

Additional File 7: Table S6 List of genes up-regulated in both Weisuobuzhi and Dong17 after exposing the plants to 5 μ M Cd for 15 d.

Annotation	Probe Set ID	Fold change*		Accession No	e-value
		(Cd vs control)			
		WS	D		
Stress and defense response					
Thaumatococcal protein TLP7 [H. vulgare]	rbaak13h13_s_at	2.68	2.01	AAK55325.1	5e-38
Gamma-thionin precursor [H. vulgare]	Contig381_x_at	2.06	2.1	S65779	2e-32
1-aminocyclopropane-1-carboxylate oxidase [P. edulis]	EBro03_SQ004_E10_at	2.31	2.13	BAB32502.1	5e-13
Methyljasmonate-inducible lipoxygenase 2 [H. vulgare]	Contig2306_s_at	2.93	2.39	T06190	5e-95
P450 [T. aestivum]	Contig15561_s_at	2.69	2.51	BAB87820.1	3e-63
Glutathione transferase [H. vulgare subsp.]	Contig20831_at	2.23	2.65	AAL73394.1	5e-60
Contains ESTs C74501, AU094804 [O. sativa (japonica)]	Contig10481_at	4.18	2.67	BAB90402.1	5e-47
Absciscic acid- and stress-induced protein [O. sativa]	Contig8961_at	3.75	3.16	T02663	9e-17
Cysteine protease component of protease-inhibitor complex [Z. mays]	Contig2554_at	2.44	3.46	BAA88898.1	2e-31
Probable chitinase [H. vulgare]	Contig25195_at	2.47	4.14	T04484	3e-53
Probable cysteine proteinase [H. vulgare]	Contig2988_s_at	5.54	4.15	T05920	9e-52
Barwin homolog wheatwin2 precursor [T. aestivum]	Contig2546_at	2.65	4.26	T06486	3e-64
18,9 KDa ABA-induced protein [H. vulgare subsp.]	Contig6276_s_at	4.01	4.91	T04417	5e-80
Putative class III chitinase [O. sativa]	Contig5024_at	5.8	7.12	AAM08776.1	4e-79
Avr9/Cf-9 rapidly elicited protein 65 [N.tabacum]	Contig19890_at	6.13	8.34	AAG43557.1	e-04
polyubiquitin (UBQ4) [A. thaliana]	Contig1058_x_at	3.31	23.47	NP_568397.1	1e-47
Transport					
Lipid transfer protein Cw(21) [H. vulgare]	rbasd16a13_s_at	2.94	2.95	S28872	9e-09
Nonspecific lipid-transfer protein 4.3 precursor [H. vulgare subsp.]	Contig959_x_at	2.09	2.03	Q42842	3e-39
Glu-tRNA(Gln) amidotransferase subunit A [A. thaliana]	Contig7597_at	2.07	2.13	AAG29095.1	9e-95
Lipid transfer protein [A. thaliana]	rbags1f20_x_at	2.01	2.21	2115353A	5e-07
Copper chaperone homolog CCH [O. sativa]	Contig6788_at	3.07	2.27	T50779	6e-29
fructosyltransferase [Lolium perenne]	rbah48h06_s_at	2.35	2.37	AAL92880.1	6e-84
Glycoprotein specific UDP-glucuronyltransferase [A. thaliana]	Contig10435_at	2.6	2.51	AAD45998.1	5e-10
Probable phospholipid transfer protein precursor [H. vulgare]	Contig871_s_at	2.96	2.59	T04407	7e-39
F23N19.15 similar to lipid transfer protein [A. thaliana]	Contig6504_s_at	2.29	2.73	AAF19544.1	1e-37
Putative serine carboxypeptidase OSJNBa0046L02.7 [O. sativa]	HK04D23r_at	2.59	2.73	AAL73563.1	3e-14
Putative uncharacterized protein At3g62660 [A. thaliana]	HVSMEc0009L17r2_at	4.27	2.99	NP_191825.2	7e-29
