

Table 1 Suppl. Summary of sequencing data.

Summary	Albino seedlings	Green seedlings
Raw reads	22940683	20474903
Clean reads	22662341	20286483
GC content [%]	51.03	52.9
Duplication [%]	46.39	48.66
Error rate [%]	0.03	0.04
Total mapped ([%])	9103213 (40.17)	8952477 (44.13)
Multiple mapped ([%])	709779 (3.13)	853564 (4.21)
Uniquely mapped ([%])	8393434 (37.04)	8098913 (39.92)

Table 2 Suppl. Differentially expressed genes that were associated with albinism in the albino and green plantlets libraries. DEGs in the *grey area* were specifically expressed in green materials respectively.

Gene_ID	RPKM_A	RPKM_G	log2.fold	Blast nr
Down-regulated in albino seedlings				
TC268856	0	695.1204	-10.744	RNase S-like protein precursor
TC263944	0.267757	202.795	-9.98891	photosystem II 10 kDa polypeptide
TC249516	1.459856	212.6653	-7.61064	NADH dehydrogenase ND4 subunit
TC268430	0	64.48255	-7.42824	HAP5 subunit of HAP complex
TC263155	0.647059	65.9571	-7.09552	light harvesting chlorophyll a/b-binding protein
TC233229	37.51421	2708.324	-6.59785	LHCI-680, photosystem I antenna protein
TC263456	23.53403	1694.203	-6.59374	chlorophyll a/b-binding protein
TC250453	20.11233	1327.762	-6.4688	phosphoribulokinase
TC264984	8.713299	566.5709	-6.44692	sedoheptulose-1,7-bisphosphatase
TC262756	39.73506	2548.975	-6.42739	putative carbonic anhydrase
TC274695	0.767227	37.46474	-6.03377	fatty acid hydroperoxide lyase
TC247042	28.26245	1355.844	-6.00819	plastid glutamine synthetase
TC235264	4.352267	178.5518	-5.78246	fructose-1,6-bisphosphatase
TC249615	59.75245	2412.48	-5.7594	RuBisCO activase A
TC257599	0.398427	14.0293	-5.56201	photosystem I P700 chlorophyll a apoprotein A1
TC246850	63.26814	1990.144	-5.39928	light-harvesting complex IIa protein
TC248057	22.94619	688.9643	-5.33213	plastocyanin precursor
TC268669	22.06527	261.0956	-3.98876	thylakoid membrane phosphoprotein 14 kDa
TC276730	5.469959	61.47025	-3.91432	MYB-related protein
TC263934	5.271023	44.06586	-3.48754	ribulose-1,5-bisphosphate carboxylase/oxygenase
TC269898	5.634137	39.7584	-3.24303	phytoene synthase
TC239455	16.95975	99.5572	-2.97744	chlorophyllide a oxygenase
TC262788	44.31878	171.1775	-2.37353	protochlorophyllide reductase
Up-regulated in albino seedlings				
TC234343	60.73937	12.4594	1.861368	pentameric polyubiquitin
TC240487	5.896081	0.153817	4.836445	RNA polymerase beta subunit
TC235598	37.85674	0.945131	4.899863	MADS box transcription factor AP1
TC263724	65.42774	2.262815	4.429683	ribosomal protein L2
TC256916	44.84992	2.618151	3.674456	isocitrate lyase
TC263685	15.1793	1.141665	3.308864	ribosomal protein L22
TC249291	68.83911	5.217875	3.297665	LEA3 protein
TC232193	107.1613	8.953447	3.157168	universal stress protein A-like protein-like
TC240625	37.32628	5.530431	2.330699	F-box protein-like
TC271302	12.95435	2.076397	2.217253	E3 ubiquitin-protein ligase ATL41-like
TC239497	162.0249	27.01433	2.160389	ubiquitin-like modifier-activating enzyme atg7-like
TC232194	56.97284	9.585691	2.147291	universal stress protein A-like protein-like
TC247326	166.2324	29.46479	2.072109	peroxidase 8

Table 3 Suppl. Differentially expressed genes in enriched GO terms.

