-120770	122.865	2.67E-34	PITG_15072	81.3	7.00E-17	serine protease family S33, putative (435 aa)	0.997 Y	0
U13679	Phyci1-217253	85.885	1.34E-20	PITG_11619	83.6	1.00E-16	FKBP-type peptidyl-prolyl cis-trans isomerase, putative (109 aa)	0.995 Y	0
U4823*	Phyci1-95833	83.959	3.20E-19	PITG_03020	80.9	2.00E-16	cysteine protease family C01A, putative (536 aa)	1 Y	0
U31945	Phyci1-270646	77.411	3.50E-17	PITG_10226	79.3	4.00E-16	Ammonium Transporter (Amt) Family (519 aa)	0.759 Y	0
U28035*	Phyci1-75976	82.804	1.15E-18	PITG_03582	79.7	7.00E-16	serine protease family S01B, putative (393 aa)	0.999 Y	0
							dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit		
U38392	Phyci1-20834	100.138	3.10E-26	PITG_18053	77.8	8.00E-16	(471 aa)	1 Y	0
							triosephosphate isomerase/glyceraldehyde-3-phosphate		
U41160	Phyci1-21101		2.09E-18	PITG_22103	78.2	9.00E-16	dehydrogenase, putative (334 aa)	0.726 Y	0
U64870	Phyci1-248391	93.204	6.24E-23	PITG_01451	75.5	4.00E-15	GPI ethanolamine phosphate transferase, putative (964 aa)	0.977 Y	0
U27410	Phyci1-19565	92.434	1.71E-23	PITG_11046	67.8	8.00E-13	creatine kinase B-type (432 aa)	0.989 Y	0

U65090*	Phyci1-71307	67.396	2.22E-14	PITG_12598	67	1.00E-12 glycerophosphoryl diester phosphodiesterase, putative (416 aa)	0.998 Y	0
U14815	Phyci1-101986	64.699	3.09E-14	PITG_20795	67	1.00E-12 ribosomal protein (112 aa)	0.887 Y	0
U29527	Phyci1-318796	73.174	4.55E-16	PITG_08421	67	3.00E-12 peroxisomal multifunctional enzyme type 2, putative (315 aa)	0.785 Y	0
U17134	Phyci1-13900	60.077	4.36E-12	PITG_09445	64.3	2.00E-11 conserved hypothetical protein (119 aa)	0.941 Y	0
U24774	Phyci1-87573	59.692	2.15E-12	PITG_20795	61.2	8.00E-11 ribosomal protein (112 aa)	0.999 Y	0
U390	Phyci1-97405	66.625	1.62E-12	PITG_07797	61.6	3.00E-10 methionyl-tRNA synthetase, putative (728 aa)	0.769 Y	0
U13438	Phyci1-101986	58.921	2.49E-12	PITG_20795	59.3	3.00E-10 ribosomal protein (112 aa)	0.999 Y	0
U17525	Phyci1-87573	59.692	2.62E-12	PITG_01041	58.5	6.00E-10 60S acidic ribosomal protein P2, putative (114 aa)	0.865 Y	0
U24532	Phyci1-87573	50.062	2.91E-09	PITG_01041	57.8	8.00E-10 60S acidic ribosomal protein P2, putative (114 aa)	0.743 Y	0
U58943	Phyci1-87573	54.684	8.85E-11	PITG_20795	56.2	2.00E-09 ribosomal protein (112 aa)	0.978 Y	0
U1196	Phyci1-98415	61.233	2.69E-11	PITG_02282	57.4	3.00E-09 acyl-CoA dehydrogenase, putative (765 aa)	0.869 Y	0
U4223	Phyci1-253206	85.5	1.81E-20	PITG_05156	55.5	4.00E-09 secretory protein OPEL (489 aa)	1 Y	0
U15439	Phyci1-101986	57.766	1.61E-11	PITG_20795	56.2	4.00E-09 ribosomal protein (112 aa)	0.998 Y	0
U15669	Phyci1-98415	60.462	4.91E-11	PITG_02282	57	4.00E-09 acyl-CoA dehydrogenase, putative (765 aa)	0.797 Y	0
U46773	Phyci1-243686	60.077	3.48E-12	PITG_10877	54.7	1.00E-08 peptidyl-prolyl cis-trans isomerase, putative (173 aa)	1 Y	0
U7812	Phyci1-101986	58.536	3.53E-12	PITG_20795	53.5	2.00E-08 ribosomal protein (112 aa)	0.998 Y	0
U22190	Phyci1-98415	58.151	2.03E-10	PITG_02282	53.1	3.00E-08 acyl-CoA dehydrogenase, putative (765 aa)	0.98 Y	0
U31765	Phyci1-87573	47.751	2.00E-08	PITG_01041	51.6	6.00E-08 60S acidic ribosomal protein P2, putative (114 aa) succinate dehydrogenase flavoprotein subunit, mitochondrial precursor	0.797 Y	0
U31021	Phyci1-224622	63.544	2.47E-12	PITG_18354	51.2	1.00E-07 (626 aa)	0.899 Y	0
U63783	Phyci1-114269	44.284	5.77E-07	PITG_11603	50.4	1.00E-07 peptidyl-prolyl cis-trans isomerase CYP19-4 precursor (207 aa)	1 Y	0
U47658	Phyci1-383688	58.921	1.16E-10	PITG_22124	50.4	2.00E-07 P-type ATPase (P-ATPase) Superfamily (1076 aa)	0.881 Y	0
U38904	Phyci1-214892	52.373	4.39E-09	PITG_06981	50.1	2.00E-07 DEAD/DEAH box RNA helicase, putative (848 aa)	0.767 Y	0
U47845	Phyci1-237827	48.521	1.20E-07	PITG_14229	49.3	3.00E-07 mannose-1-phosphate guanyltransferase beta, putative (360 aa)	0.834 Y	0
U15626	Phyci1-91772	46.595	3.30E-07	PITG_09722	48.9	4.00E-07 thioredoxin H-type (272 aa) peptidylprolyl isomerase domain and WD repeat-containing protein 1	1 Y	0
U20733	Phyci1-255156	50.062	3.87E-08	PITG_13079	48.5	5.00E-07 (631 aa)	1 Y	0
U17026	Phyci1-119828	48.521	9.38E-08	PITG_20350	47	2.00E-06 D-amino acid dehydrogenase small subunit, putative (609 aa)	0.905 Y	0
U22336	Phyci1-119828	47.751	1.71E-07	PITG_20350	46.6	2.00E-06 D-amino acid dehydrogenase small subunit, putative (609 aa)	0.949 Y	0
U3775	Phyci1-91772	46.98	4.96E-07	PITG_09722	47.8	2.00E-06 thioredoxin H-type (272 aa)	1 Y	0
U63436	NA	NA	NA	PITG_21336	46.2	3.00E-06 patatin like protein (1142 aa)	1 Y	0
U66640	Phyci1-73206	43.899	3.82E-06	PITG_03966	45.4	4.00E-06 NhaC Na :H Antiporter (NhaC) Family (685 aa)	0.997 Y	0
U70117	Phyci1-95572	60.462	4.64E-12	PITG_07051	45.1	6.00E-06 Poly(A)-specific ribonuclease PARN-like protein (590 aa)	0.895 Y	0
U64718	NA	NA	NA	PITG_18728	45.1	6.00E-06 conserved hypothetical protein (511 aa)	0.863 Y	0
U18773	Phyci1-206169	43.513	2.71E-06	PITG_13614	43.9	1.00E-05 malate dehydrogenase, mitochondrial precursor (336 aa)	0.913 Y	0
U27715	Phyci1-113116	41.587	1.73E-05	PITG_08531	43.9	1.00E-05 conserved hypothetical protein (180 aa)	0.847 Y	0
U15102	Phyci1-242322	44.284	1.51E-05	PITG_21447	44.7	2.00E-05 ribosomal large subunit pseudouridine synthase A, putative (364 aa)	1 Y	0

