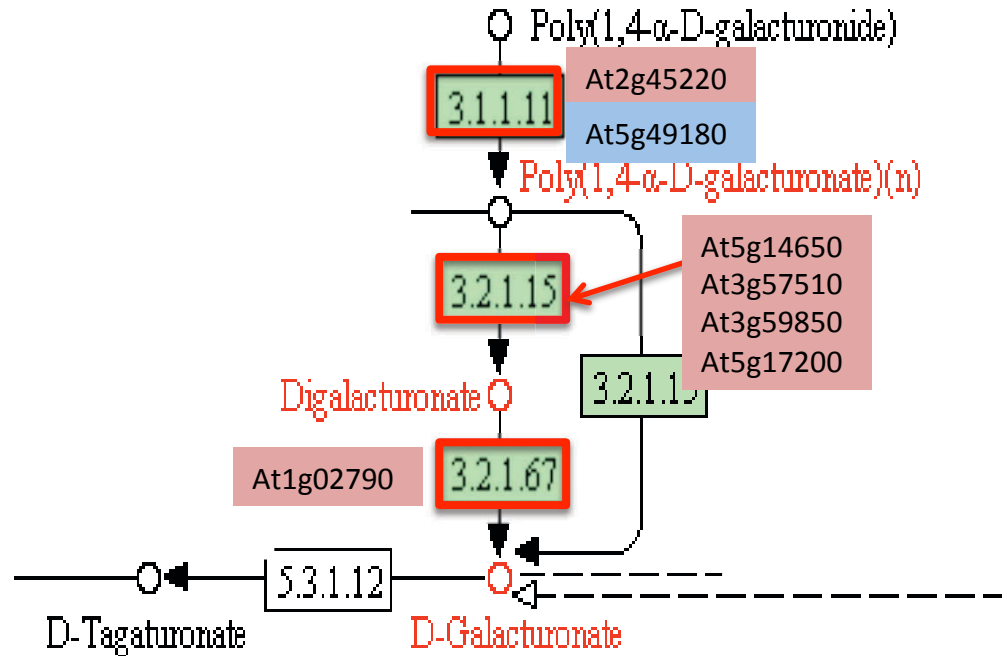


Supplemental Figure 1: Hierarchic clustering of metabolite changes between *atg5* mutants and controls show salicylic dependence of metabolite classes.

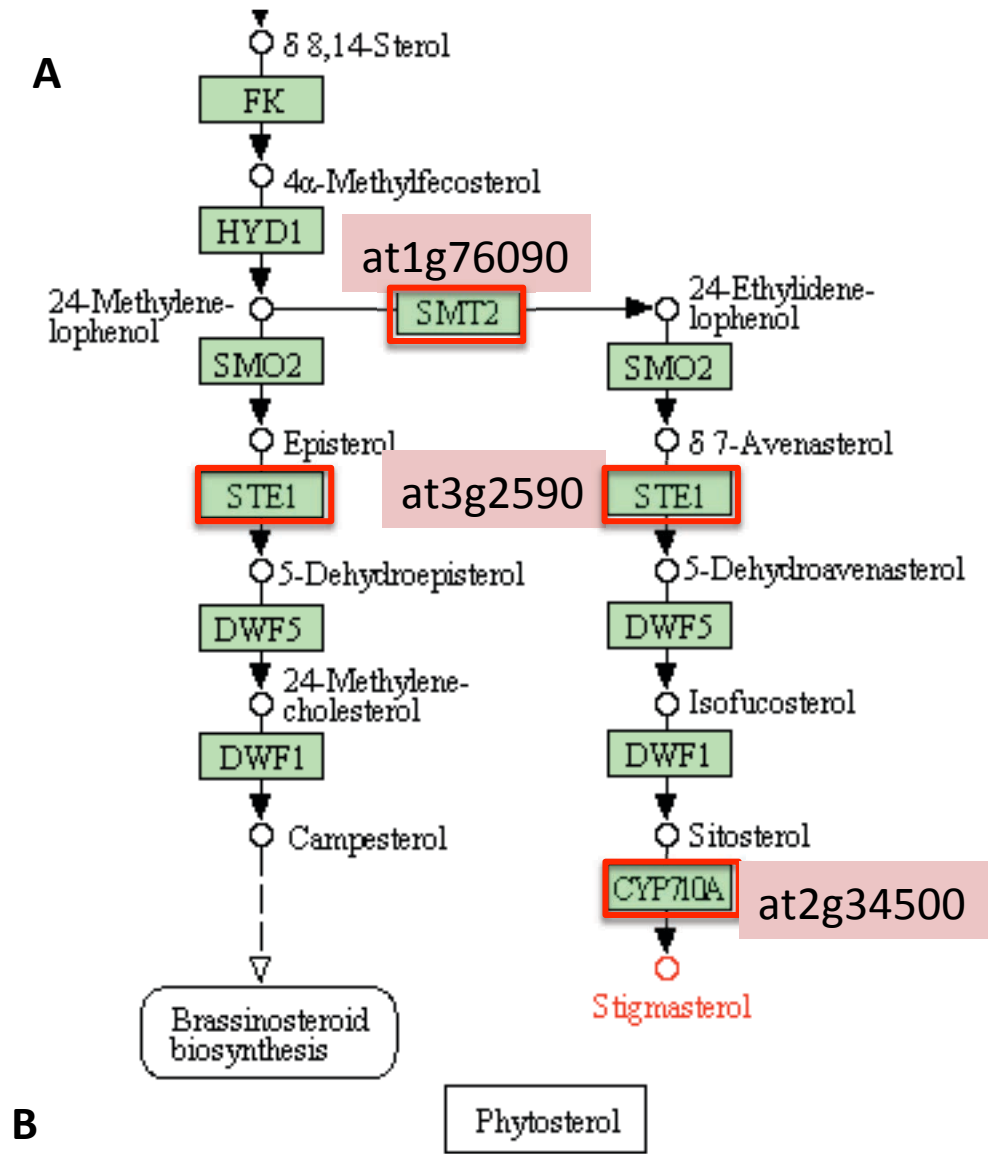
Metabolite relative contents in the rosettes of *atg5*, *atg5.sid2*, *atg5.NahG*, *Col*, *NahG* and *sid2* genotypes, grown under low nitrate conditions for 60 days after sowing are analysed using hierarchic clustering tool (MEV4.0). Clusters show gradation for salicylic acid genotype dependencies. Metabolites that accumulate in *atg5* mutants whatever *Col* wild type, *NahG* and *sid2* genetic background are salicylic acid independent (deep green cluster). Metabolites that accumulate in *atg5* mutants but not in *atg5.sid2*, *atg5.NahG*, are salicylic acid dependent (deep red cluster). The two other clusters (light green and light red) are in between.

A**B**

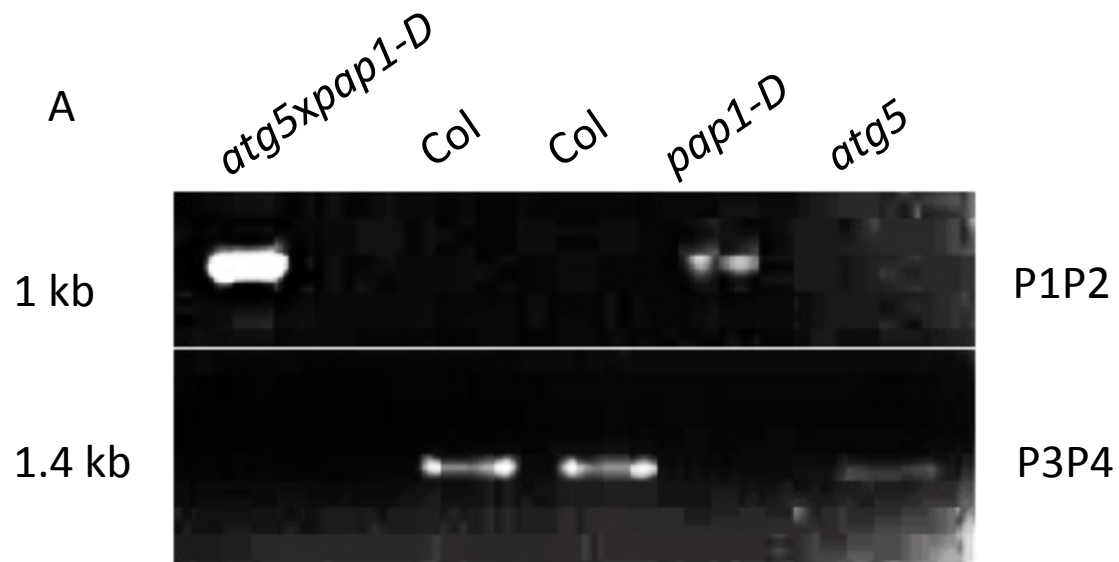
AGI	Name and Function	<i>atg5</i> lowN 30DAS	<i>atg5</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT2G45220	pectinesterase	3.55	8.14	6.14
AT5G14650	polygalacturonase, putative	1.59	2.45	1.27
AT3G57510	ADPG1; polygalacturonase	0.86	8.73	5.49
AT3G59850	polygalacturonase, putative	-2.23	3.06	-0.52
AT5G17200	polygalacturonase	-0.48	0.10	1.25
AT1G02790	PGA4 (POLYGALACTURONASE 4); polygalacturonase	0.51	2.64	0.40
AT5G49180	pectinesterase family protein	-1.07	-1.30	-0.47

Supplemental Figure 2: Genes involved in galacturonate biosynthesis are up-regulated in *atg5*. (A) D-galacturonate pathway was adapted from the KEGG galacturonate pathway available online (<http://www.genome.jp/kegg/pathway.html>). Most of the genes identified on KEGG as coding for the pectine esterases (EC.3.1.1.11) and polygalacturonases (EC.3.2.1.67 and EC.3.2.1.15) involved in the galacturonate pathway are up-regulated (pink boxes) in *atg5* relative to wild type as shown in (B). Relative gene expression in *atg5* compared to wild type is presented as Log₂(fold change) Significant up- or down-regulations (FDR%<10⁻⁵) are indicated by yellow or blue colored cells respectively.

Supplemental Figure 3: Phytosterol pathway is up-regulated in *atg5*. (A) Phytosterol pathway was adapted from the KEGG (<http://www.genome.jp/kegg/pathway.html>). Genes coding for SMT2, STE1 and CYP710A enzymes (pink boxes) are up-regulated in *atg5* relative to wild type (B): the relative expressions of SMT2, STE1 and CYP710A genes in *atg5* are presented as Log2(fold change). Significant up- or down-regulations (FDR%<10⁻⁵) are indicated by yellow or blue colored cells respectively.



