

Supplemental materials

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Table S1. Summary of RNA-Seq results

Sample	Raw Reads (M)	Clean Reads (M)	Clean Bases (G)	Q30 (%)	GC (%)	Total mapped ratio (%)
NP1	48.64	47.32	6.70	92.87	44.91	96.87
NP2	48.80	47.3	6.70	92.75	44.95	96.79
NP3	50.52	49.12	6.96	92.75	44.93	96.79
HP1	47.13	45.73	6.47	92.86	45.03	96.89
HP2	47.65	46.12	6.49	92.78	44.82	96.94
HP3	47.83	46.61	6.64	92.78	44.91	97.20
TP1	47.60	46.14	6.47	92.92	44.99	96.88
TP2	50.70	49.23	6.94	92.92	45.12	96.93
TP3	51.07	49.43	6.96	92.68	45.18	96.92

Table S2. The top 30 of up regulated DEGs of gene ontology in group HP vs TP

Id	Term	Category	ListHits	p-value	Enrichment score	geneID
GO:0010226	response to lithium ion	biological_	2	4.75E-05	187.9906323	<i>Pg_S1983.2;Pg_S6590.1</i>
GO:0016051	carbohydrate	process	2	0.000235549	87.72896175	<i>Pg_S0007.3;Pg_S0368.2</i>
GO:0016042	biosynthetic process	biological_	4	0.001100585	8.861511288	<i>Pg_S0093.55;Pg_S1983.2;Pg_S6336.2;Pg_S6590.1</i>
GO:0006000	lipid catabolic process	process	2	0.001384556	36.55373406	<i>Pg_S0007.3;Pg_S0368.2</i>
GO:0009838	fructose metabolic process	biological_	1	0.007576475	131.5934426	<i>Pg_S7392.1</i>
GO:0019252	abscission	process	2	0.008893983	14.14983254	<i>Pg_S0007.3;Pg_S0368.2</i>
GO:0007091	starch biosynthetic process	biological_	1	0.010591231	93.99531616	<i>Pg_S1646.4</i>
GO:0010922	metaphase/anaphase transition of mitotic cell cycle	process	1	0.010591231	93.99531616	<i>Pg_S6577.8</i>
GO:0042326	positive regulation of phosphatase activity	biological_	1	0.010591231	93.99531616	<i>Pg_S6577.8</i>
GO:0009751	negative regulation of phosphorylation	process	3	0.011401985	6.450658952	<i>Pg_S0055.11;Pg_S1983.2;Pg_S6590.1</i>
GO:0031410	response to salicylic acid	biological_	3	0.000243277	24.9860967	<i>Pg_S0637.13;Pg_S1015.3;Pg_S2513.2</i>
GO:0009705	cytoplasmic vesicle	cellular_co	4	0.000945106	9.234627552	<i>Pg_S2763.11;Pg_S3162.8;Pg_S4250.10;Pg_S7392.1</i>
GO:0000323	plant-type vacuole membrane	mponent	1	0.013596978	73.10746812	<i>Pg_S0055.11</i>
GO:0000325	lytic vacuole	cellular_co	2	0.015151578	10.69865387	<i>Pg_S3162.8;Pg_S4250.10</i>
GO:0031428	plant-type vacuole	mponent	1	0.028491511	34.62985332	<i>Pg_S3834.4</i>
GO:0048226	box C/D snoRNP complex	cellular_co	1	0.029968741	32.89836066	<i>Pg_S3518.15</i>
GO:0005749	Casparian strip	mponent	1	0.031443761	31.33177205	<i>Pg_S3342.1</i>
GO:0045273	mitochondrial respiratory chain complex II, succinate dehydrogenase complex (ubiquinone)	cellular_co	1	0.031443761	31.33177205	<i>Pg_S3342.1</i>
GO:0000326	respiratory chain complex II	mponent	1	0.035855597	27.41530055	<i>Pg_S0055.11</i>
	protein storage vacuole	cellular_co				
		mponent				

