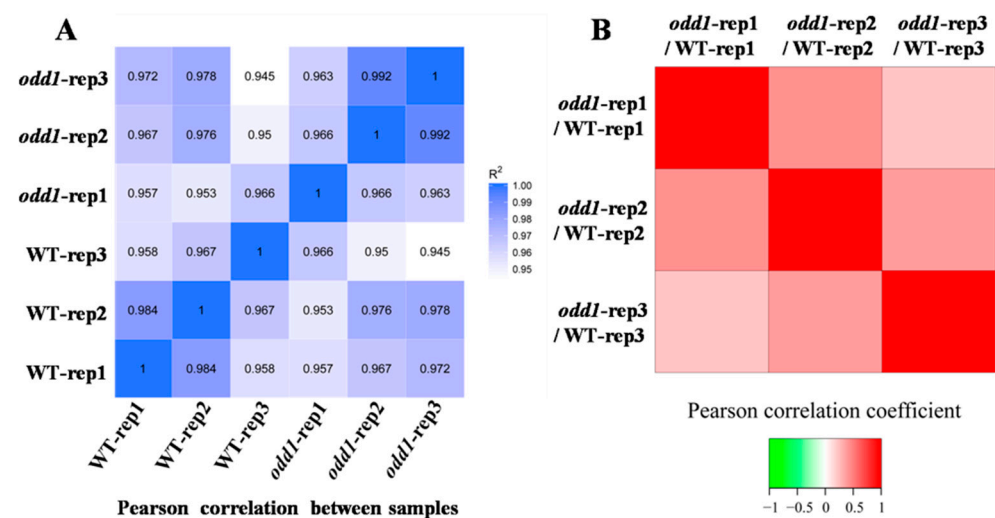
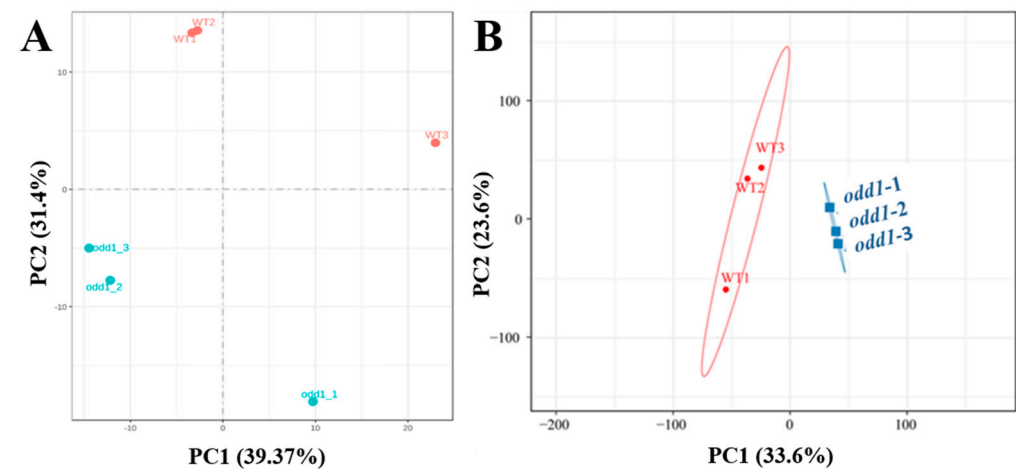


