Supplementary Table S1. Primers used for qRT PCR and screening of SSH library

Gene name	**Primer pair F/R (5’-3’)**
Reference gene	
Actin (*ScACT*) (JS807771)	*F* 5’-GAGAGGTTACATGTTCACCAC-3’ *R* 5’-CTGATATCCACATCACACTTC-3’
Candidate genes [a]	
γ-glutamylcysteine synthetase (*ScCAD2*) (JS807772)	*F* 5’-GAYATGACAGCTGACTGGAC-3’ *R* 5’-TGTCCCCAYTYTCCATKGT-3’
Heavy metal translocating P-type ATPase (*ScHMA1*) (JS807773)	*F* 5’-GCATTAGCWRMWGCTGATATTGG-3’ *R* 5’-CATCWGCAAGAACRGCTGCCCAA-3’
Metallothionein (*ScMT2B*) (JS807774)	*F* 5’-TGCAAGAKGTACCCTGACHTG-3’ *R* 5’-TCATTTRCARGTGCADGGRTRGCA-3’
Metallothionein (*ScMT3*) (JS807775)	*F* 5’-ATGTCTAGCAMCTGCGRCA-3’ *R* 5’-GTGCAGKTRGTGCARGTGCA-3’
Metal tolerance protein (*ScMTP1*) (JS807776)	*F* 5’-CTGGTGAACATCATAATGGCT-3’ *R* 5’-GCAGATCAGATCAATTATCTTCC-3’
O-acetylserine lyase (*ScOASA1*) (JS807777)	*F* 5’-AGAGTGTCCTGATTGAGCC-3’ *R* 5’-GCACTTTCAACCGGTTCTAC-3’
Phytochelatin synthase 1 (*ScPCS1*) (JS807778)	*F* 5’-TGTMRGGAAACWTGYGTGAAATG-3’ *R* 5’-GAAGGAACCAGCACATCAA-3’
Phytochelatin synthase 2 (*ScPCS2*) (JS807779)	*F* 5’-TGTMRGGAAACWTGYGTGAAATG-3’ *R* 5’-TCTTTGATMCCWGACCACGT-3’
Serine-o-acetyl transferase (*ScSAT1*) (JS807780)	*F* 5’-GACGGWGTGTTGATTGGAGC-3’ *R* 5’-ATATAATCTGACCATCVGAKATA-3’
Zrt-Irt-like protein (*ScZIP6*) (JS807781)	*F* 5’-GGCTCTGTTGGTTGATTTA-3’ *R* 5’-GCAATGCAGCCGCCAAGA-3’
SSH library genes [b]	
Cell wall-associated kinase-like (*ScWAKL1*)	*F* 5’-CAAGGGACTTTAGGCTACTTGGA-3’ *R* 5’-TCCCCTAACAAGTATTCCGTCT-3’
Heavy metal-associated domain-containing protein (*ScHMAD1*)	*F* 5’-ACAAAATACTGCTATACCCAC-3’ *R* 5’-CTTGATGTCGTAGCCTTCTC-3’-3’
Metallothionein (*ScMT2A*)	*F* 5’-ACATACCGCATCCATTGC-3’ *R* 5’-TCAGTTTCCAAGTAAAATCCC-3’
Mitochondrial copper transporter (*ScMCT1*)	*F* 5’-CAAAAAATAGTGCTCAGGGTGCAG-3’ *R* 5’-TGCCCAACTTTCTTCCTCAACCT-3’
Pectin methylesterase (*ScPME1*)	*F* 5’-TGTCCAGACATGGCTTAGCGCT-3’ *R* 5’-CTCCCATCCCTGGCCACCAC-3’
Polyphenol oxidase (*ScPPO3*)	*F* 5’-GATTGGCTTAATGCCTCATTC-3’ *R* 5’-CTGCTTTTTGCTTCTCGATTTC-3’
Predicted expressed membrane protein (*ScPMP1*)	*F* 5’-GCCAACAATAGCAGAAAGGATAG-3’ *R* 5’-CTCAGGGTTTCACTAAGTCGCT-3’
Rapid alkalinisation factor-like (*ScRALFL1*) [c]	*F* 5’-TCAGCGATATTGCGTGGCTCCAC-3’ *R* 5’-TCAAGATCCACTCGATCCAGC-3’
Thaumatin/Osmotin-like protein 21 (*ScTOL21*)	*F* 5’-GACCCTGTACCGCTACCATCG-3’ *R* 5’-AGGCAGCCAACTTTGAAATCC-3’
Thylakoid membrane phosphoprotein (*ScTMP14*)	*F* 5’-GAAGATAGCTCGCAATGTTATG-3’ *R* 5’-CAATCTCAAAAACCCCAGGAATC-3’
Primers for differential screening	
M13	*F* 5’-GTAAAACGACGGCCAGT-3’ [d] *R* 5’-CAGGAAACAGCTATGAC-3’

[a] Primers were designed as degenerate using D=A/G/T; H=A/C/T; K=G/T; M=A/C; R=A/G; V=A/C/G; W=A/T; Y=C/T

[b] Primers specific for the *S. caprea* genes identified in the SSH library screening

[c] Reverse primer located in 3’UTR region which was obtained by 3’RACE from the initial SSH library fragment

[d] M13-F was used for sequencing the inserts of the selected clones

Supplementary Table S2. Full list of ESTs identified from a Zn+Cd induced *S. caprea* KH21 suppression subtractive hybridization (SSH) library. Genes selected for qRT-PCR are marked bold. Only one representative of the 120 cDNAs encoding the partial ScRALFL ortholog is listed (M-E-H5).