GO:0005680	anaphase-promoting complex	cellular_component	1	0.038785833	25.30643127	<i>Pg_S1646.4</i>
GO:0008234	cysteine-type peptidase activity	molecular_function	3	0.000156019	29.02796528	<i>Pg_S0637.13;Pg_S1015.3;Pg_S2513.2</i>
GO:0016788	hydrolase activity, acting on ester bonds	molecular_function	3	0.001601162	13.07219629	<i>Pg_S1983.2;Pg_S6336.2;Pg_S6590.1</i>
GO:0019200	carbohydrate kinase activity	molecular_function	2	0.001707527	32.89836066	<i>Pg_S0007.3;Pg_S0368.2</i>
GO:0008865	fructokinase activity	molecular_function	2	0.002252523	28.60727014	<i>Pg_S0007.3;Pg_S0368.2</i>
GO:0008309	double-stranded DNA exodeoxyribonuclease activity	molecular_function	1	0.007576475	131.5934426	<i>Pg_S7228.3</i>
GO:0034002	(R)-limonene synthase activity	molecular_function	1	0.007576475	131.5934426	<i>Pg_S2552.4</i>
GO:0043765	T/G mismatch-specific endonuclease activity	molecular_function	1	0.007576475	131.5934426	<i>Pg_S7228.3</i>
GO:0000104	succinate dehydrogenase activity	molecular_function	1	0.009084981	109.6612022	<i>Pg_S3342.1</i>
GO:0008177	succinate dehydrogenase (ubiquinone) activity	molecular_function	1	0.009084981	109.6612022	<i>Pg_S3342.1</i>
GO:0019902	phosphatase binding	molecular_function	1	0.010591231	93.99531616	<i>Pg_S6577.8</i>

Table S3. The top 30 of up regulated DEGs of gene ontology in group NP vs TP

Id	Term	Category	ListHits	p-value	Enrichment score	geneID
GO:0030643	cellular phosphate ion homeostasis	biological_process	4	1.61E-08	121.993921	<i>Pg_S0930.37;Pg_S1865.23;Pg_S3218.5;Pg_S6826.5</i>
GO:0006071	glycerol metabolic process	biological_process	4	0.000173497	14.47385503	<i>Pg_S0930.37;Pg_S1865.23;Pg_S3218.5;Pg_S6826.5</i>
GO:0009737	response to abscisic acid	biological_process	13	0.00026578	3.175471055	<i>Pg_S0015.23;Pg_S0086.24;Pg_S0271.2;Pg_S0386.12;Pg_S0519.15;Pg_S2035.9;Pg_S2835.16;Pg_S2984.3;Pg_S3260.5;Pg_S5077.6;Pg_S5400.12;Pg_S5778.1;Pg_S6098.1</i>
GO:0006979	response to oxidative stress	biological_process	9	0.000314127	4.232167963	<i>Pg_S0374.50;Pg_S1619.2;Pg_S2116.17;Pg_S3099.12;Pg_S3152.4;Pg_S3511.16;Pg_S5778.1;Pg_S6529.2;Pg_S9260.2</i>
GO:0080040	positive regulation of cellular response to phosphate starvation	biological_process	2	0.000323341	71.16312057	<i>Pg_S3574.8;Pg_S4039.5</i>
GO:0010226	response to lithium ion	biological_process	2	0.000451281	60.99696049	<i>Pg_S1983.2;Pg_S6590.1</i>
GO:0016036	cellular response to phosphate starvation	biological_process	5	0.000753011	7.069184162	<i>Pg_S2471.12;Pg_S3574.8;Pg_S4039.5;Pg_S4611.1;Pg_S9493.1</i>
GO:0016114	terpenoid biosynthetic process	biological_process	3	0.001409243	13.62698053	<i>Pg_S0639.1;Pg_S3711.2;Pg_S7152.2</i>

