

Additional file 2

File format: PDF

Title: Supplementary Table S1

Description:

Table S1. Proteins identified in poplar (*P. deltoides*) leaf apoplast using 2-D PAGE MS/MS.

Poplar protein ID	Poplar transcript ID	Poplar new ID	Spot number	Mr/pl (theor.)	Number of matching peptides	Protein score	Protein identity/similarity	Glyco- protein**	Sequence similarity	Accession number	Organism	Signal peptide (SP)	Non- classical SP
Cell wall metabolism													
297914#*	gw1.88.36.1	POPTR_0017s08470.1	177	98.5/6.2	14	163	Beta-galactosidase		77%	Q5CCQ1	<i>Pyrus pyrifolia</i>	SA	yes
297914#*	gw1.88.36.1	POPTR_0017s08470.1	55	98.5/6.2	15	260	Beta-galactosidase		77%	Q5CCQ1	<i>Pyrus pyrifolia</i>	SA	yes
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	60	90.0/6.3	15	194	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	62	90.0/6.3	15	238	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	92	90.0/6.3	12	205	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	11	90.0/6.3	8	143	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	57	90.0/6.3	12	469	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
209993#	gw1.V.5394.1	POPTR_0005s20280.1	57	85.3/9.0	4	106	Beta-galactosidase 16		63%	Q8GX69	<i>Arabidopsis thaliana</i>	no	yes
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	58	90.0/6.3	11	428	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
209993#	gw1.V.5394.1	POPTR_0005s20280.1	58	85.3/9.0	4	106	Beta-galactosidase 16		63%	Q8GX69	<i>Arabidopsis thaliana</i>	no	yes
204338#*	gw1.IX.4803.1	POPTR_0009s01780.1	59	90.0/6.3	7	206	Beta-galactosidase		77%	Q93X57	<i>Fragaria ananassa</i>	yes	
209993#	gw1.V.5394.1	POPTR_0005s20280.1	59	85.3/9.0	7	80	Beta-galactosidase 16		63%	Q8GX69	<i>Arabidopsis thaliana</i>	no	yes
786149*	fgenesh4_pg.C_scaffold_164000005	POPTR_0018s14920.1	75	40.0/4.9	14	366	Alpha-galactosidase		83%	Q84VQ7	<i>Helianthus annuus</i>	no	yes
254860#	gw1.XVI.799.1	POPTR_0016s01920.1	102	36.9/6.1	7	66	Pectinesterase		78%	A2Q4U8	<i>Medicago truncatula</i>	no	yes
718566*	estExt_Genewise1_v1.C_LG_VII1401	POPTR_0007s04020.1	66	62.1/6.3	10	333	Pectin methylesterase-like protein		66%	Q9FXW9	<i>Arabidopsis thaliana</i>	yes	
718566*	estExt_Genewise1_v1.C_LG_VII1401	POPTR_0007s04020.1	176	62.1/6.3	7	226	Pectin methylesterase-like protein		66%	Q9FXW9	<i>Arabidopsis thaliana</i>	yes	
718566*	estExt_Genewise1_v1.C_LG_VII1401	POPTR_0007s04020.1	175	62.1/6.3	5	115	Pectin methylesterase-like protein		66%	Q9FXW9	<i>Arabidopsis thaliana</i>	yes	
718566*	estExt_Genewise1_v1.C_LG_VII1401	POPTR_0007s04020.1	173	62.1/6.3	9	113	Pectin methylesterase-like protein		66%	Q9FXW9	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	173	114.7/5.8	15	81	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
570444*	eugene3.00121097	POPTR_0012s13090.1	72	43.7/5.1	7	63	Pectinacetyl esterase	box e	64%	Q9FF93	<i>Arabidopsis thaliana</i>	yes	
570444*	eugene3.00121097	POPTR_0012s13090.1	73	43.7/5.1	6	309	Pectinacetyl esterase	box e	64%	Q9FF93	<i>Arabidopsis thaliana</i>	yes	
570444*	eugene3.00121097	POPTR_0012s13090.1	76	43.7/5.1	7	268	Pectinacetyl esterase	box e	64%	Q9FF93	<i>Arabidopsis thaliana</i>	yes	
570444*	eugene3.00121097	POPTR_0012s13090.1	122	43.3/5.1	9	74	Pectinacetyl esterase		64%	Q9FF93	<i>Arabidopsis thaliana</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	12	73.3/5.5	10	138	Alpha-L-arabinofuranosidase		74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	27	73.3/5.5	10	146	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	28	73.3/5.5	10	146	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	29	73.3/5.5	9	161	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	30	73.3/5.5	10	138	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
207219#*	gw1.V.2620.1	POPTR_0005s07020.1	129	71.2/4.9	11	73	Beta-galactosidase	box a	72%	A5AXS9	<i>Vitis vinifera</i>	no	yes
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	129	73.3/5.5	12	84	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	133	73.3/5.5	12	84	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	134	73.3/5.5	9	149	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	135	73.3/5.5	9	102	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	136	73.3/5.5	10	280	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	137	73.3/5.5	12	239	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	138	73.3/5.5	11	194	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	