#	**Name (bold: selected for qPCR)**	**Accession No.**	**Best hit in Populus Phyozome BLAST**	**Chromosomal Position in Populus (Phytozome)**	**Best hit in NCBI BLAST** (grey: hit to full genome only)	**Identical to** (grey: only domains shared)	**GO_biological process**	**Putative function**
1	M-E-A2	JK747487	POPTR_0007s05960	scaffold 7	XM_002309957.1		Photosynthesis	**Cytochrome P450** CYP2 subfamily
2	M-E-A5	JK747488	POPTR_0002s24070	scaffold 2	XM_002302988.1	G-3-C5	Photosynthesis	**Photosystem I reaction centre subunit XI**
3	M-E-A7	JK747489	POPTR_0005s15660	scaffold 5	EF148461.1	MT-B-2, MT-B-3, M-E-B11, M-2-D6, M-14-A7, M-16-D9, G-3-H10	Carbon fixation	**Rubisco** (Ribulose bisphosphate carboxylase, small chain)
4	M-E-A8	JK747490	POPTR_0002s19710	scaffold 2	XM_002302728	M-20-B8	Carbon fixation	**CP12 domain-containing protein**
5	M-E-A11	JK747491	POPTR_0017s13120	scaffold 17	AC212848	M-E-C10, M-7-E8	Kinase activity (molecular function)	**Serine/threonine kinase**
6	M-E-A12	JK747492	POPTR_0554s00210	scaffold 554	XM_002324086.1		Predicted protein of unknown function	**Unknown**
7	M-E-B6	JK747493	POPTR_0008s03550	scaffold 8	XM_002311039.1		Protein transport	**Vacuolar protein-sorting protein 33-homolog** (VPS33) (ortholog of At3g54860)
8	M-E-B11	JK747494	POPTR_0004s09910	scaffold 4	EF148461.1	MT-B-2, MT-B-3, M-E-A7, M-2-D6, M-14-A7, M-16-D9, G-3-H10	Carbon fixation	**Rubisco** (Ribulose bisphosphate carboxylase)
9	M-E-B12	JK747495	POPTR_0019s15200	scaffold 19	XM_002325597.1		Regulation of protein metabolism	**Ubiquitin conjugating enzyme E2**
10	**M-E-C5**	JK747496	POPTR_0014s14720	scaffold 14	CU224046.1	M-6-D7, G-1-H7	Cell wall modification	**Pectinesterase** (*PME*)
11	**M-E-C10**	JK747484	POPTR_0004s20330	scaffold 4	XM_002328164.1	M-E-A11, M-7-E8	Kinase activity (molecular function)	**Wall Associated Serine/Threonine kinase** (*WAKL*)
12	M-E-D7	JK747497	POPTR_0007s09630	scaffold 7	CU232059.1		Energy homeostasis	**Oxidoreductase**
13	M-E-E8	JK747498	POPTR_0010s20810	scaffold 10	XM_002315174.1		Carbon fixation	**Rubisco activase**
14	M-E-E9	JK747499	-	scaffold 1	AC208048.1		Predicted protein of unknown function	**Chloroplast Protein**
15	M-E-E12	JK747500	POPTR_0016s12420	scaffold 16	EF145076.1		Regulation of transcription	**PHD finger family protein**
16	M-E-F2	JK747501	POPTR_0010s16330	scafold 10	XM_002314957.1		Amino acid metabolism	**S-Adenosylmethionine Synthetase** (*SAM*)
17	M-E-F4	JK747485	POPTR_0017s13220	scaffold 17	CU223227.1		Signaling	**Rapid alkalinization factor 4**
18	M-E-F11	JK747502	POPTR_0015s07340	scaffold 15	EF148354.1	M-E-H7, C-2-G1, G-1-C12	Photosynthesis	**Chlorophyll a/b binding protein**
19	M-E-G3a	JK747503	POPTR_0011s04710	scaffold 11	AY665682.1	M-E-H9	Oxidation-reduction process	**Polyphenol oxidase** (*PPO3*)
20	M-E-G3b	JK747504	POPTR_0005s22780	scaffold 5	GU282643.1		Photosynthesis	**Photosystem 2 family protein**
21	**M-E-H5**	JK747486	POPTR_0554s00210	scaffold 554	XM_002324086.1		Signaling	**Rapid alkalinization factor-like** (*RALFL*)
22	M-E-H6	JK747505	POPTR_0005s21750	scaffold 5	XM_002306680.1		Oxidation-reduction process	**Peroxidase** (*POD*)
23	M-E-H7	JK747506	POPTR_0015s07340	scaffold 5	EF148354.1	M-E-F11, C-2-G1, G-1-C12	Photosynthesis	**Chlorophyll a/b binding protein**
24	**M-E-H9**	JK747507	POPTR_0011s04710	scaffold 11	XM_002316596.1	M-E-G3	Oxidation-reduction process	**Polyphenol oxidase**
25	MT-A-7	JK747508	POPTR_0005s27550	scaffold 5	XM_002307770.1	M-4-D3	Glycolysis	**Glyceraldehyde-3-phosphate dehydrogenase**
26	MT-B-2	JK747509	POPTR_0005s15660	scaffold 5	EF148627.1	M-E-A7, M-E-B11, MT-B-3, M-2-D6, M-14-A7, M-16-D9, G-3-H10	Carbon fixation	**Rubisco** (beginning)
27	MT-B-3	JK747510	POPTR_0005s15660	scaffold 5	XM_002329248.1	M-E-A7, M-E-B11, MT-B-2, M-2-D6, G-3-H10	Carbon fixation	**Rubisco** (end)
28	M-1-C6	JK747511	POPTR_0004s20960	scaffold 4	CU226848.1		Photosynthesis	**Photosystem I subunit O**
29	M-1-C10	JK747512	POPTR_0015s10770	scaffold 15	XM_002321667.1		Development	**Mitochondrial/chloroplast 50S ribosomal protein L21**
30	M-1-F4	JK747513	POPTR_0010s05210	scaffold 10	XM_002315654.1		Predicted protein of unknown function	**Unknown protein**
31	M-1-F7a	JK747514	POPTR_0004s05920	scaffold 4	XM_002305694.1		Regulation of transcription and unknown	**Transcription factor WRKY65**
32	M-1-F7b	JK747515	POPTR_1046s00010	scaffold 1046	AP008956.1		Predicted protein of unknown function	**Unknown protein**
33	M-2-D5a	JK747516	POPTR_0009s08370	scaffold 9	XM_002313175.1	M-2-E8, M-8-F11	Regulation of transcription	**PB1 domain-containing protein** (*A. thaliana* octicosapeptide/Phox/Bem1p (PB1) domain-containing protein)
34	M-2-D5b	JK747517	POPTR_0010s16030	scaffold 10	CU227229.1		Signaling	**Stress-responsive A/B barrel domain-containing protein**
35	M-2-D6a	JK747518	POPTR_0006s02750	scaffold 6	XM_002307900.1		Signaling	**Calmodulin**
36	M-2-D6b	JK747519	POPTR_0005s15660	scaffold 5	XM_002329248.1	M-E-A7, M-E-B11, MT-B-2, MT-B-3, M-14-A7, M-16-D9, G-3-H10	Carbon fixation	**Rubisco**
37	M-2-E8a	JK747520	POPTR_0009s08370	scaffold 9	XM_002313175.1	M-2-D5, M-8-F11	Regulation of transcription	**PB1 domain-containing protein** (*A. thaliana* octicosapeptide/Phox/Bem1p (PB1) domain-containing protein)
38	M-2-E8b	JK747521	POPTR_0010s16100	scaffold 10	XM_002314940.1		Signaling	**Stress-responsive A/B barrel domain-containing**
39	M-2-G1	JK747522	-	-	GQ245470.1		Translation	**Salix viminalis tRNA from chloroplast**
40	**M-3-A2**	JK747523	POPTR_0014s10200	scaffold 14	XM_002320200.1	M-16-B5, M-17-G12, C-1-C9, C-3-C12, C-4-A10, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein** (*TMP14*)