GO:0006817	phosphate ion transport	biological_process	3	0.001785241	12.55819775	<i>Pg_S0519.15;Pg_S2471.12;Pg_S2984.3</i>
GO:0046244	salicylic acid catabolic process	biological_process	2	0.001913769	30.49848024	<i>Pg_S0219.9;Pg_S2438.4</i>
GO:0005576	extracellular region	cellular_component	20	4.64E-06	3.224914829	<i>Pg_S0123.13;Pg_S0144.17;Pg_S0253.12;Pg_S0274.4;Pg_S0374.50;Pg_S0769.1;Pg_S1619.2;Pg_S1983.2;Pg_S2116.17;Pg_S2207.36;Pg_S2400.1;Pg_S3152.4;Pg_S3247.3;Pg_S3506.2;Pg_S4721.2;Pg_S5400.12;Pg_S5631.1;Pg_S6257.2;Pg_S6590.1;Pg_S9260.2</i>
GO:0005618	cell wall	cellular_component	15	0.000337953	2.806608611	<i>Pg_S0123.13;Pg_S0144.17;Pg_S0349.1;Pg_S0760.2;Pg_S0769.1;Pg_S1619.2;Pg_S2400.1;Pg_S2901.1;Pg_S3152.4;Pg_S3247.3;Pg_S3506.2;Pg_S4721.2;Pg_S5400.12;Pg_S6001.10;Pg_S6257.2</i>
GO:0005887	integral component of plasma membrane	cellular_component	5	0.011139696	3.758615523	<i>Pg_S1530.3;Pg_S3260.5;Pg_S4898.14;Pg_S7757.1;Pg_S8289.3</i>
GO:1990298	bub1-bub3 complex	cellular_component	1	0.027779095	35.58156028	<i>Pg_S5702.2</i>
GO:0005773	vacuole	cellular_component	10	0.035366823	1.939049607	<i>Pg_S0103.3;Pg_S0349.1;Pg_S0519.15;Pg_S1619.2;Pg_S2447.1;Pg_S2468.26;Pg_S2984.3;Pg_S5400.12;Pg_S5860.6;Pg_S8289.3</i>
GO:0033597	mitotic checkpoint complex	cellular_component	1	0.036867142	26.68617021	<i>Pg_S5702.2</i>
GO:0005905	clathrin-coated pit	cellular_component	2	0.045045217	5.930260047	<i>Pg_S1485.7;Pg_S2386.14</i>
GO:0005828	kinetochore microtubule	cellular_component	1	0.045870684	21.34893617	<i>Pg_S5702.2</i>
GO:0031410	cytoplasmic vesicle	cellular_component	2	0.053165816	5.404793967	<i>Pg_S1015.3;Pg_S2513.2</i>
GO:0005816	spindle pole body	cellular_component	1	0.059219258	16.42225859	<i>Pg_S1749.17</i>
GO:0008889	glycerophosphodiester phosphodiesterase activity	molecular_function	4	1.06E-06	50.23279099	<i>Pg_S0930.37;Pg_S1865.23;Pg_S3218.5;Pg_S6826.5</i>
GO:0033759	flavone synthase activity	molecular_function	2	0.000323341	71.16312057	<i>Pg_S0219.9;Pg_S2438.4</i>
GO:0034785	salicylate 5-hydroxylase activity	molecular_function	2	0.000323341	71.16312057	<i>Pg_S0219.9;Pg_S2438.4</i>
GO:0020037	heme binding	molecular_function	11	0.000335385	3.520814061	<i>Pg_S0266.27;Pg_S0374.50;Pg_S0762.28;Pg_S1157.11;Pg_S1619.2;Pg_S1952.7;Pg_S2116.17;Pg_S2275.6;Pg_S3716.6;Pg_S5024.11;Pg_S9260.2</i>
GO:0004497	monooxygenase activity	molecular_function	8	0.000558709	4.356925749	<i>Pg_S0252.42;Pg_S0266.27;Pg_S0762.28;Pg_S1157.11;Pg_S1952.7;Pg_S2275.6;Pg_S2835.16;Pg_S5024.11</i>
GO:0045549	9-cis-epoxycarotenoid dioxygenase activity	molecular_function	2	0.002201403	28.46524823	<i>Pg_S1728.5;Pg_S5203.1</i>
GO:0010436	carotenoid dioxygenase activity	molecular_function	2	0.002833837	25.11639549	<i>Pg_S1728.5;Pg_S5203.1</i>
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	molecular_function	6	0.00292232	4.298443524	<i>Pg_S0266.27;Pg_S0762.28;Pg_S1157.11;Pg_S1952.7;Pg_S2275.6;Pg_S5024.11</i>
GO:0000287	magnesium ion binding	molecular_function	7	0.004227543	3.491648439	<i>Pg_S0491.1;Pg_S0639.1;Pg_S0930.37;Pg_S1865.23;Pg_S3218.5;Pg_S3711.2;Pg_S6826.5</i>

