Supplementary Materials:.

Table S1. Primers for qPCR.

Gene	Primer	Sequence(5′-3′)	Tm(°C)	Product(bp)
RIB1	F	GCTCGTATCCCAACCACACA	58.8	109
	R	GCGACCGTATGTCTTCACCA	59	
PGI1	F	AAGTTGGGTCGGTGGTCGTT	61.5	134
	R	ATGGGGTTTGGGTGAAGTGG	61.6	
EOL1	F	GACGCAACCGATGGAGACA	59.6	400
	R	TGAACCTAAGCAATCCTCACACT	58.5	
ADH2	F	AATCCAACTGTCCTCACGCT	56.8	269
	R	GACTCTGTAACCCATCGCCT	56.5	
PFK2	F	GTTTGTGGTGGTGACGGTTC	58	254
	R	TGAGAGTTGGCAGTGGCTTC	58.4	
GRE3	F	CGGGCTCTGGAAGAATGTGT	59.8	216
	R	TTGAGGACCGAAGGAGGAGT	58.4	
SFA1	F	GAGTGTGGAAAGGCTCTGCT	56.7	128
	R	TTCTTTGAATGGTCTCCTGTGA	57.3	
HXK1	F	GGATACCTCCTACCCAGCAA	56.6	181
	R	AGCGGCAATACCACAAACAG	58.7	
SSA2	F	CTACACTTCCATCACCAGAGC	54.6	142
	R	AGAACCACCGACCAAGACAA	57.5	
PDA1	F	CCAGGCTTCTATGGTGGTAATG	59.1	198
	R	CTCACAGCAAAACACGACGG	59.8	
PYC1	F	TTCGTCAAGCAAGCCAAGGA	61.6	97
	R	TCACAGCATCTACACCGACC	56.2	
ALD4	F	TTGAAGACTGCCGAATCCAC	58.2	347
	R	CTTGAACCCGCACAACAGAC	58.6	
GND2	F	TGAGAGGCTACCAGCAAACT	55	94
	R	CAAATGGGCAGAAGCACA	55.4	
NRG1	F	AGAAAATGGCTCTGAAAAGTGG	58.2	351
	R	TGCCTTGCTAAATGACCCGA	61.5	
RCK2	F	GGACAAAGGGAAGGACAGCA	59.8	83
	R	CAGCGGAAACCGTCTTATGTA	58.2	
CMK2	F	GCGTCACACATTCGTTGGA	57.9	171
	R	CGTCTTCCTCTTCACCAGCC	59.5	
CYC8	F	TTCTCCCTCAACCTCCTGCT	58.6	90
	R	CACCTTGCCACTCTCCCAT	57.7	
SUC2	F	AACAAGGGCTGGATGAATGA	57.7	290
	R	GTCCAAATCGCAACGCATCT	60.9	
MAL31	F	GTATGATTGCCGTGGGACAG	58.4	157
	R	GCAGCGAAAAGTTGACCGAA	61.3	
MAL32	F	GAAGACCAATCCGAAGCGTG	60.4	239

	R	CCAGCCAAAATCCAACAGCA	61.7	
IMA2	F	TCTACCAGACGCTCCTGTGAT	57.1	276
	R	TTTTGACGGAACTTGGGCGA	63.7	
PMA1	F	CCTTACTCTCCAAAGCCCGT	58.6	162
	R	CATAATACCGTTCATAGCACCG	57.9	

Table S2. Base information of genome sequencing before filter.

Sample	Clean_Data(bp)	Q20(%)	Q30(%)	N(%)	GC(%)
WT	1,223,448,300	1,187,316,227(97.05%)	1,124,541,384(91.92%)	4009(0.0%)	464,455,756(37.96%)
MT	1,077,144,300	1,046,481,321(97.15%)	992,611,414(92.15%)	3798(0.0%)	413,524,155(38.39%)

Table S3. Base information of genome sequencing after filter.

