

Table S1. Checklist of known genes in the F library and R library.

Seq. Name	Seq. Description	Length	#Hits	E-value	Similarity
H543	Zinc finger protein	372	20	4.58E-33	69.80%
H884	Xyloglucan endotransglycosylase-related protein XTR-7	309	20	1.87E-34	75.60%
H1092	Vacuolar H ⁺ -translocating inorganic pyrophosphatase	482	16	1.33E-05	64.56%
H684	Uncharacterized protein	247	20	7.28E-39	77.30%
H767	Uncharacterized protein	641	2	7.24E-05	38.00%
H779	Uncharacterized protein	641	2	7.24E-05	38.00%
H690	Uncharacterized protein	640	20	1.83E-96	78.25%
H556	Ubiquitin-protein ligase E3	471	20	1.44E-62	95.00%
H858	Ubiquitin-conjugating enzyme E2	314	20	1.58E-35	97.30%
H1207	Sugar transport protein 14	447	20	1.47E-56	87.50%
H545	Sugar transport protein 14	428	20	8.71E-51	87.85%
H572	Soluble inorganic pyrophosphatase	393	20	3.04E-66	97.55%
H264	Senescence-associated protein	252	20	1.07E-36	89.95%
H348	Senescence-associated protein	340	20	7.04E-59	96.90%
H583	Ring-h2 finger protein	431	20	2.89E-42	86.55%
H1065	RIN4-like protein	517	20	2.61E-34	57.05%
H521	Reversibly glycosylated polypeptide	700	20	5.46E-157	95.15%
H1174	Receptor-like cytosolic serine threonine-protein kinase RBK1-like	326	20	1.84E-31	72.50%
H597	Rapid alkalization factor	192	20	1.90E-12	68.45%
H1038	RAB-like protein	689	20	2.35E-53	95.15%
H1234	RAB-like protein	689	20	2.35E-53	95.15%
H283	Proton pump interactor 1	862	20	6.57E-93	78.00%
H1037	Protein cobra	515	20	7.13E-36	72.60%
H1024	Uncharacterized protein	539	20	1.65E-37	58.40%
H1208	Uncharacterized protein	547	20	4.02E-36	57.70%
H164	Uncharacterized protein	572	20	1.50E-40	57.85%
H226	Uncharacterized protein	487	20	2.23E-31	86.55%
H699	Uncharacterized protein	252	20	5.06E-11	64.70%
H770	Uncharacterized protein	545	20	4.02E-36	57.70%
H782	Uncharacterized protein	545	20	4.02E-36	57.70%
H889	Uncharacterized protein	451	20	5.76E-31	86.40%
H1099	Probable polyol transporter 3-like	363	20	4.27E-30	83.75%
H102	Pollen coat-like protein	488	20	2.23E-31	86.55%
H128	Pollen allergen Pla o1	526	20	1.80E-35	57.85%
H1206	Pectin esterase PPME1-like	1245	20	6.00E-87	79.05%
H1019	Pectate lyase-like	481	16	1.29E-05	64.56%

Table S1. Cont.

Seq. Name	Seq. Description	Length	#Hits	E-value	Similarity
H1128	Pectate lyase-like	654	20	5.51E-29	66.90%
H708	Pectate lyase-like	549	20	3.56E-14	67.65%
H761	Pectate lyase-like	634	20	3.69E-25	67.10%
H813	Pectate lyase-like	489	20	5.54E-06	66.70%
H868	Pectate lyase family protein	848	20	2.95E-61	70.80%
H293	Pectate lyase	955	20	6.23E-80	72.30%
H783	Pectate lyase	882	20	1.51E-65	70.90%
H1191	NADH dehydrogenase	701	20	1.56E-67	81.80%
H865	Monosaccharide transporter	263	20	9.97E-19	86.85%
H984	Monosaccharide transporter	266	20	4.46E-17	86.95%
H986	Mitochondrial processing peptidase	684	20	2.87E-64	94.85%
H580	MADS box	441	20	2.58E-48	89.95%
H431	Glycosyl transferase	180	20	6.89E-26	94.65%
H748	Glucan endo- β -glucosidase	333	20	1.02E-35	69.35%
H1125	GDP-D-mannose-3 -epimerase	863	20	2.31E-149	98.30%
H933	GDP-D-mannose-3 -epimerase	863	20	2.31E-149	98.30%
H1166	Fructose-bisphosphate	389	20	7.16E-68	94.15%
H304	F-box family protein	446	20	3.04E-23	87.80%
H997	Endo- α -glucanase	503	20	2.77E-70	79.50%
H409	DNA double-strand break repair Rad 50	554	11	6.39E-12	59.73%
H447	Carbonic anhydrase	561	20	1.05E-57	67.35%
H115	Calcium-dependent phospholipid binding protein	805	20	3.67E-112	86.40%
H749	β -galactosidase 7-like	342	20	6.16E-26	68.70%
H549	β -glucanase	410	20	4.27E-37	68.30%
H601	Aldose 1-epimerase	656	20	5.18E-70	76.80%
H931	Aldose 1-epimerase	277	20	3.43E-13	85.50%
H576	Adenylate translocator	439	20	3.96E-25	94.05%
H428	Actin depolymerizing	612	20	6.19E-85	93.75%
H557	60s acidic ribosomal protein	671	20	3.59E-28	86.75%
F580	Zinc finger (C ₂ H ₂ type) family protein	373	20	3.56E-22	75.20%
F822	WD-40 repeat protein-like	465	20	6.61E-41	94.25%
F279	Universal stress protein family protein	596	20	1.86E-47	87.75%
F883	Universal stress protein family protein	595	20	7.51E-47	87.35%
F197	Sugar transport protein 14	447	20	1.47E-56	87.50%
F277	Sugar transport protein 14	447	20	1.47E-56	87.50%
F303	Sugar transport protein 14	372	20	3.10E-57	86.25%
F304	Sugar transport protein 14	567	20	6.63E-81	85.25%

