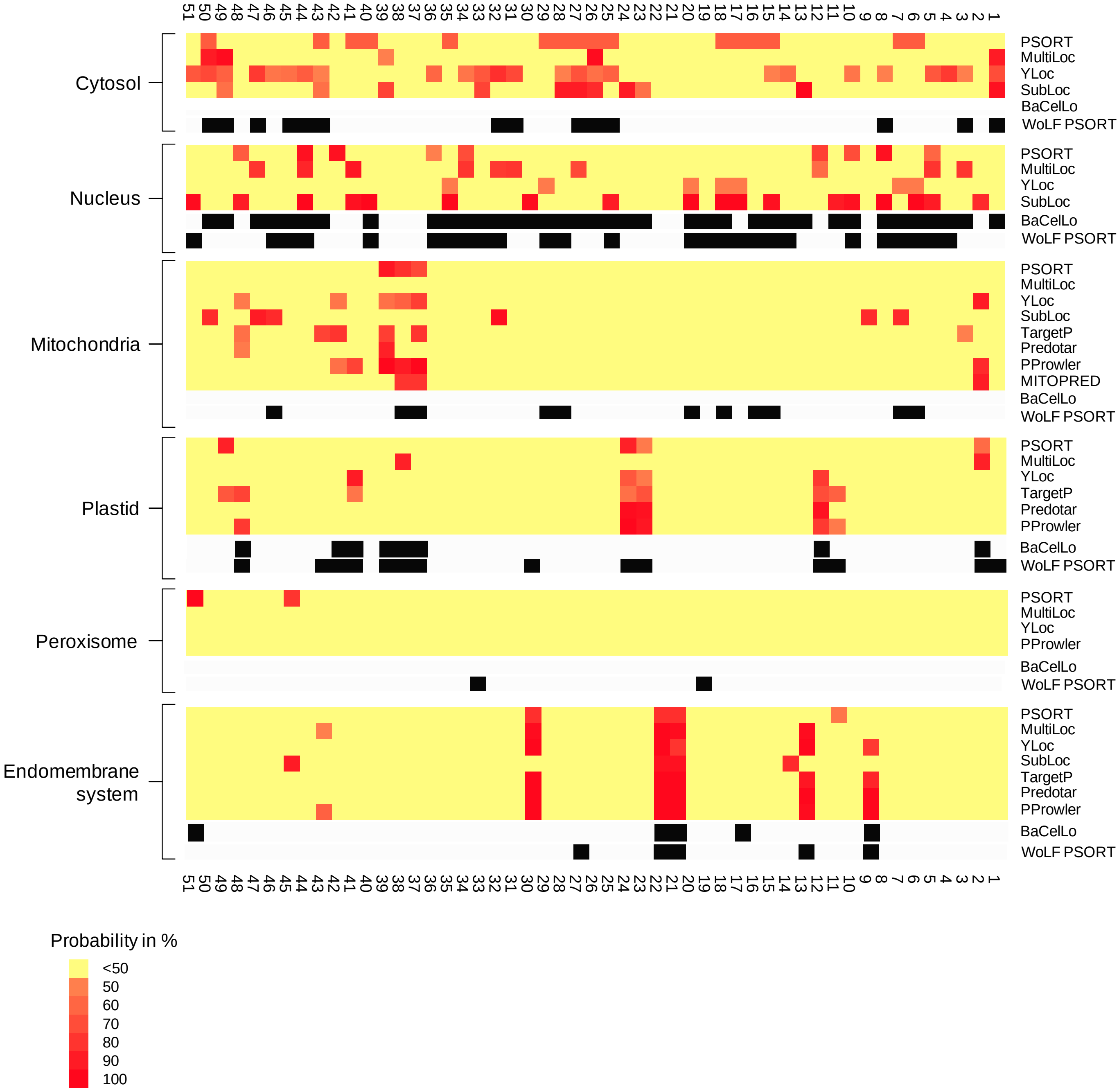
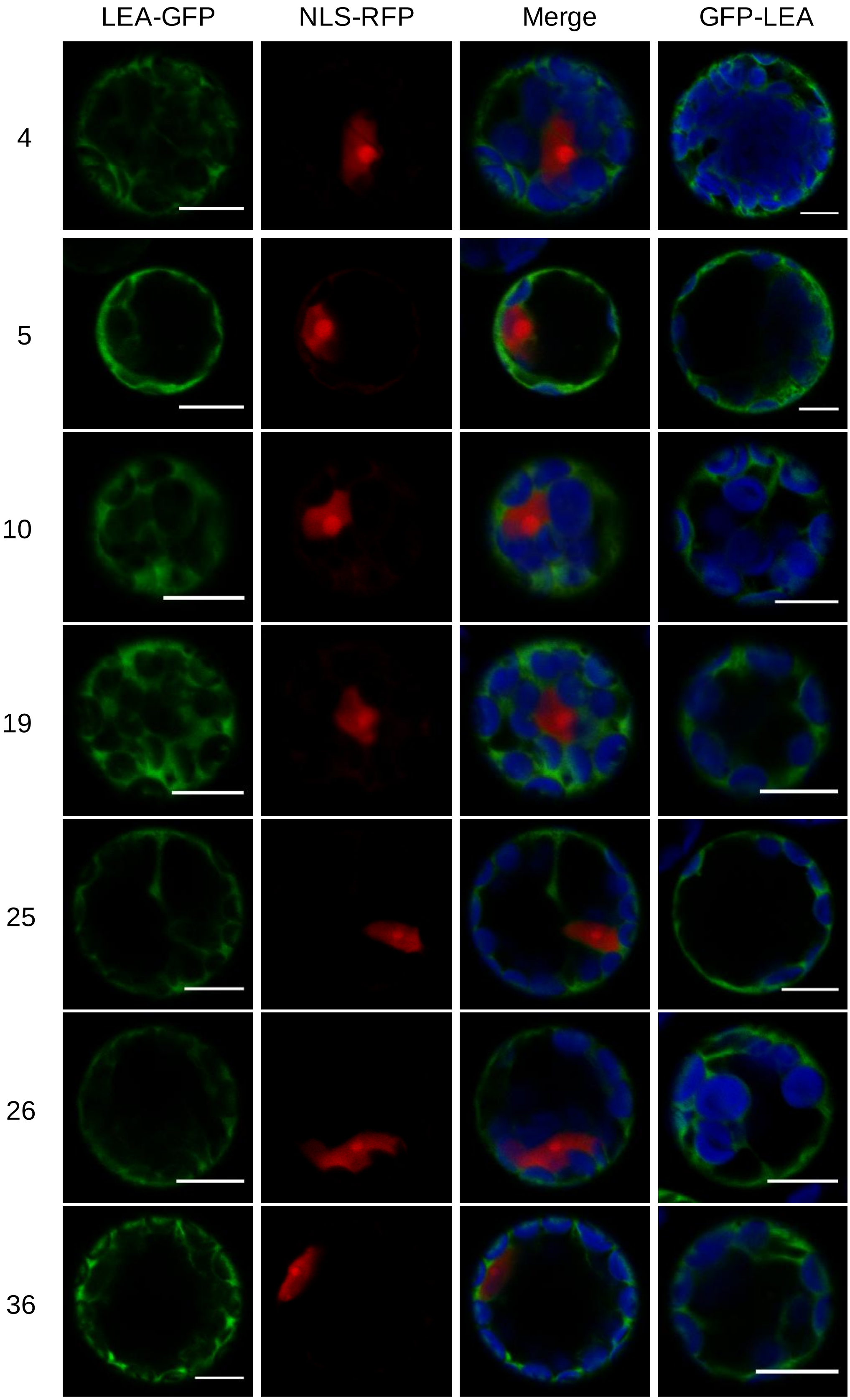
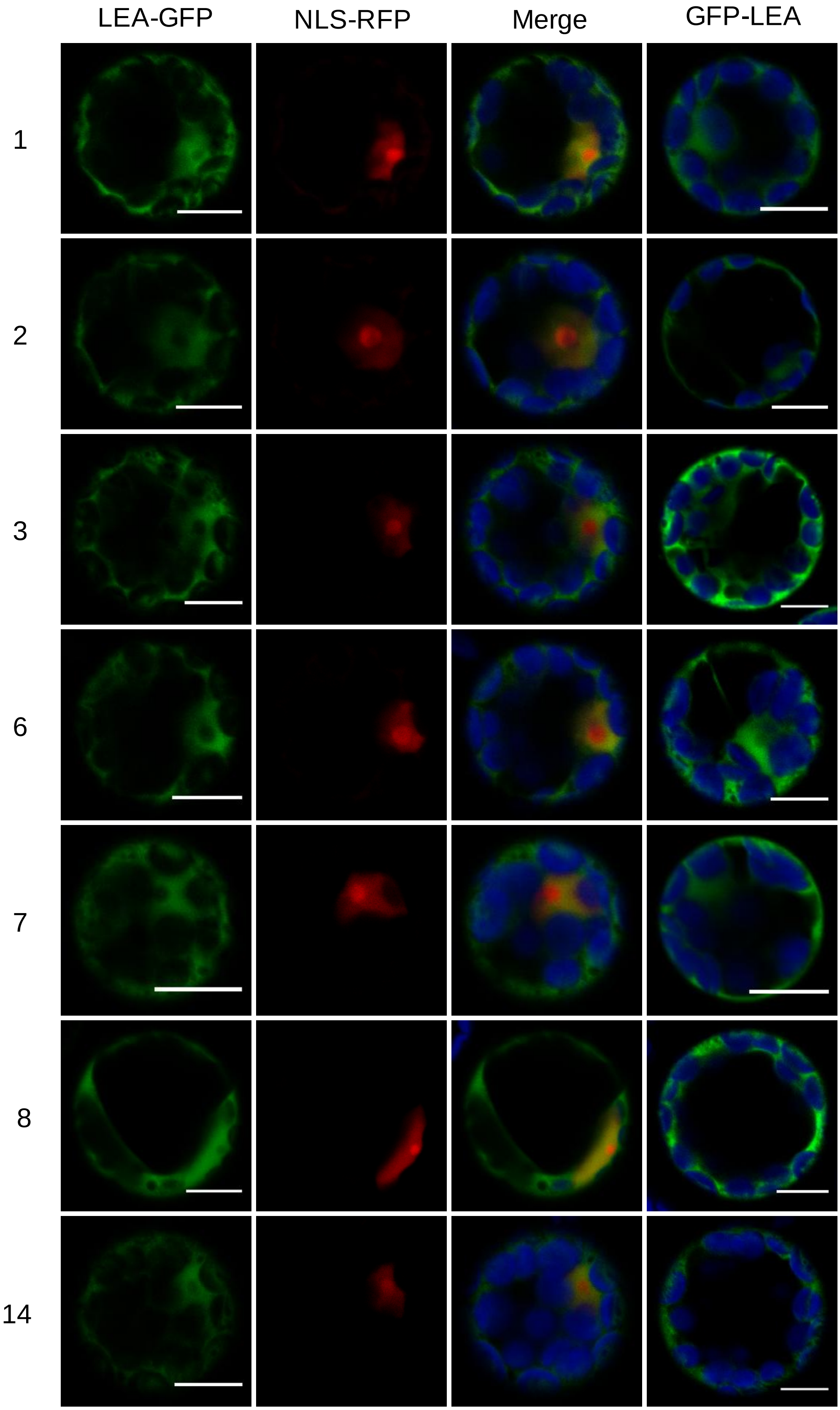


