

Table S1. Primers of random transcripts used in this study

Gene ID	Forward primer	Reverse primer
β -actin	GCATGAAGATCAAGGTGGTG	CATCTGCTGGAAGGTGCTAA
Unigene_000586	TCCCGCCATCTTGTTCCTGTCT	GCAACCACGGCTTCTTCCCTT
Unigene_004587	TCGGCATTGATCCTCGTAGC	GCCTGAATGGCCTTAGTGGT
Unigene_006313	CAGGAACGGTAGGCCACAAA	TGGCTCTGTGAATGTTGCGA
Unigene_006706	AGGATCTGTTGTCGAGGCCA	GCTTCACCCACTATATGCCTGTT
Unigene_006918	AGCCACTTCAACCATGTCGT	GAGTCCAGCAGCATCTCGTT
Unigene_007109	ACCACCCGGAGTTCAATCAC	TGTGCCCAACAAGATCCACAT
Unigene_007147	TTCGTCACCTTGACGGCAA	CCGGCTTTGGTGCAGTATTCTTA
Unigene_007785	AGTGGATATTACTCAGGCTTTGC	TGACGGTGAGGGAGTGCAT
Unigene_008442	AGCTCAAGTGCAAGCTCCAT	CATCACCACATCAAGTGCCTATT
Unigene_008551	GCAGTCCTACCACTTCGTTG	TCCTGCCCTTTCATGTGTCTC
Unigene_009084	ATCTACCACTTGCTTGCCC	CCCACCACATTTCGTCTTGATG
Unigene_009354	GACATCCTCGCTCAGACCAC	TTGCGTCCAAGTCTCACCTTG
Unigene_009369	ATAACCAACAAGGGGCTCGG	AGCAACCCGACTGCGTT
Unigene_010800	AGAACCGCTTCCTTCTCTGT	CAATGTGTCCTGGTAGCCGT
Unigene_047133	TTGAGACCGCCACACACTAC	GCTTCCTCCGACTTACAGCA
Unigene_050704	GCTTGGAAGGAGGGTGTCATGT	GGGCAGTAGCAGTTGGAGGGTA
Unigene_093648	ACCAACTCAGTCCCTCTTGG	TCGTATCTGCTCTCCACCTCT
Unigene_098130	GGAAGAGAGGGAGCGCATTT	TCGCCTAGCTCCGTAGATGA
Unigene_098084	GGTGCCGAAAGGGGTATTCA	AAGCCAATCCAGGTATCGCC
Unigene_098284	CACTTCGCCAACCTCACCAACT	ACTGCTTCTCCTCCACCCACTT
Unigene_093116	TGCTTCAGTCACCTTGCCCTCT	AACTTTCATTCTGCCCCGTCC

Table S2. Summary of de novo transcriptome assembly

Length Range	All Unigenes	T01_T02 Unigenes	T03_T04 Unigenes
200-300bp	31,911(31.85%)	37,482(41.64%)	29,040(38.05%)
300-500bp	25,894(25.85%)	22,954(25.50%)	19,821(25.97%)
500-1000bp	19,126(19.09%)	14,157(15.73%)	12,408(16.26%)
1000-2000bp	12,738(12.72%)	9,085(10.09%)	8,563(11.22%)
>2000bp	10,508(10.49%)	6,346(7.05%)	6,488(8.50%)
Total Number	100,177	90,024	76,320
Total Length(bp)	82,311,264	60,025,175	55,500,233
N50 Length(bp)	1,555	1,182	1,377
Mean Length(bp)	821.66	666.77	727.20