Sample	HQ_Clean_Data(bp)	HQ_Q20(%)	HQ_Q30(%)	HQ_N(%)	HQ_GC(%)
WT	1,219,208,533	1,184,169,438(97.13%)	1,121,835,425(92.01%)	3996(0.0%)	462,308,743(37.92%)
MT	1,073,751,375	1,044,084,572(97.24%)	990,585,693(92.25%)	3758(0.0%)	411,831,035(38.35%)

Table S4. Alignment to the reference genome.

Sample	Total read	Total unmapped	Total mapped	Total pair mapped	Total single mapped
WT	8,136,772	469,482(5.77%)	7,667,290(94.23%)	7,555,584(92.86%)	111,706(1.37%)
MT	7,164,538	465,628(6.50%)	6,698,910(93.50%)	6,598,452(92.10%)	100,458(1.40%)

Table S5. Statistics of genome coverage.

Sample	1×(%)	4×(%)	10×(%)	20×(%)	30×(%)
WT	99.08	98.60	98.19	97.56	96.97
MT	98.75	98.36	97.84	97.00	96.25

Table S6. Locations of SNPs on the genome.

Sample	Downstream	Exonic	Intergenic	Intronic	Upstream	Upstream.downstream	UTR3	Total
WT	3314	30,412	1132	394	4940	7645	58	47,895
MT	3746	35,358	1346	421	5792	8686	62	55,411

Table S7. Coding information of SNPs.

Sample	Nonsynonymous. SNV	Stopgain	Synonymous. SNV	Unknow	Total
WT	10,652	65	19,643	52	30,412
MT	11,790	72	23,444	52	35,385

Table S8. Location of InDels on the genome.

Sample	Downstream	Exonic	Intergenic	Intronic	Splicing	Upstream	Upstream. downstream	UTR3	UTR5	Total
WT	705	482	199	70	1	857	1476	11	1	3802
MT	782	573	204	73	1	923	1587	14	1	4154

Table S9. Coding information of InDels.

Sample	Frameshift.deletion	Frameshift. insertion	Nonframeshift. deletion	Nonframeshift. insertion	Stopgain	Unknpwn	Total
WT	102	90	155	123	3	9	482
MT	126	112	168	154	5	8	573

Table S10. Hybrid information of SNPs and InDels.

Sample	SNP. Hom	SNP. Het	InDel. Hom	InDel. Het
WT	47,160	735	3644	158
MT	54,220	1191	3984	174

Table S11. Base information of RNA-Seq.

Sample	RawData(bp)	CleanData(bp	*AF_Q20(%)	AF_Q30(%)	AF_N(%)	AF_GC(%)
WT-T1-1	6,668,616,900	6,614,944,991	97.68	93.36	15,503(0.00%)	44.22
WT-T1-2	5,828,627,100	5,791,112,963	97.69	93.41	13,438(0.00%)	44.23
WT-T1-3	6,434,889,600	6,380,780,124	97.66	93.36	19,002(0.00%	44.42
MT-T1-1	10,412,181,600	10,333,826,850	97.76	93.57	23,807(0.00%)	44.40
MT-T1-2	9,679,800,300	9,612,309,032	97.78	93.62	22,472(0.00%)	44.58
MT-T1-3	5,875,123,200	5,830,482,985	97.97	94.07	13,754(0.00%)	44.28
WT-T2-1	7,246,543,500	7,183,453,832	97.44	92.86	16,486(0.00%)	44.26
WT-T2-2	9,426,709,500	9,358,149,097	97.66	92.86	21,979(0.00%)	44.01
WT-T2-3	10,604,002,200	10,519,130,214	97.41	92.76	24,365(0.00%)	44.08
MT-T2-1	11,869,559,400	11,773,095,758	97.28	92.44	26,922(0.00%)	44.47
MT-T2-2	7,505,652,300	7,386,865,191	97.68	93.42	21,497(0.00%)	44.40
MT-T2-3	6,867,680,100	6,741,757,241	97.63	93.33	20,550(0.00%)	44.38
WT-T3-1	6,767,549,700	6,699,313,334	97.18	92.30	53,764(0.00%)	45.15
WT-T3-2	5,985,458,400	5,915,100,780	97.47	92.94	47,633(0.00%)	44.84
WT-T3-3	6,558,156,900	6,492,962,720	97.48	93.03	51,590(0.00%)	44.57
MT-T3-1	7,171,195,500	7,076,495,536	96.91	91.83	58,287(0.00%)	45.10
MT-T3-2	7,043,041,200	6,959,028,044	97.00	92.05	57,490(0.00%)	45.01
MT-T3-3	6,905,925,300	6,826,555,345	97.45	92.89	54,829(0.00%）	45.30

