



**Supplementary Figure S1.** Expression profiles of 18 representative ESTs in seedlings of the resistant (Lanmai) and susceptible (Polan305) varieties under *S. avenae* damage at different times. RT-qPCR was used to detect the expression levels of the candidate genes. *TaActin* was used as an internal control. Each value represents the mean  $\pm$  SE of three biological replicates. psbP-like protein 1 (A), light-harvesting complex-like protein OHP2 (B), ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (C), Fructose-bisphosphate aldolase (D), protein CHUP1, chloroplastic-like (E), protein thylakoid formation 1 (F), fructose-1,6-bisphosphatase (G), alpha-L-arabinofuranosidase 1 (H), glyceraldehyde-3-phosphate dehydrogenase (I), protein phosphatase 2C (J), translation machinery-associated protein (K), chlorophyllide, an oxygenase (L), probable aquaporin TIP2-2 (M), anion transporter 5 (N), calcium-transporting ATPase 9 (O), serine/threonine protein phosphatase (P), RAN-binding protein 1 (Q), S-adenosylmethionine decarboxylase (R).

**Supplementary Table S1.** The list of ESTs of SSH cDNA library from tetraploid wheat infected by *S. avenae* feeding

d b U se E r S T I - I d - d	Nr annotation		wheat function annnotation		Mapman function annotation		Gene_Ontology
	Protein name/organism	P E va lu e t	gene ID	annnotation	BI N co de	name	
Photosy nthesis and energy							
75 S 91 0 12 0 04 9	JK7 psbP-like protein 1, chloroplastic [Triticum aestivum]	5. 9 Traes 9. CS4A 00 1 03G0 E- 7 77860 80 % 0	PsbP-like protein 1	1.1 PS.lightreaction.phot .1. osystem II.PSII 2 polypeptide subunits	GO:0005509 MF: calcium ion binding;GO:0009523 CC: photosystem II;GO:0009654 CC: photosystem II oxygen evolving complex;GO:0015979 BP: photosynthesis;GO:0019898 CC: extrinsic component of membrane		
75 S 91 0 12 1 07 3	JK7 light-harvesting complex- like protein OHP2, chloroplastic [Triticum dicoccoides]	5. 0 Traes 00. CS2D E- 0 03G1 29 0 32930 % 0	Photosystem II CP43 reaction center protein	1.1 PS.lightreaction.phot .1. osystem II.PSII 2 polypeptide subunits	GO:0009521 CC: photosystem;GO:0009767 BP: photosynthetic electron transport chain;GO:0016020 CC: membrane;GO:0016168 MF: chlorophyll binding;GO:0019684 BP: photosynthesis, light reaction		
75 S 91 0 12 1 09 5	JK7 protein curvature thylakoid 1B, chloroplastic-like [Triticum dicoccoides]	2. 0 Traes 00. CS1B E- 0 03G0 07 0 62500 % 0	Protein curvature thylakoid chloroplastic-like	1.1 PS.lightreaction.phot .2. osystem I.PSI 2 polypeptide subunits	Unknown		
75 S 91 0 12 2 17 3	JK7 SKP1-like protein 1[Triticum dicoccoides]	3. 9 Traes 007. CS7D E- 2 03G0 13 8 03670 6 % 0	SKP1-like protein	1.1 PS.lightreaction.oth .5. r electron carrier 3 (ox/red).ferredoxin reductase	GO:0006511 BP: ubiquitin-dependent protein catabolic process		
75 S 91 0 12 3 31 7	JK7 photosystem I reaction center subunit N, chloroplastic-like [Triticum dicoccoides]	9. 9 Traes 00 7. CS2D E- 4 03G0 49 7 24090 % 0	Photosystem I reaction center subunit N	1.1 PS.lightreaction.phot .2. osystem I.PSI 2 polypeptide subunits	GO:0009522 CC: photosystem I;GO:0015979 BP: photosynthesis		

75 S	JK7	Chlorophyll a-b binding	4. 0 Traes	Chlorophyll a-b	1.1 PS.lightreaction.phot	Unknown
91 0	160	protein 1C, chloroplastic	000. CS1B	binding protein,	.1. osystem II.LHC-II	
12 5	82	[Triticum urartu]	E- 0 03G0	chloroplastic	1	
46 2			27 0 87120			
			% 0			
75 S	JK7	Chlorophyll a-b binding	7. 0 Traes	Chlorophyll a-b	1.1 PS.lightreaction.phot	Unknown
91 0	160	protein 1C, chloroplastic	000. CS5B	binding protein,	.1. osystem II.LHC-II	
12 5	83	[Triticum urartu]	E- 0 03G0	chloroplastic	1	
47 3			25 0 88440			
			% 0			
75 S	JK7	photosystem II 10 kDa	6. 8 Traes	Photosystem II 10	1.1 PS.lightreaction.phot	GO:0009523 CC: photosystem II;GO:0009654 CC: photosystem II oxygen evolving complex;GO:0015979 BP: photosynthesis;GO:0042651 CC: thylakoid membrane
91 0	160	polypeptide, chloroplastic	00 9. CS6A	kDa polypeptide	.1. osystem II.PSII	
12 6	91	[Triticum dicoccoides]	E- 2 03G0	family protein	2 polypeptide subunits	
55 1			55 1 95100			
			% 0			
75 S	JK7	protein THYLAKOID	6. 0 Traes	Protein	1.1 PS.lightreaction.phot	GO:0010207 BP: photosystem II assembly;GO:0015979 BP: photosynthesis
91 0	160	FORMATION1,	000. CS2B	THYLAKOID	.1. osystem II.PSII	
12 6	99	chloroplastic [Triticum	E- 0 03G0	FORMATION1,	2 polypeptide subunits	
63 9		dicoccoides]	23 0 56040	chloroplastic		
			% 0			
75 S	JK7	vulgare photosystem II	7. 9 Traes	Photosystem II	1.1 PS.lightreaction.phot	GO:0010207 BP: photosystem II assembly
91 1	161	repair protein PSB27-H1,	009. CS4D	Psb27 protein	.1. osystem II.PSII	
13 1	48	chloroplastic[Hordeum	E- 0 03G0		2 polypeptide subunits	
12 8		vulgare]	15 2 42910			
			2 % 0			
75 S	JK7	ribulose-1,5-bisphosphate	9 Traes	Ribulose	1.3 PS.calvin	GO:0000287 MF: magnesium ion binding;GO:0015977 BP: carbon fixation;GO:0016984 MF: ribulose-bisphosphate carboxylase activity
91 0	161	carboxylase/oxygenase	7. CS3B	bisphosphate	cycle.rubisco large	
13 0	65	large subunit [Triticum	0 8 03G0	carboxylase large	.1 subunit	
29 1		aestivum]	6 44620	chain		
			% 0			
75 S	JK7	ribulose-1,5-bisphosphate	1 Traes	Ribulose	1.3 PS.calvin	GO:0000287 MF: magnesium ion binding;GO:0015977 BP: carbon fixation;GO:0016984 MF: ribulose-bisphosphate carboxylase activity
91 0	160	carboxylase/oxygenase	2. 0 CS5D	bisphosphate	cycle.rubisco large	
11 0	33	large subunit [Hordeum	000. 03G0	carboxylase large	.1 subunit	
97 2		brachyantherum]	E- 0 01600	chain		
			47 0 0			
			% 0			