		<i>atg5</i> lowN 30DAS	<i>atg5</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT1G76090	SMT3 (STEROL METHYLTRANSFERASE 3)	-0.441	1.187	0.450
AT3G02590	delta 7-sterol-C5-desaturase, putative	-1.151	1.627	0.608
AT2G34500	CYP710A1 (cytochrome P450, family 710,	0.998	3.991	2.936

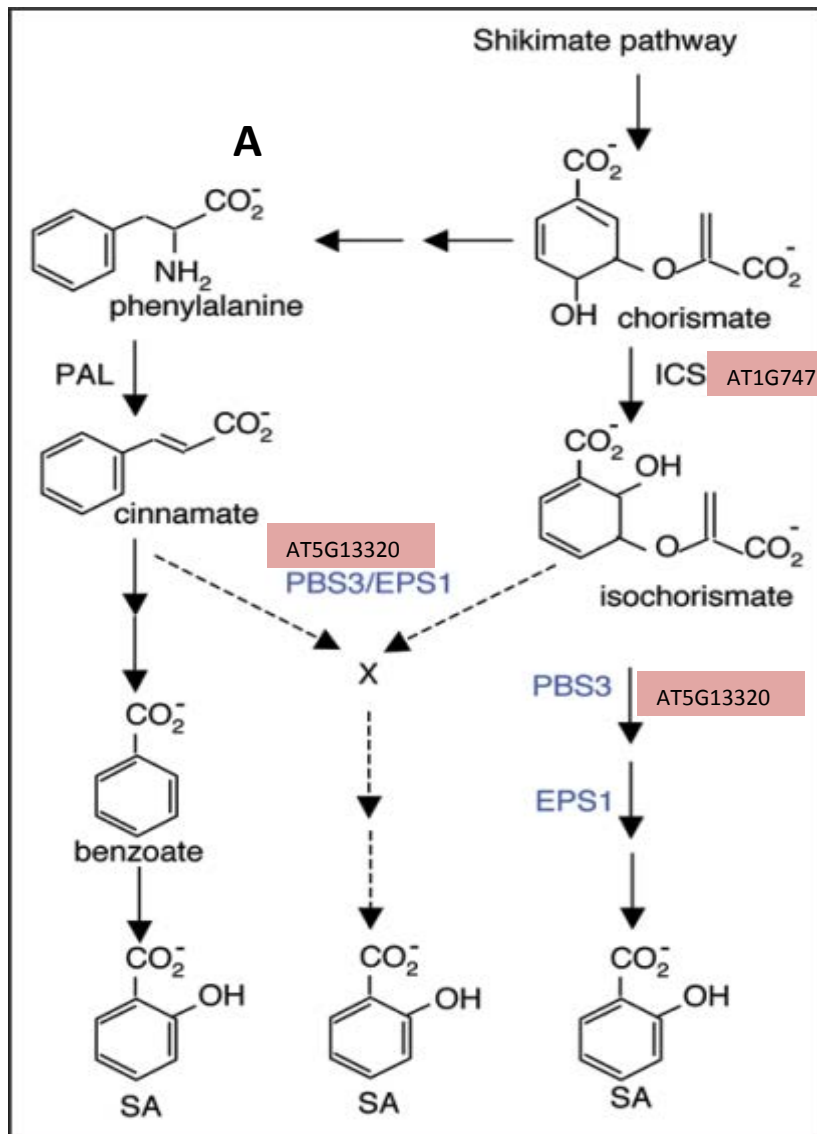


B P1: 5'-TGAGACTTTTCAACAAAGGG-3'
P2: 5'-ACG GAA TAT CTG GAC AGC CGG A-3'
P3: 5'-ACG GAA TAT CTG GAC AGC CGG A-3'
P4: 5'-TGC AGA GAC TAC TCC CTC GTG C-3'

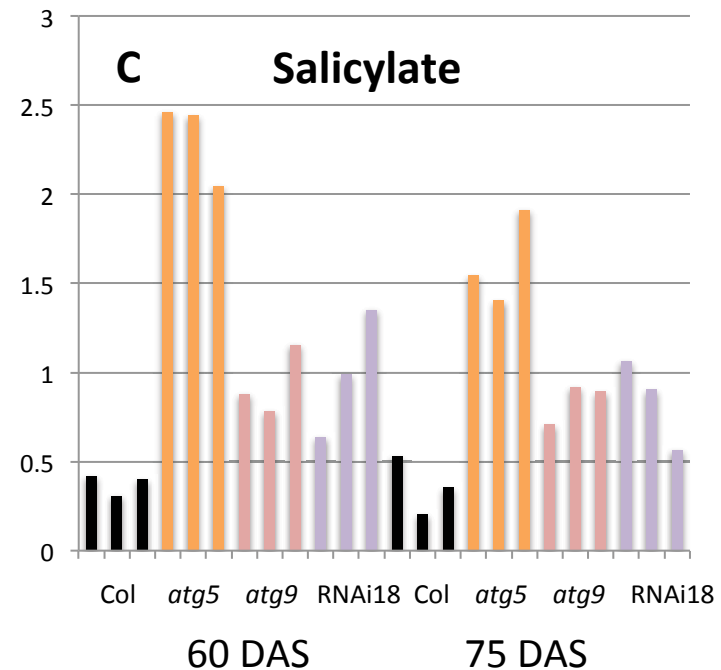
P3P4 amplification reveals *PAP1* wild type allele

P1P2 amplification reveals *pap1-D* dominant allele

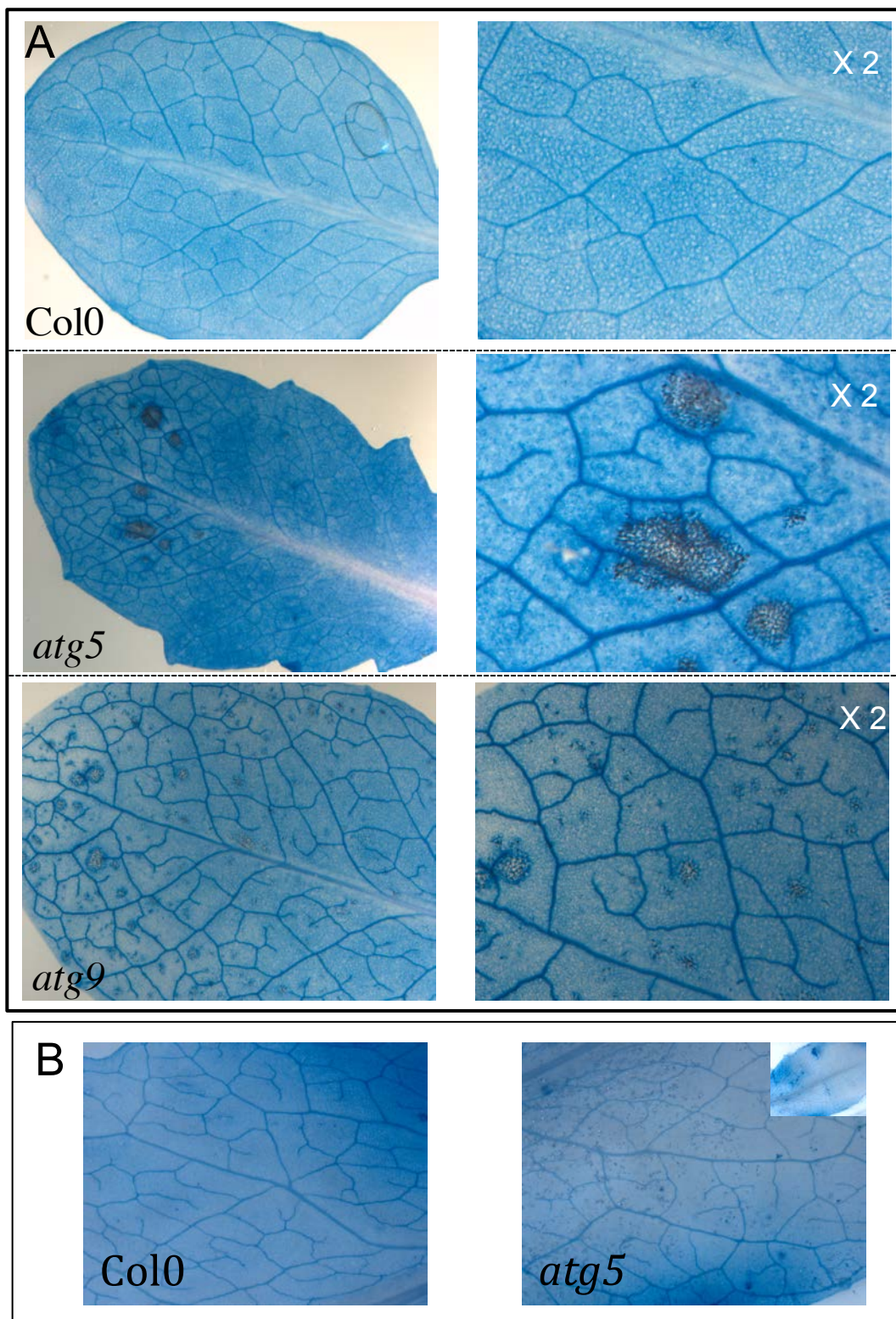
Supplemental Figure 4: PCR genotyping of *atg5.pap1-D* double mutant. A: PCR products on gel. B: Primers used to amplify wild type *PAP1* (P3 and P4) and *pap1-D* (P1 and P2) alleles.



Supplemental Figure 5: Overexpression of isochorismate synthase (ICS) 1 and PBS3 genes in *atg5* relative to wild type explain SA accumulation in autophagy mutants. A: SA biosynthesis pathway showing steps catalysed by ICS and PBS3. B: Genes involved in SA biosynthesis are up-regulated in *atg5* relative to wild type; relative gene expressions in *atg5* compared to wild type are presented as Log₂(fold change) Significant up-regulation (FDR%<10⁻⁵) is indicated by red cells. C: Relative SA concentrations in Col wild type, *atg* mutants and RNAi line grown under low nitrate supply for 60 and 75 days after sowing.

**B**

AGI	function or name	<i>atg5</i> & <i>atg9</i> 30DAS LowN	<i>atg5</i> & <i>atg9</i> 60DAS LowN	<i>atg5</i> 60DAS HighN
at1g74710	isochorismate synthase 1 (ICS1) / isochorismate mutase	-0.106	2.197	1.131
at5g13320	PBS3 (AVRPPHB SUSCEPTIBLE 3)	3.759	4.058	2.899



Supplemental Figure 6: Cell death area on leaves of autophagy mutants. Cell death regions were revealed after boiling leaves in trypan blue staining solution (glycerol 10 mL, lactic acid 10 mL, phenol 9.5 mL and trypan blue 10 mg) for 1 min and incubating at room temperature for 24 h afterward. Destaining was performed by transferring samples into chloral hydrate (1 g.mL⁻¹). A: Col, *atg5*, *atg9* leaves of plants grown under low nitrate conditions for 60 days. B: Col and *atg5* leaves of plants grown under high nitrate conditions for 75 days. Dead cells appear as black clouds in leaf blades.

Supplemental Table 1: Flavonoid compounds identified and quantified using LC-MS.

