

Table Supplement 3 Drought stress response of CaWDT-2 and Tavee 60. Expression analysis were analyzed by MapMan software from differentially expressed genes (DEGs) with $p \leq 0.05$ and \log_2 (fold change) ≥ 1 or ≤ -1 .

Drought stress response of CaWDT-2

BIN	Name	Element	<i>p</i> -value
26.4	misc.beta 1,3 glucan hydrolases	8	0.0027290285891613526
20.2.1	stress.abiotic.heat	47	0.005428732396115077
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	22	0.006494283574969284
17.3		16	0.012011922371220275
16		126	0.012584995271690467
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	11	0.016689649729772604
20.2	stress.abiotic	98	0.030829325446406486
20.1.3	stress.biotic.signalling	4	0.052022041854786844
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	23	0.06941872766535706
17.5		23	0.08580074811700467
26.9	misc.glutathione S transferases	28	0.08808083655038024
17.1		15	0.10459417812136551
20.1.1	stress.biotic.respiratory burst	1	0.20383358583157793
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	12	0.2798156172177251
21		38	0.41180903373538913
17.8		4	0.42090325883574886
17.2	hormone metabolism.auxin	34	0.45720698422557404
17.7		8	0.5850579348408347
30.6	signalling.MAP kinases	11	0.629699170996791
20.1.7	stress.biotic.PR-proteins	29	0.6745820942458097
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	9	0.7180612609035628
30		247	0.7243140094268286
10		127	1.0050773902682205E-6
26.12	misc.peroxidases	24	4.28639277149004E-5
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	21	6.059239125000282E-5
29.5	protein.degradation	275	8.385167375664082E-4

Drought stress response of Tavee 60

BIN	Name	Element	p-value
26.12	misc.peroxidases	19	0.004974905899964787
29.5	protein.degradation	189	0.0058041943015825215
17.3		13	0.016490740749035393
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	5	0.024685751539544665
26.9	misc.glutathione S transferases	24	0.030928610672054768
17.1		11	0.033089300287005186
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	20	0.03938865621956622
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	15	0.03954878576738863
10		81	0.04570396653277434
17.5		16	0.12547701204884532
16		83	0.15427972689523126
20.1.1	stress.biotic.respiratory burst	1	0.2026645596214906
20.1.3	stress.biotic.signalling	5	0.21330157319445792
26.4	misc.beta 1,3 glucan hydrolases	7	0.3915806326715136
30		179	0.4008689537629786
30.6	signalling.MAP kinases	4	0.47958809732369656
17.7		6	0.5991559519659402
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	8	0.6039935948798085
17.8		4	0.6040776933752254
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	6	0.6059870960347324
20.1.7	stress.biotic.PR-proteins	12	0.6138383429217164
20.1.2	stress.biotic.receptors	1	0.6676605957701791
20.2.1	stress.abiotic.heat	29	0.8018851550980791
17.2	hormone metabolism.auxin	18	0.8491328761816551
21		37	0.9362155722323154
20.2	stress.abiotic	61	0.9905341037916671
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	18	3.2494999457455265E-5