

Supplementary data Table S1. Gene specific primers used in this study

Item	Gene Name	Gene ID number	Primer sequence
Vector construction	TsPIP1::GFP	JX133234	F: 5'-AAGCTTATGGACGGCAAAGAAGA-3' R: 5'-GGATCCGCTCTTGAAAGGAATG-3'
	<i>TsPIP1;1</i>	JX133234	F: 5'-GTACACCTGGCGACAATTCC-3' R: 5'-GGTCCAACCCAGAAAATCCA-3'
	<i>ERF109</i>	Os09G0457900	F: 5'-GGATAGATGAGATTCTGTGAG-3' R: 5'-GTTGAGTTCTGCATTGAGGTC-3'
	<i>bHLH35</i>	Os04g0301500	F: 5'-GTCATTTTTGCGACACCCCA-3' R: 5'-CCTCGCAAGAAAACAACCACC-3'
	<i>GLK1</i>	Os06G0348800	F: 5'-AGCTGCGAGATTTCTGCTC-3' R: 5'-ATAGCTGCGTCGATGCTCTC-3'
	<i>CaATP2</i>	Os03g0203700	F: 5'-GGAATGCGGCATTTTGACTG-3' R: 5'-CTTGGTTCTGAAATCCGGTCCT-3'
RT-PCR	<i>RBCS2</i>	Os12g0274700	F: 5'-CAACTAAGCCGTCATCGTC-3' R: 5'-CCTCACCCAACAACATATAGTC-3'
	<i>RBCS3</i>	Os12g0291100	F: 5'-CAATGGCCTCTGCTCTTAAC-3' R: 5'-GCCGACGAATTTATCAGATATG-3'
	<i>RBCS4</i>	Os12g0292400	F: 5'-TACTACA ACTATCGGTCTATCGTTC-3' R: 5'-TGTCGACGGATTCAGATATG-3'
	<i>RBCS5</i>	Os12g0291400	F: 5'-AGCTTTGAACGTTTGAATC-3' R: 5'-CATAACACAGCTGATGTTGACAC-3'
	<i>LHCA4</i>	Os08G0435900	F: 5'-CTACCTTCCTAGGGCAATCC-3' R: 5'-TTGAGGTAGGTGGGAGAAGG-3'
	<i>UBQ3</i>	Os02g0634800	F: 5'-AAGGCATGGCTGATTCATGT-3' R: 5'-CAGATGTTACATGGTGACAGTA-3'

Supplementary data Table S2. Expression profiles of up- and down-regulated differentially expressed genes.