41	M-4-C7	JK747524	-	scaffold 12	AC149575.1		no hit	no hit
42	M-4-D3	JK747525	POPTR_0014s13660	scaffold 14	XM_002321029.1	MT-A-7	Glycolysis	**Glyceraldehyde-3-phosphate dehydrogenase**
43	M-4-D4	JK747526	POPTR_0010s05530	scaffold 10	XM_002315639.1	M-4-D7, M-5-D2, C-1-A12, C-1-C5, C-5-H3	Amino acid metabolism	**Alanine aminotransferase**
44	M-4-D6	JK747527	-	scaffold 9	AJ849558.1	M-12-A6, M-17-D8	Translation	**Salix babylonica chloroplast partial tRNA-Leu gene**
45	M-4-D7	JK747528	POPTR_0010s05530	scaffold 10	CU226008.1	M-4-D4, M-5-D2, C-1-A12, C-1-C5, C-5-H3	Amino acid metabolism	**Alanine aminotransferase**
46	M-4-E5a	JK747529	POPTR_0002s20940	scaffold 2	XM_002320601.1		Translation	**Eukaryotic translation initiation factor 2-alpha kinase-related**
47	M-4-E5b	JK747530	POPTR_0018s02460	scaffold 18	XM_002324290.1		Kinase activity (molecular function)	**CBL-interactin protein kinase 5** (*CIPK5*)
48	M-5-D2	JK747531	POPTR_0010s05530	scaffold 10	CU226008.1	M-4-D4, M-4-D7, C-1-A12, C-1-C5, C-5-H3	Amino acid metabolism	**Alanine aminotransferase**
49	M-6-B7	JK747532	POPTR_0010s16080	scaffold 10	XM_002314943.1	C-4-H1	Unknown	**Unknown protein**
50	M-6-C3	JK747533	POPTR_0010s16640	scaffold 10	XM_002316054.1		Cell wall modification	**Glycosyl hydrolase family protein**
51	M-6-D6	JK747534	POPTR_0001s28350	scaffold 9	CU230955.1		Regulation of transcription	**Transcription factor Abd-B**, contains HOX (=homeobox) domain
52	M-6-D7	JK747535	POPTR_0014s14720	scaffold 14	EF146911.1	M-E-C5, G-1-H7	Cell wall modification	**Pectinesterase**
53	M-6-G8	JK747536	POPTR_0016s03490	scaffold 16	XM_002322582.1		Other catalytic activity	**Dual specificity protein phosphatase** (Protein-tyrosine-phosphatase; Serine/threonine specific protein phosphatase)
54	M-7-A9	JK747537	POPTR_0011s15350	scaffold 11	XM_002317013.1	M-7-H3	Oxidation-reduction process	**Fe/ascorbate family oxidoreductase**
55	M-7-C3	JK747538	POPTR_0002s19960	scaffold 2	XM_002301463.1		Translation	**Arginyl-tRNA synthetase**
56	M-7-E7	JK747539	POPTR_0018s09210	scaffold 18	XM_002324087.1		Other catalytic activity	**Nucleolar GTPase/ATPase**
57	M-7-E8	JK747540	POPTR_0017s09230	scaffold 17	XM_002316582.1	M-E-C10, M-E-A11	Kinase activity (molecular function)	**Serine-theorenine protein kinase**
58	M-7-E9	JK747541	POPTR_0003s14290	scaffold 8	AK109513.1		Kinase activity (molecular function)	**HUA enhancer 3 (HEN3) kinase** (Cyclin C-dependent kinase CDK8)
59	M-7-F9	JK747542	POPTR_0009s07490	scaffold 9	XM_002299945.1		Unknown	**RING-finger domain containing protein**
60	M-7-H2	JK747543	POPTR_0004s24210	scaffold 4	XM_002328797.1		Cell wall modification	**Pectin acetylesterase**
61	M-7-H3	JK747544	POPTR_0011s15350	scaffold 11	XM_002317013.1	M-7-A9	Oxidation-reduction process	**Fe/ascorbate family oxidoreductase**
62	M-8-D11a	JK747545	POPTR_0008s18250	scaffold 8	AB048260.1		Cell wall modification	**Pectate lyase**
63	M-8-D11b	JK747546	POPTR_0005s10760	scaffold 5	XM_002327681.1		Predicted protein of unknown function	**Expressed protein in *A. thaliana*** (At2g17695)
64	M-8-D11c	JK747547	POPTR_0001s04840	scaffold 3	AB260989.1		Oxidation-reduction process	**Peroxidase**
65	M-8-E11a	JK747548	POPTR_0007s03270	scaffold 7	XM_002310452.1		Regulation of transcription	**Populus trichocarpa MIKC mads-box transcription factor** (*MADS12*)
66	M-8-E11b	JK747549	POPTR_0007s02460	scaffold 7	FJ438462.1		Regulation of protein metabolism	**Ubiquitin and ubiquitin-like protein**
67	M-8-F10	JK747550	POPTR_0010s00640	scaffold 10	XM_002315440.1		Lipid metabolic process	**(acyl-CoA) thioesterase** family member related (HGG-motif containing)

68	M-8-F11a	JK747551	POPTR_0004s03230	scaffold 4	XM_002305609.1	M-2-D5, M-2-E8	Signaling	**Octicosapeptide/Phox/Bem1p**
69	M-8-F11b	JK747552	POPTR_0007s14350	scaffold 7	XM_002530641.1		Regulation of transcription	**Glycosylphosphatidylinositol anchor synthesis protein**
70	M-9-D6	JK747553	POPTR_0017s02580	scaffold 17	XM_002302894.1		Disease resistance	**NBS-LRR resistance-like protein**
71	M-9-D7	JK747554	POPTR_0010s20060	scaffold 8	CU225007.1		Carbohydrate metabolism	**Sedoheptulose-1,7-bisphosphatase**
72	M-9-D8	JK747555	POPTR_0016s00410	scaffold 16	XM_002329902.1		Carbohydrate metabolism	**Raffinose synthase or seed imbibition protein** Sip1
73	M-10-A12	JK747556	POPTR_0012s12820	scaffold 13	EF146768.1	M-13-D10, M-15-D8, C-4-G10	Photosynthesis	**Photosystem II protein D1**
74	M-10-D2	JK747557	POPTR_0015s01610	scaffold 15	XM_002321963.1		Cell wall modification	**Pectin methylesterase**
75	M-10-D8	JK747558	POPTR_0010s00670	scaffold 10	XM_002315441.1		Regulation of transcription	**Chromatin modeling SNF5**
76	M-10-D11	JK747559	POPTR_0001s44700	scaffold 1	XM_002317549.1		no hit	**Unknown protein**
77	M-10-E4a	JK747560	POPTR_0002s03280	scaffold 2	XM_002300711.1		Regulation of protein metabolism	**26S proteasome AAA-ATPase subunit**
78	M-10-E4b	JK747561	POPTR_0001s41080	scaffold 1	CU226725.1	M-16-E8, G-1-A2, G-1-A10	Metal ion transport	**Metallothionein MT3**
79	M-10-E8	JK747562	POPTR_0001s16170	scaffold 1	XM_002326588.1		Kinase activity (molecular function)	**Leucine-rich repeat transmembrane protein kinase 1**
80	M-10-E9	JK747563	POPTR_0010s02830	scaffold 10	XM_002311780.1		Unknown	**Expressed protein in *A. thaliana*** (At3g21570)
81	M-11-C10	JK747564	POPTR_0001s41780	scaffold 1	XM_002330356.1	M-12-E2, M-13-E9, M-16-F1, G-2-H12	Photosynthesis	**Chlorophyll A-B binding protein**
82	M-12-A6	JK747565	-	scaffold 9	AJ849558.1	M-4-D6, M-17-D8	Translation	**Salix babylonica chloroplast partial tRNA-Leu gene**
