Supplementary Table 5. Transcript specifically responsive to MV, significantly elevated/suppressed (>3-fold).

Probe set name	Gene	TAIR description	Ratio $\log_2$ MV 2 h/ control
261443_at	At1g28480	glutaredoxin, putative similar to glutaredoxin GI:2244924 from [Arabidopsis thaliana]; supported by cDNA: gi_13358219_gb_AF325030.2_AF325030	3.365
261394_at	At1g79680	wall-associated kinase 2, putative similar to wall-associated kinase 2 GI:4826399 from [Arabidopsis thaliana]	3.283
245005_at	rps14	ribosomal protein S14	3.086
261899_at	At1g80820	cinnamoyl CoA reductase, putative similar to cinnamoyl CoA reductase GB:AAF43141 GI:7239228 from [Populus tremuloides]; supported by full-length cDNA: Ceres: 32255.	3.071
244990_s_at	rpl23-01	hypothetical protein	2.899
250149_at	At5g14700	cinnamoyl CoA reductase - like protein cinnamoyl CoA reductase, Populus tremuloides, EMBL:AF217958; supported by full-length cDNA: Ceres:17229.	2.842
260005_at	At1g67920	unknown protein; supported by full-length cDNA: Ceres:13102.	2.834
256306_at	At1g30370	lipase, putative contains Pfam profile: PF01764: Lipase	2.833
263783_at	At2g46400	member of WRKY Transcription Factor; Group III, WRKY46	2.726
260668_at	At1g19530	unknown protein; supported by full-length cDNA: Ceres:39579.	2.606
247293_at	At5g64510	putative protein similar to unknown protein (pir |T03813)	2.599
261474_at	At1g14540	anionic peroxidase, putative similar to anionic peroxidase GI:170202 from [Nicotiana sylvestris]	2.549
249264_s_at	At5g41740	disease resistance protein-like	2.548
267451_at	At2g33710	member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family	2.513
259428_at	At1g01560	MAP kinase, putative similar to MAP kinase 5 GI:4239889 from [Zea mays]	2.487
259792_at	At1g29690	Significant homology to the MACPF (membrane attack complex and perforin) domain of complements and perforin proteins	2.464
252487_at	At3g46660	glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819; supported by cDNA: gi_15081808_gb_AY048297.1_	2.438
256181_at	At1g51820	light repressible receptor protein kinase, putative similar to light repressible receptor protein kinase GI:1321686 from (Arabidopsis thaliana)	2.419
267384_at	At2g44370	DC1 domain-containing protein; similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G17740.1)	2.396
252345_at	At3g48640	hypothetical protein	2.383
261037_at	At1g17420	lipoxygenase identical to GB:CAB56692 from (Arabidopsis thaliana)	2.380
245209_at	At5g12340	putative protein similarity to predicted protein, Arabidopsis thaliana	2.344
252346_at	At3g48650	At14a-related protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	2.328
248814_at	At5g46910	transcription factor jumonji (jmj) family protein; similar to REF6 (RELATIVE OF EARLY FLOWERING 6), transcription factor [Arabidopsis thaliana] (TAIR:AT3G48430.1)	2.318
250796_at	At5g05300	putative protein similar to unknown protein (gb|AAF01528.1)	2.298
263570_at	At2g27150	aldehyde oxidase identical to GP:3172044:gnl:PID:d1029570:AB010080; supported by cDNA: gi_5672671_dbj_AB016622.1_AB016622	2.285
247215_at	At5g64905	PROPEP3 (Elicitor peptide 3 precursor); Identical to Elicitor peptide 3 precursor (PEP3) [Arabidopsis Thaliana]; supported by full-length cDNA: Ceres: 3657.	2.256
259298_at	At3g05370	putative disease resistance protein similar to Cf-2 disease resistance protein GB:AAC15780 from [Lycopersicon pimpinellifolium]	2.228
247145_at	At5g65600	receptor protein kinase-like protein	2.217
