

Supplemental Table 2. All identified proteins in thylakoid and envelopes. These proteins were collectively identified in this and other experimental proteomics studies (9,25) (7,24,34). All thylakoid proteins (322+64) and envelope proteins (429) as used for the functional classification in Fig. 5B,C. Proteins were identified by large scale proteomics studies or in more 'classical' biochemical tools or forward or reverse genetics. The presence of a predicted cTP, curated TMD prediction by TMHMM, functional classification (BIN) and assignment into more general functional categories is listed for each accession. These proteins are grouped in 6 fractions, as follows: 1) only thylakoid (150), 2) only thylakoid and envelope (25), 3) thylakoid and envelope and total chloroplast (74), 4) only envelope (222), 5) only envelope and total chloroplast (108), 6) only thylakoid and total chloroplast (135)

only Thylakoid (150)	accession no.	lab annotation	cTP	TMHMM - curated	MapMan bin	Simplified functional categories
only Thylakoid (150)	At4g37220.1	cold acclimation protein homolog		5	20.2.2 stress.abiotic.cold	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At2g21970.1	Sep2 or Lil5		2	20.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At1g45474.1	LHCI-5 - new		3	1.1.2 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At2g05620.1	PGR5		0	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g08550.1	Violaxanthin Deepoxidase (VDE)		0	16.1.1 secondary metabolism	terpenoids & tetrapyrrole synthesis & degradation
only Thylakoid (150)	At5g55330.1			8	16.7 secondary metabolism.v	terpenoids & tetrapyrrole synthesis & degradation
only Thylakoid (150)	At1g03675.1				21.1 redox.thioredoxin	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At2g30860.1	Glutathione S-transferase		0	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At3g48890.1	cytochrome b5 domain-containing pr		1	21.3 redox.heme	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At5g53560.1	cytochrome b5		1	26.1 misc.misc2	unknown function
only Thylakoid (150)	At2g37230.1	pentatricopeptide (PPR) repeat-contai		0	26.15 misc. Pentapeptide rep	unknown function
only Thylakoid (150)	At5g18180.1	glycine-rich protein		0	27 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
only Thylakoid (150)	At3g03920.1	glycine-rich protein		0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
only Thylakoid (150)	At2g21160.1	signal sequence receptor, alpha subun		1	29.3 protein.targeting	protein fate
only Thylakoid (150)	At2g29080.1	FtsH3 - mitochondrial predicted		0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At1g07510.1	FtsH10 - mTP predicted		0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At3g16540.1	DegP protease		0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At3g12340.1	immunophilin / FKBP-type peptidyl-]		0	29.6 protein.(un)foldin	(incl)protein fate
only Thylakoid (150)	At1g06870.1	TPP-1 lumen (LepB1 homologue)		0	29.7 protein. processing	protein fate
only Thylakoid (150)	At1g52410.1	myosin-related, Poly-adenylate bindin		0	31.1 cell.organisation	other developmental & signalling functions
only Thylakoid (150)	At5g65020.1	Annexin - AnnAt2		0	31.1 cell.organisation	other developmental & signalling functions
only Thylakoid (150)	At1g14830.1	dynamine ADL1-thylakoid		0	31.4 cell. vesicle transport	other developmental & signalling functions
only Thylakoid (150)	At5g11710.1			0	31.4 cell. vesicle transport	other developmental & signalling functions
only Thylakoid (150)	At3g20660.1	organic cation transporter family		11	34.14 transport.unspecified c	transport ions & small organic molecules
only Thylakoid (150)	At2g01870.1	expressed protein		1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g49720.1	expressed protein		1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g43750.1	expressed protein		1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g52780.1	expressed protein		2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g15110.1	expressed protein		2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g16640.1	TCTP homolog - tumor protein homo		0	35.2 not assigned.unknown	unknown function
only Thylakoid (150)	At3g23840.1	transferase family I		0	35.2 not assigned.unknown	unknown function
only Thylakoid (150)	At2g45180.1	protease inhibitor/seed storage/lipid t		1	35.2 not assigned.unknown	unknown function
only Thylakoid (150)	At4g20990.1	carbonic anhydrase		0	8.3 TCA / org. transformatio	other metabolic functions
only Thylakoid (150)	At3g15640.1	cytochrome c oxidase subunit Vb		0	9.7 mitochondrial electron tr	mitochondria and other non-chloroplast functions
only Thylakoid (150)	At3g52300.1	ATP synthase D chain		0	9.9 mitochondrial electron tr	mitochondria and other non-chloroplast functions
only Thylakoid (150)	At4g34190.1	Sep1 or Lil4	yes	2	20.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At4g22260.1	IMMUTANS/alt oxidase	yes	1	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At3g25480.1	rhodanese-like domain	yes	1	26.16 misc. Rhodanese doma	unknown function
only Thylakoid (150)	At1g22700.1	tetratricopeptide repeat (TPR)-contair	yes	1	26.17 misc. tetratricopeptide	unknown function
only Thylakoid (150)	At2g28800.1	Alb3 (Albino 3)	yes	6	29.3 protein.targeting	protein fate
only Thylakoid (150)	At2g18710.1	cpSecY	yes	10	29.3 protein.targeting	protein fate
only Thylakoid (150)	At5g15250.1	FtsH6 (formerly pflp)	yes	2	29.5 protein.degradation	protein fate
only Thylakoid (150)	At3g26580.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	ATCG00070	psbK	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00080	psbI	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00220	psbM	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00550	psbJ	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00560	psbL	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00580	psbE cytb559a	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00690	psbT/yef8	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00700	psbN	-encode	1	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00300	psbZ/yef9	-encode	2	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00270	psbD D2	-encode	5	1.1.1 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00510	psaI - subunit IX	-encode	1	1.1.2 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00630	psaJ - subunit VIII	-encode	1	1.1.2 PS.lightreaction - Phot	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00210	petN - ycf6	-encode	1	1.1.3 PS.lightreaction - Cyt	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00590	petL - ycf7 - ORF31	-encode	1	1.1.3 PS.lightreaction - Cyt	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00600	petG -	-encode	1	1.1.3 PS.lightreaction - Cyt	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00730	petD - subIV	-encode	3	1.1.3 PS.lightreaction - Cyt	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00140	CFO-III - atpH	-encode	2	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG00150	CFO-IV - atpI	-encode	5	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlorores

only Thylakoid (150)	ATCG00440	NDH C (3)	-encode	3	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG01070	NDH E (4L)	-encode	3	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG01100	NDH A (1)	-encode	6	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG01250	NDH B (2)	-encode	9	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	ATCG01000	YCF1.2 essential	-encode	6	29.8 protein assembly and co	protein fate
only Thylakoid (150)	At3g22840.1	Lil1.1 - Elip1	yes	2	20.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At5g11450.1	OEC23-like Tat ltp TP21.5	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g54190.1	PORA - down regulated in light; high	yes	0	19 tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
only Thylakoid (150)	At2g22360.1	DnaJ domain family	yes	0	26.14 misc. DnaJ domain wit	unknown function
only Thylakoid (150)	At2g34860.1	DnaJ central domain (4 repeats)	yes	0	26.14 misc. DnaJ domain wit	unknown function
only Thylakoid (150)	At1g49970.1	ClpR1 (nClpP5)	yes	0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At5g39830.1	DegP8 - HhoA homologue or DegQ	yes	0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At1g18170.1	Isomerases TAT ITP	yes	0	29.6 protein.(un)folding (incl	protein fate
only Thylakoid (150)	At1g20810.1	Isomerases - lumen	yes	0	29.6 protein.(un)folding (incl	protein fate
only Thylakoid (150)	At4g19830.1	Isomerases Tat ltp	yes	0	29.6 protein.(un)folding (incl	protein fate
only Thylakoid (150)	At2g43560.1	Isomerases	yes	0	29.6 protein.(un)folding (incl	protein fate
only Thylakoid (150)	At3g57680.1	CtpA-3	yes	0	29.7 protein. processing	protein fate
only Thylakoid (150)	At5g45680.1	AtFKBP13 - ITP-TAT (involved with	yes	0	29.8 protein assembly and co	protein fate
only Thylakoid (150)	At5g42765.1	Expressed protein ITP?	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g53560.1	chloroplast lumen common protein fa	yes	0	35.2 not assigned.unknown	unknown function
only Thylakoid (150)	At4g14690.1	Lil1.2 - Elip2	yes	3	20.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At1g76100.1	PC-2	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At2g06520.1	psbX precursor 1 TM ITP but spontar	yes	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At2g30570.1	psbW - 'LTP' but spontaneous	yes	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g67740.1	psbY1+2	yes	2	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g08380.1	psaO	yes	2	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g30380.1	psaK - subunit X	yes	2	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At2g26500.1	petM - 4 kDa Tat ltp	yes	1	1.1.3 PS.lightreaction - Cyto	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g21430.1	DnaJ domain family	yes	1	26.14 misc. DnaJ domain wit	unknown function
only Thylakoid (150)	At3g56010.1	expressed protein CHLOROPLAST 3	yes	1	29.2.1 protein.synthesis.chlor	(Regulation) DNA organization,transcription and translation
only Thylakoid (150)	At3g53470.1	S40 ribosomal protein S25	yes	1	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only Thylakoid (150)	At2g01110.1	TATC-like	yes	6	29.3 protein.targeting	protein fate
only Thylakoid (150)	At5g05740.1	expressed protein similar to unknown	yes	3	29.5 protein.degradation	protein fate
only Thylakoid (150)	At1g50020.1	tubulin alpha-6 chain	yes	1	31.1 cell.organisation	other developmental & signalling functions
only Thylakoid (150)	At5g21930.1	PAA2 - ATP-Copper transport - thyl	yes	3	34.12 transport.metal	transport ions & small organic molecules
only Thylakoid (150)	At1g73885.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At1g78915.1	unknown protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At2g17972.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At2g29180.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At2g42975.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g02160.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g37360.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g17930.1	expressed protein C/M	yes	2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At4g11960.1	expressed protein	yes	2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At4g38100.1	expressed protein	yes	2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g36120.1	expressed protein - YGGT family	yes	2	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g55710.1	expressed protein - C/M	yes	3	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g47110.1	Lil3.1	yes	2	20.2.5 stress abiotic light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At4g17600.1	Lil3.2	yes	2	20.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At3g56690.1	calmodulin-binding protein	yes	0	30.3 signalling.calcium	other developmental & signalling functions
only Thylakoid (150)	At1g10960.1	Fd1-leaf	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g60950.1	Fd2-leaf	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At4g05390.1	FNR-3	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g45040.1	cytochrome c6	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g02120.1	Ohp1 or Lil2/Hlip/Scp	yes	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At2g34420.1	LHCII-1.5	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g76570.1	putative lhcb3 or putative lhcb5	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g51400.1	psbTn-2	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At3g01440.1	PsbQ domain Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At4g28660.1	psbW -like sequencing project	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At3g21055.1	psbTn-1 - ITP	yes	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At3g16140.1	psaH-1 - subunit VI	yes	1	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At1g19150.1	LHCI-1-2 - LHC-730	yes	3	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At3g26650.1	glyceraldehyde 3-phosphate dehydrog	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only Thylakoid (150)	At1g68830.1	Stt7-At1 kinase state transition thylak	yes	0	1.5 PS. lightreaction state tra	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g01920.1	Stt7-At2 kinase state transition thylal	yes	0	1.5 PS. lightreaction state tra	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only Thylakoid (150)	At5g01600.1	Ferritin 1	yes	0	15.2 metal handling.binding,	metal handling.binding, chelation and storage
only Thylakoid (150)	At2g15570.1	thioredoxin m3	yes	0	21.1 redox.thioredoxin	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At1g80030.1	DnaJ domain family	yes	0	26.14 misc. DnaJ domain wit	unknown function
only Thylakoid (150)	At2g42130.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At3g26080.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response

only Thylakoid (150)	At3g58010.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only Thylakoid (150)	At3g53460.1	RNA binding protein CP29 A'	yes	0	28 (Regulation) transcription (Regulation) DNA organization,	transcription and translation
only Thylakoid (150)	At1g78630.1	30S ribosomal protein S5	yes	0	29.2.2 protein.synthesis.misc (Regulation) DNA organization,	transcription and translation
only Thylakoid (150)	At3g63190.1	Putative ribosome recycling factor	yes	0	29.2.99 protein.synthesis.mis (Regulation) DNA organization,	transcription and translation
only Thylakoid (150)	At2g45770.1	cpFtsY	yes	0	29.3 protein.targeting	protein fate
only Thylakoid (150)	At2g47940.1	DegP2 - HhoA homologue or DegQ	yes	0	29.5 protein.degradation	protein fate
only Thylakoid (150)	At4g17740.1	CtpA-1 - Satoh - spinach	yes	0	29.7 protein. processing	protein fate
only Thylakoid (150)	At5g46390.1	CtpA-2 - (also CtpC) barley - Pakrasf	yes	0	29.7 protein. processing	protein fate
only Thylakoid (150)	At2g27290.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At4g28025.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g09050.1	unknown protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At1g74880.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At2g36145.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At3g47860.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g42070.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At1g71480.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At2g21530.1	unknown protein	yes	0	35.2 not assigned. unknown	unknown function
only Thylakoid (150)	At5g04740.1	ACT domain-containing protein	yes	0	35.2 not assigned. unknown	unknown function