83	M-12-A7	JK747566	POPTR_0003s10270	scaffold 3	XM_002303433.1		Lipid metabolic process	**acyl-CoA-binding protein**
84	M-12-E2	JK747567	POPTR_0001s41780	scaffold 1	XM_002330356.1	M-11-C10, M-13-E9, M-16-F1, G-2-H12	Photosynthesis	**Chlorophyll A-B binding protein**
85	M-12-E3	JK747568	POPTR_0003s02620	scaffold 3	XM_002327489.1		Cellular response to unfolded protein	**Unfolded protein binding**
86	M-12-G6	JK747569	POPTR_0001s14310	scaffold 1	XM_002299246.1	G-1-A7, G-3-E2	Secondary metabolism	**Naringenin chalcone synthase**
87	M-13-D9	JK747570	POPTR_0010s05210	scaffold 10	XM_002315654.1	M-16-C1	Beginning: Unknown; end: regulation of	**Plant protein 1589 of unknown function**
88	M-13-D10	JK747776	POPTR_0012s12820	scaffold 13	EF146768.1	M-10-A12, M-15-D8, C-4-G10	Photosynthesis	**Photosystem II protein D1**
89	M-13-E9	JK747571	POPTR_0001s41780	scaffold 1	XM_002330356.1	M-11-C10, M-12-E2, M-16-F1, G-2-H12	Photosynthesis	**Chlorophyll A-B binding protein**
90	M-13-F8	JK747572	POPTR_0004s15440	scaffold 4	EF147107.1		Photosynthesis	**Cytochrome b6f complex subunit** (petM)
91	M-13-H9	JK747573	-	scaffold 1	AC213083.1		Photosynthesis	**Chloroplast PSII cytochrome b559**
92	M-14-A7	JK747574	POPTR_0005s15660	scaffold 5	EF148627.1	MT-B-2, MT-B-3, M-E-A7, ,M-E-B11, M-2-D6, M-16-D9, G-3-H10	Carbon fixation	**Rubisco**
93	M-14-C10a	JK747575	POPTR_0004s01950	scaffold 4	XM_002305564.1		Disease resistance	**Pathogenesis-related protein** Bet v I family
94	M-14-C10b	JK747576	-	scaffold 4	JF937588.1		Translation	**Chloroplast 50S ribosomal protein L2**
95	**M-15-A8**	JK747577	POPTR_0006s00390	scaffold 6	XM_002307806.1		Metal ion transport	**Metal ion binding/ heavy Metal ion transporter** (COPPER TRANSPORT PROTEIN ATOX1-RELATED) (*MCT1*)
96	M-15-B9	JK747578	POPTR_0011s09360	scaffold 11	XM_002317315.1		Metal ion transport	**ABC (ATP-binding cassette) transporter**
97	M-15-C9	JK747579	POPTR_0005s18820	scaffold 5	XM_002306459.1		Regulation of protein metabolism	**Beta catenin-related armadillo reapeat containing protein**
98	M-15-D8	JK747580	POPTR_0012s12820	scaffold 13	EF146768.1	M-10-A12, M-13-D10, C-4-G10	Photosynthesis	**Photosystem II D1 protein**
99	M-15-D9	JK747581	POPTR_0002s22220	scaffold 2	XM_002301546.1	C-5-D5, C-5-E7, C-6-A4, G-3-A2, G-3-F10	Photosynthesis	**Chlorophyll a-b binding protein**
100	M-15-D12	JK747582	POPTR_0001s08410	scaffold 1	EF148007.1		Secondary metabolism	**Leucoanthocyanidin dioxygenase**
101	M-16-A1	JK747583	POPTR_0005s27330	scaffold 5	XM_002300605.1		Kinase activity (molecular function)	**Serine/threonine protein kinase**
102	M-16-A5	JK747584	POPTR_0002s21340	scaffold 2	XM_002302836.1		Lipid metabolic process	**Aspartic endopeptidase**
103	M-16-A10	JK747585	POPTR_0007s07690	scaffold 7	XM_002310613.1	G-3-F7	Regulation of protein metabolism	**Serine carboxypeptidase**
104	M-16-B5	JK747586	POPTR_0014s10200	scaffold 14	XM_002320200.1	M-3-A2, M-17-G12, C-1-C9, C-3-C12, C-4-A10, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein**
105	M-16-C1	JK747587	POPTR_0010s05210	scaffold 10	XM_002315654.1	M-13-D9	Beginning: Unknown; end: regulation of	**Plant protein 1589 of unknown function**
106	M-16-C9	JK747588	POPTR_0006s12710	scaffold 6	XM_002326158.1	C-1-A2, C-2-E3	Unknown	**Predicted membrane protein**
107	M-16-D1	JK747589	POPTR_0007s14560	scaffold 7	XM_002326158.1		Unknown	**Unknown**
108	M-16-D9a	JK747590	POPTR_0004s09910	scaffold 4	EF148461.1	For Rubisco part: MT-B-2, MT-B-3, M-E-A7, M-E-B11, M-2-D6, M-14-A7, G-3-H10	Carbon fixation	**Rubisco**
109	M-16-D9b	JK747591	POPTR_0004s01470	scaffold 4	EF148017.1		Energy homeostasis	**ATP synthase gamma chain 1**
110	M-16-E7	JK747592	POPTR_0006s19530	scaffold 6	EF145552.1		Translation	**60S ribosomal protein RL5**
111	M-16-E8	JK747593	POPTR_0001s41080	scaffold 1	CU226725.1	M-10-E4b, G-1-A2, G-1-A10	Metal ion transport	**Metallothionein MT3**
112	M-16-F1	JK747594	POPTR_0014s03400	scaffold 14	-		Photosynthesis	**Uroporphyrinogen-3 synthase**
113	M-16-F2	JK747595	POPTR_0001s41780	scaffold 1	XM_002330356.1	M-11-C10, M-12-E2, M-13-E9, G-2-H12	Photosynthesis	**Chlorophyll A-B binding protein**
114	M-16-F4	JK747596	POPTR_0013s13510	scaffold 13	XM_002330595.1		Cell wall modification	**Hydroxyproline-rich glycoprotein**
115	M-16-G4	JK747597	POPTR_0027s00440	scaffold 27	XM_002303159.1		Unknown	**Expressed protein in *A. thaliana*** (At1g15780, At1g15770)
116	M-17-D7	JK747598	POPTR_0125s00210	scaffold 125	AC212848.1		Kinase activity (molecular function)	**Serine/threonine protein kinase**
117	M-17-D8	JK747599	POPTR_0011s07340	scaffold 11	AJ849563.1	M-4-D6, M-12-A6	Unknown	**Expressed protein in *A. thaliana*** (At1g29195)
118	M-17-D11	JK747600	POPTR_0001s19170	scaffold 1	XM_002304189.1		Cytoskeleton organization	**Profilin-3 pollen allergen Hev b 8.0201**
119	M-17-D12	JK747601	POPTR_0006s05980	scaffold 6	XM_002330972.1		Unknown	**Serine-rich protein**
120	M-17-E7	JK747602	POPTR_0018s01620	scaffold 18	XM_002324820.1		Nucleic acid metabolic process (RNA)	**RNA Helicase**
121	M-17-F12	JK747603	-	scaffold 8	GU363535.1		Unknown	**Chloroplast protein**
122	M-17-G12	JK747604	POPTR_0014s10200	scaffold 14	XM_002320200.1	M-3-A2, M-16-C1, C-1-C9, C-3-C12, C-4-A10, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
123	M-19-A7	JK747605	POPTR_0015s13910	scaffold 15	XM_002321838.1		Cellular response to unfolded protein	**BCL2-associated athanogene-like protein**
124	M-19-B8	JK747606	POPTR_0019s14100	scaffold 19	XM_002325648.1		Photosynthesis	**Photosynthetic electron transfer C**