*AF, after filter.

Table S12. Alignment to the reference genome.

Sample	Total	Unmapped(%)	Unique_Mapped(%)	Multiple_Mapped(%)	Tatal_Mapped(%)
WT-T1-1	44,113,274	4.19	93.35	2.47	95.81
WT-T1-2	38,560,776	4.15	93.51	2.35	95.85
WT-T1-3	42,506,642	4.09	93.44	2.48	95.91
MT-T1-1	68,585,240	3.89	92.55	3.56	96.11
MT-T1-2	63,780,760	3.85	92.30	3.85	96.15
MT-T1-3	38,654,816	3.91	92.40	3.69	96.09
WT-T2-1	24,975,946	5.10	87.09	7.81	94.90
WT-T2-2	38,987,798	4.58	89.03	6.39	95.42
WT-T2-3	44,132,336	4.95	88.04	7.01	95.05
MT-T2-1	41,750,132	6.02	86.41	7.57	93.98
MT-T2-2	26,971,294	5.04	88.77	6.19	94.96
MT-T2-3	24,038,958	5.46	88.07	6.47	94.54
WT-T3-1	16,408,314	6.35	86.56	7.10	93.65
WT-T3-2	17,740,012	6.51	86.42	7.08	93.49
WT-T3-3	21,500,872	5.18	89.30	5.52	94.82
MT-T3-1	19,555,136	8.95	82.78	8.28	91.05
MT-T3-2	18,205,808	8.83	82.56	8.62	91.17
MT-T3-3	17,668,984	10.62	81.13	8.25	89.38

Table S13. Location of alignment to the reference genome.

Sample	Exon	Intron	Intergenic
WT-T1-1	40,170,986(95.06%)	66,938(0.16%)	2,028,211(4.80%)
WT-T1-2	35,148,242(95.09%)	53,948(0.15%)	1,760,023(4.76%)
WT-T1-3	38,746,087(95.04%)	69,522(0.17%)	1,954,574(4.79%)
MT-T1-1	62,801,181(95.28%)	184,292(0.28%)	2,929,573（4.44%）
MT-T1-2	58,528,742(95.44%)	142,768(0.23%)	2,655,895(4.33%)
MT-T1-3	35,408,430(95.33%)	98,494(0.27%)	1,637,756(4.41%)
WT-T2-1	18,917,694(79.81%)	669,290(2.82%)	4,116,084(17.37%)
WT-T2-2	31,792,372(85.46%)	852,044(2.29%)	4,558,006(12.25%)

WT-T2-3	34,974,391(83.37%)	943,996(2.25%)	6,031,598(14.38%)
MT-T2-1	32,317,511(82.37%)	382,779(0.98%)	6,536,243(16.66%)
MT-T2-2	22,179,444(86.59%)	295,055(1.15%)	3,138,365(12.25%)
MT-T2-3	18,995,801(83.59%)	269,465(1.19%)	3,460,312(15.23%)
WT-T3-1	11,507,476(74.89%)	437,051(2.84%)	3,422,010(22.27%)
WT-T3-2	12,882,124(77.67%)	388,669(2.34%)	3,315,074(19.99%)
WT-T3-3	16,649,646(81.67%)	427,530(2.10%)	3,309,810(16.23%)
MT-T3-1	13,604,563(76.41%)	152,592(0.86%)	4,048,252(22.74%)
MT-T3-2	12,665,124(76.30%)	142,567(0.86%)	3,791,450(22.84%)
MT-T3-3	11,900,951(75.36%)	143,917(0.91%)	3,747,060(23.73%)

Table S14. Gene number detection.

