

Table S3. Groups of functionally related genes up-regulated in roots of the *oas-a1* mutant when compared with wild type

Genes with a fold change (\log_2 [ratio between *oas-a1* roots and wild type roots]) higher than 2 and P value < 0.05 are shown in the table grouped by functional categories. Raw data can be found in the Supplemental material. The three genes more highly expressed in the mutant are highlighted.

Functional category (Locus identifier)	Annotation	Fold change	P value
Stress			
AT3G54420	Class IV chitinase (CHIV)	3.47	0.001
AT5G45070	Disease resistance protein (TIR class), putative	3.37	0.000
AT3G14200	DNAJ heat shock N-terminal domain-containing protein	2.69	0.007
AT5G49910	Heat shock protein 70 / HSP70 (HSC70-7)	2.09	0.005
AT2G17060	Disease resistance protein (TIR-NBS-LRR class), putative	2.07	0.003
AT3G13650	Disease resistance response protein-related/ similar to pathogenesis-related protein	2.04	0.027
Oxidative stress-related			
AT2G36690	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	4.30	0.000
AT1G19250	Flavin-containing monooxygenase family protein / FMO family protein	3.33	0.001
AT5G45340	Cytochrome P450 family protein	2.84	0.002
AT4G36430	Peroxidase, identical to cDNA class III peroxidase ATP31	2.49	0.005
AT1G78340	Gutathione S-transferase, putative	2.42	0.015
AT4G37400	Cytochrome P450 family protein, similar to cytochrome P450 monooxygenase CYP91A2	2.29	0.000
Hormone signaling and metabolism			
AT3G24500	Putative ethylene-responsive transcriptional coactivator MBF1	4.19	0.013
AT5G62920	Two-component responsive regulator / response regulator 6 (ARR6)	2.56	0.018
AT4G34000	ABA-responsive element-binding protein / (ABRE) / (ABF3)	2.19	0.040
AT5G51310	Gibberellin 20-oxidase-related	2.06	0.025
Development			
AT3G30720	Expressed protein, highly expressed in senescent leaves and mature pollen	4.04	0.000
AT5G47060	Senescence-associated protein-related, similar to SAG102	2.31	0.034
RNA			
AT1G10480	Zinc finger (C2H2 type) family protein	3.02	0.002

AT5G62430	Dof-type zinc finger domain-containing protein	2.89	0.027
AT5G24120	RNA polymerase sigma subunit SigE	2.24	0.024
AT1G07350	Transformer serine/arginine-rich ribonucleoprotein, putative	2.13	0.014
CHO metabolism			
AT5G11110	Similar to sucrose-phosphate synthase	2.77	0.036
AT1G78090	Trehalose-6-phosphate phosphatase (TPPB)	2.31	0.001
Pentose-phosphate pathway			
AT1G24280	Plastidic glucose-6-phosphate dehydrogenase	2.94	0.000
Lipid metabolism			
AT3G15650	Phospholipase/carboxylesterase family protein	2.55	0.007
AT2G38180	GDSL-motif lipase/hydrolase family protein	2.52	0.001
Secondary metabolism			
AT5G66690	UDP-glucuronosyl/UDP-glucosyl transferase family protein	2.54	0.003
AT3G51240	Naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H)	2.38	0.040
AT3G50300	Transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase	2.35	0.000
Metal handling			
AT5G01600	Ferritin 1 (FER1)	2.19	0.017
Transport			
AT5G44110	ABC transporter family protein	3.16	0.002
AT4G10310	Sodium transporter AtHKT1	2.78	0.004
AT3G27170	Chloride channel protein (CLC-b)	2.58	0.000
AT3G62270	Anion exchange family protein	2.32	0.019
AT1G59740	Proton-dependent oligopeptide transport (POT) family protein	2.07	0.003
AT4G10380	Major intrinsic family protein / MIP family protein	2.03	0.004
AT5G02270	ABC transporter family protein, NBD-like protein POP	2.01	0.044
Miscellaneous			
AT5G54040	DC1 domain (rich in cysteines and histidines)-containing protein	2.28	0.000
AT2G39380	Exocyst subunit EXO70 family protein, putative exocyst subunits	2.25	0.000
AT1G67360	Rubber elongation factor (REF) family protein	2.23	0.047
Not assigned			
AT3G07090	Expressed protein	2.63	0.006
AT1G17090	Expressed protein	2.29	0.023
AT3G02910	Expressed protein	2.25	0.004