Compound name (other name)	Ion molecular mass (g.mol ⁻¹)	fragment mass (g.mol ⁻¹)	retention time (min)
Cyanidin 3-O-[2''-O-(xylosyl)-6''-O-(p-coumaroyl) glucoside] 5-O-malonylglucoside (A974)	975	535.2 [Cy + Glc + Mal]+ 727.2 [Cy + Glc + Xyl + Cou]+ 975.2 [Cy + 2Glc + Xyl + Cou + Mal]+	20
Cyanidin 3-O-[2''-O-(xylosyl) 6''-O-(p-O-(glucosyl) p-coumaroyl) glucoside] 5-O-[6'''-O-(malonyl) glucoside] (A1136)	1137	535.2 [Cy + Glc + Mal]+ 889.2 [Cy + 2Glc + Xyl + Cou]+ 1137.2 [Cy + 3Glc + Xyl + Cou + Mal]+	16
Cyanidin 3-O-[2''-O-(2'''-O-(sinapoyl) xylosyl) 6''-O-(p-O-coumaroyl) glucoside] 5-O-[6'''-O-(malonyl) glucoside] (A1182)	1183	535.2 [Cy + Glc + Mal]+ 933.2 [Cy + Glc + Xyl + Sin + Cou]+ 1183.2 [Cy + 2Glc + Xyl + Sin + Cou + Mal]+	23
Cyanidin 3-O-[2''-O-(2'''-O-(synapoyl) xylosyl) 6''-O-(p-O-(glucosyl) p-coumaroyl) glucoside] 5-O-glucoside (A1256)	1257	1095.2 [Cy + 2Glc + Xyl + Cou + Sin]+ 1257.2 [Cy + 3Glc + Xyl + Cou + Sin]+	17
Cyanidin 3-O-[2''-O-(6'''-O-(sinapoyl) xylosyl) 6''-O-(p-O-(glucosyl)-p-coumaroyl) glucoside] 5-O-(6'''-O-malonyl) glucoside (A1342)	1343	535.2 [Cy + Glc + Mal]+ 1095.2 [Cy + 2Glc + Xyl + Cou + Sin]+ 1343.2 [Cy + 3Glc + Xyl + Cou + Sin + Mal]+	17 and 20 for isomer
Km-3,7-di-O-Rha	579	287.2 [Km + H]+ 433.2 [Km + Rha + H]+ 579.2 [Km + 2Rha + H]+	21
Km-3-O-Glc-7-O-Rha	595	287.2 [Km + H]+ 433.2 [Km + Rha + H]+ 595.2 [Km + Rha + Glc + H]+	19
Km-3-O-Rha(1-2)Glc-7-O-Rha	741	287.2 [Km + H]+ 433.2 [Km + Rha + H]+ 741.2 [Km + 2Rha + Glc + H]+	15
Qr-3,7-di-Rha	303		19
Qr-3-O-Glc-7-O-Rha	611	303.2 [Qr + H]+ 449.2 [Qr + Rha + H]+ 611.2 [Qr + Rha + Glc + H]+	17
Qr-3-O-Rha(1-2)Glc-7-O-Rha	757	303.2 [Qr + H]+ 449.2 [Qr + Rha + H]+ 757.2 [Qr + 2Rha + Glc + H]+	6
I-Glc-Rha	625	317.2 [I + H]+ 463.2 [I + Rha + H]+ 625.2 [I + Rha + Glc + H]+	19
Isomère Cyanidin 3-O-[2''-O-(6'''-O-(sinapoyl) xylosyl) 6''-O-(p-O-(glucosyl)-p-coumaroyl) glucoside] 5-O-(6'''-O-malonyl) glucoside	A1342 2		

Supplemental Table 2: Metabolites significantly more or less concentrated in *atg5*, *atg5.sid2*, *atg5.NahG* compared to Col, *sid2*, or NahG controls are listed. Plants were grown under low or high nitrate conditions for 60 days after sowing. Significant differences were tested using T-tests (n=3) and probability is presented (*Pr*). Fold changes are also presented (FC). Yellow cells indicate increased concentrations in *atg5*. Blue cells indicate decreased concentrations in *atg5*. Black cells indicate non significant difference. Deep and light purple cells indicate metabolite on which differences that have been previously found between wild type and *atg5*, *atg9* and *RNAi18*. Deep purple indicates difference that are nitrate condition independent.

Metabolites	Low Nitrate (2 mM)						Metabolites	High Nitrate (10 mM)					
	<i>atg5/Col</i>		<i>atg5-3.sid2/sid2</i>		<i>atg5.NahG/NahG</i>			<i>atg5/Col</i>		<i>atg5-3.sid2/sid2</i>		<i>atg5.NahG/NahG</i>	
	<i>Pr</i>	FC	<i>Pr</i>	FC	<i>Pr</i>	FC		<i>Pr</i>	FC	<i>Pr</i>	FC	<i>Pr</i>	FC
Glycosylsalicylate	0.000	15.587	0.006	2.000	-	-	Melibiose	0.0086	0.277	0.009	0.394	0.017	0.374
γ -tocopherol	0.000	4.230	0.018	4.416	-	-	Galactosylglycerol	0.0064	0.671	0.031	0.667	0.031	0.622
myo-Inositol	0.000	1.277	0.021	1.158	-	-	Xylose	0.0230	0.777	-	-	0.029	0.743
Campesterol	0.001	1.303	0.015	1.191	-	-	Campesterol	0.0115	1.3	0.025	1.2	-	-
Aspartate	0.000	2.189	0.046	1.232	0.001	1.859	Monopalmitine	0.0231	1.4	0.014	1.2	-	-
Rhamnose	0.001	1.918	0.004	1.364	0.032	1.443	Glutamate	0.0107	1.4	0.026	1.3	-	-
Glycerol-3-P	0.000	1.471	0.021	1.364	0.002	1.735	β -Sitosterol	0.0005	1.4	0.004	1.4	-	-
β -Sitosterol	0.000	1.428	0.004	1.365	0.003	1.356	Glycosylsalicylate	0.0158	2.3	0.022	1.5	-	-
Ascorbate/Dehydro	0.002	1.507	0.005	1.383	0.006	1.672	Homoserine	0.0011	1.5	0.043	1.7	-	-
Tryptophan	0.002	1.656	0.034	1.387	0.040	1.258	Raffinose	0.0434	1.9	0.001	2.2	-	-
Fructose-6-P	0.003	1.632	0.026	1.405	0.002	1.837	Shikimate	0.0002	1.5	0.001	1.7	0.047	1.3
α -Tocopherol	0.019	1.315	0.042	1.427	0.002	1.331	Sinapinate-cis	0.0173	1.1	-	-	0.047	1.2
Shikimate	0.000	2.247	0.003	1.445	0.004	1.929	Threonine	0.0135	1.3	-	-	0.022	1.2
Methionine	0.000	2.275	0.011	1.459	0.003	1.994	Pipecolate	0.0005	6.9	-	-	0.005	2.3
Linoleic acid	0.017	1.323	0.002	1.514	0.001	1.363							
Digalactosylglycerol	0.001	1.781	0.002	1.564	0.000	1.893							
Ribonate	0.000	1.857	0.000	1.637	0.002	1.607							
Glutamate	0.000	1.623	0.000	1.698	0.001	1.716							
Sucrose	0.023	1.634	0.018	2.490	0.019	1.711							
Raffinose	0.000	2.805	0.000	2.850	0.000	3.398							
Pipecolate	0.000	49.057	0.001	14.446	0.001	41.247							
Fumarate	0.004	0.601	-	-	0.024	0.659							
Threonine	0.001	1.498	-	-	0.041	1.266							
Monopalmitine	0.004	1.252	-	-	0.001	1.414							
Salicylate	0.000	2.707	-	-	0.009	1.455							
Asparagine	0.001	1.864	-	-	0.019	1.483							
Ethanolamine	0.000	2.146	-	-	0.007	1.597							
Glucose-6-P	0.002	1.639	-	-	0.003	1.679							
Arginine	0.003	1.255	-	-	0.018	1.788							
Stigmasterol	0.000	4.777	-	-	0.003	1.909							
GABA	0.021	1.709	-	-	0.008	1.912							
Galactonate	0.003	1.624	-	-	0.000	2.159							
Galactinol	0.000	1.944	-	-	0.000	2.253							
myo-Inositol-1-P	0.040	1.791	-	-	0.002	3.461							