only envelope (222)	accession no.	lab annotation	CTP	TMHMM - curated	MapMan bin	Simplified functional cetergies
only envelope (222)	At4g12020.1	disease resistance protein -related DN		0	20.1 stress.biotic	redox proteins & oxidative defense & stress response
only envelope (222)	At5g40100.1	disease resistance protein (TIR-NBS-		0	20.1 stress biotic	redox proteins & oxidative defense & stress response
only envelope (222)	At5g23190.1	P450 monooxygenase (CYP86B1 in f		2	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
only envelope (222)	At2g01220.1	expressed protein		0	11.3 lipid metabolism.Phospl	hormone and lipid metabolism
only envelope (222)	At3g55030.1	PG-phosphate synthase 1 -		3	11.3 lipid metabolism.Phospl	hormone and lipid metabolism
only envelope (222)	At5g16010.1	3-oxo-5-alpha-steroid 4-dehydrogena		5	11.8 lipid metabolism.exotic	hormone and lipid metabolism
only envelope (222)	At1g52570.1	phospholipase D		0	11.9.3 lipid metabolism.lipid	hormone and lipid metabolism
only envelope (222)	At1g66200.1	glutamine synthetase		0	12.2 N-metabolism.ammonia N,	S, aa and nucleotide metabolism
only envelope (222)	At1g11840.1	glyoxalase I, putative (lactoylglutathi		0	13.3.2.2 amino acid metaboli	N, S, aa and nucleotide metabolism
only envelope (222)	At4g33010.1	glycine decarboxylase/glycine cleava		0	13.5.2.1 amino acid metaboli	N, S, aa and nucleotide metabolism
only envelope (222)	At1g11860.1	aminomethyltransferase-related precu		0	13.5.2.2 amino acid metaboli	N, S, aa and nucleotide metabolism
only envelope (222)	At1g60690.1	aldo/keto reductase family		0	17.2.3 hormone metabolism.h	hormone and lipid metabolism
only envelope (222)	At2g47750.1	auxin-responsive protein -related		0	17.2.3 hormone metabolism.h	hormone and lipid metabolism
only envelope (222)	At1g07420.1	C-4 methyl sterol oxidase identical to		4	17.3 hormone metabolism.br:	hormone and lipid metabolism
only envelope (222)	At5g14220.1	protoporphyrinogen oxidase (PPO) (F		0	19 tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At4g35460.1	NADPH-dependent thioredoxin reduc		0	21.1 redox.thioredoxin	redox proteins & oxidative defense & stress response
only envelope (222)	At4g35000.1	ascorbate peroxidase, putative (APX)		1	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only envelope (222)	At3g27820.1	monodehydroascorbate reductase (MI		1	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only envelope (222)	At1g20630.1	catalase 1		0	21.6 redox.dismutases and ca	redox proteins & oxidative defense & stress response
only envelope (222)	At1g80270.1	DNA binding protein, PPR repeat		0	26.15 misc. Pentapeptide rep	unknown function
only envelope (222)	At2g44490.1	glycosyl hydrolase family 1		1	26.3 misc.gluco-, galacto-	an unknown function
only envelope (222)	At3g06510.1	glycosyl hydrolase family 1		2	26.3 misc.gluco-, galacto-	an unknown function
only envelope (222)	At2g47250.1	RNA helicase, putative		0	27.1 RNA.processing	(Regulation) DNA organization,transcription and translation
only envelope (222)	At4g35460.1	transcriptional factor B3 family		0	27.2 RNA.transcription	(Regulation) DNA organization,transcription and translation
only envelope (222)	At5g35210.1	PHD finger transcription factor		5	27.3 RNA.regulation of trans	(Regulation) DNA organization,transcription and translation
only envelope (222)	At4g13130.1	CHP-rich zinc finger protein		0	28 (Regulation) transcription	(Regulation) DNA organization,transcription and translation
only envelope (222)	At2g41130.1	bHLH protein family		0	28. DNA.unspecified	(Regulation) DNA organization,transcription and translation
only envelope (222)	At3g60170.1	expressed protein		0	28.1 DNA.synthesis/chromat	(Regulation) DNA organization,transcription and translation
only envelope (222)	At5g43530.1	SNF2 domain/helicase domain/RING		0	28.2 DNA.repair	(Regulation) DNA organization,transcription and translation
only envelope (222)	At1g13930.1	expressed protein		0	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only envelope (222)	At1g26910.1	60S ribosomal protein L10 (RPL10B)		0	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only envelope (222)	At1g33140.1	60S ribosomal protein L9 (RPL90A/C		0	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only envelope (222)	At4g34620.1	30S ribosomal protein S16p family		0	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only envelope (222)	At5g29771.1	putative ribosomal protein S1		0	29.2.2 protein.synthesis.misc	(Regulation) DNA organization,transcription and translation
only envelope (222)	At4g26670.1	expressed protein		0	29.3 protein targeting	protein fate
only envelope (222)	At3g49560.1	expressed protein		0	29.3 protein.targeting	protein fate
only envelope (222)	At5g24650.1	expressed protein		0	29.3 protein.targeting	protein fate
only envelope (222)	At1g02280.1	Toc33		0	29.3 protein.targeting	protein fate
only envelope (222)	At2g16640.1	Toc132		0	29.3 protein.targeting	protein fate
only envelope (222)	At4g09080.1	Toc75-IV		0	29.3 protein.targeting	protein fate
only envelope (222)	At4g15440.1	Hydroperoxide Lyase (HPL) like prot		0	29.3 protein.targeting	protein fate
only envelope (222)	At5g55510.1	expressed protein		0	29.3 protein.targeting	protein fate
only envelope (222)	At3g17960.1	HP64b (TOC64 homolog) Toc64-III		0	29.3 protein.targeting	protein fate
only envelope (222)	At1g76370.1	protein kinase,		0	29.4 protein.postranslational	protein fate
only envelope (222)	At1g64520.1	26S proteasome regulatory subunit (R		0	29.5 protein.degradation	protein fate
only envelope (222)	At5g63110.1	histone deacetylase		0	31.1 cell.organisation	other developmental & signalling functions
only envelope (222)	At2g40060.1	expressed protein		0	31.4 cell. vesicle transport	other developmental & signalling functions
only envelope (222)	At3g19720.1	Arc5-1		0	31.5 plastid division	plastid division and plastid vesicles
only envelope (222)	At3g19730.1	Arc5-2		0	31.5 plastid division	plastid division and plastid vesicles
only envelope (222)	At3g52750.1	FtsZ2.2 plastid division - tubulin mot		0	31.5 plastid division	plastid division and plastid vesicles

only envelope (222)	At1g24490.1	artemis- ALBINO3 -related	4	31.5 plastid division	plastid division and plastid vesicles
only envelope (222)	At4g38510.1	probable H ⁺ -transporting ATPase	0	34.1 transport.p- and v-ATPa	transport ions & small organic molecules
only envelope (222)	At1g26130.1	haloacid dehalogenase-like hydrolase	10	34.1 transport.p- and v-ATPa	transport ions & small organic molecules
only envelope (222)	At4g37270.1	ATPase, E1-E2 type family	5	34.12 transport.metal	transport ions & small organic molecules
only envelope (222)	At2g01980.1	sodium proton exchanger, putative (N	9	34.14 transport.unspecified c	transport ions & small organic molecules
only envelope (222)	At4g00630.1	K ⁺ efflux antiporter	11	34.15 transport.potassium	transport ions & small organic molecules
only envelope (222)	At4g25450.1	ABC transporter family	5	34.16 transport.ABC transpo	transport ions & small organic molecules
only envelope (222)	At5g58270.1	ABC transporter family protein	5	34.16 transport.ABC transpo	transport ions & small organic molecules
only envelope (222)	At3g61430.1	plasma membrane intrinsic protein 1/	6	34.19.1 transport.Major Intriit	transport ions & small organic molecules
only envelope (222)	At2g36830.1	major intrinsic protein (MIP) family	7	34.19.2 transport.Major Intriit	transport ions & small organic molecules
only envelope (222)	ATCG00530	YCF10 - cemA envelope - carbon tra	3	34.8 transport.metabolite trar	transport ions & small organic molecules
only envelope (222)	At1g19800.1	TDG1 - permease	5	34.8 transport.metabolite trar	transport ions & small organic molecules
only envelope (222)	At3g26570.1	PH2;1 Phosphate translocator - Na ⁺ /	13	34.8 transport.metabolite trar	transport ions & small organic molecules
only envelope (222)	At2g35800.1	mitochondrial carrier protein family	0	34.9 transport.metabolite trar	mitochondria and other non-chloroplast function
only envelope (222)	At4g28390.1	mitochondrial ADP,ATP carrier prote	3	34.9 transport.metabolite trar	mitochondria and other non-chloroplast function
only envelope (222)	At1g15500.1	adenine nucleotide translocase	11	34.9 transport.metabolite trar	mitochondria and other non-chloroplast function
only envelope (222)	At2g11910.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At1g03780.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At1g19100.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g11600.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g37930.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g40550.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g12570.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g27100.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At4g24150.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At5g39410.1	expressed protein	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At5g02940.1	expressed protein	2	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g22620.1	protease inhibitor/seed storage/lipid t	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g02980.1	expressed protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g07120.1	expressed protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g45170.1	OEP24-II	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g67120.1	expressed protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g67700.1	auxin-regulated protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g76405.1	OEP21-I	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At3g06940.1	mudrA protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At3g10840.1	hydrolase, alpha/beta fold family	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g07780.1	athila transposon protein -related	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g08020.1	transposon protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g23430.1	short-chain dehydrogenase/reductase	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g24450.1	expressed protein hypothetical protei	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At5g51320.1	expressed protein	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At5g64430.1	octicosapeptide/Phox/Bem1p (PB1)	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At3g28220.1	expressed protein	1	35.2 not assigned.unknown	unknown function
only envelope (222)	At2g42770.1	peroxisomal membrane protein famil	2	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g00290.1	expressed protein	4	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g70410.1	carbonic anhydrase	0	8.3 TCA / org. transformatio	other metabolic functions
only envelope (222)	At5g08690.1	H ⁺ -transporting ATP synthase beta cl	0	9.9 mitochondrial electron tr	mitochondria and other non-chloroplast functions
only envelope (222)	At2g07698.1	expressed protein	3	9.9 mitochondrial electron tr	mitochondria and other non-chloroplast functions
only envelope (222)	At4g30950.1	FD6C = omega-6 fatty acid desaturas	yes 2	11.2 lipid metabolism.FA des	hormone and lipid metabolism
only envelope (222)	At4g03320.1	Tic20-IV	yes 4	29.3 protein.targeting	protein fate
only envelope (222)	At2g26900.1	bile acid:sodium symporter family	yes 9	34.1 transport.nucleotides	transport ions & small organic molecules
only envelope (222)	At5g03910.1	ABC transporter family protein	yes 2	34.16 transport.ABC transpo	transport ions & small organic molecules
only envelope (222)	At3g51140.1	expressed protein hypothetical protei	yes 4	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g61870.1	expressed protein hypothetical protei	yes 4	35.2 not assigned. unknown	unknown function
only envelope (222)	At5g03900.1	expressed protein predicted protein, S	yes 2	35.2 not assigned.unknown	unknown function
only envelope (222)	At2g38550.1	putative non-green plastid inner envel	yes 3	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g24360.1	3-oxoacyl-[acyl-carrier protein] reduc	yes 0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
only envelope (222)	At5g17990.1	anthranilate phosphoribosyltransferas	yes 0	13.6.3.1 amino acid metaboli	N, S, aa and nucleotide metabolism
only envelope (222)	At5g67030.1	zeaxanthin epoxidase precursor (LOS	yes 0	16.1.1 secondary metabolis	terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At5g47190.1	50S ribosomal protein L19	yes 0	29.2.1 protein.synthesis.chlor	(Regulation) DNA organization,transcription and translation
only envelope (222)	At2g37400.1	chloroplast lumen protein?	yes 0	35.2 not assigned.unknown	unknown function
only envelope (222)	At5g05580.1	Temperature-sensitive omega-3 fatty	yes 3	11.2 lipid metabolism.FA des	hormone and lipid metabolism
only envelope (222)	At3g11170.1	F9F8.4 omega-3 fatty acid desaturase	yes 3	11.2 lipid metabolism.FA des	hormone and lipid metabolism
only envelope (222)	At2g39290.1	Phosphatidylglycero-phosphate synth	yes 1	11.3 lipid metabolism.Phosphl	hormone and lipid metabolism
only envelope (222)	At4g30580.1	LPAAT (ACT2) = plastidial lysophos	yes 2	11.3 lipid metabolism.Phosphl	hormone and lipid metabolism
only envelope (222)	At1g78620.1	expressed protein	yes 3	11.3 lipid metabolism.Phosphl	hormone and lipid metabolism
only envelope (222)	At3g60620.1	phosphatidate cytidyllyltransferase	yes 6	11.3 lipid metabolism.Phosphl	hormone and lipid metabolism
only envelope (222)	At1g08640.1	DnaJ domain family	yes 3	26.14 misc. DnaJ domain wit	unknown function
only envelope (222)	At1g04940.1	Tic20-I - ok	yes 3	29.3 protein.targeting	protein fate
only envelope (222)	At5g64940.1	ABC transporter-related	yes 1	34.16 transport.ABC transpo	transport ions & small organic molecules
only envelope (222)	At5g22830.1	magnesium transporter protein (GMN	yes 2	34.18 transport.unspecified a	transport ions & small organic molecules

