**Table S5**. *Groups of functionally related genes down-regulated in roots of the* oas-a1 *mutant when compared with wild type* Genes with a fold change (log2[ratio between *oas-a1* roots and wild type roots]) lower than 0.5 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 with the lowest expression in the mutant are highlighted.

Functional category	Annotation	Fold change	P Value
(Locus identifier)			
Stress			
AT5G47240	MutT/nudix family protein, jasmonic-responsive, senescence induced	0.20	0.000
AT5G39890	Expressed protein, strongly induced by anoxia and hypoxia	0.24	0.015
AT3G30775	Proline oxidase, mitochondrial /Osmotic stress-responsive proline dehydrogenase (POX)	0.30	0.001
AT1G80920	DNAJ heat shock N-terminal domain-containing protein	0.37	0.016
AT1G56300	DNAJ heat shock N-terminal domain-containing protein	0.49	0.012
Hormone signaling a	nd metabolism		
AT1G72360	Member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor		
	family	0.30	0.016
AT4G37390	IAA-amido synthase, auxin-responsive	0.37	0.004
AT1G59500	IAA-amido synthase	0.37	0.004
AT5G61590	Member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor		
	family	0.40	0.047
AT5G08350	GRAM domain-containing protein / ABA-responsive protein-related	0.49	0.009
Development			
AT4G35770	Senescence-associated protein (SEN1)	0.06	0.009
AT1G15040	Glutamine amidotransferase-related, senescence induced	0.13	0.023
AT2G20670	Expressed protein, strongly induced by senescence	0.22	0.014
AT4G08300	Nodulin MtN21 family protein	0.29	0.005
AT2G32150	Haloacid dehalogenase-like hydrolase family protein, strongly induced by senescence	0.31	0.005
AT5G66170	Senescence-associated family protein	0.44	0.045
AT4G08290	Nodulin MtN21 family protein	0.46	0.028
Redox regulation			
AT5G61440	Thioredoxin family protein	0.44	0.029
RNA	· -		
AT1G13260	DNA-binding protein RAV1 (RAV1)	0.32	0.004
AT2G25900	Putative Cys3His zinc finger protein (ATCTH)	0.35	0.010
AT5G28770	bZIP transcription factor family protein	0.36	0.005

	A TE C 27 5 40	A classification of the control of t	0.45	0.020
	AT5G37540	Aspartyl protease family protein, weak similarity to chloroplast nucleoid DNA binding protein	0.45	0.030
m	AT5G47390	Myb family transcription factor	0.48	0.042
r	Protein	Time fines and (COLICA types PINIC fines and femily mastering	0.20	0.000
	AT5G22920 AT4G03510	Zinc finger (C3HC4-type RING finger) family protein Zinc finger (C3HC4-type RING finger) family protein (RMA1)	0.20 0.26	0.000
		Protein kinase family protein	0.28	
	AT4G38470	* *	0.28	0.000
	AT5G24490	30S ribosomal protein, putative		0.006
	AT3G23880	F-box family protein, contains F-box domain	0.35	0.007
	AT1G23390	Kelch repeat-containing F-box family protein	0.36	0.004
	AT1G80440	Kelch repeat-containing F-box family protein	0.37	0.016
	AT4G37610	TAZ zinc finger family protein / BTB/POZ domain-containing protein	0.37	0.005
	AT4G28270	Zinc finger (C3HC4-type RING finger) family protein	0.37	0.003
	AT3G48360	Speckle-type POZ protein-related	0.41	0.025
	AT1G61590	Protein kinase, putative	0.41	0.007
	AT3G59940	Kelch repeat-containing F-box family protein	0.46	0.004
	AT4G11360	RING-H2 finger protein RHA1b	0.48	0.025
	AT1G24440	Expressed protein, similar to MTD2	0.49	0.013
	AT3G43430	Zinc finger (C3HC4-type RING finger) family protein (RMA1)	0.50	0.009
(	CHO metabolism			
	AT2G19800	MIOX2- Myoinositol oxygenase 2	0.25	0.000
	AT5G18670	Beta-amylase, putative (BMY3)	0.30	0.001
	AT5G56870	Beta-galactosidase, putative / lactase, putative	0.32	0.024
	AT1G70290	Trehalose-6-phosphate synthase, putative, (UDP-forming)	0.35	0.001
	AT5G20250	Similar to alkaline alpha galactosidase, putative	0.38	0.014
	AT1G80380	Phosphoribulokinase/uridine kinase-related	0.39	0.001
	AT1G61820	Glycosyl hydrolase family 1 protein	0.46	0.013
	AT3G57520	Alkaline alpha galactosidase, putative	0.48	0.033
F	ermentation			
	AT4G33070	Pyruvate decarboxylase, putative	0.10	0.008
I	ipid metabolism			
	AT5G41080	Glycerophosphoryl diester phosphodiesterase family protein	0.14	0.000
S	-assimilation			
	AT5G67520	Adenylylsulfate kinase, chloroplast precursor (APS kinase)	0.44	0.008
N	ucleotide metabolis			
	AT1G30820	CTP synthase, putative / UTPammonia ligase, putative	0.39	0.003
S	econdary metabolis			
	AT5G48110	Terpene synthase/cyclase family protein	0.42	0.025
(	Cell			
	AT1G52250	Dynein light chain type 1 family protein	0.23	0.004
	· <del></del> -			