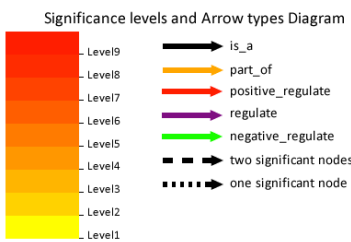
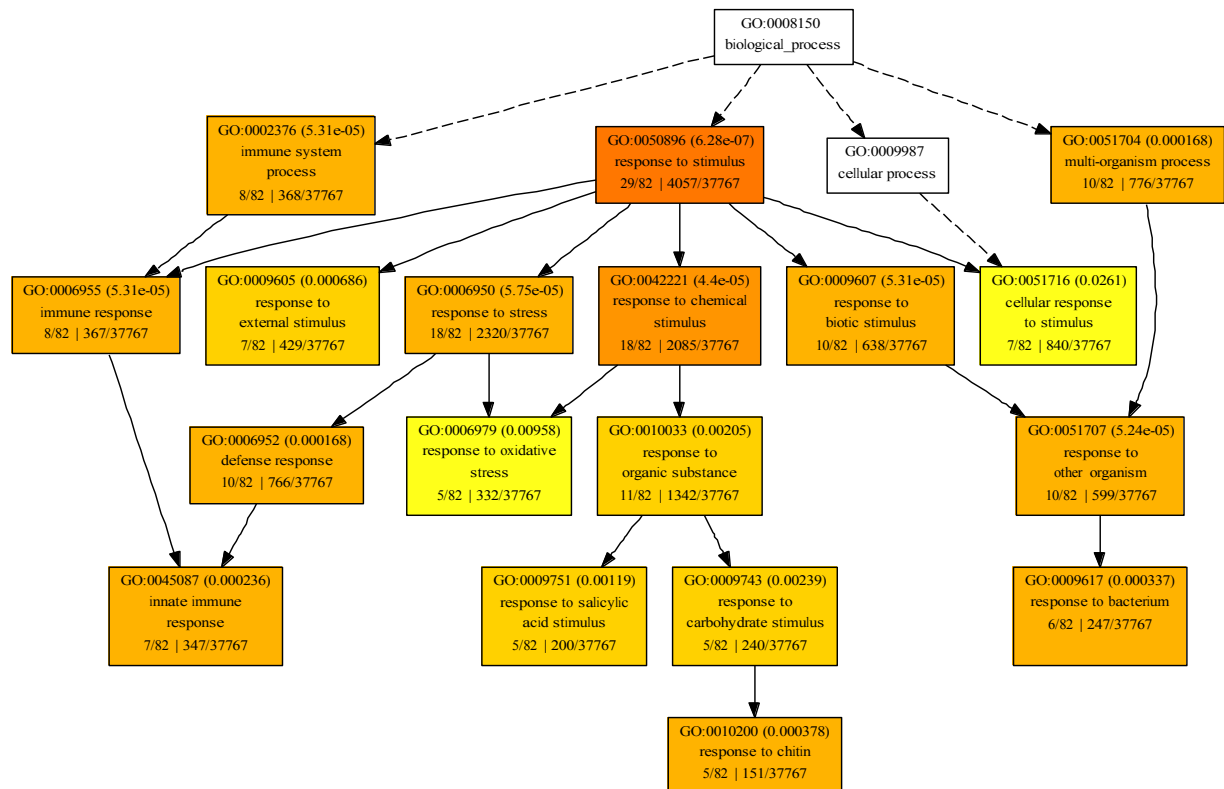
AGI	Annotation	has/involved in/located in	Function	atg5 & atg9 30DAS	atg5 & atg9 60DAS	atg5 60DAS 10mM	References
At3g28580	P-loop containing nucleoside triphosphate hydrolases	ATPase activity	hydrolase activity/ stress response	2.19	2.86	2.72	
At2g22470	AGP2 arabinogalactan protein 2	anchored to membrane	other membranes/cell wall	3.48	3.05	1.49	
At1g35230	AGP5, arabinogalactan protein 5	innate immune response	response to stress/ cell wall	3.06	4.88	2.99	
At1g33960	AIG1 ATPase	response to bacterium	response to abiotic or biotic stimulus	4.00	5.75	1.88	
At1g79450	ALISS, ALA-interacting subunit 5	amino acid transport	transport	2.20	3.25	1.98	
At1g02220	ANAC003	protein desumoylation	other metabolic processes	3.48	4.09	2.71	
At2g17040	ANAC036	leaf morphogenesis	developmental processes	2.67	2.24	1.95	Slocombe et al. 2009
At3g44350	ANAC061	DNA binding	DNA or RNA binding	2.76	2.32	2.25	
At5g22380	ANAC090	nucleus	nucleus	3.06	1.69	1.51	
At5g20230	ATBCB, SAG14, blue-copper-binding protein	response to fungus/ senescence	response to abiotic or biotic stimulus	2.42	3.65	2.99	
At1g01340	ACBK1, CNGC10, cyclic nucleotide gated channel 10	plasma membrane	CA2+ and Mg2+ transport	3.38	2.06	1.71	Guo et al. 2010
At3g54420	ATCHITIV, chitinase	chitin binding	other binding	3.79	2.12	2.23	
At1g07000	EXO70B2, exocyst subunit	cell wall apposition	respond to chitin and ER stress	2.72	1.64	1.39	Pecenkova et al. 2011
At4g25110	AtMC2, MC2, metacaspase 2	cysteine-type endopeptidase activity	hydrolase activity	3.36	3.93	2.53	
At3g13100	ATMRP7, multidrug resistance-associated protein 7	tonoplast/plasma membrane	ABC transporter/ cadmium	3.42	3.52	2.13	Wojas et al. 2009
At1g20350	TIM17-1, translocase inner membrane subunit 17-1	mitochondrial inner membrane presequence translocase	stress response	4.00	4.95	3.66	Uggalla et al. 2009
At3g01290	SPFH membrane-associated protein family	mitochondrion	mitochondria	2.68	3.18	2.57	
At1g11190	BFN1, ENDO1, bifunctional nuclease 1	senescent leaf/ abscission zone	nuclease	2.13	3.52	4.14	Farage-Barhom et al. 2008
At5g56870	BGAL4, beta-galactosidase 4	lactose catabolic process via UDP-galactose	other metabolic processes	2.84	3.71	4.45	
At3g22910	ATPase E1-E2 type family protein	ATP biosynthetic process	other cellular processes	2.85	2.70	2.29	
At3g01830	Calcium-binding EF-hand family protein	salicylic acid mediated signaling pathway	signal transduction	6.30	4.58	3.43	
At5g47850	CCR4, CRINKLY4 related 4	protein phosphorylation	cell division/pericycle/lateral roots	2.82	4.00	3.45	Smet et al. 2008
At2g43570	CHI, chitinase, putative	chitinase activity	hydrolase activity	2.39	5.00	2.82	
At1g09500	NAD(P)-binding Rossmann-fold superfamily protein	cellular metabolic process	other cellular processes	3.22	4.27	5.73	
At5g42380	CML37, CML39, calmodulin like 37	endoplasmic reticulum unfolded protein response	signal transduction	6.69	3.48	2.72	
At5g50260	CEP1 KDEL-tailed cysteine endopeptidase	endoderm lateral roots	endopeptidase/ PCD/cell wall	2.32	2.49	2.19	Helm et al. 2008
At3g49620	DIN11, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase	cellular response to starvation	dark induced	2.68	3.44	1.63	
At3g60140	BGLU30, DIN2, SRG2, Glycosyl hydrolase	response to sucrose stimulus	dark induced	2.91	7.35	6.64	
At1g57630	Toll-Interleukin-Resistance (TIR) domain family protein	response to molecule of bacterial origin	response to abiotic or biotic stimulus	5.35	4.34	2.46	
At2g18660	PNP-A, plant natriuretic peptide A	response to endoplasmic reticulum stress	regulator leaf dark respiration	3.82	5.24	2.90	Ruzvidzo et al. 2011, Wang et al. 2011
At1g26420	FAD-binding Berberine family protein	UDP-N-acetylmuramate dehydrogenase activity	other enzyme activity	3.07	6.32	2.69	
At1g30700	FAD-binding Berberine family protein	toxin catabolic process	other cellular processes	2.92	6.22	9.18	
At1g02400	ATGA2OX6, gibberellin 2-oxidase 6	GA inactivation/ oxidoreductase activity	induced by low temperature and ABA	1.69	1.46	1.05	Kendall et al. 2011
At4g14630	GLP9, germin-like protein 9	response to salt stress	response to stress	2.28	4.63	6.63	
At3g62950	Thioredoxin superfamily protein	cytoplasm	other cytoplasmic components	5.18	2.31	2.82	
At4g37900	Protein of unknown function	biological_process	response to salt stress	3.21	2.74	4.74	
At2g35710	Nucleotide-diphospho-sugar transferases	biosynthetic process	other metabolic processes	2.87	3.74	2.32	
At4g39670	Glycolipid transfer protein (GLTP) family protein	cytoplasm	acyl lipid metabolism	3.36	4.80	3.18	
At5g64790	O-Glycosyl hydrolases family 17 protein	anchored to membrane	other membranes	2.87	1.31	2.16	
At5g52760	Copper transport protein family	regulation of hydrogen peroxide metabolic process	MAPK	2.77	4.10	2.46	
At3g50480	HR4, homolog of RPW8 4	response to other organism	interaction with beneficial microbes	2.44	2.81	2.06	Saenz-Mata et al. 2012
At1g68620	alpha/beta-Hydrolases superfamily protein	toxin catabolic process	other cellular processes	4.24	3.89	4.52	
At2g34600	JAZ7, jasmonate-zim-domain protein 7	jasmonic acid mediated signaling pathway	cambium regulator	2.80	2.53	2.07	Sehr et al. 2010
At1g16420	MCS8, metacaspase 8	hydrogen peroxide-mediated programmed cell death	response to UV	3.38	2.90	1.79	He et al. 2008
At1g62490	mTERF	mTERF	unknown molecular functions	3.24	2.47	2.52	Kleine 2012
At3g23250	MYB15, myb domain protein 15	sequence-specific DNA binding transcription factor	Cold stress	4.37	4.33	2.66	Chen et al. 2010
At2g47190	MYB2, myb domain protein 2	transcription factor	Plant senescence/ Cytokinin/ IPT/ response	2.23	2.16	2.65	Guo and Gan, 2011
At3g26830	CYP71B15, PAD3, Cytochrome P450	defense response to bacterium	camalexin production	2.15	3.56	2.09	Beets et al. 2012
At3g52430	ATPAD4, PAD4, alpha/beta-Hydrolases	detection of external stimulus	lipase/ SA signalling	2.51	2.80	2.27	Jirage et al. 1999
At5g13320	PBS3	GH3 amino acid conjugase	SA metabolism	3.76	4.06	2.90	Okrent and Wildermuth, 2011
At2g26560	PLA2A, phospholipase A 2A	response to ethylene stimulus	Phospholipase A/ water loss	3.54	1.65	2.15	Yang et al. 2012
At2g14610	PR1, pathogenesis-related gene 1	regulation of plant-type hypersensitive response	other cellular processes	2.42	5.02	2.17	Glazebrook et al. 1996
At5g25440	Protein kinase superfamily protein	regulation of plant-type hypersensitive response	other cellular processes	2.39	2.41	1.83	
At1g72540	Protein kinase superfamily protein	plasma membrane	plasma membrane	1.78	5.36	1.11	
At3g48650	pseudogene, At14a-related protein	#N/A	#N/A	3.45	2.69	3.32	
At4g02380	SAG21, senescence-associated gene 21	cellular response to water deprivation	response to abiotic or biotic stimulus	3.43	1.83	2.22	
At5g43580	UPI Serine protease inhibitor	UPI Unusual serine protease inhibitor	response to necrotrophe/ induced by stress	2.20	7.02	5.77	Laluk and Mengiste 2011
At1g48210	Protein kinase	protein kinase activity	kinase activity	2.90	1.59	2.30	
At3g51680	SDR2 NAD(P)-binding Rossmann-fold superfamily protein	oxidoreductase activity	ABA	2.37	3.44	2.02	
At2g41100	ATCAL4, TCH3, Calcium-binding EF hand family protein	vacuolar membrane	other membranes	1.87	1.83	1.47	
At2g32140	transmembrane receptors	ethylene biosynthetic process	other cellular processes	2.86	3.24	2.68	
At4g04300	transposable element gene	#N/A	#N/A	4.11	3.42	3.68	
At2g13310	transposable element gene	#N/A	#N/A	3.48	4.70	4.14	
At3g11340	UGT76B1 UDP-Glycosyltransferase	transferase activity	conjugates Isoleucic acid/ JA and SA re	2.81	5.85	5.38	von Saint Paul et al. 2011
At3g53150	UGT73D1, UDP-glucosyl transferase	metabolic process	other metabolic processes	2.38	4.52	1.89	
At2g43820	UGT74F2, UDP-glucosyltransferase 74F2	benzoate metabolic process	coronatine signalling	2.83	2.65	2.24	Uppalapati et al. 2010
At1g20180	unknown protein	molecular_function	unknown molecular functions	3.27	4.24	3.89	
At3g13950	unknown protein	defense response to fungus	response to abiotic or biotic stimulus	2.99	4.46	3.46	
At3g48640	unknown protein	defense response to fungus	response to abiotic or biotic stimulus	3.41	6.31	2.58	
At4g28460	unknown protein	extracellular region	extracellular	2.15	3.86	2.05	
At1g13340	unknown protein	cytoplasm	other cytoplasmic components	3.39	3.26	2.85	
At1g76230	unknown protein	biological_process	unknown biological processes	1.88	4.14	4.91	
At3g12510	unknown protein	molecular_function	unknown molecular functions	3.81	2.78	2.58	
At2g04025	unknown protein	growth factor activity	receptor binding or activity	3.33	2.46	3.50	
At4g32870	unknown protein	molecular_function	unknown molecular functions	2.69	3.09	2.95	
At2g22880	VQ motif-containing protein	response to UV-B	response to abiotic or biotic stimulus	4.35	2.99	3.76	
At1g78410	VQ motif-containing protein	response to chitin	other biological processes	4.22	1.75	1.76	
At1g21240	WAK3 (wall associated kinase 3)	protein phosphorylation	wall associated kinase	4.25	3.55	2.60	He et al. 1999
At4g31800	WRKY18; transcription factor	transcription factor	bacterial volatile response	2.30	2.56	1.87	Wenkeet al. 2012
At5g22570	WRKY38; transcription factor	defense response to bacterium	response to abiotic or biotic stimulus	4.40	5.58	2.22	Kim et al. 2008
At1g04600	MYA2 XIA (MYOSIN XI A); motor/ protein binding	myosin complex	transport peroxisomes, mitochondria,	4.29	2.02	1.46	Walter and Holweg, 2008
At5g57550	XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3)	xyloglucan:xyloglucosyl transferase activity	transferase activity	2.04	3.38	3.42	
At1g59590	ZCF37	mitochondrion	mitochondria	3.64	2.41	2.16	
At5g04390	zinc finger (C2H2 type)	zinc ion binding	other binding	2.56	2.18	2.29	
At1g08050	zinc finger (C3HC4-type RING finger)	systemic acquired resistance, salicylic acid mediated	other cellular processes	1.58	2.53	2.78	
At4g14365	zinc finger (C3HC4-type RING finger)	jasmonic acid mediated signaling pathway	signal transduction	2.29	2.95	1.97	