GO accession	Description	Term type	P-value	Gene names
Up-regulated GO terms in the albino seedlings				
GO:0006412	translation	biological_process	3.46E-05	TC264563,TC252850,TC233144,TC264114,TC264730,TC249932,TC232284,TC246775,TC246764,TC262720,TC236813,TC264222,TC264424,TC250346,TC264335,TC264422,TC232139,TC249326,TC233131,TC232131,TC262752,TC264427,TC264435,TC233173,TC232344,TC263956,TC251145,TC263724,TC232809
GO:0006812	cation transport	biological_process	0.0046295	TC237562,TC238365,TC270627,TC239528,TC236747,TC239233,TC266628,TC255999,TC268328
GO:0005840	ribosome	cellular_component	1.96E-05	TC264563,TC252850,TC233144,TC264114,TC264730,TC249932,TC232284,TC246775,TC246764,TC262720,TC248496,TC264222,TC264424,TC250346,TC264335,TC264422,TC232139,TC249326,TC233131,TC232131,TC262752,TC264427,TC264435,TC233173,TC232344,TC263956,TC251145,TC263724,TC232809
GO:0015934	large ribosomal subunit	cellular_component	0.0008115	TC264563,TC264114,TC262720,TC263956,TC263724
GO:0005730	nucleolus	cellular_component	0.0044349	TC235682,TC232284,TC246775,TC246764,TC262720,TC246802,TC264422,TC234588,TC232139,TC233809,TC232131,TC262752,TC264979,TC264435,TC247036,TC248026,TC232403,TC232775
GO:0022626	cytosolic ribosome	cellular_component	0.0178845	TC264563,TC252850,TC263917,TC249932,TC262738,TC246775,TC262720,TC233154,TC264222,TC232139,TC232158,TC262752,TC264435,TC262814,TC264087
GO:0005622	intracellular	cellular_component	0.0193147	TC264563,TC233144,TC264114,TC264730,TC249932,TC250586,TC246775,TC246764,TC248496,TC264222,TC264424,TC250346,TC264335,TC266943,TC232139,TC249326,TC233131,TC232131,TC262752,TC264979,TC264427,TC264435,TC232344,TC235250,TC251973,TC247628,TC266944,TC251145,TC263724,TC232809
GO:0003735	structural constituent of ribosome	molecular_function	1.48E-05	TC264563,TC252850,TC233144,TC264114,TC264730,TC249932,TC232284,TC246775,TC246764,TC262720,TC248496,TC236813,TC264222,TC264424,TC250346,TC264335,TC264422,TC232139,TC249326,TC233131,TC232131,TC262752,TC264427,TC264435,TC233173,TC232344,TC263956,TC251145,TC263724,TC232809
GO:0015299	solute:hydrogen antiporter activity	molecular_function	0.0056122	TC270627,TC255999,TC248043
GO:0005509	calcium ion binding	molecular_function	0.0158072	TC274405,TC262722,TC252006,TC255319,TC248321,TC235123,TC252299,TC242486,TC239147,TC248695,TC234416
Down-regulated GO terms in the albino seedlings				
GO:0042742	defense response to bacterium	biological_process	2.87E-05	TC250453,TC250679,TC249532,TC247025,TC249812,TC234551,TC236883,TC232403,TC262897,TC234416,TC269312
GO:0009765	photosynthesis, light harvesting	biological_process	4.54E-05	TC248661,TC249806,TC262736,TC233229,TC246850,TC249808
GO:0008299	isoprenoid biosynthetic process	biological_process	0.0014263	TC262734,TC266198,TC234723,TC269469,TC251974
GO:0008152	metabolic process	biological_process	0.0100649	TC263452,TC237562,TC247045,TC249785,TC250453,TC248020,TC238135,TC239528,TC246795,TC253156,TC251736,TC262839,TC256916,TC239233,TC262784,TC264131,TC266198,TC247951,TC268328,TC240212,TC232419,TC248332,TC247185,TC267654,TC266533,TC265041,TC232269,TC238592,TC232403,TC236843,TC265273,TC268302
GO:0009579	thylakoid	cellular_component	1.27E-08	TC234620,TC248661,TC250453,TC263917,TC249806,TC262738,TC262736,TC249532,TC247025,TC264595,TC233229,TC232823,TC234551,TC246850,TC232269,