Table S1. *Cont.*

Seq. Name	Seq. Description	Length	#Hits	E-value	Similarity
F354	Sugar transport protein 14	447	20	1.47E-56	87.50%
F573	Sugar transport protein 14	567	20	6.63E-81	85.25%
F647	Sugar transport protein 14	568	20	6.63E-81	85.25%
F1197	Sugar transport protein	606	20	1.94E-97	82.50%
F477	Sugar transport protein	251	20	9.39E-17	86.80%
F905	Sugar transport protein	501	20	1.08E-78	83.50%
F960	Sexual differentiation process protein isp4-like	840	20	7.23E-67	83.80%
F1234	Self-incompatibility S1 family protein	440	12	1.38E-09	62.83%
F78	Self-incompatibility S1 family protein	440	12	1.38E-09	62.83%
F91	Self-incompatibility S1 family protein	441	12	1.38E-09	62.83%
F966	Seed maturation protein PM37	246	20	5.47E-26	87.90%
F465	Ribonuclease HII family protein	344	17	6.15E-18	77.24%
F666	Ribonuclease H2, subunit a	345	17	6.15E-18	77.24%
F785	Ribonuclease H2, subunit a	345	17	6.15E-18	77.24%
F1002	Receptor-like cytosolic serine threonine-protein kinase RAB1-like	244	20	4.51E-22	72.25%
F391	RAB1-like protein	689	20	2.35E-53	95.15%
F327	Protein-tyrosine-phosphatase IBR5	239	20	2.55E-29	80.05%
F503	Protein SKU5-like 11	443	20	2.06E-70	85.20%
F869	Protein RER1B	394	20	1.19E-49	88.90%
F1001	Uncharacterized protein	479	20	2.08E-36	85.60%
F1031	Uncharacterized protein	543	20	3.42E-37	58.75%
F1032	Uncharacterized protein	339	20	6.79E-52	82.15%
F1057	Uncharacterized protein	448	20	5.56E-31	86.40%
F1072	Uncharacterized protein	436	20	7.87E-17	59.65%
F1169	Uncharacterized protein	422	20	1.18E-57	77.75%
F1238	Uncharacterized protein	334	20	6.41E-17	68.45%
F269	Uncharacterized protein	424	18	6.88E-15	59.83%
F350	Uncharacterized protein	465	20	1.24E-18	74.65%
F447	Uncharacterized protein	546	20	4.16E-36	57.70%
F475	Uncharacterized protein	338	20	2.57E-51	82.65%
F586	Uncharacterized protein	548	20	4.16E-36	57.70%
F637	Uncharacterized protein	292	20	1.76E-35	90.10%
F839	Uncharacterized protein	364	14	1.54E-13	65.64%
F922	Uncharacterized protein	229	19	1.76E-08	68.47%
F972	Uncharacterized protein	393	20	2.66E-19	75.65%
F1029	Probable polyol transporter 3-like	366	20	4.43E-30	83.75%
F1415	Probable β -D-xylosidase 5-like	231	10	3.09E-15	68.20%