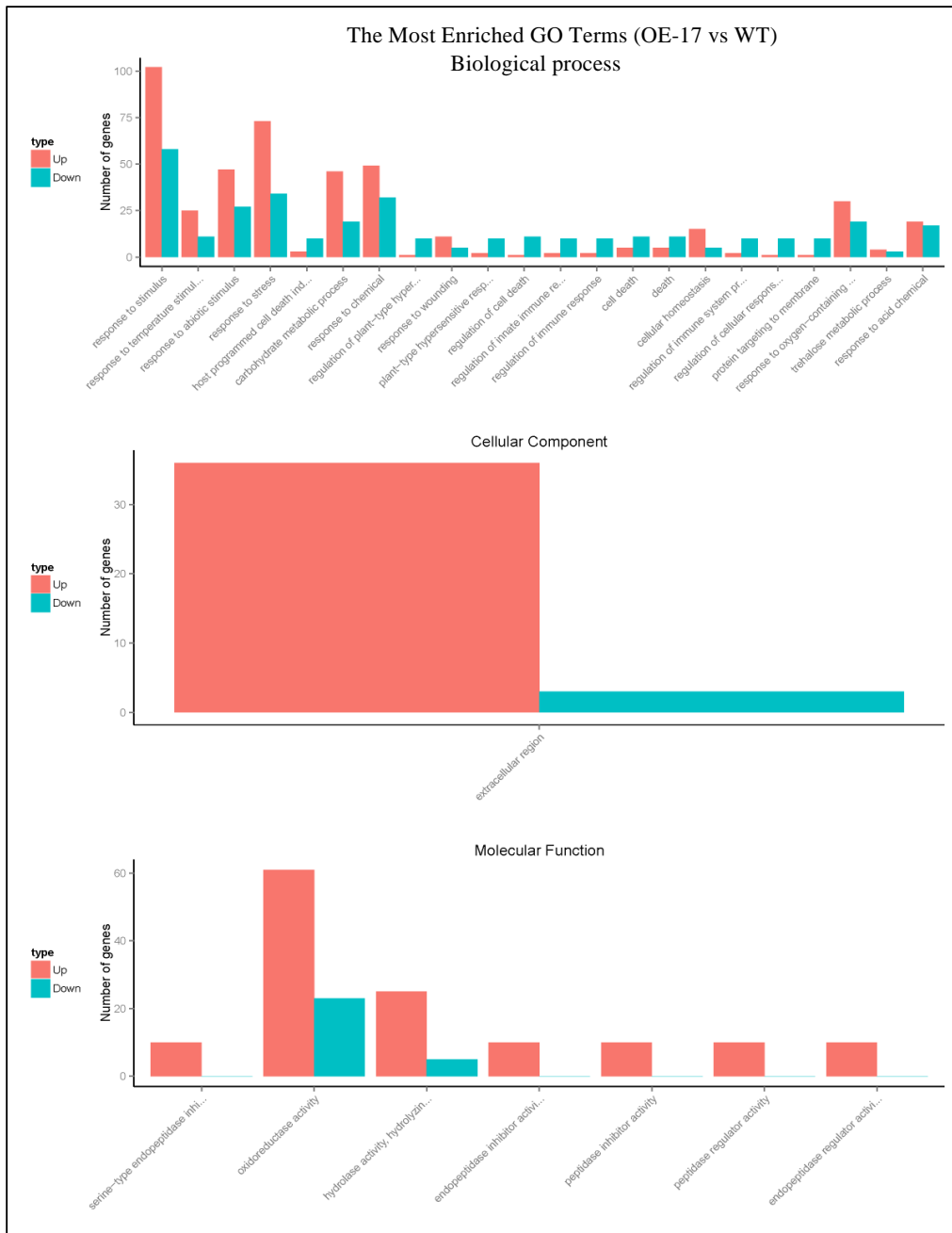
Gene name	Gene ID	log ₂ fold	Corrected P-Value	Up or down regulation
C2H2	Os03G0820400	-1.5215	3.9322E-16	down
	Os03G0786400	1.9505	2.1642E-07	up
	Os07G0581366	1.2388	0.000097158	up
	Os02G0775600	1.2769	0.001385	up
AP2/ERF	Os02G0752800	-1.0239	0.00065716	down
	Os04G0546800	-1.1621	9.6123E-09	down
	Os06G0166400	-1.0514	0.000086157	down
	Os08G0474000	3.101	0.00094189	up
	Os09G0457900	3.0104	1.3651E-10	up
WRKY	Os05G0322900	1.1052	0.000053685	up
	Os05G0474800	-1.199	2.2212E-19	down
	Os09G0417600	3.2151	3.1913E-23	up
	Os09G0417800	3.4388	0.00015673	up
	Os01G0584900	-2.1061	4.4308E-08	down
	Os01G0656400	-2.1875	9.742E-16	down
	Os02G0462800	-1.4191	7.7888E-06	down
bHLH	Os01G0566800	2.4709	0.00076773	up
	Os01G0575200	-1.059	0.00020205	down
	Os03G0741100	1.3511	3.18E-23	up
	Os03G0782500	1.3074	0.00021517	up
	Os04G0301500	2.8469	9.4279E-18	up
	Os09G0455300	-1.4075	0.0013425	down
MYB	Os01G0874300	-1.1476	0.00016325	down
	Os02G0641300	-2.3503	9.0618E-07	down
	Os06G0348800	1.205	1.6305E-15	up
	Os06G0637500	-1.1787	0.000043914	down
	Os12G0564100	1.7919	1.1506E-13	up
CDPK	Os01G0557500	-1.2106	2.7248E-09	down
	Os01G0955100	-1.2151	1.5419E-17	down
	Os02G0122600	-1.6934	0.000016445	down
	Os03G0128700	1.1971	0.00021544	up
	Os03G0203700	2.9559	1.2509E-06	up
	Os03G0319300	-1.0086	1.1761E-18	down
	Os06G0172200	-1.1592	1.4453E-06	down
	Os07G0678300	1.4697	3.4663E-06	up
	Os08G0441100	-1.509	8.6226E-07	down