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Supplemental Table 4: Frequency of Gene Ontology terms (GO) represented in the 86 genes (see Table 4) up regulated in both atg5 and atg9 independently of nitrate conditions or plant age. Below is AGRIGO representation of the GO terms.

Term	Observed Frequency	Expected Frequency	p-value
GO:0050896	response to stimulus 30 out of 81 genes, 37%	3498 out of 27870 genes, 12.6%	9.77E-06
GO:0006950	response to stress 20 out of 81 genes, 24.7%	2058 out of 27870 genes, 7.4%	0.000235
GO:0042221	response to chemical stimulus 19 out of 81 genes, 23.5%	1824 out of 27870 genes, 6.5%	0.000235
GO:0051707	response to other organism 10 out of 81 genes, 12.3%	551 out of 27870 genes, 2%	0.000652
GO:0006952	defense response 11 out of 81 genes, 13.6%	734 out of 27870 genes, 2.6%	0.000722
GO:0006955	immune response 7 out of 81 genes, 8.6%	260 out of 27870 genes, 0.9%	0.000722
GO:0009607	response to biotic stimulus 10 out of 81 genes, 12.3%	603 out of 27870 genes, 2.2%	0.000722
GO:0045087	innate immune response 7 out of 81 genes, 8.6%	256 out of 27870 genes, 0.9%	0.000722
GO:0051704	multi-organism process 10 out of 81 genes, 12.3%	581 out of 27870 genes, 2.1%	0.000722
GO:0002376	immune system process 7 out of 81 genes, 8.6%	292 out of 27870 genes, 1%	0.00134
GO:0010200	response to chitin 5 out of 81 genes, 6.2%	127 out of 27870 genes, 0.5%	0.00194
GO:0009751	response to salicylic acid stimulus 5 out of 81 genes, 6.2%	144 out of 27870 genes, 0.5%	0.00316
GO:0009617	response to bacterium 6 out of 81 genes, 7.4%	251 out of 27870 genes, 0.9%	0.00371
GO:0009863	salicylic acid mediated signaling pathway 3 out of 81 genes, 3.7%	29 out of 27870 genes, 0.1%	0.00371
GO:0071446	NA 3 out of 81 genes, 3.7%	29 out of 27870 genes, 0.1%	0.00371



Supplemental Data. Masclaux-Daubresse et al. Plant Cell (2014) 10.1105/tpc.114.124677

Supplemental Table 5: Gene Ontology terms (GO) represented in the list of genes significantly up regulated in (i) *atg5* and *atg9* [*atg5&atg9*] grown under low nitrate conditions for 30 DAS, (ii) *atg5* and *atg9* [*atg5&atg9*] grown under low nitrate conditions for 60 DAS and (iii) *atg5* grown under high nitrate conditions for 60 DAS. Only GO terms with high significance (FDR<10-5) in at least one of the three gene lists are presented. Yellow to Orange colour intensities are relative to significance and inversely proportional to the FDR values.

GO Information		<i>atg5&atg9</i> 30DAS lowN	<i>atg5&atg9</i> 60DAS lowN	<i>atg5</i> 60DAS highN
GO Term	Description	FDR	FDR	FDR
GO:0006952	defense response	1.10E-09	3.10E-26	1.80E-20
GO:0009607	response to biotic stimulus	4.40E-07	8.90E-18	7.40E-15
GO:0051707	response to other organism	9.30E-06	3.20E-17	1.00E-13
GO:0050896	response to stimulus	1.70E-07	1.70E-15	3.50E-14
GO:0006950	response to stress	3.10E-06	5.10E-15	2.90E-15
GO:0006955	immune response	6.80E-06	5.10E-15	5.30E-10
GO:0002376	immune system process	7.10E-06	5.10E-15	5.40E-10
GO:0045087	innate immune response	9.90E-06	3.10E-14	7.00E-09
GO:0051704	multi-organism process	7.30E-06	4.10E-14	6.40E-13
GO:0009617	response to bacterium	0.00086	1.20E-13	1.40E-11
GO:0010200	response to chitin	3.30E-08	2.20E-13	1.50E-17
GO:0031347	regulation of defense response	0.033	7.50E-12	0.0001
GO:0042221	response to chemical stimulus	3.20E-05	2.70E-11	2.40E-10
GO:0042742	defense response to bacterium	0.0018	5.40E-10	5.10E-09
GO:0080134	regulation of response to stress	---	6.90E-10	7.50E-05
GO:0010033	response to organic substance	2.70E-07	1.80E-09	2.20E-08
GO:0009620	response to fungus	---	5.00E-09	7.50E-05
GO:0009743	response to carbohydrate stimulus	3.20E-05	9.30E-09	2.80E-13
GO:0050832	defense response to fungus	---	1.30E-08	9.00E-06
GO:0003824	catalytic activity	3.20E-06	2.60E-07	1.20E-06
GO:0016798	hydrolase activity, acting on glycosyl bonds	---	1.70E-06	0.00021
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compo	---	1.70E-06	0.00055
GO:0009814	defense response, incompatible interaction	---	2.30E-06	4.60E-06
GO:0016787	hydrolase activity	0.022	8.40E-06	0.00055
GO:0016301	kinase activity	5.80E-08	1.60E-05	1.20E-06
GO:0016265	death	---	2.50E-05	0.031
GO:0008219	cell death	---	2.50E-05	0.031
GO:0009751	response to salicylic acid stimulus	---	4.30E-05	4.50E-05
GO:0019825	oxygen binding	---	4.70E-05	0.0015
GO:0048583	regulation of response to stimulus	---	5.30E-05	---
GO:0006979	response to oxidative stress	---	0.00014	2.30E-05
GO:0009816	defense response to bacterium, incompatible int	---	0.00014	2.40E-05
GO:0016740	transferase activity	1.70E-06	0.00028	5.40E-06
GO:0006468	protein amino acid phosphorylation	1.70E-10	0.00046	8.40E-08
GO:0009605	response to external stimulus	---	0.00048	5.70E-05
GO:0016772	transferase activity, transferring phosphorus-con	7.90E-07	0.001	7.40E-05
GO:0019748	secondary metabolic process	---	0.0011	6.60E-06
GO:0006793	phosphorus metabolic process	5.10E-08	0.002	4.80E-06
GO:0043687	post-translational protein modification	1.50E-08	0.0021	9.00E-06
GO:0009611	response to wounding	---	0.0026	1.10E-05
GO:0006796	phosphate metabolic process	5.10E-08	0.0029	7.80E-06
GO:0016310	phosphorylation	3.50E-09	0.0037	4.40E-06
GO:0010876	lipid localization	7.20E-14	0.0047	7.20E-14
GO:0006464	protein modification process	7.30E-08	0.021	0.0015
GO:0001883	purine nucleoside binding	6.10E-09	---	0.0017
GO:0001882	nucleoside binding	6.10E-09	---	0.0017
GO:0030554	adenyl nucleotide binding	6.10E-09	---	0.0017
GO:0017076	purine nucleotide binding	1.20E-08	---	0.011
GO:0000166	nucleotide binding	1.70E-08	---	---
GO:0005524	ATP binding	7.50E-08	---	0.012
GO:0032559	adenyl ribonucleotide binding	9.50E-08	---	0.013
GO:0032555	purine ribonucleotide binding	2.50E-07	---	0.046
GO:0032553	ribonucleotide binding	2.50E-07	---	0.046
GO:0009791	post-embryonic development	2.80E-07	---	---
GO:0043412	macromolecule modification	9.10E-07	---	0.027
GO:0003700	transcription factor activity	3.20E-06	---	0.033
GO:0003677	DNA binding	6.90E-06	---	---
GO:0004674	protein serine/threonine kinase activity	7.90E-05	---	---
GO:0004672	protein kinase activity	7.90E-05	---	---
GO:0030528	transcription regulator activity	7.90E-05	---	---
GO:0005488	binding	9.10E-05	---	---

Supplemental Table 6: Gene Ontology terms (GO) represented in the list of genes significantly down regulated in (i) *atg5* and *atg9* [*atg5&atg9*] grown under low nitrate conditions for 30 DAS, (ii) *atg5* and *atg9* [*atg5&atg9*] grown under low nitrate conditions for 60 DAS and (iii) *atg5* grown under high nitrate conditions for 60 DAS. Blue colour shows GO terms represented in at least two of these lists.

