

**Supplemental Figure 1: Thiol levels of genetically complemented** *sir1-1* **plants** (A) Cysteine and (B) Glutathione steady state levels in leaves of 7 week old wild type (black), *sir1-1* (white) and three complemented *sir1-1* lines (gray) grown on soil under short day conditions. Mean  $\pm$  SE (n = 5) are shown. Asterisks indicate statistical significance (P < 0.05). FW, fresh weight



#### Supplemental Figure 2: Spectrum of glucosinolates in *sir1-1* plants

Steady state levels of the major glucosinolates in leaves of 7 week old wild type (black) and *sir1-1* (white) plants grown on soil in a growth chamber under short day conditions. Mean  $\pm$  SE (n = 5) are shown. Asterisks indicate statistical significance (P < 0.05). 1: glucoibarin, 2: glucoeurocin, 3: glucohirsutin, 4: glucobrassicin, 5: 4-methoxy.glucobrassicin, 6: neuglucobrassin, 7: glucoiberin, 8: glucoalyssin.



### Supplemental Figure 3: Contribution of anions to total sulfur and nitrogen content

(A) The Content of sulfate in % of dry weight was calculated on the basis of means of sulfate steady-state levles in leaves of 7 week old plants grown on soil under short day conditions and a ratio of fresh to dry weight of 13.81 for wild type and 13.16 for *sir1-1* plants. (Fig. 4A). The contribution of other S-compounds was calculated by difference of sulfate content to the total content of sulfur in wild type and *sir1-1* (Fig. 4F, n = 5). (B) Same calculation for contribution of nitrate to total content of nitrogen as in A.





Steady state levels of amino acids in leaves of 7 week old wild type (black) and *sir1-1* (white) plants grown on soil in a growth chamber under short day conditions. Mean  $\pm$  SE (n = 5) are shown. Asp: aspartic acid, Glu: glutamic acid, Ser: serine, Asn: asparagine, Gly: glycine, Gln: glutamine, Thr: threonine, His: histidine, Ala: alanine, Arg: arginine, Pro: proline, Tyr: tyrosine, Val: valine, Met: methionine, Ile: isoleucine, Leu: leucine, Lys: lysine, Phe: phenylalanine, FW, fresh weight



## Supplemental Figure 5: Immunological detection of sulfite oxidase (SO) in *sir1-1* plants

Soluble proteins were extracted from leaves of 7 week old wild type (Col-0) and *sir1-1* plants grown on soil in a growth chamber under short day conditions (n=3). Total soluble proteins (10  $\mu$ g) were separated by SDS-PAGE (12% acrylamide) and transferred to a nitrocellulose membrane as described in the Methods. The abundance of Sulfite oxidase was tested with a polyclonal antiserum according to Lang et al., (2007).



### Supplemental Figure 6: Incorporation rates of sulfate in wild type and *sir1-1* plants grown on soil

Leaf pieces of 7 week old wild type (black circles) and *sir1-1* (white circles) from plants grown on soil at short day conditions were incubated with  ${}^{35}SO_4{}^2$ -spiked  $\frac{1}{2}$  Hoagland solution for 15 min (pulse) and subsequently kept on the same medium without radiolabel for 30 min (chase). Time point 0 was defined by transfer of leaf pieces to  ${}^{35}SO_4{}^2$ -spiked  $\frac{1}{2}$  Hoagland solution. Samples were taken at indicated time points. (A) Cysteine and (B) GSH were extracted and separated by HPLC. The incorporated  ${}^{35}S$ -label was quantified by scintillation counting. The mean  $\pm$  SE from 4 independent extractions of wild type and *sir1-1* are shown. Asterisks indicate statistical significance (P < 0.05). FW, fresh weight



# Supplemental Figure 7: Transcript levels of *APR2* in *sir 1-1* determined by qRT-PCR

Total mRNA was extracted from leaves of *sir1-1* and wild type plants grown on soil under short day conditions for 7 weeks (n = 3) and analysed for transcript levels of *APR2* by qRT-PCR as described in the Methods. Ef1a served as reference. Means ± SE are shown. Asterisks indicate statistically significant differences.