U71742	Phyci1-24773	39.661	9.81E-05	PITG_09932	43.5	2.00E-05	translation initiation factor eIF-2B subunit epsilon, putative (743 aa)	0.814 Y	0
U36029	NA	NA	NA	PITG_18375	44.3	2.00E-05	UDP-glucose 6-dehydrogenase (476 aa)	0.709 Y	0
U13826	Phyci1-98415	46.98	7.92E-07	PITG_02282	43.1	3.00E-05	acyl-CoA dehydrogenase, putative (765 aa)	0.938 Y	0
U16996	Phyci1-91772	41.973	1.16E-05	PITG_09722	41.2	8.00E-05	thioredoxin H-type (272 aa)	0.992 Y	0
U61525	Phyci1-35881	41.587	3.22E-05	PITG_03700	41.6	9.00E-05	enolase (455 aa)	0.998 Y	0
U15167	Phyci1-229975	41.202	7.23E-05	NA	NA	NA	NA	0.989 Y	0
U19168	Phyci1-585339	40.817	5.78E-05	NA	NA	NA	NA	0.872 Y	0
U24069	Phyci1-243801	67.781	6.40E-13	NA	NA	NA	NA	0.874 Y	0
U58247	Phyci1-243801	167.548	5.19E-50	NA	NA	NA	NA	0.968 Y	0
U5155	Phyci1-316587	51.603	7.37E-09	NA	NA	NA	NA	0.742 Y	0
U12323	Phyci1-77786	44.669	5.84E-06	NA	NA	NA	NA	0.999 Y	0
U37984	Phyci1-78043	41.973	9.19E-06	NA	NA	NA	NA	0.741 Y	0
U32988	Phyci1-99044	41.202	1.69E-05	NA	NA	NA	NA	0.711 Y	0
U54017	Phyci1-87573	37.35	5.65E-05	NA	NA	NA	NA	1 Y	0
U55798	Phyci1-167931	37.35	5.98E-05	NA	NA	NA	NA	0.99 Y	0
U40431	Phyci1-304486	39.276	6.38E-05	NA	NA	NA	NA	0.858 Y	0

*Pathogenicity transcripts listed in Table 2