

Table 1. Length distribution of transcripts and unigenes in *L. japonica* transcriptome

Length Range	Transcripts	Unigenes
201-400	133,539 (32.70%)	91,643 (46.79%)
401-800	96,759 (23.69%)	53,265 (27.20%)
801-1200	45,868 (11.23%)	18,007 (9.19%)
1201-2000	56,871 (13.93%)	15,704 (8.02%)
2000+	75,372 (18.46%)	17,231 (8.80%)
Total number	408,409	195,850
Total length	475,591,847	154,102,626
Average length	1164.5	786.84
N50 length	2099	1310

Table 2. Summary statistics of functional annotation for *L. japonica* unigenes in public databases

Annotation Database	Annotated Number	percentage
GO	56,184	66.37%
KEGG	36,592	43.22%
Nr	65,332	77.17%
Pfam	40,282	47.58%
STRING	54,151	63.97%
Swiss-Prot	56,610	66.87%
Total	84,657	100%

Table 3. The primers used for Real time PCR.

Unigene	Name	Forward Primer (5'-3')	Reverse Primer(5'-3')
TRINITY_DN48871_c1_g2	AGL24	TCGTCAAATTTCCACGTT	TTGTGATGCTGAGGTTGCTC
TRINITY_DN49620_c0_g1	SOC1	ATCCAACCCTTGGAGCTCTT	TGAACAGCCATGTCTTGAGC
TRINITY_DN82380_c0_g1	FLC	GAGATCAAGGCCATCAAGGA	ATGACGGCGACGTCTACTG
TRINITY_DN47340_c3_g1	AP1	CCTAATTCGTCCCATTCTCT	AGTGGCTCGAGTGTGAGGTC
TRINITY_DN43630_c7_g4	MVK	TTCTGGTGAGCATGATTTGG	CTCAGCTTTCCACCGATAA
TRINITY_DN48885_c3_g1	MVD	CCCATTCTGCGATTCTCT	TATCCACCCACACATTTGGA
TRINITY_DN52905_c2_g3	PSY	ACCCTTCCTCTTCTGGCACT	TGTTTGTGCCTTGCTTCTTG
TRINITY_DN50419_c0_g1	PAL	GAGAGCTGCACCCATCTAGG	CAACCAGGACTTGCCTTAGC
TRINITY_DN52586_c2_g4	IDS	TTGGATTGACAGCGAGAAGA	CAAGGGAGAGAGGTGCAATC
TRINITY_DN52168_c3_g2	HDS	TGGTGTCTCGAATTGGACTG	AATGGAGCAAGCTACCGATG
TRINITY_DN41892_c1_g1	ANS	GTTCAGGAGGTGCCAAGAAG	GCCCCAAACACAACCTCTAA
TRINITY_DN51090_c5_g2	CHS	GAAGGTCCACGAAAGTGAC	ATGTACCAGCAAGGCTGCTT
TRINITY_DN51352_c1_g7	Actin7	GCCGTGCTTTCTCTATACGC	CATTAGGGCATCCGTGAGAT