Putative flavonol glucosyltransferase [O. sativa (japonica)]	Contig11602_at	2.24	3.05	BAB68083.1	2e-51
Mitochondrial carrier protein family [A. thaliana]	Contig6913_x_at	2.36	3.13	NP_568060.1	7e-96
Aquaporin 2 [Samanea saman]	Contig19393_at	2.16	3.21	AAC17529.1	7e-57
Nonspecific lipid-transfer protein 4.1 precursor [H. vulgare]	Contig972_x_at	3.47	3.6	Q43767	2e-41
Herbicide safener binding protein 1 [Z. mays]	Contig4910_at	16.08	4.11	T01354	4e-62
Probable lipid transfer protein [H. vulgare]	Contig6042_at	4.17	4.25	T06199	3e-41
Putative protein; protein id: At5g14910.1 [A. thaliana]	Contig10306_s_at	2.78	4.74	NP_568306.1	3e-23
Trigger factor-like protein; protein id: At5g55220.1, [A. thaliana]	Contig7069_at	2.27	4.85	NP_200333.2	2e-79
Putative protein; protein id: At5g14910.1 [A. thaliana]	Contig10306_at	2.96	5.17	NP_568306.1	3e-23
Herbicide safener binding protein 1 [Z. mays]	Contig4911_at	12.6	8.32	T01354	1e-60
Putative seven transmembrane protein [O. sativa (japonica)]	HVSMEb0006O01r2_at	2.14	44.8	BAB92639.1	2e-06
Putative fatty acid condensing enzyme CUT1 [O. sativa (japonica)]	HVSMEb0010E16r2_s_at	2.46	2.3	BAB91850.1	1e-25
THA4 [Z. mays]	Contig18499_at	2.04	2.5	AAD31522.1	5e-18
Transcription					
At1g02150/T7I23.8 [A. thaliana]	Contig6600_at	2.11	2.12	AAM19786.1	2e-50
Probable RNA-binding protein cp33 precursor [H. vulgare subsp.]	Contig7834_at	2.28	2.48	T05730	e-153
Contains ESTs D47958 [O. sativa (japonica)]	Contig6169_at	2.37	2.59	BAB78620.1	2e-35
Putative nascent polypeptide associated complex alpha chain [O. sativa (japonica)]	Contig11109_at	3.15	4.03	AAM52321.1	2e-46
F22G5.34 [A. thaliana]	Contig9938_at	2.17	4.14	AAF79563.1	5e-78
Transducin-like enhancer protein 4 [Mus musculus]	Contig13990_at	2.06	5.19	Q62441	0.029
Contains ESTs D47958 [O. sativa (japonica)]	Contig6170_s_at	3.12	2.81	BAB78620.1	4e-30
Putative mitotic control protein dis3 [O. sativa (japonica)]	HV_CEB0018G22r2_at	2	3.75	AAN17392.1	2e-31
Carbohydrate metabolism					
Putative purple acid phosphatase [O. sativa (japonica)]	Contig26476_at	2.83	2.06	BAC07354.1	6e-20
Fatty acyl coA reductase [T. aestivum]	Contig10274_at	2.52	2.18	CAD30694.1	1e-59
Probable vacuolar hydrolase, beta-fructosidase [T. aestivum]	Contig2490_at	3.7	2.31	T06338	e-131
Beta-D-xylosidase [H. vulgare]	Contig13674_at	2.78	2.34	AAK38482.1	1e-80
Putative arabinogalactan-like protein [O. sativa (japonica)]	Contig6782_at	3.03	2.36	BAB84493.1	3e-23

Putative NAD dependent epimerase [<i>A. thaliana</i>]	Contig16221_at	2.71	2.38	NP_189024.1	8e-55
Endo-1,4-beta-glucanase Cel1 [<i>H. vulgare subsp.</i>]	HVSMEn0019D12r2_s_at	3.25	2.52	BAA94257.1	2e-10