Sample	Refer_genes	Sequenced_ refer_gene(%)	Novel_genes	Sequenced_ Novol_genes(%)	Total_genes	Sequenced_ Tatol_genes(%)
all	6600	6383(96.71%)	36	36(100%)	6636	6419(96.73%)
WT-T1-1	6600	6018(91.18%)	36	34	6636	6052(90.28%)
WT-T1-2	6600	5962(90.33%)	36	29(80.56%)	6636	5991(90.28%)
WT-T1-3	6600	6001(90.92%)	36	30(83.33%)	6636	6031(90.88%)
MT-T1-1	6600	6031(91.38%)	36	28(77.78%)	6636	6059(91.31%)
MT-T1-2	6600	5982(90.64%)	36	30(83.33%)	6636	6012(90.60%)
MT-T1-3	6600	6014(91.12%)	36	28(77.78%)	6636	6042(91.05%)
WT-T2-1	6600	5911(89.56%)	36	33(91.67%)	6636	5944(89.57%)
WT-T2-2	6600	6059(91.80%)	36	34(94.44%)	6636	6093(91.82%)
WT-T2-3	6600	6011(91.08%)	36	32(88.89%)	6636	6043(91.06%)
MT-T2-1	6600	5737(86.92%)	36	28(77.78%)	6636	5765(86.87%)
MT-T2-2	6600	5204(78.85%)	36	26(72.22%)	6636	5230(78.81%)
MT-T2-3	6600	5517(83.59%)	36	25(69.44%)	6636	5542(83.51%)
WT-T3-1	6600	5857(88.47%)	36	32(88.89%)	6636	5889(88.74%)
WT-T3-2	6600	5951(90.17%)	36	34(94.44%)	6636	5985(90.19%)
WT-T3-3	6600	6013(91.11%)	36	34(94.44%)	6636	6047(91.12%)
MT-T3-1	6600	5236(79.33%)	36	25(69.44%)	6636	5261(79.28%)
MT-T3-2	6600	5300(80.30%)	36	27(75.00%)	6636	5327(80.27%)
MT-T3-3	6600	5364(81.27%)	36	27(75.00%)	6636	5391(81.24%)

Table S15. Gene coverage of each sample.

Sample	00-20%	20-40%	40-60%	60-80%	80-100%
WT-T1-1	33(0.50%)	51(0.78%)	117(1.79%)	186(2.84%)	6160(94.09%)
WT-T1-2	40(0.61%)	76(1.16%)	134(2.05%)	203(3.10%)	6086(93.07%)
WT-T1-3	26(0.40%)	66(1.01%)	145(2.22%)	216(3.31%)	6079(93.06%)
MT-T1-1	29(0.44%)	46(0.7%)	74(1.13%)	109(1.66%)	6295(96.06%)
MT-T1-2	35(0.54%)	58(0.89%)	85(1.30%)	131(2.00%)	6233(95.28%)