GO Information		<i>atg5&atg9</i> 30DAS lowN	<i>atg5&atg9</i> 60DAS lowN	<i>atg5</i> 60DAS highN
GO Term	Description	FDR	FDR	FDR
GO:0010876	lipid localization		0.00025 ---	0.0055
GO:0005199	structural constituent of cell wall		0.0038 ---	---
GO:0003700	transcription factor activity		0.016 ---	---
GO:0004091	carboxylesterase activity		0.029 ---	---
GO:0030528	transcription regulator activity		0.035 ---	---
GO:0012505	endomembrane system		0.0072 ---	0.048
GO:0031225	anchored to membrane		0.023 ---	---
GO:0042545	cell wall modification	---		0.0097 ---
GO:0042547	cell wall modification during multidimensional cell growth	---		0.025 ---
GO:0009831	plant-type cell wall modification during multidimensional cell growth	---		0.025 ---
GO:0009631	cold acclimation	---		0.025 ---
GO:0009828	plant-type cell wall loosening	---		0.025 ---
GO:0009827	plant-type cell wall modification	---		0.035 ---
GO:0009698	phenylpropanoid metabolic process	---	---	0.001
GO:0009699	phenylpropanoid biosynthetic process	---	---	0.0034
GO:0010584	pollen exine formation	---	---	0.0093
GO:0019748	secondary metabolic process	---	---	0.01
GO:0008299	isoprenoid biosynthetic process	---	---	0.015
GO:0010927	cellular component assembly involved in morphogenesis	---	---	0.02
GO:0042398	cellular amino acid derivative biosynthetic process	---	---	0.02
GO:0010208	pollen wall assembly	---	---	0.02
GO:0006575	cellular amino acid derivative metabolic process	---	---	0.02
GO:0009813	flavonoid biosynthetic process	---	---	0.02
GO:0005982	starch metabolic process	---	---	0.033
GO:0019438	aromatic compound biosynthetic process	---	---	0.04
GO:0009812	flavonoid metabolic process	---	---	0.04
GO:0006720	isoprenoid metabolic process	---	---	0.046
GO:0016798	hydrolase activity, acting on glycosyl bonds	---	---	0.0054
GO:0016746	transferase activity, transferring acyl groups	---	---	0.017
GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	---	---	0.017
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---	0.025
GO:0019825	oxygen binding	---	---	0.034
GO:0046527	glucosyltransferase activity	---	---	0.034

Supplemental Table 7: Differential expression in *atg5* and *atg9* relative to wild type of genes involved in the nitrogen assimilation pathway and in aspartate and glutamate metabolism. The Log₂(fold change) values of the significantly differentially expressed genes are presented (FDR%<10⁻⁵). Comparisons are in *atg5* and *atg9* relative to wild type under Low nitrate (LowN) conditions, 30 and 60 days after sowing (DAS) and under High nitrate (HighN) conditions 60 days after sowing. ns is non significant.

	<i>atg5</i> & <i>atg9</i>		<i>atg5</i>
	LowN 30DAS	LowN 60DAS	HighN 60DAS
AT1G77760 <i>NIA1</i> (NITRATE REDUCTASE 1)	ns	1.19	ns
AT1G37130 <i>NIA2</i> (NITRATE REDUCTASE 2)	ns	ns	ns
AT2G15620 <i>NIR1</i> (NITRITE REDUCTASE 1)	ns	ns	ns
AT5G04140 <i>GLU1</i> (Fd-GLUTAMATE SYNTHASE)	ns	ns	ns
AT2G41220 <i>GLU2</i> (Fd-GLUTAMATE SYNTHASE)	2.30	ns	ns
AT5G53460 <i>GLT1</i> (NADH-GLUTAMATE SYNTHASE)	ns	ns	ns
AT5G35630 <i>GS2</i> (chloroplast GLUTAMINE SYNTHETASE 2)	ns	ns	ns
AT5G37600 <i>GLN1;1</i> (cytosol GLUTAMINE SYNTHETASE)	ns	ns	1.34
AT1G66200 <i>GLN1;2</i> (cytosol GLUTAMINE SYNTHETASE)	ns	ns	ns
AT3G17820 <i>GLN1;3</i> (cytosol GLUTAMINE SYNTHETASE)	ns	ns	ns
AT5G16570 <i>GLN1;4</i> (cytosol GLUTAMINE SYNTHETASE)	ns	ns	1.71
AT1G48470 <i>GLN1;5</i> (cytosol GLUTAMINE SYNTHETASE)	ns	ns	ns
AT5G18170 <i>GDH1</i> (GLUTAMATE DEHYDROGENASE 1)	ns	ns	ns
AT5G07440 <i>GDH2</i> (GLUTAMATE DEHYDROGENASE 2)	ns	2.12	ns
AT3G03910 <i>GDH3</i> (GLUTAMATE DEHYDROGENASE 3)	ns	0.98	ns
AT1G51720 glutamate dehydrogenase, putative	ns	0.27	ns
AT3G47340 <i>ASN1</i> (ASPARAGINE SYNTHASE 1)	ns	2.73	ns
AT5G65010 <i>ASN2</i> (ASPARAGINE SYNTHETASE 2)	ns	ns	ns
AT5G10240 <i>ASN3</i> (ASPARAGINE SYNTHETASE 3)	ns	ns	ns
AT2G30970 <i>ASP1</i> (ASPARTATE AMINOTRANSFERASE 1)	ns	ns	ns
AT5G19550 <i>ASP2</i> (ASPARTATE AMINOTRANSFERASE 2)	ns	ns	ns
AT5G11520 <i>ASP3</i> (ASPARTATE AMINOTRANSFERASE 3)	ns	1.33	1.25
AT1G62800 <i>ASP4</i> (ASPARTATE AMINOTRANSFERASE 4)	ns	-1.13	ns
AT4G31990 <i>ASP5</i> (ASPARTATE AMINOTRANSFERASE 5)	ns	ns	ns

Supplemental Table 8: Differential expression in *atg5* relative to wild type of genes involved in the shikimate and flavonoid pathways and reported by Lillo et al. (2008). The Log₂(fold change) values of the differentially expressed genes are presented (FDR%<10-5). Yellow and blue colours indicate significant up and down regulations, respectively.

Shikimate pathway		<i>atg5</i> lowN 30DAS	<i>atg5</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT4G39980	DHS1	-0.020	-0.532	-0.417
AT4G33510	DHS2	0.516	0.236	-0.218
AT1G22410	DHS3	0.166	1.132	0.382
AT5G66120	3-dehydroquinate synthase	0.114	-0.060	-0.222
AT3G06350	MEE32 3-dehydroquinate dehydratase	0.260	-0.012	-0.099
AT2G35500	shikimate kinase-related	0.454	-0.541	-0.597
AT2G21940	shikimate kinase, putative	1.970	-0.520	-0.328
AT4G39540	shikimate kinase family protein	0.119	-0.433	-0.374
AT2G16790	shikimate kinase family protein	0.166	1.169	0.465
AT3G26900	shikimate kinase family protein	0.186	0.303	0.044
AT5G47050	protein binding / zinc ion binding	0.098	-0.387	0.045
AT1G06890	transporter-related	0.413	-0.656	-0.258
AT2G45300;A	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phc	-0.219	-0.232	-0.061
AT1G48850	EMB1144 chorismate synthase	0.083	-0.172	-0.292
AT3G29200	CM1 (CHORISMATE MUTASE 1)	-0.373	0.197	0.227
AT5G10870	ATCM2 (chorismate mutase 2)	-0.103	-0.304	-0.090
AT2G20610	SUR1 S-alkylthiohydroximate lyase/ carbon-sulfur lyase/ transaminase	-0.359	-0.359	-0.157
AT2G38400	AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3)	0.549	2.727	2.103
AT5G22630	ADT5 (arogenate dehydratase 5)	0.201	0.407	0.328
AT1G11790	ADT1 (arogenate dehydratase 1)	-0.029	-0.066	-0.172
AT3G07630	ADT2 (arogenate dehydratase 2)	1.328	0.296	-0.083
AT3G44720	ADT4 (arogenate dehydratase 4)	0.430	1.298	1.172
AT1G08250	ADT6 (arogenate dehydratase 6)	0.615	0.020	-0.159
AT2G27820	PD1 (PREPHENATE DEHYDRATASE 1)	-0.415	-0.441	-0.571
Flavonoid pathway		<i>atg5</i> lowN 30DAS	<i>atg5</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT3G10340	PAL4 (Phenylalanine ammonia-lyase 4)	-0.122	0.574	0.762
AT5G04230	PAL3 (PHENYL ALANINE AMMONIA-LYASE 3); phenylalanine ammonia-lyase	-0.796	-0.900	-0.116
AT3G53260	PAL2; phenylalanine ammonia-lyase	-0.104	-0.270	-1.053
AT2G37040	pal1 (Phe ammonia lyase 1)	0.664	0.397	-1.021
AT2G30490	C4H (CINNAMATE 4-HYDROXYLASE)	0.133	-0.003	-0.254
AT1G51680	4CL1 (4-COUMARATE:COA LIGASE 1)	0.017	-0.040	-0.051
AT1G65060	4CL3; 4-coumarate-CoA ligase	0.361	-0.541	-1.475
AT3G21230	4CL4 4CL5 (4-coumarate:CoA ligase 5)	-0.145	-0.191	-0.137
AT3G21240	4CL2 (4-COUMARATE:COA LIGASE 2)	-0.818	-0.333	-0.074
AT1G20490	4CL AMP-dependent synthetase and ligase family protein	-0.336	-1.412	-1.554
AT5G13930	TT4 (TRANSPARENT TESTA 4)	0.101	-1.103	-1.012
AT3G55120	TT5 (TRANSPARENT TESTA 5)	-0.056	-1.060	-1.836
AT3G51240	TT6 F3H (FLAVANONE 3-HYDROXYLASE)	0.370	-0.479	-1.509
AT5G07990	TT7 (TRANSPARENT TESTA 7)	-0.278	-1.982	-3.424
AT5G08640	FLS (FLAVONOL SYNTHASE)	0.205	-0.468	-0.983
AT3G50210	FLS 2-oxoacid-dependent oxidase, putative	-0.290	-0.304	-0.173
AT5G63580	FLS2 (FLAVONOL SYNTHASE 2)	-0.466	-0.778	-0.462
AT5G63590	FLS3 (FLAVONOL SYNTHASE 3)	0.778	1.384	0.922
AT5G63600	FLS5 (FLAVONOL SYNTHASE 5)	1.929	0.988	2.287
AT1G06000	FGT UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.411	0.111	-0.179
AT1G30530	FGT UGT78D1 (UDP-GLUCOSYL TRANSFERASE 78D1)	-0.058	-0.827	-0.369
at2g22590	FGT transferase, transferring glycosyl groups	-0.698	0.262	0.124
at4g15480	FGT UGT84A1; UDP-glycosyltransferase	2.536	2.142	0.406
at5g17030	FGT UGT78D3 (UDP-GLUCOSYL TRANSFERASE 78D3)	-0.897	-0.850	-0.239
at5g17050	FGT UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2)	-0.295	-0.301	-1.580
at5g42800	DFR (TT3, DIHYDROFLAVONOL 4-REDUCTASE)	-0.157	-1.598	-2.842
AT4G22870;A	LDOX, ANS [AT4G22870, leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase]	-0.331	-1.331	-2.684
at5g17050	AGT UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2)	-0.295	-0.301	-1.580
at4g14090	AGT UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.130	-1.699	-2.729
at5g40600	AGT UF3GT (udp-glucose:flavonoid 3-O-glucosyltransferase)	-0.440	-2.162	-2.874
at3g21560	AGT UGT84A2; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase	0.170	-0.673	-0.888
at2g29750	AGT UGT71C1 (UDP-GLUCOSYL TRANSFERASE 71C1); UDP-glycosyltransferase	2.307	-0.525	0.690
at4g01070	AGT GT72B1; UDP-glycosyltransferase	-0.042	-0.288	-0.134
at1g22370	AGT AUGC85A5 (UDP-glucosyl transferase 85A5)	0.668	-0.002	-0.431
at3g29590	AAT AT5MAT; O-malonyltransferase/ transferase	0.002	-1.457	-2.547
AT1G03940;A	transferase/ transferase, transferring acyl groups other than amino-acyl group:	-0.195	-1.137	-2.740
at5g17220	GST ATGSTF12 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE 12)	-0.086	-2.032	-2.997
at1g02940	GSTF5 (GLUTATHIONE S-TRANSFERASE (CLASS PHI) 5)	-1.204	-1.067	-0.893
AT5G61160	AACT1 (anthocyanin 5-aromatic acyltransferase 1)	-2.025	-4.154	2.105
Flavonoid Regulation		<i>atg5</i> lowN 30DAS	<i>atg5</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT1G12910	ATAN11 (ANTHOCYANIN11)	-0.311	0.441	0.074
AT1G56650	PAP1 (PRODUCTION OF ANTHOCYANIN PIGMENT 1)	-0.162	-1.559	-2.094
AT4G00730	ANL2 (ANTHOCYANINLESS 2)	0.243	-0.805	-0.097
AT5G24520	TTG1 (TRANSPARENT TESTA GLABRA 1)	-0.026	0.251	0.561
AT5G40330	MYB23 (MYB DOMAIN PROTEIN 23)	0.999	-0.402	-0.187
AT1G66370	MYB113 (myb domain protein 113)	-0.120	-0.825	-0.358
AT1G66380	MYB114 (myb domain protein 114)	3.171	-1.216	-0.914
AT4G09820	TT8 (TRANSPARENT TESTA 8)	1.525	-2.672	-3.381
AT1G66390	PAP2 MYB90 (MYB DOMAIN PROTEIN 90)	3.377	-1.472	-1.309
AT1G63650	EGL3 (ENHANCER OF GLABRA 3)	-0.467	-0.416	-1.153
AT3G27920	GL1 ATMYB0 (MYB DOMAIN PROTEIN 0)	0.260	-0.180	-3.016
AT5G14750	WER ATMYB66 (MYB DOMAIN PROTEIN 66)	0.769	-0.150	1.734
AT1G61720	BAN (BANYULS)	-0.544	-0.411	-0.200