GO:0009535	chloroplast thylakoid membrane	cellular_component	1.05E-05	TC265171,TC247042,TC249808,TC265273,TC262897,TC234416,TC263709,TC269312,TC248253,TC238743,TC257599,TC264087
GO:0009534	chloroplast thylakoid	cellular_component	0.0001174	TC234620,TC248661,TC250453,TC263613,TC262794,TC263917,TC249806,TC235608,TC262736,TC249532,TC233229,TC234551,TC264979,TC246850,TC249808,TC234416,TC263709,TC269312,TC248253,TC238743,TC257599,TC264087
GO:0016020	membrane	cellular_component	0.0002167	TC234620,TC248661,TC262794,TC235608,TC262736,TC233229,TC232823,TC264979,TC270203,TC262814,TC246850,TC249808,TC234416,TC263709,TC269312,TC248253,TC238743,TC257599,TC263956
GO:0048046	apoplast	cellular_component	0.0002718	TC234620,TC237562,TC253649,TC251083,TC236560,TC248661,TC256284,TC274405,TC246844,TC268807,TC250453,TC252850,TC263613,TC262794,TC252205,TC263917,TC264730,TC257652,TC249932,TC239528,TC267415,TC237099,TC252682,TC249806,TC246795,TC263824,TC251736,TC262736,TC249532,TC246775,TC262720,TC265405,TC264595,TC264222,TC234990,TC239233,TC249812,TC253621,TC271907,TC246817,TC233229,TC251184,TC232158,TC234551,TC233809,TC232131,TC232620,TC264979,TC239620,TC268425,TC234689,TC264435,TC262814,TC246901,TC246850,TC248332,TC267348,TC264301,TC236173,TC236722,TC265171,TC247042,TC248026,TC239147,TC237797,TC249808,TC263610,TC232775,TC248695,TC263709,TC269312,TC248253,TC238743,TC257599,TC264087,TC263724
GO:0009941	chloroplast envelope	cellular_component	0.0007082	TC250453,TC263613,TC240513,TC263917,TC246795,TC262738,TC264994,TC249532,TC264595,TC232823,TC264979,TC263620,TC264790,TC247951,TC262814,TC248332,TC249088,TC247042,TC265273,TC262897,TC234416,TC264087
GO:0009507	chloroplast	cellular_component	0.0070615	TC234620,TC252323,TC251251,TC248661,TC250453,TC252850,TC263613,TC262794,TC240513,TC249806,TC235608,TC249532,TC248578,TC264595,TC234990,TC253621,TC232823,TC264131,TC234551,TC264979,TC240212,TC248332,TC265273,TC253903,TC238743,TC257599,TC264087
				TC263452,TC234620,TC270110,TC257572,TC252323,TC251251,TC248661,TC257627,TC250453,TC253555,TC252850,TC263613,TC270669,TC262794,TC240513,TC263917,TC234262,TC268231,TC249806,TC246795,TC263824,TC235608,TC262738,TC262736,TC249532,TC253638,TC246775,TC255912,TC247025,TC262734,TC254908,TC265405,TC248578,TC264595,TC234990,TC249812,TC253621,TC236533,TC266675,TC232139,TC233229,TC232823,TC264131,TC234551,TC236883,TC236658,TC264979,TC264790,TC256019,TC270203,TC254014,TC262814,TC240212,TC246850,TC248332,TC249088,TC263479,TC241081,TC232269,TC268698,TC265171,TC247042,TC249808,TC266944,TC269469,TC265273,TC248695,TC262897,TC234416,TC263709,TC269312,TC240487,TC248253,TC238743,TC257599,TC264087,TC263956,TC249516

Table 4 Suppl. Differentially expressed proteins in the albino and green plantlets. DEPs in the *grey area* were specifically expressed in albino and green materials respectively.