MT-T1-3	27(0.41%)	57(0.87%)	91(1.39%)	111(1.70%)	6257(95.63%)
WT-T2-1	69(1.06%)	154(2.36%)	280(4.29%)	379(5.81%)	5638(86.47%)
WT-T2-2	32(0.49%)	70(1.07%)	124(1.89%)	254(3.87%0	6086(92.69%)
WT-T2-3	33(0.50%)	69(1.05%)	126(1.92%)	270(4.11%)	6077(92.43%)
MT-T2-1	114(1.76%)	262(4.05%)	366(5.66%)	494(7.64%)	5230(80.88%)
MT-T2-2	346(5.74%)	591(9.81%)	561(9.31%)	637(10.57%)	3890(64.56%)
MT-T2-3	228(3.62%)	395(6.27%)	49597.86%）	620(9.85%)	4557(72.39%)
WT-T3-1	120(1.85%)	272(4.19%)	454(7.00%)	623(9.61%)	5016(77.35%)
WT-T3-2	71(1.08%)	159(2.43%)	332(5.07%)	502(7.67%)	5480(83.74%)
WT-T3-3	47(0.72%)	128(1.95%)	260(3.97%)	463(7.07%)	5651(86.29%)
MT-T3-1	342(5.63%)	583(9.60%)	632(10.41%)	677(11.15%)	3838(63.21%)
MT-T3-2	311(5.08%)	536(8.76%)	570(9.31%)	641(10.47%)	4062(66.37%)
MT-T3-3	290(4.68%)	536(8.65%)	578(9.33%)	715(11.55%)	4074(65.78%)

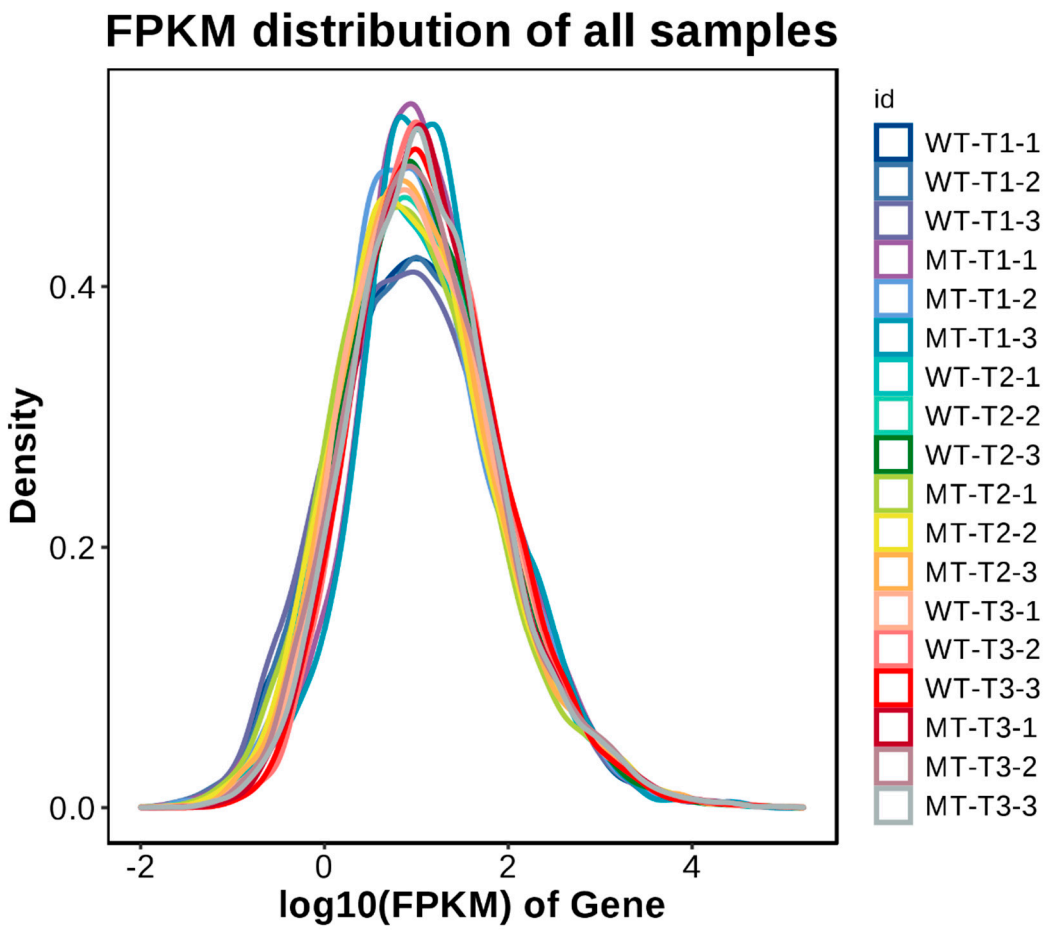

Figure S1. Distribution of gene expression abundance.

