De novo Transcriptome Sequencing of MeJA-Induced *Taraxacum koksaghyz Rodin* to Identify Genes Related to Rubber Formation

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Supplementary Fig S5. KOG function classification of the transcriptome from 26 terms. The Y-axis showed the percentage genes accounted for.

Supplementary Fig S6. DEGs statistics between 0 h and 6h-treated lines (A) and between 0 h and 24 h-treated lines (B). The color red means genes up-regulated and the green means genes down-regulated and the color blue means the expression level of genes showed no obvious change.

Supplementary Fig S7. Enriced terms of gene ontology for the DEGs between the 0 h and 6 h-treated line (A) and between the 0 h and 24 h-treated line (B). Distribution of differential expressed genes in 0 h vs 6h-treated line and 0 h vs 24h-treated line from the categories of biological process (BP) and molecular function (MF); The color red means up-regulated and the blue means down-regulated terms. The Y-axis showed the number of genes for different terms.

Supplementary Fig S8A. The identification of *ERF* transgenic TKS seedlings by genomic pcr. M means DNA Mark Ⅲ; 1 means the positive control and the 2 means the WT, 3-13 means different transgenic seedlings.

Supplementary Fig S8B. The identification of *DREB* transgenic TKS seedlings by genomic pcr. M means DNA Marker Ⅲ and number 1-8 means different transgenic seedlings, 9 means the positive control.
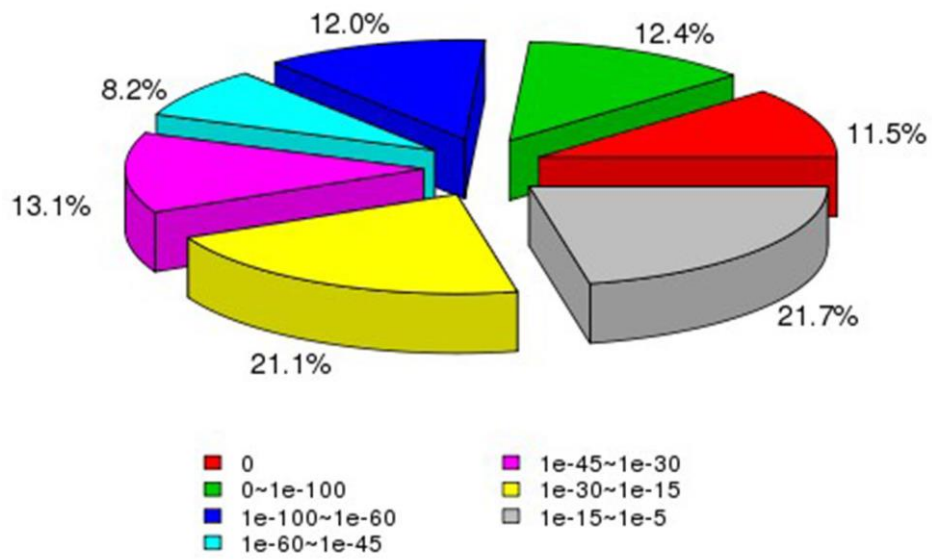
Supplementary Table:

