

**Table S1.** Quality assessment of sequencing data of *Eleusine indica* (L.) Gaertn.

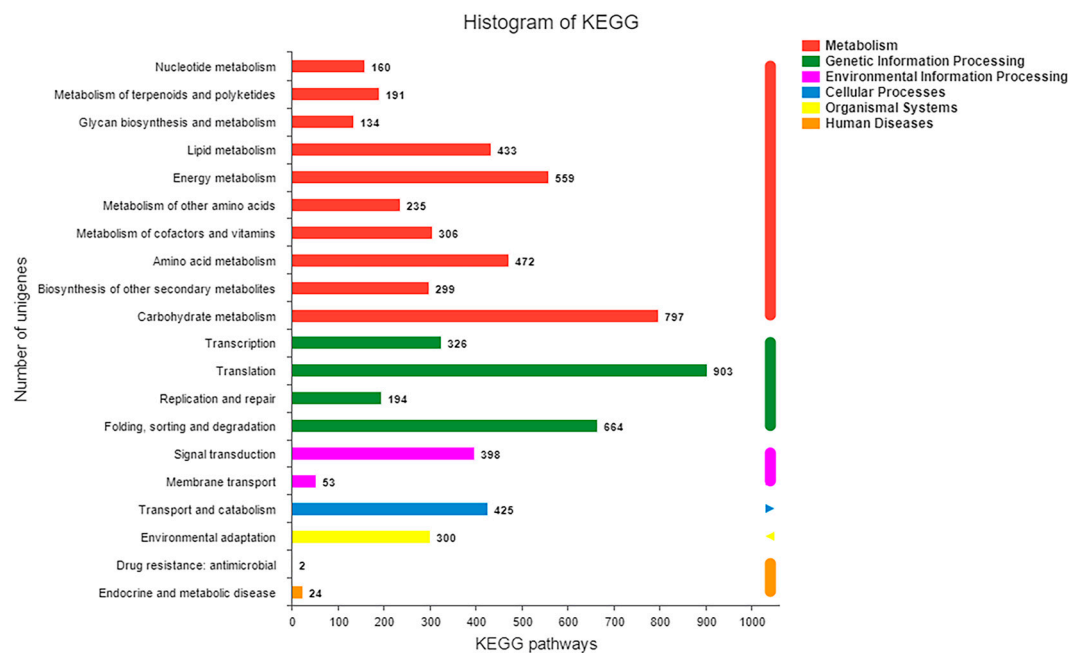
Sample	Raw reads	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
CK_R1_1	49273852	48742578	7.26G	0.0245	98.15	94.75	55.51
CK_R1_2	57156216	56682684	8.43G	0.0243	98.26	94.94	56.64
CK_R1_3	55572836	55093634	8.24G	0.0241	98.33	95.12	56.89
CK_R2_1	57667286	57193890	8.51G	0.0242	98.3	95.02	55.95
CK_R2_2	51420504	51009050	7.61G	0.0243	98.25	94.86	56.39
CK_R2_3	55534526	55077946	8.20G	0.024	98.37	95.19	56.65
CK_S_1	53870186	53394964	7.98G	0.0241	98.33	95.15	56.97
CK_S_2	50375378	50002742	7.46G	0.024	98.37	95.21	57.24
CK_S_3	49032528	48661402	7.26G	0.0241	98.36	95.15	55.2
T_R1_1	58414340	57972622	8.64G	0.0241	98.34	95.11	56.43
T_R1_2	56729902	56308918	8.37G	0.0241	98.32	95.07	55.56
T_R1_3	58332378	57808062	8.62G	0.0244	98.22	94.8	55.54
T_R2_1	58248166	57734872	8.60G	0.0244	98.23	94.81	55.59
T_R2_2	55698446	55273330	8.22G	0.0243	98.24	94.85	55.89
T_R2_3	52302004	51757640	7.69G	0.0243	98.25	94.88	54.35
T_S_1	48742902	48312828	7.20G	0.0243	98.26	94.9	55.08
T_S_2	55139630	54707748	8.15G	0.0243	98.28	94.94	54.54
T_S_3	56623568	56180024	8.37G	0.0242	98.32	95.04	55.29