125	M-19-D4a	JK747607	POPTR_0002s06070	scaffold 2	XM_002306703.1		Development	**Protein Mei2** (essential for commitment to meiosis)
126	M-19-D4b	JK747608	POPTR_0002s21750	scaffold 2	CU225456.1		Oxidation-reduction process	**1-aminocyclopropane-1-carboxylate oxidase** (Fe(II)/ascorbate oxidase superfamily)
127	M-19-D11	JK747609	POPTR_0008s06580	scaffold 8	XM_002312111.1		Transport	**Plasma membrane intrinsic protein 1-1** (aquaporin)
128	M-19-E10	JK747610	POPTR_0010s07340	scaffold 10	CU229144.1	G-4-C2	Carbohydrate metabolism	**Beta-amylase 1** (Glycosyl hydrolase family 14)
129	M-19-F3	JK747611	POPTR_0006s13980	scaffold 6	EF148722.1		Oxidation-reduction process	**Peroxiredoxin Q** (*PrxQ*)
130	M-19-G1a	JK747612	POPTR_0006s24570	scaffold 6	XM_002308526.1		Carbon fixation	**Glycine decarboxylase**
131	M-19-G1b	JK747613	POPTR_0001s11990	scaffold 1	EF148743.1		Unknown	**Unknown**
132	M-20-B6	JK747614	POPTR_0001s12220	scaffold 1	GU363535.1		Photosynthesis	**Chloroplast Protein**
133	M-20-B7	JK747615	-	scaffold 18	EF145515.1		no hit	**Unknown**
134	M-20-B8	JK747616	POPTR_0014s11580	scaffold 14	CU224938.1	M-E-A8	Carbon fixation	**CP12 domain-containing protein**
135	C-1-A2	JK747617	POPTR_0005s10030	scaffold 5	EF148057.1	M-16-C9, C-2-E3	Unknown	**Expressed protein in *A. thaliana*** (At1g16520) located in plasma membrane
136	C-1-A3	JK747618	POPTR_0107s00220	scaffold 107	EF146768.1	C-1-C12, C-6-E9	Photosynthesis	**Photosystem II PsbA protein** (PSBA)
137	C-1-A4	JK747619	POPTR_0019s09140	scaffold 19	EF148726.1		Photosynthesis	**Chlorophyll A/B binding protein CP26**
138	C-1-A6	JK747620	POPTR_0014s17070	scaffold 14	EF148813.1		Photosynthesis	**Chlorophyll A/B binding protein**
139	C-1-A12	JK747621	POPTR_0010s05530	scaffold 10	CU226008.1	M-4-D4, M-4-D7, M-5-D2, C-1-C5, C-5-H3	Amino acid metabolism	**Alanine aminotransferase**
140	C-1-C5	JK747622	POPTR_0010s05530	scaffold 10	CU226008.1	M-4-D4, M-4-D7, M-5-D2, C-1-A12, C-5-H3	Amino acid metabolism	**Alanine aminotransferase**
141	C-1-C6	JK747623	POPTR_0005s11030	scaffold 5	EF147096.1		Signaling	**Protein phosphatase 2C/pyruvate dehydrogenase** (*KAPP*)
142	C-1-C9	JK747624	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-C1, M-17-G12, C-3-C12, C-4-A10, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
143	C-1-C12	JK747625	POPTR_0107s00220	scaffold 107	EF146768.1	C-1-A3, C-6-E9	Photosynthesis	**Photosystem II PsbA protein** (PSBA)
144	C-1-F4	JK747626	POPTR_0014s02300	scaffold 14	AC217034.1		Amino acid metabolism	**L-asparaginase** (ortholog of At3g16150)

145	**C-2-C9**	JK747627	POPTR_0001s09030	scaffold 1	XM_002299511.1	G-3-C11	Disease resistance	**Protein P21; Thaumatin- or osmotin-like protein** (*TOL21*)
146	C-2-E2	JK747628	POPTR_0002s10640	scaffold 2	BT034242.1		Cellular nitrogen compound metabolism	**Argininosuccinat lyase**
147	**C-2-E3**	JK747629	POPTR_0019s13860	scaffold 19	XM_002314845.1	M-16-C9, C-1-A2	Unknown	**Predicted expressed membrane protein** (At1g25520, At1g68650)
148	C-2-F4	JK747630	POPTR_0009s15560	scaffold 9	AM483989.2		Other catalytic activity	**Aldehyde oxidase 3; Xanthin dehydrogenase**
149	C-2-F8	JK747631	POPTR_0014s02400	scaffold 14	-		Nucleic acid metabolic process (DNA)	**Nuclear receptor binding protein-related**
150	C-2-F9	JK747632	POPTR_0009s12710	scaffold 9	EF147567.1		Glycolysis	**Fructose biphosphate aldolase**
151	C-2-F11	JK747633	POPTR_0010s22970	scaffold 10	XM_002315268.1		Other catalytic activity	**N-acetyltransferase**
152	C-2-G1	JK747634	POPTR_0015s07340	scaffold 15	EF148354.1	M-E-F11, M-E-H7, G-1-C12	Photosynthesis	**Chlorophyll A/B binding protein**
153	C-2-G6	JK747635	POPTR_0004s18570	scaffold 4	EF146997.1		Other catalytic activity	**UDP-glucuronosyl/glucosyl transferase**
154	C-2-H12	JK747636	POPTR_0019s13710	scaffold 19	XM_002329362.1		Protein binding	**Ankyrin-repeat contaning protein**
155	C-3-A1	JK747637	POPTR_0011s14870	scaffold 11	XM_002317598.1		Protein transport	**Predicted membrane protein**
156	C-3-A4	JK747638	POPTR_0014s11190	scaffold 14	XM_002320240.1		Photosynthesis	**Pentatricopeptide repeat-containing protein**; cytochrome c heme binding site; electron transporter activity
157	C-3-A5	JK747639	POPTR_0001s23950	scaffold 1	XM_002330871.1		Unknown	**Hypothetical protein**
158	**C-3-A12a**	JK747640	POPTR_0003s00500	scaffold 10	XM_002299837.1		Metal ion transport	**Metallothionein** (*MT2A*)
159	C-3-A12b	JK747641	POPTR_0001s24660	scaffold 1	JN872551.1		Energy homeostasis	**Cytochrome C oxidase subunit**
160	C-3-C12	JK747642	POPTR_0014s10200	scaffold 14	XM_002320200.1	M-3-A2, M-16-B5, M-17-G12, C-1-C9, C-4-A10, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
161	C-3-D9	JK747643	POPTR_0004s08380	scaffold 4	XM_002305849.1	G-5-E1	Cellular nitrogen compound metabolism	**Glutamine synthetase** (glutamine-ammonia ligase)
162	C-3-E9	JK747644	POPTR_0016s13210	scaffold 16	EF144186.1		Translation	**40S ribosomal protein S4**
163	C-3-F9	JK747645	POPTR_0001s33990	scaffold 1	XM_002298578.1		Unknown	**Expressed protein in *A. thaliana*** (At3g01860)
164	C-3-F12	JK747646	POPTR_0006s28990	scaffold 6	XM_002330768.1		Energy homeostasis	**Plasma membrane H+ ATPase**
165	C-3-G9	JK747647	POPTR_0008s10060	scaffold 8	XM_002312271.1		Nucleic acid metabolic process (RNA)	**RNA binding protein**
166	C-3-H7	JK747648	POPTR_0006s11140	scaffold 6	EF146078.1		Regulation of protein metabolism	**20S proteasome regulatory subunit alpha**
167	C-4-A2	JK747649	POPTR_0004s16860	scaffold 4	XM_002313727.1		Regulation of transcription	**Zinc finger transcription factor** (GATA-4/5/6)
