

Figure S1

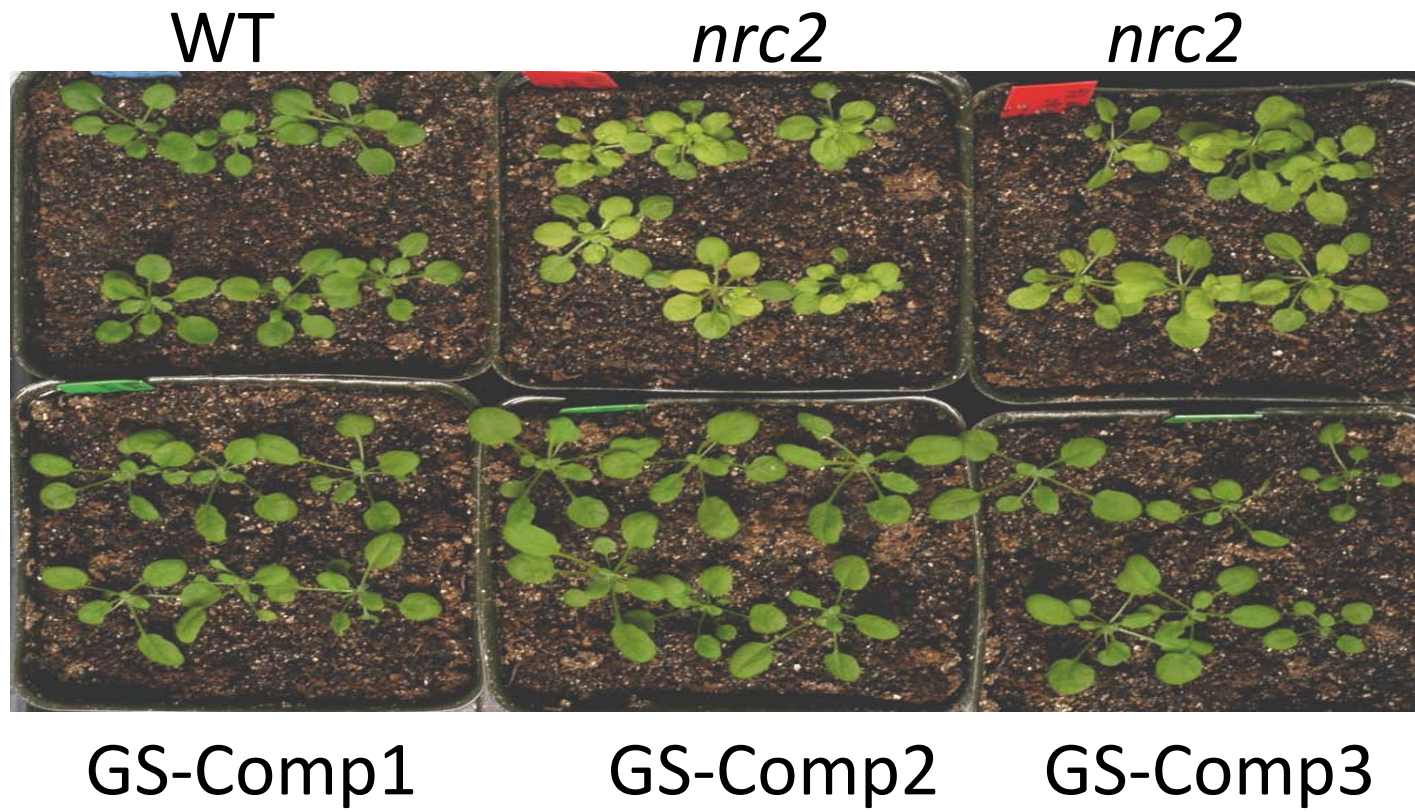


Table S1

Cadmium Control Fold Induction Locus				Description
1294.5	34.1	38.0	At2g44460	putative beta-glucosidase
881.1	34.3	25.7	At3g49580	putative protein
733.5	30	24.5	At5g48850	MALE STERILITY MS5 FAMILY PROTEIN
4999.3	566.4	8.8	At1g78000	high affinity sulphate transporter, putative
963	137.6	7.0	At1g69920	glutathione transferase, putative
214.3	31.7	6.8	At1g23730	putative carbonic anhydrase
281.5	41.8	6.7	At3g45460	putative protein
2461.7	374.7	6.6	At1g17170	glutathione transferase, putative
232.7	35.7	6.5	At4g17710	GLABRA2 like protein
1494.4	277.4	5.4	At2g23270	hypothetical protein
494.4	93	5.3	At1g74310	heat shock protein 101 (HSP101)
3968.7	756.1	5.2	At4g04610	5-adenylylsulfate reductase
271.2	55.7	4.9	At1g10980	membrane protein PTM1 precursor isolog
561	121	4.6	At5g26220	CHAC-LIKE FAMILY PROTEIN
821	192.1	4.3	At4g23600	tyrosine transaminase like protein
4766.1	1132.5	4.2	At4g04830	Similar to METHIONINE SULFOXIDE REDUCTASE
287.2	68.9	4.2	At3g16330	unknown protein
1058.7	259.3	4.1	At1g21140	tonoplast intrinsic protein, alpha (alpha-TIP)
5125.7	1270.5	4.0	At4g21990	5-adenylylsulfate reductase
1944.3	501.6	3.9	At3g12580	heat shock protein 70
253.2	65.8	3.8	At1g65390	disease resistance protein (TIR class), putative
613.4	159.6	3.8	At4g33040	GLUTAREDOXIN FAMILY PROTEIN
3730.1	979.1	3.8	At1g62180	5-adenylylsulfate reductase
2312.7	610.7	3.8	At3g25190	integral membrane protein, putative
868.4	233.9	3.7	At2g37430	putative C2H2-type zinc finger protein
388.4	104.8	3.7	At2g18210	unknown protein
2537.7	688.9	3.7	At1g78340	glutathione transferase, putative
1790.7	494.4	3.6	At3g45140	lipoxygenase AtLOX2
488.1	135.1	3.6	At3g28220	Similar to UBIQUITIN-SPECIFIC PROTEASE 12
554	154.2	3.6	At2g02010_s	glutamate decarboxylase