75 S	JK7	ribulose biphosphate	7. 9 Traes	Ribulose	1.3	PS.calvin	GO:0000287 MF: magnesium ion binding;GO:0015977 BP: carbon fixation;GO:0016984 MF: ribulose-bisphosphate carboxylase activity
91 0	160	carboxylase large chain-like	00 9. CS5D	bisphosphate	.1	cycle.rubisco large	
11 0	34	[Triticum aestivum]	E- 2 93640	carboxylase large		subunit	
98 3			63 % 0	chain			
75 S	JK7	ribulose 1,5-bisphosphate	4. 9 Traes	Ribulose	1.3	PS.calvin	GO:0000287 MF: magnesium ion binding;GO:0015977 BP: carbon fixation;GO:0016984 MF: ribulose-bisphosphate carboxylase activity
91 0	160	carboxylase/oxygenase	00 3. CS5D	bisphosphate	.1	cycle.rubisco large	
11 0	35	large subunit, Rubisco	E- 7 03G0	carboxylase large		subunit	
99 4		[Triticum aestivum]	11 % 0	chain			
75 S	JK7	ribulose bisphosphate	1. 9 Traes	Ribulose	1.3	PS.calvin	Unknown
91 0	160	carboxylase small chain	00 1. CS5D	bisphosphate	.2	cycle.rubisco small	
12 0	38	PW9, chloroplastic-like	E- 4 03G0	carboxylase small		subunit	
02 7		[Triticum dicoccoides]	10 3 41420	chain			
			9 % 0				
75 S	JK7	ribulose bisphosphate	5. 9 Traes	Ribulose	1.3	PS.calvin	Unknown
91 0	160	carboxylase small chain	00 8. CS2A	bisphosphate	.2	cycle.rubisco small	
12 0	39	PW9, chloroplastic-like	E- 5 03G0	carboxylase small		subunit	
03 8		[Triticum dicoccoides]	43 % 0	chain			
75 S	JK7	ribulose bisphosphate	1. 9 Traes	Ribulose	1.3	PS.calvin	GO:0005524 MF: ATP binding
91 0	161	carboxylase/oxygenase	00 6. CS4B	bisphosphate	.13	cycle.rubisco	
13 1	66	activase A, chloroplastic-	E- 8 03G0	carboxylase/oxygena.		interacting	
30 1		like isoform X1 [Triticum	E- 4 32750	se activase			
		dicoccoides]	64 % 0				
75 S	JK7	ribulose-1,5-bisphosphate	1. 9 Traes	Ribulose	1.3	PS.calvin	GO:0000287 MF: magnesium ion binding;GO:0015977 BP: carbon fixation;GO:0016984 MF: ribulose-bisphosphate carboxylase activity
91 0	160	carboxylase/oxygenase	00 0. CS3B	bisphosphate	.1	cycle.rubisco large	
12 3	66	large subunit [Triticum	E- 0 03G0	carboxylase large		subunit	
30 6		turgidum]	75 0 44620	chain			
			% 0				
75 S	JK7	fructose-1,6-bisphosphatase,	3. 9 Traes	Fructose-1,6-	1.3	PS.calvin	GO:0005975 BP: carbohydrate metabolic process;GO:0016791 MF: phosphatase activity;GO:0042132 MF: fructose 1,6-bisphosphate 1-phosphatase activity
91 0	160	cytosolic-like [Triticum	00 4. CS3D	bisphosphatase class	.7	cycle.FBPase	
12 4	76	dicoccoides]	E- 4 03G0	1			
40 6			11 1 81950				
			9 % 0				
75 S	JK7	phospholipase A1-II 7-like	2. 9 Traes	Fructose-	1.3	PS.calvin	GO:0003824 MF: catalytic activity;GO:0004332 MF: fructose-bisphosphate aldolase activity;GO:0006096 BP: glycolytic process
91 0	161	[Triticum dicoccoides]	00 6. CS4D	bisphosphate	.6	cycle.aldolase	
12 7	09		E- 6 03G0	aldolase			
73 9			65				

		4 21190 % 0						
Cell organisation and division								
75 S 91 0 12 1 13 9	JK7 cell division control protein 48 homolog E-like [Triticum dicoccoides]	6. 9 Traes 7. 00 CS4B 2 03G0 6 71320 25% 0	Cell division cycle protein 48-like protein	31. 2	cell.division		GO:0005524 MF: ATP binding;GO:0016787 MF: hydrolase activity	
75 S 91 0 12 5 44 0	JK7 protein CHUP1, chloroplastic-like [Triticum dicoccoides]	6. 9 Traes 7. 00 CS1B 2 03G1 6 19540 92% 0	Protein CHUP1, chloroplastic	31. 1	cell.organisation		GO:0005179 MF: hormone activity;GO:0005576 CC: extracellular region	
75 S 91 0 12 5 45 1	JK7 protein CHUP1, chloroplastic-like [Triticum dicoccoides]	3. 9 Traes 8. 00 CS1A 1 03G1 3 01410 63% 0	Protein CHUP1, chloroplastic	31. 1	cell.organisation		GO:0005179 MF: hormone activity;GO:0005576 CC: extracellular region	
75 S 91 0 12 9 84 0	JK7 MOB kinase activator-like 1A [Hordeum vulgare]	6. 9 Traes 7. 00 CS6D 9 03G0 6 36970 60% 0	MOB kinase activator-like 1A	31. 2	cell.division		Unknown	
Cel 1 wal 1								
75 S 91 0 12 7 65 1	JK7 probable aquaporin TIP2-2 [Triticum dicoccoides]	4. 8 Traes 6. 00 CS7A 2 03G0 4 81690 90% 0	Aquaporin	10. 7	cell wall.modification		GO:0005215 MF: transporter activity;GO:0006810 BP: transport;GO:0016020 CC: membrane	
75 S 91 0 12 9 90 6	JK7 expansin-B6-like [Triticum dicoccoides]	1. 9 Traes 4. 00 CS1B 8 03G0 7 65130 43% 0	Expansin protein	10. 7	cell wall.modification		GO:0005576 CC: extracellular region;GO:0019953 BP: sexual reproduction	