### Supplemental Data. Khan et al. Plant Cell. (2010). 10.1105/tpc.110.074088

UND 00IndexOutputModuleModul		I		I	median fitted	median fitted			
Add [1170]Sex (0.1019)Sex (0.1019) <th>MIPs code</th> <th>NCBI GeneID:</th> <th>Identity, description</th> <th>Catagory</th> <th>data Col-0</th> <th>data sir</th> <th>Change</th> <th>Change in % of wild type</th> <th>P- value</th>	MIPs code	NCBI GeneID:	Identity, description	Catagory	data Col-0	data sir	Change	Change in % of wild type	P- value
Ardy2000Rev20.132167WingwardenBauterial cythese33276WindU.1.6U.1.6U.0.1Ardy2000Free StabilityConsolidit synthese37.620.0810.0210.021Ardy2000Free StabilityVanchum F490, CPT24Consolidit synthese1.0810.0210.021Ardy2000Free StabilityVanchum F490, CPT24Consolidit synthese1.0810.0210.021Ardy2000Free StabilityVanchum F490, CPT24Consolidit synthese2.0810.110.011Ardy2100Free StabilityVanchum F490, CPT24Consolidit synthese2.0810.110.1100.011Ardy2100Free StabilityVanchum F490, CPT24Consolidit synthese2.0810.110.0110.011Ardy2100Free StabilityVanchum F190, FT2100Consolidit synthese1.0100.0110.0110.011Ardy2100StabilityVanchum F190, FT2100Consolidit synthese1.0100.0110.0110.011Ardy2100StabilityVanchum F190, FT2100Consolidit synthese1.0100.0110.01	At3g19710	GeneID:821508	branched-chain amino transferase	Glucosinolat-synthesis	5594	9639	1,72	172,0	0,004
Mag 2000     Genetic 3,2565     Improvise     Quality of prediction     1,252     1,558     1,538     1,538     0,500       ALALLIO     Construct Anticolation     Construct Anticolati	At5g25980	GeneID:832667	myrosinase	Glucosinolat-synthesis	35276	56689	1,61	161,0	0,031
Add 11/0     Conception P4/9     Quantitation profiles     2664     1.000     1.51     1.53     0.50       Add 1240     Conception profiles     Quantitation profiles     2.000     1.20     1.20     1.20     0.000       Add 2240     Conception profiles     Quantitation profiles     2.000     1.20     1.20     0.000       Add 2240     Conception profiles     Quantitation profiles     1.20     1.20     0.000       Add 22400     Conception profiles     Quantitation profiles     1.100     1.10     1.10     0.000       Add 22400     Conception profiles     Quantitation profiles     1.100     1.10     1.10     1.10     0.000       Add 22400     Conception profiles     Quantitation profiles     1.100     1.10     <	At5g26000	GeneID:832669	myrosinase	Glucosinolat-synthesis	5726	9084	1,59	159,0	0,004
Aligheod     Seriol Skillin     Operations 440, OPPUP     Enclosed synthesis     2010     1.11     1.10     1.10     0.00       Aligheod     Seriol Skillin     Operations     Obcessmele synthesis     1.10     1.10     0.00       Aligheod     Seriol Skillin     Operations     Obcessmele synthesis     1.10     1.10     0.00       Aligheod     Seriol Skillin     Operations     Obcessmele synthesis     1.10     1.10     0.00       Aligheod     Seriol Skillin     Seriol Skillin     Operations     0.00	At4g13770	GenelD:827011	cytochrom P450	Glucosinolat-synthesis	7864	12020	1,53	153,0	0,022
Add BLOB     Evol D. 2013     Department of the second synthesis     1440     1740     1	At1g16400	GenelD:838210	cytochrom P450, CYP79F2	Glucosinolat-synthesis	2083	2957	1,42	142,0	0,022
All (24.10)     Annu Statut     Decomposition     Decompositio	At4g03060	GenelD:828102	AOP2	Glucosinolat-synthesis	1948	2476	1,27	127,0	0,006