251054_at	At5g01540	receptor like protein kinase receptor like protein kinase - Arabidopsis thaliana, EMBL:ATLECGENE; supported by cDNA: gi_13605542_gb_AF361597.1_AF361597	2.162
265008_at	At1g61560	Mlo protein, putative similar to Mlo protein GI:1877220 from [Hordeum vulgare]; supported by cDNA: gi_14091581_gb_AF369567.1_AF369567	2.160
263228_at	At1g30700	putative reticuline oxidase-like protein similar to GB:P30986 from [Eschscholzia californica] (berberine bridge-forming enzyme), ESTs gb|F19886, gb|Z30784 and gb|Z30785 come from this gene; supported by cDNA: gi_16930506_gb_AF419607.1_AF419607	2.156
258787_at	At3g11840	U-box domain-containing protein	2.149
247848_at	At5g58120	resistance protein - like disease resistance protein RPP1-WsA, Arabidopsis thaliana, EMBL:AF098962	2.135

262360_at	At1g73080	receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from [Arabidopsis thaliana]	2.122
265093_at	At1g03905	ABC transporter family protein; Identical to Non-intrinsic ABC protein 4 (GCN-related protein 2) (NAP4) [Arabidopsis Thaliana] (GB:Q3EDJ0;GB:Q9ZWB0); similar to POP1 [Arabidopsis thaliana] (TAIR:AT5G44110.1)	2.113
266992_at	At2g39200	similar to Mlo proteins from H. vulgare; supported by cDNA: gi_14091593_gb_AF369573.1_AF369573	2.107
267381_at	At2g26190	calmodulin-binding family protein; similar to EDA39 (embryo sac development arrest 39), calmodulin binding [Arabidopsis thaliana] (TAIR:AT4G33050.3); supported by cDNA: gi_16930468_gb_AF419588.1_AF419588	2.100
251259_at	At3g62260	putative protein phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423; supported by full-length cDNA: Ceres:20050.	2.096
253181_at	At4g35180	amino acid permease - like protein Lily mRNA, Lilium longiflorum, gb:D21814; supported by full-length cDNA: Ceres:36461.	2.090
258947_at	At3g01830	hypothetical protein similar to calmodulin-like protein GB:CAB42906 [Arabidopsis thaliana]; Pfam HMM hit: EF hand; supported by full-length cDNA: Ceres: 7252.	2.085
252470_at	At3g46930	protein kinase 6-like protein protein kinase 6 - Glycine max,PIR2:S29851	2.082
265737_at	At2g01180	putative phosphatidic acid phosphatase; supported by full-length cDNA: Ceres:19163.	2.041
264660_at	At1g09940	putative glutamyl-tRNA reductase 2 precursor similar to GB:P49294 and to A. thaliana HEMA2 (gb|U27118)	2.029
262930_at	At1g65690	hypothetical protein similar to hin1 GB:Y07563 GI:1619320 Nicotiana tabacum; supported by full-length cDNA: Ceres:21639.	2.029
249339_at	At5g41100	DNA binding; similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT3G26910.2)	2.021
253737_at	At4g28703	Expressed protein; supported by full-length cDNA: Ceres: 38545.	2.015
266615_s_at	At2g29720	putative monooxygenase; supported by full-length cDNA: Ceres:34214.	2.014
252533_at	At3g46110	putative protein predicted proteins, Arabidopsis thaliana	1.995
257919_at	At3g23250	myb-related transcription factor, putative similar to myb-related transcription factor GB:CAA66952 from [Lycopersicon esculentum]	1.986
261650_at	At1g27770	envelope Ca2+-ATPase identical to envelope Ca2+-ATPase GB:AAD10212 GI:516118 from (Arabidopsis thaliana); supported by cDNA: gi_493621_dbj_D13983.1_ATHRCECAA	1.976
246465_at	At5g17000	quinone oxidoreductase - like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611	1.967
261476_at	At1g14480	hypothetical protein contains similarity to alpha-latroinsectotoxin precursor GI:9537 from [Latrodectus tredecimguttatus]	1.954
249903_at	At5g22690	disease resistance protein-like	1.938
267289_at	At2g23770	putative protein kinase contains a protein kinase domain profile (PDOC00100)	1.937