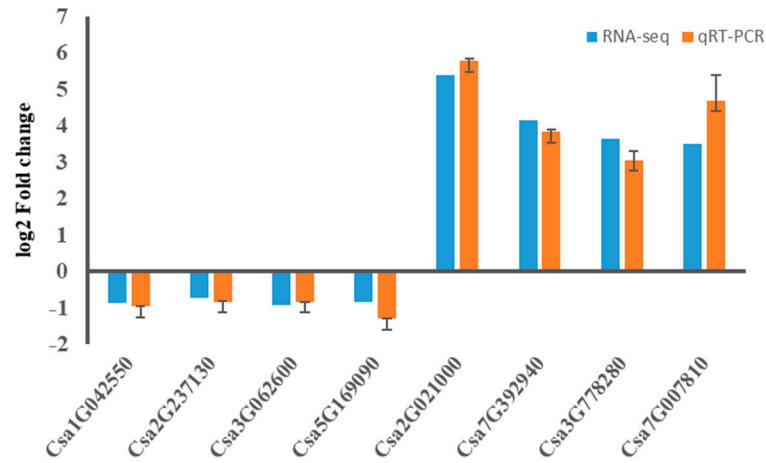
# Supplementary figures and tables



**Figure S1.** Pearson correlation analysis of transcriptomic and proteomic data between all samples, respectively. (A) Pearson correlation analysis of transcriptomic data. (B) Pearson correlation analysis of proteomic data. The color code indicates Pearson correlation coefficient value and the color scale of the heat map ranges from saturated green (value, -1) to saturated red (value, 1).

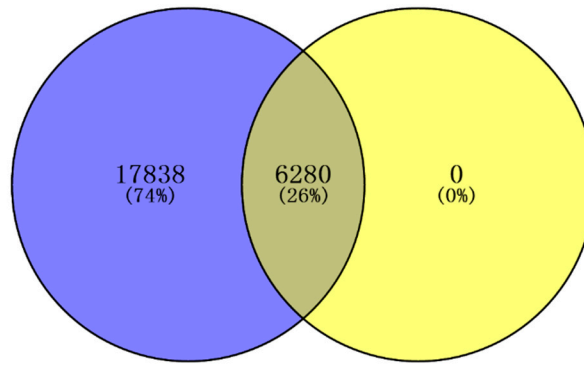


**Figure S2.** Principal component analysis of transcriptomic and proteomic data between all samples, respectively. (A) Principal component analysis at the transcriptome level. (B) Principal component analysis at the proteome level.



**Figure S3.** qRT-PCR validation of DEGs identified by RNA-seq.

**Transcriptomics** **Proteomics**



**Figure S4.** Transcriptomics and proteomics identified compared venn diagram.

**Table S1.** The quality of re-sequencing data.

Sample	Raw reads	Clean bases	Mapped (%)	Q20 (%)	Q30 (%)	GC content (%)
<i>odd1</i>	48664295	45992885	92.4	95.77	90.79	37.65

**Table S2.** Summary of transcriptome sequencing data.

Sample	Raw reads	Clean reads (Clean/All)	Mapped Reads (Mapped/Clean)	Uniquely mapped (Unique/Clean)	Q20 (%)	GC content (%)
WT-rep1	56857254	54862040(96.49%)	52588770 (95.86%)	51649382 (94.14%)	97.23	42.93
WT-rep2	63656560	62760600(98.59%)	60223314 (95.96%)	59122631 (94.20%)	97.11	43.16
WT-rep3	52118766	51169978(98.18%)	49175600 (96.10%)	48348213 (94.49%)	98.08	42.08
<i>odd1</i> -rep1	42777848	41132430(96.15%)	39215014 (95.34%)	38549174 (93.72%)	97.85	42.00
<i>odd1</i> -rep2	51930126	51164624(98.53%)	49059426 (95.89%)	48200934 (94.21%)	97.17	42.99
<i>odd1</i> -rep3	55159510	54155680(98.18%)	52063995 (96.14%)	51135218 (94.42%)	97.31	43.18

**Table S3.** Mapped regions distribution in the reference genome.

Sample	Intergenic (%)	Exon (%)	Intron (%)
WT-rep1	5.8	92.1	2.1
WT-rep2	6.0	92.0	2.0
WT-rep3	6.9	90.7	2.4
<i>odd1</i> -rep1	6.6	91.5	1.9
<i>odd1</i> -rep2	5.9	91.8	2.3
<i>odd1</i> -rep3	5.8	92.0	2.2