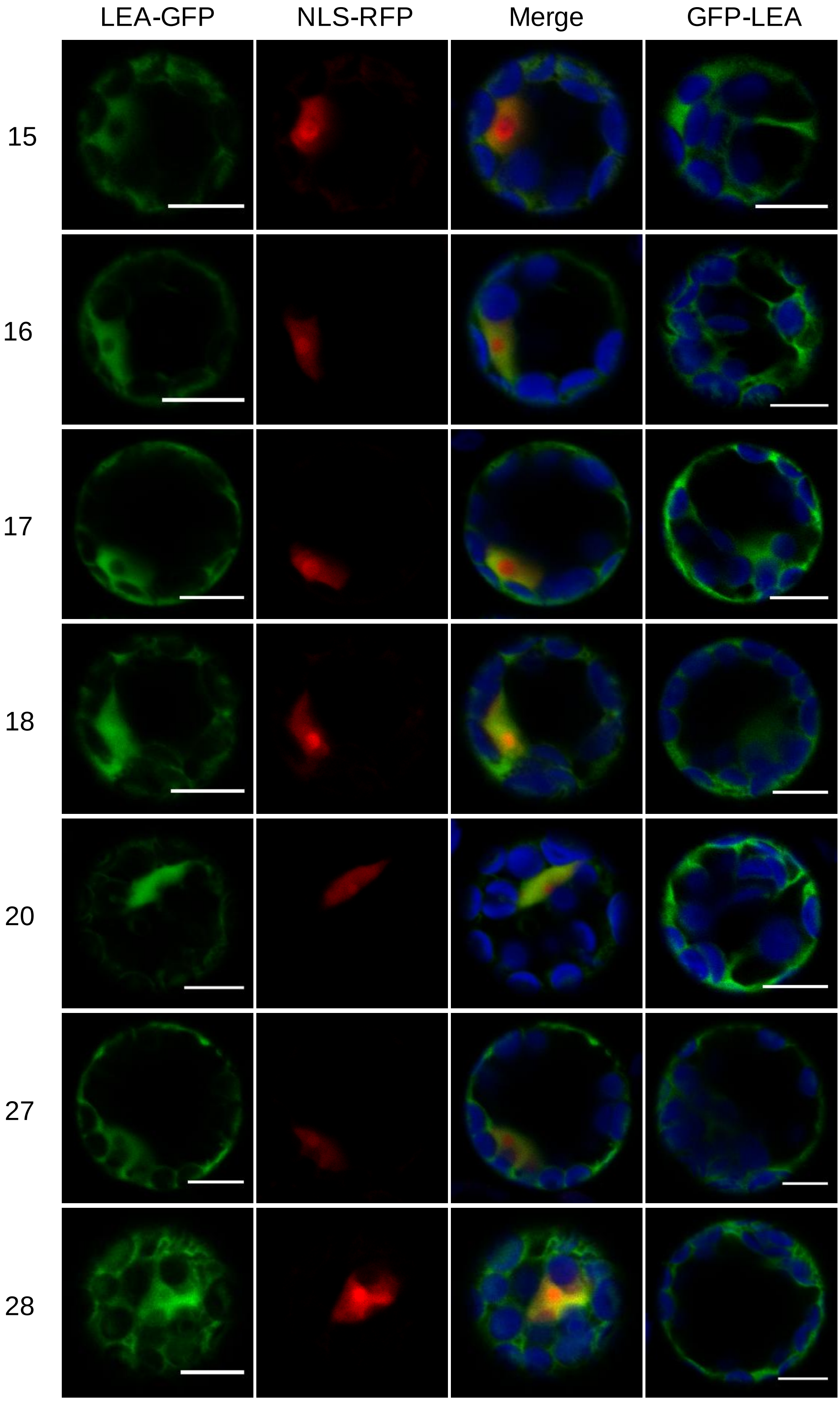
Supplemental Figure 1. Heatmap of subcellular localization predictions of the 51 Arabidopsis LEA proteins. The heatmap illustrates probability over 50 % of LEA protein targeting to various cellular compartments given by the different software indicated on the right. LEA proteins are numbered from 1 to 51, and the color coding represents the targeting probability below 50 % (yellow) or between 50 to 100% (red). The two qualitative predictors BaCelLo and WoLF PSORT were included with black square indicating a positive prediction.



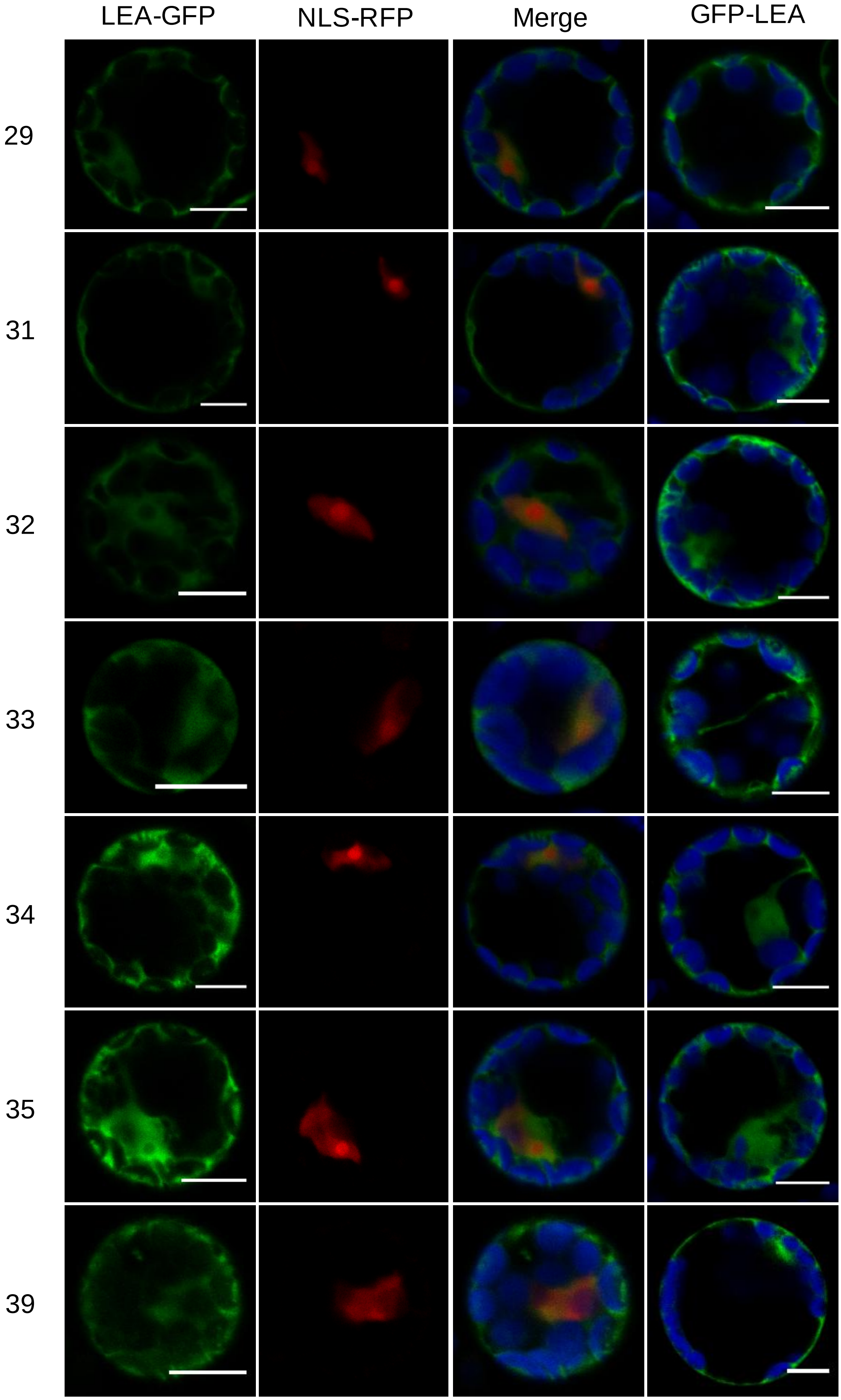
Supplemental Figure 2. Transient expression of cytosolic LEA protein in Arabidopsis protoplasts. Representative examples of LEA-GFP and GFP-LEA fusion proteins localized either in the cytosol only or both in the cytosol and the nucleus were co-expressed with a RFP nuclear marker in Arabidopsis mesophyll protoplasts. Numbers refer to the corresponding LEA proteins. Green, GFP; Red, RFP; Blue, chlorophyll. Bar = 10 µm.



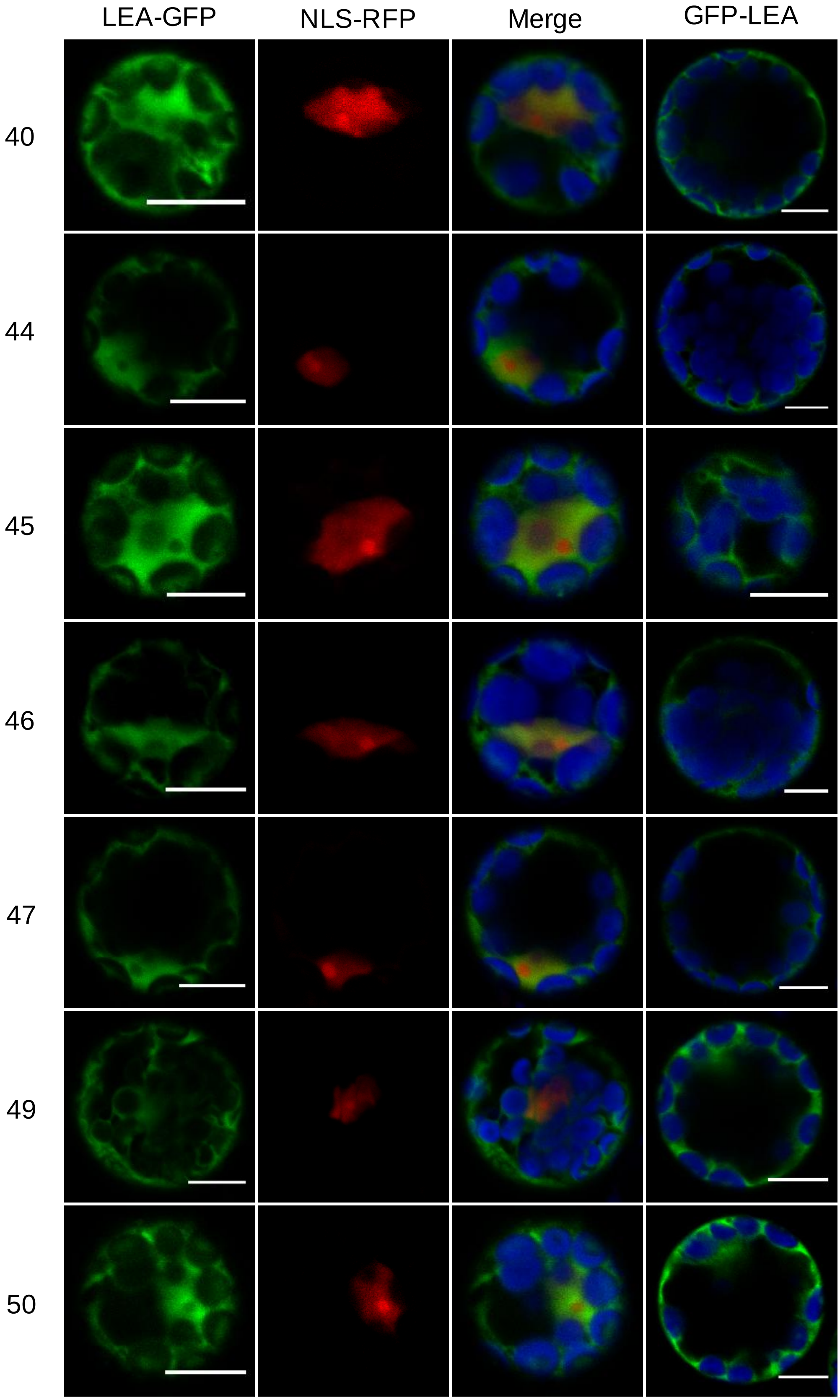
Supplemental Figure 2. (continued).



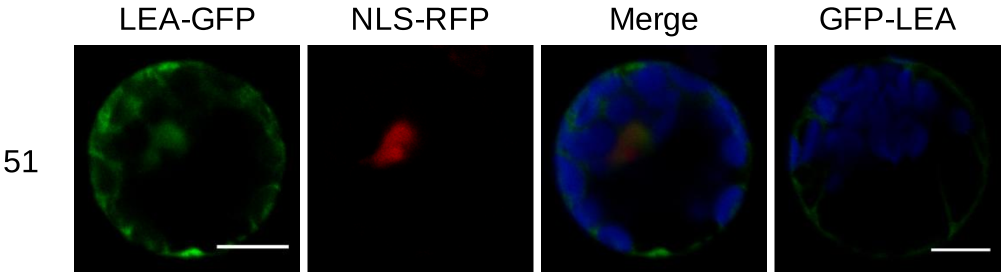
Supplemental Figure 2. (continued).



