Table S4. *Groups of functionally related genes up-regulated in shoots of the* oas-a1 *mutant when compared with wild type*

Genes with a fold change (log2[ratio between *oas-a1* shoots and wild type shoots]) 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			
AT5G24780	Vegetative storage protein 1 precursor (VSP1), response to jasmonic acid stimulus	6.18	0.002
AT5G37260	Myb family transcription factor, response to salt stress; to abscisic acid, auxin, ethylene, gibberellic acid, jasmonic acid and salicylic acid stimuli	4.37	0.002
AT2G34810	FAD-binding domain-containing protein, response to wounding and jasmonic acid stimulus	3.21	0.007
AT2G33380	Calcium-binding RD20 protein (RD20), induced by abscisic acid during dehydration	2.86	0.016
AT3G19680	Expressed protein, response to heat stress	2.77	0.002
AT1G73010	Expressed protein, similar to phosphatase, strong response to isoxaben and senescence	2.47	0.052
AT1G55260	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	2.44	0.031
AT2G04030	Heat shock protein, putative	2.34	0.001
AT5G15950	Adenosylmethionine decarboxylase family protein, spermidine biosynthetic process	2.32	0.035
AT4G19530	Disease resistance protein (TIR-NBS-LRR class), putative	2.25	0.012
AT4G23600	Cystine lyase, coronatine-responsive tyrosine aminotransferase, response to wounding, jasmonic acid and abscisic acid stimuli, hyperosmotic salinity, microbial phytotoxin	2.16	0.014
AT3G28270	Expressed protein, response to norflurazon, syringolin, and biotic stress	2.13	0.004
AT4G37260	Transcription factor activity, response to salt stress, abscisic acid, auxin, ethylene, gibberellic acid, jasmonic acid and salicylic acid stimuli, response to cadmium ion	2.06	0.035
AT4G09350	DNAJ heat shock N-terminal domain-containing protein	2.02	0.003
Oxidative stress-related			
AT5G24770	Vegetative storage protein 2 precursor (VSP2), response to oxidative stress	6.18	0.002
AT1G56650	Member of the R2R3 factor gene family, removal of superoxide radicals, response to salt stress and jasmonic acid stimulus	3.83	0.007
AT3G42570	Peroxidase-related, response to oxidative stress	2.54	0.000
AT3G17070	Peroxidase, putative, response to oxidative stress	2.54	0.000
AT2G34490	Cytochrome P450 family protein	2.52	0.005
AT1G13080	Cytochrome P450 family protein, identical to cytochrome P450 monooxygenase	2.41	0.004

Hormone signaling and metabolism			
AT1G72430	Auxin-responsive protein-related	2.99	0.006
AT5G24150	Squalene monooxygenase 1,1	2.75	0.004
AT1G75080	Brassinosteroid signalling positive regulator	2.02	0.010
AT1G19350	Brassinosteroid signalling positive regulator	2.02	0.010
Development			
AT5G65870	Phytosulfokines 5 (PSK5), cell proliferation, cell differentiation, organ morphogenesis	3.18	0.006
AT1G22160	Senescence-associated protein-related	2.69	0.008
AT2G02450	No apical meristem (NAM) family protein	2.28	0.027
Signaling			
AT4G33660	Expressed protein, G-protein coupled receptor protein signaling pathway	2.55	0.004
AT2G02950	Phytochrome kinase substrate 1 (PKS1)	2.13	0.012
AT2G30520	Signal transducer of phototropic response (RPT2)	2.06	0.003
Redox regulation			
AT3G62950	Glutaredoxin family protein	2.20	0.011
RNA			
AT1G51140	Basic helix-loop-helix (bHLH) family protein	3.68	0.000
AT5G43270	Squamosa promoter-binding protein-like 2 (SPL2)	3.18	0.001
AT2G34620	Mtochondrial transcription termination factor-related	3.03	0.002
AT5G67420	LOB domain protein 37	2.99	0.009
AT1G68520	Zinc finger (B-box type) family protein	2.62	0.000
AT5G67480	TAZ zinc finger family protein / BTB/POZ domain-containing protein	2.54	0.001
AT3G02830	Zinc finger (CCCH-type) family protein	2.54	0.000
AT3G54810	Zinc finger (GATA type) family protein	2.37	0.017
AT3G20810	Transcription factor jumonji (jmjC) domain-containing protein	2.30	0.000
AT3G07650	Zinc finger (B-box type) family protein	2.07	0.022
AT1G49010	Myb family transcription factor	2.01	0.017
AT2G18300	Basic helix-loop-helix (bHLH) family protein	2.01	0.008
Protein			
AT5G58140	Protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1)	2.72	0.001
AT2G24280	Serine carboxypeptidase S28 family protein	2.54	0.000
AT3G20340	Expressed protein, N-terminal protein myristoylation	2.54	0.017
AT5G59130	Subtilase family protein	2.51	0.015
AT3G05640	Protein phosphatase 2C, putative	2.25	0.031
AT1G49200	Zinc finger (C3HC4-type RING finger) family protein	2.23	0.000
AT4G02630	Protein kinase family protein	2.18	0.031
AT5G45650	Subtilase family protein	2.07	0.007
AT1G73390	Expressed protein, N-terminal protein myristoylation	2.04	0.022