Table S2

Primer Name	Sequence (5' - 3')	AGI	Purpose
DS451	TCTGCAATAGCACACTCCAGCTT	AHg23100	sequencing primer (CAD2 γ -ECS)
DS452	GTGAATGGTAGATAATGAATCACCA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS453	CATGGAATTTGAAGGATTTTGTGA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS454	AGAAACAATCAAAATTCGTGTATCA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS455	CTCTTCTTCTTCGCTTTCGTGA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS456	TGAAGCTAACATGTTTCTACAGGCT	AHg23100	sequencing primer (CAD2 γ -ECS)
DS457	CGAGCTTCTTAATGGTATCGCT	AHg23100	sequencing primer (CAD2 γ -ECS)
DS458	C GTTGGCTATGTAGAATCAGA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS459	GCATGTCGCTGAAGATGTCTCT	AHg23100	sequencing primer (CAD2 γ -ECS)
DS460	AACTTCCACTACACAGCCTAGA	AHg23100	sequencing primer (CAD2 γ -ECS)
DS566	GTATTATGAGCCAAAGTGATTGT	A5g27380	sequencing primer (GS)
DS567	GAACATTTCTGATTTCTGTGA	A5g27380	sequencing primer (GS)
DS568	ATCACTGATCTTGATTTGTGTT	A5g27380	sequencing primer (GS)
DS569	TATTTGAAACGGTCTTTCAGTA	A5g27380	sequencing primer (GS)
DS570	TTTCAGACATTCGTTGATTCAT	A5g27380	sequencing primer (GS)
DS461-F	GATGTGAATTGACTTCAGCACAA	AHg23100	γ -ECS RT-PCR
DS600-R	GAGGAGTAAAGAGGGCATCAA	AHg23101	γ -ECS RT-PCR
DS462-F	ATAAGCAGCCTAGCATTCCTAT	A5g27380	GS RT-PCR
DS601-R	GCATAGACTCTGAACGTGTACCTA	A5g27380	GS RT-PCR
TJ198-F	CACCATGGCAGTGGCTGCTCTCTCTCT	A5g27380	Cloning of GS
TJ198-R	TCAAATCAGATATATGCTGTCCAAAGACTCC	A5g27381	Cloning of GS
TJ199-F	CACCATGGCCTTGTCTCAAGCAGGAG	AHg23100	Cloning of γ -ECS
TJ199-R	TTAGTACAGCAGCTCTTCGAACACG	AHg23100	Cloning of γ -ECS
RDS129	CGCGATCCAGTGAAGCCAAATTTCTGAAGTTACA	At1g74310	Promoter cloning primers to pPZP \times omegal+
RDS130	CGCGATCCCTTCGATGACTTTTGTAAATCCCTG	At1g74310	Promoter cloning primers to pPZP \times omegal+
RDS131	CGCGATCCAAAGGCGTGTAAATACATTGCAAT	AHg21990	Promoter cloning primers to pPZP \times omegal+
RDS132	CGCGATCCCTTCACTCCAAACCAAATCTCTC	AHg21990	Promoter cloning primers to pPZP \times omegal+
RDS133	CGCGATCCCGCTTGTGATGTTCTTGCTTAGT	At1g78000	Promoter cloning primers to pPZP \times omegal+
RDS134	CGCGATCCAGTATGTAACCTCTGCAAAACAGAACA	At1g78000	Promoter cloning primers to pPZP \times omegal+
RDS135	CGCGATCCAAACGGAAATCGACCAATAAGTATAA	AHg04610	Promoter cloning primers to pPZP \times omegal+
RDS136	CGCGATCCCTTTCACAGCAAAATTTGGATT	AHg04610	Promoter cloning primers to pPZP \times omegal+