Table S1. continued

207219#*	gw1.V.2620.1	POPTR_0005s07020.1	139	71.2/4.9	8	91	Beta-galactosidase	box a	72%	A5AXS9	<i>Vitis vinifera</i>	no	yes
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	139	73.3/5.5	9	78	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	144	73.3/5.5	10	118	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	145	73.3/5.5	9	255	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	146	73.3/5.5	10	96	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	147	73.3/5.5	12	105	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	148	73.3/5.5	12	118	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	149	73.3/5.5	7	98	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	151	73.3/5.5	5	137	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	152	73.3/5.5	9	121	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	153	73.3/5.5	11	146	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	154	73.3/5.5	12	140	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	155	73.3/5.5	6	209	Alpha-L-arabinofuranosidase		74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	156	73.3/5.5	10	154	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	157	73.3/5.5	11	63	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	158	73.3/5.5	12	130	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	159	73.3/5.5	11	79	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	160	73.3/5.5	11	101	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
255102*	gw1.XVI.1041.1	POPTR_0016s02620.1	162	73.3/5.5	9	68	Alpha-L-arabinofuranosidase	box a	74%	Q7X9G7	<i>Malus domestica</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	21	114.8/5.8	15	212	Alpha-mannosidase	box h	71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	105	114.8/5.8	5	90	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	125	114.8/5.8	15	129	Alpha-mannosidase	box d	71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	126	114.8/5.8	17	110	Alpha-mannosidase	box d	71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	132	114.8/5.8	17	326	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	140	114.8/5.8	15	90	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	141	114.8/5.8	16	291	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	142	114.8/5.8	16	327	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	128	114.8/5.8	13	217	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	67	114.8/5.8	16	243	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
572859*	eugene3.00140904	POPTR_0014s14050.1	127	113.8/6.3	9	81	Alpha-mannosidase		70%	Q9FFX7	<i>Arabidopsis thaliana</i>	yes	
816882*	estExt_fgenesh4_pg.C_LG_II2363	POPTR_0002s23920.1	130	114.7/5.8	18	369	Alpha-mannosidase		71%	P94078	<i>Arabidopsis thaliana</i>	yes	
595225	eugene3.68730001	POPTR_0003s13160.1	107	38.7/4.9	4	136	Polygalacturonase-like protein	box b	75%	Q84L17	<i>Fragaria ananassa</i>	no	yes
413310#*	gw1.III.413.1	POPTR_0003s13160.1	108	47.1/4.7	5	157	Polygalacturonase-like protein	box b	74%	Q84L17	<i>Fragaria ananassa</i>	no	yes
662785*	grail3.0016022201	POPTR_0013s02730.2	33	41.7/6.1	6	143	Lipolytic enzyme, G-D-S-L		75%	Q2HTP0	<i>Medicago truncatula</i>	yes	
662785*	grail3.0016022201	POPTR_0013s02730.2	35	41.7/6.1	11	266	Lipolytic enzyme, G-D-S-L		75%	Q2HTP0	<i>Medicago truncatula</i>	yes	
662785*	grail3.0016022201	POPTR_0013s02730.2	24	41.7/6.1	9	280	Lipolytic enzyme, G-D-S-L	box k	75%	Q2HTP0	<i>Medicago truncatula</i>	yes	
827727	estExt_fgenesh4_pg.C_1210040	POPTR_0006s18230.1	24	30.0/4.8	3	128	Proline-rich protein	box k	46%	Q94J26	<i>Oryza sativa subsp. japonica</i>	yes	
662785*	grail3.0016022201	POPTR_0013s02730.2	36	41.7/6.1	9	93	Lipolytic enzyme, G-D-S-L		75%	Q2HTP0	<i>Medicago truncatula</i>	yes	
827727	estExt_fgenesh4_pg.C_1210040	POPTR_0006s18230.1	36	30.0/4.8	4	92	Proline-rich protein		46%	Q94J26	<i>Oryza sativa subsp. japonica</i>	yes	
580490	eugene3.01210029	POPTR_0006s18240.1	36	42.3/5.1	7	75	GDSL-motif lipase/hydrolase-like protein		43%	Q9FK75	<i>Arabidopsis thaliana</i>	yes	