RuBisCO large subunit-binding protein subunit beta, chloroplastic [<i>Secale cereale</i>]	Contig807_at	2.79	2.75	Q43831	4e-98
Glucan endo-1,3-beta-glucosidase [<i>H. vulgare subsp.</i>]	Contig1632_at	2.31	2.8	AAA32960.1	e-169
Putative xylanase inhibitor protein [<i>O. sativa</i> (japonica)]	Contig5996_s_at	3.42	3.06	BAC10141.1	1e-30
Xyloglucan endo-1,4-beta-D-glucanase [<i>H. vulgare subsp.</i>]	HVSMEn00004L16r2_at	4.63	3.54	T06201	1e-64
Xyloglucan endo-1,4-beta-D-glucanase [<i>H. vulgare subsp.</i>]	Contig2670_x_at	7.42	3.67	T06201	e-154
Putative acid phosphatase [<i>H. vulgare subsp.</i>]	Contig2433_s_at	2.48	4.73	CAB71336.1	e-112
Apyrase GS52 [<i>Glycine soja</i>]	Contig3332_at	3.88	6.52	AAG32960.1	4e-55
RuBisCO subunit binding-protein alpha subunit, chloroplast precursor [<i>S. cereale</i>]	rbags36a18_s_at	6.46	11	P08823	5e-08
Cell growth, division					
Porphobilinogen deaminase [<i>T. aestivum</i>]	Contig5956_at	2.1	2.16	AAL12220.1	e-122
Expansin [<i>Festuca pratensis</i>]	Contig3675_at	4.48	2.4	CAC06433.1	e-92
23 kDa jasmonate-induced protein 1 [<i>H. vulgare</i>]	Contig1679_s_at	4.52	3.23	P32024	8e-93
Fat metabolism					
Similar to latex allergen from <i>Hevea brasiliensis</i> [<i>A. thaliana</i>]	Contig4196_at	2.82	2.85	AAM63157.1	2e-53
GDSL-motif lipase/hydrolase-like protein [<i>A. thaliana</i>]	Contig15_s_at	3.4	3.05	NP_200316.1	3e-15
Allene oxide synthase [<i>H. vulgare subsp.</i>]	Contig3096_s_at	3.48	3.46	CAB86384.1	e-121
Similar to lipases [<i>A. thaliana</i>]	Contig6611_at	4.26	10.74	AAF63138.1	e-71
Photosynthesis					
Coproporphyrinogen III oxidase, chloroplast precursor [<i>H. vulgare</i>]	Contig5401_s_at	2.35	2.36	Q42840	e-110
Putative protoporphyrinogen IX oxidase [<i>O. sativa</i> (japonica)]	Contig7919_at	2.23	3.12	BAB39998.1	e-115
Chloroplast Cpn21 protein [<i>A. thaliana</i>]	Contig3840_at	2.57	3.65	NP_197572.1	5e-87
Chlorophyll a/b-binding protein WCAB precursor [<i>T. aestivum</i>]	Contig949_at	2.1	11.44	AAB18209.1	e-125
Protein synthesis					
Strictosidine synthase-related protein [<i>A. thaliana</i>]	Contig9052_at	2.31	2.04	NP_563818.1	1e-83
Chloroplast 50S ribosomal protein L2 [<i>H. vulgare</i>]	ChlorContig17_s_at	2.09	2.75	P41096	e-129
50S ribosomal protein L24, chloroplast precursor [<i>A. thaliana</i>]	Contig6148_at	2.01	2.86	NP_200271.1	3e-55
50S ribosomal protein L12-1, chloroplast precursor [<i>S. cereale</i>]	Contig8125_at	2.04	3.24	Q06030	7e-46
30S ribosomal protein S17, chloroplast precursor [<i>O. sativa</i>]	Contig4490_s_at	2.08	3.41	Q9ZST1	6e-45
50S ribosomal protein L5 [<i>O. sativa</i>]	Contig5775_at	2.23	3.49	AAC64970.1	e-106