Supplementary Table S1. Primers of 12 selected genes designed by Primer Premier 5.0 used for qPCR analysis
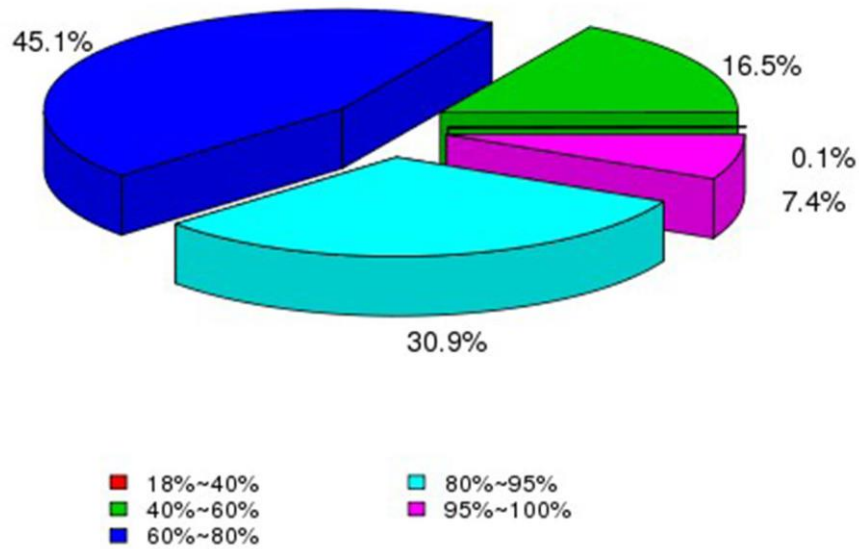
Species classification
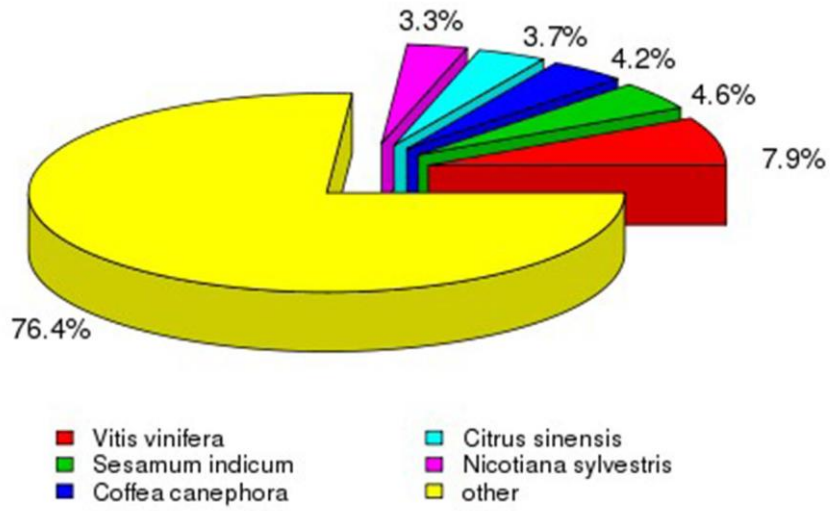
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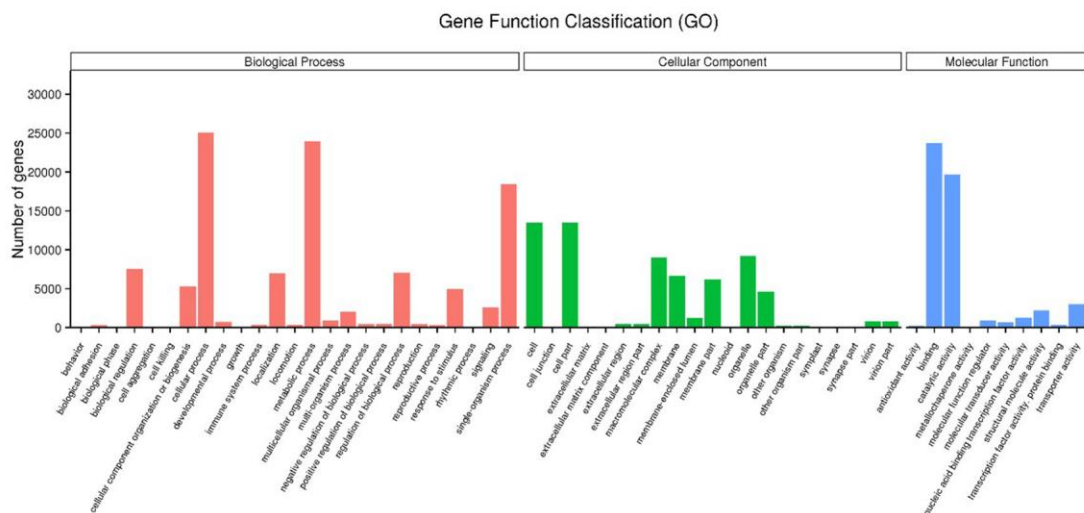
E-value Distribution

Legend:
- 0
- 0~1e-100
- 1e-100~1e-60
- 1e-60~1e-45
- 1e-45~1e-30
- 1e-30~1e-15
- 1e-15~1e-5