75 S	JK7	probable aquaporin PIP2-2	3. 8 Traes	Bifunctional					
91 1	161	[Triticum dicoccoides]	00 7. CS4B	inhibitor/lipid-	35.	not			
13 2	51		E- 9 03G0	transfer protein/seed	2	assigned.unknown			Unknown
15 1			85 9 03730	storage 2S albumin					
			% 0	superfamily protein					
Metabo									
lism									
75 S	JK7	4-hydroxyphenylpyruvate	5. 9 Traes						
91 0	160	dioxygenase-like [Triticum	00 2. CS6B	4-	12.	N-metabolism.misc			GO:0003868 MF: 4-hydroxyphenylpyruvate dioxygenase activity;GO:0009072 BP: aromatic
12 0	37	dicoccoides]	E- 8 03G0	hydroxyphenylpyruv	4				amino acid family metabolic process;GO:0016701 MF: oxidoreductase activity, acting on
01 6			05 6 43370	ate dioxygenase					single donors with incorporation of molecular oxygen;GO:0055114 BP: oxidation-reduction
			% 0						process
75 S	JK7	glucose-6-phosphate	2. 8 Traes						
91 0	160	isomerase 1, chloroplastic-	00 4. CS5D	Glucose-6-phosphate	4.2	glycolysis.plastid			GO:0004347 MF: glucose-6-phosphate isomerase activity;GO:0006094 BP:
12 2	57	like [Triticum	E- 1 03G0	isomerase	.3	branch.glucose-6-			gluconeogenesis;GO:0006096 BP: glycolytic process
21 7		dicoccoides]	58 3 58420			phosphate isomerase			
			% 0						
75 S	JK7	photosystem II 22 kDa	5. 9 Traes		13.	amino acid			
91 0	160	protein 1, chloroplastic-like	00 5. CS6B	AT-rich interactive	1.4	metabolism.synthesis			
12 2	58	[Triticum dicoccoides]	E- 2 03G0	domain protein	.1.	.branched chain			GO:0003677 MF: DNA binding
22 8			46 4 88410		1	group.common.aceto			
			% 0			lactate synthase			
75 S	JK7	malate dehydrogenase,	1. 9 Traes			TCA / org.			GO:0003824 MF: catalytic activity;GO:0005975 BP: carbohydrate metabolic
91 0	160	cytoplasmic-like [Triticum	00 6. CS1B	Malate	8.2	transformation.other			process;GO:0006108 BP: malate metabolic process;GO:0016491 MF: oxidoreductase
12 3	60	dicoccoides]	E- 0 03G0	dehydrogenase	.9	organic acid			activity;GO:0016615 MF: malate dehydrogenase activity;GO:0016616 MF: oxidoreductase
24 0			99 8 50910			transformaitons.cyt			activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0019752 BP:
			% 0			MDH			carboxylic acid metabolic process;GO:0030060 MF: L-malate dehydrogenase
									activity;GO:0055114 BP: oxidation-reduction process
75 S	JK7	glyceraldehyde-3-phosphate	1. 9 Traes			glycolysis.plastid			
91 0	160	dehydrogenase 1, cytosolic-	00 5. CS7D	Glyceraldehyde-3-	4.2	branch.Glyceraldehy			GO:0006006 BP: glucose metabolic process;GO:0016620 MF: oxidoreductase activity, acting
12 3	68	like [Triticum dicoccoides]	E- 7 03G0	phosphate	.3	de 3-phosphate			on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0050661 MF: NADP
32 8			52 4 73750	dehydrogenase		dehydrogenase			binding;GO:0051287 MF: NAD binding;GO:0055114 BP: oxidation-reduction process
			% 0						
75 S	JK7	ATP synthase CF1 alpha	4. 9 Traes			mitochondrial			GO:0005524 MF: ATP binding;GO:0015986 BP: ATP synthesis coupled proton
91 0	160	subunit [Triticum	00 5. CS5D	ATP synthase	9.9	electron transport /			transport;GO:0015992 BP: proton transport;GO:0045261 CC: proton-transporting ATP
12 4	77	turgidum]	E- 5 03G1	subunit alpha		ATP synthesis.F1-			synthase complex, catalytic core F(1);GO:0046034 BP: ATP metabolic process;GO:0046933
41 7			48 1 01600			ATPase			MF: proton-transporting ATP synthase activity, rotational mechanism
			% 0						

75 S 91 0 12 4 42 8	JK7 160 78 X1 [Triticum dicoccoides]	carbonic anhydrase, chloroplastic-like isoform X1 [Triticum dicoccoides]	3. 9 Traes 00 6. CS3A 7 03G0 E- 5 59360 80 % 0	Carbonic anhydrase	8.3 transformation.carbo nic anhydases	TCA / org.	GO:0004089 MF: carbonate dehydratase activity;GO:0008270 MF: zinc ion binding;GO:0015976 BP: carbon utilization
75 S 91 0 12 6 61 7	JK7 160 97 vulgare]	vulgare mRNA for predicted protein [Hordeum vulgare]	6. 9 Traes 00 9. CS6D E- 1 03G0 16 1 31880 8 % 0	Aldose 1-epimerase family protein			GO:0003824 MF: catalytic activity;GO:0005975 BP: carbohydrate metabolic process;GO:0016853 MF: isomerase activity;GO:0030246 MF: carbohydrate binding
75 S 91 0 12 7 71 7	JK7 161 07 [Triticum turgidum]	kinetochore-associated protein KNL-2 homolog [Triticum turgidum]	9. 9 Traes 00 6. CS2A E- 6 03G0 10 1 68220 5 % 0	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha		Unknown	
75 S 91 0 12 8 77 3	JK7 161 13 [Triticum dicoccoides]	malate dehydrogenase [NADP] 1, chloroplastic- like [Triticum dicoccoides]	2. 9 Traes 00 9. CS7B E- 1 03G0 16 2 54600 4 % 0	Malate dehydrogenase	35. not 2 assigned.unknown		GO:0003824 MF: catalytic activity;GO:0005975 BP: carbohydrate metabolic process;GO:0006108 BP: malate metabolic process;GO:0016491 MF: oxidoreductase activity;GO:0016615 MF: malate dehydrogenase activity;GO:0016616 MF: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0046554 MF: malate dehydrogenase (NADP+) activity;GO:0055114 BP: oxidation-reduction process
75 S 91 0 12 8 80 6	JK7 161 16 chloroplastic-like [Triticum dicoccoides]	carbamoyl-phosphate synthase small chain, chloroplastic-like [Triticum dicoccoides]	9. 9 Traes 00 7. CS5D E- 2 03G0 12 1 39540 3 % 0	Carbamoyl- phosphate synthase small chain	23. metabolism.synthesis 1.1 .pyrimidine.carbamo .1 yl phosphate synthetase amino acid 13. metabolism.synthesis 1.4 .branched chain .1 group.common.aceto lactate synthase		GO:0004088 MF: carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;GO:0006207 BP: 'de novo' pyrimidine nucleobase biosynthetic process;GO:0006541 BP: glutamine metabolic process
75 S 91 0 12 9 87 3	JK7 161 23 [Triticum dicoccoides]	adenosylhomocysteinase [Triticum dicoccoides]	2. 9 Traes 00 8. CS2B E- 8 03G1 11 4 30790 7 % 0	Adenosylhomocystei nase			GO:0004013 MF: adenosylhomocysteinase activity;GO:0006730 BP: one-carbon metabolic process;GO:0019510 BP: S-adenosylhomocysteine catabolic process;GO:0051287 MF: NAD binding
75 S 91 1 12 0 94 0	JK7 161 30 [Triticum dicoccoides]	alpha-L-arabinofuranosidase 1-like isoform X2 [Triticum dicoccoides]	9. 9 Traes 00 9. CS4B E- 3 03G0 10 2 30100 1 % 0	Alpha-L- arabinofuranosidase 1	35. not 2 assigned.unknown		GO:0046373 BP: L-arabinose metabolic process;GO:0046556 MF: alpha-L- arabinofuranosidase activity
75 S 91 1 12 0 97 3	JK7 161 33 [Triticum dicoccoides]	sucrose synthase 2-like [Triticum dicoccoides]	4. 9 Traes 00 3. CS4A E- 9 03G1 10 4 11630 10 % 0	Sucrose synthase	2.2 major CHO .1. metabolism.degradat 5 ion.sucrose.Susy		GO:0005985 BP: sucrose metabolic process;GO:0016157 MF: sucrose synthase activity