Ribosomal protein L29 [<i>Z. mays</i>]	Contig9437_at	2.88	3.61	AAD50383.1	2e-50
Plastid ribosomal protein L11 [<i>O. sativa</i> (japonica)]	Contig8084_at	2.57	3.72	BAB21483.1	6e-77
RuBisCO subunit binding-protein beta subunit [<i>S. cereale</i>]	Contig807_s_at	2.61	3.9	Q43831	4e-98
Putative ribonucleoprotein [<i>O. sativa</i>]	Contig5988_at	3.81	4	AAL82527.1	6e-76
Ribosomal protein L12.1 precursor, chloroplast [<i>S. cereale</i>]	Contig12793_at	2.38	4.03	S30199	2e-53
Expressed protein; protein id: At4g29060.1, [<i>A. thaliana</i>]	Contig3659_s_at	2.67	4.13	NP_567820.1	2e-54
Expressed protein; protein id: At4g29060.1, [<i>A. thaliana</i>]	Contig3659_at	2.37	4.56	NP_567820.1	2e-54
Putative ribosomal protein L18 [<i>O. sativa</i>]	Contig5585_s_at	2.6	4.58	AAL79739.1	5e-62
Plastid-specific ribosomal protein 2 precursor [<i>S. oleracea</i>]	Contig9436_at	2.89	4.83	AAF64167.1	3e-50
Putative elongation factor P [<i>A. thaliana</i>]	Contig17155_at	2.84	5.99	NP_566333.1	5e-74
Adenosine diphosphate glucose pyrophosphatase [<i>H. vulgare subsp.</i>]	Contig2769_s_at	15.54	42.64	CAC32847.1	4e-72
Signal transduction					
33 kDa secretory protein [<i>O. sativa</i>]	Contig20580_at	2.04	2.09	AAC36744.1	4e-40
Putative leucine-rich repeat transmembrane protein kinase [<i>A. thaliana</i>]	Contig13334_at	2.92	2.15	NP_192248.1	3e-63
Unknown classified					
(AY088630) unknown [<i>A. thaliana</i>]	Contig18643_at	2	2.39	AAM66952.1	3e-15
Hypothetical protein [<i>O. sativa</i> (japonica)]	Contig17412_at	2.14	2.42	BAB89418.1	5e-33
Putative protein [<i>A. thaliana</i>]	Contig5364_at	2.01	2.42	NP_194537.1	2e-45
Hypothetical protein [<i>Anabaena</i> sp. (strain PCC 7120)]	Contig6063_s_at	2.28	2.42	NP_487053.1	9e-34
Putative protein [<i>A. thaliana</i>]	Contig5475_s_at	2.65	2.43	NP_568160.1	1e-23
Hypothetical protein [<i>O. sativa</i>]	Contig504_x_at	2.03	2.48	AAG46123.1	5e-38
Unnamed protein product [<i>O. sativa</i> (japonica)]	Contig228_s_at	2.55	2.64	BAA96147.1	9e-67
Hypothetical protein [<i>O. sativa</i> (japonica)]	Contig10379_at	2.67	2.78	BAB16875.1	8e-07
Expressed T31J12.3 protein [<i>A. thaliana</i>]	Contig6804_at	4.79	2.83	NP_563841.1	9e-37
Expressed protein [<i>A. thaliana</i>]	Contig18991_at	2.61	3.55	NP_680449.1	4e-17
Hypothetical protein [<i>O. sativa</i> (japonica)]	Contig7338_at	2.05	3.56	AAL58119.1	1e-43
Putative protein [<i>A. thaliana</i>]	Contig20033_at	2.8	3.65	NP_198202.1	2e-19
Unknown protein [<i>O. sativa</i>]	Contig13271_at	3.01	3.81	AAL58188.1	e-103
Expressed protein [<i>A. thaliana</i>]	Contig5487_s_at	4.65	3.87	NP_564683.1	1e-19