CHO metabolism			
AT4G15210	Beta-amylase (BMY1)	4.95	0.019
AT4G39330	Mannitol dehydrogenase, putative	3.44	0.034
AT4G10120	Sucrose-phosphate synthase, putative	2.70	0.015
AT2G37760	Aldo/keto reductase family protein, similar to chalcone reductase	2.44	0.001
AT4G39800	Inositol-3-phosphate synthase isozyme 1/myo-inositol-1-phosphate synthase 1	2.27	0.013
AT2G37770	Aldo/keto reductase family protein, similar to chalcone reductase	2.21	0.013
AT1G02850	Glycosyl hydrolase family 1 protein	2.16	0.013
AT3G23920	Beta-amylase, putative	2.15	0.028
Cell wall			
AT4G24000	Cellulose synthase family protein	2.96	0.029
AT2G01850	Endoxyloglucan transferase	2.63	0.000
AT4G19420	Pectinacetylesterase family protein	2.61	0.004
AT1G57590	Similar to pectinacetylesterase, putative	2.45	0.004
TCA/C1-metabolism			
AT3G52720	Carbonic anhydrase family protein	2.27	0.001
AT1G53310	Phosphoenolpyruvate carboxylase, putative, response to water deprivation	2.20	0.007
AT3G55630	Dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS4)	2.11	0.036
Lipid metabolism			
AT5G45950	GDSL-motif lipase/hydrolase family protein	2.96	0.009
AT3G11670	Digalactosyldiacylglycerol synthase 1 (DGD1)/galactolipid galactosyltransferase	2.38	0.022
AT2G11810	1,2-Diacylglycerol 3-beta-galactosyltransferase, putative/identical to monogalactosyldiacylglycerol synthase type C	2.12	0.045
AT1G28660	Lipase	2.08	0.018
AT1G28670	Lipase	2.08	0.018
Nucleotide metabolism			
AT2G18230	Inorganic pyrophosphatase (soluble) (PPase)	3.12	0.000
Secondary metabolism			
AT4G03070	2-Oxoglutarate-dependent dioxygenase (AOP1.2), 2OG-Fe(II) oxygenase superfamily domain, glucosinolate biosynthesis	2.14	0.000
AT5G57800	CER1 protein, putative (WAX2)	2.06	0.009
AT2G29290	Tropinone reductase, putative / tropine dehydrogenase, putative, oxidoreductase activity	2.01	0.012
Cell			
AT5G10470	Kinesin motor protein-related, TH65 protein	2.39	0.002
Photosynthesis			
ATCG00270	PSII D2 protein	2.45	0.008
Metal handling			
AT5G01600	Ferritin 1 (FER1)	2.78	0.002

AT3G56090	Ferritin, putative	2.54	0.005
AT2G40300	Ferritin, putative	2.17	0.019
Transport			
AT5G06530	ABC transporter family protein	3.16	0.004
AT2G36830	Major intrinsic family protein, water channel activity	3.15	0.003
AT2G37170	Plasma membrane intrinsic protein 2B/aquaporin PIP2.2	2.97	0.002
AT2G37180	Plasma membrane intrinsic protein 2C/aquaporin PIP2.3	2.97	0.002
AT2G36590	Proline transporter, putative	2.69	0.036
AT4G22200	Potassium channel protein	2.62	0.000
AT4G00430	Plasma membrane intrinsic protein, water channel activity, response to water deprivation	2.40	0.012
AT2G26690	Nitrate transporter (NTP2), response to wounding and jasmonic acid stimulus	2.22	0.004
AT3G05030	Sodium proton exchanger, putative (NHX2)	2.14	0.004
AT1G64780	Ammonium transporter 1, member 2 (AtAMT1;2)	2.13	0.029
AT2G47800	Glutathione-conjugate transporter (MRP4), response to nematode and water deprivation	2.09	0.008
AT4G37270	Cadmium/zinc-transporting ATPase, putative (HMA1), copper-exporting ATPase activity	2.06	0.035
AT3G53420	Plasma membrane intrinsic protein 2A (PIP2A) / aquaporin PIP2.1	2.03	0.001
AT2G45960	Plasma membrane intrinsic protein 1B (PIP1B) / aquaporin PIP1.2	2.01	0.000
Miscellaneous			
AT5G02230	Haloacid dehalogenase-like hydrolase family protein	3.42	0.001
AT5G58770	Dehydrodolichyl diphosphate synthase, putative	2.63	0.026
AT1G01320	Tetratricopeptide repeat (TPR)-containing protein	2.51	0.000
AT3G61220	Short-chain dehydrogenase/reductase (SDR) family protein, oxidoreductase activity	2.47	0.009
AT4G33670	L-galactose dehydrogenase (L-GalDH)	2.31	0.006
AT5G19130	GPI transamidase component family protein	2.30	0.012
AT4G14930	Acid phosphatase survival protein SurE, putative, acid phosphatase activity	2.12	0.006
AT1G22370	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2.06	0.016
Not assigned			
AT3G30720	Expressed protein	4.06	0.000
AT5G62140	Expressed protein	2.94	0.000
AT4G28080	Expressed protein	2.70	0.001
AT1G69760	Expressed protein	2.40	0.021
AT4G33666	Expressed protein	2.31	0.006
AT5G19120	Expressed protein	2.30	0.012
AT1G56580	Expressed protein	2.01	0.022