75 S	JK7	alpha-L-arabinofuranosidase 1-like isoform X2	1. 9 Traes 00 1. CS4A 04 03G0 E- 3 50680 52 % 0	Alpha-L-arabinofuranosidase 1	35. 2	not assigned.unknown	GO:0046373 BP: L-arabinose metabolic process;GO:0046556 MF: alpha-L-arabinofuranosidase activit
75 S	JK7	formamidase-like	2. 9 Traes 00 9. CS3A 01 03G0 E- 8 74710 79 % 0	Acetamidase/formamidase, putative	26. 1	misc.misc2	GO:0016811 MF: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
<b>Protein degradation</b>							
75 S	JK7	ATP-dependent Clp protease ATP-binding subunit clpA-like protein CD4B, chloroplastic	1. 9 Traes 00 6. CS5B 06 03G0 E- 1 29950 27 % 0	ATP-dependent Clp protease ATP-binding subunit	29. 5.5	protein.degradation.serine protease	GO:0005515 MF: protein binding;GO:0005524 MF: ATP binding;GO:0019538 BP: protein metabolic process
75 S	JK7	ATP-dependent Clp protease proteolytic subunit 3, chloroplastic-like	7. 9 Traes 00 8. CS3A E- 2 03G0 16 2 49990 1 % 0	ATP-dependent Clp protease proteolytic subunit	29. 5.5	protein.degradation.serine protease	GO:0004252 MF: serine-type endopeptidase activity;GO:0006508 BP: proteolysis
75 S	JK7	protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1	3. 9 Traes 00 5. CS3A 08 03G0 E- 3 11270 22 % 0	Katanin p60 ATPase-containing subunit, putative	29. 5.9	protein.degradation.AAA type	GO:0005524 MF: ATP binding
75 S	JK7	protein HHL1, chloroplastic-like	3. 9 Traes 00 9. CS6B 00 0 03G0 E- 2 71270 62 % 0	Protein HHL1, chloroplastic	29. 5.1	protein.degradation.ubiquitin.proteasom	Unknown
75 S	JK7	20S proteasome beta 4 subunit	4. 9 Traes 00 5. CS4B 08 03G0 E- 3 07800 23 % 0	Proteasome subunit beta type	29. 5.1	protein.degradation.ubiquitin.proteasom	GO:0004175 MF: endopeptidase activity;GO:0004298 MF: threonine-type endopeptidase activity;GO:0005839 CC: proteasome core complex;GO:0051603 BP: proteolysis involved in cellular protein catabolic process



75 S	JK7	coiled-coil domain- containing protein 12-like [Triticum dicoccoides]	1. 9 Traes 00 4. CS7A 12 9 03G1 85 1 E- 4 37230 61 % 0	Coiled-coil domain- containing protein 12 5	protein.degradation	Unknown
75 S	JK7	ubiquitin carboxyl-terminal hydrolase 12-like isoform 22 X1 [Triticum dicoccoides]	2. 9 Traes 00 9. CS5A 12 9 03G0 86 2 E- 9 27520 90 % 0	Ubiquitin carboxyl- terminal hydrolase, putative	29. protein.degradation.u 5.1 biquitin.ubiquitin 1.5 protease	GO:0005515 MF: protein binding;GO:0006511 BP: ubiquitin-dependent protein catabolic process;GO:0016579 BP: protein deubiquitination;GO:0036459 MF: thiol-dependent ubiquitinyl hydrolase activity
75 S	JK7	E3 ubiquitin-protein ligase RNF25-like [Triticum dicoccoides]	3. 0 Traes 00 0. CS4B 13 0 03G0 00 6 E- 0 40780 49 0 % 0	E3 ubiquitin-protein ligase RNF25	29. 5.1 protein.degradation.u 1.4 biquitin.E3.RING .2	GO:0005515 MF: protein binding;GO:0008270 MF: zinc ion binding
75 S	JK7	E3 ubiquitin-protein ligase At1g63170-like isoform X1 40 [Triticum dicoccoides]	3. 9 Traes 00 8. CS5A 13 1 03G0 04 0 E- 4 48460 59 % 0	RING/U-box superfamily protein	29. 5.1 protein.degradation.u 1.4 biquitin.E3.RING .2	O:0005515 MF: protein binding;GO:0008270 MF: zinc ion binding
<b>Protein synthesis</b>						
75 S	JK7	40S ribosomal protein S15- like [Triticum dicoccoides]	1. 9 Traes 00 5. 0 CS5A 12 2 03G1 18 4 E- 0 04530 13 0 % 0	30S ribosomal protein S19	29. 2.1 protein.synthesis.ribo somal .2. protein.eukaryotic.40 1.1 S subunit.S15 5	GO:0003723 MF: RNA binding;GO:0003735 MF: structural constituent of ribosome;GO:0005840 CC: ribosome;GO:0006412 BP: translation;GO:0015935 CC: small ribosomal subunit
75 S	JK7	vulgare mRNA for predicted protein[Hordeum vulgare]	2. 9 Traes 00 8. CS7B 12 2 03G0 20 6 E- 4 29100 65 % 0	Receptor-like protein kinase	GO:0004672 MF: protein kinase activity;GO:0005515 MF: protein binding;GO:0005524 MF: ATP binding;GO:0006468 BP: protein phosphorylation	
75 S	JK7	protein SGT1 homolog [Triticum dicoccoides]	1. 1 Traes 00 0. CS3D 12 2 03G0 23 9 E- 0. 53920 54 0 0	SGT1	29. protein.postranslatio 4 nal modification	GO:0005515 MF: protein binding

			0 %				
75 S	JK7	CTD small phosphatase-like	5. 9 Traes	CTD small			
91 0	160	protein 2 [Triticum	006. CS5B	phosphatase-like	26. misc.acid and other		GO:0016791 MF: phosphatase activity
12 3	63	dicoccoides]	E- 1 03G1	protein	13 phosphatases		
27 3			11 3 30880				
			0 % 0				
75 S	JK7	neurogenic locus Notch	1. 9 Traes	Neurogenic locus			
91 0	160	protein-like [Triticum	00 1. CS4B	notch homolog	29. protein.synthesis.elo		GO:0005515 MF: protein binding
12 4	72	dicoccoides]	E- 6 03G0	protein 2	2.4 ngation		
36 2			55 7 73610				
			% 0				
75 S	JK7	putative prefoldin subunit 3	9. 8 Traes	Prefoldin subunit 3	29. protein.folding		GO:0006457 BP: protein folding;GO:0016272 CC: prefoldin complex
91 0	160	[Triticum urartu]	00 8. CS5B		6		
12 4	75		E- 6 03G0				
39 5			47 4 23270				
			% 0				
75 S	JK7	elongation factor 1-delta 1-	8. 9 Traes	Elongation factor 1-	29. protein.synthesis.elo	GO:0003746 MF: translation elongation factor activity;GO:0005853 CC: eukaryotic translation	
91 0	160	like isoform X2 [Triticum	00 5. CS2B	beta	2.4 ngation	elongation factor 1 complex;GO:0006414 BP: translational elongation	
12 5	89	dicoccoides]	E- 0 03G0				
53 9			44 6 47320				
			% 0				
75 S	JK7	chlorophyllide a oxygenase,	3. 9 Traes	Chlorophyllide a		GO:0005506 MF: iron ion binding;GO:0010277 MF: chlorophyllide a oxygenase [overall]	
91 0	161	chloroplastic-like	00 9. CS3B	oxygenase,	29.protein.targeting.chlo	activity;GO:0016491 MF: oxidoreductase activity;GO:0016705 MF: oxidoreductase activity,	
12 8	17	[Triticum dicoccoides]	E- 3 03G1	chloroplastic	3.3 roplast	acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0051537 MF:	
81 7			98 1 43490			2 iron, 2 sulfur cluster binding;GO:0055114 BP: oxidation-reduction process	
			% 0				
75 S	JK7	40S ribosomal protein S27	4. 9 Traes	40S ribosomal	29. protein.synthesis.ribo		
91 0	161	isoform X1 [Triticum	00 8. CS4B	protein S27	2.1 somal	GO:0003735 MF: structural constituent of ribosome;GO:0005622 CC:	
12 9	27	dicoccoides]	E- 8 03G0		2. protein.eukaryotic.40	intracellular;GO:0005840 CC: ribosome;GO:0006412 BP: translation	
91 7			34 2 18730		1.2 S subunit.S27		
			% 0				
75 S	JK7	RGS domain-containing	2. 9 Traes	Protein kinase family			
91 0	161	serine/threonine-protein	00 7. CS4B	protein, putative,	29. protein.postranslatio	GO:0004672 MF: protein kinase activity;GO:0005524 MF: ATP binding;GO:0006355 BP:	
12 9	28	kinase A-like isoform X1	E- 4 03G0	expressed	4 nal modification	regulation of transcription, DNA-templated;GO:0006468 BP: protein phosphorylation	
92 8		[Hordeum vulgare]	06 4 30030				
			% 0				
75 S	JK7	40S ribosomal protein S6-	6. 9 Traes	40S ribosomal	29.protein.synthesis.ribo	GO:0003735 MF: structural constituent of ribosome;GO:0005622 CC:	
91 1	161	like [Triticum	00 7. CS2D	protein S6	2.1 somal	intracellular;GO:0005840 CC: ribosome;GO:0006412 BP: translation	
	31	dicoccoides]	00 0 03G0				