Table S1. continued

827727	estExt_fgenesh4_pg.C_1210040	POPTR_0006s18230.1	37	30.0/4.8	6	164	Proline-rich protein GDSL-motif lipase/hydrolase-like protein Phenylcoumaran benzylic ether reductase Glucan endo-1,3-beta-glucosidase 7	46%	Q94J26	<i>Oryza sativa</i> subsp. <i>japonica</i>	yes	
580490	eugene3.01210029	POPTR_0006s18240.1	37	42.3/5.1	7	147		43%	Q9FK75	<i>Arabidopsis thaliana</i>	yes	
830063*	estExt_fgenesh4_pm.C_LG_II0164	POPTR_0002s03580.1	98	33.9/5.5	19	465		100%	O65904	<i>Populus trichocarpa</i>	no no	
648596	grail3.0045003902	POPTR_0004s16120.2	97	40.3/5.8	11	141		74%	Q9M069	<i>Arabidopsis thaliana</i>	yes	
209602#*	gw1.V.5003.1	POPTR_0005s16590.1	124	32.8/5.0	11	211	Glucan 1,3-beta-glucosidase	68%	Q8RU06	<i>Oryza sativa</i> subsp. <i>japonica</i>	no yes	
569295	eugene3.00111309	POPTR_0011s15750.1	116	102.5/7.1	5	65	Alpha-glucosidase 1	64%	Q9LYF8	<i>Arabidopsis thaliana</i>	SA yes	
570444*	eugene3.00121097	POPTR_0012s13090.1	80	43.7/5.1	6	145	Pectinacetyl esterase	64%	Q9FF93	<i>Arabidopsis thaliana</i>	yes	
Cell wall and stress related												
547681*	eugene3.00010122	POPTR_0001s05050.1	1	36.8/4.5	5	140	Peroxidase	box c	98%	Q43101	<i>Populus trichocarpa</i>	yes
817694*	estExt_fgenesh4_pg.C_LG_III1873	POPTR_0003s21660.1	65	33.4/5.8	8	146	Peroxidase N		67%	Q42517	<i>Armoracia rusticana</i>	no yes
817694*	estExt_fgenesh4_pg.C_LG_III1873	POPTR_0003s21660.1	69	33.4/5.8	11	145	Peroxidase N	box i	67%	Q42517	<i>Armoracia rusticana</i>	no yes
817694*	estExt_fgenesh4_pg.C_LG_III1873	POPTR_0003s21660.1	70	33.4/5.8	10	297	Peroxidase N	box m	67%	Q42517	<i>Armoracia rusticana</i>	no yes
817694*	estExt_fgenesh4_pg.C_LG_III1873	POPTR_0003s21660.1	74	33.4/5.8	10	197	Peroxidase N	box i	67%	Q42517	<i>Armoracia rusticana</i>	no yes
679511	grail3.0064002301	POPTR_0017s06550.2	7	32.0/8.7	5	75	Peroxidase a	box v	76%	Q66RM0	<i>Eucommia ulmoides</i>	yes
679511	grail3.0064002301	POPTR_0017s06550.2	150	32.0/8.7	6	65	Peroxidase a	box v	76%	Q66RM0	<i>Eucommia ulmoides</i>	yes
777213*	fgenesh4_pg.C_LG_XVI00455	POPTR_0016s05860.1	77	33.0/5.3	2	173	Peroxidase	box g	93%	Q08IT3	<i>Populus alba</i>	no yes
825400*	estExt_fgenesh4_pg.C_LG_XVI1240	POPTR_0016s14030.1	54	33.4/8.1	9	72	Cationic peroxidase 1	box u	69%	P22195	<i>Arachis hypogaea</i>	yes
800693	fgenesh4_pm.C_LG_IV000380	POPTR_0004s14240.1	25	34.6/5.2	8	201	Peroxidase ATP17a like protein		68%	Q67XK7	<i>Arabidopsis thaliana</i>	yes