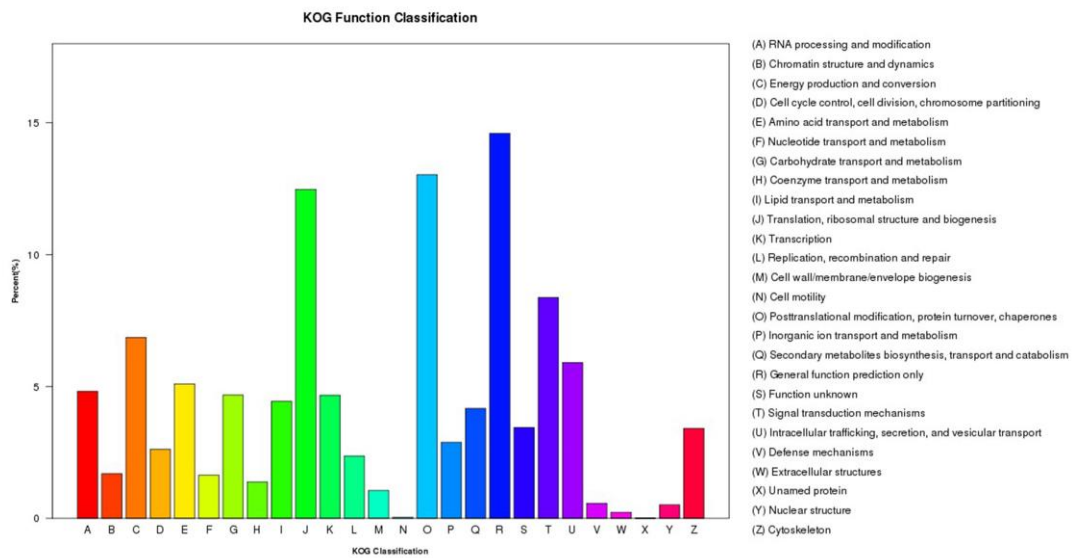**Supplementary Fig S2.** E-value distribution of NR database annotation of the transcriptome

Similarity Distribution

Supplementary Fig S3. Similarity distribution of NR database annotation of the transcriptome
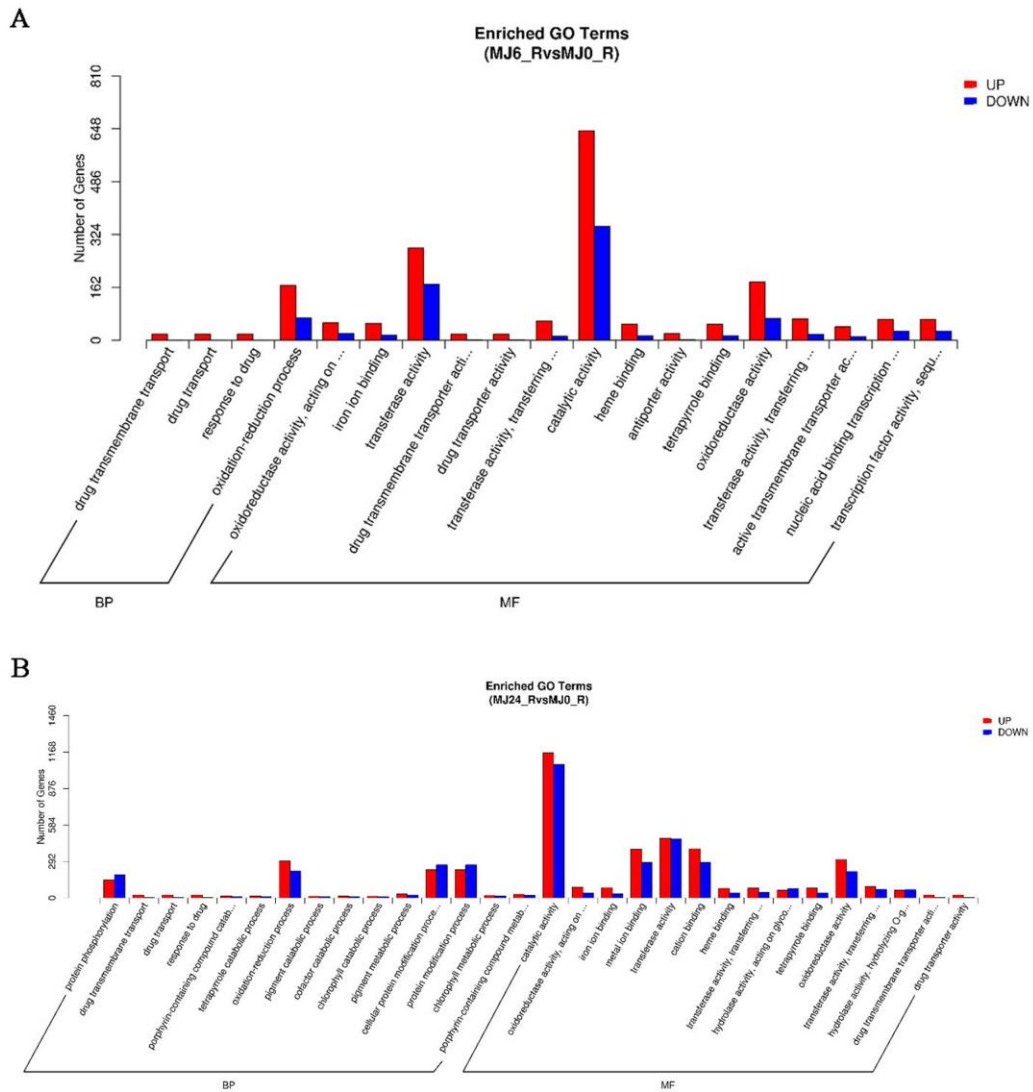