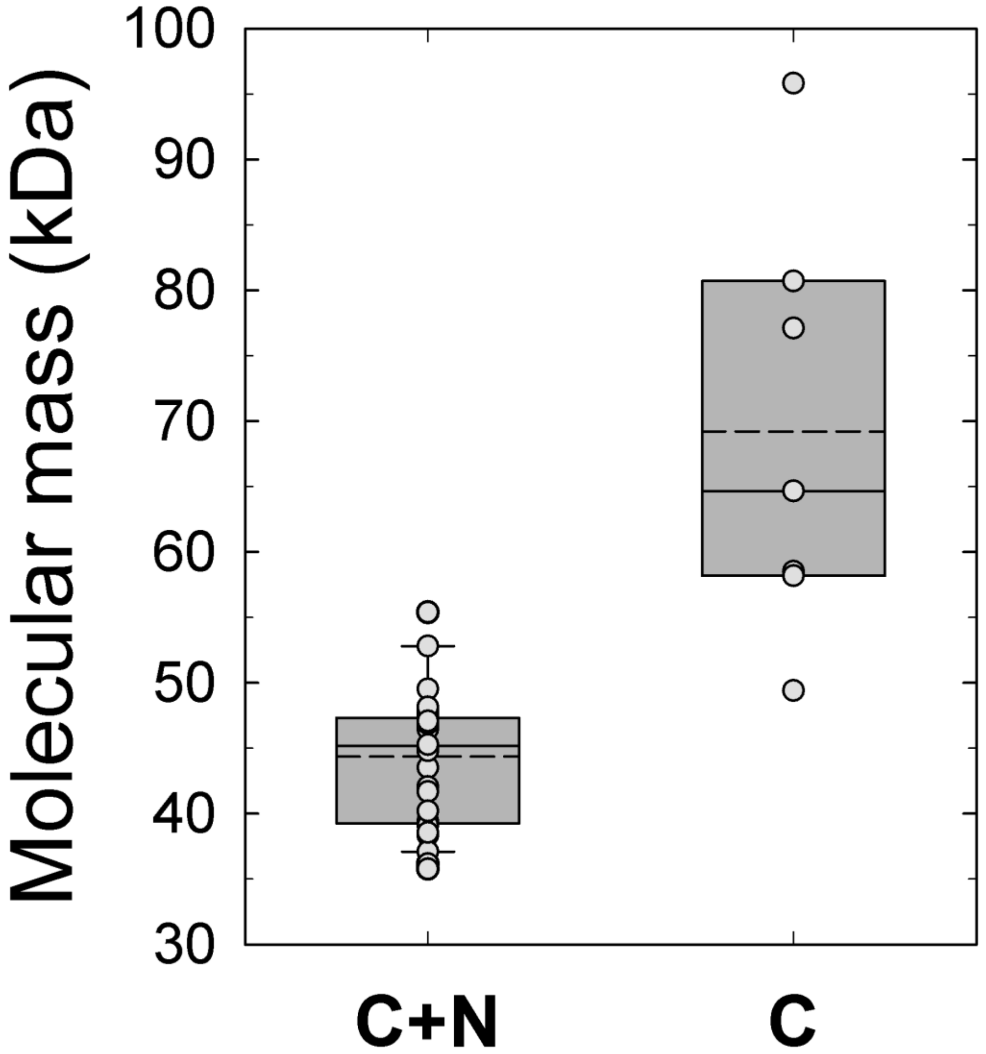
Supplemental Figure 2. (continued).



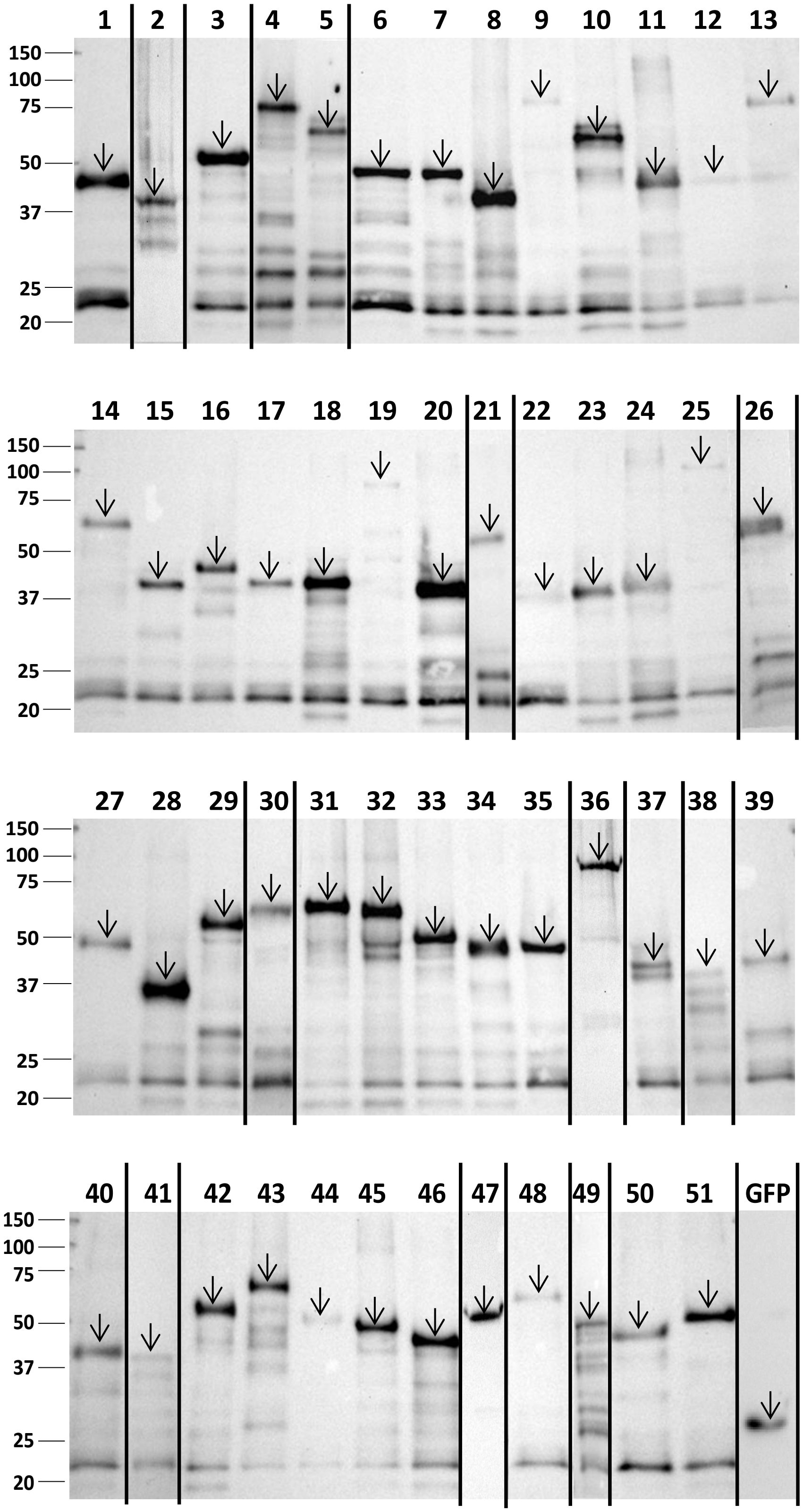
Supplemental Figure 2. (continued).



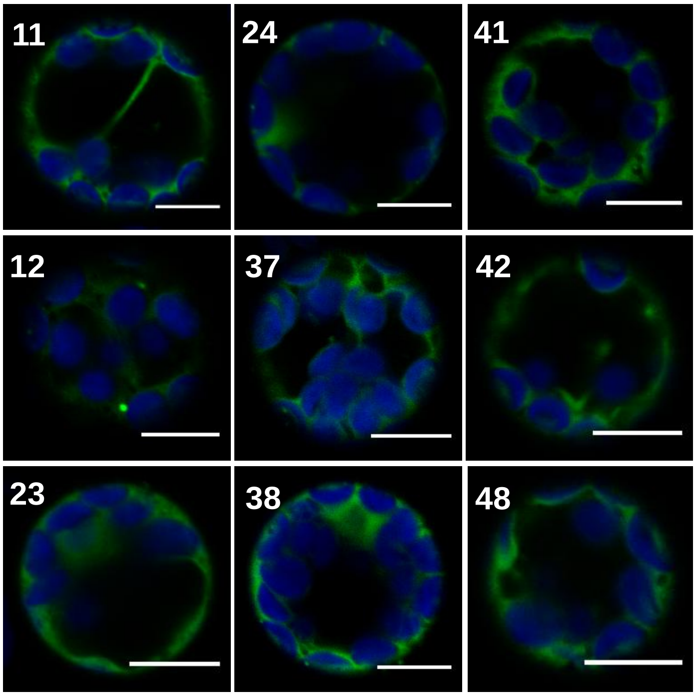
Supplemental Figure 2. (continued).



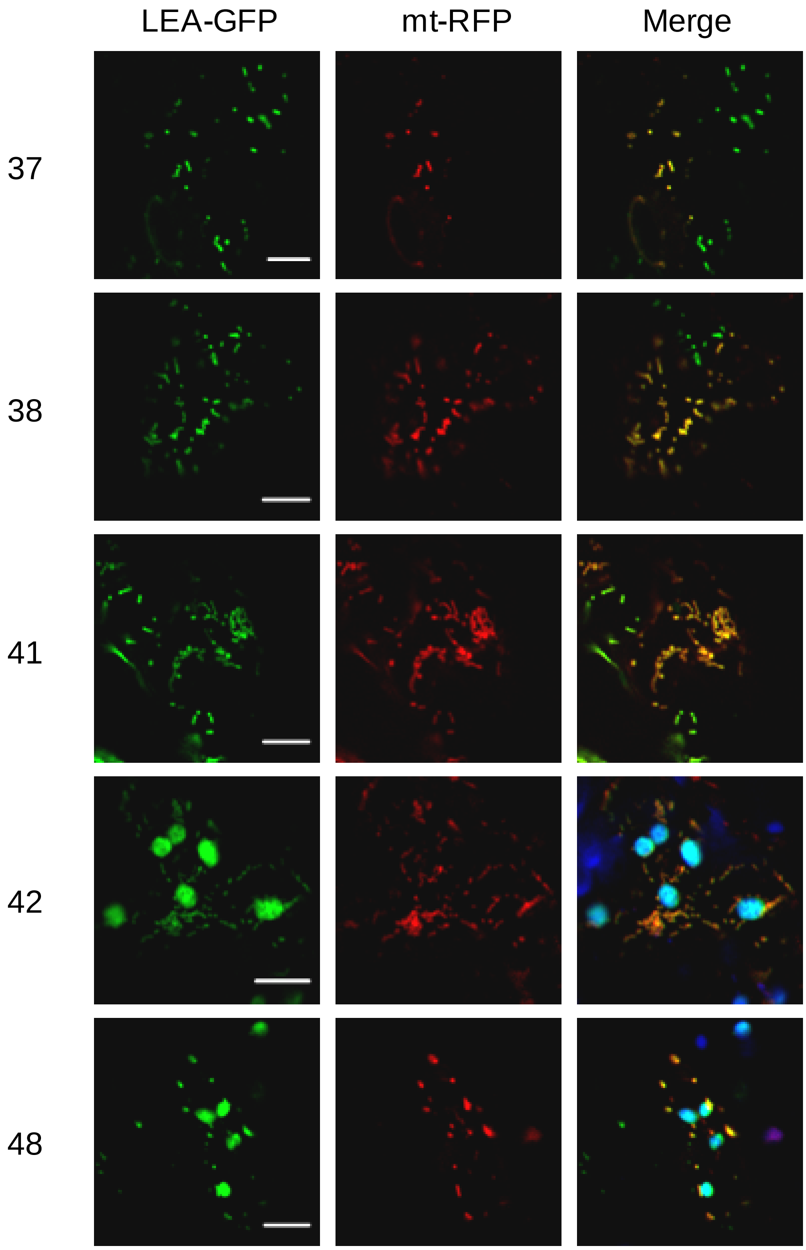
Supplemental Figure 3. Diffusion of cytosolic LEA-GFP proteins in the nucleus.
The graph shows the distribution of LEA protein fusions between cytosolic only (C) or cytosolic-nuclear (C+N) compartments as a function of their molecular mass. Each box encloses 50% of the data with the median value of the variable displayed as a line. The mean is indicated as a dashed line. The top and bottom of the box mark the limits of ± 25% of the variable population. The lines extending from the top and bottom of each box mark the minimum and maximum values within the data set that fall within an acceptable range.



