

Supplementary Table S1. The 50 most highly abundant transcripts in *Arabidopsis* vegetative tissues.

SAGE Tag ID ¹	Tag sequence ²	Tag number ³		Total tags	GenBank Accession	Corresponding gene ⁴
		WT	Pti4			
1	CAGGTGTGGC	257	287	544	BE039377	putative rubisco small subunit
2	GGCCTTCGCC	245	241	486	X03909	chlorophyll a/b binding protein AB 140
3	GGAGCTGTTG	211	257	468	X64460 ⁵	photosystem II type I chlorophyll a/b binding protein
4	AAGGTGTGGC	200	146	346	BE039376	rubisco small subunit 2b
5	AGGAGAAAGA	162	182	344	T04019	putative photosystem II type I chlorophyll a /b binding protein
6	AACAAATTTG	160	157	317	M63931 ⁵	light-harvesting chlorophyll a/b binding protein
7	CTCGGAGCCC	124	162	286	X64460 ⁵	putative photosystem II type I chlorophyll a/b binding protein
8	CTTGTGATGG	155	111	266	X14212	rubisco activase
9	GCACAACAAC	110	92	202	X56062	photosystem I chlorophyll a/b binding
10	GGTTTGGTTG	98	96	194	AF134126	chlorophyll a/b binding protein Lhcb3
11	CACCTGAACG	78	75	153	AA597587	photosystem I subunit X precursor
12	TTTGCGATGC	58	62	120	AF134129	chlorophyll a/b binding protein Lhcb5
13	AGGCTTGTTT	62	54	116	AA597854	similar to chlorophyll binding protein (<i>Petunia hybrida</i>)
14	TGGCAACAGT	53	62	115	M63931 ⁵	light-harvesting chlorophyll a/b binding protein
15	GTCACCTCCTA	61	48	109	X98108.1	23 kDa polypeptide precursor psbP of oxygen-evolving complex
16	AAAGTTCTCG	41	58	99	U32176.1	photosystem I reaction centre subunit psaN precursor PSI-N
17	TTTGTACAAA	57	37	94	AF134120.1	chlorophyll a/b binding protein Lhca2
18	TGCCTCACCA	41	49	90	AF446350	similar to photosystem I subunit XI precursor (Spinach)
19	ATAGAACCTT	52	35	87	BE038487	unknown protein
20	TTCTCTATGT	55	32	87	AF134124	chlorophyll a/b binding protein Lhcb2
21	AACCCAGCCG	43	42	85	AF004393	salt stress induced tonoplast intrinsic protein
22	GCAATAGAAG	45	39	84	AJ271355	putative plastocyanin

23	TGTTTTATG	42	41	83	U01103	putative photosystem I type III chlorophyll a/b binding protein
24	TCAAATCATT	47	36	83	AV439495	similar to fructose-bisphosphate aldolase (rice)
25	TGAGATTCTA	37	45	82	X71878	chlorophyll a/b binding protein Lhcb4
26	GGATGACCAC	37	42	79	X75883	plasma membrane intrinsic protein 2a
27	AAAGCTTTCT	46	25	71	AJ245629	putative photosystem I subunit III precursor
28	ATTCGGAATG	39	30	69	T04005	putative calcium-binding protein calreticulin
29	GTTTGAAGGA	34	33	67	BE038725	similar to translationally controlled tumor protein (<i>Hevea brasiliensis</i>)
31	TTTCTATAAA	40	23	63	X55970	photosystem II 10 kDa polypeptide
32	ACCATCCATC	31	29	60	X65541	carbonic anhydrase
33	TAATGATGTA	27	32	59	AF134127	chlorophyll a/b binding protein Lhcb4.2
34	TTGAGACAAA	33	23	56	AF134131	putative photosystem II 22kDa protein
35	ACATTAAATT	20	35	55	AA720059	chlorophyll a/b binding protein CP29
36	TCCGAATCTT	22	33	55	X98313	peroxidase prxr1
37	GTGCGTTTGT	20	34	54	AV820031	putative glycine-rich protein
38	TTAATTTTTA	21	33	54	AJ245906	putative photosystem I reaction center subunit II precursor
39	AGGCAGACCG	22	31	53	X16432	EF-1 alpha-A4 gene for elongation factor 1-alpha
40	GGCCTTCGCT	26	26	52	X64459	photosystem II type I chlorophyll a/b binding protein Lhb1B1
41	ATGATGCGGC	32	20	52	AV550460	putative chlorophyll a/b binding protein
42	ATGTTTTTGA	29	21	50	AF134130	chlorophyll a/b binding protein Lhcb6
43	TGGAGTCAAT	21	28	49	AF159798	lipid transfer protein 1
44	AACACTGCTG	29	20	49	U17589	thiamine biosynthesis gene Thi1
45	AACGCACACC	29	19	48	AV532739	chloroplast PSI P700 apoprotein A2
46	GGCAGGCAAG	24	23	47	AY096798	23S ribosomal RNA coding sequence
47	GCGAAAAGGA	21	23	44	X58149	ribulose-5-phosphate kinase
48	CCTAAGATCT	23	19	42	X52428	33 kDa oxygen-evolving protein

49	AAGATGAGGA	26	16	42	T41733	photosystem II 5 KD protein
50	AGAGTTTGTA	22	19	41	AV535384	putative glyceraldehyde-3-phosphate dehydrogenase
51	TGGATCTTCT	23	18	41	X64271.1	catalase

¹The SAGE tag ID corresponding to a particular tag sequence or gene.

²The 10 bp SAGE tag sequence, excluding the 5' adjacent Nla III site (CATG).

³The number of tags of a particular sequence counted in the WT and Pti4 libraries.

⁴The gene corresponding to a particular tag. Most of the tags corresponded to annotated genes, or to ESTs with an assigned function. In the cases where the ESTs bore similarity to predicted proteins from other organisms, the name of the organism is indicated in parentheses.

⁵Tags #3 and 7 were found on the same gene and tags #6 and 14 were found on the same gene. All 4 tags corresponded to chlorophyll a/b binding genes. We believe that these tags correspond to nearly identical, independent transcripts that belong to a gene family, or could be products of alternate splicing of a single gene.