12 0		E- 1 35680		.2. protein.eukaryotic.40	
95 1		18% 0		1.6 S subunit.S6	
75 S		6. 9 Traes			
91 1	JK7	00 5. CS3B	Translation	29.protein.synthesis.initi	GO:0003743 MF: translation initiation factor activity;GO:0006413 BP: translational initiation
12 0	161	7 03G0	machinery-	2.3 ation	
99 5	35	E- 3 28550	associated protein 22		
		70% 0			
75 S		1. 8 Traes		29. protein.synthesis.ribo	
91 1	JK7	00 3. CS1B		2.1 somal	GO:0003735 MF: structural constituent of ribosome;GO:0005622 CC: intracellular;GO:0005840 CC: ribosome;GO:0006412 BP: translation
13 0	161	E- 1 03G0	Ribosomal protein	.2. protein.eukaryotic.60	
03 9	39	33% 0		2.1 S subunit.L10	
75 S		2. 9 Traes			
91 1	JK7	00 9. CS2B	Protein phosphatase	29. protein.postranslatio	GO:0003824 MF: catalytic activity
13 1	161	E- 0 03G1	2c, putative	4 nal modification	
10 6	46	70% 0			
75 S		5. 9 Traes			
91 1	JK7	00 3. CS1D	Protein translation	29.protein.synthesis.initi	GO:0003743 MF: translation initiation factor activity;GO:0006413 BP: translational initiation
13 2	161	E- 3 03G0	factor SUI1-like	2.3 ation	
19 5	55	09% 0	protein		
75 S		1 4. 0 Traes		29.protein.synthesis.ribo	
91 1	JK7	000. CS2B	30S ribosomal	2.1 somal	GO:0003735 MF: structural constituent of ribosome;GO:0005840 CC: ribosome;GO:0006412 BP: translation
13 2	161	E- 0 03G0	protein S8	.2. protein.eukaryotic.30	
22 8	58	31 0 70330		1.6 S subunit.S8	
75 S		8. 9 Traes		29. protein.synthesis.ribo	
91 1	JK7	00 0. CS4D	40S ribosomal	2.1 somal	GO:0003735 MF: structural constituent of ribosome;GO:0005622 CC: intracellular;GO:0005840 CC: ribosome;GO:0006412 BP: translation
13 3	161	E- 5 03G0	protein S21	.2. protein.eukaryotic.40	
24 0	60	49% 0		1.2 S subunit.S21	
75 S		8. 9 Traes			
91 1	JK7	00 9. CS7A	receptor kinase 1	29. protein.postranslatio	GO:0004672 MF: protein kinase activity;GO:0005515 MF: protein binding;GO:0005524 MF: ATP binding;GO:0006468 BP: protein phosphorylation
13 3	161	E- 2 03G1		4 nal modification	
26 2	62	63% 0			

75 S	JK7	5.8S ribosomal RNA (LOC119351432), rRNA[Triticum dicoccoides]	1.0 000.03G0 E-032540 6100 %	1 Traes CS4D	Kinase family protein	GO:0004672 MF: protein kinase activity;GO:0005524 MF: ATP binding;GO:0006468 BP: protein phosphorylation
Cell stress response and defence						
75 S	JK7	S-adenosylmethionine decarboxylase [Triticum dicoccoides]	1.0 000.03G0 E-086970 1400 %	1 Traes CS2A	S-adenosylmethionine decarboxylase proenzyme	22. polyamine metabolism.synthesis 1.2.SAM decarboxylase
91 0	160					GO:0004014 MF: adenosylmethionine decarboxylase activity;GO:0006597 BP: spermine biosynthetic process;GO:0008295 BP: spermidine biosynthetic process
12 1	46					
10 6						
75 S	JK7	heat shock factor-binding protein [Triticum dicoccoides]	1.0 000.03G0 E-047440 4900 %	1 Traes CS7D	Heat shock factor-binding protein 1	20. stress.abiotic.heat 2.1
91 0	160					GO:0003714 MF: transcription corepressor activity
12 2	51					
15 1						
75 S	JK7	putative BPI/LBP family protein Atlg04970 isoform X1 [Triticum dicoccoides]	3.9 003.03G0 E-367430 81% 0	9 Traes CS5B	Lipid-binding serum glycoprotein	35. not assigned.unknown
91 0	160					GO:0005615 CC: extracellular space;GO:0008289 MF: lipid binding
12 5	85					
49 5						
75 S	JK7	heat shock protein 90-5, chloroplastic-like [Triticum dicoccoides]	3.9 007.03G0 E-159590 1016 %	9 Traes CS5D	Chaperone protein htpG family protein	20. stress.abiotic.heat 2.1
91 0	160					GO:0005524 MF: ATP binding;GO:0006457 BP: protein folding;GO:0006950 BP: response to stress;GO:0051082 MF: unfolded protein binding
12 5	87					
51 7						
75 S	JK7	unnamed protein product [Triticum turgidum]	2.9 008.03G0 E-192740 1197 %	9 Traes CS1A	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	35. not assigned.unknown
91 0	160					GO:0016491 MF: oxidoreductase activity;GO:0055114 BP: oxidation-reduction process
12 6	92					
56 2						
75 S	JK7	UV-B-induced protein At3g17800, chloroplastic-like [Triticum aestivum]	5.9 007.03G0 E-699490 74% 0	9 Traes CS2D	UV-B-induced protein, chloroplastic	20. stress.abiotic
91 0	160					Unknown
12 6	94					
58 4						

75 S	JK7	unnamed protein product	1.0	Traes					
91 0	160	[Triticum turgidum]	00.0	CS6B	Superoxide				
12 6	98		E-0	03G0	dismutase [Cu-Zn]				Unknown
62 8			75 0	97190					
			%	0					
75 S	JK7	cytochrome B5-like protein	9.4	Traes					
91 0	161	[Triticum aestivum]	00.4	CS5D	Cytochrome B5-like	21. redox.ascorbate and			
12 7	02		E-4	03G0	protein	2 glutathione			GO:0020037 MF: heme binding
66 2			13 0	45370					
			6 1	0					
75 S	JK7	beta purothionin [Triticum	5.6	Traes					
91 0	161	urartu]	00.0	CS1D	Beta purothionin	20. stress.abiotic			GO:0006952 BP: defense response
12 7	04		E-2	03G0		2			
68 4			26 4	94380					
			%	0					
75 S	JK7	unnamed protein product	1.0	Traes					
91 0	161	[Triticum turgidum]	00.0	CS6B	Superoxide				
12 7	05		E-0	03G0	dismutase [Cu-Zn]				Unknown
69 5			36 0	97190					
			%	0					
75 S	JK7	wPR4a gene [Triticum	2.8	Traes					
91 0	161	aestivum]	00.3	CS3D	Pathogenesis-related	20. stress.biotic			GO:0042742 BP: defense response to bacterium;GO:0050832 BP: defense response to fungus
12 8	10		E-6	03G1	protein PR-4	1			
74 0			34 0	16060					
			%	0					
75 S	JK7	quinolinate synthase,	1.9	Traes					
91 0	161	chloroplastic-like isoform	00.8	CS5A	Quinolinate synthase	35. not			GO:0008987 MF: quinolinate synthetase A activity;GO:0009435 BP: NAD biosynthetic
12 8	14	X1 [Triticum dicoccoides]	E-1	03G0	A	2 assigned.unknown			process;GO:0051539 MF: 4 iron, 4 sulfur cluster binding
78 4			14 7	29800					
			9 %	0					
75 S	JK7	cytochrome b5-like	2.9	Traes					
91 1	161	[Triticum dicoccoides]	00.7	CS3D	Cytochrome b5	21. redox.ascorbate and			GO:0020037 MF: heme binding
13 1	44		E-5	03G1		2 glutathione			
08 4			50 6	16990					
			%	0					

