

Supplementary Materials

Table S1. Primers sequence used in qRT-PCR.

	Gene ID	Primers sequences (5'-3')	
		Forward	Reverse
RNA-Seq verify	Os03g0757000	GCGGAAGGGCAGCACATCAT	TGGAAGGAGTTGCAGACGGTCAT
	Os10g0530900	CGCAGGTCATCGTGCAGTACATCG	TCTCCTCCTCCGTCTTGCTCCC
	Os01g0696701	GACCTGGCCGAAGATGACGG	CACGGACCTGCTGCTGATGG
	Os01g0692100	CTCCTCCCTGCCGATCCCTA	ACCTGAACAGCACTTTCCACGAC
	Os01g0949750	CTGCTGCTCAACCACAACCC	GCTTCCCTCACGAAACAATCC
	Os04g0178400	CAAGAGCCCACAAGACCACG	GCCCTCCACAATCTCATACCCT
	Os04g0570500	CCTAGTTGCCAAGAAGTTGA	ATCGGTAGAATGATGTCCCT
	Os01g0854800	GGGCACAAGGTGGAGCAGAAG	GTGGTAGTCGGTATCACGAGGGAG
	Os01g0356400	CTTCCAGAGTATGTCGGTTTGTCG	CTGCCTCAGATGGGATGTTCCG
	Os01g0173900	TTCAACGGATCAAAGCGAAGT	TACCAGAAGCAGGCAGCAAG
	Os04g0206500	AACCGCATGGGAGATTGGTG	TTGTGCTGCTTCCTTGGCTTT
	Os07g0606800	TCCGCGTCAGGATGTTCTTTCCG	CCGCCTTGCCGTCGTCGTAG
	Os05g0295300	CTCAGAATGGCTGCGAAAGG	GATTGCTGGTTGGTGGGAAA
	Os01g0628700	TGGTGGACAAGTGGAAGGTTT	ACCTAAACCAGCCGTCCACATA
	Os11g0635500	AGCATGGTGAGGCAGGTGTT	CGGCTCATCAGCACGCTTCAT
	Os08g0508000	CCTCGTGTCTGAACGCCTTCTT	AAACGGCTGTTGGTTATGTTGTCC
Potential FE metabolic-rela ted genes	Os10g0530900	CGCAGGTCATCGTGCAGTACATCG	TCTCCTCCTCCGTCTTGCTCCC
	Os11g0441500	TTCGGCACCCCTCGTCTCCAT	GTGGACTACTAGGAGGGAGACG
	Os03g0757000	GCGGAAGGGCAGCACATCAT	TGGAAGGAGTTGCAGACGGTCAT
	Os06g0220500	GTCGTTGTCGTTGGCGTTGGC	GCTTCAGCGTCGGGTTGATGTG
	Os02g0208300	ACAGCACTGATGGGTGTTAG	TCATGTCTCCCTGAGCATTT
	Os01g0696600	CACGGACCTGCTGCTGATGG	TGACCTGGCCGAAGATGACG
	Os01g0696701	GACCTGGCCGAAGATGACGG	CACGGACCTGCTGCTGATGG
	Os02g0634700	CCTGGGTGTTTCGTCTGTTGG	GTCGCTACATCTTCAGCACTCTAA
	Os01g0332800	GTCAACAATGTTTGCGACTT	TTATCGTGCCTAGTATGGGA

	Os08g0191700	GTGGTATGGCTCCTGTCTTC	TTAGACGCCACTATTAGACC
Reference	<i>UBQ5</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
gene			

Table S2. Summary of rice transcriptome sequencing, assembly, and comparison with the reference genome.