GO:0004553 hydrolase activity,
hydrolyzing O-glycosyl
compounds molecular_f
unction 3 0.004397374 9.149544073 *Pg_S0760.2;Pg_S5075.8;Pg_S6001.10*

Table S4. The top 20 of up regulated DEGs of KEGG in group HP vs TP

Id	Term	Classification level1	Classification level2	ListHits	p-value	Enrichment score	geneID	hyperlink only excel
ko03008	Ribosome biogenesis in eukaryotes	Genetic Information Processing	Translation	2	0.027715	7.582054	<i>Pg_S3834.4;Pg_S5175.1</i>	ko03008
ko00750	Vitamin B6 metabolism	Metabolism	Metabolism of cofactors and vitamins	1	0.052131	18.72303	<i>Pg_S6053.3</i>	ko00750
ko00520	Amino sugar and nucleotide sugar metabolism	Metabolism	Carbohydrate metabolism	2	0.053465	5.287773	<i>Pg_S0368.2;Pg_S1347.27</i>	ko00520
ko00073	Cutin, suberine and wax biosynthesis	Metabolism	Lipid metabolism	1	0.067578	14.33482	<i>Pg_S2835.16</i>	ko00073
ko00260	Glycine, serine and threonine metabolism	Metabolism	Amino acid metabolism	1	0.186607	4.879939	<i>Pg_S1096.2</i>	ko00260
ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	1	0.191096	4.753516	<i>Pg_S0303.1</i>	ko03050
ko00051	Fructose and mannose metabolism	Metabolism	Carbohydrate metabolism	1	0.191991	4.729013	<i>Pg_S0368.2</i>	ko00051
ko00020	Citrate cycle (TCA cycle)	Metabolism	Carbohydrate metabolism	1	0.203545	4.432022	<i>Pg_S3342.1</i>	ko00020
ko00630	Glyoxylate and dicarboxylate metabolism	Metabolism	Carbohydrate metabolism	1	0.218422	4.095663	<i>Pg_S1096.2</i>	ko00630
ko04120	Ubiquitin mediated proteolysis	Genetic Information Processing	Folding, sorting and degradation	1	0.293767	2.912472	<i>Pg_S3592.1</i>	ko04120
ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	1	0.317088	2.659213	<i>Pg_S3342.1</i>	ko00190
ko00500	Starch and sucrose metabolism	Metabolism	Carbohydrate metabolism	1	0.369464	2.205357	<i>Pg_S0368.2</i>	ko00500
ko04626	Plant-pathogen interaction	Organismal Systems	Environmental adaptation	1	0.406102	1.956138	<i>Pg_S6285.3</i>	ko04626
ko04144	Endocytosis	Cellular Processes	Transport and catabolism	1	0.420721	1.86849	<i>Pg_S0226.20</i>	ko04144
ko03040	Spliceosome	Genetic Information Processing	Transcription	1	0.494753	1.50152	<i>Pg_S3683.10</i>	ko03040
ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	1	0.500508	1.477341	<i>Pg_S1844.26</i>	ko04075

