

Supplemental Table 1. Prominent upregulated genes in steroid-inducible *MKK3DD* plants.

	AGI number ^b	Discription ^c	Experiment 1 ^a (Transgenic line 5)		Experiment 2 (Transgenic line 3)	
			Fold change ^d	P value ^e	Fold change ^d	P value ^e
Metabolism	At1g43800	stearoyl acyl carrier protein desaturase, putative	5.6	1.6E-24		
	At3g45140	lipoxygenase AtLOX2			7.0	4.11E-27
	At4g12290	copper amine oxidase -like protein	2.0	3.4E-08	5.3	1.34E-22
	At1g05530	UDP-glycosyltransferase family			7.3	2.60E-26
	At1g05560	UDP-glucose transferase(UGT1)	1.7	1.3E-07	8.1	2.02E-28
	At1g55850	cellulose synthase catalytic subunit, putative			5.4	2.52E-23
	At2g29420	glutathione transferase, putative			6.2	4.07E-26
	At5g07560	glycine-rich protein GRP20	5.6	7.9E-25	2.3	8.45E-09
	At5g20740	ripening-related protein - like	24.2	2.4E-33	5.2	2.95E-24
	At5g50030	putative protein	5.3	1.1E-23		
Transcription	At5g66320	GATA zinc finger protein	6.5	1.2E-24	1.5	1.72E-03
	At1g01300	chloroplast nucleoid DNA binding protein, putative	5.9	5.9E-23	1.7	5.24E-03
	At1g01720	NAC domain protein, putative (ATAF1)	5.1	3.7E-21	3.0	6.86E-14
	At1g53170	ethylene responsive element binding factor 8	5.9	2.7E-25	1.4	1.26E-03
Protein fate	At4g33490	nucellin -like protein			5.6	8.53E-24
Transport	At2g38170	high affinity Ca ²⁺ antiporter			5.4	5.80E-24
	At2g38540	putative nonspecific lipid-transfer protein	8.1	1.5E-27	1.9	3.13E-06
	At4g13510	ammonium transport protein (AMT1)	6.7	5.8E-26	2.7	8.51E-13
	At5g59310	nonspecific lipid-transfer protein precursor - like	12.2	1.6E-31		
Signal transduction	At1g10430	serine/threonine protein phosphatase, PP2A	6.2	1.3E-05		
	At2g36570	leucine-rich repeat transmembrane protein kinase, putative	6.0	1.4E-25	1.6	3.00E-05
Defense	At1g52400	glycosyl hydrolase family 1, beta-glucosidase (BG1)			6.3	1.45E-24
	At1g75940	glycosyl hydrolase family 1, beta-glucosidase(ATA27)	3.3	4.4E-08	21.3	8.04E-32
	At2g21130	cyclophilin (CYP2)	5.8	1.8E-23	2.9	6.43E-12
	At2g28190	copper/zinc superoxide dismutase (CSD2)	5.1	1.6E-24		
	At5g25610	dehydration-induced protein RD22	5.7	2.9E-24		
	At5g44420	plant defensin protein, putative (PDF1.2a)	12.6	3.9E-31	6.1	2.69E-25
Unknown	At1g12570	hypothetical protein	6.3	7.3E-26	2.6	4.32E-09
	At1g19960	hypothetical protein	6.5	6.4E-27	1.3	9.88E-05
	At1g78020	expressed protein	5.5	3.9E-25	2.2	6.46E-12
	At2g20870	expressed protein	5.9	2.9E-25	2	2.87E-08
	At2g25510	expressed protein	5.1	8.2E-23	2.3	1.05E-09
	At3g04720	hevein-like protein precursor (PR-4)	5.7	7.3E-23		
	At3g15400	anther development protein, ATA20	9.8	1.2E-28	6.1	1.26E-23
	At3g22240	expressed protein	6.3	4.2E-26	1.5	4.91E-04
	At3g57690	arabinogalactan-protein, putative (AGP23)	5.7	3.9E-25		
	At5g20790	putative protein	6.1	1.1E-25		
	At5g22430	expressed protein	6.3	1.6E-26	5.4	4.14E-22
	At5g22460	putative protein	1.6	9.5E-05	5.4	9.17E-21

^a Upregulated genes in DEX-inducible *MKK3DD* transgenic plants (*MKK3DD/Cont.*).

^b AGI, Arabidopsis Genome Initiative.

^c Description as given by The Institute for Genomic Research database.

^d Median of fold change

^e corrected-P values < 0.05 were studied.