Gene Function Classification (GO)

Supplementary Fig S4. Gene function classification of GO dantabase of the transcriptome from three categories of Biological Process, Cellular Component and Molecular Function. The X-axis showed the concrete terms of three categories and the Y-axis showed the number of genes in different terms.

KOG Function Classification

(A) RNA processing and modification
(B) Chromatin structure and dynamics
(C) Energy production and conversion
(D) Cell cycle control, cell division, chromosome partitioning
(E) Amino acid transport and metabolism
(F) Nucleotide transport and metabolism
(G) Carbohydrate transport and metabolism
(H) Coenzyme transport and metabolism
(I) Lipid transport and metabolism
(J) Translation, ribosomal structure and biogenesis
(K) Transcription
(L) Replication, recombination and repair
(M) Cell wall/membrane/envelope biogenesis
(N) Cell motility
(O) Posttranslational modification, protein turnover, chaperones
(P) Inorganic ion transport and metabolism
(Q) Secondary metabolites biosynthesis, transport and catabolism
(R) General function prediction only
(S) Function unknown
(T) Signal transduction mechanisms
(U) Intracellular trafficking, secretion, and vesicular transport
(V) Defense mechanisms
(W) Extracellular structures
(X) Unamed protein
(Y) Nuclear structure
(Z) Cytoskeleton

Supplementary Fig S5. KOG function classification of the transcriptome from 26 terms. The Y-axis showed the percentage genes accounted for.
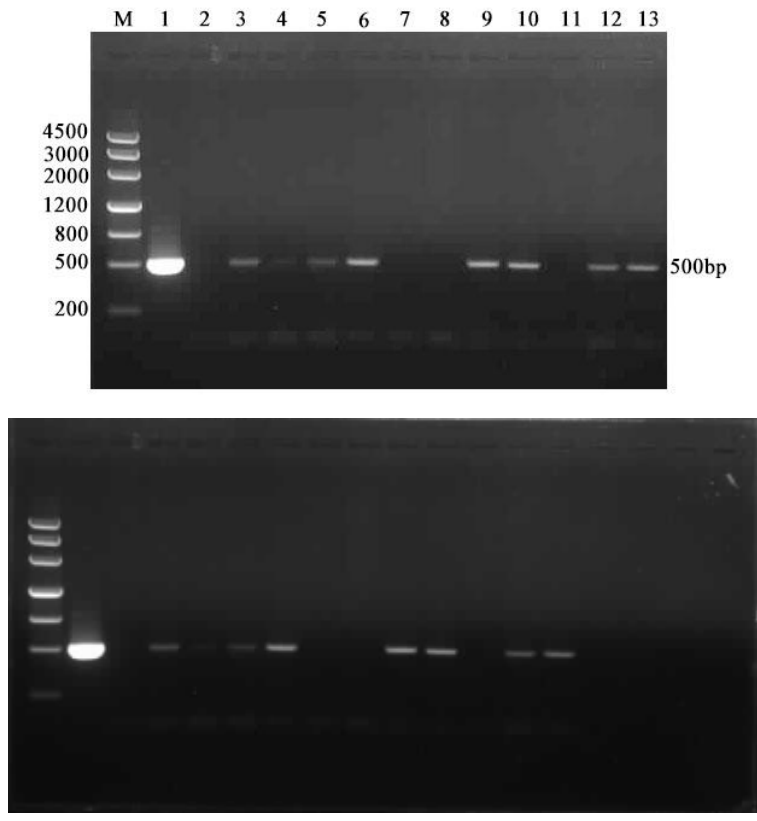
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Supplementary Fig S7. Enriced terms of gene ontology for the DEGs between the 0 h and 6 h-treated line (A) and between the 0 h and 24 h-treated line (B). Distribution of differential expressed genes in 0 h vs 6h-treated line and 0 h vs 24h-treated line from the categories of biological process (BP) and molecular function (MF); The color red means up-regulated and the blue means down-regulated terms. The Y-axis showed the number of genes for different terms.