718485*	estExt_Genewise1_v1.C_LG_VII1054	POPTR_0007s02580.1	53	35.9/8.6	8	244	Peroxidase		74%	Q9ZNZ5	<i>Glycine max</i>	yes
654740	grail3.0011011501	POPTR_0007s05100.1	96	36.5/5.3	15	288	Peroxidase 17		75%	Q9SJZ2	<i>Arabidopsis thaliana</i>	yes
Stress/defense												
549955*	eugene3.00012396	POPTR_0001s30680.1	11	25.0/7.0	7	273	NtPRP27		72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
549955*	eugene3.00012396	POPTR_0001s30680.1	3	25.0/7.0	6	289	NtPRP27	box p	72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
549955*	eugene3.00012396	POPTR_0001s30680.1	4	25.0/7.0	6	193	NtPRP27	box p	72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
549955*	eugene3.00012396	POPTR_0001s30680.1	6	25.0/7.0	10	217	NtPRP27	box p	72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
549955*	eugene3.00012396	POPTR_0001s30680.1	121	25.0/7.0	5	295	NtPRP27		72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
549955*	eugene3.00012396	POPTR_0001s30680.1	17	25.0/7.0	8	107	NtPRP27		72%	Q9XIY9	<i>Nicotiana tabacum</i>	yes
201948#	gw1.IX.2413.1	POPTR_0009s09750.1	48	23.7/5.0	9	239	NtPRP27-like protein		66%	Q84XQ4	<i>Solanum tuberosum</i>	no no
735049	estExt_Genewise1_v1.C_LG_XVI1825	POPTR_0016s05800.1	51	22.5/7.8	1	83	Beta-1,3 glucanase		90%	Q9M5I9	<i>Populus tremula x Populus alba</i>	no yes
735049	estExt_Genewise1_v1.C_LG_XVI1825	POPTR_0016s05800.1	52	22.5/7.8	1	111	Beta-1,3 glucanase		90%	Q9M5I9	<i>Populus tremula x Populus alba</i>	no yes
290846#	gw1.5405.1.1	POPTR_0001s26210.1	38	34.7/4.7	8	192	Beta-1,3-glucanase		69%	Q84RT6	<i>Fragaria ananassa</i>	no yes
290846#	gw1.5405.1.1	POPTR_0001s26210.1	40	34.7/4.7	8	277	Beta-1,3-glucanase		69%	Q84RT6	<i>Fragaria ananassa</i>	no yes
574380*	eugene3.00190854	POPTR_0019s12360.1	40	28.9/4.7	2	123	Class IV chitinase		70%	Q7X9F8	<i>Galega orientalis</i>	yes
290846#	gw1.5405.1.1	POPTR_0001s26210.1	41	34.7/4.7	8	397	Beta-1,3-glucanase		69%	Q84RT6	<i>Fragaria ananassa</i>	no yes
652688*	grail3.0024032801	POPTR_0006s04670.1	43	31.6/4.7	7	245	Beta-1,3-glucanase		80%	Q9M5I9	<i>Populus tremula x Populus alba</i>	yes
259952	gw1.XVIII.493.1	POPTR_0018s14060.1	153	109.4/5.9	21	71	Salt-inducible protein	box a	52%	Q9LVD3	<i>Arabidopsis thaliana</i>	no yes
828660*	estExt_fgenesh4_pg.C_1970027	POPTR_0015s05980.1	56	31.7/8.4	7	199	Hevamine-A	box t	80%	P23472	<i>Hevea brasiliensis</i>	yes

