

## Supplementary Materials

**Table S1.** Comparison of agronomic traits between the mutants and wild-type plants

Material	Height (cm)	Stem diameter (mm)	Fresh weight (g)	Dry weight (g)
MT	42.14+9.07b	9.75+0.34a	102.79+9.10b	6.96+0.30b
F <sub>2</sub> (YGL)	36.84+4.65b	9.74+0.22a	107.70+21.48b	6.78+1.21b
F <sub>2</sub> (GL)	81.26+5.68a	11.02+1.20a	371.23+56.99a	26.64+3.85 a
WT	74.86+11.36a	10.4 1+1.05a	345.81+54.09a	22.88+4.31a
F1	79.80+14.46a	10.94+0.57a	293.17+81.55a	19.40+5.94a

Note: Different lowercase letters indicate significant difference at p<0.05 level. MT: yellow-green mutant phenotype plants; F<sub>2</sub> (YGL): plants with yellow-green leaves in F<sub>2</sub> population; F<sub>2</sub> (GL): plants with green leaf in F<sub>2</sub> population; WT: wild type plants with green leaves.

**Table S2.** Summary of sequencing reads

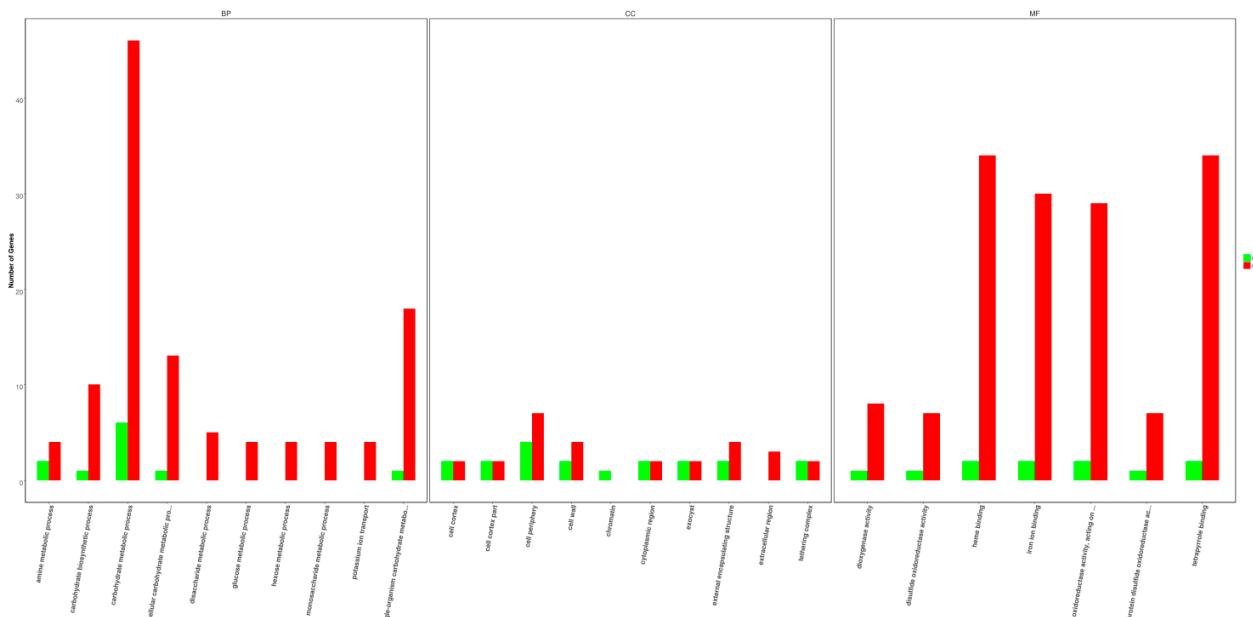
sample	Raw reads	Clean reads	Clean bases	Error rate	Q20(%)	Q30(%)	GC(%)
WT_1	43,403,482	42,646,942	6.4G	0.03	97.17	92.07	42.4
WT_2	47,531,044	46,707,718	7.01G	0.03	97.44	92.59	43.75
WT_3	46,970,892	45,568,742	6.84G	0.03	97.43	92.59	43.27
MT_1	48,891,598	47,415,702	7.11G	0.03	97.35	92.39	43.05
MT_2	42,645,236	41,467,018	6.22G	0.03	97.1	91.97	42.81
MT_3	43,136,424	42,406,444	6.36G	0.03	97.48	92.65	43.66

Note: WT: wild type plants with green leaves; MT: yellow-green mutant phenotype plants.