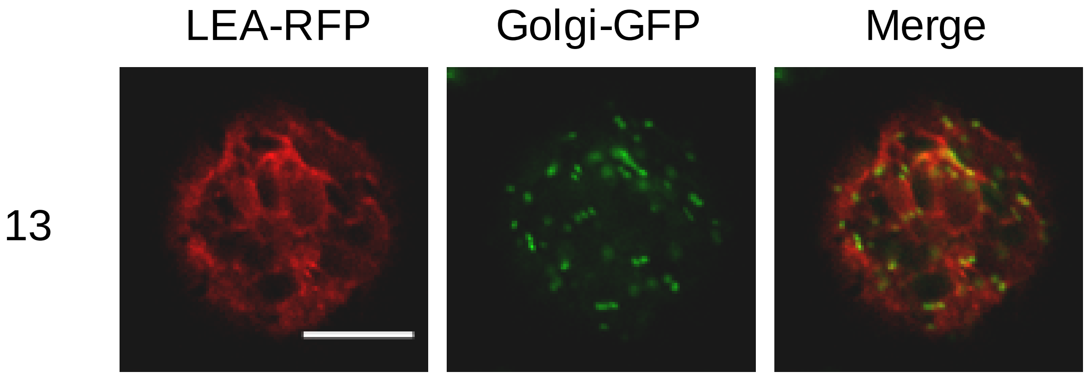
Supplemental Figure 4. Western blot analysis of LEA protein expressed in protoplasts.
Total proteins extracted from protoplasts expressing LEA-GFP fusions were separated by SDS-PAGE and transferred on a nylon membrane. LEA-GFP were immuno-detected with a specific anti-GFP antibody. Each LEA protein is indicated by its number. The molecular mass in the scale is in kDa. Lanes between black bars (2, 4, 5, 21, 26, 30, 36, 38, 41, 47 and 49) were obtained from a second western blot analysis and were merged in the figure for more clarity. Arrows indicate the bands of interest.



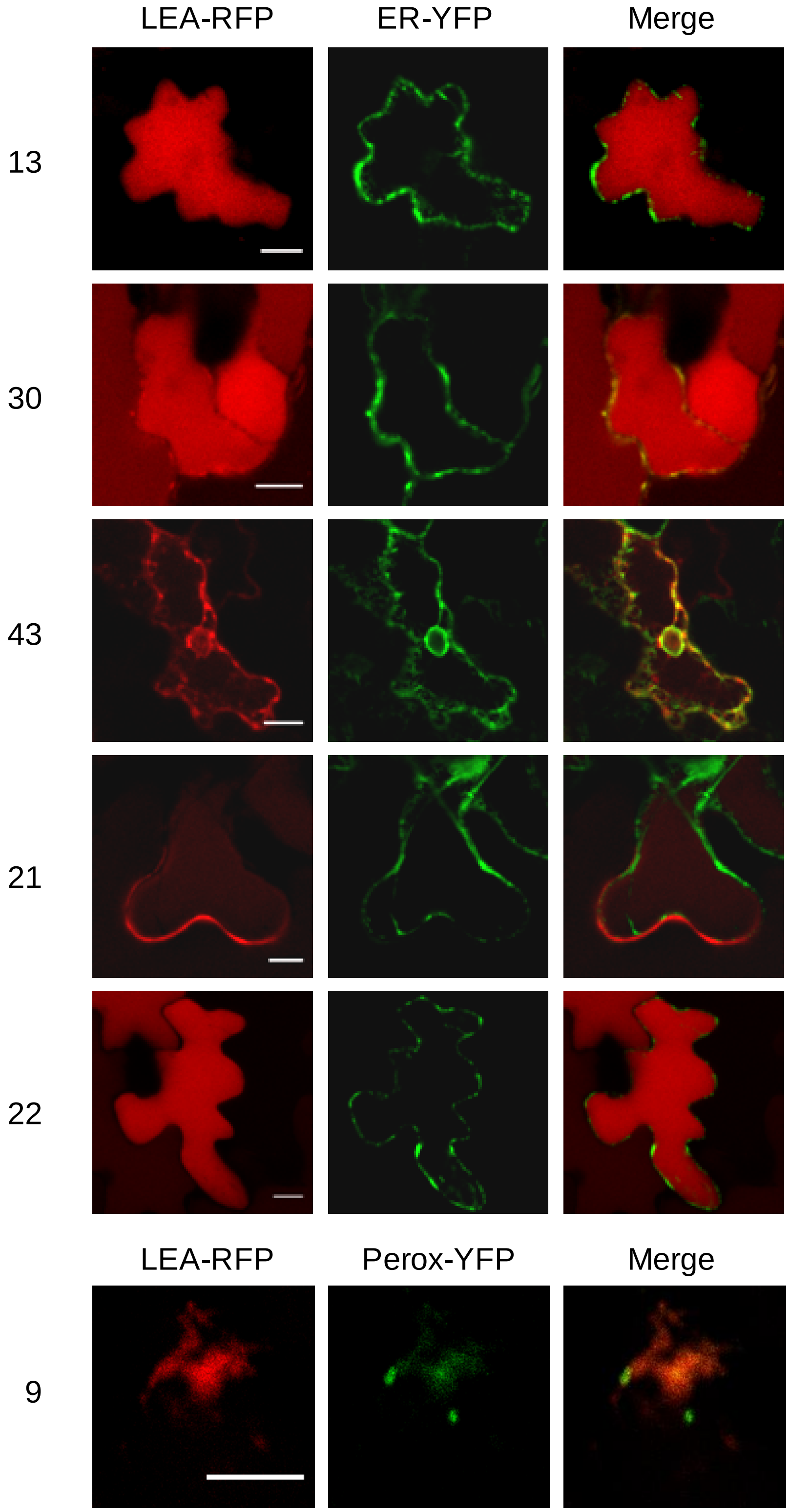
Supplemental Figure 5. Cytosolic localization of GFP-LEA fusions for proteins localized in mitochondria or plastid when expressed as LEA-GFP fusions (see Figures 3 and 4).
Representative images of GFP-LEA fusion proteins expressed in wild type Arabidopsis mesophyll protoplasts. Numbers refer to different LEA proteins for which LEA-GFP fusions were localized in plastid or mitochondria . Green, GFP; Blue, chlorophyll. Bar = 10 µm.



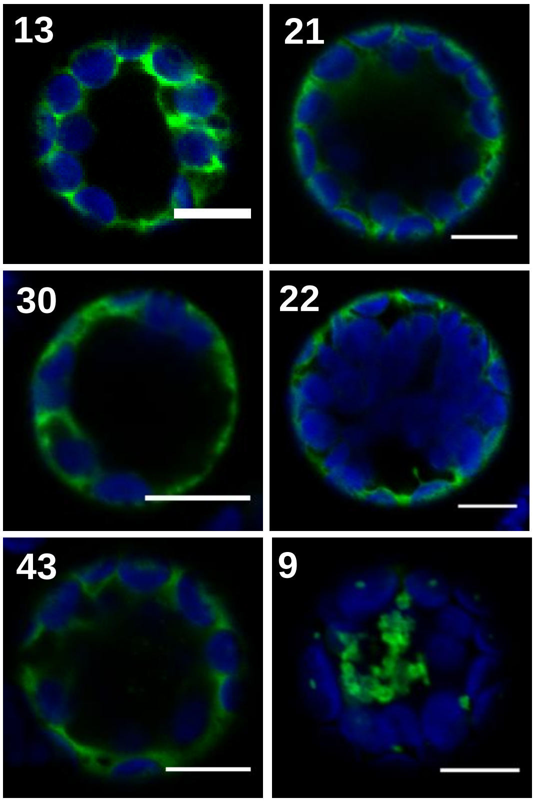
Supplemental Figure 6. Leaf cells from Arabidopsis transgenic lines expressing LEA proteins targeted to mitochondria or dual targeted to mitochondria and plastid.
Representative images of LEA-GFP fusion proteins expressed in transgenic lines expressing a RFP mitochondrial marker. In the merged images fro LEA42 and 48, chlorophyll autofluorescence is also shown (in blue). Numbers refer to different LEA proteins. Green, GFP; Red, RFP; Blue, chlorophyll. Bar = 10 µm.



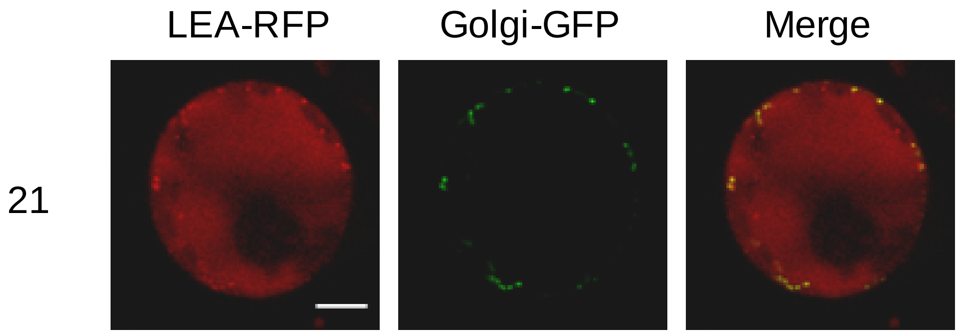
Supplemental Figure 7. LEA13-RFP does not co-localize with Golgi in Arabidopsis protoplasts. LEA13-RFP fusion protein was expressed in Arabidopsis mesophyll protoplasts carrying a Golgi marker (GFP). Bar = 10 µm.



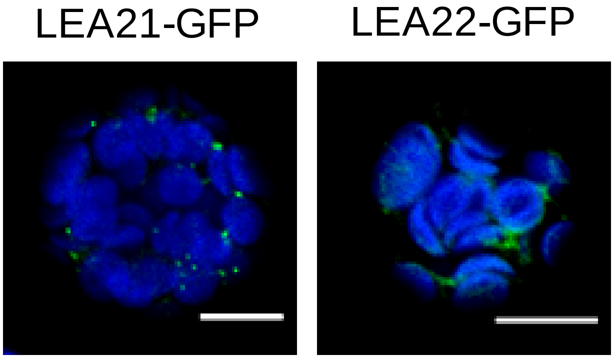
Supplemental Figure 8. Arabidopsis leaf cells from transgenic lines expressing LEA proteins targeted to the secretory pathway or the pexophagosome.
Representative images of LEA-RFP fusion proteins expressed in transgenic lines expressing a YFP ER marker (ER-YFP) or a YFP peroxisome marker (Perox-YFP). Numbers refer to different LEA proteins. Green, YFP; Red, RFP. Bar = 10 µm.



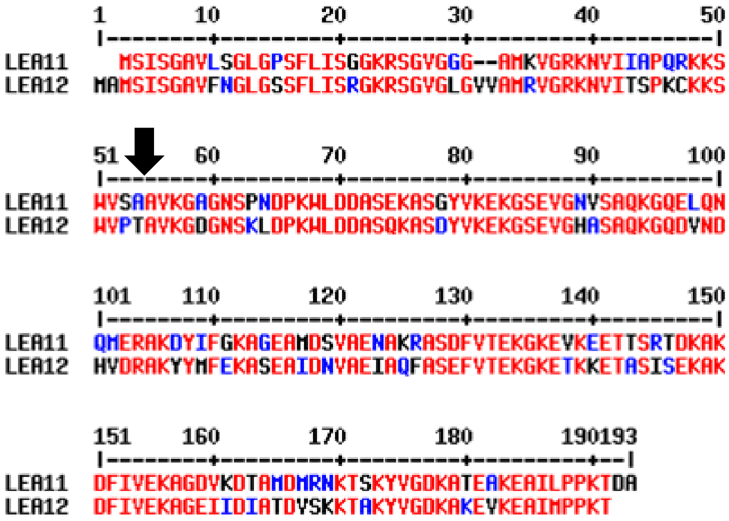
Supplemental Figure 9. Transient expression in Arabidopsis protoplasts of GFP-LEA fusions for proteins which are targeted to the secretory pathway as LEA-GFP fusions.
Representative images of GFP-LEA fusion proteins expressed in wild type Arabidopsis mesophyll protoplasts. Numbers refer to different LEA proteins for which LEA-GFP fusions were targeted to the secretory pathway. Green, GFP; Blue, chlorophyll. Bar = 10 µm.



Supplemental Figure 10. Vacuolar and Golgi localization of LEA 21 in Arabidopsis protoplasts. LEA21-RFP fusion protein was expressed in Arabidopsis mesophyll protoplasts carrying a Golgi marker (GFP). Bar = 10 µm.