Samples	Clean reads	Mapped Reads	Uniq Mapped Reads	Multiple Mapped Reads	GC Content (%)	%≥Q30
RCK-1	25,092,502	46,334,056 (92.33%)	44,988,139 (89.64%)	1,345,917 (2.68%)	51.98	93.79
RCK-2	23,520,406	43,647,138 (92.79%)	42,467,880 (90.28%)	1,179,258 (2.51%)	51.82	93.48
RCK-3	26,325,799	48,726,936 (92.55%)	47,370,320 (89.97%)	1,356,616 (2.58%)	52.41	93.52
RCK-4	25,490,533	47,292,009 (92.76%)	45,999,229 (90.23%)	1,292,780 (2.54%)	52.22	93.77
RT1-1	25,335,658	46,879,095 (92.52%)	45,542,012 (89.88%)	1,337,083 (2.64%)	52.78	93.81
RT1-2	23,415,165	43,415,648 (92.71%)	42,254,003 (90.23%)	1,161,645 (2.48%)	53.08	93.98
RT1-3	23,906,937	44,183,421 (92.41%)	42,935,155 (89.80%)	1,248,266 (2.61%)	52.13	93.56
RT1-4	25,359,466	46,940,887 (92.55%)	45,588,994 (89.89%)	1,351,893 (2.67%)	51.86	93.54
RT2-1	23,859,190	44,010,959 (92.23%)	42,739,241 (89.57%)	1,271,718 (2.67%)	51.47	93.61
RT2-2	24,290,301	44,837,627 (92.30%)	43,621,690 (89.79%)	1,215,937 (2.50%)	51.83	93.55
RT2-3	21,882,776	40,360,224	39,255,820	1,104,404	52.44	93.5

		(92.22%)	(89.70%)	(2.52%)		
RT2-4	25,841,069	47,853,634	46,521,532	1,332,102	51.79	93.82
		(92.59%)	(90.01%)	(2.58%)		
SCK-1	21,101,964	39,168,519	37,963,537	1,204,982	50.58	93.52
		(92.81%)	(89.95%)	(2.86%)		
SCK-2	20,741,692	38,509,459	37,358,069	1,151,390	50.93	93.91
		(92.83%)	(90.06%)	(2.78%)		
SCK-3	23,246,118	43,023,811	41,752,747	1,271,064	51.83	93.72
		(92.54%)	(89.81%)	(2.73%)		
SCK-4	23,198,848	42,849,585	41,549,271	1,300,314	50.99	93.68
		(92.35%)	(89.55%)	(2.80%)		

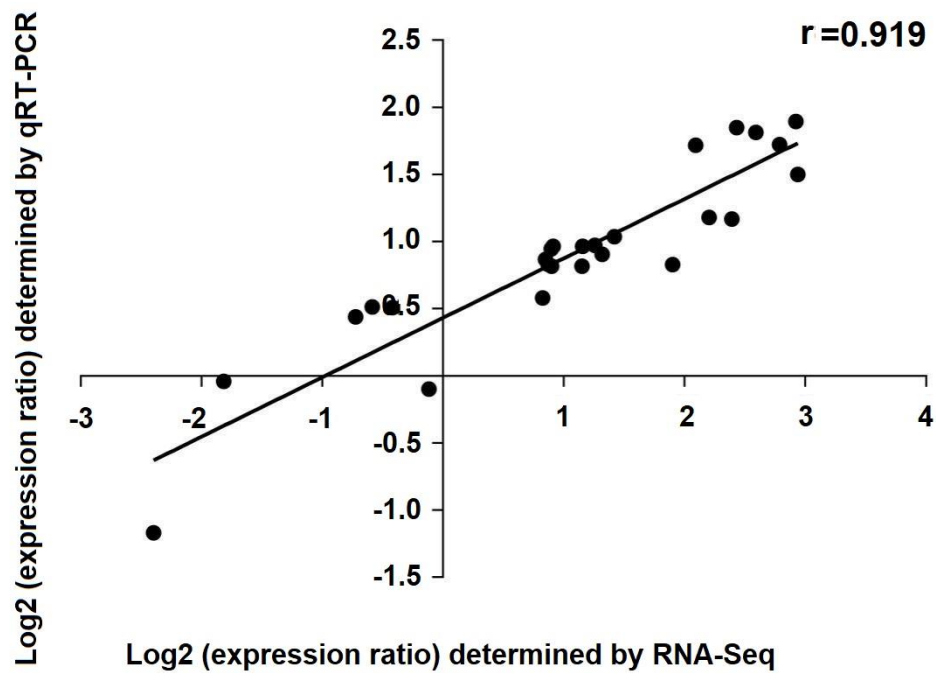


Figure S1. Correlation between qRT-PCR and RNA Seq results. A simple linear regression between the RNA-Seq data and the qRT-PCR validation was shown in scatterplots. The correlation coefficient was expressed in r .