Table S1. continued

828660*	estExt_fgenesh4_pg.C_1970027	POPTR_0015s05980.1	31	31.7/8.4	6	166	Hevamine-A	80%	P23472	<i>Hevea brasiliensis</i>	yes
233978#	gw1.XI.1958.1	POPTR_0012s01160.1	83	28.6/5.2	N-TS		Pathogenesis-related protein 8	75%	Q00MX4	<i>Malus domestica</i>	no yes
746640*	estExt_Genewise1_v1.C_1970084	POPTR_0015s05990.1	83	30.8/4.4	N-TS		Acidic class III chitinase	72%	Q09Y38	<i>Citrullus lanatus</i>	yes
669475*	grail3.0020019002	POPTR_0018s10490.1	87	24.7/7.8	N-TS		Thaumatin-like protein	76%	Q5ND92	<i>Actinidia deliciosa</i>	yes
669475*	grail3.0020019002	POPTR_0018s10490.1	88	24.7/7.8	N-TS		Thaumatin-like protein	76%	Q5ND92	<i>Actinidia deliciosa</i>	yes
574380*	eugene3.00190854	POPTR_0019s12360.1	50	28.9/4.7	2	123	Class IV chitinase	70%	Q7X9F8	<i>Galega orientalis</i>	yes
270686#*	gw1.142.209.1	POPTR_0013s12870.1	2	27.1/4.4	5	184	Class IV chitinase	80%	Q9M2U5	<i>Arabidopsis thaliana</i>	no yes
572334	eugene3.00140379	POPTR_0014s08860.1	100	29.9/6.9	9	112	Class III chitinase	54%	Q19AL0	<i>Panax ginseng</i>	yes
586585	eugene3.01970027	POPTR_0015s06000.1	68	30.8/4.3	3	116	Acidic class III chitinase	69%	Q09Y38	<i>Citrullus lanatus</i>	yes
586585	eugene3.01970027	POPTR_0015s06000.1	90	30.8/4.3	3	88	Acidic class III chitinase	69%	Q09Y38	<i>Citrullus lanatus</i>	yes
811643*	fgenesh4_pm.C_scaffold_163000009	POPTR_0011s01280.1	103	21.6/6.4	5	114	Superoxide dismutase [Cu-Zn]	99%	A9PJW9	<i>Populus jackii</i>	no yes
595511	eugene3.00700152	POPTR_0005s04590.1	111	15.3/5.6	6	70	Superoxide dismutase [Cu-Zn]	100%	A3FM77	<i>Populus trichocarpa</i>	no yes
822230	estExt_fgenesh4_pg.C_LG_X1353	POPTR_0010s16050.1	34	13.0/5.7	4	71	<i>P.trichocarpa X P.deltoides</i> wound-responsive	98%	Q7DM48	<i>Populus trichocarpa</i>	no no
819386*	estExt_fgenesh4_pg.C_LG_VI1270	POPTR_0006s19310.1	10	13.8/8.9	6	77	Blight-associated protein p12	49%	Q6K4C4	<i>Oryza sativa subsp. japonica</i>	yes
825296*	estExt_fgenesh4_pg.C_LG_XVI0953	POPTR_0016s10140.1	9	11.9/8.1	7	62	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	74%	A9XNQ1	<i>Sonneratia caseolaris</i>	yes
819822	estExt_fgenesh4_pg.C_LG_VII0502	POPTR_0007s05650.1	84	18.6/4.7	3	377	Dehydration stress-induced protein	68%	Q9AXN5	<i>Brassica napus</i>	yes
832078	estExt_fgenesh4_pm.C_LG_VI0650	POPTR_0006s24030.1	119	17.5/6.2	3	99	Cytosolic class II low molecular weight heat shock protein	88%	Q9XGS6	<i>Prunus dulcis</i>	no no
723969	estExt_Genewise1_v1.C_LG_X0701	POPTR_0010s16030.1	174	12.4/4.9	6	182	<i>Populus x generosa</i> pop3 peptide	100%	Q41049	<i>Populus jackii</i>	no yes
272681#*	gw1.152.150.1	POPTR_0006s06100.2	101	56.8/6.0	14	553	Heparanase-like protein 3	66%	Q9FZP1	<i>Arabidopsis thaliana</i>	no yes
201272	gw1.IX.1737.1	POPTR_0009s12090.1	98	34.1/7.8	3	90	Isoflavone reductase related protein	80%	O81355	<i>Pyrus communis</i>	no yes