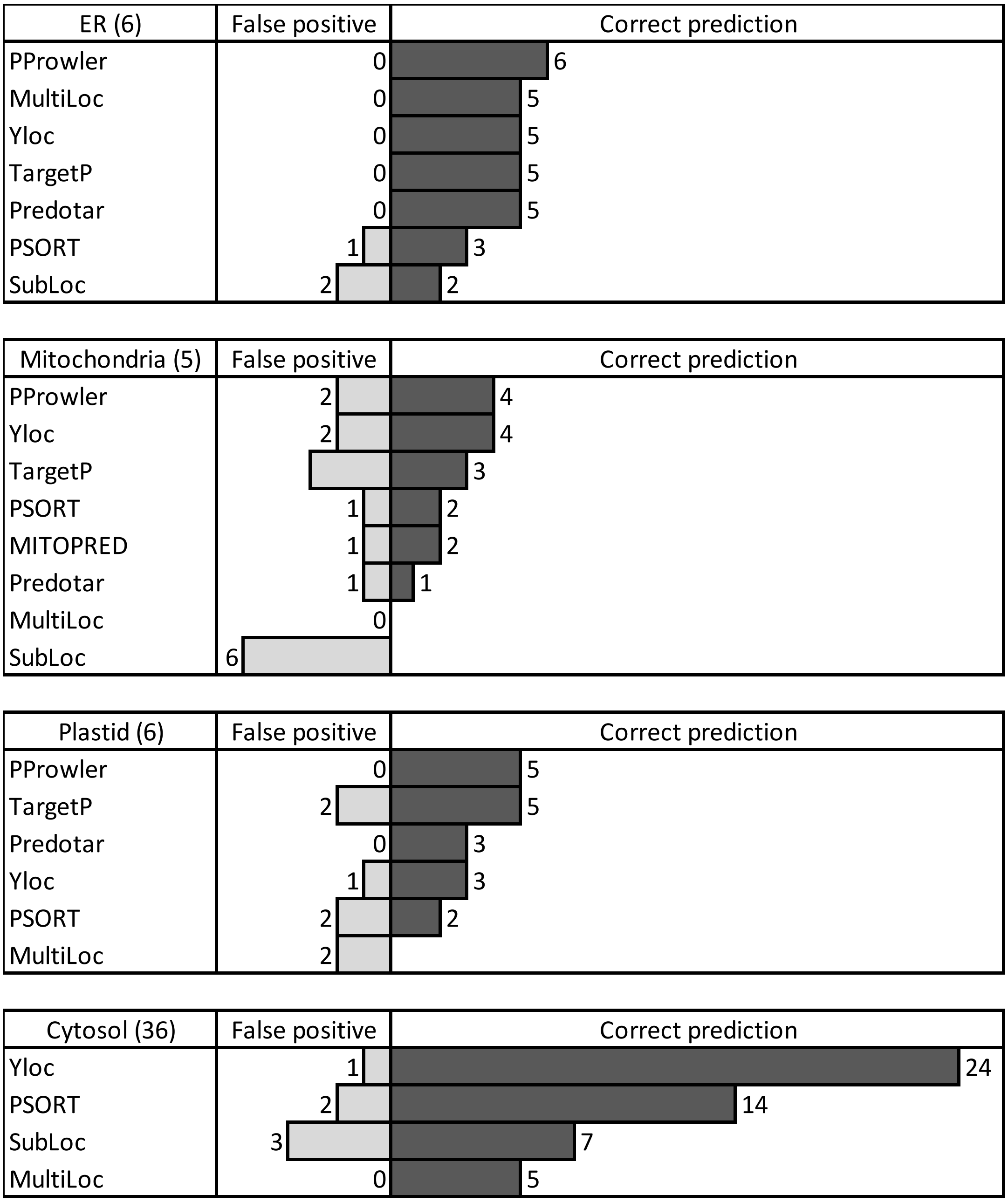


Supplemental Figure 11. Localization of LEA 21-GFP and LEA22-GFP in Arabidopsis protoplasts. GFP fusion protein was expressed in wild type Arabidopsis mesophyll protoplasts. In the case of LEA22-GFP, the fluorescence signal was very weak. Bar = 10 µm.

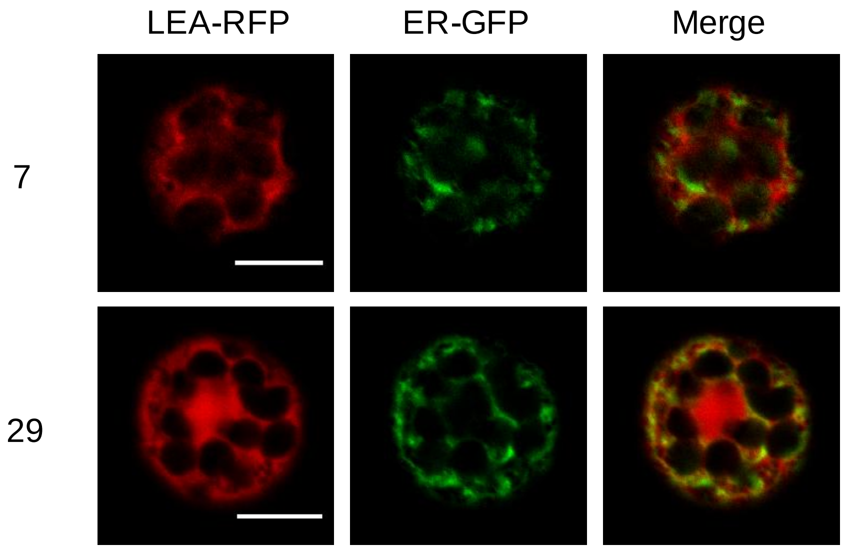


```
          1       10        20        30        40        50
          |--------+---------+---------+---------+---------|
LEA11       MSISGAVLSGLGPSFLISGGKRSGVGGG--AMKVGRKNVIIAPQRKKS
LEA12     MAMSISGAVFNGLGSSFLISRGKRSGVGLGVVAMRVGRKNVITSPKCKKS

          51      60        70        80        90       100
          |--------+---------+---------+---------+---------|
LEA11     WVSAAVKGAGNSPNDPKWLDDASEKASGYVKEKGSEVGNVSAQKGQELQN
LEA12     WVPTAVKGDGNSKLDPKWLDDASQKASDYVKEKGSEVGHASAQKGQDVND

          101    110       120       130       140       150
          |--------+---------+---------+---------+---------|
LEA11     QMERAKDYIFGKAGEAMDSVAENAKRASDFVTEKGKEVKEETTSRTDKAK
LEA12     HVDRAKYYMFEKASEAIDNVAEIAQFASEFVTEKGKETKKETASISEKAK

          151    160       170       180       190193
          |--------+---------+---------+---------+--|
LEA11     DFIVEKAGDVKDTAMDMRNKTSKYVGDKATEAKEAILPPKTDA
LEA12     DFIVEKAGEIIDIATDVSKKTAKYVGDKAKEVKEAIMPPKT
```

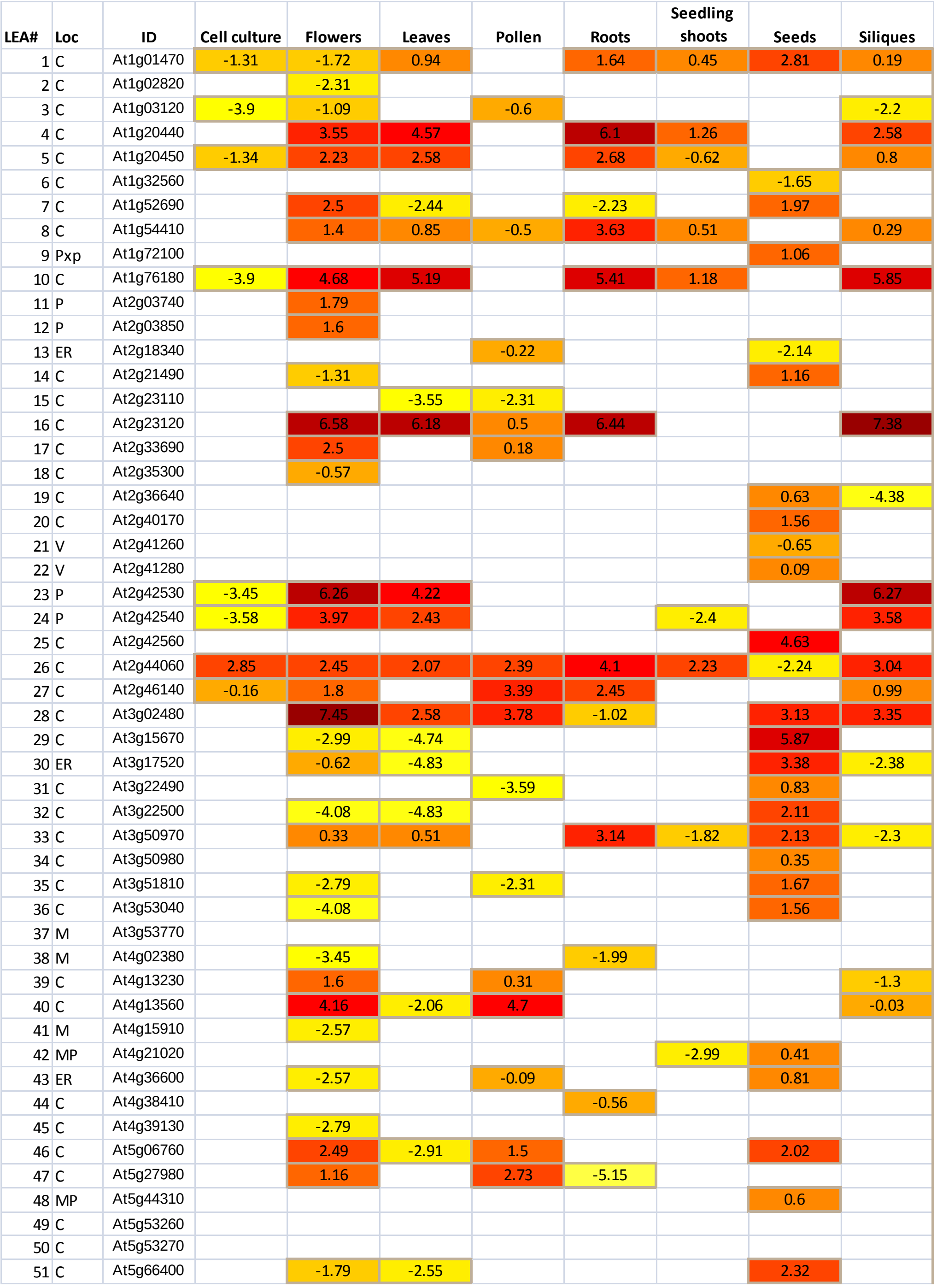
Supplemental Figure 12. LEA11 and LEA12 sequence alignment. Sequences were aligned using the MultAlin software (http://multalin.toulouse.inra.fr/multalin/) using default parameters. The targeting peptide cleavage site of LEA11 is indicated with a black arrow.



Supplemental Figure 13. Estimation of prediction software efficiency. The bar graph shows the number of proteins with correct or false predictions by the different software. For each compartment, the total number of experimentally identified proteins is indicated between brackets. Correct predictions were achieved when the experimental subcellular localization matched with the prediction. False positives correspond to erroneous subcellular compartment attribution with a strong prediction.

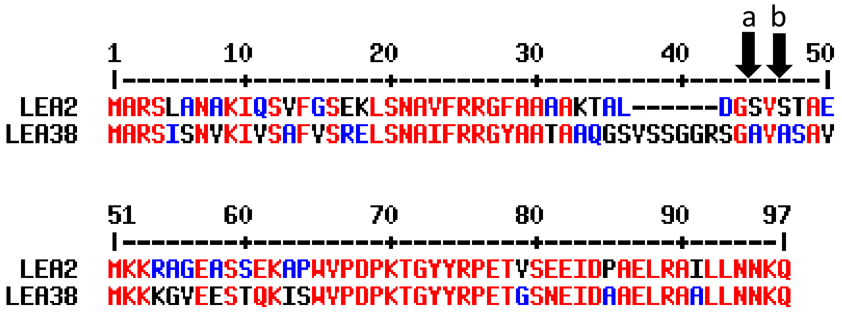


Supplemental Figure 14. Cytosolic localization of LEA7 and LEA29 in Arabidopsis protoplasts. LEA-RFP fusion proteins were expressed in Arabidopsis mesophyll protoplasts carrying a ER marker (GFP). Bar = 10 µm.