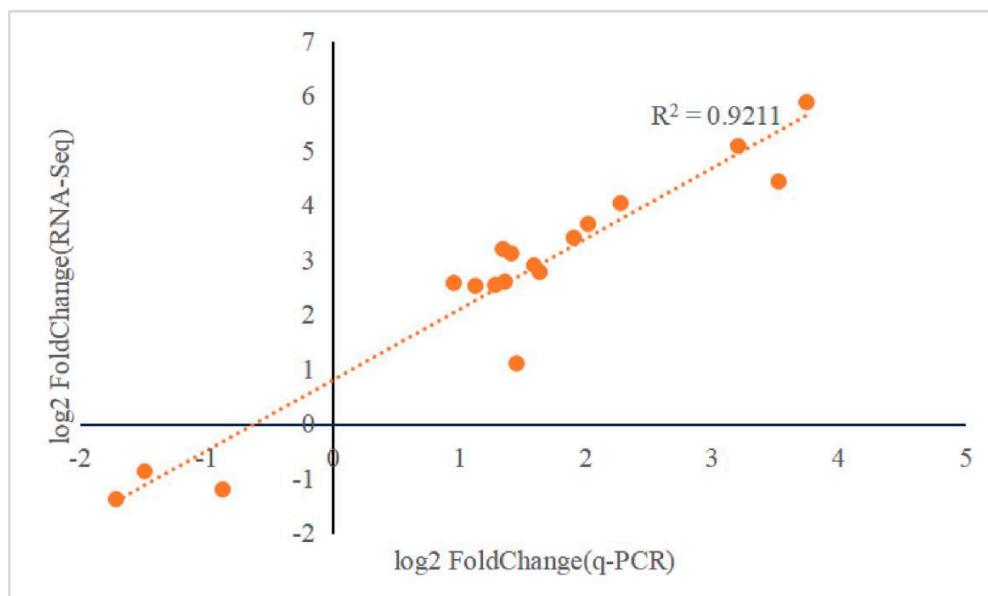
**Table S3.** Primer information

Gene name	log <sub>2</sub> FC (RNA-Seq)	log <sub>2</sub> FC (q-PCR)	Primer information used in the experimental process(F-R)
PCK	3.203406709	5.083333333	TTGAGAATGTGGTGGATG CAACGCAGGGGATTAG
PPDK	1.590354001	2.9	GAAAAGGAAGGAGTGAGGGT CAGTTGAGATGGTGAGTCCA
PEPC	1.903984312	3.403333333	GCCACAAGACGAAATGAGA TGAAAACTGAATAAGAGGAGCA
FBP	1.409818715	3.116666667	TGGAAGGTATTCTGTGGTGT TAGGTTAGGTTCGTGGCTGT
TIM	1.283908764	2.536666667	ATCACAGCCCAACCAAAC GGAAGAGGAGAACATCGGAGA
MDH	1.451763137	1.1	TTGCCACCTTGAACCTTT CTGAACCTTGAGGGAGTGT
SUS5	3.744939345	5.883333333	AAACACACCTTCCAAACTCC CAATCTCCCCATCCTCTCT
TPP	3.522988072	4.433333333	CACTCTCTGCTCCGATGA TGAATCCGTAAACCTGTCTCT
BAM3	2.016480218	3.653333333	GTCCTGTGTTGTTATGCTTC GTCCATCTTCTCCACTAATCC
SDHB	0.955743318	2.573333333	CCGATAGTCCTCCAAACC AAGCCAACCCATTACATCC
ICDH	2.27491789	4.036666667	TGTTTGTTGTTGTCCTGATG TATGCTGTTGCTGGTT
HK1	1.635563564	2.773333333	GGAACTGGAACAAATGCTG CTCGGTGAAGGGAAGATG
UGP1	1.35962417	2.596666667	TAAAGTGGTTGGCGATGTT TGAAAGAGTTGTGAAAGGCA
CoAOMT	1.487127562	0.873333333	GGCTATTGCTCCTCACA TTACTCCACCAACCTTCACC
CYP98A2	0.870067651	1.206666667	CAAACCTTACCAACCGTCTCC ACCTCCCTCGCTAACTCC
GSHPx	1.344567314	3.196666667	CCTGCTCAAGGTTCAAGG AAAAGGCGATGTTGTTGG
ODC1	1.713576754	1.383333333	CCTTACCACTTTGATTCCG GCCGTATTGTTCCCAA
PWD	1.127128268	2.52	TACACACATACAGCCCAACC ACTACACCACAAACTCCCA