only envelope (222)	At1g80300.1	ATP/ADP translocator (AATP1)	yes	9	34.8 transport.metabolite trar transport ions & small organic molecules
only envelope (222)	At2g29650.1	ANTR1 - anion transporter	yes	10	34.8 transport.metabolite trar transport ions & small organic molecules
only envelope (222)	At5g52540.1	expressed protein	yes	10	34.8 transport.metabolite trar transport ions & small organic molecules
only envelope (222)	At4g00370.1	ANTR2 - anion transporter	yes	10	34.8 transport.metabolite trar transport ions & small organic molecules
only envelope (222)	At5g16150.1	IIEP62 (putative sugar transporter)	yes	10	34.8 transport.metabolite trar transport ions & small organic molecules
only envelope (222)	At4g39460.1	mitochondrial carrier protein family	yes	5	34.9 transport.metabolite trar mitochondria and other non-chloroplast function
only envelope (222)	At1g20830.1	expressed protein	yes	1	35.2 not assigned. unknown unknown function
only envelope (222)	At5g22790.1	expressed protein	yes	1	35.2 not assigned. unknown unknown function
only envelope (222)	At5g43745.1	expressed protein	yes	2	35.2 not assigned. unknown unknown function
only envelope (222)	At5g19750.1	??expressed protein 22kDa peroxisom	yes	2	35.2 not assigned. unknown unknown function
only envelope (222)	At5g13720.1	expressed protein	yes	3	35.2 not assigned. unknown unknown function
only envelope (222)	At5g23040.1	expressed protein	yes	3	35.2 not assigned. unknown unknown function
only envelope (222)	At2g15290.1	expressed protein	yes	3	35.2 not assigned. unknown unknown function
only envelope (222)	At1g67080.1	expressed protein	yes	4	35.2 not assigned. unknown unknown function
only envelope (222)	At1g48460.1	expressed protein	yes	5	35.2 not assigned. unknown unknown function
only envelope (222)	At3g20320.1	expressed protein	yes	1	35.2 not assigned.unknown unknown function
only envelope (222)	At3g08640.1	glycine-rich protein	yes	2	35.2 not assigned.unknown unknown function
only envelope (222)	At5g62720.1	IIEP18 unknown function	yes	4	35.2 not assigned.unknown unknown function
only envelope (222)	At4g13590.1	expressed protein	yes	4	35.2 not assigned.unknown unknown function
only envelope (222)	At3g56160.1	expressed protein	yes	5	35.2 not assigned.unknown unknown function
only envelope (222)	At5g17520.1	root cap 1 (RCP1) identical to GI:613	yes	9	35.2 not assigned.unknown unknown function
only envelope (222)	At2g42530.1	cold-regulated protein (cor15b)	yes	0	20.2.2 stress.abiotic.cold redox proteins & oxidative defense & stress response
only envelope (222)	At1g19870.1	expressed protein	yes	0	30.8 signalling.misc other developmental & signalling functions
only envelope (222)	At5g38420.1	Rubisco small subunit 2b (RBCS-2b)	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only envelope (222)	At5g61410.1	ribulose-5-phosphate-3-epimerase	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only envelope (222)	At5g46290.1	3-oxoacyl-[acyl-carrier-protein] syntf	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At1g77590.1	LACS9 - acyl-CoA synthetase -	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At3g15690.1	biotin carboxylase (BC) - part of ACC	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At4g25050.1	acyl carrier protein family similar to /	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At5g15530.1	biotin carboxyl carrier protein BCCP-	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At5g16390.1	biotin carboxyl carrier protein BCCP-	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At1g35360.1	acetyl-CoA carboxylase	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism
only envelope (222)	At5g01220.1	UDP-sulfoquinovose:DAG sulfoquin-	yes	0	11.3 lipid metabolism.Phospl hormone and lipid metabolism
only envelope (222)	At4g31780.1	MGD1 - monogalactosyldiacylglycer	yes	0	11.3 lipid metabolism.Phospl hormone and lipid metabolism
only envelope (222)	At1g74040.1	2-isopropylmalate synthase -related	yes	0	13.4.2.1 amino acid metaboli N, S, aa and nucleotide metabolism
only envelope (222)	At1g80560.1	3-isopropylmalate dehydrogenase	yes	0	13.4.2.1 amino acid metaboli N, S, aa and nucleotide metabolism
only envelope (222)	At2g33740.1	CUTA - copper chaperone	yes	0	15.2 metal handling.binding, Co-factor and vitamine metabolism, metal handling & storage
only envelope (222)	At2g40300.1	ferritin -related	yes	0	15.2 metal handling.binding, Co-factor and vitamine metabolism, metal handling & storage
only envelope (222)	At3g56090.1	expressed protein ferritin 2	yes	0	15.2 metal handling.binding, Co-factor and vitamine metabolism, metal handling & storage
only envelope (222)	At3g04870.1	zeta-carotene desaturase (ZDS) [carot	yes	0	16.1.1 secondary metabolism terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At3g53130.1	LUT1-cytochrome P450-type monoo:	yes	0	16.1.1 secondary metabolism terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At5g18660.1	isoflavone reductase-related	yes	0	16.3 secondary metabolism.fl terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At5g54770.1	TH11 -involved in thiamine synthesis	yes	0	18 Co-factor and vitamine mCo-factor and vitamine metabolism, metal handling & storage
only envelope (222)	At1g80560.1	uroporphyrinogen decarboxylase (UP	yes	0	19 tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At5g08280.1	hydroxymethylbilane synthase	yes	0	19 tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At4g37000.1	red chlorophyll catabolite reductase (l	yes	0	19.1 tetrapyrrole degradation terpenoids & tetrapyrrole synthesis & degradation
only envelope (222)	At5g19220.1	ADP-glucose pyrophosphorylase) (Al	yes	0	2.1.2 major CHO metabolism Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only envelope (222)	At1g76080.1	thioredoxin family	yes	0	21.1 redox.thioredoxin redox proteins & oxidative defense & stress response
only envelope (222)	At2g47730.1	glutathione transferase, putative (GST	yes	0	21.2 redox.ascorbate and glutaredox proteins & oxidative defense & stress response
only envelope (222)	At5g63310.1	NDPK2-stromal	yes	0	23.4 nucleotide metabolism.fN, S, aa and nucleotide metabolism
only envelope (222)	At3g23790.1	AMP-binding protein, putative simila	yes	0	26.1 misc.misc2 unknown function
only envelope (222)	At3g18420.1	expressed protein contains TPR doma	yes	0	26.17 misc. tetratricopeptide unknown function
only envelope (222)	At5g50250.1	31 kDa ribonucleoprotein (AtRBP33)	yes	0	28 (Regulation) transcription (Regulation) DNA organization,transcription and translation
only envelope (222)	At3g52170.1	PEND - PD2 - DNA binding - nucleo	yes	0	28 DNA.unspecified (Regulation) DNA organization,transcription and translation
only envelope (222)	At3g48420.1	haloacid dehalogenase-like hydrolase	yes	0	28.1 DNA.synthesis/chromat (Regulation) DNA organization,transcription and translation
only envelope (222)	At1g75350.1	50S ribosomal protein L31 chloroplas	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only envelope (222)	At4g17560.1	50S ribosomal protein L19	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only envelope (222)	At1g48350.1	50S ribosomal protein L18p	yes	0	29.2.2 protein.synthesis.misc (Regulation) DNA organization,transcription and translation
only envelope (222)	At1g17220.1	translation initiation factor IF-2	yes	0	29.2.3 protein.synthesis.initia (Regulation) DNA organization,transcription and translation
only envelope (222)	At5g19620.1	Toc75-V- putative protein outer mem	yes	0	29.3 protein.targeting protein fate
only envelope (222)	At5g55220.1	Trigger Factor	yes	0	29.3 protein.targeting protein fate
only envelope (222)	At3g04340.1	expressed protein	yes	0	29.5 protein.degradation protein fate
only envelope (222)	At5g64580.1	FtsH putative????	yes	0	29.5 protein.degradation protein fate
only envelope (222)	At3g16290.1	FtsH hypothetical	yes	0	29.5 protein.degradation protein fate
only envelope (222)	At3g47060.1	FtsH7	yes	0	29.5 protein.degradation protein fate
only envelope (222)	At3g13470.1	Cpn60-beta-1	yes	0	29.6 protein.(un)folding (incl protein fate
only envelope (222)	At5g51070.1	ClpD (Erd1)	yes	0	29.6 protein.(un)folding (incl protein fate
only envelope (222)	At5g10470.1	kinesin-related protein TH65 protein	yes	0	31.1 cell.organisation other developmental & signalling functions
only envelope (222)	At4g33650.1	dynamidin ADL 2-envelope	yes	0	31.4 cell. vesicle transport other developmental & signalling functions
only envelope (222)	At5g42480.1	Arc6 (AtFN2) DnaJ family	yes	0	31.5 plastid division plastid division and plastid vesicles
only envelope (222)	At1g69390.1	MinE	yes	0	31.5 plastid division plastid division and plastid vesicles

only envelope (222)	At2g36250.1	FtsZ2.1 plastid division - tubulin mot	yes	0	31.5 plastid division	plastid division and plastid vesicles
only envelope (222)	At5g24020.1	MinD	yes	0	31.5 plastid division	plastid division and plastid vesicles
only envelope (222)	At4g33520.1	PAA1 - copper transport envelope	yes	0	34.12 transport.metal	transport ions & small organic molecules
only envelope (222)	At4g33460.1	ABC transporter family protein	yes	0	34.16 transport.ABC transpo	transport ions & small organic molecules
only envelope (222)	At5g01500.1	mitochondrial carrier protein family	yes	0	34.17 transport.peroxisomes	transport ions & small organic molecules
only envelope (222)	At3g11560.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At4g27990.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At1g06380.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At1g16080.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g21385.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g36835.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At2g44640.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g32930.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g59840.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At3g63170.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At5g01590.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
only envelope (222)	At1g10510.1	expressed protein similar to ribonucle	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g04420.1	aldo/keto reductase family	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g15140.1	oxidoreductase NAD-binding domain	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g16720.1	expressed protein	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g80380.1	auxin-regulated protein	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At2g27680.1	aldo/keto reductase family	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At2g43950.1	OE37	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At3g07430.1	expressed protein	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g30620.1	expressed protein hypothetical protein	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At4g39970.1	haloacid dehalogenase-like hydrolase	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At5g38520.1	hydrolase	yes	0	35.2 not assigned.unknown	unknown function
only envelope (222)	At1g01090.1	E1alpha - pyruvate dehydrogenase co	yes	0	8.1 TCA / org. transformatio	other metabolic functions
only envelope (222)	At1g30120.1	E1 beta- pyruvate dehydrogenase con	yes	0	8.1 TCA / org. transformatio	other metabolic functions
only envelope (222)	At5g58330.1	malate dehydrogenase [NADP]	yes	0	8.2 TCA / org. transformatio	other metabolic functions

Only Thylakoid & Envelope (25)	accession no.	lab annotation	cTP	TMHMM - curated	MapMan bin	Simplified functional categories
ly Thylakoid & Envelope	At5g22640.1	expressed protein		0	30.4 signalling.phosphinositi	other developmental & signalling functions
ly Thylakoid & Envelope	At4g13010.1	ceQORH - oxidoreductase, Zn bindin		0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
ly Thylakoid & Envelope	At1g16790.1	expressed protein		0	35.2 not assigned. unknown	unknown function
ly Thylakoid & Envelope	At1g33810.1	expressed protein		0	35.2 not assigned. unknown	unknown function
ly Thylakoid & Envelope	At3g47070.1	phosphoprotein -peripheral thylakoid		0	35.2 not assigned.unknown	unknown function
ly Thylakoid & Envelope	At3g52230.1	OM24 orthologue		0	35.2 not assigned.unknown	unknown function
ly Thylakoid & Envelope	At5g14740.1	carbonic anhydrase 2		0	8.3 TCA / org. transformatio	other metabolic functions
ly Thylakoid & Envelope	At1g65260.1	Vipp1 - mutant HCF155	yes	0	29.3 protein.targeting	protein fate
ly Thylakoid & Envelope	At5g28750.1	Tha4 Tata/E	yes	1	29.3 protein.targeting	protein fate
ly Thylakoid & Envelope	At5g16660.1	expressed protein - C/M	yes	1	35.2 not assigned. unknown	unknown function
ly Thylakoid & Envelope	At3g27690.1	LHCII-2.4	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesi
ly Thylakoid & Envelope	At5g09650.1	Inorganic phosphatase like	yes	0	23.4 nucleotide metabolism.†N, S, aa and nucleotide	metabolism
ly Thylakoid & Envelope	At5g35170.1	adenylate kinase	yes	0	23.4 nucleotide metabolism.†N, S, aa and nucleotide	metabolism
ly Thylakoid & Envelope	At2g37220.1	RNA binding protein CP29 B'	yes	0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
ly Thylakoid & Envelope	At5g16620.1	Tic40	yes	0	29.3 protein.targeting	protein fate
ly Thylakoid & Envelope	At1g02560.1	ClpP5 (nClpP1)	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At1g09130.1	ClpR3 (nClpP8)	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At1g12410.1	ClpR2 (nClpP2)	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At1g66670.1	ClpP3 (nClpP3)	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At4g12060.1	ClpS2	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At4g17040.1	ClpR4 (nClpP9)	yes	0	29.5 protein.degradation	protein fate
ly Thylakoid & Envelope	At2g43630.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
ly Thylakoid & Envelope	At5g08540.1	expressed protein	yes	0	35.2 not assigned. unknown	unknown function
ly Thylakoid & Envelope	At1g74640.1	expressed protein contains Pfam profi	yes	0	35.2 not assigned.unknown	unknown function
ly Thylakoid & Envelope	At2g24020.1	expressed protein	yes	0	35.2 not assigned.unknown	unknown function