LEA#	Loc	ID	Cell culture	Flowers	Leaves	Pollen	Roots	Seedling shoots	Seeds	Siliques
1	C	At1g01470	-1.31	-1.72	0.94		1.64	0.45	2.81	0.19
2	C	At1g02820		-2.31						
3	C	At1g03120	-3.9	-1.09		-0.6				-2.2
4	C	At1g20440		3.55	4.57		6.1	1.26		2.58
5	C	At1g20450	-1.34	2.23	2.58		2.68	-0.62		0.8
6	C	At1g32560							-1.65	
7	C	At1g52690		2.5	-2.44		-2.23		1.97	
8	C	At1g54410		1.4	0.85	-0.5	3.63	0.51		0.29
9	Pxp	At1g72100							1.06	
10	C	At1g76180	-3.9	4.68	5.19		5.41	1.18		5.85
11	P	At2g03740		1.79						
12	P	At2g03850		1.6						
13	ER	At2g18340				-0.22			-2.14	
14	C	At2g21490		-1.31					1.16	
15	C	At2g23110			-3.55	-2.31				
16	C	At2g23120		6.58	6.18	0.5	6.44			7.38
17	C	At2g33690		2.5		0.18				
18	C	At2g35300		-0.57						
19	C	At2g36640							0.63	-4.38
20	C	At2g40170							1.56	
21	V	At2g41260							-0.65	
22	V	At2g41280							0.09	
23	P	At2g42530	-3.45	6.26	4.22					6.27
24	P	At2g42540	-3.58	3.97	2.43			-2.4		3.58
25	C	At2g42560							4.63	
26	C	At2g44060	2.85	2.45	2.07	2.39	4.1	2.23	-2.24	3.04
27	C	At2g46140	-0.16	1.8		3.39	2.45			0.99
28	C	At3g02480		7.45	2.58	3.78	-1.02		3.13	3.35
29	C	At3g15670		-2.99	-4.74				5.87	
30	ER	At3g17520		-0.62	-4.83				3.38	-2.38
31	C	At3g22490				-3.59			0.83	
32	C	At3g22500		-4.08	-4.83				2.11	
33	C	At3g50970		0.33	0.51		3.14	-1.82	2.13	-2.3
34	C	At3g50980							0.35	
35	C	At3g51810		-2.79		-2.31			1.67	
36	C	At3g53040		-4.08					1.56	
37	M	At3g53770								
38	M	At4g02380		-3.45			-1.99			
39	C	At4g13230		1.6		0.31				-1.3
40	C	At4g13560		4.16	-2.06	4.7				-0.03
41	M	At4g15910		-2.57						
42	MP	At4g21020						-2.99	0.41	
43	ER	At4g36600		-2.57		-0.09			0.81	
44	C	At4g38410					-0.56			
45	C	At4g39130		-2.79						
46	C	At5g06760		2.49	-2.91	1.5			2.02	
47	C	At5g27980		1.16		2.73	-5.15			
48	MP	At5g44310							0.6	
49	C	At5g53260								
50	C	At5g53270								
51	C	At5g66400		-1.79	-2.55				2.32	

Supplemental Figure 15. Proteomic quantification of LEA proteins in different organs of Arabidopsis.
Proteomic data were obtained from the pep2pro database (http://fgcz-pep2pro.uzh.ch/) and the subcellular localizations were added from our experimental observations: C, cytosol ; P, plastid ; M, mitochondria ; MP, mitochondria and plastid ; ER, Endoplasmic Reticulum ; V, vacuole ; Pxp, pexophagosome. Values are expressed as Log2 of spectral counts and normalized (single hits were previously removed). Results were color coded as a function of values from yellow to red with Excel.

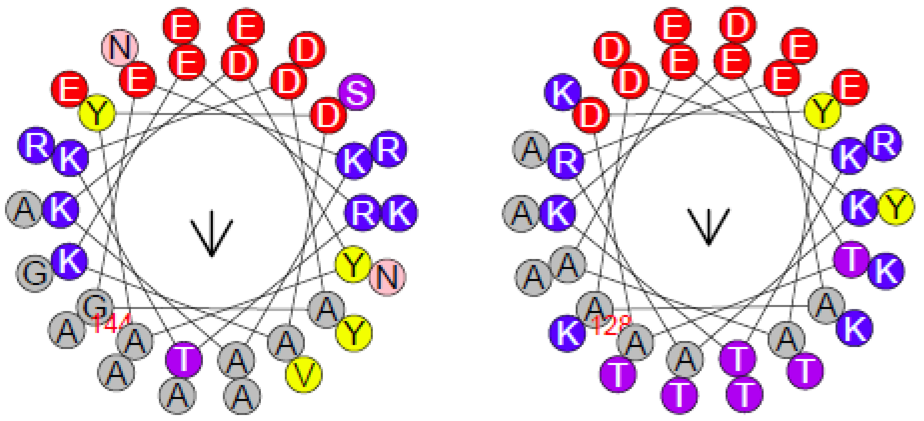


```
                                                   a  b
       1       10        20        30        40        50
       |--------+---------+---------+---------+---------|
LEA2   MARSLANAKIQSVFGSEKLSNAVFRRGFAAAAKTAL------DGSVSTAE
LEA38  MARSISNVKIVSAFVSRELSNAIFRRGYAATAAQGSVSSGGRSGAVASAV

       51      60        70        80        90     97
       |--------+---------+---------+---------+------|
LEA2   MKKRAGEASSEKAPWVPDPKTGYYRPETVSEEIDPAELRAILLNNKQ
LEA38  MKKKGVEESTQKISWVPDPKTGYYRPETGSNEIDAAELRAALLNNKQ
```

Supplemental Figure 16. LEA2 and LEA38 sequence alignment. Sequences were aligned using the MultAlin software (http://multalin.toulouse.inra.fr/multalin/) using default parameters. The targeting peptide cleavage sites of LEA38 shown as black arrows were predicted using the MitoProt (a) and TargetP (b) software.

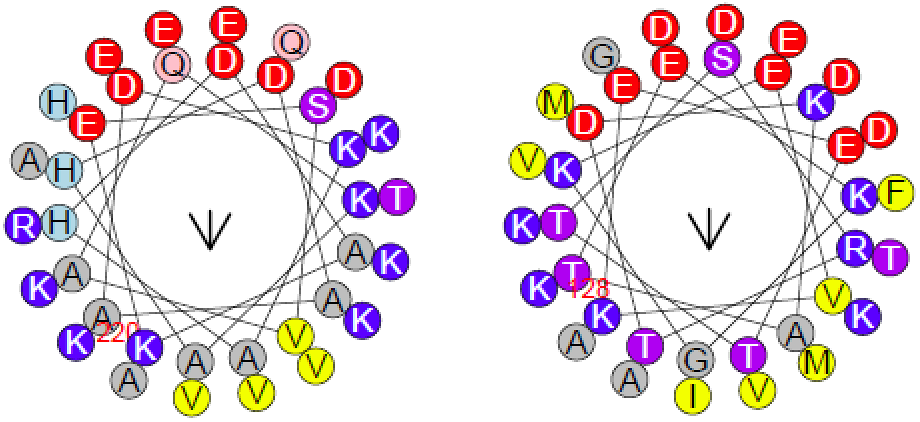
PsLEAM (144-179)
Mitochondria

LEA36 (128-163)
Cytosol



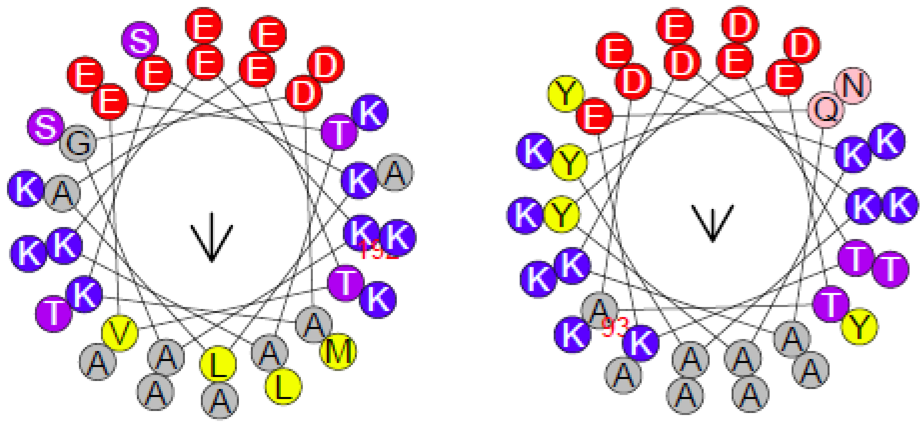
LEA9 (220-255)
Pexophagosome

LEA11(128-163)
Plastid

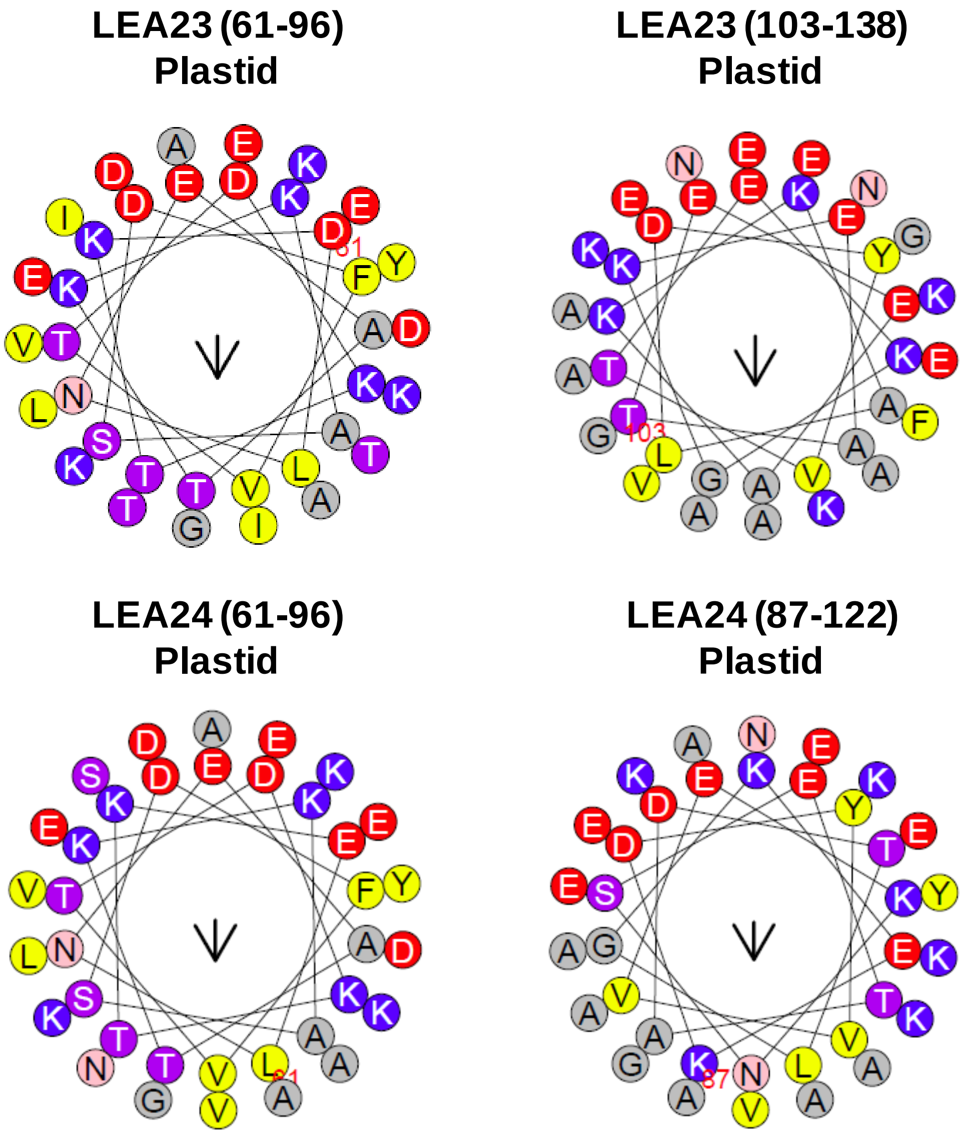


LEA30 (192-227)
ER

LEA42 (93-128)
Mitochondria-Plastid



Supplemental Figure 17. Modeling of class A α-helix motif of LEA proteins.
Helical projections of α-helices were obtained using the HeliQuest webserver (http://heliquest.ipmc.cnrs.fr/). Each wheel was obtained with a 36 amino acids window. Residues are color coded with blue for positively (K, R) and red (D, E) for positively charged residues. Non polar residues are shown in yellow or grey, and others in purple, light blue or light pink colors. The arrow shows the hydrophobic moment.



