

Supplementary information for following article

The ERF transcription factor family in cassava: genome-wide characterization and expression analyses against drought stress

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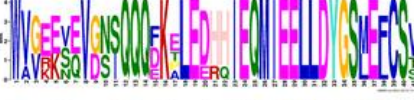
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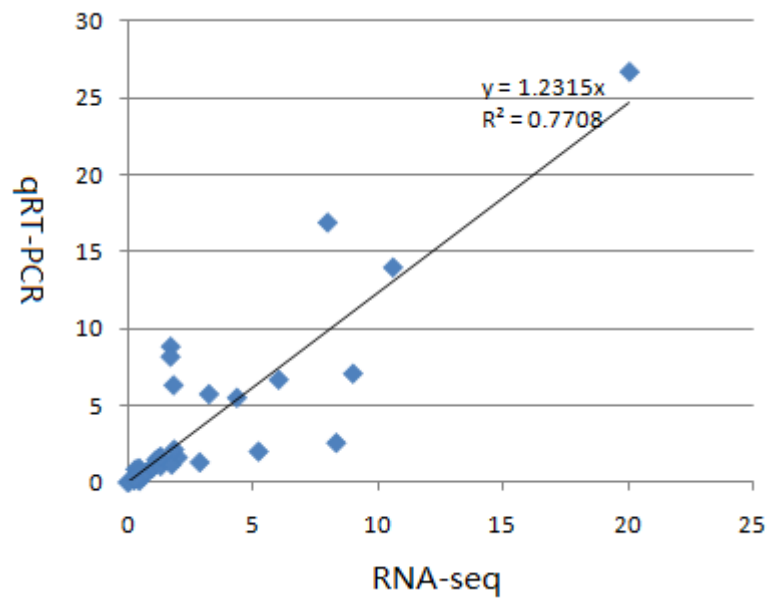
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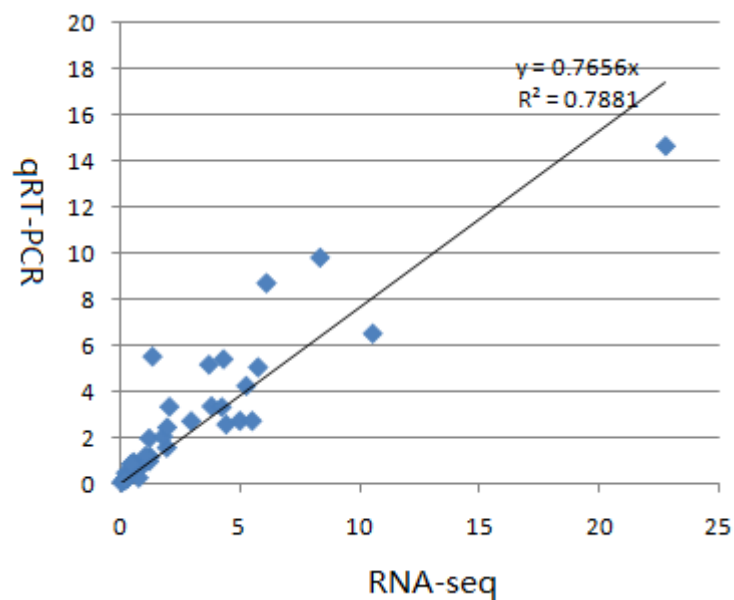
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Motif 1	• 3.0e-2421 • 147 sites	
Motif 2	• 3.1e-1227 • 145 sites	
Motif 3	• 1.4e-859 • 141 sites	
Motif 4	• 3.3e-629 • 143 sites	
Motif 5	• 2.4e-181 • 29 sites	
Motif 6	• 5.5e-118 • 11 sites	
Motif 7	• 1.6e-100 • 6 sites	
Motif 8	• 2.6e-094 • 17 sites	
Motif 9	• 4.2e-087 • 5 sites	
Motif 10	• 4.8e-074 • 4 sites	
Motif 11	• 1.3e-107 • 5 sites	
Motif 12	• 1.6e-071 • 14 sites	

Supplementary Figure S1. The conserved motifs of cassava ERFs identified by MEME database with the complete amino acid sequences of cassava ERFs. 12 conserved motifs sharing high E-value were adopted.

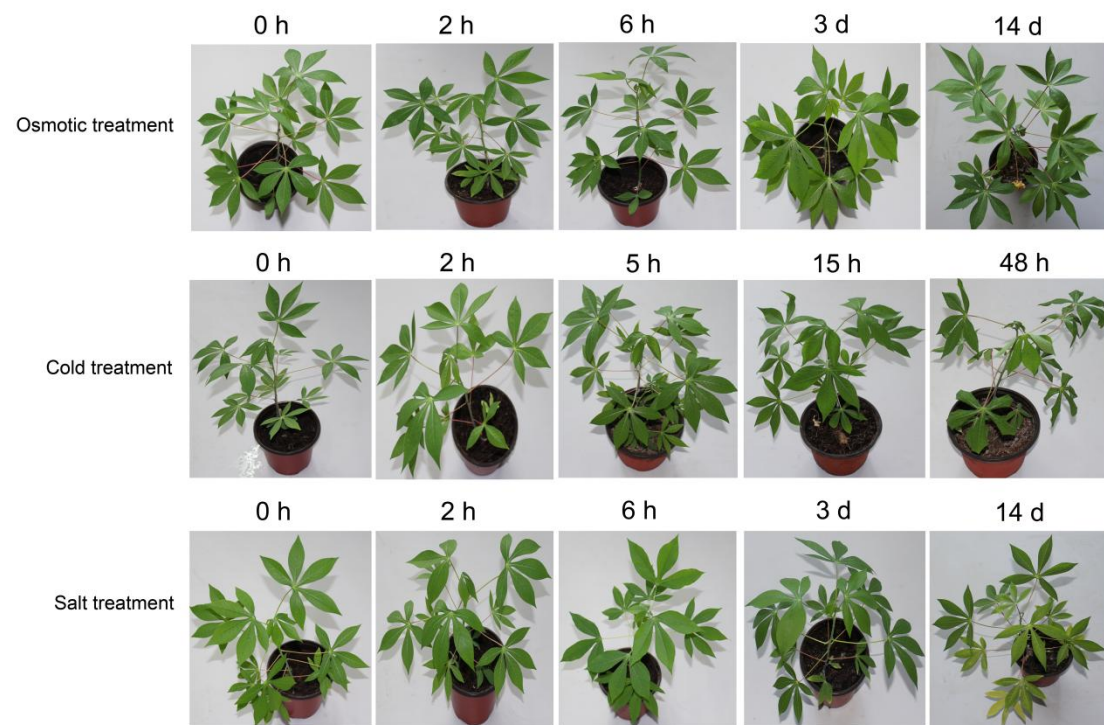


Supplementary Figure S2. Validation of the expression data in different organs of Arg7 and W14 by qRT-PCR analysis. Seven genes were randomly selected in the RNA-seq data for qRT-PCR analysis. Value of each RNA-seq expression data was plotted against that from qRT-PCR analysis.



Supplementary Figure S3. Validation of the expression data related to drought treatment in Arg7, SC124, and W14 by qRT-PCR analysis. Seven genes were randomly selected in the RNA-seq data for qRT-PCR analysis. Value of each

RNA-seq expression data was plotted against that from qRT-PCR analysis.



Supplementary Figure S4. Phenotypic changes of cassava treated with various stresses for different time. Time point of sampling was determined based on a moderate level of stress.