Table S5. The top 20 of up regulated DEGs of KEGG in group NP vs TP

Id	Term	Classification_1 evel1	Classification_1 evel2	ListH its	p- value	Enrichment_s core	geneID	hyperlink_only_ excel
ko00940	Phenylpropanoi d biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	8	5.38E- 05	5.890392	<i>Pg_S0123.13;Pg_S0266.27;Pg_S0374.50;Pg_S0762.28;Pg_S1619.2;Pg_S2116.17 ;Pg_S3506.2;Pg_S9260.2</i>	ko00940
ko00564	Glycerophosph olipid metabolism	Metabolism	Lipid metabolism	4	0.0224 97	3.704911	<i>Pg_S0930.37;Pg_S1865.23;Pg_S3218.5;Pg_S6826.5</i>	ko00564
ko00909	Sesquiterpenoid and triterpenoid biosynthesis	Metabolism	Metabolism of terpenoids and polyketides	2	0.0226 14	8.594179	<i>Pg_S0639.1;Pg_S3711.2</i>	ko00909
ko00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	0.0240 18	8.321348	<i>Pg_S0266.27;Pg_S0762.28</i>	ko00945
ko00941	Flavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	0.0398 9	6.316204	<i>Pg_S0266.27;Pg_S0762.28</i>	ko00941
ko00906	Carotenoid biosynthesis	Metabolism	Metabolism of terpenoids and polyketides	2	0.0416 48	6.167587	<i>Pg_S1728.5;Pg_S5203.1</i>	ko00906
ko00130	Ubiquinone and other terpenoid- quinone biosynthesis	Metabolism	Metabolism of cofactors and vitamins	2	0.0499 09	5.577073	<i>Pg_S0266.27;Pg_S0762.28</i>	ko00130
ko00350	Tyrosine metabolism	Metabolism	Amino acid metabolism	2	0.0499 09	5.577073	<i>Pg_S0500.38;Pg_S2707.6</i>	ko00350
ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	3	0.0560 24	3.44898	<i>Pg_S0813.6;Pg_S4064.8;Pg_S5244.3</i>	ko00710
ko00604	Glycosphingoli pid biosynthesis - ganglio series	Metabolism	Glycan biosynthesis and metabolism	1	0.0665 31	14.56236	<i>Pg_S3630.2</i>	ko00604
ko00010	Glycolysis / Gluconeogenesi s	Metabolism	Carbohydrate metabolism	4	0.0694 61	2.569828	<i>Pg_S0491.1;Pg_S0813.6;Pg_S2707.6;Pg_S4064.8</i>	ko00010
ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	5	0.0866 4	2.110487	<i>Pg_S2566.5;Pg_S4931.9;Pg_S5077.6;Pg_S5602.1;Pg_S6397.3</i>	ko04075
ko00592	alpha-Linolenic acid metabolism	Metabolism	Lipid metabolism	2	0.1044 31	3.64059	<i>Pg_S0615.14;Pg_S2707.6</i>	ko00592
ko00603	Glycosphingoli pid biosynthesis - globo and isoglobo series	Metabolism	Glycan biosynthesis and metabolism	1	0.1118 64	8.455563	<i>Pg_S3630.2</i>	ko00603

ko00591	Linoleic acid metabolism	Metabolism	Lipid metabolism	1	0.118644	7.943105	<i>Pg_S3814.3</i>	ko00591
ko00531	Glycosaminoglycan degradation	Metabolism	Glycan biosynthesis and metabolism	1	0.164706	5.577073	<i>Pg_S3630.2</i>	ko00531
ko00760	Nicotinate and nicotinamide metabolism	Metabolism	Metabolism of cofactors and vitamins	1	0.171091	5.349438	<i>Pg_S1174.9</i>	ko00760
ko00630	Glyoxylate and dicarboxylate metabolism	Metabolism	Carbohydrate metabolism	2	0.210348	2.340379	<i>Pg_S0885.9;Pg_S3458.1</i>	ko00630
ko00040	Pentose and glucuronate interconversions	Metabolism	Carbohydrate metabolism	2	0.217357	2.289279	<i>Pg_S0144.17;Pg_S2400.1</i>	ko00040
ko00073	Cutin, suberine and wax biosynthesis	Metabolism	Lipid metabolism	1	0.217476	4.095663	<i>Pg_S2835.16</i>	ko00073