168	C-4-A9	JK747650	POPTR_0009s02250	scaffold 9	XM_002313462.1		Regulation of transcription	**MEIS1 transcription factor** (contains homeobox (HOX) domain)
169	C-4-A10	JK747651	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-B5, M-17-G12, C-1-C9, C-3-C12, C-5-D2,C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
170	C-4-B2a	JK747652	POPTR_0001s41410	scaffold 1	XM_002329113.1		Unknown	**Expressed protein in *A. thaliana*** (At4g27435, At3g15480, At1g52910)
171	C-4-B2b	JK747653	POPTR_0008s04580	scaffold 8	NM_115358.4		Cytoskeleton organization	**Tonneau 1B protein phosphatase**
172	C-4-B9	JK747654	POPTR_0012s07880	scaffold 12	XM_002318602.1		Unknown	**Hypothetical protein**
173	C-4-D1	JK747655	POPTR_0002s17120	scaffold 2	XM_002301371.1		Transport	**Cyclic nucleotide gated channel 1** (*CNGC1*)
174	C-4-D9	JK747656	POPTR_0012s08320	scaffold 12	CU228754.1		Cellular nitrogen compound metabolism	**Nitrogen fixation protein** (*NIFU*)
175	C-4-G3a	JK747657	POPTR_0005s23980	scaffold 5	XM_002306781.1		Translation	**Auxin-induced protein** (*AUX28*)
176	C-4-G3b	JK747658	POPTR_0014s04310	scaffold 14	XM_002526462.1		Protein transport	**Dynamin-like protein 4**
177	C-4-G10	JK747659	POPTR_0012s12820	scaffold 13	EF146768.1	M-10-A12, M-13-D10, M-15-D8	Photosynthesis	**Photosystem II protein D1**
178	C-4-G11	JK747660	POPTR_0006s23610	scaffold 6	XM_002324161.1		Signaling	**GTP-binding regulatory protein** alpha chain 2
179	C-4-H1	JK747661	POPTR_0010s16080	scaffold 10	XM_002314944.1	M-6-B7	Unknown	**Contains a stress-responsive A/B barrel domain**
180	C-4-H3	JK747662	-	scaffold 17	X61277.1		Translation	**18S ribosomal rRNA** (mitochondrial)
181	C-5-A2	JK747663	POPTR_0007s13020	scaffold 7	XM_002310207.1		Regulation of transcription	**Centromere-binding protein** (*CBP1*)
182	C-5-B1	JK747664	POPTR_0009s05720	scaffold 9	XM_002314040.1		Photosynthesis	**Similarity to photosystem II 5 kD protein**
183	C-5-C2a	JK747665	POPTR_0001s13800	scaffold 1	CU225621.1		Photosynthesis	**Chlorophyll A/B binding protein** Lhca2-1
184	C-5-C2b	JK747666	POPTR_0004s10660	scaffold 4	EF147068.1		Other catalytic activity	**S-Adenosylmethionine decarboxylase**
185	C-5-D2	JK747667	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-B5, M-17-G12,C-1-C9, C-3-C12, C-4-A10, C- 5-G4, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
186	C-5-D5	JK747668	POPTR_0002s22220	scaffold 2	XM_002301546.1	M-15-D9, C-5-E7, C-6-A4, G-3-A2, G-3-F10	Photosynthesis	**Chlorophyll A/B binding protein Lhcb2-2**
187	C-5-E2	JK747669	POPTR_0006s14510	scaffold 6	-		Unknown	**Cupin domain containing protein**
188	C-5-E7	JK747670	POPTR_0002s22220	scaffold 2	XM_002301546.1	M-15-D9, C-5-D5, C-6-A4, G-3-A2, G-3-F10	Photosynthesis	**Chlorophyll A/B binding protein Lhcb2-2**
189	C-5-G4	JK747671	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-B5, M-17-G12,C-1-C9, C-3-C12, C-4-A10, C-5-D2, C-6-E3, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
190	C-5-G5	JK747672	POPTR_0005s02980	scaffold 5	XM_002332598.1		Protein transport	**RAB GDP dissociation inhibitor**
191	C-5-G6	JK747673	-	-	-		no hit	**Unknown**
192	C-5-H3	JK747674	POPTR_0010s05530	scaffold 10	CU226008.1	M-4-D4, M-4-D7, M-5-D2, C-1-A12, C-1-C5	Amino acid metabolism	**Alanine aminotransferase**
193	C-6-A1	JK747675	-	-	AP008956.1		no hit	no hit
194	C-6-A4	JK747676	POPTR_0002s22220	scaffold 2	XM_002301546.1	M-15-D9, C-5-D5, C-5-E7, G-3-A2, G-3-F10	Photosynthesis	**Chlorophyll A/B binding protein Lhcb2-2**
195	C-6-A11	JK747677	-	scaffold 2	EF489041.1		no hit	no hit
196	C-6-C2	JK747678	POPTR_0002s11250	scaffold 2	AY180376.1		Cytoskeleton organization	**Alpha-tubulin**
197	C-6-E1	JK747679	POPTR_0008s11140	scaffold 8	XM_002311379.1		Signaling	**Phosphatidylinositol 3- and 4-kinase family protein**
198	C-6-E3	JK747680	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-B5, M-17-G12,C-1-C9, C-3-C12, C-4-A10, C-5-D2,C-5-G4,, C-6-G2	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
199	C-6-E9	JK747681	POPTR_0107s00220	scaffold 107	EF146768.1	C-1-A3, C-1-C12	Photosynthesis	**Photosystem II PsbA protein** (PSBA)
200	C-6-F1	JK747682	POPTR_0001s34950	scaffold 1	CU231959.1		Oxidation-reduction process	**Carbonic anhydrase**
201	C-6-G1	JK747683	POPTR_0003s18380	scaffold 3	XM_002304706.1		Lipid metabolic process	**Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase**
202	C-6-G2	JK747684	POPTR_0014s10200	scaffold 14	EF148481.1	M-3-A2, M-16-B5, M-17-G12,C-1-C9, C-3-C12, C-4-A10, C-5-D2,C-5-G4, C-6-E3	Photosynthesis	**Thylakoid membrane phosphoprotein 14**
203	C-6-G3a	JK747685	POPTR_0004s03380	scaffold 4	XM_002305614.1		Protein binding	**Armadillo/beta-catenin-like repeats**
204	C-6-G3b	JK747686	POPTR_0014s15880	scaffold 14	NM_126484.4		Translation	**ELAC-related; CPZ**; 3'-tRNA processing endoribonuclease
205	C-6-G5	JK747687	POPTR_0004s03340	scaffold 4	XM_002304960.1		Protein binding	**Putative receptor-interacting protein (PRIP)**
206	C-6-H9	JK747688	POPTR_0017s14330	scaffold 17	XM_002305267.1		Development	**Late embryogenesis abundant (LEA)**
207	G-1-A2	JK747689	POPTR_0001s41080	scaffold 1	CU226725.1	M-10-E4b, M-16-E8, G-1-A10	Metal ion transport	**Metallothionein** family 15
208	G-1-A4	JK747690	POPTR_0010s00320	scaffold 10	XM_002328574.1		Signaling	**Two-component response regulator ARR2**
209	G-1-A7	JK747691	POPTR_0001s14310	scaffold 1	XM_002299246.1	M-12-G6, G-3-E2	Secondary metabolism	**Naringenin chalcone synthase**
210	G-1-A10	JK747692	POPTR_0001s41080	scaffold 1	CU226725.1	M-10-E4b, M-16-E8, G-1-A2	Metal ion transport	**Metallothionein** family 15
