

**Table S1.** RNA sequencing statistics. CK: normal watering. CK-1, CK-2, CK-3: three replications of normal watering. T: drought stress. T-1, T-2, T-3: three replications of drought stress. Raw reads (Rr): raw sequencing data. Clean reads (Cr): number of reads after culling low-quality reads, adaptors and ambiguous reads. Clean bases (Cb): number of sequenced sequences multiplied by its length, and converted to units of G. Error rate (Er): base error rate. Q20 and Q30: the ratio of bases with *Phred*-value > 20 and *Phred*-value 30 to the total number of bases, respectively. GC content: G and C ratio considering the all bases.

Group	Rr	Cr	Cb (Gb)	Er (%)	Q20 (%)	Q30 (%)	GC (%)
CK-1	54,230,138	53,229,668	7.98	0.03	97.32	92.6	46.24
CK-2	48,422,264	47,233,114	7.08	0.03	96.64	91.16	46.00
CK-3	53,158,862	52,212,380	7.83	0.03	97.16	92.26	45.86
T-1	50,790,984	49,932,386	7.49	0.03	97.3	92.6	45.78
T-2	55,499,302	54,787,806	8.22	0.03	97.36	92.69	45.8
T-3	64,926,978	63,723,460	9.56	0.03	97.66	93.35	45.62

**Table S2.** Lengths of transcripts and unigenes. N50/N90: The spliced transcripts were arranged from long to short according to length, then these spliced transcripts were accumulated until more than 50%/90% of the total length of the spliced transcripts , which was N50/N90.

	Transcripts	Unigenes
Minimum length	201	201
Mean length	966	1107
Median length	615	789
Maximum length	26,379	26,379
N50	1554	1628
N90	398	503
Total nucleotides	320,982,757	30,6097,014
Total number	332,420	276,423