Only Env and Chlor (108)	accession no.	lab annotation	cTP	TMHMM - curated	MapMan bin	Simplified functional categories
Only Env and Chlor (108)	At2g42540.1	cold-regulated protein (cor15a)		0	20.2.2 stress.abiotic.cold	redox proteins & oxidative defense & stress response
Only Env and Chlor (108)	At3g14210.1	myrosinase-associated protein		1	11.9.1 lipid metabolism.lipid hormone and lipid	metabolism
Only Env and Chlor (108)	At3g03780.1	methionine synthase		0	13.3.4.1 amino acid metaboli	N, S, aa and nucleotide metabolism
Only Env and Chlor (108)	At2g26080.1	glycine dehydrogenase [decarboxylat		0	13.5.2.2 amino acid metaboli	N, S, aa and nucleotide metabolism
Only Env and Chlor (108)	At2g43940.1	thiol methyltransferase		0	16.5 secondary metabolism.s	terpenoids & tetrapyrrole synthesis & degradation
Only Env and Chlor (108)	At4g01690.1	protoporphyrinogen oxidase (PPO) (F		0	19 tetrapyrrole synthesis	hormone and lipid metabolism
Only Env and Chlor (108)	At1g20620.1	catalase 3		0	21.6 redox.dismutases and care	redox proteins & oxidative defense & stress response
Only Env and Chlor (108)	At1g15690.1	inorganic pyrophosphatase		14	23.4 nucleotide metabolism.†N, S, aa and nucleotide	metabolism
Only Env and Chlor (108)	At3g11950.1	UbiA prenyltransferase family		7	26.5.1 misc. prenyltransferas	unknown function
Only Env and Chlor (108)	At1g09340.1	RNA-binding protein		0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
Only Env and Chlor (108)	At4g02510.1	OE37 (TOC159) (putative chloropla		0	29.3 protein.targeting	protein fate

Only Env and Chlor (108)	At5g05000.1	Toc34, component of the import appa	0	29.3 protein.targeting	protein fate	
Only Env and Chlor (108)	At1g56410.1	HSP70t-1	0	29.6 protein.(un)folding (incl protein fate		
Only Env and Chlor (108)	At1g78900.1	ATPase 70 kDa	0	34.1 transport.p- and v-ATPase	transport ions & small organic molecules	
Only Env and Chlor (108)	At5g13490.1	mitochondrial ADP,ATP carrier prote	3	34.14 transport.unspecified c	transport ions & small organic molecules	
Only Env and Chlor (108)	At1g01790.1	K+ efflux antiporter, putitive (KEA1)	11	34.15 transport.potassium	transport ions & small organic molecules	
Only Env and Chlor (108)	At5g15090.1	voltage-dependent anion-selective ch	0	34.18 transport.unspecified a	transport ions & small organic molecules	
Only Env and Chlor (108)	At3g16240.1	delta tonoplast integral protein (delta-	6	34.19.2 transport.Major Intriit	transport ions & small organic molecules	
Only Env and Chlor (108)	At3g01280.1	porin-related	0	34.2 transport.porins	transport ions & small organic molecules	
Only Env and Chlor (108)	At5g67500.1	porin-related protein	0	34.2 transport.porins	transport ions & small organic molecules	
Only Env and Chlor (108)	At5g19760.1	oxoglutarate/malate translocator	0	34.8 transport.metabolite trar	transport ions & small organic molecules	
Only Env and Chlor (108)	At5g46110.1	TPT - IEP30 = Phosphate/triose-phos	9	34.8 transport.metabolite trar	transport ions & small organic molecules	
Only Env and Chlor (108)	At2g28900.1	OEP16 - HP15	0	34.9 transport.misc	transport ions & small organic molecules	
Only Env and Chlor (108)	At3g08580.1	mitochondrial ADP,ATP carrier prote	3	34.9 transport.metabolite trar	mitochondria and other non-chloroplast function	
Only Env and Chlor (108)	At3g60590.1	expressed protein	5	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At3g22520.1	expressed protein	0	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At5g17670.1	expressed protein	0	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At4g00640.1	expressed protein	0	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At1g30360.1	ERD4 protein	10	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At5g42960.1	OEP24-II	0	35.2 not assigned.unknown	unknown function	
Only Env and Chlor (108)	At3g13930.1	acetyltransferase-related	0	8.1 TCA / org. transformatio	other metabolic functions	
Only Env and Chlor (108)	At5g09660.1	malate dehydrogenase, glyoxysomal i	0	8.2 TCA / org. transformatio	other metabolic functions	
Only Env and Chlor (108)	At5g33320.1	PPT - IEP33 = Phosphate/phosphoen	yes	6	34.8 transport.metabolite trar	transport ions & small organic molecules
Only Env and Chlor (108)	At5g12860.1	IEP45 = 2-oxoglutarate/malate transl	yes	13	34.8 transport.metabolite trar	transport ions & small organic molecules
Only Env and Chlor (108)	At2g04030.1	HSP90	yes	0	20.2.1 stress.abiotic.heat	redox proteins & oxidative defense & stress response
Only Env and Chlor (108)	At3g16950.1	dihydroliipoamide dehydrogenase 1, p	yes	0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
Only Env and Chlor (108)	At1g23740.1	oxidoreductase, zinc-binding dehydre	yes	0	17.2.3 hormone metabolism.h	hormone and lipid metabolism
Only Env and Chlor (108)	At4g25080.1	magnesium-protoporphyrin IX methy	yes	0	19 tetrapyrrole synthesis	hormone and lipid metabolism
Only Env and Chlor (108)	At1g06950.1	Tic110	yes	1	29.3 protein.targeting	protein fate
Only Env and Chlor (108)	At4g33350.1	Tic22	yes	0	29.3 protein.targeting	protein fate
Only Env and Chlor (108)	At5g49910.1	cpHSP70-2 (Dnak homologue)	yes	0	29.6 protein.(un)folding (incl	protein fate
Only Env and Chlor (108)	At4g25650.1	Rieske [2Fe-2S] domain-containing p	yes	2	26.18 misc. other Ferredoxin	unknown function
Only Env and Chlor (108)	At2g24820.1	Tic55 (putative Rieske iron-sulfur prc	yes	2	29.3 protein.targeting	protein fate
Only Env and Chlor (108)	At2g47840.1	IEP16 (low homology TIC20)	yes	4	29.3 protein.targeting	protein fate
Only Env and Chlor (108)	At1g59870.1	ABC transporter family	yes	13	34.16 transport.ABC transpo	transport ions & small organic molecules
Only Env and Chlor (108)	At3g51870.1	putative carrier protein peroxisomal C	yes	2	34.17 transport.peroxisomes	transport ions & small organic molecules
Only Env and Chlor (108)	At5g59250.1	sugar transporter family	yes	9	34.2 transporter.sugars	transport ions & small organic molecules
Only Env and Chlor (108)	At5g64290.1	2-oxoglutarate/malate translocator (D	yes	9	34.8 transport.metabolite trar	transport ions & small organic molecules
Only Env and Chlor (108)	At3g63410.1	APG1 (putative chloroplast inner env	yes	1	35.2 not assigned.unknown	unknown function
Only Env and Chlor (108)	At3g57280.1	expressed protein	yes	3	35.2 not assigned.unknown	unknown function
Only Env and Chlor (108)	At3g43520.1	expressed protein	yes	4	35.2 not assigned.unknown	unknown function
Only Env and Chlor (108)	At1g32080.1	HP45 unknown function	yes	12	35.2 not assigned.unknown	unknown function
Only Env and Chlor (108)	At1g12900.1	calcium-binding protein, calreticulin	yes	0	30.3 signalling.calcium	other developmental & signalling functions
Only Env and Chlor (108)	At3g60750.1	transketolase - like protein transketol	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At2g21330.1	fructose-bisphosphate aldolase	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At3g12780.1	phosphoglycerate kinase-related	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At3g55800.1	sedoheptulose-bisphosphatase precur	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At4g38970.1	fructose-bisphosphate aldolase	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At3g38430.1	Rubisco small subunit 1b (RBCS-1b)	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At2g34590.1	E1beta pyruvate dehydrogenase comp	yes	0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
Only Env and Chlor (108)	At2g38040.1	putative alpha-carboxyltransferase ;	yes	0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
Only Env and Chlor (108)	At3g25860.1	E2 pyruvate dehydrogenase complex	yes	0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
Only Env and Chlor (108)	At4g16155.1	dihydroliipoamide dehydrogenase 2 (f	yes	0	11.1 lipid metabolism.FA syr	hormone and lipid metabolism
Only Env and Chlor (108)	At2g41220.1	ferredoxin-dependent glutamate syntf	yes	0	12.2 N-metabolism.ammonia N, S, aa	and nucleotide metabolism
Only Env and Chlor (108)	At5g04140.1	ferredoxin-dependent glutamate syntf	yes	0	12.2 N-metabolism.ammonia N, S, aa	and nucleotide metabolism
Only Env and Chlor (108)	At4g31990.1	aspartate aminotransferase, chloropla:	yes	0	13.1.2.1 amino acid metaboli N, S, aa	and nucleotide metabolism
Only Env and Chlor (108)	At3g58610.1	ketol-acid reductoisomerase	yes	0	13.4.1.1 amino acid metaboli N, S, aa	and nucleotide metabolism
Only Env and Chlor (108)	At2g43750.1	cysteine synthaser	yes	0	13.5.3.1 amino acid metaboli N, S, aa	and nucleotide metabolism
Only Env and Chlor (108)	At5g04590.1	sulphite reductase	yes	0	14 S-assimilation	N, S, aa and nucleotide metabolism
Only Env and Chlor (108)	At3g09580.1	amine oxidase family	yes	0	16.1 secondary metabolism.t	terpenoids & tetrapyrrole synthesis & degradation
Only Env and Chlor (108)	At4g14210.1	phytoene dehydrogenase precursor [p	yes	0	16.1.1 secondary metabolism	terpenoids & tetrapyrrole synthesis & degradation
Only Env and Chlor (108)	At5g60600.1	GcpE protein	yes	0	16.2 secondary metabolism.t	terpenoids & tetrapyrrole synthesis & degradation
Only Env and Chlor (108)	At3g48730.1	glutamate-1-semialdehyde 2,1-amino	yes	0	19 tetrapyrrole synthesis	hormone and lipid metabolism
Only Env and Chlor (108)	At5g63570.1	glutamate-1-semialdehyde 2,1-amino	yes	0	19 tetrapyrrole synthesis	hormone and lipid metabolism
Only Env and Chlor (108)	At3g44880.1	Phosphoribide a oxygenase (PaO) or /	yes	0	19.1 tetrapyrrole degradation	hormone and lipid metabolism
Only Env and Chlor (108)	At1g10760.1	Sex1 - R1 protein - controls starch ph	yes	0	2.1.2 major CHO metabolism	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At5g1820.1	phosphoglucomutase (starch free mut	yes	0	2.1.2 major CHO metabolism	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At5g16710.1	dehydroascorbate reductase (DHAR)	yes	0	21.2 redox.ascorbate and glui	redox proteins & oxidative defense & stress response
Only Env and Chlor (108)	At4g14070.1	AMP-binding protein, putative simila	yes	0	26.1 misc.misc2	unknown function
Only Env and Chlor (108)	At5g19940.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
Only Env and Chlor (108)	At1g01080.1	RNA-binding protein cp33	yes	0	27 (Regulation) transcription (Regulation)	DNA organization,transcription and translation
Only Env and Chlor (108)	At3g63140.1	mRNA binding protein precursor	yes	0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation

Only Env and Chlor (108)	At5g35970.1	DNA helicase-related	yes	0	28 DNA.unspecified (Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g05190.1	50S ribosomal protein L6p family	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g32990.1	50S ribosomal protein L11p	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g35680.1	50S ribosomal protein L21	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g79850.1	30S ribosomal protein S17 chloroplas	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At4g01310.1	50S ribosomal protein L5p family	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At5g14320.1	30S ribosomal protein S13	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At5g65220.1	50S ribosomal protein L29p family	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g74970.1	30S ribosomal protein S9	yes	0	29.2.2 protein.synthesis.misc (Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At1g62750.1	elongation factor Tu family	yes	0	29.2.4 protein.synthesis.elong(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At4g29060.1	expressed protein	yes	0	29.2.99 protein.synthesis.mis(Regulation) DNA organization,transcription and translation
Only Env and Chlor (108)	At5g46740.1	OEP75 (TOC75) = Chloroplast impo	yes	0	29.3 protein.targeting protein fate
Only Env and Chlor (108)	At1g63770.1	aminopeptidase	yes	0	29.5 protein.degradation protein fate
Only Env and Chlor (108)	At3g19170.1	metalloprotease	yes	0	29.5 protein.degradation protein fate
Only Env and Chlor (108)	At1g55490.1	Cpn60-beta-2	yes	0	29.6 protein.(un)folding (incl protein fate
Only Env and Chlor (108)	At3g48870.1	ClpC2	yes	0	29.6 protein.(un)folding (incl protein fate
Only Env and Chlor (108)	At5g24690.1	expressed protein	yes	0	35.2 not assigned. unknown unknown function
Only Env and Chlor (108)	At5g12470.1	expressed protein similarity to predict	yes	0	35.2 not assigned. unknown unknown function
Only Env and Chlor (108)	At1g11430.1	DAG protein -related	yes	0	35.2 not assigned. unknown unknown function
Only Env and Chlor (108)	At1g52510.1	hydrolase, alpha/beta fold family	yes	0	35.2 not assigned.unknown unknown function
Only Env and Chlor (108)	At2g21280.1	expressed protein	yes	0	35.2 not assigned.unknown unknown function
Only Env and Chlor (108)	At4g31530.1	expressed protein hypothetical protein	yes	0	35.2 not assigned.unknown unknown function
Only Env and Chlor (108)	At2g21170.1	triosephosphate isomerase	yes	0	4 glycolysis Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At4g24620.1	glucose-6-phosphate isomerase gluco	yes	0	4 glycolysis Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
Only Env and Chlor (108)	At1g34430.1	E2 pyruvate dehydrogenase complex	yes	0	8.1 TCA / org. transformatioi other metabolic functions
Only Env and Chlor (108)	At3g47520.1	malate dehydrogenase [NAD]	yes	0	8.2 TCA / org. transformatioi other metabolic functions