211	G-1-A11	JK747693	POPTR_0001s10880	scaffold 1	XM_002297931.1		Unknown	**Predicted protein**
212	G-1-A12	JK747694	POPTR_0019s05620	scaffold 19	XM_002325402.1		Amino acid transport	**Cationic amino acid transporter** (*PtrCAT3*)
213	G-1-B1	JK747695	POPTR_0003s17980	scaffold 3	XM_002303809.1		Secondary metabolism	**Cinnamoyl-CoA reductase**
214	G-1-B8	JK747696	POPTR_0013s01250	scaffold 13	CU227974.1		Drought response	**Drought-responsive family protein Di19**
215	G-1-B10	JK747697	POPTR_0002s10400	scaffold 2	XM_002302296.1		Protein binding	**Multifunctional chaperone, 14-3-3 protein**
216	G-1-C8	JK747698	POPTR_0018s02590	scaffold 18	XM_002324877.1		Signaling	**Signal transducer activity NPH3**
217	G-1-C12	JK747699	POPTR_0015s07340	scaffold 15	XM_002330091.1	M-E-F11, M-E-H7, C-2-G1	Photosynthesis	**Chlorophyll a/b binding protein**
218	**G-1-E11**	JK747700	POPTR_0016s00850	scaffold 16	EF147807.1		Metal ion transport	**Heavy-metal-associated domain-containing protein** copper transport protein ATOX1-related (*HMAD1*)
219	G-1-F11	JK747701	POPTR_0004s08380	scaffold 4	XM_002305849.1		Cellular nitrogen compound metabolism	**Glutamine synthetase**
220	G-1-H7	JK747702	POPTR_0014s14720	scaffold 14	XM_002320412.1	M-E-C5, M-6-D7	Cell wall modification	**Pectinesterase**

221	G-1-H10a	JK747703	POPTR_0012s07620	scaffold 12	AC216684.1		Regulation of transcription	**MOT2 transcription factor**; contains Zinc finger, C3HC4 type (RING finger)
222	G-1-H10b	JK747704	POPTR_0013s12690	scaffold 13	AC213156.1		Unknown	**Unknown**
223	G-1-H12	JK747705	POPTR_0004s22900	scaffold 4	AC216689.1		Regulation of protein metabolism	**Ubiquitin family protein**
224	G-2-A2	JK747706	POPTR_0016s01720	scaffold 16	XM_002338972.1		Development	**Protease inhibitor/seed storage/lipid transfer protein family**
225	G-2-B3	JK747707	POPTR_0006s04560	scaffold 6	EF147170.1		Methane metabolism	**Esterase D**
226	G-2-C3	JK747708	POPTR_0010s06190	scaffold 10	EF148588.1		Photosynthesis	**Photosystem II core complex protein** psbY
227	G-2-C9	JK747709	POPTR_0003s19210	scaffold 3	XM_002336095.1		Photosynthesis	**Prolin rich family protein**
228	G-2-D3a	JK747710	POPTR_0200s00220	scaffold 200	AC182663.2		Kinase activity (molecular function)	**Serine/threonine protein kinase**
229	G-2-D3b	JK747711	POPTR_0008s13180	scaffold 8	XM_002311481.1		Carbohydrate metabolism	**Phosphohexomutase**
230	G-2-D4	JK747712	POPTR_0017s01640	scaffold 17	XM_002305206.1		Disease resistance	**Expressed protein in *A. thaliana*** (At4g25690, At5g52550, At4g25670)
231	G-2-D8	JK747713	POPTR_0001s27320	scaffold 1	XM_002298396.1		Cell wall modification	**Cellulose synthase**
232	G-2-E7	JK747714	POPTR_0006s28640	scaffold 6	XM_002309666.1		Disease resistance	**CC-NBS-LRR Resistance Protein**
233	G-2-E8	JK747715	POPTR_0005s13330	scaffold 5	XM_002307255.1		Kinase activity (molecular function)	**Serine/threonine protein kinase, Pto-like kinase**
234	G-2-F7	JK747716	POPTR_0004s07630	scaffold 4	XM_002305882.1		Oxidation-reduction process	**Microsomal glutathione s-transferase**
235	G-2-F8	JK747717	POPTR_0015s11500	scaffold 15	XM_002321704.1		Lipid metabolic process	**Serine palmitoyltransferase**
236	G-2-H1	JK747718	POPTR_0017s04300	scaffold 7	XM_002323670.1		Unknown	**Expressed protein**
237	G-2-H4	JK747719	POPTR_0001s12390	scaffold 1	-		Unknown	**Endomembrane-associated protein**
238	G-2-H12	JK747720	POPTR_0001s41780	scaffold 1	XM_002330356.1	M-11-C10, M-12-E2, M-13-E9, M-16-F2	Photosynthesis	**Chlorophyll A-B binding protein** (Lhcb3)
239	G-3-A2	JK747721	POPTR_0002s22220	scaffold 2	XM_002301546.1	M-15-D9, C-5-D5, C-5-E7, C-6-A4, G-3-F10	Photosynthesis	**Chlorophyll A-B binding protein** Lhcb2-2
240	G-3-B2	JK747722	POPTR_0010s14740	scaffold 10	XM_002314878.1		Regulation of transcription	**Basic helix-loop-helix (bHLH) family protein**
241	G-3-B3	JK747723	POPTR_0003s16160	scaffold 3	XM_002333900.1		no hit	**Unknown**
242	G-3-C2	JK747724	POPTR_0006s01060	scaffold 6	XM_002307833.1		Photosynthesis	**Plastocyanin-like Protein**
243	G-3-C5	JK747725	POPTR_0002s24070	scaffold 2	XM_002302988.1	M-E-A5	Photosynthesis	**Photosystem I reaction center subunit XI**
244	G-3-C11	JK747726	POPTR_0001s09570	scaffold 1	XM_002299511.1	C-2-C9	Disease resistance	**Thaumatin family protein**
245	G-3-D11	JK747727	POPTR_0005s26040	scaffold 5	XM_002307686.1		Development	**Gibberellin-regulated protein** (GASA family)
246	G-3-E2	JK747728	POPTR_0001s14310	scaffold 1	XM_002299246.1	M-12-G6, G-1-A7	Secondary metabolism	**Naringenin chalcone synthase**
247	G-3-E10	JK747729	POPTR_0008s15060	scaffold 10	XM_002311580.1		Circadian rhythm	**Expressed protein**
248	G-3-F7	JK747730	POPTR_0007s13810	scaffold 7	XM_002333293.1	M-16-A10	Regulation of protein metabolism	**Serine Carboxypeptidase**
249	G-3-F10	JK747731	POPTR_0002s22220	scaffold 2	XM_002301546.1	M-15-D9, C-5-D5, C-5-E7, C-6-A4, G-3-A2	Photosynthesis	**Chlorophyll A-B binding protein** Lhcb2-2
250	G-3-G7	JK747732	-	-	AC210554.1		no hit	**Unknown**
251	G-3-H3	JK747733	POPTR_0001s15740	scaffold 1	CT028217.1		Nucleic acid metabolic process (RNA)	**RNA binding protein**
252	G-3-H5a	JK747734	POPTR_0018s12810	scaffold 18	XM_002324605.1		Protein binding	**WD-40 repeat family protein**
253	G-3-H5b	JK747735	POPTR_0016s11610	scaffold 16	XM_002322910.1		Carbohydrate metabolism	**Fructose 1,6 bisphosphatase**
254	G-3-H10	JK747736	POPTR_0004s09910	scaffold 4	CT029820.1	M-E-A7, MT-B-2, MT-B-3, M-E-B11, M-2-D6, M-14-A7, M-16-D9	Carbon fixation	**Rubisco**
255	G-4-B4	JK747737	POPTR_0009s04850	scaffold 9	XM_002314080.1		Regulation of transcription	**Zn-finger (C2H2 type) family protein**