RDS137	CGCGATCCAGCGGATATATACAGTTTCTTTTCAT	At1g62180	Promoter cloning primers to pPZP \times omegal+
RDS138	CGCGATCCCTTCAATCAAAAAAAGGATGCTC	At1g62180	Promoter cloning primers to pPZP \times omegal+
RDS141	CGCGATCCCTGGAATGCTTATGATGTTTGCTAC	A5g45140	Promoter cloning primers to pPZP \times omegal+
RDS142	GCCCAAGCTTATTTTTCTCTTCTATAAGGCTTACA	A5g45140	Promoter cloning primers to pPZP \times omegal+
RDS143	GCCCAAGCTTTTAGAGGATGTTGTGTAGAG	A5g12580	Promoter cloning primers to pPZP \times omegal+
RDS144	GCCCAAGCTTTTATTAGAGATCAGAAATGTTCCG	A5g12580	Promoter cloning primers to pPZP \times omegal+
RDS153	CGCGATCCCTGTTTGTGTTTTTCTTCTTCTC	At1g69920	Promoter cloning primers to pPZP \times omegal+
RDS154	CGCGATCCCTGGACTGAAGATTTGTGTTTGT	At1g69920	Promoter cloning primers to pPZP \times omegal+
RDS155	CGCGATCCGCAATCGGAATCCTAAATCAG	At1g17170	Promoter cloning primers to pPZP \times omegal+
RDS156	CGCGATCCGTTGCTTGTGATTAAGCTTCACTA	At1g17170	Promoter cloning primers to pPZP \times omegal+
DS244	CCGTTTTTGGGCTCACTC	At1g69920	AIGSTU12 RT-PCR
DS245	GGCAACGGTAGGCAATGTAA	At1g69920	AtGSTU12 RT-PCR
DS246	CAAAAAGGTGAATGTACGGC	At1g17170	AIGSTU24 RT-PCR
DS247	CAAAAGCAACAACAGATCAACATA	At1g17170	AIGSTU24 RT-PCR
DS224	GCGGCTTCTCTGAGTTTGTG	AHg21990	APR3 RT-PCR
DS225	CCGGGTGATGATCTTTCCT	AHg21990	APR3 RT-PCR
DS226	TGGGACGTAACATACACTTTCAC	At1g78000	SULTRI:2 RT-PCR
DS227	AAGGCAAGGGGAGATATTC	At1g78000	SULTRI:2 RT-PCR
DS228	TTCGCTTCTGGGATCAAAA	AHg04610	APR1 RT-PCR
DS229	ACCGGAATCTCAGACCTTGT	AHg04610	APR1 RT-PCR
DS230	AAGCTTTTTCAGTATCATAGAGACA	At1g62180	APR2 RT-PCR
DS231	CTGGGTCAAAGACCTGTAC	At1g62180	APR2 RT-PCR
DSelfa-F	TAGCCGCAAGACTCCTTTTCAGATTC	A5g60390	EF1- α RT-PCR
DSelfa-R	GATGTCCTGGGGCATCAATGACT	A5g60391	EF1- α RT-PCR

Supplementary Information Legends

Figure S1: Visual phenotype of 20 day-old *nrc2* mutant plants grown in soil. Compared to Col-0 (WT), the *nrc2* mutants have pale yellow leaves. In contrast, the complemented T2 seedlings (GS-Comp1 to 3) have healthy green leaves similar to WT. This observation was made for six transformant lines.

Table S1: A list of the 30 genes most influenced by cadmium exposure ranked in order of decreasing induction. The entries highlighted represent the nine genes selected for promoter analysis in this study. Microarray data can be found at the Gene Omnibus (GEO) website, <http://www.ncbi.nlm.nih.gov/geo/>.

Table S2: A list of primers used for RT-PCR, promoter cloning, gene sequencing and complementation experiments.