Proteolysis												
835003*	estExt_fgenesh4_pm.C_LG_XIV0520	POPTR_0014s17580.1	49	55.6/5.4	7	130	Serine carboxypeptidase-like 20	72%	Q8L7B2	<i>Arabidopsis thaliana</i>	yes	
560367*	eugene3.00060326	POPTR_0006s03490.1	39	51.1/4.9	6	240	Serine carboxypeptidase family protein	65%	Q2R3G8	<i>Oryza sativa subsp. japonica</i>	yes	
199556#*	gw1.IX.21.1	POPTR_0009s00820.1	42	49.0/5.4	7	87	Serine carboxypeptidase-like 51	67%	Q67Y83	<i>Arabidopsis thaliana</i>	no yes	
560367*	eugene3.00060326	POPTR_0006s03490.1	19	51.1/4.9	6	478	Serine carboxypeptidase family protein	65%	Q2R3G8	<i>Oryza sativa subsp. japonica</i>	yes	
797202	fgenesh4_pm.C_LG_I000205	POPTR_0001s13140.1	19	50.9/5.6	3	101	Serine carboxypeptidase-like 45	79%	Q93Y09	<i>Arabidopsis thaliana</i>	yes	
835003*	estExt_fgenesh4_pm.C_LG_XIV0520	POPTR_0014s17580.1	117	55.6/5.4	4	152	Serine carboxypeptidase-like 20	box r	72%	Q8L7B2	<i>Arabidopsis thaliana</i>	yes
835003*	estExt_fgenesh4_pm.C_LG_XIV0520	POPTR_0014s17580.1	115	55.6/5.4	6	202	Serine carboxypeptidase-like 20	72%	Q8L7B2	<i>Arabidopsis thaliana</i>	yes	
835003*	estExt_fgenesh4_pm.C_LG_XIV0520	POPTR_0014s17580.1	45	55.6/5.4	7	305	Serine carboxypeptidase-like 20	72%	Q8L7B2	<i>Arabidopsis thaliana</i>	yes	
835003*	estExt_fgenesh4_pm.C_LG_XIV0520	POPTR_0014s17580.1	46	55.6/5.4	8	239	Serine carboxypeptidase-like 20	72%	Q8L7B2	<i>Arabidopsis thaliana</i>	yes	
199556#*	gw1.IX.21.1	POPTR_0009s00820.1	44	49.0/5.4	3	98	Serine carboxypeptidase-like 51	67%	Q67Y83	<i>Arabidopsis thaliana</i>	no yes	
249095#*	gw1.XIX.1495.1	POPTR_0019s08160.1	109	52.4/5.2	10	159	Wound-inducible carboxypeptidase	box s	64%	Q9M513	<i>Solanum lycopersicum</i>	no yes
263224#	gw1.10474.1.1	POPTR_0019s08160.1	109	9.1/5.1	4	104	Serine carboxypeptidase-like 20	box s	83%	Q8L7B2	<i>Arabidopsis thaliana</i>	no no
249095#*	gw1.XIX.1495.1	POPTR_0019s08160.1	110	52.4/5.2	5	170	Wound-inducible carboxypeptidase	box s	64%	Q9M513	<i>Solanum lycopersicum</i>	no yes
263224#	gw1.10474.1.1	POPTR_0019s08160.1	110	9.1/5.1	3	140	Serine carboxypeptidase-like 20	box s	83%	Q8L7B2	<i>Arabidopsis thaliana</i>	no no
249095#*	gw1.XIX.1495.1	POPTR_0019s08160.1	112	52.4/5.2	6	92	Wound-inducible carboxypeptidase		64%	Q9M513	<i>Solanum lycopersicum</i>	no yes
825802*	estExt_fgenesh4_pg.C_LG_XVIII0531	POPTR_0018s03020.1	76	49.9/7.4	6	89	41 kD chloroplast nucleoid DNA binding protein		45%	Q8H9F4	<i>Nicotiana sylvestris</i>	yes