Spot No.	Protein Name	Acc. No.	Protein Mr/PI	Protein score	C.I. [%]	Total ion score	C.I. [%]	Peptide count
Up-regulated proteins in albino seedlings								
3	HSP70	gi 2827002	71385/5.14	374	100	277	100	17
17	aldehyde dehydrogenase 7b	gi 300087069	55057/5.9	425	100	344	100	13
18	lipoxygenase 2	gi 239923157	96624/6.18	555	100	244	100	34
1	RuBisCO large subunit-binding protein	gi 326513802	64237/4.83	371	100	295	100	13
2	Protein disulfide isomerase 3 precursor	gi 13925728	56879/4.96	571	100	412	100	20
4	HSP70	gi 87241037	71445/5.11	514	100	426	100	16
5	RuBisCO large subunit-binding protein	gi 2493650	53721/4.88	950	100	784	100	19
6	ATP synthase subunit beta	gi 114421	59933/5.95	83	99.48	60	99.90	6
7	vacuolar proton-ATPase subunit A	gi 90025017	68753/5.23	1120	100	845	100	28
8	arabinoxylan arabinofuranohydrolase	gi 381142340	72495/5.22	304	100	276	100	8
9	metacaspase 1	gi 356463686	44371/5.17	732	100	564	100	19
10	predicted protein	gi 326490934	48600/5.39	614	100	458	100	18
11	phosphoglycerate mutase	gi 32400802	29615/5.43	642	100	540	100	13
12	phosphoglycerate mutase	gi 32400802	29615/5.43	510	100	391	100	14
13	phosphoglycerate mutase, partial	gi 32400802	29615/5.43	492	100	358	100	16
14	predicted protein	gi 326490934	48600/5.39	614	100	458	100	18
16	methionine synthase 1 enzyme	gi 68655495	84853/5.74	1050	100	883	100	23
19	40S ribosomal protein SA-like	gi 357113738	33384/4.94	681	100	543	100	15
22	predicted protein	gi 326517094	47337/5.34	289	100	231	100	10
23	glutamine synthetase	gi 40317418	38918/5.34	369	100	310	100	9
25	lactoylglutathione lyase-like	gi 357144699	32843/5.34	516	100	395	100	15
26	malate dehydrogenase 1	gi 357132456	35599/8.54	343	100	279	100	9
27	predicted protein	gi 326505556	32023/5.25	371	100	319	100	8
28	chitinase 2	gi 18146827	35227/6.06	567	100	498	100	9
29	ascorbate peroxidase	gi 15808779	27963/5.10	685	100	600	100	10
30	ascorbate peroxidase	gi 15808779	27963/5.10	506	100	420	100	10
31	triophosphat-isomerase	gi 11124572	27013/5.38	709	100	587	100	13
34	glycine-rich protein	gi 40363759	19555/5.63	456	100	356	100	10
Down-regulated proteins in albino seedlings								
15	chaperone protein ClpC2	gi 357160412	101791/6.62	748	100	538	100	31
20	plastid glutamine synthetase 2	gi 251832993	46985/5.75	921	100	765	100	17
21	succinyl-CoA ligase	gi 357150216	45518/6.50	854	100	713	100	18
24	fructose-bisphosphate aldolase	gi 343173173	42784/6.26	509	100	446	100	10
32	oxygen-evolving enhancer protein 2	gi 131394	27423/8.84	973	100	871	100	11
33	thioredoxin peroxidase	gi 3328221	28400/6.34	456	100	378	100	7
35	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gi 61378660	53626/6.13	915	100	617	100	24
36	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gi 61378609	53399/6.22	883	100	561	100	26
37	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gi 31087879	53738/6.22	1160	100	791	100	28
38	30S ribosomal protein S5	gi 357126676	33662/5.01	209	100	169	100	8
39	chloroplast oxygen-evolving enhancer protein 1	gi 147945622	34718/6.08	806	100	602	100	20

40	putative peptidyl-prolyl cis-trans isomerase	gi 13486733	25272/8.05	108	99.99	79	99.994	5
41	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	gi 132099	19783/8.52	639	100	504	100	13
42	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	gi 11990901	19733/8.81	505	100	384	100	12
43	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	gi 62176930	19322/8.59	627	100	475	100	14

Table 5 Suppl. Differentially expressed proteins in the functional groups.