**Table S2.** Transcriptional splicing data statistics

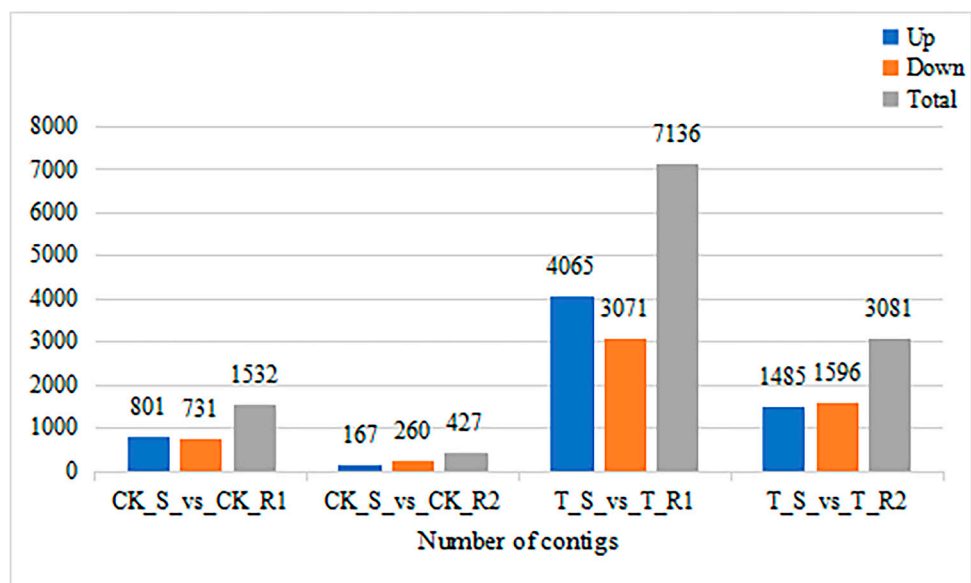
Assembly quality parameters	Transcripts	Unigenes
200-500bp	12998	14928
500-1kbp	11709	17032
1k-2kbp	9739	21979
>2kbp	10843	25179
Maximum length	36898	36898
Minimum length	201	201
Average length	1406.78	1683.30
N50 value	2318	2454
N90 value	2978	2410
Total nucleotides	63711510	133179639

**Table S3.** Primers for fluorescent quantitative of *Eleusine indica* (L.) Gaertn.

Primer	Sequence (5'—3')
<i>ABCB2</i> -F	GGCGTGGAGTTCCGTTACCC
<i>ABCB2</i> -R	CCCGATCATCATAAGCCTTGCA
<i>ABCC4</i> -F	GGGTTGATGTGGAGGTGAGGA
<i>ABCC4</i> -R	ACAAGCACGTATGACTTCGGAATAT
<i>ABCG50</i> -F	ACTGCTCAGGTTATACTTGCTAC
<i>ABCG50</i> -R	TCGGAAGAATACGGACATTGC
<i>ABCG11</i> -F	GGAGGAGCAGTGGTGAAGAA
<i>ABCG11</i> -R	CGAACCGCAGCCAGTAGTA
<i>ABCA</i> -F	ACAAGCACGTATGACTTCGGAATAT
<i>ABCA</i> -R	GCGACACTTAGCCTTCTCTTC
<i>AKR4C10</i> -F	ACCGCAACGAGAAGGAGGTAGGA
<i>AKR4C10</i> -R	CGGGATGTCGGATGGGATGA
<i>AKR2</i> -F	ATATGCCTAGACTTCGACCAGA
<i>AKR2</i> -R	TCTCAGAATCCCACAAGGTG
<i>CYP88</i> -F	AAACAGGTGCTGATGGATGACGA
<i>CYP88</i> -R	GATGAAGCCGAGGTAGGTGGTG
<i>CYP89</i> -F	AGACGACAACAACGCTGGTGGAG
<i>CYP89</i> -R	CGAACGGCATCATCTTGATCTCC
<i>GST1</i> -F	TGTCTGCTTGGCTAAATGT
<i>GST1</i> -R	CTATCCTCAATCCTGGTCAC



**Figure. S1** Classification of KEGG function annotation *Eleusine indica*. The y-axis lists the various KEGG pathways. The x-axis indicates the number of genes. According to participation in KEGG pathways, unigenes were classified into six categories: Metabolism, Genetic Information Processing, Environmental Information Processing, Cellular Process, Organismal Systems and Human Diseases.



**Figure. S2** The number of DEGS between the different groups