Table S1. Primers for qPCR amplification of differentially expressed genes.

Code	Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')
1	Glyma.12G063400	AGGAGCACCCAGTTCTGCTA	TATGGCTGACACCATCTCCA
2	Glyma.08G230400	CGAGTCGATCAAACACTGGA	GCCATACGGAGGATCAACAT
3	Glyma.17G260600	AGCCAAGAGCTGAAACTCCA	AGGGGCTCCCAAGTATCAGT
4	Glyma.09G185500	TCGCAAGGTTGACGAGTATG	CCGTAGGCATTGGTGGTATC
5	Glyma.08G171100	TTGGATCCCCAATATGCACT	CTGCAAGACGCAGGTATTCA
6	Glyma.08G137000	CATCGCCGTAACCGTTAGAT	CCCATGCTTCGAGGTTTTTA
7	Glyma.05G218100	CGGACATGGACGAGGTTACT	ACTCCTTGCCCTTGGAAACT
8	Glyma.07G115400	AATAATCCAGCGTTGGTTGC	CTGGAAACACTGTGGCAAGA
9	Glyma.06G297600	ATTGTGGAGGCCTTGAAAGA	GGACCCCAGCAGCTTAAGTA
10	Glyma.13G098600	CAACTCCACCTCCGATGATT	TTTGGGGGTAACTGAACTCG
11	Glyma.07G202300	AGCATGGCCCCTTATTCTCT	AGCTTCCTCACGAACTTCCA
12	Glyma.17G260500	AGCCTCAGTTGGCCCTTAAT	CCTCTGCGATATGCTTAGCC
13	Glyma.16G165800	TTGGTGTTGGAAGGGTTAGC	CCCATCTGGAGTGGATGACT
14	Glyma.20G204500	TTGGTATGTGGTGCAGCATT	CCAACCCAATCGTTCTCACT
15	Glyma.10G147700	GATTGCGTCTTGGAGAAAGC	CTTCCAAGGAAAGCCCTCTT
16	Glyma.10G184600	CCGAGTGCAAAGGTAAGAGC	ACCCAAACCCAAACCCTATC
17	Glyma.10G050800	TGGAAGCCTTGATTCCAAAC	CCACGGTGGGGTATAATCTG
18	Glyma.15G174200	GGCTTCCACTTCTGCAGTTT	AGGCCCTCACTTGAAACCTT
19	Glyma.04G255400	TTGGGGATGAGGATCAAGAG	ACGGCTCCTCCTTTGAATTT
20	Glyma.07G007000	GCCTTCGCCTTGTGATAGAG	ACCATGACCCTTCTCCACAG
21	Glyma.12G198100	CAAGGACATGGGTGTGTGAG	ATGAATATGCCTGGCAAAGG
22	Glyma.14G048000	GAAGTCACGAGAAGGCCAAG	AGCGGAGTTTGCAGTGACTT
23	Glyma.16G210600	CGATGTGTTCCTCAGCTTCA	GGAATCTTGAATTGCCTCCA
24	Glyma.05G150400	AGCCCCAGCACATCATATTC	GGTGCTTTGGACCAATCAGT
25	Glyma.15G026400	CGTATGCAACTCCTGGGTTT	TTATCTGGATCGCCCAAGTC
26	Tubulin	GGAGTTCACAGAGGCAGAG	CACTTACGCATCACATAGCA

Table S2. Data assembly for transcriptome sequencing.

Sample name	Clean reads	Clean bases/Gb	GC %	Uniquely mapped reads	Total mapped rate	Unique mapped rate	Q30/%
Z1-1	51646008	7.24	45.03	43365372	93.89%	83.96%	93.44
Z1-2	56687883	8.23	45.10	50904628	94.74%	89.79%	93.28
Z1-3	50855848	7.29	44.79	44437578	94.69%	87.37%	93.37
Z2-1	48507535	6.99	44.79	41507757	91.75%	85.56%	93.50
Z2-2	44496599	6.42	44.96	37559769	90.55%	84.41%	93.74
Z2-3	49045426	7.12	44.78	40564086	88.01%	82.70%	93.85
Z3-1	51884179	7.08	45.47	41566688	96.16%	80.11%	93.68
Z3-2	42501763	5.89	45.57	34883920	95.62%	82.07%	93.78
Z3-3	47217908	6.47	45.69	37567100	95.18%	79.56%	93.54
Z4-1	52894437	7.63	44.74	46647255	94.13%	88.18%	94.01
Z4-2	55420552	7.99	44.87	49144380	94.72%	88.67%	93.35
Z4-3	52899465	7.64	44.66	46876108	94.36%	88.61%	93.68
Average	50338134	7.17	45.04	42918720	93.65%	85.08%	93.60

Note: Q30 means percentage of quality values of bases involved clean reads is equal or greater than 30.