Artice 2015     Participating Provings     Discover 1	At1g24100	GenelD:839022	glucosyl transferase	Glucosinolat-synthesis	3025	3591	1,19	119,0	0,016
Balance     Participant Networks     Difference of the second sec	AL1g54040	GenelD:841842	epithiospecifier protein,	Glucosinolat-synthesis	2408	2/51	1,14	114,0	0,03
And Sci 2000     International Control     1940     5545     1.14     1.140     0.000       And Sci 2000     Serie D 231545     AMPC 1     Serie D 23156     AMPC 1     Serie D 23156     AMPC 1     Serie D 23157     LAID 2	At2g22550	GenelD:824772	mandelonitrile lyase like protein	Glucosinolat-synthesis	2126	2400	-1.2	54.2	0,04
AT322.20     sense D 2115 4     AtMPT 3     atMpre atMPT 3     Sense D 2115 4     AtMPT 3     atMpre atMPT 3     AtMPT 3     atMpre atMPT 3	AT5663980	GenelD:836519	PAPS Phosphatase	Sulfur-metabolism	3942	5354	1 36	136.0	0,034
ArtAG0120     Semi-D 24097     MA2     With matheding     5372     0.77     1.22     1.20     0.033       Artg5120     Semi-D 24078     Aptice metallymysion     Suffic matheding     1.28     2.73     1.31     6.80     6.80       Artg5120     Semi-D 24077     Cycle Sing Hethian     Suffic matheding     1.28     2.924     1.24     6.80     6.82       Artg51200     Semi-D 24077     Cycle Sing Hethian     Suffic matheding     1.22     1.24     4.93     6.01     6.01       ArtG51200     Semi-D 24077     Cycle Sing Hethian     Suffic matheding     1.22     1.24     4.93     6.01       ArtG51200     Semi-D 23078     Suffic matheding     1.24     4.94     6.01       ArtG51200     Semi-D 23078     Suffic matheding     1.937     1.17     0.02     0.01       ArtG51200     Semi-D 24078     Suffic matheding     1.937     1.22     0.940     0.01       ArtG51200     Suffic matheding     Suffic matheding     1.041     1.010     0.02     0.01     0.01 <t< td=""><td>AT3G22740</td><td>GenelD:821845</td><td>AtHMT-3</td><td>Sulfur-metabolism</td><td>1580</td><td>1937</td><td>1,30</td><td>130,0</td><td>0.03</td></t<>	AT3G22740	GenelD:821845	AtHMT-3	Sulfur-metabolism	1580	1937	1,30	130,0	0.03
Alg.S202     Gene DataBase     All enclasation     D238     1.16     D350     Quant       Alg.S2070     Gene DatAsia     Suff-metabolism     D288     D431     L.12     D48.6     D033       Alg.S2070     Gene DatAsia     Suff-metabolism     D2785     Quant     D432     D436     D033       Alg.S2080     Gene DatAsia     Suff-metabolism     D2785     Quant     D433     D436     D406     D630	AT4G01850	GenelD:826987	SAM2	Sulfur-metabolism	5572	6779	1.22	122.0	0.033
Addgo 200Send D35000Cyclesine desult/mylosieSuffic-metacloimD238D2731.130.010.01Addgo 201Send D34300Pylochelisin synthaseSuffic-metacloimD4880.031D4221.230.031ATGS 202Sinfi Crimites Embry DotteSuffic-metacloimD728D2281.230.031ATGS 202Sinfi Crimites Embry DotteSuffic-metacloimD378D3821.420.003ATGS 202Sinfi Crimites Embry DotteSuffic-metacloimD378D3821.420.003ATGS 202Sinfi Crimites Embry DotteSuffic-metacloimD378D3281.22D3100.013ATGS 202Sinfi CrimitesSuffic-metacloimD378D321D412D310D310ATGS 202Sinfi CrimitesSuffic-metacloimD312D312D412D310D310ATGS 202Sinfi CrimitesSuffic-metacloimD325D312D412D310D310ATGS 202Sinfi CrimitesSuffic-metacloimD325D312D412D410D310ATGS 202Sinfi CrimitesSinfi CrimitesD320D312D312D412D310D310ATGS 202Sinfi CrimitesSinfi CrimitesD320D312D413D410D310ATGS 202Sinfi CrimitesD300D312D312D413D414D300ATGS 202Sinfi Crimites Embry D310Affi-CrimitesD300D312D413D414D410ATGS	At1g62180	GenelD:842514	APR2	Sulfur-metabolism	6278	5390	-1,16	86,2	0,034