Supplemental Table 9: Differential expression in *atg5* & *atg9* relative to wild type of senescence associated genes (SAG). The Log₂(fold change) values of the differentially expressed genes are presented (FDR%<10⁻⁵). Yellow and blue colours indicate significant up and down regulations respectively. Yellow and blue colours indicate significant up and down regulations respectively.

	<i>atg5&atg9</i> lowN 30DAS	<i>atg5&atg9</i> lowN 60DAS	<i>atg5</i> highN 60DAS
AT4G35770 SEN1 (SENESCENCE 1)	1.2109	4.5786	2.8685
AT2G29350 SAG13	1.1511	4.4036	3.0423
AT3G02040 SRG3	2.3063	2.7765	0.1033
AT1G19200 senescence-associated protein	-0.2973	2.8885	2.1315
AT5G13170 SAG29	2.9157	2.0904	1.1636
AT1G17020 SRG1 (SENESCENCE-RELATED GENE)	1.5573	2.1439	1.7822
AT5G45890 SAG12 (SENESCENCE-ASSOCIATED C	3.8548	3.8737	6.6250
AT4G02380 SAG21 (SENESCENCE-ASSOCIATED C	3.4321	1.8345	2.2178
AT3G10985 SAG20 (SENESCENCE ASSOCIATED C	1.8256	0.7924	0.6194
AT3G51250 senescence/dehydration-associated	-0.0972	0.4199	0.2193
AT3G48140 senescence-associated protein	0.0231	0.3727	0.3074
AT1G66330 senescence-associated family	-0.0382	0.0985	-0.1359
AT5G14930 SAG101 (SENESCENCE-ASSOCIATED	0.4348	0.7193	0.6426
AT4G35985 senescence/dehydration-associated	0.9390	0.3842	0.1568
AT1G20780 SAUL1 (SENESCENCE-ASSOCIATED E	0.8330	0.3910	1.7061
AT1G71190 SAG18 (SENESCENCE ASSOCIATED C	0.0263	-0.2102	-0.0385
AT2G25690 senescence-associated protein-relat	-0.7395	-0.3859	-0.7205
AT5G49120 senescence-associated protein-relat	-0.0494	-0.6251	-0.2357
AT3G21600 senescence/dehydration-associated	-0.7806	-0.7152	-0.2542
AT5G47060 senescence-associated protein-relat	0.2747	-0.4382	-0.3322
AT2G44670 senescence-associated protein-relat	0.2771	-0.3222	-0.0042
AT1G78020 senescence-associated protein-relat	-0.4244	-0.6136	-0.1015
AT1G74940 senescence-associated protein-relat	-0.0313	-0.3845	-0.2532
AT4G17670 senescence-associated protein-relat	-0.3637	0.3240	0.5174
AT5G11460 senescence-associated protein-relat	-0.4533	-0.7064	-0.5761
AT5G65040 senescence-associated protein-relat	-0.2106	-0.9072	-0.3758
AT3G22550 senescence-associated protein-relat	-0.3742	-1.1482	-0.6552
AT1G22160 senescence-associated protein-relat	0.2276	-0.7947	-0.1513
AT5G20700 senescence-associated protein-relat	0.5614	-0.9248	-0.3382

Supplemental Table 10: Differential expression (in *atg5* and *atg9* relative to wild type) of genes responding to salicylic acid (SA), jasmonic acid (JA), pathogen/wounding/ethylen or involved in camalexin biosynthesis in rosettes grown under low (lowN) or high (highN) nitrate conditions for 30 (30DAS) or 60 (60DAS) days after sowing. The log₂(fold change) values of the differentially expressed genes are presented, yellow and blue colours indicate significant up and down regulations, respectively (FDR%<10-5). Adapted from Leeuwen et al. 2007 Plant Cell

Gene Name ^a	AGI code	log ₂ (FC)			
		<i>atg5</i> and <i>atg9</i> lowN 30DAS	<i>atg5</i> and <i>atg9</i> lowN 60DAS	<i>atg5</i> highN 60DAS	
EDS1	At3g48090	0.76	1.77	1.37	SA regulated
PAD4	At3g52430	2.51	2.80	2.27	SA regulated
AtWRKY18	At4g31800	2.30	2.56	1.87	SA regulated
EDS5 (SID1)	At4g39030	0.30	1.98	1.33	SA regulated
PR1	At2g14610	2.42	5.02	2.17	SA regulated
PLDgamma1	At4g11850	0.45	0.95	1.41	SA regulated
WAK1	At1g21250	0.91	1.72	1.46	SA regulated
AtERF1	At4g17500	1.65	2.00	2.56	SA regulated
PR5	At1g75040	0.39	4.04	1.64	SA regulated
PAD3	At3g26830	2.15	3.56	2.09	SA regulated
RAR047	At2g03760	1.11	1.84	1.25	SA regulated
ap4.3a	At2g32800	0.73	0.89	0.77	SA regulated
PR2 (BGL2)	At3g57260	2.55	3.35	1.76	SA regulated
HEL (PR4)	At3g04720	0.75	0.00	0.37	SA regulated
NHL3	At5g06320	0.60	1.17	1.63	SA regulated
PDF1.2	At5g44420	2.08	-0.03	1.96	JA regulated
AtERT13	At2g44840	2.08	0.23	3.70	JA regulated
LOX1	At1g55020	-0.18	2.15	1.17	JA regulated
THI2.1	At1g72260	-0.95	-1.00	-1.18	JA regulated
LOX2	At3g45140	0.49	-0.34	-0.53	JA regulated
PLDbeta	At2g42010	0.97	-0.04	0.32	pathogen/wounding/ethylen
bg3	At3g57240	1.58	3.22	3.09	pathogen/wounding/ethylen
PR3 (CHIA4)	At3g54420	3.79	2.12	2.23	pathogen/wounding/ethylen
PAL2	At3g53260	-0.14	-0.30	-1.05	pathogen/wounding/ethylen
PAL1	At2g37040	0.57	0.22	-1.02	pathogen/wounding/ethylen
ECS1 (CXc750)	At1g31580	0.21	0.07	0.13	pathogen/wounding/ethylen
NPR1/NIM1	At1g64280	0.04	1.14	0.99	pathogen/wounding/ethylen
4CL	At1g51680	-0.13	-0.27	-0.05	pathogen/wounding/ethylen
ELI3	At4g37980	0.12	-0.65	-0.32	pathogen/wounding/ethylen
ASA1	At5g05730	0.16	1.13	0.99	pathogen/wounding/ethylen
AtCMPG1	At1g66160	2.04	1.78	1.17	pathogen/wounding/ethylen
PLDalpha1	At3g15730	-0.02	-0.39	-0.16	pathogen/wounding/ethylen
ap3.3a	At3g50360	0.52	-0.61	-0.33	pathogen/wounding/ethylen
DHS1	At4g39980	-0.03	-0.50	-0.42	pathogen/wounding/ethylen
CYP79B2; electron car	AT4G39950	0.00	1.99	1.97	camalexin biosynthesis
CYP79B3; electron car	AT2G22330	0.63	-0.38	-0.02	camalexin biosynthesis
CYP71A16; electron c:	AT5G42590	-0.91	-0.02	0.62	camalexin biosynthesis
CYP71A13 (cytochrom	AT2G30770	0.00	3.08	1.75	camalexin biosynthesis
cytochrome P450	AT4G13310;AT4G	1.05	1.85	0.97	camalexin biosynthesis
WRKY33; transcriptio	AT2G38470	1.49	1.17	1.19	camalexin biosynthesis
PAD3 (PHYTOALEXIN I	AT3G26830	2.15	3.56	2.09	camalexin biosynthesis

Supplemental Table 11: Differential expression of WRKY genes in rosettes of *atg5* relative to wild type, grown under low (lowN) or high (highN) nitrate conditions for 30 (30DAS) or 60 (60DAS) days after sowing.The log₂(fold change) values of the differentially expressed genes are presented, Yellow and blue colours indicate significant up and down regulations, respectively (FDR%<10⁻⁵). Breeze et al. 2011