251109_at	At5g01600	ferritin 1 precursor; supported by full-length cDNA: Ceres:1100.	1.937
257074_at	At3g19660	unknown protein	1.932
260239_at	At1g74360	putative receptor protein kinase similar to brassinosteroid insensitive 1 GB:AAC49810 (putative receptor protein kinase); contains Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats), PF00069 Eukaryotic protein kinase domain; supported by cDNA: gi_15810516_gb_AY056297.1_	1.930
266775_at	At2g29060	putative SCARECROW gene regulator	1.916
246327_at	At1g16670	receptor-like serine/threonine kinase, putative similar to receptor-like serine/threonine kinase GI:2465923 from [Arabidopsis thaliana]; supported by cDNA: gi_16649102_gb_AY059921.1_	1.907
260869_at	At1g43800	stearoyl acyl carrier protein desaturase, putative similar to stearoyl acyl carrier protein desaturase Lldd3A20 GB: AAD28287 GI:4704824 from [Lupinus luteus]; supported by full-length cDNA: Ceres:12758.	1.861
251428_at	At3g60140	beta-glucosidase-like protein several beta-glucosidases - different species; supported by cDNA: gi_10834547_gb_AF159376.1_AF159376	1.861
259297_at	At3g05360	putative disease resistance protein similar to Cf-2 disease resistance protein GB:AAC15780 from [Lycopersicon pimpinellifolium]	1.843
264083_at	At2g31230	ethylene reponse factor-like AP2 domain transcription factor	1.833
263230_at	At1g05665	putative indole-3-acetate beta-glucosyltransferase similar to indole-3-acetate beta-glucosyltransferase GB:AAD32293	1.827
265327_at	At2g18210	unknown protein	1.795
246001_at	At5g20790	putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:267031.	1.793
254652_at	At4g18170	member of WRKY Transcription Factor; Group II-c, WRKY28	1.792
252825_at	At4g39890	small GTP-binding protein - like SR1 Nt-rab6, Nicotiana tabacum, L29273; supported by cDNA: gi_14423429_gb_AF386952.1_AF386952	1.786
256968_at	At3g21070	Encodes a protein with NAD(H) kinase activity.	1.784

246108_at	At5g28630	putative protein retinal glutamic acid-rich protein, bovine, PIR:A40437; supported by full-length cDNA: Ceres:24151.	1.780
264953_at	At1g77120	alcohol dehydrogenase identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 4033.	1.779
254215_at	At4g23700	putative Na+/H+-exchanging protein Na+/H+-exchanging protein slr1595 - Synechocystis sp., EMBL:D90902	1.778
266155_at	At1g64950	cytochrome p450, putative similar to cytochrome p450 GI:438242 from [Solanum melongena]; supported by cDNA: gi_14334809_gb_AY035078.1_	1.775
258682_at	At3g08720	putative ribosomal-protein S6 kinase (ATPK19) identical to putative ribosomal-protein S6 kinase (ATPK19) GB:D42061 [Arabidopsis thaliana] (FEBS Lett. 358 (2), 199-204 (1995)); supported by cDNA: gi_15292784_gb_AY050826.1_	1.774
252214_at	At3g50260	putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982; supported by cDNA: gi_15010555_gb_AY045579.1_	1.769
265797_at	At2g35710	glycogenin glucosyltransferase (glycogenin)-related; similar to glycogenin glucosyltransferase (glycogenin)-related [Arabidopsis thaliana] (TAIR:AT4G16600.1); supported by full-length cDNA: Ceres: 9996.	1.768
256583_at	At3g28850	glutaredoxin family protein; similar to glutaredoxin family protein [Arabidopsis thaliana] (TAIR:AT5G39865.1)	1.757
257644_at	At3g25780	Encodes allene oxide cyclase (AOC3), one of the enzymes involved in jasmonic acid biosynthesis; supported by full-length cDNA: Ceres:3457.	1.756
252652_at	At3g44720	putative chloroplast prephenate dehydratase similar to bacterial PheA gene products	1.754