only thyl and chlo (135)	accession no.	lab annotation	cTP	TMHMM - curated	MapMan bin	Simplified functional cetergies
only thyl and chlo (135)	At2g35370.1	GCSH protein		0	1.2 PS.photorepiration	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only thyl and chlo (135)	At5g14780.1	Formate dehydrogenase		0	25 C1-metabolism	other metabolic functions
only thyl and chlo (135)	At4g39960.1	DnaJ domain family		0	26.14 misc. DnaJ domain wit	unknown function
only thyl and chlo (135)	At1g73990.1	SppA		0	29.5 protein.degradation	protein fate
only thyl and chlo (135)	At5g51540.1	expressed protein		3	29.5 protein.degradation	protein fate
only thyl and chlo (135)	At1g21750.1	PDI Calsequestrin and thioredoxin do		0	29.6 protein.(un)folding (incl protein fate	
only thyl and chlo (135)	At1g35720.1	Annexin - AnnA11		0	31.1 cell.organisation	other developmental & signalling functions
only thyl and chlo (135)	At2g10940.1	protease inhibitor/seed storage/lipid tr		0	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	At4g39730.1	expressed protein		0	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	At5g07020.1	proline-rich protein family		0	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	At1g22450.1	cytochrome c oxidase subunit 6b		0	9.7 mitochondrial electron tr	mitochondria and other non-chloroplast function
only thyl and chlo (135)	At4g22890.1	expressed protein TPP/C/M	yes	2	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At1g54780.1	thylakoid lumen 18.3 kDa	yes	1	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	ATCG00280	psbC CP43	-encode	6	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00570	psbF cytb559b	-encode	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00680	psbB CP47	-encode	6	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00710	psbH-phospho	-encode	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00020	psbA D1	-encode	5	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00340	psaB - subunit Ib	-encode	11	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00350	psaA - subunit Ia	-encode	11	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG01060	psaC - subunit VII - stromal side	-encode	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00540	petA - cytochrome f (cleavable ss of f	-encode	1	1.1.3 PS.lightreaction - Cytoth	ylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00720	petB - Cytochrome b6	-encode	4	1.1.3 PS.lightreaction - Cytoth	ylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00120	CF1a - atpA	-encode	0	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00130	CF0P1 - atpF	-encode	1	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00470	CF1e - atpE	-encode	0	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00480	CF1b - atpB	-encode	0	1.1.4 PS.lightreaction - ATP	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG00490	Rubisco large subunit (RBCL)	-encode	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only thyl and chlo (135)	ATCG00890	NDHB (1)	-encode	9	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG01090	NDHI	-encode	0	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG01110	NDH 7	-encode	0	1.4 PS Cyclic electron flow-c	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	ATCG01240	30S ribosomal protein S7	-encode	0	29.2.2 protein.synthesis.misc (Regulation) DNA organization,transcription and translation	
only thyl and chlo (135)	ATCG00670	ClpP1 (pClpP)	-encode	0	29.5 protein.degradation	protein fate
only thyl and chlo (135)	ATCG01040	YCF5 CCSA heme attachment	-encode	7	29.8 protein assembly and co	protein fate
only thyl and chlo (135)	ATCG01130	YCF1.2	-encode	6	29.8 protein assembly and co	protein fate
only thyl and chlo (135)	At1g03600.1	PSII Lumen Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	At1g14150.1	PsbQ domain TAT ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	At1g34000.1	Ohp2	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	At1g76450.1	OEC23-like Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj
only thyl and chlo (135)	At2g39470.1	OEC23-like Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlororesj

only thyl and chlo (135)	At3g50820.1	psbO OEC33-like	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At3g55330.1	OEC23-like Tat ITP TL25.6	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g15510.1	OEC23-like Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g21280.1	psbQ OEC16 Tat Itp	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At5g66570.1	psbO OEC33	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g28750.1	psaE-1 subunit IV - stromal side	yes	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At5g64040.1	psaN - TAT LTP	yes	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At5g14910.1	expressed protein - also in CN-PAGE	yes	0	15.2 metal handling.binding, metal handling.binding, chelation and storage	
only thyl and chlo (135)	At3g52960.1	Peroxioredoxin II E	yes	0	21.5 redox.peroxioredoxins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At1g12250.1	thylakoid lumen pentapeptide repeat	yes	0	26.15 misc. Pentapeptide rep	unknown function
only thyl and chlo (135)	At2g44920.1	thylakoid lumen pentapeptide repeat	yes	0	26.15 misc. Pentapeptide rep	unknown function
only thyl and chlo (135)	At3g63490.1	ribosomal protein L1p family	yes	0	29.2.1 protein.synthesis.chlor	(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At1g50250.1	FtsH1 (Var1)	yes	2	29.5 protein.degradation	protein fate
only thyl and chlo (135)	At4g18370.1	DegP5 - HhoA homologue or DegQ	yes	0	29.5 protein.degradation	protein fate
only thyl and chlo (135)	At3g01480.1	Tlp-40	yes	0	29.6 protein.(un)foldng (incl	protein fate
only thyl and chlo (135)	At3g10060.1	Isomerases TAT ITP	yes	0	29.6 protein.(un)foldng (incl	protein fate
only thyl and chlo (135)	At3g15520.1	Isomerases	yes	0	29.6 protein.(un)foldng (incl	protein fate
only thyl and chlo (135)	At4g39710.1	Isomerases	yes	0	29.6 protein.(un)foldng (incl	protein fate
only thyl and chlo (135)	At5g23120.1	HCF136 Tat Itp	yes	0	29.8 protein assembly and co	protein fate
only thyl and chlo (135)	At3g16000.1	MFP1 - nucleoid binding	yes	0	28 DNA.unspecified	(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At4g02530.1	thylakoid lumen protein TL16.5	yes	0	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	At4g24930.1	thylakoid lumen 17.9 kDa protein	yes	0	35.2 not assigned.unknown	unknown function
only thyl and chlo (135)	At1g20340.1	PC-1	yes	1	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g79040.1	psbR	yes	1	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At2g40100.1	LHCII-4.3 -CP29	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g77490.1	thylakoid bound APX	yes	1	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At1g75690.1	DnaJ domain family	yes	1	26.14 misc. DnaJ domain wit	unknown function
only thyl and chlo (135)	At4g14870.1	cpSecE	yes	1	29.3 protein.targeting	protein fate
only thyl and chlo (135)	At5g52440.1	hcf106 TatB	yes	1	29.3 protein.targeting	protein fate
only thyl and chlo (135)	At1g54500.1	rubredoxin	yes	1	29.8 protein assembly and co	protein fate
only thyl and chlo (135)	At1g14345.1	expressed protein	yes	1	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At1g52220.1	expressed protein	yes	2	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At1g74730.1	expressed protein	yes	2	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At3g51510.1	expressed protein - C/M	yes	2	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At5g08050.1	expressed protein	yes	2	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At5g23060.1	expressed protein - C/M	yes	1	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At5g38660.1	expressed protein similar to unknown	yes	1	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At5g44650.1	expressed protein TMs in PPDB	yes	1	35.2 not assigned. unknown	unknown function
only thyl and chlo (135)	At1g20020.1	FNR-2	yes	0	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g29910.1	LHCII-1.1 - 100% identical to lhcb-1	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g29920.1	LHCII-1.2 - 100% identical to lhcb-1	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g29930.1	LHCII-1.3 - 100% identical to lhcb-1	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g44575.1	psbS	yes	4	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g77090.1	OEC23-like Tat ITP TL29.8	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At2g30790.1	psbP OEC23 Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At3g56650.1	OEC23-like	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g05180.1	psbQ OEC16-like Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g10340.1	LHCII-5 - CP26	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At5g01530.1	LHCII-4.1-CP29	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At5g54270.1	LHCII-3	yes	3	1.1.1 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g52230.1	psaH-2 - subunit VI	yes	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g61520.1	LHCI-3 - LHCI-680A CAB4	yes	3	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At2g20260.1	psaE-2 subunit IV - stromal side	yes	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At3g61470.1	LHCI-2.1 - LHCI-680B	yes	3	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At4g02770.1	psaD-2 subunit II - stromal side-tight	yes	0	1.1.2 PS.lightreaction - Photc	thylakoid (cyclic) electron transport, ATP synthesis and chlorores
only thyl and chlo (135)	At1g73110.1	activase-related	yes	0	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,
only thyl and chlo (135)	At4g32770.1	cyclase/sxd1- vit E biosynthesis	yes	0	18 Co-factor and vitamine m	Co-factor and vitamine metabolism, metal handling & storage
only thyl and chlo (135)	At1g03680.1	thioredoxin m1	yes	0	21.1 redox.thioredoxin	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At4g03520.1	thioredoxin m2	yes	0	21.1 redox.thioredoxin	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At4g09010.1	Putative Asc-perox lumen Tat Itp	yes	0	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At5g03880.1	auxin-regulated protein predicted prot	yes	0	21.2 redox.ascorbate and glut	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At5g53490.1	peptapptide repeat TL17.4	yes	0	26.15 misc. Pentapeptide rep	unknown function
only thyl and chlo (135)	At2g42220.1	rhodanese-like domain protein contain	yes	0	26.16 misc. Rhodanese doma	unknown function
only thyl and chlo (135)	At4g27700.1	rhodanese-like domain protein	yes	0	26.16 misc. Rhodanese doma	unknown function
only thyl and chlo (135)	At1g51110.1	fibrillin (similar to PAP2 B. rapa)	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At2g35490.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At3g23400.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At3g26070.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At4g04020.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At4g22240.1	fibrillin	yes	0	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
only thyl and chlo (135)	At2g35410.1	putative RNA binding protein	yes	0	28 (Regulation) transcription (Regulation)	DNA organization,transcription and translation

only thyl and chlo (135)	At1g07320.1	50S ribosomal protein L4	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At1g64510.1	30S ribosomal protein S6 (changed at	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At1g68590.1	PSRP-3A small	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At2g33800.1	30S Ribosomal p S5 Isolog L13	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At3g27830.1	50S ribosomal protein L12-A	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At3g27850.1	50S ribosomal protein L12-C	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At5g40950.1	50S ribosomal protein L27	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation
only thyl and chlo (135)	At3g27925.1	DegP1 - HhoA homologue or DegQ	yes	0	29.5 protein.degradation protein fate
only thyl and chlo (135)	At1g74070.1	Isomerases TAT ITP	yes	0	29.6 protein.(un)foldng (incl protein fate
only thyl and chlo (135)	At3g60370.1	Isomerases	yes	0	29.6 protein.(un)foldng (incl protein fate
only thyl and chlo (135)	At5g13120.1	peptidyl-prolyl isomerase protein - TI	yes	0	29.6 protein.(un)foldng (incl protein fate
only thyl and chlo (135)	At5g13410.1	Isomerases TAT ITP	yes	0	29.6 protein.(un)foldng (incl protein fate
only thyl and chlo (135)	At3g24590.1	TPP-2 lumen	yes	0	29.7 protein. processing protein fate
only thyl and chlo (135)	At4g37200.1	HCF164 Fd like	yes	0	29.8 protein assembly and co protein fate
only thyl and chlo (135)	At1g18730.1	unknown protein	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At1g72640.1	expressed protein	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At2g23670.1	ycf37 Synechocystis -stromal predict	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At2g26340.1	stromal predicted??	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At4g13200.1	expressed protein ITP? C/M	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At4g23890.1	expressed protein hypothetical protei	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At5g58250.1	similar to unknown protein (spP7277	yes	0	35.2 not assigned. unknown unknown function
only thyl and chlo (135)	At3g10130.1	expressed protein	yes	0	35.2 not assigned.unknown unknown function
only thyl and chlo (135)	At5g20140.1	expressed protein	yes	0	35.2 not assigned.unknown unknown function
only thyl and chlo (135)	At5g52970.1	thylakoid lumen 15 kDa protein	yes	0	35.2 not assigned.unknown unknown function