Supplementary data Table S3. Profiles of the differentially expressed genes specifically involved in the transcription regulation or photosynthetic system in the KEGG pathways.

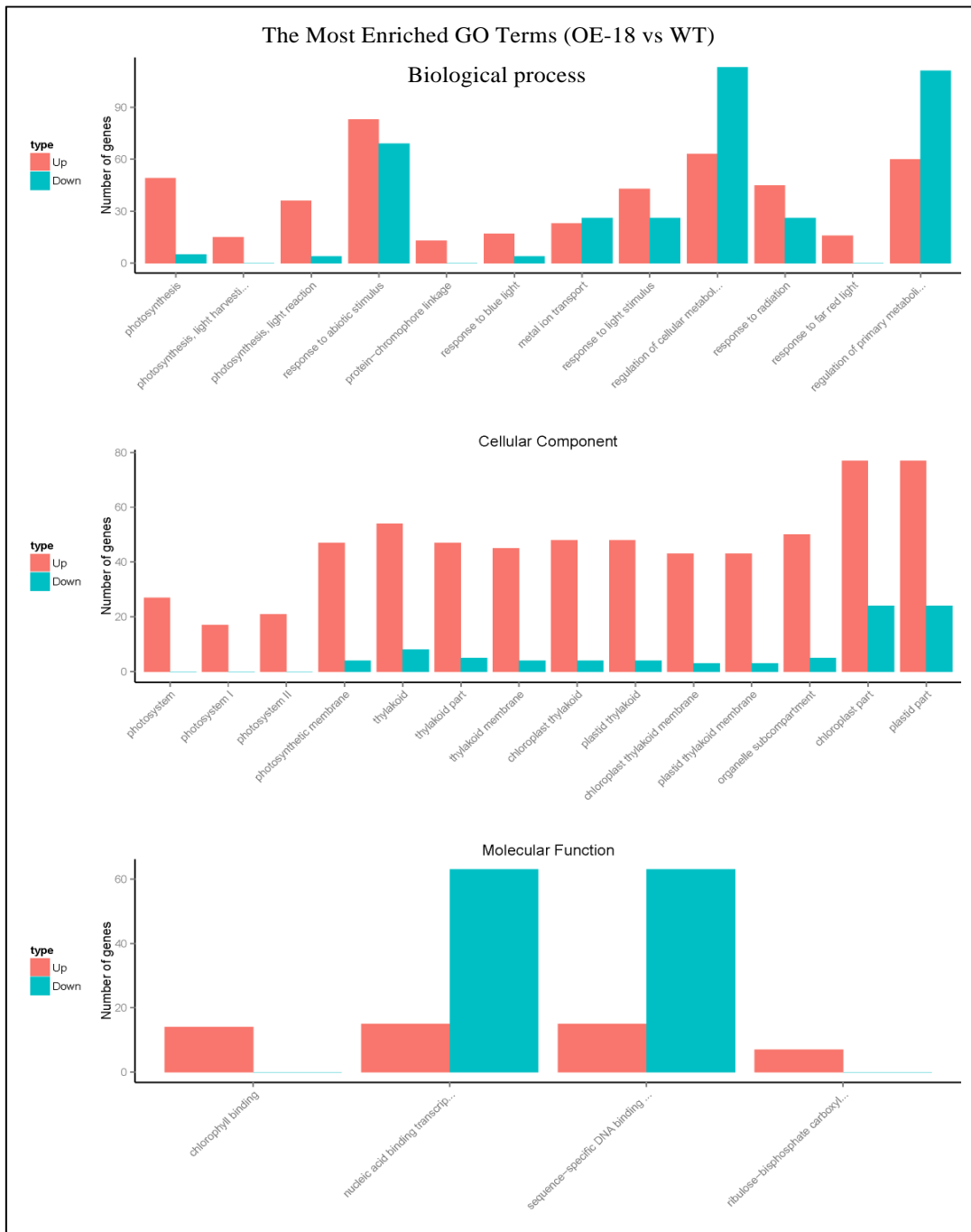
Gene name	Gene ID	Log2fold	P value	Q value	Function annotation	Transgenic line
<i>RBCS2</i>	OS12G0274700	1.9532	5.95E-168	1.25E-164	ribulose biphosphate carboxylase small chain, chloroplastic	OE-17
<i>RBCS3</i>	OS12G0291100	1.025	5.62E-80	3.72E-77	ribulose biphosphate carboxylase small chain, chloroplastic	OE-17
<i>RBCS4</i>	OS12G0292400	1.0522	2.33E-33	5.42E-31	ribulose biphosphate carboxylase small chain, chloroplastic	OE-17
<i>RBCS5</i>	OS12G0291400	1.8712	2.93E-43	1.01E-40	ribulose biphosphate carboxylase small chain, chloroplastic	OE-17
<i>LHCA4</i>	OS08G0435900	1.3138	1.63E-15	1.35E-13	light-harvesting complex I chlorophyll a/b binding protein 4	OE-17
<i>GLK1</i>	OS06G0348800	1.9077	4.60E-56	7.57E-54	probable transcription factor	OE-18
<i>RBCS2</i>	OS12G0274700	2.562	0	0	ribulose biphosphate carboxylase small chain, chloroplastic	OE-18
<i>RBCS3</i>	OS12G0291100	1.9574	0	0	ribulose biphosphate carboxylase small chain, chloroplastic	OE-18
<i>RBCS4</i>	OS12G0292400	2.1745	3.44E-236	3.21E-233	ribulose biphosphate carboxylase small chain, chloroplastic	OE-18