252414_at	At3g47420	putative protein sn-glycerol-3-phosphate permease - Haemophilus influenzae,PID:g3603157; supported by cDNA: gi_13430515_gb_AF360170.1_AF360170	1.751
256266_at	At3g12310	unknown protein; supported by cDNA: gi_15293280_gb_AY051074.1_	1.751
260015_at	At1g67980	putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase similar to S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase GB:AAA62426 [Arabidopsis thaliana] (function=disease resistance); supported by cDNA: gi_682727_gb_L40031.1_ATHORF	1.745
245151_at	At2g47550	putative pectinesterase; supported by full-length cDNA: Ceres:111254.	1.742
265276_at	At2g28400	hypothetical protein predicted by genscan and genefinder	1.731
264867_at	At1g24150	Formin homologue 4 (ATFH4); encodes a group I formin. Localized to cell junctions. Polymerizes actin. Binds profilin.	1.724
251479_at	At3g59700	serine/threonine-specific kinase lecRK1 precursor,lectin receptor-like	1.717
244953_s_at	nad6	NADH dehydrogenase subunit 6	1.715
245119_at	At2g41640	unknown protein; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579	1.715
249032_at	At5g44910	putative protein contains similarity to disease resistance protein	1.709
248322_at	At5g52760	heavy-metal-associated domain-containing protein; similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:AT5G52750.1)	1.704
252739_at	At3g43250	cell cycle control protein-related; similar to cell cycle control protein-related [Arabidopsis thaliana] (TAIR:AT2G32050.1)	1.699
246340_s_at	At3g44860	AtPP -like protein AtPP protein, Brassica napus, EMBL:BNA245479; supported by cDNA: gi_15293070_gb_AY050969.1_	1.683
246418_at	At5g16960	quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611; supported by full-length cDNA: Ceres:7898.	1.677
260662_at	At1g19540	2-hydroxyisoflavone reductase, putative similar to PIR:T08106 from [Betula pendula]	1.669
262369_at	At1g73010	phosphoric monoester hydrolase; similar to phosphoric monoester hydrolase [Arabidopsis thaliana] (TAIR:AT1G17710.1); supported by full-length cDNA: Ceres:19976.	1.665
256050_at	At1g07000	leucine zipper protein, putative similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana]	1.663
249260_at	At5g41680	Pto kinase interactor 1-like protein	1.659
264757_at	At1g61360	receptor protein kinase (IRK1), putative similar to receptor protein kinase (IRK1) GI:836953 from [Ipomoea trifida]	1.658
247240_at	At5g64660	U-box domain-containing protein	1.655
258752_at	At3g09520	ATEXO70H4; a member of EXO70 gene family, putative exocyst subunits, conserved in land plants.	1.650
252234_at	At3g49780	Phytosulfokine 3 precursor (ATPSK4), coding for a unique plant peptide growth factor; supported by full-length cDNA: Ceres: 40302.	1.647
257785_at	At3g26980	geranylgeranylated protein, putative similar to ATGP4 GB:AAD00115 from [Arabidopsis thaliana]	1.643
249485_at	At5g39020	receptor protein kinase - like protein receptor-protein kinase-like protein, Arabidopsis thaliana, PIR:T45786	1.642

258941_at	At3g09940	putative monodehydroascorbate reductase (NADH) similar to monodehydroascorbate reductase (NADH) GB:JU0182 [Cucumis sativus]; supported by full-length cDNA: Ceres: 11160.	1.638
255512_at	At3g05710	SYNTAXIN 43 (SYP43); member of SYP4 Gene Family; supported by cDNA: gi_5059351_gb_AF154574.1_AF154574	1.635
249072_at	At5g44060	putative protein similar to unknown protein (gb|AAD10670.1)	1.635
251336_at	At3g61190	Bon association protein 1 (BAP1); encodes a protein with a C2 domain that binds to BON1 in yeast two hybrid analyses; supported by full-length cDNA: Ceres:30454.	1.631