common in thy-env-chl (74)	accession no.	lab annotation	cTP	TMHMM - curated	MapMan bin	Simplified functional categories
common in thy-env-chl (74)	At1g15820.1	LHCII-6 - CP24		3	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g25100.1	FE-SOD -		0	21.6 redox.dismutases and caredox proteins & oxidative defense & stress response	
common in thy-env-chl (74)	At1g06430.1	FtsH8 TAT ITP		2	29.5 protein.degradation protein fate	
common in thy-env-chl (74)	At3g63160.1	OEP6		1	35.2 not assigned. unknown unknown function	
common in thy-env-chl (74)	At4g37920.1	expressed protein		0	35.2 not assigned. unknown unknown function	
common in thy-env-chl (74)	At3g01500.1	carbonic anhydrase		0	8.3 TCA / org. transformatioi other metabolic functions	
common in thy-env-chl (74)	At1g13330.1	psaF- subunit III - LTP - hydrophobic	yes	1	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At3g14110.1	Flu gene - TPR motif, regulation tetra	yes	1	19. tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation	
common in thy-env-chl (74)	At2g30950.1	FtsH2 (VAR2 and Pftf)	yes	2	29.5 protein.degradation protein fate	
common in thy-env-chl (74)	At1g06680.1	psbP OEC23 Tat ITP	yes	0	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g32260.1	CFO-II - atpG	yes	1	1.1.4 PS.lightreaction - ATP thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g09650.1	CFI d - atpD	yes	0	1.1.4 PS.lightreaction - ATP thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g27440.1	PORB - constitutive expression - mai	yes	0	19 tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation	
common in thy-env-chl (74)	At4g01050.1	expressed protein ITP? Rhodanese-lik	yes	0	26.16 misc. Rhodanese doma unknown function	
common in thy-env-chl (74)	At3g52150.1	PSRP-2 small	yes	0	29.2.1 protein.synthesis.chlor(Regulation) DNA organization,transcription and translation	
common in thy-env-chl (74)	At5g42270.1	FtsH5 (VAR1)	yes	0	29.5 protein.degradation protein fate	
common in thy-env-chl (74)	At2g28000.1	Cpn60-alpha-1	yes	0	29.6 protein.(un)foldng (incl protein fate	
common in thy-env-chl (74)	At4g24280.1	cpHSP70-1 (DnaK homologue)	yes	0	29.6 protein.(un)foldng (incl protein fate	
common in thy-env-chl (74)	At1g16880.1	expressed protein	yes	0	35.2 not assigned. unknown unknown function	
common in thy-env-chl (74)	At3g04790.1	ribose 5-phosphate isomerase	yes	0	7.2 OPP.non-reductive PP Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,	
common in thy-env-chl (74)	At1g55670.1	psaG - subunit V- stromal side	yes	2	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g12800.1	psaL - subunit XI (also named V)	yes	2	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g03280.1	petC - Rieske Fe-S protein - LTP	yes	1	1.1.3 PS.lightreaction - Cytoct.thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At5g17170.1	expressed protein Rubredoxin and PE	yes	1	29.8 protein assembly and co protein fate	
common in thy-env-chl (74)	At1g42960.1	Hp17	yes	1	35.2 not assigned. unknown unknown function	
common in thy-env-chl (74)	At4g01150.1	expressed protein C/M	yes	2	35.2 not assigned. unknown unknown function	
common in thy-env-chl (74)	At5g23890.1	expressed protein	yes	1	35.2 not assigned.unknown unknown function	
common in thy-env-chl (74)	At5g66190.1	FNR-1	yes	0	1.1 PS.lightreaction thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At2g05070.1	LHCII-2.2	yes	3	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At2g05100.1	LHCII-2.1	yes	3	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At2g34430.1	LHCII-1.4	yes	3	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At3g08940.1	LHCII-4.2 - CP29	yes	3	1.1.1 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At3g54890.1	LHCI-1-1 - LHCI-730	yes	3	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At1g03130.1	psaD-1 subunit II - stromal side-tight	yes	0	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At3g47470.1	LHCI-4 - LHCI-730	yes	3	1.1.2 PS.lightreaction - Photc thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At4g04640.1	CFI y - atpC	yes	0	1.1.4 PS.lightreaction - ATP thylakoid (cyclic) electron transport, ATP synthesis and chlororesj	
common in thy-env-chl (74)	At1g32060.1	phosphoribulokinase precursor	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,	
common in thy-env-chl (74)	At1g42970.1	glyceraldehyde-3-phosphate dehydro	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,	
common in thy-env-chl (74)	At1g67090.1	Rubisco small subunit (RBCS) - very	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,	
common in thy-env-chl (74)	At3g39730.1	Rubisco activase	yes	0	1.3 PS.calvin cyle Calvin cycle, photorespiration, minor carbohydrates, starch, OPP,	
common in thy-env-chl (74)	At2g05990.1	Enoyl-ACP reductase	yes	0	11.1 lipid metabolism.FA syr hormone and lipid metabolism	
common in thy-env-chl (74)	At5g35630.1	glutamate-ammonia ligase, chloropl:	yes	0	12.2 N-metabolism.ammonia N, S, aa and nucleotide metabolism	
common in thy-env-chl (74)	At1g74470.1	geranylgeranyl reductase (GGDR)	yes	0	16.1 secondary metabolism.t terpenoids & tetrapyrrole synthesis & degradation	
common in thy-env-chl (74)	At2g34460.1	flavin reductase-related	yes	0	16.3 secondary metabolism.f terpenoids & tetrapyrrole synthesis & degradation	
common in thy-env-chl (74)	At3g25760.1	allene oxide cyclase family (ERD12)	yes	0	17.7.1 hormone metabolism.j hormone and lipid metabolism	

common in thy-env-chl (74):At3g25770.1	allene oxide cyclase family - (ERD12	yes	0	17.7.1 hormone metabolism.jhormone and lipid metabolism
common in thy-env-chl (74):At3g45140.1	lipoygenase AtLOX2	yes	0	17.7.1 hormone metabolism.jhormone and lipid metabolism
common in thy-env-chl (74):At5g42650.1	allene oxide synthase	yes	0	17.7.1 hormone metabolism.jhormone and lipid metabolism
common in thy-env-chl (74):At1g03630.1	PORC- ~constitutive expression	yes	0	19 tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation
common in thy-env-chl (74):At3g56940.1	CHL27 or Crd1	yes	0	19 tetrapyrrole synthesis terpenoids & tetrapyrrole synthesis & degradation
common in thy-env-chl (74):At3g15360.1	thioredoxin m4	yes	0	21.1 redox.thioredoxin redox proteins & oxidative defense & stress response
common in thy-env-chl (74):At2g25080.1	glutathione peroxidase putative	yes	0	21.2 redox.ascorbate and glutiredox proteins & oxidative defense & stress response
common in thy-env-chl (74):At3g11630.1	2-Cys PerA	yes	0	21.5 redox.periredoxins redox proteins & oxidative defense & stress response
common in thy-env-chl (74):At3g26060.1	Peroxioredoxin Q	yes	0	21.5 redox.periredoxins redox proteins & oxidative defense & stress response
common in thy-env-chl (74):At4g13670.1	DnaJ domain family	yes	0	26.14 misc. DnaJ domain wit unknown function
common in thy-env-chl (74):At1g71500.1	Rieske [2Fe-2S] domain	yes	0	26.18 misc. other Ferredoxin unknown function
common in thy-env-chl (74):At4g24770.1	RNA binding protein CP31	yes	0	28 (Regulation) transcription (Regulation) DNA organization,transcription and translation
common in thy-env-chl (74):At3g56910.1	PSRP-5 large	yes	0	29.2.1 protein.synthesis.chlori(Regulation) DNA organization,transcription and translation
common in thy-env-chl (74):At4g20360.1	elongation factor Tu, chloroplast prec	yes	0	29.2.3 protein.synthesis.initia(Regulation) DNA organization,transcription and translation
common in thy-env-chl (74):At2g47450.1	cpSRP43	yes	0	29.3 protein.targeting protein fate
common in thy-env-chl (74):At3g48890.1	UOS1	yes	0	11.8 hormone and lipid metalhormone and lipid metabolism
common in thy-env-chl (74):At4g01800.1	cpSecA	yes	0	29.3 protein.targeting protein fate
common in thy-env-chl (74):At1g11750.1	ClpP6 (nClpP6)	yes	0	29.5 protein.degradation protein fate
common in thy-env-chl (74):At4g25370.1	ClpS1	yes	0	29.5 protein.degradation protein fate
common in thy-env-chl (74):At5g45390.1	ClpP4 (nClpP4)	yes	0	29.5 protein.degradation protein fate
common in thy-env-chl (74):At3g62030.1	peptidylprolyl isomerase ROC4	yes	0	29.6 protein.(un)folding (incl protein fate
common in thy-env-chl (74):At5g20720.1	Cpn21	yes	0	29.6 protein.(un)folding (incl protein fate
common in thy-env-chl (74):At5g50920.1	ClpC1	yes	0	29.6 protein.(un)folding (incl protein fate
common in thy-env-chl (74):At2g46820.1	expressed protein - C/M	yes	0	35.2 not assigned. unknown unknown function
common in thy-env-chl (74):At1g55480.1	expressed protein	yes	0	35.2 not assigned. unknown unknown function
common in thy-env-chl (74):At2g20890.1	expressed protein sII1414 homologue	yes	0	35.2 not assigned. unknown unknown function
common in thy-env-chl (74):At3g46780.1	expressed protein	yes	0	35.2 not assigned. unknown unknown function
common in thy-env-chl (74):At1g06690.1	aldo/keto reductase family	yes	0	35.2 not assigned.unknown unknown function
common in thy-env-chl (74):At5g58260.1	similar to unknown protein (pir S755	yes	0	35.2 not assigned.unknown unknown function

only in chloropl (370)	accession no.	TAIR annotation	cTP	TMHMM - curated
only in chloropl (370)	At1g51040.1	phosphatidylinositol 4-kinase, putativ		0
only in chloropl (370)	At1g07660.1	histone H4 identical to histone H4 fro		0
only in chloropl (370)	At1g07920.1	elongation factor 1-alpha (EF-1-alpha		0
only in chloropl (370)	At1g09590.1	60S ribosomal protein L21 (RPL21A'		0
only in chloropl (370)	At1g20260.1	vacuolar H+-ATPase subunit B -relat		0
only in chloropl (370)	At1g24300.1	expressed protein similar to hypotheti		0
only in chloropl (370)	At1g33120.1	60S ribosomal protein L9 (RPL90B)		0
only in chloropl (370)	At1g55650.1	hypothetical protein		0
only in chloropl (370)	At2g40510.1	40S ribosomal protein S26 (RPS26A)		0
only in chloropl (370)	At3g08530.1	clathrin heavy chain -related similar t		0
only in chloropl (370)	At3g11940.1	40S ribosomal protein S5 (RPS5B) si		0
only in chloropl (370)	At3g14420.1	glycolate oxidase -related similar to g		0
only in chloropl (370)	At4g02520.1	glutathione transferase, putative		0
only in chloropl (370)	At4g08900.1	arginase		0
only in chloropl (370)	At5g26000.1	glycosyl hydrolase family 1, myrosin:		0
only in chloropl (370)	At3g14590.1	C2 domain-containing protein low sir		2
only in chloropl (370)	At5g46090.1	hypothetical protein similar to unkno		4
only in chloropl (370)	At2g37170.1	plasma membrane intrinsic protein 2E		6
only in chloropl (370)	At1g08890.1	sugar transporter family similar to suç		10
only in chloropl (370)	ATCG00430	psbG NADH dehydrogenase subunit		0
only in chloropl (370)	At2g13360.1	alanine-glyoxylate aminotransferase		0
only in chloropl (370)	At4g37930.1	glycine hydroxymethyltransferase lik		0
only in chloropl (370)	At1g13440.1	glyceraldehyde-3-phosphate dehydroç		0
only in chloropl (370)	At4g26530.1	fructose-bisphosphate aldolase, putati		0
only in chloropl (370)	At1g49750.1	leucine rich repeat protein family con		0
only in chloropl (370)	At4g39260.1	glycine-rich RNA-binding protein 8 (0
only in chloropl (370)	At1g68560.1	glycosyl hydrolase family 31 (alpha-)		0
only in chloropl (370)	At5g02260.1	expansin, putative (EXP9) similar to ç		0
only in chloropl (370)	At2g06850.1	xyloglucan endotransglycosylase (ext		1
only in chloropl (370)	At1g29670.1	GDSL-motif lipase/hydrolase protein		0
only in chloropl (370)	At2g42690.1	lipase, putative similar to lipase [Diar		0
only in chloropl (370)	At3g15730.1	Phospholipase D, putative similar to I		0
only in chloropl (370)	At4g11830.1	phospholipase D-gamma, putative sin		0
only in chloropl (370)	At2g33150.1	acetyl-CoA C-acyltransferase (3-keto		0
only in chloropl (370)	At1g17290.1	alanine aminotransferase, putative sin		0
only in chloropl (370)	At1g23310.1	alanine aminotransferase -related sim		0
only in chloropl (370)	At4g08870.1	arginase -related similar to arginases ç		0
only in chloropl (370)	At5g62530.1	delta-1-pyrroline-5-carboxylate dehyç		0
only in chloropl (370)	At3g61440.1	cysteine synthase (O-acetylserine (thi		0

