

Supplemental Table 2. Prominent upregulated genes in steroid-inducible *MKK4DD* plants.

	AGI number <sup>b</sup>	Discription <sup>c</sup>	Experiment 1 <sup>a</sup>		Experiment 2		
			(Transgenic line 7)		(Transgenic line 2)		
			Fold change <sup>d</sup>	P value <sup>e</sup>	Fold change <sup>d</sup>	P value <sup>e</sup>	
Metabolism	At1g02920	glutathione transferase, putative	7.9	1.8E-28	6.1	8.7E-26	
	At1g02930	glutathione transferase, putative (GST1)	23.0	3.6E-33	8.2	2.5E-28	
	At3g54640	tryptophan synthase alpha chain	6.1	4.1E-26	3.2	1.7E-18	
	At4g11280	ACC synthase (AtACS-6)	8.4	6.3E-28	2.3	1.8E-08	
	At4g15210	glycosyl hydrolase family 14 (beta-amylase)	5.3	7.5E-20			
	At4g20830	FAD-linked oxidoreductase family	5.1	7.5E-22	2.1	6.5E-07	
	At4g27070	tryptophan synthase beta-subunit (TSB2)	7.6	3.0E-28	2.4	5.2E-14	
	At4g39940	adenosine-5-phosphosulfate-kinase	6.6	1.6E-26	4.6	1.0E-22	
	At5g38900	frnE protein - like	10.1	6.9E-29	3.5	3.9E-18	
	At5g38910	germin - like protein	6.7	9.7E-26			
	At5g57220	cytochrome p450 family	9.5	2.3E-24	9.6	1.3E-26	
	At5g65140	trehalose-6-phosphate phosphatase	6.5	7.2E-24	2.8	3.1E-09	
	At1g21100	O-methyltransferase 1, putative	7.3	2.4E-27	5.2	9.2E-24	
	At1g21110	O-methyltransferase 1, putative	5.5	1.7E-22	2.0	7.3E-07	
	At1g21120	O-methyltransferase 1, putative	8.5	1.5E-27	3.8	2.3E-17	
	At1g21130	O-methyltransferase 1, putative	5.3	3.7E-24	2.5	1.2E-12	
	At1g23730	putative carbonic anhydrase	6.4	2.3E-25	1.3	7.8E-03	
	At1g26380	FAD-linked oxidoreductase family	23.6	3.1E-33	13.5	5.6E-31	
	At1g26410	FAD-linked oxidoreductase family	5.3	1.1E-23	5.4	2.3E-21	
	At1g26420	FAD-linked oxidoreductase family	17.0	2.2E-31	11.2	6.1E-28	
	At1g69920	glutathione transferase, putative	5.7	7.4E-25	3.2	1.2E-14	
	At1g74590	glutathione transferase, putative	6.1	4.3E-25	2.7	3.4E-14	
	At2g02010	glutamate decarboxylase	29.4	2.8E-33	21.1	2.5E-30	
	At2g04400	putative indole-3-glycerol phosphate synthase	6.7	2.0E-25	3.4	3.0E-16	
	At2g29350	putative tropinone reductase	15.3	2.6E-31	1.7	4.3E-04	
	At2g29720	monooxygenase family	7.7	7.9E-27	3.3	1.2E-16	
	At5g40990	gDSL-motif lipase/hydrolase-like protein	3.6	3.5E-15	6.0	6.7E-24	
	At2g26560	similar to latex allergen from <i>Hevea brasiliensis</i>	6.8	9.1E-27	3.9	1.7E-20	
	Transcription	At2g38470	WRKY family transcription factor	5.1	1.9E-23	2.8	1.2E-14
		At5g13080	WRKY family transcription factor	6.5	1.2E-26	2.6	3.8E-14
		At1g18570	myb family transcription factor	18.8	2.0E-32	7.6	6.0E-27
		At1g27730	salt-tolerance zinc finger protein	5.7	4.2E-25	2.6	2.5E-14
At1g74080		putative transcription factor	5.5	1.7E-21	3.5	2.1E-11	
At1g80840		WRKY family transcription factor	7.4	5.4E-27	3.8	1.1E-19	
At2g43000		NAM (no apical meristem)-like protein	8.4	2.2E-22	6.8	9.2E-25	
At4g23810		WRKY family transcription factor	6.2	1.5E-26	3.4	2.0E-17	
Protein fate	At3g12580	heat shock protein 70	5.8	2.1E-24	1.7	3.0E-06	
	At1g24140	putative metalloproteinase	8.1	5.5E-27	4.6	1.2E-23	
	At2g31980	putative cysteine proteinase inhibitor B (cystatin B)	6.7	1.3E-25	1.7	3.0E-05	
	At2g32020	putative alanine acetyl transferase	5.0	2.3E-23	1.9	7.3E-08	
	At2g38860	expressed protein	6.0	4.9E-25	3.9	2.3E-18	
Transport	At4g13420	potassium transporter - like protein	12.5	5.4E-31			
	At1g74360	leucine-rich repeat transmembrane protein kinase, putative	6.2	1.4E-24	3.9	4.1E-18	
	At3g28510	hypothetical protein	5.9	5.6E-25			
	At4g12120	putative protein	5.2	3.7E-18	2.1	2.4E-06	
	At4g39670	putative protein	7.2	5.3E-25	1.9	2.4E-06	
Signal transduction	At2g19190	putative receptor-like protein kinase	8.9	6.0E-27	1.6	2.4E-03	
	At3g16530	putative lectin	15.6	1.3E-31	5.5	1.7E-23	
	At5g25930	receptor-like protein kinase - like	9.9	9.3E-30	5.1	1.2E-24	
	At5g18470	putative protein	5.6	2.8E-22	4.2	2.6E-17	
Defense	At2g43590	glycosyl hydrolase family 19 (chitinase)	9.7	3.5E-29	2.9	9.4E-16	
	At3g47540	glycosyl hydrolase family 19 (chitinase)	12.7	3.3E-30	3.1	7.8E-14	
	At4g14630	germin precursor oxalate oxidase	5.7	5.3E-24			
	At5g02780	In2-1 protein, putative	5.2	6.5E-21	2.7	2.5E-09	
	At5g47910	respiratory burst oxidase protein	5.4	1.6E-23	1.9	3.2E-06	
	At1g14540	anionic peroxidase, putative	6.2	1.3E-24	2.6	1.5E-03	
	At1g57630	disease resistance protein (TIR class), putative	18.8	8.9E-32	2.9	1.0E-12	
	At1g61810	glycosyl hydrolase family 1	11.7	1.3E-27	4.2	1.2E-15	
At1g65970	type 2 peroxiredoxin, putative	22.5	4.3E-33	6.7	6.1E-27		