252827_at	At4g39950	cytochrome P450 - like protein cytochrome P450, Sinapis alba, AF069494; supported by cDNA: gi_15028134_gb_AY046017.1_	1.630
256793_at	At3g22160	VQ motif-containing protein; similar to VQ motif-containing protein [Arabidopsis thaliana] (TAIR:AT4G15120.1); supported by full-length cDNA: Ceres:8081.	1.629
255549_at	At4g01950	Glycerol-3-phosphate acyltransferase 3 (gpat3); encodes a member of a family of proteins with glycerol-3-phosphate acyltransferase activity	1.627
260206_at	At1g70740	putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain	1.618
251603_at	At3g57760	putative protein wall-associated kinase 1, Arabidopsis thaliana, AJ009696; supported by cDNA: gi_13937221_gb_AF372966.1_AF372966	1.614
265620_at	At2g27310	F-box family protein; similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT2G36090.1)	1.611
245329_at	At4g14360	dehydration-responsive protein-related; similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:AT1G04430.1); supported by full-length cDNA: Ceres: 37809.	1.608
247026_at	At5g67080	protein kinase-like protein	1.607
255568_at	At4g01250	member of WRKY Transcription Factor; Group II-e, WRKY22	1.605
262238_at	At1g48300	similar to soluble diacylglycerol acyltransferase [Arachis hypogaea] (GB:AAX62735.1)	-1.601
256598_at	At3g30180	cytochrome P450 homolog, putative similar to cytochrome P450 homolog GB:U54770 GI:1421740 from [Lycopersicon esculentum]; supported by full-length cDNA: Ceres:11278.	-1.620
266322_at	At2g46690	putative auxin-regulated protein	-1.649
257008_at	At3g14210	myrosinase-associated protein, putative similar to GB:CAA71238 from [Brassica napus], conatains Pfam profile:PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_15450434_gb_AY052318.1_	-1.653
244932_at	AtC01060	PSI 9KDa protein	-1.654
263688_at	At1g26920	unknown protein Location of EST 228A16T7A, gb|N65686; supported by full-length cDNA: Ceres:24946.	-1.681
245861_at	At5g28300	GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963	-1.690
262682_at	At1g75900	anter-specific proline-rich -like protein (APG-like) similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-ear cress)]; supported by cDNA: gi_15054385_gb_AY028611.1_	-1.698
252607_at	At3g44990	xyloglucan endo-transglycosylase; supported by cDNA: gi_15810248_gb_AY056163.1_	-1.726
249309_at	At5g41410	Homeodomain protein involved in ovule morphogenesis, BEL1	-1.735
248921_at	At5g45950	GDSL-motif lipase/hydrolase-like protein	-1.798
255028_at	At4g09890	putative protein Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, gene T30B22.22, PID:g2529679	-1.842
248961_at	At5g45650	subtilisin-like protease	-1.992
267361_at	At2g39920	acid phosphatase class B family protein; Identical to Hypothetical protein At2g39920 [Arabidopsis Thaliana] (GB:O04195); similar to acid phosphatase, putative [Arabidopsis thaliana] (TAIR:AT4G25150.1); supported by full-length cDNA: Ceres:33701.	-2.002
246275_at	At4g36540	BEE2 (BR ENHANCED EXPRESSION 2); DNA binding / transcription factor; similar to basic helix-loop-helix (bHLH) family protein	-2.047
247252_at	At5g64770	unknown protein	-2.115
263402_at	At2g04050	MATE efflux family protein; similar to ATDTX1, antiporter/ multidrug efflux pump/ multidrug transporter/ transporter [Arabidopsis thaliana] (TAIR:AT2G04040.1)	-2.226
252965_at	At4g38860	putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099	-2.459
256060_at	At1g07050	hypothetical protein contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from [Oryza sativa]; supported by full-length cDNA: Ceres:1955.	-2.476