

Supplementary Table 1. Summary of Illumina RNA sequencing results for twenty-four samples isolated from maize leaves

Samples ¹	Raw reads ²	Clean reads ³	Total mapped ⁴	Uniquely mapped ⁵	Q30(%) ⁶	GC content(%) ⁷
NDC1	48035096	47610098	43143631(90.62%)	41372616(86.90%)	96.33	55.80
NDC2	54486068	54166538	50258591(92.79%)	48336953(89.24%)	96.56	57.05
NDC3	44542680	44085504	38332401(86.95%)	36372979(82.51%)	96.50	54.60
NDC4	42548972	41544188	35311007(85.00%)	30342991(73.04%)	94.50	55.95
NDC5	40734384	39783580	35423813(89.04%)	33861471(85.11%)	94.46	55.80
NDC6	41127584	40153870	35629542(88.73%)	34012429(84.71%)	94.51	55.30
NDCA	59925726	59580188	55088277(92.46%)	51854517(87.03%)	96.69	58.59
NDCB	73048054	72636578	67511922(92.94%)	64399057(88.66%)	96.71	57.78
NDCC	51946220	51558264	47579146(92.28%)	45066907(87.41%)	96.30	58.68
NDCa	55342254	54963524	50467490(91.82%)	48503647(88.25%)	96.44	57.27
NDCb	59161562	58848272	54571986(92.73%)	52363482(88.98%)	96.75	56.40
NDCc	58430550	58068856	53792336(92.64%)	51774291(89.16%)	96.62	56.59
NDD1	57502078	57188372	53180180(92.99%)	51087820(89.33%)	96.62	56.84
NDD2	60217732	59870224	55618716(92.90%)	53420048(89.23%)	96.48	56.63
NDD3	54959348	54580992	49427404(90.56%)	47440596(86.92%)	96.56	56.35
NDD4	27793124	27549536	25314496(91.89%)	24277425(88.12%)	95.54	55.15
NDD5	47563710	46494702	41046147(88.28%)	38920912(83.71%)	94.64	55.33
NDD6	23219294	23029648	21253143(92.29%)	20432633(88.72%)	96.15	55.61
NDDA	56338684	55977752	52008434(92.91%)	49705362(88.79%)	96.14	58.20
NDDb	59760736	59414606	55036131(92.63%)	52216093(87.88%)	96.63	57.84
NDDC	65312034	64915948	60089140(92.56%)	56803851(87.5%)	96.68	58.48
NDDa	54746454	54424602	50537680(92.86%)	48566518(89.24%)	96.63	57.66
NDDb	59668746	59322012	53685546(90.50%)	51419976(86.68%)	96.26	56.81
NDDc	56185708	55801650	51513215(92.31%)	49344332(88.43%)	96.45	56.89

¹Samples, sample name of drought-tolerant genotype leaf tissues collected from four stages both of control and drought treatment; ²Raw reads, the reads amount before filtering; ³Clean reads, the reads amount after filtering; ⁴Total mapped:the percentage of mapped clean reads; ⁵Uniquely reads: the percentage of reads that map to only one location of the reference; ⁶Q30, the Q30 value for the raw bases/Calculate the percentage of bases that have greater than 30 Phred values; ⁷GC content: the ratio of GC bases for the raw bases.

Supplementary Table 2. Summary of the functional annotation of assembled genes

Database categories¹	Gene Number²	Percentage³
GO	133525	69.41%
KEGG	82758	43.02%
COG	169691	88.21%
NR	179093	93.10%
Swiss-Prot	137849	71.66%
All	192366	100%

¹Annotated database, the database used for functional annotation; ²Gene number, the number of genes predicted by the corresponding database's annotation information; ³ Percentage, the percentage of annotated gene number to the total genes. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; COG, clusters of orthologous groups ; NR, non-redundant protein sequence; Swiss-Prot, a manually annotated protein sequence database; All, the total of differentially expressed genes in the data set/comparison group.