[illegible]

75 S	JK7	ran-binding protein 1	3. 0	1 Traes					
91 0	160	homolog c-like [Triticum	000.	CS1B	Ran-binding protein	30.	signalling.G-proteins	GO:0046907 BP: intracellular transport	
12 1	48	dicoccoides]	E- 0	03G0	1	5			
12 8			26 0	67810					
			%	0					
75 S	JK7	serine/threonine protein	1. 9	1 Traes					
91 0	160	phosphatase 2A 55 kDa	00 1.	CS3B	Late embryogenesis	33.	development.late		
12 3	61	regulatory subunit B beta	E- 7	03G1	abundant protein	2	embryogenesis	Unknown	
25 1		isoform [Triticum aestivum]	47 8	46470			abundant		
			%	0					
75 S	JK7	probable pyridoxal 5'-	2. 9	1 Traes					
91 0	160	phosphate synthase subunit	00 8.	CS6B	Pyridoxal 5'-	30.		GO:0004359 MF: glutaminase activity;GO:0042819 BP: vitamin B6 biosynthetic	
12 3	65	PDX2 [Triticum	E- 1	03G0	phosphate synthase	11	signalling.light	process;GO:0042823 BP: pyridoxal phosphate biosynthetic	
29 5		dicoccoides]	19 8	29080	subunit PdxT				
			%	0					
75 S	JK7	aspartate aminotransferase,	2. 9	1 Traes					
91 0	160	chloroplast-like isoform	00 6.	CS6D	Aspartate	30.		GO:0003824 MF: catalytic activity;GO:0006520 BP: cellular amino acid metabolic	
12 4	70	X2 [Triticum dicoccoides]	E- 5	03G0	aminotransferase	3	signalling.calcium	process;GO:0008483 MF: transaminase activity;GO:0009058 BP: biosynthetic	
34 0			75 5	79700				process;GO:0030170 MF: pyridoxal phosphate binding	
			%	0					
75 S	JK7	lipoxygenase 2.1,	8. 8	1 Traes			hormone	GO:0005515 MF: protein binding;GO:0016491 MF: oxidoreductase activity;GO:0016702 MF:	
91 0	160	chloroplast-like	00 7.	CS5D	Lipoxygenase	17.	metabolism.jasmonat	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen,	
12 4	74	[Triticum dicoccoides]	E- 6	02890		7.1	e.synthesis-	incorporation of two atoms of oxygen;GO:0046872 MF: metal ion binding;GO:0055114 BP:	
38 4			51 0			.2	degradation.lipoxyge	oxidation-reduction process	
			%	0			nase		
75 S	JK7	calcium-dependent protein	2. 9	1 Traes					
91 0	160	kinase [Arachis hypogaea]	00 3.	CS2B	2-oxoglutarate		hormone	GO:0016491 MF: oxidoreductase activity;GO:0055114 BP: oxidation-reduction process	
12 4	79		E- 3	03G0	(2OG) and Fe(II)-	17.	metabolism.ethylene.		
43 9			27 3	14270	dependent oxygenase5.1		synthesis-		
			%	0	superfamily protein		degradation		
75 S	JK7	transcript variant X1,	2. 9	1 Traes					
91 0	160	mRNA[Triticum	00 6.	CS5B	Transducin/WD-like	33.	development.unspeci	GO:0005515 MF: protein binding	
12 6	96	dicoccoides]	E- 5	03G1	repeat-protein	99	fied		
60 6			17 6	33610					
			3 %	0					
75 S	JK7	Programmed cell death	1. 9	1 Traes					
91 0	161	protein 4 [Triticum urartu]	00 0.	CS2B	Programmed cell	28.	DNA.unspecified	GO:0005488 MF: binding	
12 7	03		E- 4	03G0	death protein 4	99			
67 3			55						

			8 92830 % 0				
75 S	JK7	zeaxanthin epoxidase, chloroplastic-like [Triticum dicoccoides]	1. 0 Traes 000. CS2B E- 03G0 39 0 87190 % 0	Zeaxanthin epoxidase, chloroplastic	17. metabolism.abscisic hormone 1.1 acid.synthesis- .1. degradation.synthesi epoxidase [overall] activity; 1 s.zeaxanthin GO:0005515 MF: protein binding;GO:0009507 CC: chloroplast;GO:0009540 MF: zeaxanthin epoxidase process;GO:0071949 MF: FAD binding		
75 S	JK7	unnamed protein product [Triticum turgidum]	2. 9 Traes 008. CS3A E- 8 03G0 10 4 50770 3 % 0	Evolutionarily conserved C- terminal region 2	30. signalling.calcium 3	GO:0003723 MF: RNA binding	
75 S	JK7	multiprotein-bridging factor 1a-like [Hordeum vulgare]	6. 9 Traes 008. CS2A E- 5 03G0 95 9 93970 % 0	Multiprotein- bridging factor, putative	17.metabolism.ethylene. 5.3 induced-regulated- responsive-activated	GO:0003677 MF: DNA binding;GO:0043565 MF: sequence-specific DNA binding	
75 S	JK7	IAA-amino acid hydrolase ILR1-like 7 [Triticum dicoccoides]	1. 9 Traes 006. CS5A E- 7 03G0 25 2 25310 76 % 0	IAA-amino acid hydrolase ILR1	17. hormone 2.1 metabolism.auxin.sy nthesis-degradation	GO:0008152 BP: metabolic process;GO:0016787 MF: hydrolase activity	
75 S	JK7	CBL-interacting protein kinase 8[Triticum dicoccoides]	5. 8 Traes 008. CSU0 E- 5 3G00 57 0 60600 % 0	Gluconokinase	35. not 2 assigned.unknown	GO:0005975 BP: carbohydrate metabolic process;GO:0016301 MF: kinase activity	
Tra nsc rip tio n							
75 S	JK7	MADS-box transcription factor 51-like isoform X2 [Triticum dicoccoides]	3. 8 Traes 009. CS4D E- 0 03G0 31 4 80300 % 0	MADS-box transcription factor	27. RNA.regulation of 3.2 transcription.MADS 4 box transcription factor family	GO:0003677 MF: DNA binding;GO:0046983 MF: protein dimerization activity	