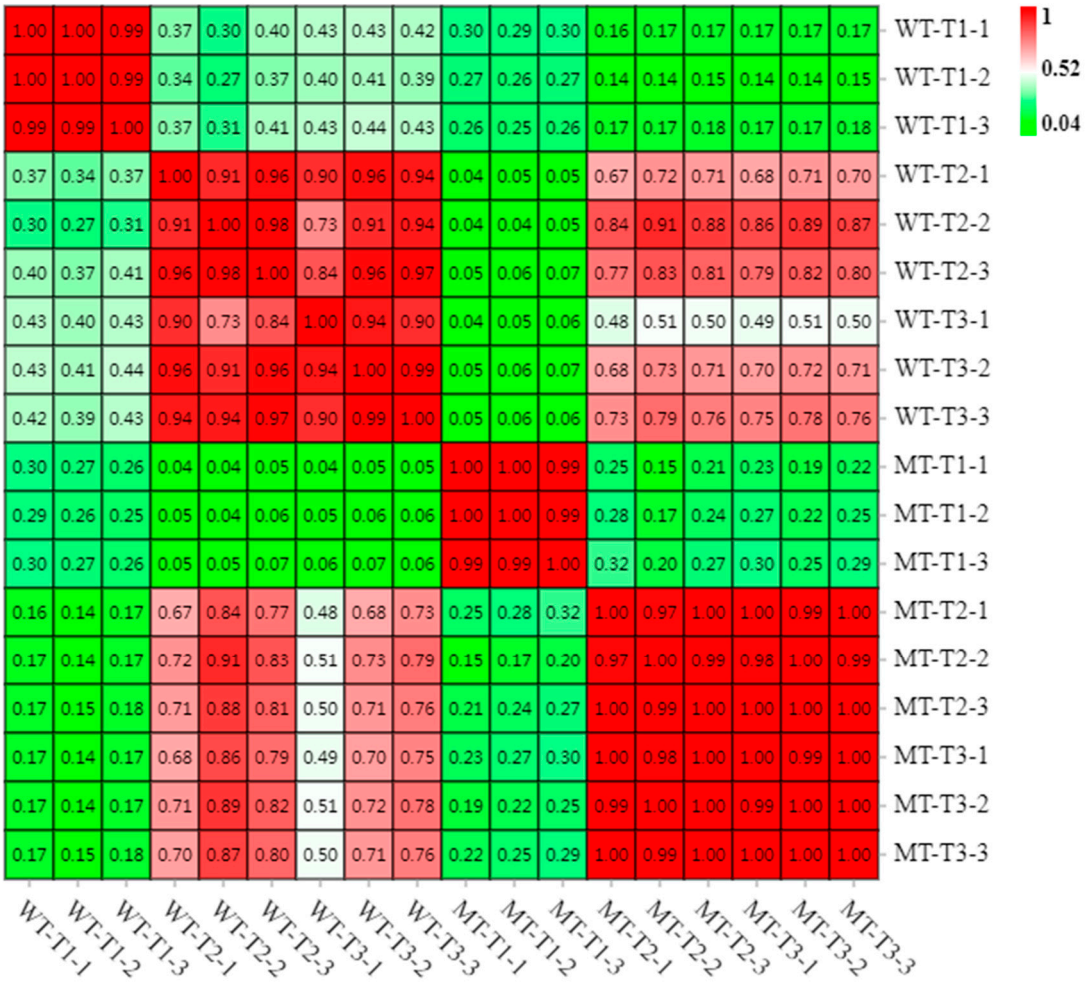

Figure S2. Heat map of the Pearson correlation coefficient R between samples.