**Table S4.** List of transcription factors that were down-regulated in *odd1* mutant.

Gene ID	Gene description	log <sub>2</sub> (fold change)	Padj (adjusted P-value)
<b>AP2-EREBP</b>			
<i>Csa5G155570</i>	Dehydration responsive element binding transcription factor 1B	5.5528	0.0051271
<i>Csa1G075060</i>	Ethylene-responsive transcription factor, putative	2.2624	0.040152
<i>Csa4G630010</i>	Ethylene-responsive transcription factor 6	1.8708	0.045959
<i>Csa7G447150</i>	Ethylene-responsive transcription factor 6	1.5621	0.0027254
<i>Csa5G612310</i>	AP2-like ethylene-responsive transcription factor	1.4571	0.01555
<i>Csa3G357110</i>	Ethylene responsive transcription factor 1a	0.90386	0.008539
<b>C2H2</b>			
<i>Csa3G141860</i>	Zinc finger C2H2-type contained transcriptional regulator superman	3.1593	0.0069897
<i>Csa7G071440</i>	Zinc finger C2H2-like contained protein	1.6484	0.044601
<i>Csa7G428260</i>	Zinc finger C2H2-type contained protein	1.4741	0.00018434
<b>HSF</b>			
<i>Csa6G169310</i>	Heat stress transcription factor A-4a	2.3722	0.0015535
<i>Csa6G490870</i>	Heat stress transcription factor	1.3613	0.0033273
<b>HB</b>			
<a href="#"><i>Csa1G042780</i></a>	WUSCHEL-related homeobox 1	2.2545	0.0000263
<i>Csa4G043850</i>	Homeobox-leucine zipper protein	1.1622	0.0023245
<b>WRKY</b>			
<i>Csa3G730800</i>	WRKY transcription factor 17	1.9597	0.034386
<i>Csa4G051470</i>	WRKY transcription factor 21	1.8208	0.0056665
<i>Csa2G297180</i>	WRKY transcription factor 16	1.4414	0.00049001
<i>Csa3G119700</i>	Putative WRKY transcription factor 30	1.1134	0.013385
<b>bHLH</b>			
<i>Csa3G354520</i>	bHLH domain-containing transcription factor	1.8743	0.004005
<b>GRAS</b>			
<i>Csa6G495010</i>	GRAS family transcription factor	1.7225	0.0017211
<i>Csa3G405510</i>	Scarecrow-like 1 transcription factor	1.3704	0.004545
<b>MYB</b>			

<i>Csa3G826690</i>	MYB family transcription factor-like protein	0.97522	0.0046356
<i>Csa1G033200</i>	MYB transcription factor	0.74405	0.036368
<b>Others</b>			
<i>Csa2G295940</i>	LOB domain-containing protein	1.6026	0.00000114
<i>Csa1G051590</i>	Squamosa promoter binding protein	1.1462	0.0045259
<i>Csa7G448770</i>	Zinc finger CCCH domain-containing protein	1.0682	0.0063682
<i>Csa7G290470</i>	FHA domain containing protein, expressed	1.0374	0.004545
<i>Csa2G223670</i>	Protein tesmin/TSO1-like CXC 2	0.99262	0.011514
<i>Csa3G645940</i>	Protein TIFY	0.79419	0.035278
<i>Csa3G113370</i>	NAC domain protein	0.79032	0.014446
<i>Csa6G445000</i>	DNA-binding protein S1FA, putative	0.75534	0.029907
<i>Csa4G051430</i>	High mobility group family, contains high mobility group (HMG) box domain	0.72699	0.025411