(The original gel image)

Supplementary Fig S8A. The identification of *ERF* transgenic TKS seedlings by genomic pcr. M means DNA Mark Ⅲ; 1 means the positive control and the 2 means the WT, 3-13 means different transgenic seedlings. The gel image acquisition was achieved by Gel Doc XR System (Bio-rad: Intas Gel Hood) and processed with Photoshop (label and clip).
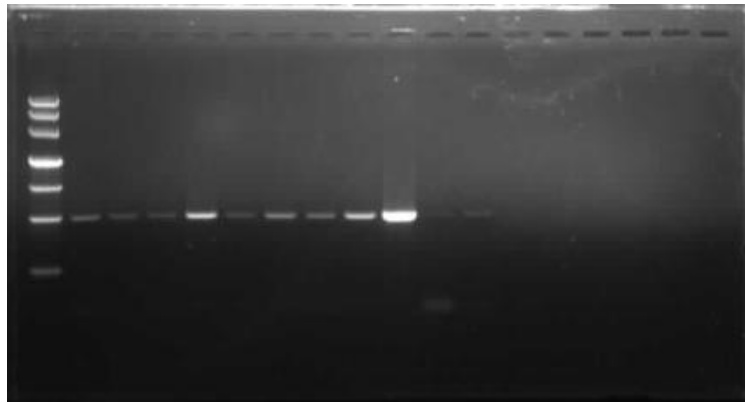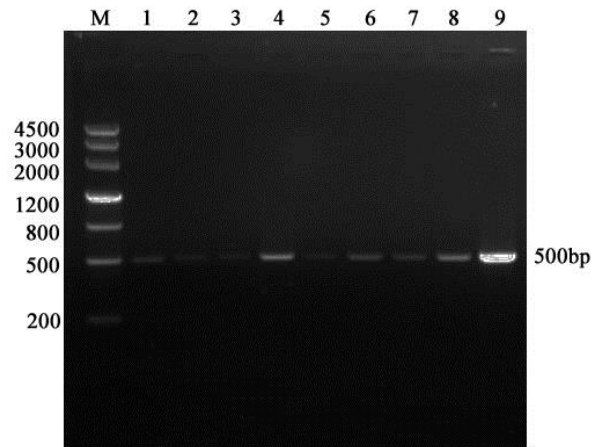
(The original gel image)

Supplementary Fig S8B. The identification of *DREB* transgenic TKS seedlings by Genomic PCR. M means DNA Marker Ⅲ and number 1-8 means different transgenic seedlings, 9 means the positive control. The gel image acquisition was achieved by Gel Doc XR System (Bio-rad: Intas Gel Hood) and processed with Photoshop (label and clip).

Supplementary Table S1. Primers of 12 selected genes designed by Primer Premier 5.0 used for qPCR analysis

Primers used for quantitative PCR analysis

Gene	Unigene ID	Forward Primer	Reverse Promer
AOS	c39329_g1	CTACGGCGAAGGTAAGGTGAC	CTGGAACCCGAATAACATCTCAC
AOC	c44998_g3	ACGGGCAGATAGCAGTCCAG	ACGGAGGAACAGGGGTGACT
LOX	c53508_g1	ATTCTCCGCCAAGCGACCAC	CAACGCCGCCAACACCTA
OPR	c49640_g1	CAGACAAAGTCGGCGTCAGAAT	TCAACTCTGCCACTTCCTCTTCA
MYC2	c46426_g2	GGCGTCGTCATCTGCTTCAA	CCATCTCCCCACCCTAACAC
DXS	c49476_g1	TGCGGGCTACTTGGATTCG	GAACCACTAATCATTCCACGAGC
ISPH	c44729_g5	TTACCTGCTTTCGGTGCTGC	CGGTTGCCACTGTCTCCTCA
HMGR	c50260_g1	TGTCTTCTTCACCGTATTCTTCTCG	CCGAAGAACCCGAGAAGGTAGAT
FPS	c48867_g1	CCTTCGAGTTCGATGACGATTC	TCCGCCTTTAAGCAACTGGTAG
IDI	c43940_g2	CTCTTCCTTCGCTGGTCTTACTCTC	CCCAACGACATTGTCATTTTCATCC
GGPS	c42408_g1	CGGTGACAACTCCAGCAAGATACT	CCTTTCAATCTCCTCGTGGCT
REF/SRPP	c41870_g1	TAATGCCTCCTGCGGTGAAAGAC	AGAGTTTTCCAAGCCGAAGAAGCGT