Supplemental Figure 18. Modeling of class A-like α-helix motif of LEA23 and LEA24. Helical projections of α-helices were obtained using the HeliQuest webserver (http://heliquest.ipmc.cnrs.fr/). Each wheel was obtained with a 36 amino acids window. Residues are color coded with blue for positively (K, R) and red (D, E) for positively charged residues. Non polar residues are shown in yellow or grey, and others in purple, light blue or light pink colors. The arrow shows the hydrophobic moment.

Supplemental Table 1. Theoretical and apparent molecular masses of LEA and fusion proteins.

LEA protein	Molecular weight (kDa)	Molecular weight with GFP (kDa)	Molecular weight with GFP deduced from Western blot (kDa)
1	16.543	45.169	43.5
2	9.827	38.453	38.5
3	18.941	47.568	51.0
4	29.896	58.523	77.5
5	29.547	58.174	64.0
6	14.890	43.517	44.0
7	18.100	46.727	46.5
8	10.795	39.422	39.0
9	52.703	81.330	80.0
10	20.786	49.412	63.0
11	20.016	48.643	44.0
12	20.578	49.204	45.0
13	49.838	78.464	78.8
14	19.297	47.924	64.0
15	9.712	38.339	39.5
16	8.482	37.108	43.5
17	7.555	36.181	40.5
18	10.480	39.107	40.5
19	48.492	77.119	87.5
20	9.933	38.560	38.5
21	23.887	52.513	56.0
22	11.431	40.058	37.5
23	14.960	43.587	38.0
24	14.605	43.231	39.0
25	67.195	95.821	99.5
26	36.036	64.662	64.0
27	17.846	46.472	48.0
28	7.144	35.771	36.0
29	24.186	52.812	55.5
30	32.559	61.185	63.0
31	26.743	55.370	65.0
32	26.778	55.405	63.0
33	20.909	49.535	50.0
34	13.434	42.061	46.0
35	16.612	45.238	46.5
36	52.084	80.710	85.0
37	14.418	43.044	42.5
38	10.291	38.918	40.0
39	13.063	41.690	43.0
40	11.584	40.210	41.0
41	10.965	39.591	39.5
42	29.422	58.048	57.0
43	37.959	66.585	68.5
44	18.255	46.881	52.0
45	16.259	44.886	48.5
46	16.178	44.805	43.5
47	19.515	48.142	52.0
48	38.451	67.077	63.5
49	18.272	46.898	50.0
50	16.660	45.287	45.0
51	18.463	47.090	53.5

Supplemental Table 2. Quantitative data about transiently transformed protoplasts.

Exp, independent transformation; FP, fluorescent protoplast number

	protoplasts	Exp 1		Exp 2		Exp 3		Exp 4		Exp 5		
LEA	number of independant transformation	Protopl. observed	FP	Protopl. observed	FP	Protopl. observed	FP	Protopl. observed	FP	Protopl. observed	FP	Total FP
1	3	25	10	67	21	38	22					53
2	3	45	11	34	12	108	53					76
3	3	44	23	10	3	46	8					34
4	3	17	4	10	4	96	31					39
5	2	125	42	147	48							90
6	2	42	13	57	23							36
7	3	20	7	53	22	17	6					35
8	3	19	6	33	15	72	26					47
9	5	9	2	34	6	12	4	13	4	19	4	20
10	3	32	8	57	26	126	42					76
11	3	56	4	28	18	99	45					67
12	2	35	4	68	3							7
13	3	25	9	29	3	53	2					14
14	3	19	7	37	11	77	23					41
15	2	49	11	137	46							57
16	2	50	9	145	48							57
17	2	50	7	154	72							79
18	2	60	30	114	17							47
19	2	30	5	164	15							20
20	2	38	26	147	18							44
21	3	27	12	23	5	25	9					26
22	3	38	6	18	3	20	5					14
23	3	36	11	26	14	15	9					34
24	3	77	45	17	5	135	9					59
25	2	8	3	96	12							15
26	2	21	5	92	7							12
27	2	47	16	170	16							32
28	2	12	8	62	10							18
29	3	9	8	24	5	110	11					24
30	3	53	7	12	4	16	2					13
31	3	45	30	10	5	128	11					46
32	3	17	7	25	12	86	9					28
33	3	18	5	19	12	82	2					19
34	3	8	5	13	7	116	14					26
35	2	46	12	53	3							15
36	2	5	2	104	8							10
37	3	18	6	33	18	5	5					29
38	3	55	29	16	7	5	3					39
39	3	115	21	12	3	79	6					30
40	2	18	10	51	3							13
41	3	22	7	19	7	15	7					21
42	2	7	5	6	4							9
43	3	4	2	13	3	32	4					9
44	3	14	6	11	3	88	2					11
45	3	39	12	19	8	58	6					26
46	2	14	6	38	4							10
47	3	72	9	9	3	117	5					17
48	2	12	4	12	6							10
49	3	4	3	72	21	38	4					28
50	2	36	18	54	5							23
51	3	32	11	13	9	69	2					22

Supplemental Table 3. Arabidopsis LEA templates used for PCR amplification.

LEA#	Accession number (TAIR)	Template	Origin
1	At1g01470	cDNA Arabidopsis seeds	MPIMP
2	At1g02820	pENTR/SD/D-TOPO (+CDS)	MPIMP
3	At1g03120	cDNA Arabidopsis seeds	MPIMP
4	At1g20440	pENTR/SD/D-TOPO (+CDS)	MPIMP
5	At1g20450	pUNI51 (U24382)	ABRC
6	At1g32560	pENTR/SD/D-TOPO (+CDS)	MPIMP
7	At1g52690	pENTR/SD/D-TOPO (+CDS)	MPIMP
8	At1g54410	pENTR/SD/D-TOPO (+CDS)	MPIMP
9	At1g72100	pENTR/SD/D-TOPO (+CDS)	MPIMP
10	At1g76180	pENTR/SD/D-TOPO (+CDS)	MPIMP
11	At2g03740	pENTR/SD/D-TOPO (+CDS)	MPIMP
12	At2g03850	pENTR/SD/D-TOPO (+CDS)	MPIMP
13	At2g18340	cDNA Arabidopsis seeds	MPIMP
14	At2g21490	pENTR/SD/D-TOPO (+CDS)	MPIMP
15	At2g23110	pENTR/SD/D-TOPO (+CDS)	MPIMP
16	At2g23120	pENTR/SD/D-TOPO (+CDS)	MPIMP
17	At2g33690	pUNI51 (U63047)	ABRC
18	At2g35300	cDNA Arabidopsis seeds	MPIMP
19	At2g36640	cDNA Arabidopsis seeds	MPIMP
20	At2g40170	pENTR/SD/D-TOPO (+CDS)	MPIMP
21	At2g41260	pUC57 (synthetic gene)	GenScript
22	At2g41280	pENTR/SD/D-TOPO (+CDS)	MPIMP
23	At2g42530	pENTR/SD/D-TOPO (+CDS)	MPIMP
24	At2g42540	pENTR/SD/D-TOPO (+CDS)	MPIMP
25	At2g42560	pENTR/SD/D-TOPO (+CDS)	MPIMP
26	At2g44060	pUNI51 (U83572)	ABRC
27	At2g46140	pENTR/SD/D-TOPO (+CDS)	MPIMP
28	At3g02480	pENTR/SD/D-TOPO (+CDS)	MPIMP
29	At3g15670	pENTR/SD/D-TOPO (+CDS)	MPIMP
30	At3g17520	pENTR/SD/D-TOPO (+CDS)	MPIMP
31	At3g22490	pENTR/SD/D-TOPO (+CDS)	MPIMP
32	At3g22500	pENTR/SD/D-TOPO (+CDS)	MPIMP
33	At3g50970	pENTR/SD/D-TOPO (+CDS)	MPIMP
34	At3g50980	cDNA Arabidopsis seeds	MPIMP
35	At3g51810	pENTR/SD/D-TOPO (+CDS)	MPIMP
36	At3g53040	pENTR/SD/D-TOPO (+CDS)	MPIMP
37	At3g53770	pENTR221 (pENTR221-AT3G53770)	ABRC
38	At4g02380	pENTR/SD/D-TOPO (+CDS)	MPIMP
39	At4g13230	cDNA Arabidopsis bud	MPIMP
40	At4g13560	pENTR/SD/D-TOPO (+CDS)	MPIMP
41	At4g15910	pUNI51 (U23419)	ABRC
42	At4g21020	pUNI51 (U20045)	ABRC
43	At4g36600	pUNI51 (S63786)	ABRC
44	At4g38410	pENTR/SD/D-TOPO (+CDS)	MPIMP
45	At4g39130	cDNA Arabidopsis seeds	MPIMP
46	At5g06760	pENTR/SD/D-TOPO (+CDS)	MPIMP
47	At5g27980	pUC57 (synthetic gene)	GenScript
48	At5g44310	pUNI51 (U66244)	ABRC
49	At5g53260	pUC57 (synthetic gene)	GenScript
50	At5g53270	cDNA Arabidopsis seeds	MPIMP
51	At5g66400	pENTR/SD/D-TOPO (+CDS)	MPIMP

Supplemental Table 4. Primers used for the construction of LEA gene fusions and markers.

