

## Supplementary information

**Table S1.** Summary of transcriptome sequencing results.

Sample	Raw Reads	Clean Reads (%)	Total Mapped	Multiple Mapped	Uniquely Mapped	Mapped to Gene
CK1_3d	47587866	45172624 (94.92%)	43508153 (96.32%)	2110132 (4.85%)	41398021 (95.15%)	39807397 (96.16%)
CK2_3d	52691688	49838978 (94.58%)	48005020 (96.32%)	1984745 (4.13%)	46020275 (95.87%)	44186681 (96.02%)
CK3_3d	46693958	44085536 (94.41%)	42448430 (96.29%)	2164413 (5.10%)	40284017 (94.90%)	38536730 (95.66%)
T1_3d	46802166	44327318 (94.71%)	42661016 (96.24%)	2314943 (5.43%)	40346073 (94.57%)	38564447 (95.58%)
T2_3d	53419312	50667326 (94.84%)	48865181 (96.44%)	6104049 (12.49%)	42761132 (87.51%)	40368190 (94.40%)
T3_3d	49736442	47153318 (94.8%)	45369714 (96.22%)	2186539 (4.82%)	43183175 (95.18%)	41242991 (95.51%)
CK1_7d	52226874	49542572 (94.86%)	47561164 (96.00%)	1566792 (3.29%)	45994372 (96.71%)	44110312 (95.90%)
CK2_7d	50044580	47454444 (94.82%)	45513468 (95.91%)	1545095 (3.39%)	43968373 (96.61%)	42245602 (96.08%)
CK3_7d	53528986	50562606 (94.45%)	48601499 (96.12%)	1709254 (3.52%)	46892245 (96.48%)	45057946 (96.09%)
T1_7d	52171250	49183054 (94.27%)	47009727 (95.58%)	1907244 (4.06%)	45102483 (95.94%)	43102722 (95.57%)
T2_7d	46930356	44313454 (94.42%)	42585515 (96.10%)	1845582 (4.33%)	40739933 (95.67%)	38872240 (95.42%)
T3_7d	47898072	45013538 (93.97%)	43250931 (96.08%)	1681499 (3.89%)	41569432 (96.11%)	39603874 (95.27%)

**Table S2.** Heatmap data of differentially coexpressed genes for different pathways.

	Gene_ID	CK3d	T3d	CK7d	T7d	Description
Chloroplast development	Os06g0229000	2.507144272	3.81647014	2.283935757	1.081524373	Similar to FtsH protease (VAR2) (Zinc dependent protease)
	Os06g0229066	2.492537311	4.204996382	2.531855759	1.085457835	Similar to ATP-dependent zinc metalloprotease FTSH 6, chloroplastic
	Os02g0680600	17.34856723	15.08299811	64.05759354	33.58087521	2-C-methyl-d-erythritol 2,4-cyclodiphosphate synthase, Isoprenoid biosynthesis, Chloroplast developmen
	Os01g0101700	3.169776747	3.556991544	85.36822722	43.28073072	Similar to chaperone protein dnaJ 20
	Os02g0553200	172.7114635	157.7783326	551.8094451	339.3388114	Thylakoid membrane-bound ascorbate peroxidase, Tolerance to bacterial blight, Response to NaC
	Os12g0182700	8.982173077	8.407778761	45.79026076	27.45719407	Histone deacetylase superfamily protein
	Os05g0401100	139.0581501	85.6517255	315.0230744	195.9694535	Protein of unknown function DUF477 family protein
	Os06g0348800	90.28883235	73.4614395	253.4926422	151.1852492	Transfactor-like protein
	Os09g0111100	1.383729502	1.277151768	2.261909662	1.334758024	Cyclin D domain containing protein
	Os04g0628900	7.59131165	6.33879206	58.20218817	27.04493927	Cyclin-P1-1
	Os06g0115300	35.49985935	27.87177242	179.0650085	84.01542779	Acyl-CoA-binding protein , Stress respons

	Os08g0162800	347.0337673	342.3995525	630.0081369	370.7295198	Acyl-CoA-binding protein , Stress respons
	Os02g0646500	0.058197725	0.011522859	0.334494271	0.114423243	Aldehyde dehydrogenase domain containing protein
Photosystem	Os07g0577600	1481.291402	1048.710528	3100.257693	1943.495819	Similar to Type II chlorophyll a/b binding protein from photosystem I precursor
	Os03g0592500	6408.609013	4232.617052	11295.7397	6982.428744	Similar to Photosystem II type II chlorophyll a/b binding protein (Fragment)
	Os12g0189400	1333.502322	824.1719244	3187.835239	1672.584076	Similar to Photosystem I reaction centre subunit N, chloroplast precursor (PSI- N)
	Os07g0141400	2165.831133	1468.853431	4339.077506	2668.966742	Similar to 23 kDa polypeptide of photosystem II
	Os03g0343900	336.419979	210.5841748	976.6654263	377.706458	Photosystem II PsbX domain containing protein
	Os08g0200300	3428.544576	2762.394648	12637.34101	7920.877467	Similar to Photosystem II 10 kDa polypeptide (Fragment)
	Os05g0508900	101.1377499	61.76798813	229.8841095	135.7639563	Similar to cDNA clone:001- 011-D03, full insert sequence
	Os01g0552300	18.96129894	17.2674077	101.4454831	60.84359591	Similar to Protein phosphatase- 2C
	Os03g0857400	105.2878054	103.3158386	644.3733258	371.6947715	tRNA-binding arm domain containing protein
	Os03g0736600	31.10844078	21.68158806	87.19416658	53.03652163	Similar to ATP synthase
Carbon fixation	Os12g0292400	87.03334497	41.83009942	664.2381668	393.9199971	Similar to Petunia ribulose 1,5- biphosphate carboxylase small subunit mRNA (clone pSSU 51), partial cds. (Fragment)
	Os03g0169100	253.119171	201.9257432	485.2512088	303.7528336	Ribulose-phosphate 3- epimerase, chloroplast precursor (EC 5.1.3.1) (Pentose-5-phosphate 3- epimerase) (PPE) (RPE) (R5P3E)
	Os07g0176900	158.1458904	132.4165777	543.9058762	309.5479391	Similar to Ribose-5-phosphate isomerase precursor (EC 5.3.1.6)
	Os03g0129300	851.1744377	631.3291556	3108.960916	1891.366772	Similar to Glyceraldehyde-3- phosphate dehydrogenase (EC 1.2.1.13) (Fragment)
	Os07g0412100	81.09768091	64.34328977	638.4340962	297.4783664	Similar to Granule-bound starch synthase Ib, chloroplast precursor (EC 2.4.1.21) (Fragment)
	Os12g0271700	21.84086757	14.17734527	60.01392902	35.50277385	Similar to prenyl transferase
	Os06g0133000	0.00853361	0.025018458	0.898675061	0.384173613	Granule-bound starch synthase, Synthesis of amylose in endosper
	Os06g0160700	13.95553778	15.48820633	69.83219195	39.16469469	Starch synthase, Starch biosynthesi
Chloroplast degradation	Os10g0389300	1.18374822	0.923567041	0.655115016	2.0174147	Similar to Red chlorophyll catabolite reductase (Fragment)
	Os08g0508800	0.212558447	0.559111268	0.220930288	0.954835412	Lipoxygenase, chloroplast precursor (EC 1.13.11.12)