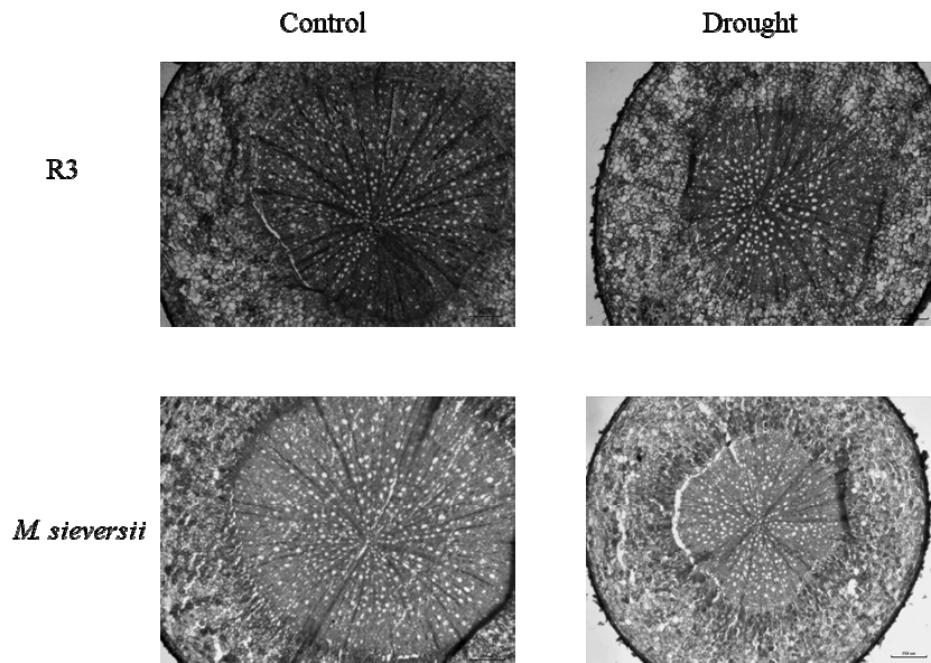


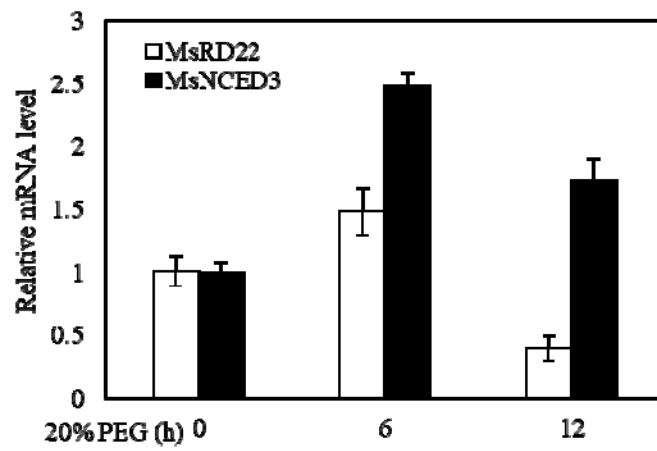
Appendix A Primers used in this study

MsMYB124 qPCR F	ACATTGCAGGCAGCCTGATTATA	qRT-PCR analysis
MsMYB124 qPCR R	GTAACCTTAATAGGAGAATTGAACTCTATAC	
MsMYB88 qPCR F	GCAGCCAGATCTATTCGACGACTCT	qRT-PCR analysis
MsMYB88 qPCR R	ACAACCTTAAAAGGAGAAGTGAACCTCGG	
MDP0000248981-qPCR F	TCAGCTACTCCGCCGAAAAAG	qPCR analysis for RNA-seq results
MDP0000248981-qPCR R	CTCCAAGGCTCAGTCCCAGAAGT	
MDP0000251424-qPCR F	GTCCTCGGAAGTTTGGTGGTTTGA	
MDP0000251424-qPCR R	AGCTGCGCCTCGTTGTTTTTGGTC	
MDP0000808163-qPCR F	GATCCGGAGCCAACGAGGTG	
MDP0000808163-qPCR R	GCGGATGTATTGGTGACGGTGGTA	
MDP0000207237-qPCR F	TTTTTCGACGGTCATGGCTGCTCT	
MDP0000207237-qPCR R	ACGATCTTCTCCGGGGTGACGA	
MDP0000247000-qPCR F	TCCGCCACAAGACAAAAGAGTTC	
MDP0000247000-qPCR R	AGCAGCATATGAGGGGAGTTGGTA	
MDP0000647167-qPCR F	CACAACCTGCCTCGGGAACG	
MDP0000647167-qPCR R	ATAAGGGTGAGACGGAGGAGGAAG	
MDP0000125095-qPCR F	AAGATGAGCTACCAAGCTGG	
MDP0000125095-qPCR R	TCATTTGTTTCATGCCGGTGG	
MDP0000161440-qPCR F	CGACGAAGCCAACCGACTGTG	
MDP0000161440-qPCR R	GGGGGCGTATGATGCTGGGTAG	
MdMYB88/124 RNAi F	CTCGAAGATCTTAAATATCTGTTAGAGGAC	Clone MdMYB88/124RNAi fragment
MdMYB88/124 RNAi	GGTTGTGAAGGATTGGTGCTT	