Table S1. *Cont.*

Seq. Name	Seq. Description	Length	#Hits	E-value	Similarity
F546	Pollen allergen Che a 1 precursor	260	20	1.67E-14	64.50%
F15	Phospholipase	248	20	7.28E-39	77.30%
F800	Pectinesterase 11	472	20	1.27E-64	75.80%
F1030	Pectate lyase-like	636	20	9.28E-26	65.35%
F18	Pectate lyase-like	489	20	5.54E-06	66.70%
F240	Pectate lyase-like	483	16	1.33E-05	64.56%
F341	Pectate lyase-like	652	20	5.51E-29	66.90%
F338	Pectate lyase family protein	847	20	2.95E-61	70.80%
F185	Pectate lyase	1235	20	1.40E-84	72.75%
F251	Pectate lyase	338	20	4.80E-21	63.75%
F339	Pectate lyase	883	20	6.66E-67	71.35%
F437	Pectate lyase	885	20	2.54E-67	71.15%
F466	Pectate lyase	1163	20	6.50E-97	73.85%
F987	Pectate lyase	487	20	5.54E-06	66.75%
F1056	Mitogen-activated protein kinase 13	573	20	2.46E-19	53.90%
F317	Magnesium transporter	427	20	4.55E-52	80.90%
F365	Lysosomal β -glucosidase-like	338	20	2.32E-46	84.10%
F481	Lysosomal β -glucosidase-like	220	20	3.03E-26	89.30%
F830	Lysosomal β -glucosidase-like	575	20	1.20E-87	80.45%
F1271	Lysine histidine transporter 1	567	20	2.10E-78	73.95%
F870	Low-temperature-induced 65 kDa protein	478	19	1.57E-27	54.37%
F111	Hypothetical protein	366	1	2.31E-04	68.00%
F1003	Hypothetical protein	638	2	1.89E-17	61.50%
F535	Hypothetical protein	637	2	1.84E-17	61.50%
F392	Hexose transporter	351	20	6.03E-33	84.50%
F843	Heat shock protein 70 kDa	282	20	4.60E-48	92.10%
F446	Glycerophosphoryl diester phosphodiesterase family protein	357	20	9.95E-30	72.75%
F1015	Glucan endo- β -glucosidase	691	20	5.72E-99	72.05%
F786	Glucan endo- β -glucosidase	251	20	1.54E-15	59.30%
F302	Gibberellin receptor	236	20	6.19E-23	67.30%
F374	Gibberellin receptor	236	20	6.19E-23	67.30%
F641	Galactose oxidase-like	361	2	3.76E-04	79.50%
F799	Galactose oxidase-like	361	2	3.76E-04	79.50%
F611	Flavanone 3-hydroxylase	798	20	0	97.00%
F65	F-box and wd40 domain protein	339	20	6.79E-52	82.15%
F248	ERD (early-responsive to dehydration stress) family protein	196	6	1.30E-06	70.17%
F1110	δ -8 sphingolipid desaturase	516	20	1.92E-52	92.70%
F396	δ -8 sphingolipid desaturase	612	20	2.29E-103	90.90%

Table S1. *Cont.*

Seq. Name	Seq. Description	Length	#Hits	E-value	Similarity
F471	Cysteine protease	246	20	1.58E-35	97.30%
F331	Copper chaperone	764	13	1.17E-23	76.69%
F418	Copper chaperone	294	13	9.18E-26	76.31%
F1019	Cell wall invertase	420	20	9.75E-50	83.65%
F425	CBS domain-containing protein CBSX5	344	8	6.11E-07	82.38%
F120	Carbonic anhydrase	380	20	7.71E-31	64.45%
F170	Carbonic anhydrase	380	20	7.71E-31	64.45%
F225	Carbonic anhydrase	357	20	4.88E-29	64.90%
F815	Carbonic anhydrase	473	20	6.71E-46	66.50%
F603	Calcium-dependent lipid-binding domain-containing protein	454	20	2.98E-36	78.70%
F1166	Ca ²⁺ -dependent membrane- binding protein annexin	212	20	1.25E-23	87.50%
F1445	β -galactosidase 7-like	342	20	5.93E-26	69.20%
F553	β -cell wall isozyme	222	20	1.75E-14	81.40%
F937	β -cell wall isozyme	221	20	1.75E-14	81.40%
F947	β -cell wall isozyme	221	20	1.75E-14	81.40%
F11	Basic form of pathogenesis -related protein 1-like	271	8	2.25E-05	61.63%
F685	Auxin-repressed protein	595	3	1.18E-09	61.67%
F731	Aquaporin NIP1-2	348	20	4.95E-21	90.75%
F896	Aquaporin NIP1-2	614	20	2.15E-113	91.05%
F499	Anther-specific protein LAT52 precursor	181	5	1.67E-06	70.80%
F250	α -glucosidase inhibitor	420	20	9.75E-50	83.65%
F636	Alpha/beta fold family protein	359	20	3.10E-53	86.45%
F965	Adenylate translocator	438	20	3.83E-25	94.05%
F519	Actin 3	692	20	4.47E-134	99.50%
F1127	Actin	692	20	4.47E-134	99.50%
F719	Actin	692	20	4.47E-134	99.50%
F938	Acid phosphatase 1	590	20	8.19E-97	77.30%
F1292	Acetyl-synthetase	594	20	1.16E-99	96.00%
F667	Acetyl-synthetase	593	20	6.70E-99	95.05%
F530	Abhydrolase domain	296	20	7.87E-36	80.50%
F242	40s ribosomal protein S17	524	20	3.86E-55	95.25%
F13	Uncharacterized protein	247	20	1.47E-26	89.80%