Functional groups	Up-regulated protein	Down-regulated protein
Catalytic activities	gi 326505556, gi 357132456, gi 300087069, gi 15808779, gi 11124572, gi 326490934, gi 32400802, gi 239923157, gi 68655495, gi 40317418, gi 2493650, gi 326513802, gi 326517094, gi 90025017, gi 18146827, gi 13925728, gi 357144699, gi 356463686, gi 381142340	gi 13486733, gi 251832993, gi 343173173, gi 61378660, gi 61378609, gi 31087879, gi 357150216, gi 3328221
Binding	gi 18146827, gi 40363759, gi 90025017, gi 357144699, gi 15808779, gi 239923157, gi 2493650, gi 32400802, gi 326490934, gi 68655495	gi 357160412, gi 147945622, gi 61378609, gi 131394, gi 31087879, gi 357126676, gi 357150216, gi 61378660
Antioxidant activity	gi 15808779	gi 3328221
Transporter activity	gi 90025017, gi 2493650	
Structural molecule activity	gi 357113738	gi 357126676



Fig. 1 Suppl. Wheat green and albino haploid plantlets that were derived from an anther culture.

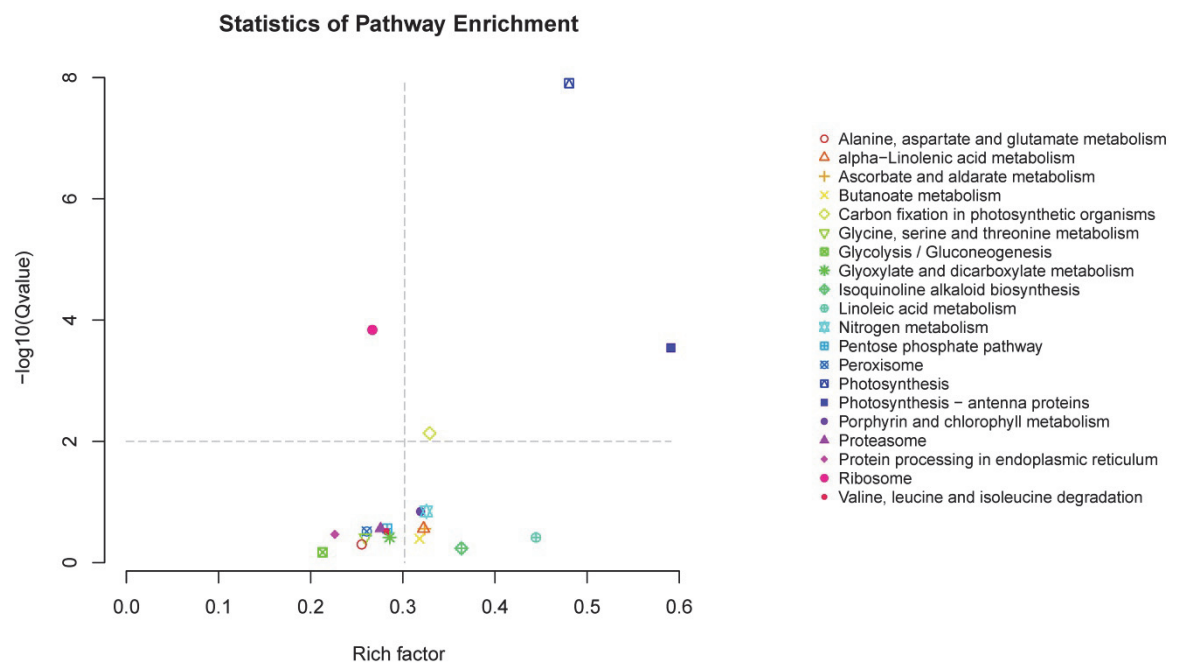


Fig. 2 Suppl. A scatter diagram of 20 of the enriched pathways. The y-axis indicates the corrected P -value of the pathways, and the x-axis indicates the enrichment factor of the pathways.