Transport			
AT5G47560	Encodes a tonoplast malate/fumarate transporter	0.47	0.004
AT2G24240	Potassium channel tetramerisation domain-containing protein	0.50	0.031
AT5G04770	Amino acid permease family protein	0.50	0.001
Miscellaneous			
AT1G09460	Glucan endo-1,3-beta-glucosidase-related	0.32	0.003
AT5G19130	GPI transamidase component family protein	0.34	0.003
AT2G02710	PAC motif-containing protein, similar to nonphototropic hypocotyl 1	0.34	0.007
AT3G61060	F-box family protein / lectin-related	0.39	0.004
AT5G52710	Heavy-metal-associated domain-containing protein	0.41	0.040
AT5G05890	UDP-glucoronosyl/UDP-glucosyl transferase family protein	0.45	0.000
AT4G18340	Glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76	0.46	0.000
AT5G62340	Invertase/pectin methylesterase inhibitor family protein	0.47	0.016
AT3G14050	RelA/SpoT protein, putative (RSH2)	0.48	0.026
AT1G62770	Invertase/pectin methylesterase inhibitor family protein	0.50	0.025
Not assigned			
AT1G33055	Expressed protein	0.21	0.030
AT2G40000	Expressed protein	0.29	0.021
AT1G76590	Zinc-binding family protein	0.32	0.003
AT4G33980	Expressed protein	0.34	0.000
AT1G05575	Expressed protein	0.34	0.029
AT5G19120	Expressed protein, low similarity to extracellular dermal glycoprotein EDGP precursor	0.34	0.003
AT4G19980	Expressed protein	0.35	0.040
AT3G07310	Expressed protein	0.36	0.003
AT5G28610	Expressed protein	0.36	0.004
AT2G15890	Expressed protein	0.36	0.000
AT1G76600	Expressed protein	0.37	0.015
AT4G19160	Expressed protein	0.39	0.003
AT4G16000	Expressed protein	0.42	0.018
AT3G10020	Expressed protein	0.42	0.010
AT5G24890	Expressed protein, weak similarity to MTD1	0.42	0.008
AT2G27830	Expressed protein	0.44	0.003
AT4G23870	Expressed protein	0.46	0.005
AT5G15120	Expressed protein	0.47	0.024
AT3G11420	Fringe-related protein	0.48	0.025
AT5G66050	Expressed protein	0.48	0.010
AT4G36500	Expressed protein	0.49	0.030
AT2G46550	Expressed protein	0.50	0.040