75 S	JK7	NAC domain-containing protein 41-like [Triticum dicoccoides]	2. 7 Traes 00 9. CS7B E- 1 03G0 4 53460 61 % 0	multimeric translocon complex in the outer envelope membrane 132	Unknown
75 S	JK7	chromatin structure-remodeling complex protein SYD-like [Triticum turgidum]	7. 1 Traes 00 0 CS7A E- 0 03G0 12 0 47720 1 % 0	Chromatin remodeling protein-like	GO:0005524 MF: ATP binding;GO:0042393 MF: histone binding
75 S	JK7	2-hydroxy-palmitic acid dioxygenase MPO1-like [Triticum dicoccoides]	2. 9 Traes 00 9. CS7A E- 4 03G0 84 4 98550 % 0	YGL010w-like protein	27. RNA.regulation of 3.1 transcription.C2H2 zinc finger family Unknown
75 S	JK7	Uncharacterized RNA-binding protein C23E6.01c [Triticum urartu]	1. 9 Traes 00 9. CS2A E- 2 03G0 72 4 47560 % 0	RNA-binding family protein	27. RNA.regulation of 3.9transcription.unclassified GO:0003676 MF: nucleic acid binding
75 S	JK7	chloroplast stem-loop binding protein of 41 kDa b, chloroplastic-like [Triticum dicoccoides]	3. 9 Traes 00 7. CS5D E- 4 03G0 42 0 11130 % 0	Chloroplast stem-loop-binding protein	27. RNA.regulation of 3.9transcription.unclassified GO:0003824 MF: catalytic activity;GO:0050662 MF: coenzyme binding
75 S	JK7	U2 small nuclear ribonucleoprotein B"-like [Triticum dicoccoides]	4. 9 Traes 00 8. CS4B E- 2 03G0 62 9 53190 % 0	Small nuclear ribonucleoprotein	27. RNA.processing.spllicing GO:0003676 MF: nucleic acid binding
75 S	JK7	ubiquitin-conjugating enzyme E2 28-like isoform X1 [Panicum virgatum]	7. 9 Traes 00 5. CS7B E- 2 03G0 05 4 66790 % 0	Ubiquitin-conjugating enzyme E2	27. RNA.regulation of 3.1 transcription.C2H2 zinc finger family Unknown
Tra nsp ort					

75 S 91 0 12 0 00 5	JK7 160 36	conserved hypothetical protein [Talaromyces stipitatus]	1. 6 Traes 00 7. CS3D E- 8 03G0 15 0 90650 % 0	ATP-binding ABC transporter	34. 16 transporters and multidrug resistance systems	GO:0005524 MF: ATP binding;GO:0006810 BP: transport;GO:0016021 CC: integral component of membrane;GO:0016887 MF: ATPase activity;GO:0042626 MF: ATPase activity, coupled to transmembrane movement of substances;GO:0055085 BP: transmembrane transport
75 S 91 0 12 2 14 0	JK7 160 50	non-specific lipid-transfer protein Cw18 [Triticum dicoccoides]	1. 8 Traes 00 3. CSU0 E- 3 3G03 07 3 42400 % 0	Non-specific lipid- transfer protein	11. 10. lipid metabolism.glycolipi d synthesis.DGDG synthase	GO:0006869 BP: lipid transport;GO:0008289 MF: lipid binding
75 S 91 0 12 2 16 2	JK7 160 52	type 1 non-specific lipid transfer protein precursor [Triticum turgidum]	5. 8 Traes 00 0. CSU0 E- 7 3G01 11 0 29800 % 0	Non-specific lipid- transfer protein	11. 10. lipid metabolism.glycolipi d synthesis.DGDG synthase	GO:0006869 BP: lipid transport;GO:0008289 MF: lipid binding
75 S 91 0 12 3 26 2	JK7 160 62	putative lipid-transfer protein DIR1 [Triticum dicoccoides]	2. 9 Traes 00 2. CSU0 E- 3 3G02 43 8 69700 % 0	Protease inhibitor/seed storage/lipid transfer protein family protein	11. 10. lipid metabolism.glycolipi d synthesis.DGDG synthase	GO:0006869 BP: lipid transport;GO:0008289 MF: lipid binding
75 S 91 0 12 3 33 9	JK7 160 69	probable calcium- transporting ATPase 9, plasma membrane-type isoform X2 [Triticum aestivum]	7. 8 Traes 00 6. CS5B E- 3 03G0 97 6 37470 % 0	Calcium-transporting ATPase	34. 3 transport.amino acids	GO:0000166 MF: nucleotide binding;GO:0005388 MF: calcium-transporting ATPase activity;GO:0005516 MF: calmodulin binding;GO:0005524 MF: ATP binding;GO:0016020 CC: membrane;GO:0016021 CC: integral component of membrane;GO:0046872 MF: metal ion binding;GO:0070588 BP: calcium ion transmembrane transport
75 S 91 0 12 4 35 1	JK7 160 71	nascent polypeptide- associated complex subunit alpha-like protein 1 [Triticum dicoccoides]	2. 8 Traes 00 8. CS1B E- 8 03G0 51 2 70150 % 0	Nascent polypeptide- associated complex subunit alpha-like protein	28. 1 DNA.synthesis/chro matin structure	Unknown
75 S 91 0 12 6 57 3	JK7 160 93	probable anion transporter 5, chloroplastic [Triticum dicoccoides]	2. 9 Traes 00 8. CS5A E- 4 03G0 73 5 85900 % 0	Phosphate transporter	34. 99 transport.misc	GO:0016021 CC: integral component of membrane;GO:0055085 BP: transmembrane transport
75 S 91 0 12 6 59 5	JK7 160 95	phosphoribulokinase, chloroplastic [Triticum dicoccoides]	9. 9 Traes 00 3. CS6B E- 8 03G0 53 3 84940 % 0	Phosphoribulokinase	34. 99 transport.misc	GO:0005524 MF: ATP binding;GO:0005975 BP: carbohydrate metabolic process;GO:0008152 BP: metabolic process;GO:0008974 MF: phosphoribulokinase activity;GO:0016301 MF: kinase activity

75 S 91 0 12 8 82 8	JK7	thylakoid membrane protein slr0575-like isoform X1 [Triticum dicoccoides]	21- 00 E- 66%	9 Traes 6. CS7A 6 03G0 7 70110 0	acclimation of photosynthesis to environment	31. 4	cell.vesicle transport	Unknown
75 S 91 0 12 9 89 5	JK7	protein detoxification like [Triticum dicoccoides]	21- 00 E- 95%	9 Traes 8. CS5A 2 03G0 0 39600 0	Protein DETOXIFICATION	34. 99	transport.misc	GO:0006855 BP: drug transmembrane transport;GO:0015238 MF: drug transmembrane transporter activity;GO:0015297 MF: antiporter activity;GO:0016020 CC: membrane;GO:0055085 BP: transmembrane transport
75 S 91 1 13 0 02 8	JK7	clathrin interactor EPSIN 1- like [Triticum dicoccoides]	1- 00 E- 72%	8 Traes 8. CS2D 2 03G0 4 98390 0	Clathrin interactor EPSIN 1	35. 2	not assigned.unknown	Unknown
75 S 91 1 13 2 16 2	JK7	probable V-type proton ATPase subunitd [Triticum dicoccoides]	2. 00 E- 39%	8 Traes 7. CS3B 5 03G0 0 62890 0	V-type proton ATPase subunit d	34. 1.1	transport.p- and v- ATPases.H+- transporting two- sector ATPase	GO:0015078 MF: hydrogen ion transmembrane transporter activity;GO:0015991 BP: ATP hydrolysis coupled proton transport;GO:0033179 CC: proton-transporting V-type ATPase, V0 domain
Un kn ow n								
75 S 91 0 12 1 08 4	JK7	testis-expressed protein 2- like [Triticum aestivum]	2- 00 E- 11%	1 Traes 0. CS6A 0. 03G1 0 02870 0	Testis-expressed sequence 2 protein			Unknown
75 S 91 0 12 1 11 7	JK7	calphotin-like [Rhopalosiphum maidis]	7. 00 E- 11%	9 Traes 7. CS2D 0 03G0 6 05930 0	ATP sulfurylase (Sulfate adenylyltransferase)	14. 1	S-assimilation.ATPS	GO:0000103 BP: sulfate assimilation;GO:0004781 MF: sulfate adenylyltransferase (ATP) activity
75 S 91 0 12 2 19 5	JK7	protein LURP-one-related 15-like [Triticum dicoccoides]	2. 00 E- 51%	9 Traes 0. CS1D 1 03G0 7 76430 0	Endonuclease 8-like 3			GO:0008270 MF: zinc ion binding