<i>RBCS5</i>	OS12G0291400	1.3714	1.98E-24	1.35E-22	ribulose biphosphate carboxylase small chain, chloroplastic	OE-18
<i>LHCA4</i>	OS08G0435900	4.4298	0	0	light-harvesting complex I chlorophyll a/b binding protein 4	OE-18
<i>ERF109</i>	OS09G0457900	3.0104	1.78E-12	1.37E-10	ethylene response factor 109	OE-19
<i>bHLH35</i>	OS04G0301500	2.8469	6.73E-20	9.43E-18	basic helix loop-helix 35	OE-19
<i>GLK1</i>	OS06G0348800	1.205	1.37E-17	1.63E-15	probable transcription factor	OE-19
<i>CaATP2</i>	OS03G0203700	2.9559	2.82E-08	1.25E-06	Calcium-transportin ATPase2	OE-19
<i>RBCS2</i>	OS12G0274700	2.0397	4.20E-202	1.51E-198	ribulose biphosphate carboxylase small chain, chloroplastic	OE-19
<i>RBCS3</i>	OS12G0291100	1.4257	1.52E-194	4.78E-191	ribulose biphosphate carboxylase small chain, chloroplastic	OE-19
<i>RBCS4</i>	OS12G0292400	1.3435	4.05E-65	3.40E-62	ribulose biphosphate carboxylase small chain, chloroplastic	OE-19
<i>RBCS5</i>	OS12G0291400	1.8271	9.27E-44	3.77E-41	ribulose biphosphate carboxylase small chain, chloroplastic	OE-19
<i>LHCA4</i>	OS08G0435900	1.7284	5.90E-32	1.63E-29	light-harvesting complex I chlorophyll a/b binding protein 4	OE-19

Supplementary data Figure S2. The distributions of the most enriched GO terms in the three KEGG pathways.