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Appendix B Micrographs of R3 and *M. sieversii* roots under control and drought. The black rulers represent 250 μm .

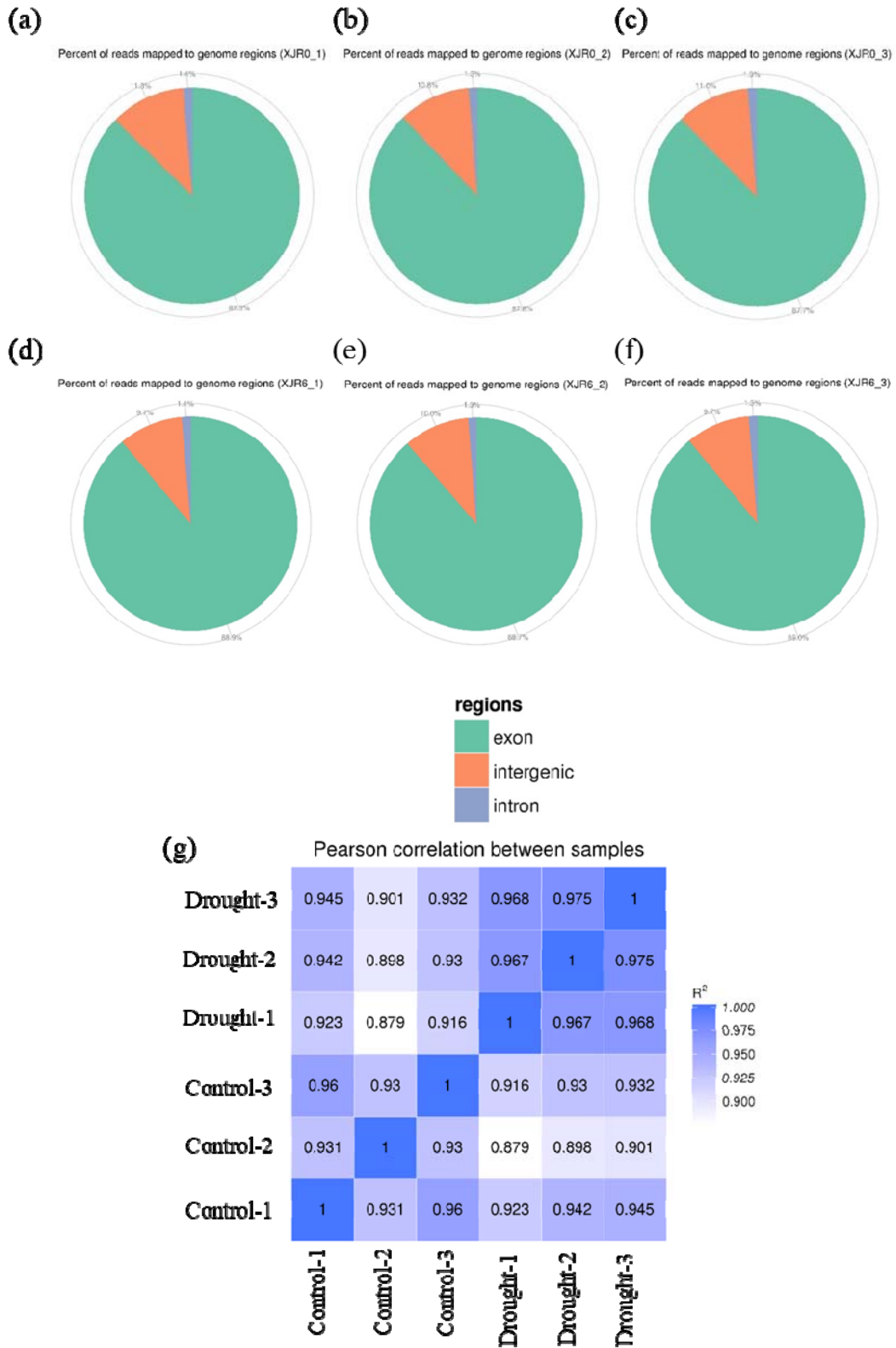


Appendix C Relative expression of *MsRD22* and *MsNCED3* in *M. sieversii* roots after simulated drought treatment determined by qRT-PCR. Error bars indicate standard deviation (n = 3).

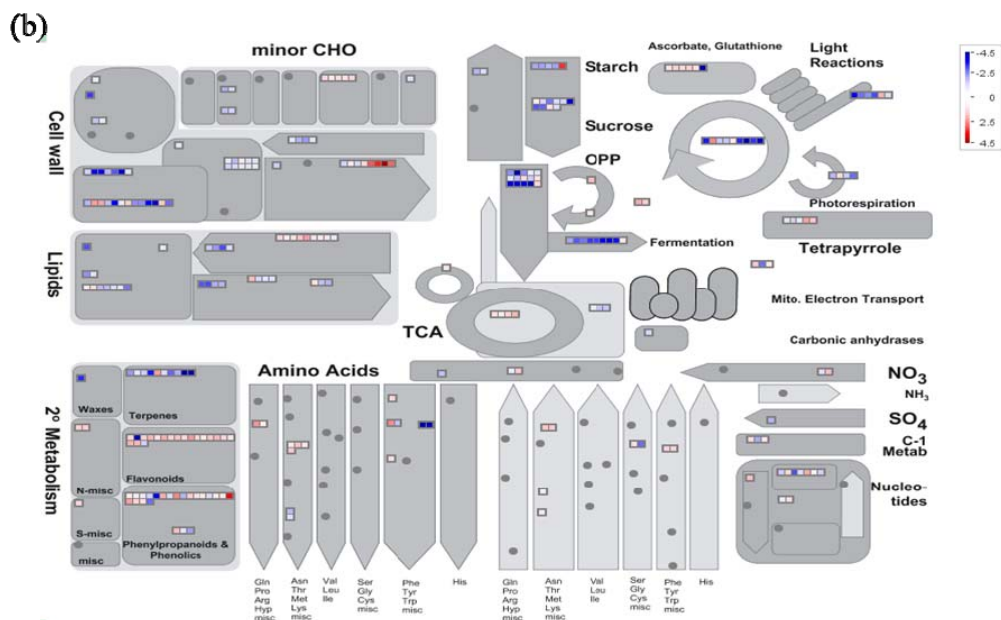
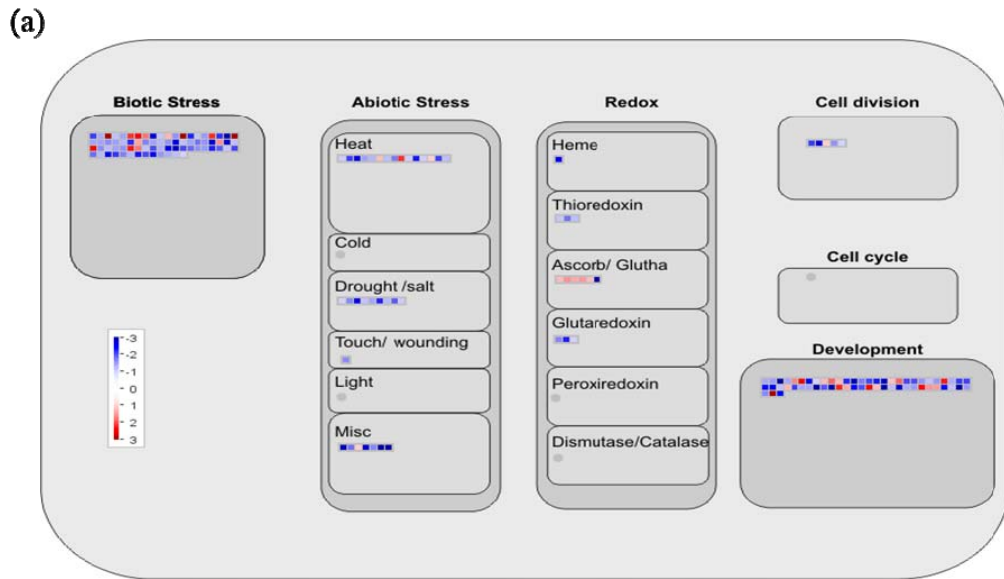
Appendix D Details of sequencing results of RNA-seq