**Table S5.** List of transcription factors that were up-regulated in *odd1* mutant.

Gene ID	Gene description	$ \log_2(\text{fold change}) $	$\text{padj}(\text{adjusted P-value})$
<b>bHLH</b>			
<i>Csa4G312280</i>	bHLH domain-containing transcription factor	3.0384	0.001786
<i>Csa6G011720</i>	Transcription factor bHLH51	1.2575	0.00014729
<i>Csa1G042340</i>	bHLH domain-containing transcription factor	1.1364	0.00079987
<i>Csa7G428890</i>	Transcription factor bHLH122	0.87739	0.024503
<b>bZIP</b>			
<i>Csa2G416070</i>	bZIP transcription factor family protein	2.4188	0.0257
<i>Csa5G642710</i>	bZIP transcription factor	1.1657	0.024835
<b>HB</b>			
<i>Csa5G635430</i>	Homeobox-leucine zipper-like protein	2.0763	0.00000000852
<i>Csa4G645830</i>	Knotted-like homeobox protein	1.5393	0.000000742
<i>Csa6G501990</i>	Homeobox-leucine zipper protein	0.73265	0.037691
<b>MYB</b>			
<i>Csa1G042350</i>	MYB transcription factor	1.8445	0.000000219
<i>Csa7G413890</i>	MYB-like transcription factor MYB 5	1.2809	0.007506
<i>Csa6G040640</i>	Putative MYB transcription factor	1.1889	0.00098148
<i>Csa2G100550</i>	MYB transcription factor	1.0642	0.020392
<b>ARF</b>			
<i>Csa6G291920</i>	Auxin response factor 5	1.7374	0.00000000000229
<i>Csa6G518210</i>	Auxin response factor, putative	1.6822	0.00000000000413
<i>Csa6G524670</i>	Auxin response factor 3	0.65105	0.045938
<b>WRKY</b>			
<i>Csa5G223070</i>	WRKY transcription factor, putative	1.6167	0.002022
<i>Csa1G547510</i>	WRKY transcription factor 14-1	1.5325	0.037691
<b>NAC</b>			
<i>Csa4G629480</i>	NAC domain protein	1.4533	0.00013625
<i>Csa1G038340</i>	NAC domain-containing protein 21/22, putative	0.87849	0.0062603
<i>Csa3G824990</i>	NAC domain protein	0.81129	0.018391

<b>C2H2</b>			
<i>Csa1G043020</i>	Putative zinc finger C2H2-type contained protein	1.343	0.00000877
<i>Csa5G092930</i>	Putative zinc finger C2H2-type contained protein	1.1256	0.00079907
<b>LOB</b>			
<i>Csa3G278920</i>	LOB domain-containing protein	1.2343	0.0000894
<i>Csa6G012240</i>	LOB domain-containing protein, putative	0.998	0.0013866
<b>TCP</b>			
<i>Csa1G020890</i>	TCP, transcription factor CYCLOIDEA	1.1351	0.013385
<i>Csa1G033030</i>	TCP transcription factor, putative	0.82854	0.024668
<b>AUX/IAA</b>			
<i>Csa7G378520</i>	Auxin-responsive protein	1.129	0.0032235
<i>Csa1G397130</i>	Auxin-responsive protein	1.032	0.001255
<i>Csa3G143570</i>	Auxin-responsive protein	0.72205	0.020911
<b>Others</b>			
<i>Csa6G040600</i>	GRAS, putative nodulation signaling pathway 2 protein	1.4767	0.00049001
<i>Csa3G904140</i>	Two-component response regulator-like protein	1.2454	0.0062603
<i>Csa1G043000</i>	G2-like	1.0396	0.0057619
<i>Csa6G039540</i>	C2C2-CO-like, CONSTANS-like zinc finger protein	0.94739	0.035103
<i>Csa6G432270</i>	SRS, short internode related sequence	0.88733	0.0066296
<i>Csa3G751470</i>	GRF, putative growth-regulating factor	0.84733	0.029301
<i>Csa6G091830</i>	AP2-EREBP, ethylene-responsive transcription factor	0.71479	0.041473

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**Table S6.** Primers for qRT-PCR.

Primer name	Sequence (5'-3')
Csa1G042550-F	GCCAGGCTAGAAGCAGAAC
Csa1G042550-R	TGCTGGTCCTCCTCAAGTTT
Csa3G062600-F	GAGACACTGCTGAAGCTG
Csa3G062600-R	CAGTTTGCTCTCTGCAAGGT
Csa2G237130-F	GAGATTGATAGAAAGCAAGCTG
Csa2G237130-R	TGGCATGGTGGTGAATACG
Csa5G169090-F	AGTGACCGGCAGATGGT
Csa5G169090-R	GATGCCAAAGCTCCAACA
Csa2G021000-F	CGATCAGTGCCCATTTTACGT
Csa2G021000-R	CGTGTTTCAAGCGTTCACCA
Csa7G392940-F	TGACATCGCCACTCGATTCC
Csa7G392940-R	GGAATCGAGTGGCGATGTCA
Csa7G007810-F	CCGCAAATACTCAACGTT
Csa7G007810-R	TTTGATGAGATCCATATC
Csa3G778280-F	CAACTACTTGGCAAAGGAG
Csa3G778280-R	GTTTGATGCCGAGGAAGACA