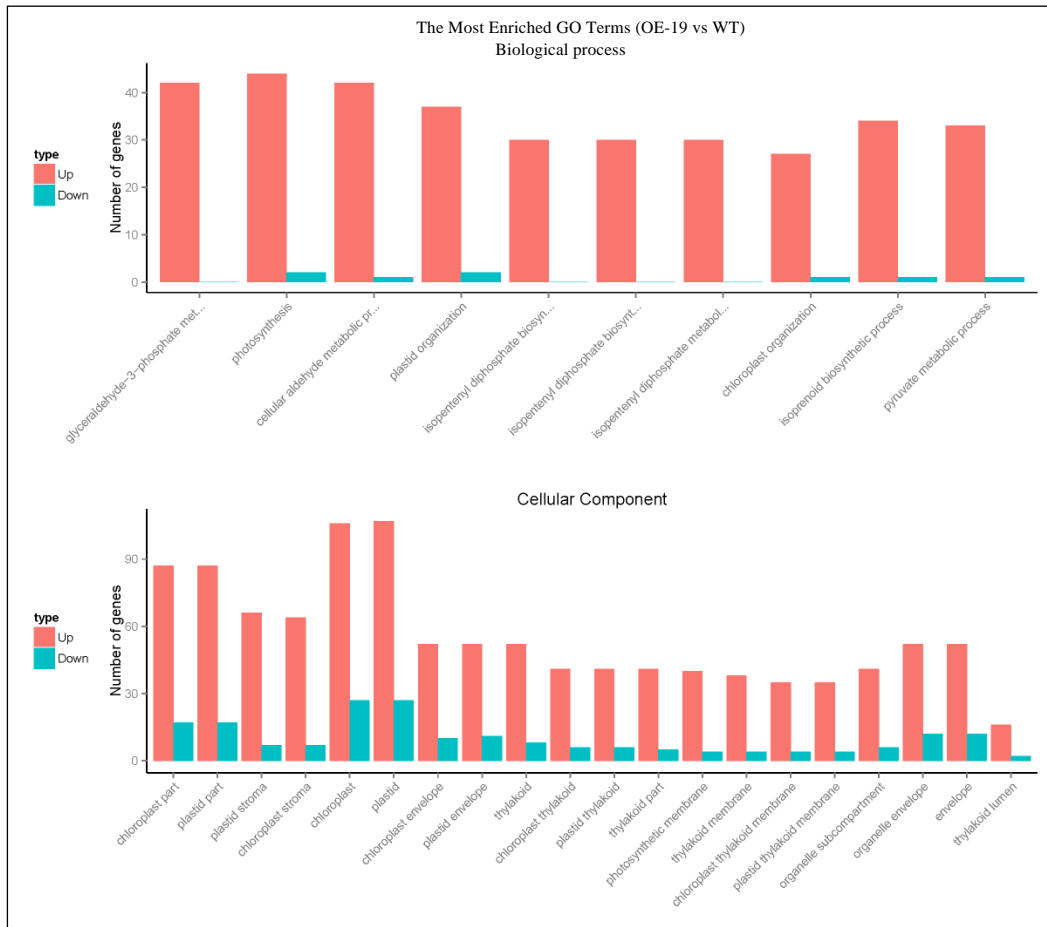
A



B



C



(A) The most enriched GO terms in the OE-17 line; (B) The most enriched GO terms in the OE-18 line; (C) The most enriched GO terms in the OE-19 line, and no enriched GO terms in molecular function were observed.