Table S1. continued

825802*	estExt_fgenesh4_pg.C_LG_XVIII0531	POPTR_0018s03020.1	18	49.9/7.4	6	205	41 kD chloroplast nucleoid DNA binding protein 41 kD chloroplast nucleoid DNA binding protein 41 kD chloroplast nucleoid DNA binding protein 41 kD chloroplast nucleoid DNA binding protein Serine carboxypeptidase family protein	box o	45%	Q8H9F4	<i>Nicotiana sylvestris</i>	yes
825802*	estExt_fgenesh4_pg.C_LG_XVIII0531	POPTR_0018s03020.1	94	49.9/7.4	4	162			45%	Q8H9F4	<i>Nicotiana sylvestris</i>	yes
825802*	estExt_fgenesh4_pg.C_LG_XVIII0531	POPTR_0018s03020.1	78	49.9/7.4	6	276		box f	45%	Q8H9F4	<i>Nicotiana sylvestris</i>	yes
825802*	estExt_fgenesh4_pg.C_LG_XVIII0531	POPTR_0018s03020.1	95	49.9/7.4	3	140			45%	Q8H9F4	<i>Nicotiana sylvestris</i>	yes
560367*	eugene3.00060326	POPTR_0006s03490.1	43	51.1/4.9	5	135			65%	Q2R3G8	<i>Oryza sativa subsp. japonica</i>	yes
709916*	estExt_Genewise1_v1.C_LG_II0461	POPTR_0002s02010.1	26	77.2/5.3	4	81	Subtilisin-like serine protease	box a	61%	Q8LAE1	<i>Arabidopsis thaliana</i>	no yes
709916*	estExt_Genewise1_v1.C_LG_II0461	POPTR_0002s02010.1	64	77.2/5.3	8	309	Subtilisin-like serine protease	box n	61%	Q8LAE1	<i>Arabidopsis thaliana</i>	no yes
709916*	estExt_Genewise1_v1.C_LG_II0461	POPTR_0002s02010.1	165	77.2/5.3	9	78	Subtilisin-like serine protease	box a	61%	Q8LAE1	<i>Arabidopsis thaliana</i>	no yes
709916*	estExt_Genewise1_v1.C_LG_II0461	POPTR_0002s02010.1	166	77.2/5.3	9	70	Subtilisin-like serine protease	box a	61%	Q8LAE1	<i>Arabidopsis thaliana</i>	no yes
551801*	eugene3.00021116	POPTR_0002s12130.1	167	82.0/6.6	16	301	Serine protease	box a	98%	Q8RVJ7	<i>Populus canadensis</i>	yes
781559*	fgenesh4_pg.C_scaffold_40000309	POPTR_0014s02650.1	164	83.4/5.3	8	163	Subtilase	box a	50%	Q84TR6	<i>Casuarina glauca</i>	yes
781559*	fgenesh4_pg.C_scaffold_40000309	POPTR_0014s02650.1	163	83.4/5.3	11	102	Subtilase	box a	50%	Q84TR6	<i>Casuarina glauca</i>	yes
781583*	fgenesh4_pg.C_scaffold_40000333	POPTR_0014s02410.1	113	50.4/5.4	9	316	Cysteine protease CP1		82%	Q52QX8	<i>Manihot esculenta</i>	yes
675847*	grail3.0028002001	POPTR_0006s14400.1	47	39.3/6.3	7	252	Cysteine protease CP1		79%	A5HIJ1	<i>Actinidia deliciosa</i>	yes
417502#	gw1.VI.1875.1	POPTR_0006s24850.1	99	49.9/5.2	7	134	Nucleoid DNA-binding protein cnd41-like protein	box l	55%	Q9LEW2	<i>Arabidopsis thaliana</i>	yes
Carbohydrate metabolism												
644125*	grail3.0033012902	POPTR_0515s00220.2	63	44.1/5.1	11	302	Alpha-amylase		78%	Q7X9T1	<i>Phaseolus angularis</i>	no yes
644125*	grail3.0033012902	POPTR_0515s00220.2	22	44.1/5.1	11	302	Alpha-amylase		78%	Q7X9T1	<i>Phaseolus angularis</i>	no yes
644125*	grail3.0033012902	POPTR_0515s00220.2	23	44.1/5.1	14	325	Alpha-amylase		78%	Q7X9T1	<i>Phaseolus angularis</i>	no yes
644125*	grail3.0033012902	POPTR_0515s00220.2	71	44.1/5.1	12	277	Alpha-amylase		78%	Q7X9T1	<i>Phaseolus angularis</i>	no yes
644125*	grail3.0033012902	POPTR_0515s00220.2	79	44.1/5.1	8	131	Alpha-amylase		78%	Q7X9T1	<i>Phaseolus angularis</i>	no yes
575698*	eugene3.00151093	POPTR_0015s14380.1	143	47.9/5.7	13	113	Enolase		100%	A9PD49	<i>Populus trichocarpa</i>	no yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	130	59.6/6.1	15	206	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	131	59.6/6.1	13	116	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	123	59.6/6.1	16	247	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	124	59.6/6.1	12	74	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	104	59.6/6.1	13	173	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
772214*	fgenesh4_pg.C_LG_XI001367	POPTR_0011s16170.1	106	59.6/6.1	15	412	Carbohydrate oxidase		59%	Q8SA59	<i>Helianthus annuus</i>	yes
287193#	gw1.40.953.1	POPTR_0014s02270.1	93	25.7/5.6	6	83	Carbohydrate esterase		57%	Q8L9J9	<i>Arabidopsis thaliana</i>	no yes
Other metabolic processes												
553231	eugene3.00002546	POPTR_0002s25070.1	59	27.1/8.6	5	168	Auxin-induced protein 12		41%	Q94BT2	<i>Arabidopsis thaliana</i>	yes
816232*	estExt_fgenesh4_pg.C_LG_II0662	POPTR_0002s07290.1	61	41.1/6.3	11	118	Alcohol dehydrogenase 2		87%	Q9FZ01	<i>Vitis vinifera</i>	no no
782655	fgenesh4_pg.C_scaffold_70000003	POPTR_0005s06140.1	61	41.1/6.1	7	84	Alcohol dehydrogenase		92%	Q19P40	<i>Dimocarpus longan</i>	no no
410110#	gw1.II.1445.1	POPTR_0002s13970.1	114	18.1/5.7	7	328	Nucleoside diphosphate kinase		99%	A9PGV1	<i>Populus trichocarpa</i>	no no
666348	grail3.0005000301	POPTR_0015s07660.1	130	28.4/6.6	10	67	(-)isopiperitenol dehydrogenase		69%	A7XDE9	<i>Mentha haplocalyx var. piperascens</i>	no no
652151*	grail3.0002074001	POPTR_0005s26740.1	45	17.0/5.1	4	85	Plastocyanin A		100%	P00299	<i>Populus nigra</i>	no yes
286504#	gw1.40.264.1	POPTR_0014s04850.1	20	16.5/5.0	1	102	Cu2+ plastocyanin-like		43%	Q6V5E4	<i>Olimarabidopsis pumila</i>	yes