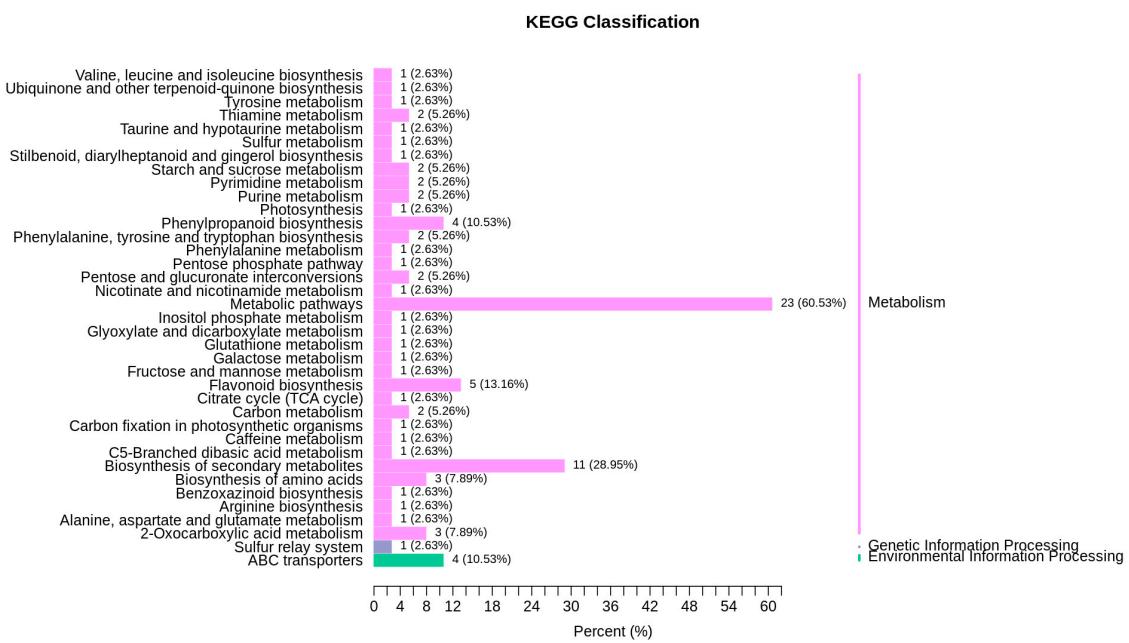
## Supplementary Material



**Figure S1.** GO annotation analysis of DEGs in MT vs. WT. BP, biological processes; CC, cellular components; MF, molecular functions. MT: yellow-green mutant phenotype plants; WT: wild type plants with green leaves.



**Figure S2.** qRT-PCR-based verification of the DEGs in MT vs. WT. MT: yellow-green mutant phenotype plants; WT: wild type plants with green leaves.



**Figure S3.** KEGG classification statistics of DAMs in MT vs. WT. MT: yellow-green mutant phenotype plants; WT: wild type plants with green leaves.