Table S1 Summary of Illumina Paired-end sequencing and assembly

Description	Value
High quality reads(Mb)	247.250754
Number of uniques	72249
Average length (bp)	820.43
Max length (bp)	10932
Min length(bp)	201
N50 (bp)	1379

Table S2 Statistics of RNA-sec results

Genes Num	GC percentage	N50	Max length	Min length	Average length
72249	40.46%	1379	10932	201	820.43

Table S3 Statistics of annotation of unigene in four databases

Total Unigenes	Nr	Swissprot	COG	Kegg	annotation unigenes	without annotation unigenes
72249	39475	29684	15051	12436	41035	31214

Table S4 Primer sequences of 20 random genes used in quantitative real-time PCR

Gene	Forward primer (5′→3′)	Reverse primer (5′→3′)
Unigene0039479	GTTGTTACGGAATAAGGC	ATACACTCCCTCGCTTTA
Unigene0008718	AGCCGAGGATAAAGGAAG	TGGTTTGCAGCAAGAAAT
Unigene0015002	AACAGGAAAGGAACAGGGAA	AGGGCAGGCTTCAGGTTT
Unigene0028013	TTACTGGTTGTTGGGACG	CGGACACCTGGAGACATT
Unigene0013621	ATAGCATTTGGGAGTGGA	TTTGGTAATAAAGGGGTG
Unigene0069399	CGACAAGAACCCAGAGGA	GCAGTGGCAGGTGAAGAG
Unigene0006315	AGGCACGATGAAGAAACAA	CGACATCCACCTTCCTAA
Unigene0057696	CATCAACTTCAACCCACCA	AAGGGAATGAGGATTACGG
Unigene0061846	GTCTTGCACCTGCTCCATC	CATCAAATCCAAAGCCTCA
Unigene0007749	ACGGCTTTGGAAGACGAGG	CACGGCAAGGATCTGGGAC
Unigene0010512	TGAGCAGCAACTTCTTGT	TCTCCAATGGGAATCTAC
Unigene0004686	CATTCAGGGTTTACTTGG	TTATGACTACAGGCAGGA
Unigene0001508	GCTCTTGCTTACGCAGTT	CACGGGTATCCTATCTTTATTT
Unigene0035641	GCTCCTCTTCCAATCTGT	GAACCCACTTAATGATAGT
Unigene0029604	ATCTCCATTGTGAGTCTGCAA	AGGGCCATAAGCCTTTCAGT
Unigene0022396	TTCCATCTCCACTTACTATTG	ATCAAGCCCCAAATTAAA
Unigene0003674	AACAACCCTCTTGGAGTC	TTCGCTCTTTCATCCTTC
Unigene0011295	CCAATGCCTAGCCCTAACAA	GGACGCTTCTTCACATCACA
Unigene0021698	GTAGCACCATACCCAAAGT	TGTTAAATGTCGGACCAAG
Unigene0025420	GTATTCGCAACTCAAACT	CTTCTATTAGCCTCCTCT
PhACTIN	TGCTGATCGAATGAGCAAGGAA	GGAGCAACAACCTTAATCTTC