Table S1. continued

816369	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	32	18.8/5.6	2	226	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes
816369	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	91	18.8/5.6	1	81	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes
816369	estExt_fgenesh4_pg.C_LG_II0927	POPTR_0002s10150.1	174	18.8/5.6	1	89	Blue copper-like protein	55%	A3F8V0	<i>Gossypium hirsutum</i>	yes
417410 [#]	gw1.VI.1783.1	POPTR_0006s06650.1	85	31.5/5.2	1	96	Dicyanin	44%	Q9M510	<i>Solanum lycopersicum</i>	yes
569314	eugene3.00111328	POPTR_0011s15950.1	104	58.7/9.3	5	65	FAD linked oxidase, N-terminal	59%	Q2HTY4	<i>Medicago truncatula</i>	yes
569314	eugene3.00111328	POPTR_0011s15950.1	106	58.7/9.3	4	74	FAD linked oxidase, N-terminal	59%	Q2HTY4	<i>Medicago truncatula</i>	yes
Unclassified											
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	17	26.4/5.8	14	199	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	5	26.4/5.8	9	135	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	14	26.4/5.8	11	288	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	86	26.4/5.8	14	213	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
562320	eugene3.00070258	POPTR_1698s00200.1	118	26.4/5.8	7	147	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
562320	eugene3.00070258	POPTR_1698s00200.1	122	26.4/5.8	9	267	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
718495	estExt_Genewise1_v1.C_LG_VII1106	POPTR_1698s00200.1	49	26.4/5.8	5	94	Cysteine-rich repeat secretory protein 38	58%	Q9LRJ9	<i>Arabidopsis thaliana</i>	yes
824970	estExt_fgenesh4_pg.C_LG_XVI0047	POPTR_0016s01210.1	120	41.9/9.6	4	87	Membrane protein	57%	Q9AR56	<i>Solanum lycopersicum</i>	no
640081 ^{#*}	grail3.0008013701	POPTR_0001s13320.1	15	17.4/9.6	5	148	Leucine-rich repeat protein	67%	A5HKK5	<i>Nicotiana tabacum</i>	no
549865 [*]	eugene3.00012306	POPTR_0001s31740.1	13	20.9/8.7	3	274	Tumor-related protein	37%	P93378	<i>Nicotiana tabacum</i>	yes
549865 [*]	eugene3.00012306	POPTR_0001s31740.1	16	20.9/8.7	5	164	Tumor-related protein	37%	P93378	<i>Nicotiana tabacum</i>	yes
814847 [*]	estExt_fgenesh4_pg.C_LG_I0347	POPTR_0001s05560.1	162	95.2/5.5	17	102	no sequence similarity to a known protein	box a			yes
814847 [*]	estExt_fgenesh4_pg.C_LG_I0347	POPTR_0001s05560.1	8	95.2/5.5	10	70	no sequence similarity to a known protein				yes
814847 [*]	estExt_fgenesh4_pg.C_LG_I0347	POPTR_0001s05560.1	82	95.2/5.5	9	529	no sequence similarity to a known protein				yes

[#] protein sequence in JGI database is incomplete^{*} protein was also identified via 2D-LC MSMS

** based on staining with specific glyco dye protein appears to be glycosylated. Boxes correspond to glycoprotein on Figure S2

N-TS - protein was identified via N-terminal sequencing

SA - protein is predicted to serve as signal anchor