Sample name ¹⁾	Raw reads	Clean reads	clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
XJR0_1	55889628	40907994	6.14G	0.01	99.49	97.51	47.43
XJR0_2	59724094	57762748	8.66G	0.01	97.07	92.88	47.02
XJR0_3	58714872	57057290	8.56G	0.01	97.26	93.13	46.77
XJR6_1	63128858	61231844	9.18G	0.01	97.19	93.05	46.48
XJR6_2	66017232	63888054	9.58G	0.01	97.01	92.67	46.98
XJR6_3	70850098	68770204	10.32G	0.01	97.21	93.06	47.15

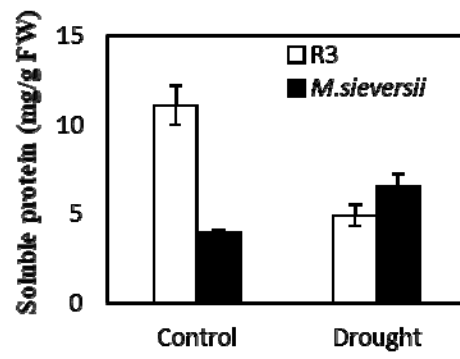
¹⁾ XJR0_1, XJR0_2, XJR0_3, roots of *M. sieversii* under control; XJR6_1, XJR6_2, XJR6_3, roots of *M. sieversii* under simulated-drought treatment for 6 h.



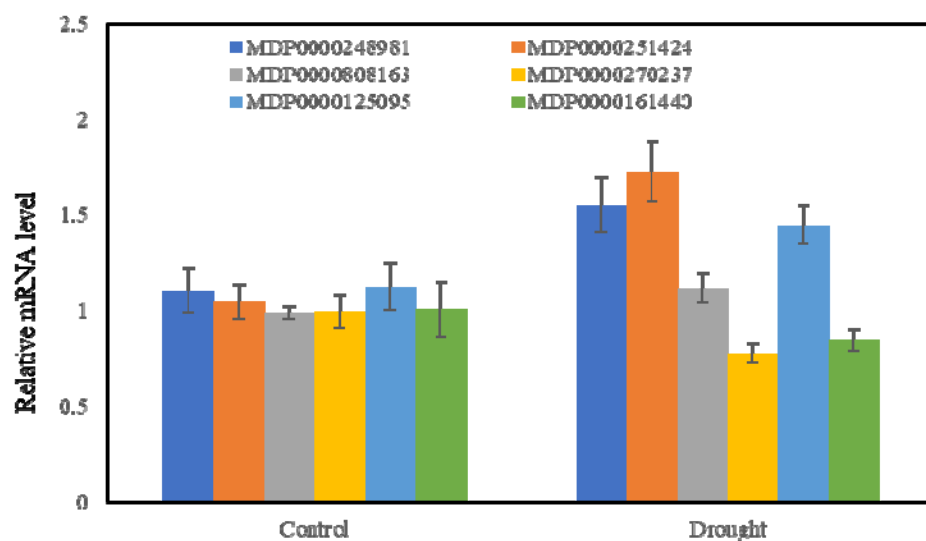
Appendix E Mapping and Pearson correlations of RNA-seq reads. (a)-(c) Mapping of control groups. (d)-(f) Mapping of drought treated groups. (g) Pearson correlations between each group.



Appendix H Overview by Mapman showing differentially expressed genes in *M. sieversii* roots after simulated drought treatment. (a) Differentially expressed genes involved in cellular response. (b) Differentially expressed genes involved in cellular metabolism. Grids represent individual genes. Up- and down-regulated genes are indicated in red and blue, respectively. Color brightness represents the degree of difference.



Appendix J Soluble protein content in roots of *M. sieversii* and R3 under long-term drought treatment. Error bars indicate standard deviation (n = 10).



Appendix K Relative expression of drought responsive genes in R3 roots after drought treatment determined by qRT-PCR. Error bars indicate standard deviation (n = 3).