256	G-4-C2	JK747738	POPTR_0014s07950	scaffold 14	XM_002320758.1	M-19-E10	Carbohydrate metabolism	**Glycosyl hydrolase** family 14
257	G-4-C8	JK747739	POPTR_0006s03720	scaffold 6	XM_002307936.1		Regulation of transcription	**bZIP transcription factor**
258	G-4-D3a	JK747740	POPTR_0013s07230	scaffold 13	XM_002319730.1		Other catalytic activity	**Transferase**
259	G-4-D3b	JK747741	POPTR_0013s10350	scaffold 13	XM_002327260.1		Other catalytic activity	**Phosphorylase**
260	G-4-D5	JK747742	POPTR_0015s10100	scaffold 6	XM_002334150.1		Oxidation-reduction process	**NADPH-dependent oxidoreductase**
261	G-4-D10	JK747743	POPTR_0018s01390	scaffold 18	XM_002324244.1		Unknown	**Expressed protein**
262	G-4-E2a	JK747744	POPTR_0004s09910	scaffold 4	CU228156.1		Carbon fixation	**Rubisco**
263	G-4-E2b	JK747745	-	-	-		no hit	**Mitochondrial DNA**
264	G-4-E3	JK747746	POPTR_0006s28350	scaffold 6	EF489041.1		Regulation of transcription	**CONSTANS-like protein 2**, GATA-4/5/6 transcription factors
265	G-4-E11a	JK747747	POPTR_0001s42970	scaffold 1	XM_002316979.1		Photosynthesis and unknown	**Photosystem II 10 kDa polypeptide**
266	G-4-E11b	JK747748	POPTR_0001s02570	scaffold 1	XM_002326482.1		Unknown	**Expressed protein**
267	G-4-F4	JK747749	POPTR_0019s03150	scaffold 19	XM_002325285.1	G-4-H4	Lipid metabolic process	**Ca-independent phospholipase A2**
268	G-4-G6	JK747750	POPTR_0274s00200	scaffold 274	XM_002301507.1		Amino acid metabolism	**S-Adenosylmethionine synthetase**
269	G-4-G8a	JK747751	POPTR_0007s12060	scaffold 7	XM_002310151.1		Resistance to abiotic stress	**Cold acclimation WCOR413-like protein** (stress-responsive protein in *O. sativa*)
270	G-4-G8b	JK747752	POPTR_0019s14100	scaffold 19	XM_002325648.1		Photosynthesis	**Photosynthetic electron transfer c** (plastoquinol-plastocyanin reductase)
271	G-4-G12	JK747753	POPTR_0003s02140	scaffold 3	XM_002327366.1		Unknown	**Expressed protein in *A. thaliana*** (At1g15780, At1g15770)
272	G-4-H1	JK747754	POPTR_0013s01640	scaffold 13	EF148733.1		Development	**Dormancy/auxin associated family protein**
273	G-4-H4	JK747755	POPTR_0001s25760	scaffold 1	XM_002299778.1	G-4-F4	Lipid metabolic process	**Phospholipase**
274	G-5-A6	JK747756	POPTR_0015s06060	scaffold 15	EF147148.1	G-5-D8	Regulation of protein metabolism	**Ubiquitin conjugating enzyme E2**
275	G-5-D1	JK747757	POPTR_0015s11580	scaffold 15	XM_002321706.1		Other catalytic activity	**Acyl carrier Zn finger protein**
276	G-5-D8	JK747758	POPTR_0004s18090	scaffold 4	XM_002305483.1	G-5-A6	Regulation of protein metabolism	**Ubiquitin conjugating enzyme E2**
277	G-5-E1	JK747759	POPTR_0004s08380	scaffold 4	XM_002305849.1	C-3-D9	Cellular nitrogen compound metabolism	**Glutamine synthetase**
278	G-5-E5	JK747760	POPTR_0001s06710	scaffold 1	EF145750.1		Energy homeostasis	**NADH dehydrogenase**
279	G-5-E12	JK747761	POPTR_0018s12260	scaffold 18	XM_002308339.1		Regulation of protein metabolism	**Ring finger and protease associated domain-containing**
280	G-5-F1	JK747762	POPTR_0001s24840	scaffold 1	XM_002299832.1		Regulation of transcription	**MYB transcription factor**
281	G-5-F5a	JK747763	POPTR_0003s09830	scaffold 3	CU225687.1		Photosynthesis	**Phosphoribulokinase**
282	G-5-F5b	JK747764	POPTR_0005s23590	scaffold 5	CT029295.1		Kinase activity	**Chlorophyllase**
283	G-5-F9a	JK747765	POPTR_0001s25410	scaffold 1	XM_002298294.1		Cytoskeleton organization	**Tubulin beta chain**
284	G-5-F9b	JK747766	POPTR_0008s04590	scaffold 8	XM_002311086.1		Energy homeostasis	**Adenylate kinase**
285	G-5-G5	JK747767	POPTR_0014s13710	scaffold 14	AC208048.1		Energy homeostasis	**Acyl-CoA synthetase**
286	G-5-G7	JK747768	POPTR_0002s04410	scaffold 2	XM_002302033.1		Nucleic acid metabolic process (DNA)	**Histone H1**
287	G-5-H10	JK747769	POPTR_0016s12090	scaffold 1	XM_002323530.1		Signaling	**Histidine-containing phosphotransfer protein**

Supplementary Table S3. Genes from the SSH screening selected for qPCR.

Accession No. (NCBI)	**Gene**	**Gene name**	**Biological process and/or molecular function**	**Best hit in *P. trichocarpa* [a]**	**Best hit in NCBI tBLASTx [a]**	**Found in library**
JK747484	Cell wall-associated kinase-like	*ScWAKL1*	Kinase activity	POPTR_0004s20330 (88 %, E = 2e-142)	XM_002325658.1 (100 %, E = 2e-64)	1
JK747700	Heavy metal-associated domain-containing protein	*ScHMAD1*	Metal ion transport	POPTR_0016s00850 (75 %, E = 9e-29)	EF147807.1 (72 %, E = 4e-22)	1
JK747640	Metallothionein MT2A	*ScMT2A*	Metal ion transport	POPTR_0001s24660 (83 %, E = 5e-38)	XM_002299837.1 (84 %, E = 4e-43)	1
JK747577	Mitochondrial copper transporter	*ScMCT1*	Metal ion transport	POPTR_0006s00390 (84 %, E = 9e-30)	XM_002307806.1 (81 %, E = 1e-57)	1
JK747496	Pectin methylesterase	*ScPME1*	Cell wall modification	POPTR_0014s14720 (85 %, E = 0)	CU224046.1 (85 %, E = 5e-86)	4
JK747507	Polyphenol oxidase	*ScPPO3*	Oxidation-reduction process	POPTR_0011s04710 (92 %, E = 0)	XM_002316596.1 (92 %, E = 0)	2
JK747629	Predicted transmembrane protein	*ScPMP1*	Unknown	POPTR_0019s13860 (86 %, E = 1e-86)	XM_002314845.1 (92 %, E = 9e-117)	1
JK747486	Rapid alkalinization factor-like	*ScRALFL1*	Signaling	POPTR_0125s00200 (81 %, E = 1e-80)	EF148634.1 (93 %, E = 2e-30)	120
JK747627	Thaumatin/Osmotin-like protein	*ScTOL21*	Disease resistance	POPTR_0001s09030 (89 %, E = 3e-108)	XM_002299511.1 (90 %, E = 6e-95)	2
JK747523	Thylakoid membrane phosphoprotein	*ScTMP14*	Photosynthesis	POPTR_0014s10200 (92 %, E = 4e-76)	XM_002320200.1 (93 %, E = 0)	10

[a] Values in brackets represent % homology and expectation value