	At2g15220	expressed protein	5.0	6.2E-23	3.6	1.3E-19
	At2g43570	glycosyl hydrolase family 19 (chitinase)	12.9	3.9E-31	4.7	3.4E-21
Unknown	At1g13520	hypothetical protein	6.7	2.1E-25	3.1	1.8E-13
	At1g24150	unknown protein	6.2	5.6E-23	2.3	4.0E-11
	At1g25083	F5A9.7	7.5	1.6E-27	3.7	1.5E-19
	At1g28190	hypothetical protein	9.6	4.2E-29	4.0	4.3E-20
	At1g55450	expressed protein	5.6	2.7E-24	3.1	1.1E-16
	At1g78410	expressed protein	7.9	1.4E-26	6.1	5.7E-22
	At2g18660	hypothetical protein	5.7	1.9E-18		
	At2g18690	expressed protein	18.1	9.6E-32	4.3	4.5E-19
	At2g30750	cytochrome p450 family	28.7	1.4E-32	19.3	8.4E-32
	At3g01830	expressed protein	14.5	8.6E-30	3.2	1.4E-08
	At3g02840	expressed protein	7.4	2.3E-26	6.5	5.6E-22
	At3g10500	expressed protein	5.1	3.3E-23	2.2	1.7E-09
	At3g15356	similar to putative lectin	12.6	3.9E-30	5.5	5.0E-23
	At3g26830	cytochrome p450 family	49.4	1.3E-34	19.0	1.8E-32
	At3g50480	expressed protein	5.2	2.5E-23	2.0	5.5E-08
	At3g54150	embryonic abundant protein -like	9.3	2.5E-28	3.7	4.7E-18
	At4g33050	putative protein	7.1	7.9E-26	3.6	2.2E-19
	At4g37290	expressed protein	5.4	5.2E-18	7.3	5.1E-25
	At4g37370	cytochrome p450 family	11.5	3.1E-30	5.9	9.8E-25
	At4g39950	cytochrome P450 - like protein	11.6	5.4E-30	5.6	6.3E-23
	At5g52760	expressed protein	5.9	8.7E-21		
	At1g67990	caffeoyl-CoA 3-O-methyltransferase, putative	11.3	2.1E-28	9.4	1.2E-18

<sup>a</sup> Upregulated genes in DEX-inducible *MKK4DD* transgenic plants (*MKK4DD/Cont.*).

<sup>b</sup> AGI, Arabidopsis Genome Initiative.

<sup>c</sup> Description as given by The Institute for Genomic Research database.

<sup>d</sup> Median of fold change

<sup>e</sup> corrected-P values < 0.05 were studied.