Sequence	Name	Forward primer	Length	Name	Reverse primer	Length
LEA1	FL1	CACCATGGCGAGCTTGCTAGAT	22	RL1	GAAGAAATCTTTAAAAGTAGG	21
	FnoL1	CACCGCGAGCTTGCTAGATAAA	22	RsL1	TCAGAAGAAATCTTTAAAAGT	21
LEA2	FL2	CACCATGGCTCGTTCTCTCGCT	22	RL2	TTGCTTGTTGTTCAAGAG	18
	FnoL2	CACCGCTCGTTCTCTCGCTAAC	22	RsL2	TTATTGCTTGTTGTTCAA	18
LEA3	FL3	CACCATGGCACAGCATCAGCATTC	24	RL3	GAGTTGTTGATTGAGCCT	18
	FnoL3	CACCGCACAGCATCAGCATTCTCC	24	RsL3	CTAGAGTTGTTGATTGAGC	19
LEA4	FL4	CACCATGGCTGAGGAGTACAAG	22	RL4	ATCATCAGACTCTTTTTCTTTC	22
	FnoL4	CACCGCTGAGGAGTACAAGAAC	22	RsL4	TTAATCATCAGACTCTTTTTCT	22
LEA5	FL5	CACCATGGCAGAAGAGTACAAGAAC	25	RL5	ATCAGACACTTTTTCTTTCTTC	22
	FnoL5	CACCGCAGAAGAGTACAAGAACACC	25	RsL5	TTAATCAGACACTTTTTCTTTC	22
LEA6	FL6	CACCATGCAATCGGCGAAACAG	22	RL6	GTAGTGATGATGATTATGATGTCC	24
	FnoL6	CACCCAATCGGCGAAACAGAAG	22	RsL6	TTAGTAGTGATGATGATTATGATG	24
LEA7	FL7	CACCATGGCGTCTCATCAAGAA	22	RL7	CTTCCTCTGTGTCTCACG	18
	FnoL7	CACCGCGTCTCATCAAGAACAG	22	RsL7	TCACTTCCTCTGTGTCTC	18
LEA8	FL8	CACCATGGCAGGACTCATCAAC	22	RL8	ATCGCTGTCGCTGTCACT	18
	FnoL8	CACCGCAGGACTCATCAACAAG	22	RsL8	TTAATCGCTGTCGCTGTC	18
LEA9	FL9	CACCATGACGAATCTTTTGGCC	22	RL9	ACAAGCGGCGCCGAGTCTCTG	21
	FnoL9	CACCACGAATCTTTTGGCCTTG	22	RsL9	TCAACAAGCGGCGCCGAGTCT	21
LEA10	FL10	CACCATGGCTGAGGAAATCAAG	22	RL10	TTCTTTATCTTTCTTCTCCTCC	22
	FnoL10	CACCGCTGAGGAAATCAAGAAT	22	RsL10	TTATTCTTTATCTTTCTTCTCC	22
LEA11	FL11	CACCATGTCGATCTCCGGAGCT	22	RL11	TGCATCAGTTTTTGGAGGC	19
	FnoL11	CACCTCGATCTCCGGAGCTGTG	22	RsL11	CTATGCATCAGTTTTTGGA	19
LEA12	FL12	CACCATGGCGATGTCGATCTCC	22	RL12	AGTTTTTGGAGGCATTATAGC	21
	FnoL12	CACCGCGATGTCGATCTCCGGA	22	RsL12	TTAAGTTTTTGGAGGCATTAT	21
LEA13	FL13	CACCATGATGGAGAGAAGAAGAAC	24	RL13	GAGCTCAGCATAACGGTC	18
	FnoL13	CACCATGGAGAGAAGAAGAACGG	23	RsL13	TTAGAGCTCAGCATAACG	18
LEA14	FL14	CACCATGGCGGATTTGAGGGAC	22	RL14	TGGGTGGTTGTGGTTATG	18
	FnoL14	CACCGCGGATTTGAGGGACGAA	22	RsL14	TCATGGGTGGTTGTGGTT	18
LEA15	FL15	CACCATGGAGGATCAGAAAAAGCC	24	RL15	CGGAACGCCCTGACGGTT	18
	FnoL15	CACCGAGGATCAGAAAAAGCCACC	24	RsL15	TCACGGAACGCCCTGACG	18
LEA16	FL16	CACCATGGAGGCCGGGAAAACA	22	RL16	CGGAGCTTTCGCATCGGT	18
	FnoL16	CACCGAGGCCGGGAAAACACCA	22	RsL16	TCACGGAGCTTTCGCATC	18
LEA17	FL17	CACCATGTCGAAGAGTGAAGAGAA	24	RL17	CTTCTTAGCTTTTTGGTTAGCG	22
	FnoL17	CACCTCGAAGAGTGAAGAGAAACA	24	RsL17	TCACTTCTTAGCTTTTTGGTTA	22
LEA18	FL18	CACCATGCAGTCGGCGAAGGAA	22	RL18	GATCTGTCCCGGCGGGTA	18
	FnoL18	CACCCAGTCGGCGAAGGAAAAG	22	RsL18	TTAGATCTGTCCCGGCGG	18
LEA19	FL19	CACCATGGCGTCAGACAAACAAAA	24	RL19	CAGCTTTCCCTTATCTTTCC	20
	FnoL19	CACCGCGTCAGACAAACAAAAGGC	24	RsL19	TCACAGCTTTCCCTTATCTT	20
LEA20	FL20	CACCATGGCGTCTCAACAAGAG	22	RL20	GGTCTTGGTCCTGAATTTGG	20
	FnoL20	CACCGCGTCTCAACAAGAGAAG	22	RsL20	TTAGGTCTTGGTCCTGAATT	20
LEA21	FL21	CACCATGGGAAACCTCAAGTCTC	23	RL21	TGGCTTAGCTTGTTGGGC	18
	FnoL21	CACCGGAAACCTCAAGTCTCTCG	23	RsL21	TCATGGCTTAGCTTGTTGG	19
LEA22	FL22	CACCATGGGAAACCTCATGTCT	22	RL22	TGGCTTAGCTTCTTCCTT	18
	FnoL22	CACCGGAAACCTCATGTCTCTC	22	RsL22	TCATGGCTTAGCTTCTTCC	19
LEA23	FL23	CACCATGGCGATGTCTTTATCAGG	24	RL23	GGACTTTGTGGCATTCTTAG	20
	FnoL23	CACCGCGATGTCTTTATCAGGAGC	24	RsL23	TCAGGACTTTGTGGCATTCT	20
LEA24	FL24	CACCATGGCGATGTCTTTCTCAGG	24	RL24	CTTTGTGGCATCCTTAGC	18
	FnoL24	CACCGCGATGTCTTTCTCAGGAGC	24	RsL24	CTACTTTGTGGCATCCTT	18
LEA25	FL25	CACCATGGCGTCAGAGCAAGCA	22	RL25	ACGTTGTCCATGTTCCCG	18
	FnoL25	CACCGCGTCAGAGCAAGCAAGG	22	RsL25	TCAACGTTGTCCATGTTC	18
LEA26	FL26	CACCATGTCGACATCTGAGGATAA	24	RL26	TTCCTCATCGTCGTCATC	18
	FnoL26	CACCTCGACATCTGAGGATAAACC	24	RsL26	TTATTCCTCATCGTCGTC	18
LEA27	FL27	CACCATGGCATCAGCGGATGAA	22	RL27	AAAGAAGTCGCGAAGGGA	18
	FnoL27	CACCGCATCAGCGGATGAAAAG	22	RsL27	TTAAAAGAAGTCGCGAAG	18
LEA28	FL28	CACCATGGACAACAAGCAAAACGC	24	RL28	GTGGCTTTTGTTCATGCC	18
	FnoL28	CACCGACAACAAGCAAAACGCGAG	24	RsL28	TTAGTGGCTTTTGTTCAT	18
LEA29	FL29	CACCATGGCATCCAACCAACAG	22	RL29	CTTCCTCTGATAAGTCTGATGA	22
	FnoL29	CACCGCATCCAACCAACAGAGC	22	RsL29	TCACTTCCTCTGATAAGTCTGA	22
LEA30	FL30	CACCATGGGGTTAGAGAGGAAA	22	RL30	GAGCTCAGCATCATCGTC	18
	FnoL30	CACCGGGTTAGAGAGGAAAGTG	22	RsL30	TCAGAGCTCAGCATCATC	18
LEA31	FL31	CACCATGAGTCAAGAAGAACAACC	24	RL31	TATATCAGCTCTCTCGTTAAGC	22
	FnoL31	CACCAGTCAAGAAGAACAACCAAA	24	RsL31	TCATATATCAGCTCTCTCGTTA	22
LEA32	FL32	CACCATGAGCCAAGAGCAACCA	22	RL32	TATATCAACTCTCTCGTTAAGC	22
	FnoL32	CACCAGCCAAGAGCAACCAAGG	22	RsL32	TCATATATCAACTCTCTCGTTA	22
LEA33	FL33	CACCATGAATTCTCACCAGAATCA	24	RL33	GTGATGACCACCGGGAAG	18
	FnoL33	CACCAATTCTCACCAGAATCAAAC	24	RsL33	CTAGTGATGACCACCGGG	18
LEA34	FL34	CACCATGGAGTCTTACCAAAACC	23	RL34	ATGATGACCACCCGGAAG	18
	FnoL34	CACCGAGTCTTACCAAAACCAG	22	RsL34	CTAATGATGACCACCCGG	18
LEA35	FL35	CACCATGGCGTCAAAGCAACTG	22	RL35	CTTGTTGGTGAACTTTGACTC	21
	FnoL35	CACCGCGTCAAAGCAACTGAGC	22	RsL35	TCACTTGTTGGTGAACTTTGA	21
LEA36	FL36	CACCATGGCATCAGGACAACGG	22	RL36	CAGCTTTTTCTCTCCCAC	18
	FnoL36	CACCGCATCAGGACAACGGGAG	22	RsL36	CTACAGCTTTTTCTCTCC	18

LEA37	FL37	CACCATGTCTCAATCACTTTTCAA	24	RL37	GCTCACTACGTACGTCTTTTG	21
	FnoL37	CACCTCTCAATCACTTTTCAATCT	24	RsL37	TTAGCTCACTACGTACGTCTT	21
LEA38	FL38	CACCATGGCTCGTTCTATCTCTAA	24	RL38	CTGCTTGTTGTTCAAGAGAGC	21
	FnoL38	CACCGCTCGTTCTATCTCTAACGT	24	RsL38	TCACTGCTTGTTGTTCAAGAG	21
LEA39	FL39	CACCATGACAAGCTTCGCGGTC	22	RL39	TTTGAGGTTCTTGGTGTTC	19
	FnoL39	CACCACAAGCTTCGCGGTCGTTG	23	RsL39	TTATTTGAGGTTCTTGGTG	19
LEA40	FL40	CACCATGTCGCAACAACAATTC	22	RL40	TTTCTTCTCGTTCATGCC	18
	FnoL40	CACCTCGCAACAACAATTCAAC	22	RsL40	TCATTTCTTCTCGTTCAT	18
LEA41	FL41	CACCATGGCCGCTCGTTCACTC	22	RL41	GAAAGACTTTGCTTTGTTTTTC	22
	FnoL41	CACCGCCGCTCGTTCACTCTCC	22	RsL41	TCAGAAAGACTTTGCTTTGTTT	22
LEA42	FL42	CACCATGGCGGCCATGCAACTAAC	24	RL42	GTTAAATGTTATGAAATCGTCC	22
	FnoL42	CACCGCGGCCATGCAACTAACAAG	24	RsL42	TCAGTTAAATGTTATGAAATCGTC	24
LEA43	FL43	CACCATGATGCTTACGACGGTG	22	RL43	AAGCTCAGCGCTACGGTC	18
	FnoL43	CACCATGCTTACGACGGTGGTG	22	RsL43	CTAAAGCTCAGCGCTACG	18
LEA44	FL44	CACCATGGCGGATCATCCTCGT	22	RL44	GGTTTCCTTCTTCTTCTCATC	21
	FnoL44	CACCGCGGATCATCCTCGTTCT	22	RsL44	CTAGGTTTCCTTCTTCTTCTC	21
LEA45	FL45	CACCATGGCGGATCTGAAAGAC	22	RL45	AAGATCATTATGGTGGCC	18
	FnoL45	CACCGCGGATCTGAAAGACGAA	22	RsL45	TCAAAGATCATTATGGTG	18
LEA46	FL46	CACCATGCAGTCGATGAAAGAA	22	RL46	TCCAGTATATCCCCCGCC	18
	FnoL46	CACCCAGTCGATGAAAGAAACA	22	RsL46	TTATCCAGTATATCCCCC	18
LEA47	FL47	CACCATGAGCGAAGAACAGCTG	22	RL47	TTTGGACTGATTGATCCG	18
	FnoL47	CACCAGCGAAGAACAGCTGCAG	22	RsL47	TCATTTGGACTGATTGAT	18
LEA48	FL48	CACCATGGCGGCTATGCAGTTAACG	25	RL48	GAACCTCTTGAAATCATCATCC	22
	FnoL48	CACCGCGGCTATGCAGTTAACGAG	24	RsL48	TTAGAACCTCTTGAAATCATCATC	24
LEA49	FL49	CACCATGGGTTCATCAAAAGATAG	24	RL49	AAGAGACGATGGATCGTG	18
	FnoL49	CACCGGTTCATCAAAAGATAGTGC	24	RsL49	TCAAAGAGACGATGGATCG	19
LEA50	FL50	CACCATGATGTTCGGGTTCGGC	22	RL50	AAGAGATACATTGCATGG	18
	FnoL50	CACCATGTTCGGGTTCGGCCTT	22	RsL50	TCAAAGAGATACATTGCA	18
LEA51	FL51	CACCATGGCGTCTTACCAGAAC	22	RL51	ACGGCCACCACCGGGAAG	18
	FnoL51	CACCGCGTCTTACCAGAACCGT	22	RsL51	TTAACGGCCACCACCGGG	18
U16034 (At3g10920)	MSD1-F	CACCATGGCGATTCGTTGTGTAGC	24	MSD1-R	GTTGTTTTCCTTCTCATAAACCTC	24
U12392 (At4g05180)	PsbQ-F	CACCATGGCTCAAGCAGTGACTTCG	25	PsbQ-R	ACCGAGCTTGGCAAGAACATTGTTC	25
U13389 (At5g38430)	RBCS1B-F	CACCATGGCTTCCTCTATGCTCT	23	RBCS1B-R	AGCATCAGTGAAGCTTGG	18
p2FGW7	FpGX	GCGAAACCCTATAAGAACC	19	RpGX	ACCACTACCAGCAGAACA	18
p2GWF7	FpXG	GTGGTGCAGATGAACTTCAG	20	RpXG	GCACAATCCCACTATCCTTC	20
				RevEGFP	TTACTTGTACAGCTCGTCCAT	21
p2GWR7	RFP-F	CACCATGGAGGGCTCCGTGAACGG	24	RevRFP	TTAGGCGCCGGTGGAGTGGC	20
	NLS-F	CACCATGCCACCAAAAAAGAAAAGAAAGGTT	31	NLS-R	AACCTTTCTTTTCTTTTTTGGTGGCAT	27
PDHA1 (NM_000284)	PDHE1-F	ATGAGGAAGATGCTCGCC	18	PDHE1t-R	CCTGGTGAGCACTGTTGTGA	20