AGI	name	<i>atg5&atg9</i> lowN 30DAS	<i>atg5&atg9</i> lowN 60DAS	<i>atg5</i> highN 60DAS	senescence related*
AT5G22570	WRKY38	4.40	5.58	2.22	no
AT5G13080	WRKY75	-0.24	5.67	4.74	yes
AT5G24110	WRKY30	1.08	5.21	3.24	yes
AT1G18860	WRKY61	-0.06	4.98	2.90	yes
AT3G01080	WRKY58	1.29	3.34	3.62	no
AT4G31800	WRKY18	2.30	2.56	1.87	no
AT3G01970	WRKY45	1.17	2.31	5.51	yes
AT2G46400	WRKY46	1.34	2.48	1.90	no
AT2G40750	WRKY54	1.78	2.67	1.46	no
AT3G56400	WRKY70	1.13	2.45	1.36	no
AT2G40740	WRKY55	0.21	2.16	1.97	yes
AT4G23810	WRKY53	1.25	2.06	2.24	no
AT1G80840	WRKY40	2.27	1.87	1.48	yes
AT5G15130	WRKY72	1.44	1.96	1.20	yes
AT1G64000	WRKY56	-0.43	2.20	-0.58	no
AT2G30250	WRKY25	0.54	1.86	1.69	yes
AT2G23320	WRKY15	0.38	1.81	1.72	yes
AT2G25000	WRKY60	-0.42	1.27	1.14	no
AT2G38470	WRKY33	1.49	1.17	1.19	yes
AT1G62300	WRKY6	1.28	0.96	1.37	yes
AT5G49520	WRKY48	1.60	0.87	1.02	yes
AT1G55600	WRKY10	-1.07	0.52	1.28	no
AT1G69810	WRKY36	-1.70	0.89	2.05	yes
AT4G01720	WRKY47	0.77	1.05	1.19	yes
AT4G04450	WRKY42	0.56	0.44	-0.41	no
AT5G46350	WRKY8	0.20	0.81	0.14	no
AT2G24570	WRKY17	1.23	0.32	1.13	no
AT4G18170	WRKY28	1.22	0.58	1.75	yes
AT3G04670	WRKY39	-0.42	0.46	0.71	no
AT1G66550	WRKY67	0.15	0.18	-0.58	no
AT1G29860	WRKY71	-0.34	0.25	1.10	no
AT4G12020	WRKY19	0.12	0.14	0.31	no
AT5G07100	WRKY26	2.32	0.33	1.05	yes
AT1G13960	WRKY4	0.45	-0.06	-0.02	yes
AT4G01250	WRKY22	1.10	-0.03	0.52	no
AT1G69310	WRKY57	1.36	-0.06	0.07	no
AT4G24240	WRKY7	-0.43	0.11	-0.10	no
AT5G28650	WRKY74	-1.38	0.38	0.35	no
AT2G30590	WRKY21	-0.21	-0.15	-0.21	no
AT4G31550	WRKY11	0.17	-0.16	0.25	no
AT1G68150	WRKY9	1.45	-0.88	1.63	no
AT3G58710	WRKY69	-0.42	-0.22	-0.21	yes
AT1G29280	WRKY65	0.81	-0.20	-0.35	yes
AT4G26640	WRKY20	-0.47	-0.47	0.03	no
AT4G26440	WRKY34	-0.46	0.62	-1.23	yes
AT4G22070	WRKY31	0.42	-0.32	0.54	no
AT4G39410	WRKY13	0.24	-0.32	0.74	no
AT4G30935	WRKY32	-0.37	-0.60	-0.46	no
AT1G80590	WRKY66	-1.15	-0.51	0.02	no
AT2G03340	WRKY3	0.24	-0.39	-0.24	yes
AT5G56270	WRKY2	-0.42	-0.47	-0.28	no
AT2G47260	WRKY23	0.11	-0.45	-0.06	no
AT5G52830	WRKY27	0.18	-0.67	0.09	no
AT2G46130	WRKY43	-0.49	-0.88	-1.58	no
AT1G30650	WRKY14	-1.22	-0.78	0.15	no
AT2G34830	WRKY35	-0.94	-1.75	0.73	no

* according to Supplemental Dataset 1. Genes differentially expressed during senescence. Breeze et al.

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Supplemental Table 12: Differential expression (in *atg5* & *atg9* relative to wild type) of NAC genes in rosettes grown under low (lowN) or high (highN) nitrate conditions for 30 (30DAS) or 60 (60DAS) days after sowing.The log₂(fold change) values of the differentially expressed genes are presented, yellow and blue colours indicate significant up and down regulations, respectively (FDR%<10 Breeze et al. 2011³).

AGI	NAC gene name	<i>atg5</i> & <i>atg9</i> lowN 30DAS	<i>atg5</i> & <i>atg9</i> lowN 60DAS	<i>atg5</i> highN 60DAS	senescence related*
AT3G15500	ANAC055 (ARABIDOPSIS NAC I	-1.37	4.79	4.35	yes
AT4G29230	anac075 (Arabidopsis NAC dor	0.04	4.19	4.60	no
AT1G02220	ANAC003 (Arabidopsis NAC dc	3.48	4.09	2.71	yes
AT2G17040	anac036 (Arabidopsis NAC dor	2.67	2.24	1.95	no
AT1G52890	ANAC019 (Arabidopsis NAC dc	0.34	2.29	2.29	yes
AT3G04060	anac046 (Arabidopsis NAC dor	0.56	2.12	2.27	yes
AT3G61910	ANAC066 (ARABIDOPSIS NAC I	0.93	2.04	-0.63	no
AT3G44350	anac061 (Arabidopsis NAC dor	2.76	2.32	2.25	no
AT5G14000	anac084 (Arabidopsis NAC dor	-0.61	2.01	2.98	yes
AT5G18270	ANAC087; transcription factor	0.87	2.16	1.43	yes
AT5G39610	ATNAC6 (ARABIDOPSIS NAC D	0.32	2.04	2.22	yes
AT3G04070	anac047 (Arabidopsis NAC dor	0.74	2.07	1.66	yes
AT3G17730	anac057 (Arabidopsis NAC dor	1.52	1.80	0.74	no
AT2G43000	anac042 (Arabidopsis NAC dor	-0.90	1.60	1.51	yes
AT5G22380	anac090 (Arabidopsis NAC dor	3.06	1.69	1.51	no
AT1G69490	NAP (NAC-like, activated by A	1.75	1.63	2.34	yes
AT1G34180	anac016 (Arabidopsis NAC dor	0.02	1.38	1.56	yes
AT5G56620	anac099 (Arabidopsis NAC dor	0.77	1.50	-0.46	no
AT5G63790	ANAC102 (ARABIDOPSIS NAC I	0.38	1.06	1.24	yes
AT3G29035	ATNAC3 (ARABIDOPSIS NAC D	0.19	0.94	0.94	yes
AT5G62380	ANAC101 (ARABIDOPSIS NAC-	0.69	0.80	1.22	no
AT4G17980	anac071 (Arabidopsis NAC dor	-1.52	0.64	0.74	no
AT1G01010	ANAC001 (Arabidopsis NAC dc	1.27	0.75	0.42	no
AT1G28470	ANAC010 (ARABIDOPSIS NAC I	-1.06	0.64	-0.16	no
AT1G32870	ANAC13 (Arabidopsis thaliana	1.18	0.69	0.39	yes
AT5G64060	anac103 (Arabidopsis NAC dor	0.12	0.93	1.02	yes
AT1G02250	anac005 (Arabidopsis NAC dor	-0.01	0.60	-0.73	yes
AT5G07680	ANAC080 (ARABIDOPSIS NAC I	2.24	0.73	2.01	yes
AT3G10500	anac053 (Arabidopsis NAC dor	-0.10	0.67	0.72	yes
AT5G61430	ANAC100 (ARABIDOPSIS NAC I	-0.22	1.00	0.71	yes
AT5G09330	anac082 (Arabidopsis NAC dor	-0.25	0.66	0.22	no
AT2G33480	ANAC041 (Arabidopsis NAC dc	0.24	0.73	0.85	yes
AT1G77450	anac032 (Arabidopsis NAC dor	0.28	0.49	0.52	yes
AT1G25580	ANAC008 (Arabidopsis NAC dc	1.26	0.66	0.61	no
AT1G33280	ANAC015 (Arabidopsis NAC dc	-0.10	0.78	1.25	no
AT1G56010	NAC1; transcription factor	2.10	0.43	0.03	yes
AT5G41090	anac095 (Arabidopsis NAC dor	-0.99	0.15	0.37	no
AT3G03200	anac045 (Arabidopsis NAC dor	-0.04	0.49	-1.59	no
AT5G04410	NAC2; transcription factor	-0.05	0.30	0.18	yes
AT5G13180	ANAC083 (ARABIDOPSIS NAC I	-0.11	0.52	0.61	yes
AT1G60280	ANAC023 (Arabidopsis NAC dc	-1.23	0.40	0.15	no
AT1G60350	anac024 (Arabidopsis NAC dor	-0.81	0.11	0.23	no
AT5G39820	anac094 (Arabidopsis NAC dor	0.14	0.10	0.84	no
AT2G24430	ANAC038 (ARABIDOPSIS NAC I	-0.50	0.10	0.82	no
AT3G49530	anac062 (Arabidopsis NAC dor	0.61	0.16	-0.18	yes
AT5G66300	NAC105 (NAC DOMAIN CONT	-0.58	-0.23	-0.66	no
AT4G10350	ANAC070 (Arabidopsis NAC dc	-0.64	-0.20	0.25	yes
AT1G65910	anac028 (Arabidopsis NAC dor	0.07	-0.08	-0.12	no
AT4G28530	anac074 (Arabidopsis NAC dor	-0.21	-0.25	-0.11	yes
AT1G32770	ANAC012 (ARABIDOPSIS NAC I	-1.10	-0.35	1.86	no
AT3G18400	anac058 (Arabidopsis NAC dor	0.10	-0.40	-0.43	no
AT1G34190	anac017 (Arabidopsis NAC dor	0.36	-0.05	0.09	yes
AT5G17260	anac086 (Arabidopsis NAC dor	-0.26	-0.33	1.86	no
AT5G04400	anac077 (Arabidopsis NAC dor	-0.72	-0.44	0.25	yes
AT5G50820	anac097 (Arabidopsis NAC dor	1.60	-0.41	-0.18	no
AT5G22290	anac089 (Arabidopsis NAC dor	-0.31	-0.32	-0.12	yes
AT1G62700	ANAC026; transcription factor	0.43	-0.53	0.15	no
AT1G54330	ANAC020 (Arabidopsis NAC dc	1.90	-0.16	1.53	no
AT4G36160	ANAC076 (ARABIDOPSIS NAC I	0.33	-0.28	-0.28	no
AT4G01550	anac069 (Arabidopsis NAC dor	0.16	-0.51	-0.51	no
AT2G02450	ANAC035 (Arabidopsis NAC dc	0.84	-0.42	0.07	no
AT3G04420	anac048 (Arabidopsis NAC dor	1.36	-0.54	-0.99	yes
AT5G46590	anac096 (Arabidopsis NAC dor	-0.92	0.02	-0.44	no
AT1G12260	ANAC007 (ARABIDOPSIS NAC I	-1.27	-0.55	2.71	no
AT3G15510	ATNAC2 (ARABIDOPSIS NAC D	0.49	-0.35	0.12	yes
AT4G28500	ANAC073 (ARABIDOPSIS NAC I	0.29	-0.73	0.04	no
AT1G61110	anac025 (Arabidopsis NAC dor	-0.11	-0.26	-0.13	no

* according to Supplemental Dataset 1. Genes differentially expressed during senescence. Breeze et al. (2011)

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