75 S	JK7	protein unc-13 homolog isoform X2 [Triticum dicoccoides]	1. 9 Traes 008. CS1A E- 7 03G0 10 8 12860 1 % 0	Mammalian uncoordinated homology 13, domain 2	35. 2	not assigned.unknown	Unknown
75 S	JK7	ubiquitin-associated protein [Triticum aestivum]	6. 9 Traes 004. CS6B E- 9 03G0 13 7 68690 2 % 0	Ubiquitin-associated protein	35. 2	not assigned.unknown	GO:0005515 MF: protein binding;GO:0008270 MF: zinc ion binding
75 S	JK7	unnamed protein product [Triticum turgidum]	1 Traes 6. 0 CS4B 000. 03G0 E- 0 67890 21 0 0 %	Nodulin-related protein 1, putative	35. 2	not assigned.unknown	Unknown
75 S	JK7	unnamed protein product [Triticum turgidum]	1 Traes 8. 0 CS6B 000. 03G1 E- 0 05100 94 0 0 %	RING finger protein			Unknown
75 S	JK7	UPF0047 protein YjbQ-like [Triticum dicoccoides]	1. 9 Traes 1. 6. CS7D 00 3 03G1 E- 6 21620 29 % 0	UPF0047 protein YjbQ			Unknown
75 S	JK7	vulgare SUMO-conjugating enzyme SCE1-like [Hordeum vulgare]	2. 9 Traes 008. CS5A E- 4 03G0 12 5 04070 3 % 0LC	Unknown			Unknown
75 S	JK7	protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB1, chloroplastic-like [Triticum dicoccoides]	2. 5 Traes 00. 0. CS3B E- 9 03G1 E- 4 34650 04 % 0	Cofactor assembly of complex C	35. 2	not assigned.unknown	Unknown

**Supplementary Table S2. List RT-PCR primers designed for the analysed wheat genes**

No.	User_Id	dbEST_Id	Nr annotation/	Sequence of Primer	
Q1	S052	JK716082	Chlorophyll a-b binding protein 1C, chloroplastic	F: TTGAGAACCTTGCCGACCAC	R: CCACACTCCCCTTACCTTGG
Q2	S069	JK716099	protein THYLAKOID FORMATION1, chloroplastic	F: CCTGAGCAATACAGGGCTGA	R: GAACCGGCTGTAGCTGAAGT
Q3	S009	JK716040	psbP-like protein 1, chloroplastic	F: TTCGTCTACCCGTTCCGATG	R: TGTGATGCTGACGCTCTCC
Q4	S013	JK716043	light-harvesting complex-like protein OHP2, chloroplastic	F: CGCCGTGCATTTGTATGGTC	R: TCCAAGACGCTGGTCTCTAAC
Q5	S046	JK716076	fructose-1,6-bisphosphatase, cytosolic-like	F: TTCCGTTCCGGCTCTTCT	R: ACTGGGACACGCCTACTGC
Q6	S036	JK716066	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	F: ACGTGCTCTACGTTTGGAGG	R: CACGTAGACACTCATAACACGC
Q7	S079	JK716109	phospholipase A1-II 7-like	F: CCGCTATGCTGACGAAGAGT	R: TACCTCCTCGAGAACCTGCT
Q8	S050	JK716080	protein CHUP1, chloroplastic-like	F: AGTGGAGCAGAGTGTTCACG	R: GCCCTGGAGAAGCAAGAA
Q9	S100	JK716130	alpha-L-arabinofuranosidase 1-like isoform X2	F: CTTGGTTCACTAGCAGAGGC	R: GTGGCGCATAACTTGCCATC
Q10	S030	JK716060	malate dehydrogenase, cytoplasmic-like	F: ACTTGTTCTTTGTTGACCAGG	R: GTTGCAACAACCTCCCTTGAGA
Q11	S038	JK716068	glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic-like	F: ACGTCGAGGAGGATTTGGTC	R: TGCTGTAACCCCACTCGTTG
Q12	S116	JK716146	probable protein phosphatase 2C 44	F: ATGAAAGGCAGAGGATTGAA	R: GTGCGTCTTGAGGCTATGGT
Q13	S109	JK716139	60S ribosomal protein L10-1	F: TCTTGAGGCTGCCCCGATTG	R: AAGCACCCCTCATACCAGTC

Q14	S125	JK716155	Protein translation factor SUI1-like protein	F: GGAGCTAGGCCAGGTCATTC	R: GCAAGACACGGTTCGACAAG
Q15	S105	JK716135	translation machinery-associated protein 22-like	F: GAAGAGGTGAAACGACTGCC	R: CACCACAGTAACACACTTGCG
Q16	S087	JK716117	chlorophyllide a oxygenase, chloroplastic-like	F: ACTTCGCACCCTGGATGAAG	R: GACTGCATCCCTCCATAGCC
Q17	S039	JK716069	probable calcium-transporting ATPase 9, plasma membrane-type isoform X2	F: TAAGCGCGACGGTGGTATTC	R: CGCTCACCAACCAGAATTGC
Q18	S063	JK716093	probable anion transporter 5, chloroplastic	F: CTGGGTCGTTGTTGCTTTCC	R: ACACCAACGATTCCAGGCAC
Q19	S121	JK716151	probable aquaporin PIP2-2	F: TTCTCCACCAAGGACTACTCG	R: TAGAGGAAGAGGAGCGTGG
Q20	S012	JK716042	MADS-box transcription factor 51-like isoform X2	F: GTGCAAGCACCAACAATGGG	R: CGTTGCGCCAACATCTTCTTG
Q21	S060	JK716090	NAC domain-containing protein 41-like	F: TCGTAGGTGCCCTGTTTCTTC	R: CACTGGAAGTGCCTCCCATC
Q22	S044	JK716074	lipxygenase 2.1, chloroplastic-like	F: GACCTCTTGTCCACGCACTC	R: CGTTGTTCCACTCATCCACC
Q23	S018	JK716048	ran-binding protein 1 homolog c-like	F: TCTCGACCACGAAGATGCAGG	R: AGCTCTCCGTCAGCAAAGTC
Q24	S031	JK716061	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	F: GAGTTGAGTCACACCTGCAAAC	R: ACGGTGAAACATCTGTGGAC
Q25	S094	JK716124	multiprotein-bridging factor 1a-like	F: GGCACAACCTTGCTCAGATGAT	R: ACTTCAAGGCATTACTTCTTGCT
Q26	S016	JK716046	S-adenosylmethionine decarboxylase	F: TACTATGCCACCGAGCAACC	R: AAGTAGCGGTTCAGGACATC
Q27	S131	JK716161	monodehydroascorbate reductase 2, peroxisomal-like	F: GGCACGTCTTTCTTGCTTTC	R: CGTTATCGGTGGTTGTCTGG
Q28	S134	JK716164	Bsi1 gene for putative protease inhibitor	F: ACGTGAACGCCGTCTATTTTC	R: CCACCAACGCACAATCATTA

Q29	S055	JK716085	putative BPI/LBP family protein At1g04970 isoform X1	F: TTTCTGGGAATAATCTTGTTGG	R: TGATGACGAAGCCCTTGATG
Q30	S080	JK716110	<a href="#">wPR4a gene</a>	F: GTAATCTAGTCGCGGCAGTC	R: ACCAAGATCGACACCAACGG

---