P0520B06.12 [<i>O. sativa</i> (japonica)]	Contig7279_at	2.98	4.42	BAB92188.1	2e-86
Expressed protein [<i>A. thaliana</i>]	HVSMEn00061H5r2_at	2.03	5.04	NP_566739.1	2e-27
P0520B06.12 [<i>O. sativa</i> (japonica)]	HVSMEn0001H24r2_s_at	2.41	5.24	BAB92188.1	6e-13

OSJNBa0086B14.7 [<i>O. sativa</i> (japonica)]	Contig11993_at	2.08	5.27	CAD40835.1	4e-12
Expressed protein [<i>A. thaliana</i>]	HVSMEd0010M122_at	2.33	7.54	NP_565093.1	3e-37
Putative protein [<i>A. thaliana</i>]	Contig5704_at	3.63	8.38	NP_190439.1	7e-44
unknown protein [<i>O. sativa</i> (japonica)]	Contig8346_at	3.9	10.16	BAC10351.1	e-113
OSJNBb0066J23.1 [<i>O. sativa</i> (japonica)]	Contig16214_at	14.32	10.93	CAD40597.1	3e-52
Unnamed protein product [<i>O. sativa</i> (japonica)]	Contig6075_at	22.66	63.82	BAA94780.1	2e-76
Putative protein [<i>A. thaliana</i>]	Contig10346_at	2.22	2.58	NP_190483.1	2e-43
None					
none	HR01A18u_x_at	2.97	2.11	none	none
none	Contig5365_s_at	2.11	2.14	none	none
none	HK06M02r_at	2.94	2.14	none	none
none	HO10P07S_at	2.04	2.15	none	none
none	HVSMEd0002K022_s_at	3.96	2.17	none	none
none	HE01D12u_at	2.9	2.28	none	none
none	HA10M12u_s_at	2.02	2.32	none	none
none	EB07_SQ002_G23_s_at	2.11	2.44	none	none
none	Contig6477_s_at	2.24	2.5	none	none
none	Contig6701_s_at	2.79	2.5	none	none
none	Contig2894_s_at	2.2	2.53	none	none
none	rbaal10d03_x_at	2.36	2.58	none	none
none	HV08L20u_x_at	3.26	2.59	none	none
none	HVSMEd0011H122_x_at	2.18	2.85	none	none
none	HVSMEd0003O11r2_at	2.26	2.93	none	none
none	Contig5807_s_at	7.22	3.11	none	none
none	Contig4031_x_at	2.16	3.13	none	none
none	HV_CEd0015F232_at	2.5	3.47	none	none
none	HW09O19u_x_at	2.64	3.51	none	none
none	HV_CEd0009D092_at	3.09	3.55	none	none
none	Contig12100_at	2.33	3.73	none	none
none	HT09C05u_at	2.42	3.77	none	none
none	HVSMEd0006H21r2_at	2.25	3.82	none	none
none	Contig16541_at	3	3.85	none	none
none	Contig25667_s_at	2.85	3.9	none	none
none	Contig2499_s_at	8.34	4.6	none	none
none	HVSMEd0019B222_x_at	2.85	4.63	none	none
none	Contig12421_at	7.5	5.32	none	none
none	Contig3122_at	2.02	5.49	none	none
none	Contig18518_at	3.58	5.7	none	none
none	basd23g06_s_at	3.09	7.17	none	none
none	Contig3082_s_at	5.49	10.09	none	none
none	Contig13115_at	3.31	11.72	none	none
none	Contig19291_at	6.38	16.45	none	none
none	HS06L16u_x_at	7.26	19.37	none	none
none	HVSMEd0001F11r2_x_at	6.15	21.16	none	none
none	HVSMEd0019B22f_x_at	3.92	52.91	none	none

* The fold change represents the mean ratio of gene expression in leaves of the two genotypes exposed to 5 μ M Cd for 15 d over those in the control. Genes were considered up-regulated and down-regulated if the induction ratio was >2.0 and <-2.0 , respectively.