only in chloropl (370)	At1g22610.1	C2 domain-containing protein contain	2
only in chloropl (370)	At1g31490.1	anthranilate N-hydroxycinnamoyl/ber	0
only in chloropl (370)	At1g33790.1	jacalin lectin family similar to myrosi	0
only in chloropl (370)	At5g25980.1	glycosyl hydrolase family 1 similar to	1
only in chloropl (370)	At5g54510.1	auxin-responsive-related protein	0
only in chloropl (370)	At1g48420.1	expressed protein contains similarity	0
only in chloropl (370)	At2g31230.1	ethylene response factor, putative sim	0
only in chloropl (370)	At3g22400.1	lipoxygenase (LOX), putative similar	0
only in chloropl (370)	At1g27170.1	disease resistance protein (TIR-NBS-	0
only in chloropl (370)	At1g33590.1	disease resistance protein-related (LR	0
only in chloropl (370)	At3g28940.1	AIG2-related protein similar to AIG2	0
only in chloropl (370)	At1g74180.1	leucine rich repeat protein family con	1
only in chloropl (370)	At2g25470.1	leucine rich repeat protein family con	1
only in chloropl (370)	At3g05660.1	disease resistance protein family cont	1
only in chloropl (370)	At1g70890.1	major latex protein (MLP)-related lov	0
only in chloropl (370)	At1g76180.1	dehydrin -related similar to dehydrin	0
only in chloropl (370)	At4g12830.1	hydrolase, alpha/beta fold family low	0
only in chloropl (370)	At5g46070.1	expressed protein contains similarity	0
only in chloropl (370)	At1g16030.1	heat shock protein hsp70b similar to H	0
only in chloropl (370)	At2g33210.1	chaperonin, putative similar to SWIS	0
only in chloropl (370)	At4g16660.1	heat shock protein hsp70, putative	0
only in chloropl (370)	At4g24190.1	shepherd (SHD) nearly identical to SI	0
only in chloropl (370)	At5g09590.1	heat shock protein mtHsc70-2 (Hsc70	0
only in chloropl (370)	At1g77510.1	protein disulfide isomerase, putative	0
only in chloropl (370)	At4g35090.1	catalase 2 identical to catalase 2 SP:P	0
only in chloropl (370)	At1g74260.1	phosphoribosylformylglycinamide	0
only in chloropl (370)	At3g09820.1	adenosine kinase 1 (ADK1)/adenosin	0
only in chloropl (370)	At1g26560.1	glycosyl hydrolase family 1 similar to	0
only in chloropl (370)	At5g63840.1	glycosyl hydrolase family 31 similar to	0
only in chloropl (370)	At2g33340.1	transducin / WD-40 repeat protein far	0
only in chloropl (370)	At3g55200.1	splicing factor, putative contains CPS	0
only in chloropl (370)	At4g35800.1	DNA-directed RNA polymerase (EC	0
only in chloropl (370)	At1g09770.1	myb family transcription factor conta	0
only in chloropl (370)	At1g72150.1	cytosolic factor -related similar to GI	0
only in chloropl (370)	At3g54400.1	nucleoid DNA-binding - like protein	0
only in chloropl (370)	At1g13230.1	leucine rich repeat protein family con	0
only in chloropl (370)	At3g49830.1	RuvB DNA helicase - like protein DN	0
only in chloropl (370)	At1g07790.1	histone H2B, putative strong similarit	0
only in chloropl (370)	At5g67630.1	RuvB DNA helicase-related protein	0
only in chloropl (370)	At1g18540.1	60S ribosomal protein L6 (RPL6A) si	0
only in chloropl (370)	At1g26880.1	60S ribosomal protein L34 (RPL34A)	0
only in chloropl (370)	At1g27400.1	60S ribosomal protein L17 (RPL17A)	0
only in chloropl (370)	At1g48830.1	40S ribosomal protein S7 (RPS7A) si	0
only in chloropl (370)	At1g58380.1	40S ribosomal protein S2 (RPS2A) si	0
only in chloropl (370)	At1g72370.1	40S ribosomal protein SA (RPSaA) ic	0
only in chloropl (370)	At2g01250.1	60S ribosomal protein L7 (RPL7B)	0
only in chloropl (370)	At2g09990.1	40S ribosomal protein S16 (RPS16A)	0
only in chloropl (370)	At2g16360.1	40S ribosomal protein S25 (RPS25A)	0
only in chloropl (370)	At2g17360.1	40S ribosomal protein S4 (RPS4A) ce	0
only in chloropl (370)	At2g18020.1	60S ribosomal protein L8 (RPL8A)	0
only in chloropl (370)	At2g31610.1	40S ribosomal protein S3 (RPS3A)	0
only in chloropl (370)	At2g36160.1	40S ribosomal protein S14 (RPS14A)	0
only in chloropl (370)	At2g36620.1	60S ribosomal protein L24 (RPL24A)	0
only in chloropl (370)	At2g42740.1	60S ribosomal protein L11 (RPL11A)	0
only in chloropl (370)	At2g44120.1	60S ribosomal protein L7 (RPL7C)	0
only in chloropl (370)	At2g47610.1	60S ribosomal protein L7A (RPL7aA)	0
only in chloropl (370)	At3g04230.1	40S ribosomal protein S16 (RPS16B)	0
only in chloropl (370)	At3g04770.1	40S ribosomal protein SA (RPSaB) ic	0
only in chloropl (370)	At3g04840.1	40S ribosomal protein S3A (RPS3aA)	0
only in chloropl (370)	At3g05590.1	60S ribosomal protein L18 (RPL18B)	0
only in chloropl (370)	At3g07110.1	60S ribosomal protein L13A (RPL13:	0
only in chloropl (370)	At3g09200.1	60S acidic ribosomal protein P0 (RPF	0
only in chloropl (370)	At3g09630.1	60S ribosomal protein L4/L1 (RPL4A	0
only in chloropl (370)	At3g13580.1	60S ribosomal protein L7 (RPL7D) si	0
only in chloropl (370)	At3g25520.1	60S ribosomal protein L5 (RPL5A) si	0
only in chloropl (370)	At3g49910.1	60S ribosomal protein L26 (RPL26A)	0
only in chloropl (370)	At3g60770.1	40S ribosomal protein S13 (RPS13A)	0
only in chloropl (370)	At4g27090.1	60S ribosomal protein L14 (RPL14B)	0
only in chloropl (370)	At4g31700.1	40S ribosomal protein S6 (RPS6A) ri	0
only in chloropl (370)	At5g02870.1	60S ribosomal protein L4/L1 (RPL4E	0
only in chloropl (370)	At5g15200.1	40S ribosomal protein S9 (RPS9B) 4C	0

only in chloropl (370)	At5g20290.1	40S ribosomal protein S8 (RPS8A) ri	0
only in chloropl (370)	At1g14850.1	nucleoporin -related similar to nuclea	0
only in chloropl (370)	At1g51980.1	mitochondrial processing peptidase al	0
only in chloropl (370)	At2g25140.1	HSP100/ClpB, putative similar to HS	0
only in chloropl (370)	At3g02090.1	mitochondrial processing peptidase -r	0
only in chloropl (370)	At5g02500.1	heat shock protein hsc70-1 (hsp70-1)	0
only in chloropl (370)	At5g53480.1	importin beta, putative similar to imp	0
only in chloropl (370)	At1g13900.1	calcineurin-like phosphoesterase fami	1
only in chloropl (370)	At1g04860.1	ubiquitin-specific protease 2 (UBP2)	0
only in chloropl (370)	At1g47128.1	cysteine proteinase RD21A identical i	0
only in chloropl (370)	At3g51260.1	20S proteasome alpha subunit D (PAL	0
only in chloropl (370)	At3g60820.1	20S proteasome beta subunit F1 (PBF	0
only in chloropl (370)	At5g10540.1	oligopeptidase A - like protein oligop	0
only in chloropl (370)	At5g66140.1	20S proteasome alpha subunit D2 (Pa	0
only in chloropl (370)	At5g65760.1	hydrolase, alpha/beta fold family simi	1
only in chloropl (370)	At1g56340.1	calreticulin 1 (CRT1) identical to calr	1
only in chloropl (370)	At5g07340.1	calnexin, putative identical to calnexi	2
only in chloropl (370)	At1g09180.1	GTP-binding protein SAR1, putative	0
only in chloropl (370)	At5g19320.1	RAN GTPase activating protein 2	0
only in chloropl (370)	At3g02520.1	14-3-3 protein GF14 nu (grf7) identic	0
only in chloropl (370)	At4g09000.1	14-3-3 protein GF14 chi (grf1) identic	0
only in chloropl (370)	At5g10450.1	14-3-3 protein GF14 lambda (grf6/Alf	0
only in chloropl (370)	At5g65430.1	14-3-3 protein GF14 kappa (grf8) ide	0
only in chloropl (370)	At1g04820.1	tubulin alpha-2/alpha-4 chain (TUA4	0
only in chloropl (370)	At1g20010.1	tubulin beta-5 chain (TUB5) nearly ic	0
only in chloropl (370)	At1g49240.1	actin 8 almost identical to actin 8 GI:	0
only in chloropl (370)	At4g31880.1	expressed protein microtubule-associi	0
only in chloropl (370)	At5g41790.1	myosin heavy chain-related protein	0
only in chloropl (370)	At3g54670.1	structural maintenance of chromosom	0
only in chloropl (370)	At1g04760.1	synaptobrevin 7B -related similar to C	1
only in chloropl (370)	At5g44020.1	vegetative storage protein-related	0
only in chloropl (370)	At1g76030.1	vacuolar ATP synthase subunit B ideo	0
only in chloropl (370)	At2g21410.1	vacuolar proton-ATPase subunit -rela	6
only in chloropl (370)	At1g17260.1	ATPase 10, plasma membrane-type (j	9
only in chloropl (370)	At1g60160.1	potassium transporter, putative (KUP	13
only in chloropl (370)	At1g01620.1	plasma membrane intrinsic protein 1c	6
only in chloropl (370)	At2g45960.1	plasma membrane intrinsic protein 1E	6
only in chloropl (370)	At3g53420.1	plasma membrane intrinsic protein 2f	6
only in chloropl (370)	At4g17340.1	major intrinsic protein (MIP) family c	6
only in chloropl (370)	At2g48020.1	sugar transporter, putative similar to I	12
only in chloropl (370)	At3g45060.1	high-affinity nitrate transporter - like	11
only in chloropl (370)	At5g02180.1	amino acid transporter family belong:	9
only in chloropl (370)	At3g08920.1	rhodanese-like domain protein contain	0
only in chloropl (370)	At5g64270.1	splicing factor, putative similar to spl	0
only in chloropl (370)	At3g48190.1	ataxia-telangiectasia mutated protein	0
only in chloropl (370)	At1g02140.1	Mago Nashi-related protein similar to	0
only in chloropl (370)	At1g03860.1	prohibitin 2 -related B-cell receptor a:	0
only in chloropl (370)	At1g09760.1	U2 small nuclear ribonucleoprotein A	0
only in chloropl (370)	At1g14320.1	60S ribosomal protein L10 (RPL10A)	0
only in chloropl (370)	At1g47260.1	transferase hexapeptide repeat family	0
only in chloropl (370)	At1g54410.1	dehydrin protein family contains Pfan	0
only in chloropl (370)	At3g27280.1	prohibitin -related similar to prohibiti	0
only in chloropl (370)	At3g48425.1	endonuclease/exonuclease/phosphata:	0
only in chloropl (370)	At3g48680.1	transferase hexapeptide repeat family	0
only in chloropl (370)	At3g54960.1	protein disulfide isomerase family sin	0
only in chloropl (370)	At4g20260.1	endomembrane-associated protein	0
only in chloropl (370)	At4g25210.1	expressed protein cyclicin II - human,	0
only in chloropl (370)	At4g29010.1	abnormal inflorescence meristem 1 (f	0
only in chloropl (370)	At5g07350.1	expressed protein p100 co-activator -	0
only in chloropl (370)	At5g22330.1	Ruv DNA-helicase-related protein	0
only in chloropl (370)	At5g52280.1	hyaluronan mediated motility recepto	0
only in chloropl (370)	At5g58230.1	WD-40 repeat protein (MSH1) contain	0
only in chloropl (370)	At5g60640.1	protein disulfide isomerase family sin	0
only in chloropl (370)	At4g27520.1	expressed protein ENOD20 gene, Me	1
only in chloropl (370)	At5g28540.1	luminal binding protein 1 precursor (I	1
only in chloropl (370)	At2g03520.1	integral membrane protein -related	9
only in chloropl (370)	At2g45740.1	expressed protein	0
only in chloropl (370)	At1g59840.1	expressed protein	0
only in chloropl (370)	At3g59780.1	expressed protein	0
only in chloropl (370)	At1g11700.1	expressed protein ESTs gb R65381 ar	0
only in chloropl (370)	At1g16290.1	expressed protein	0

only in chloropl (370)	At1g20750.1	hypothetical protein		0
only in chloropl (370)	At1g22530.1	expressed protein		0
only in chloropl (370)	At1g48090.1	predicted protein		0
only in chloropl (370)	At1g50450.1	expressed protein		0
only in chloropl (370)	At1g61730.1	expressed protein similar to hypotheti		0
only in chloropl (370)	At1g69840.1	expressed protein similar to hypotheti		0
only in chloropl (370)	At1g77550.1	tubulin-tyrosine ligase family contain		0
only in chloropl (370)	At1g79280.1	expressed protein		0
only in chloropl (370)	At1g80190.1	hypothetical protein		0
only in chloropl (370)	At2g31670.1	expressed protein		0
only in chloropl (370)	At2g38770.1	expressed protein		0
only in chloropl (370)	At3g18790.1	expressed protein		0
only in chloropl (370)	At3g20820.1	disease resistance protein family (LR)		0
only in chloropl (370)	At3g23020.1	pentatricopeptide (PPR) repeat-contai		0
only in chloropl (370)	At3g42630.1	pentatricopeptide (PPR) repeat-contai		0
only in chloropl (370)	At3g44780.1	hypothetical protein		0
only in chloropl (370)	At3g48500.1	expressed protein		0
only in chloropl (370)	At4g20130.1	expressed protein		0
only in chloropl (370)	At4g30840.1	WD-40 repeat protein family contains		0
only in chloropl (370)	At4g33690.1	hypothetical protein		0
only in chloropl (370)	At4g39680.1	expressed protein		0
only in chloropl (370)	At5g01750.1	expressed protein		0
only in chloropl (370)	At5g03350.1	expressed protein		0
only in chloropl (370)	At5g23710.1	hypothetical protein		0
only in chloropl (370)	At5g26260.1	expressed protein various predicted p		0
only in chloropl (370)	At5g47690.1	hypothetical protein strong similarity		0
only in chloropl (370)	At5g52840.1	expressed protein		0
only in chloropl (370)	At5g63430.1	expressed protein similar to unknown		0
only in chloropl (370)	At5g62620.1	galactosyltransferase family contains		1
only in chloropl (370)	At2g37290.1	hypothetical protein and genefinder		1
only in chloropl (370)	At1g61790.1	hypothetical protein		5
only in chloropl (370)	At1g66770.1	nodulin MTN3 family protein contains		6
only in chloropl (370)	At1g23190.1	phosphoglucomutase -related similar		0
only in chloropl (370)	At4g34240.1	aldehyde dehydrogenase, putative (Al		0
only in chloropl (370)	At3g48000.1	mitochondrial aldehyde dehydrogena		0
only in chloropl (370)	At4g15530.1	pyruvate,orthophosphate dikinase		0
only in chloropl (370)	At3g17240.1	dihydroliipoamide dehydrogenase 2, n		0
only in chloropl (370)	At5g03290.1	isocitrate dehydrogenase [NAD ⁺], pu		0
only in chloropl (370)	At2g13560.1	malate oxidoreductase (malic enzyme		0
only in chloropl (370)	At4g00570.1	malate oxidoreductase -related		0
only in chloropl (370)	At5g11670.1	NADP dependent malic enzyme - like		0
only in chloropl (370)	ATCG00420	ndhJ NADH dehydrogenase subunit J		0
only in chloropl (370)	At3g54110.1	uncoupling protein (ucp/PUMP)		0
only in chloropl (370)	At2g33040.1	mitochondrial F1-ATPase, gamma su		0
only in chloropl (370)	At1g54520.1	expressed protein	yes	1
only in chloropl (370)	ATCG00190	rpoB RNA polymerase beta chain	-encode	0
only in chloropl (370)	ATCG00180	rpoC1 RNA polymerase beta	-encode	0
only in chloropl (370)	ATCG00170	rpoC2 RNA polymerase beta	-encode	0
only in chloropl (370)	ATCG00160	30S rps2 ribosomal protein S2	-encode	0
only in chloropl (370)	ATCG00800	30S rps3 ribosomal protein S3	-encode	0
only in chloropl (370)	ATCG00380	30S rps4 ribosomal protein S4	-encode	0
only in chloropl (370)	ATCG00830	50S rpl2.1 ribosomal protein L2	-encode	0
only in chloropl (370)	ATCG00520	YCF4 PSI assembly	-encode	2
only in chloropl (370)	At2g22170.1	expressed protein	-encode	1
only in chloropl (370)	At3g52930.1	Aldolase	-encode	0
only in chloropl (370)	At5g08670.1	H ⁺ -transporting ATP synthase beta cl-encode		0
only in chloropl (370)	At3g54050.1	fructose-bisphosphatase precursor	yes	0
only in chloropl (370)	At3g59760.1	cysteine synthase, mitochondrial (O-a	yes	0
only in chloropl (370)	At1g58290.1	glutamyl-tRNA reductase 1 (GluTR)	yes	0
only in chloropl (370)	At1g69740.1	porphobilinogen synthase (delta-amin	yes	0
only in chloropl (370)	At1g32900.1	starch synthase, putative similar to st	yes	0
only in chloropl (370)	At3g23700.1	expressed protein	yes	0
only in chloropl (370)	At4g30910.1	leucyl aminopeptidase - like protein li	yes	0
only in chloropl (370)	At5g20930.1	protein kinase, putative nearly identic	yes	0
only in chloropl (370)	At3g26740.1	light regulated protein -related similar	yes	0
only in chloropl (370)	At5g36700.1	phosphoglycolate phosphatase, putati	yes	0
only in chloropl (370)	At2g47390.1	expressed protein	yes	0
only in chloropl (370)	At3g55760.1	expressed protein predicted protein, Δ	yes	0
only in chloropl (370)	At4g13500.1	expressed protein	yes	1
only in chloropl (370)	At3g07900.1	auxin-independent growth promoter -	yes	1
only in chloropl (370)	At1g15210.1	ABC transporter family protein Simil	yes	13

