

Supplementary Table S1 The RNA-seq information of samples

Samples	Clean reads	Raw reads	GC Content(%)	Q30(%)	Q20(%)
S1-1	26,106,241	7,795,073,918	43.91%	94.75%	98.22%
S1-2	24,994,294	7,471,209,736	44.05%	94.75%	98.22%
S1-3	19,732,995	5,901,746,064	50.23%	93.25%	97.50%
S2-1	24,297,537	7,261,929,592	44.48%	94.99%	98.33%
S2-2	24,538,852	7,328,067,880	43.97%	94.95%	98.30%
S2-3	24,449,078	7,303,179,402	44.42%	94.72%	98.21%
S3-1	26,142,023	7,802,113,090	44.47%	94.47%	98.12%
S3-2	25,535,308	7,627,852,280	44.57%	94.98%	98.31%
S3-3	23,984,043	7,160,680,780	44.47%	94.93%	98.27%
S4-1	24,625,010	7,356,395,422	44.34%	94.76%	98.22%
S4-2	24,194,907	7,229,370,362	44.24%	94.03%	97.99%
S4-3	27,148,833	8,111,302,590	44.21%	94.84%	98.27%

Supplementary Table S2 The primers information of genes in this study

Gene ID	Forward Primer (5'–3')	Reverse Primer (5'–3')
c186613.graph_c0	ACCTTCACATTTCTCCAC	TGCTTCAGGGTATGCTCAG
c237436.graph_c0	CAGCATCTGTAGTTCGTCC	CTAATGGTGGCACATCCCT
c193003.graph_c0	GTGCCTTGTGATACATTTGG	CCCCTTTACTTGTGTCTTG
c205540.graph_c0	AATCTGGTCTTCCCGCTAC	ACCTTCCATCAACAACCTC
c218337.graph_c0	ACTGTGCCATAGAGCCTGTC	AGTGGGCAACTGAGCGAAT
c222258.graph_c1	GTAATGGATTGGGGCGTAA	AACACCCTGATCTTGATGC
NsActin	GCAAAGACCTCTACGCCAACACG	CTTGATCTTCATCGTGCTGGGTG