only in chloropl (370)	At2g21960.1	expressed protein	yes	3
only in chloropl (370)	At4g21700.1	hypothetical protein	yes	6
only in chloropl (370)	AtMg01190	atp1 ATPase subunit 1	i-encod	0
only in chloropl (370)	AtMg00480	orfB \N	i-encod	1
only in chloropl (370)	AtMg00160	cox2 cytochrome c oxidase subunit 2	i-encod	2
only in chloropl (370)	At3g46870.1	pentatricopeptide (PPR) repeat-contai	yes	0
only in chloropl (370)	At4g08510.1	hypothetical protein	yes	0
only in chloropl (370)	At4g09040.1	RNA recognition motif (RRM) - cont	yes	0
only in chloropl (370)	At4g12610.1	hypothetical protein transcription initi	yes	0
only in chloropl (370)	At4g29920.1	hypothetical protein predicted protein	yes	0
only in chloropl (370)	At5g04780.1	hypothetical protein crp1 protein, mai	yes	0
only in chloropl (370)	At5g30510.1	ribosomal protein S1	yes	0
only in chloropl (370)	At3g62410.1	CP12 protein precursor-related protei	yes	0
only in chloropl (370)	At1g32470.1	glycine cleavage system H protein pri	yes	0
only in chloropl (370)	At1g56190.1	phosphoglycerate kinase -related simi	yes	0
only in chloropl (370)	At2g01140.1	fructose-bisphosphate aldolase, putati	yes	0
only in chloropl (370)	At2g45290.1	transketolase precursor -related	yes	0
only in chloropl (370)	At5g38410.1	Rubisco small subunit 3b) (Rbes 3b)	yes	0
only in chloropl (370)	At2g22230.1	beta-hydroxyacyl-ACP dehydratase fi	yes	0
only in chloropl (370)	At5g36880.1	acetyl-CoA synthetase (acetate-CoA l	yes	0
only in chloropl (370)	At2g15620.1	ferredoxin--nitrite reductase	yes	0
only in chloropl (370)	At5g53460.1	glutamate synthase [NADH], chlorop	yes	0
only in chloropl (370)	At1g29900.1	carbamoylphosphate synthetase -relat	yes	0
only in chloropl (370)	At1g80600.1	acetylmethionine aminotransferase, mit	yes	0
only in chloropl (370)	At4g24830.1	argininosuccinate synthase -related pr	yes	0
only in chloropl (370)	At3g23940.1	dihydroxyacid dehydratase -related si	yes	0
only in chloropl (370)	At3g03630.1	cysteine synthase, chloroplast (O-acet	yes	0
only in chloropl (370)	At4g19170.1	9-cis-epoxycarotenoid dioxygenase [r	yes	0
only in chloropl (370)	At2g44050.1	6,7-dimethyl-8-ribityllumazine syntha	yes	0
only in chloropl (370)	At1g03475.1	coproporphyrinogen III oxidase (copr	yes	0
only in chloropl (370)	At2g30390.1	ferrochelatase precursor -related	yes	0
only in chloropl (370)	At5g13630.1	cobalamin biosynthesis protein	yes	0
only in chloropl (370)	At2g36390.1	1,4-alpha-glucan branching enzyme (yes	0
only in chloropl (370)	At4g18240.1	starch synthase-related protein contai	yes	0
only in chloropl (370)	At3g54090.1	pfkB type carbohydrate kinase protein	yes	0
only in chloropl (370)	At1g69830.1	alpha-amylase (1,4-alpha-D-glucan gl	yes	0
only in chloropl (370)	At3g29320.1	glucan phosphorylase, putative simila	yes	0
only in chloropl (370)	At5g04360.1	pullulanase (starch debranching enzy	yes	0
only in chloropl (370)	At2g41680.1	thioredoxin reductase, putative The la	yes	0
only in chloropl (370)	At3g06730.1	thioredoxin family contains Pfam pro	yes	0
only in chloropl (370)	At1g63940.1	monodehydroascorbate reductase, put	yes	0
only in chloropl (370)	At3g54660.1	glutathione reductase, chloroplast nea	yes	0
only in chloropl (370)	At4g23100.1	gamma-glutamylcysteine synthetase	yes	0
only in chloropl (370)	At5g06290.1	2-cys peroxiredoxin-related protein	yes	0
only in chloropl (370)	At2g28190.1	copper/zinc superoxide dismutase (C	yes	0
only in chloropl (370)	At5g51100.1	iron superoxide dismutase, putative si	yes	0
only in chloropl (370)	At1g09830.1	phosphoribosylglycinamide synthetas	yes	0
only in chloropl (370)	At3g57610.1	adenylosuccinate synthetase	yes	0
only in chloropl (370)	At1g80070.1	splicing factor Prp8 -related similar t	yes	0
only in chloropl (370)	At2g47680.1	helicase conserved C-terminal domain	yes	0
only in chloropl (370)	At3g03710.1	polyribonucleotide nucleotidyltransfe	yes	0
only in chloropl (370)	At2g27100.1	C2H2 zinc-finger protein SERRATE	yes	0
only in chloropl (370)	At4g19490.1	expressed protein probable membran	yes	0
only in chloropl (370)	At4g36060.1	bHLH protein family contains Pfam f	yes	0
only in chloropl (370)	At3g10690.1	DNA gyrase subunit A -related simil	yes	0
only in chloropl (370)	At2g25840.1	tryptophanyl-tRNA synthetase -related	yes	0
only in chloropl (370)	At3g48110.1	glycine--tRNA ligase precursor, chlor	yes	0
only in chloropl (370)	At4g04350.1	leucyl tRNA synthetase -related	yes	0
only in chloropl (370)	At5g16715.1	valine--tRNA ligase-related protein sr	yes	0
only in chloropl (370)	At5g49030.1	isoleucyl-tRNA synthetase	yes	0
only in chloropl (370)	At2g43030.1	ribosomal protein L3p family	yes	0
only in chloropl (370)	At3g15190.1	chloroplast 30S ribosomal protein S2l	yes	0
only in chloropl (370)	At3g25920.1	50S ribosomal protein L15, chloropla	yes	0
only in chloropl (370)	At3g44890.1	50S ribosomal protein L9, chloroplast	yes	0
only in chloropl (370)	At5g24490.1	PSRP-1 small	yes	0
only in chloropl (370)	At3g27160.1	expressed protein contains Pfam profi	yes	0
only in chloropl (370)	At3g44610.1	protein kinase family similar to viroic	yes	0
only in chloropl (370)	At4g33500.1	protein phosphatase 2C (PP2C) -relat	yes	0
only in chloropl (370)	At4g20850.1	expressed protein tripeptidyl-peptidas	yes	0
only in chloropl (370)	At5g65770.1	nuclear matrix constituent protein 1 (l	yes	0
only in chloropl (370)	At5g40200.1	DegP9 - HhoA homologue or DegQ	yes	0

only in chloropl (370)	At5g56500.1	Cpn60-beta-3	yes	0
only in chloropl (370)	At4g09160.1	expressed protein polyphosphoinosit	yes	0
only in chloropl (370)	At1g67560.1	lipoxygenase family similar to 13-lip	yes	0
only in chloropl (370)	At3g63130.1	RAN GTPase activating protein 1 prc	yes	0
only in chloropl (370)	At5g14040.1	mitochondrial phosphate transporter i	yes	0
only in chloropl (370)	At3g16250.1	ferredoxin - related contains Pfam prc	yes	0
only in chloropl (370)	At3g20390.1	translational inhibitor protein -related	yes	0
only in chloropl (370)	At3g52140.1	tetratricopeptide repeat (TPR)-contair	yes	0
only in chloropl (370)	At4g14970.1	hypothetical	yes	0
only in chloropl (370)	At4g20160.1	Glu-rich protein mature-parasite-infe	yes	0
only in chloropl (370)	At5g61210.1	syntaxin SNAP33	yes	0
only in chloropl (370)	At1g15980.1	expressed protein	yes	0
only in chloropl (370)	At2g05120.1	expressed protein	yes	0
only in chloropl (370)	At5g51200.1	expressed protein contains similarity	yes	0
only in chloropl (370)	At5g55610.1	expressed protein	yes	0
only in chloropl (370)	At1g18060.1	expressed protein	yes	0
only in chloropl (370)	At1g21600.1	expressed protein similar to hypotheti	yes	0
only in chloropl (370)	At1g48620.1	expressed protein contains DNA-bind	yes	0
only in chloropl (370)	At1g64770.1	expressed protein	yes	0
only in chloropl (370)	At1g73060.1	expressed protein	yes	0
only in chloropl (370)	At1g74850.1	pentatricopeptide (PPR) repeat-contai	yes	0
only in chloropl (370)	At1g76560.1	expressed protein	yes	0
only in chloropl (370)	At2g04039.1	expressed protein	yes	0
only in chloropl (370)	At2g28605.1	expressed protein	yes	0
only in chloropl (370)	At2g34640.1	expressed protein	yes	0
only in chloropl (370)	At2g37660.1	expressed protein	yes	0
only in chloropl (370)	At2g39020.1	GCN5-related N-acetyltransferase (G	yes	0
only in chloropl (370)	At2g42750.1	DnaJ protein family low similarity to	yes	0
only in chloropl (370)	At3g04760.1	pentatricopeptide (PPR) repeat-contai	yes	0
only in chloropl (370)	At3g07480.1	expressed protein HMM hit: 2Fe-2S i	yes	0
only in chloropl (370)	At3g15840.1	expressed protein	yes	0
only in chloropl (370)	At3g20550.1	expressed protein	yes	0
only in chloropl (370)	At3g26050.1	expressed protein	yes	0
only in chloropl (370)	At4g00690.1	Ulp1 protease family similar to SUM0	yes	0
only in chloropl (370)	At4g34120.1	CBS domain containing protein conta	yes	0
only in chloropl (370)	At4g35250.1	vestitone reductase-related low simila	yes	0
only in chloropl (370)	At4g36970.1	expressed protein	yes	0
only in chloropl (370)	At5g47870.1	expressed protein similar to unknown	yes	0
only in chloropl (370)	At5g57460.1	expressed protein	yes	0
only in chloropl (370)	At5g62140.1	hypothetical protein	yes	0
only in chloropl (370)	At5g63420.1	hydrolase family	yes	0
only in chloropl (370)	At3g22960.1	pyruvate kinase, putative similar to p	yes	0
only in chloropl (370)	At4g10750.1	aldolase -related similar to 2,4-dihydr	yes	0
only in chloropl (370)	At5g26570.1	expressed protein pyruvate water diki	yes	0
only in chloropl (370)	At5g13420.1	transaldolase - like protein transaldol	yes	0
only in chloropl (370)	At2g05710.1	aconitate hydratase (citrate hydro-lya	yes	0
only in chloropl (370)	At1g15700.1	ATP synthase gamma-subunit -relate	yes	0