Addgatory     Genetic 33420     Cynthechaetan synthesie     Suffar metabolism     4365     <	At5g65720	GenelD:836701	cysteine desulfhydrylase	Sulfur-metabolism	3258	2731	-1,19	84,0	0,043
AlfaCodeOptime/BBAS synthesizeSuffar metabolism172629491,120.00AlfaClaudGeneb 33282AlfaCrandezas taminy portenSuffar metabolism12138904,430.00AlfaClaudGeneb 33283AlfaCrandezas taminy portenSuffar metabolism12148904,430.00AlfaClaudGeneb 33303SRSuffar metabolism1613100011771.111.00AlfaClaudGeneb 33303SRSuffar metabolism1613100011771.121.00AlfaClaudGeneb 33303Geneb 33303Suffar metabolism161310001.121.001000AlfaClaudGeneb 33303Geneb 33303Geneb 33303Geneb 333031.111.121.00 </td <td>At5g44070</td> <td>GeneID:834430</td> <td>Phytochelatin synthase</td> <td>Sulfur-metabolism</td> <td>4958</td> <td>4081</td> <td>-1,21</td> <td>82,6</td> <td>0,032</td>	At5g44070	GeneID:834430	Phytochelatin synthase	Sulfur-metabolism	4958	4081	-1,21	82,6	0,032
ArtigizitionOracle 30700Alformatabolam307307073707370707070ArtigizitionSerie 033400AFSSuffar-metabolam1234098904.450.003ArtigizitionSerie 033400AFSSuffar-metabolam1613460001.7171.711.010.013ArticizitionSerie 033030simular to ACC ordebreSuffar-induced660011.7171.711.710.013ArticizitionSerie 033000Suffar-induced633071.3131.4.20.0200.0014ArticizitionSerie 033000Suffar-induced1.3355.904251.1.11.1.100.0014ArticizitionSuffar-induced1.0201.020421.1.11.1.100.0014ArtigizitionSuffar-induced1.02041.02141.1.11.1.100.0014ArtigizitionSuffar-induced1.02041.02141.1.11.1.10.0124ArtigizitionSuffar-induced1.02041.02141.1.11.1.10.0124ArtigizitionSuffar-induced1.02041.02131.1.11.1.10.0124ArtigizitionSuffar-induced1.02041.02131.1.11.1.10.0124ArtigizitionSuffar-induced1.02041.02131.1.11.1.10.0124ArtigizitionSuffar-induced1.02041.02131.1.11.1.10.0124ArtigizitionSuffar-induced1.02141.02141.02141.0.12 <t< td=""><td>AT3G56300</td><td>GenelD:824797</td><td>Cysteinyl-tRNA synthetase</td><td>Sulfur-metabolism</td><td>37265</td><td>29949</td><td>-1,24</td><td>80,6</td><td>0,048</td></t<>	AT3G56300	GenelD:824797	Cysteinyl-tRNA synthetase	Sulfur-metabolism	37265	29949	-1,24	80,6	0,048
ATTG1320Gene 33290Solfar neutrabolismSIGur metabolismSIGUBestBidline <td>At5g10180</td> <td>GeneID:830882</td> <td>Sultr2;1</td> <td>Sulfur-metabolism</td> <td>3738</td> <td>2728</td> <td>-1,37</td> <td>73,0</td> <td>0,018</td>	At5g10180	GeneID:830882	Sultr2;1	Sulfur-metabolism	3738	2728	-1,37	73,0	0,018
AlegatizeGenetic 3:4.000PS4Sulfur-metabolism355410.251.4.855.40.001ATG52505Genetic 3:1038Sinfur to ACC ordsareSulfur-induced630211.7111.7.00.035ATG524505Genetic 3:1038Sinfur transfer and in any proteinSinfur induced357733121.1.20.03ATG524707Genetic 3:8556Genetic 1:8556Genetic 1:8556Genetic 1:8556Genetic 1:85560.0210.025ALG24707Genetic 3:8556Vict Transfer Sinfur induced20261.8836.060.001ALG24707Genetic 3:8556Vict Transfer Sinfur induced20261.8836.060.001ALG24707Genetic 3:8556Vict Transfer Sinfur induced20261.8836.060.002ALG24708Genetic 3:8556Vict Transfer Sinfur induced20262.8321.161.61.00.002ALG24709Genetic 3:8556Vict Transfer Sinfur induced2.8022.8321.161.60.00.002ALG24800Genetic 3:8558Vict Transfer Sinfur Induced2.8323.8371.161.60.00.002ALG24800Genetic 3:8558Vict Transfer Sinfur Induced2.8022.8321.161.60.00.002ALG25800Genetic 3:8558Vict Transfer Sinfur Induced2.8022.8321.161.60.00.002ALG25800Genetic 3:8588Vict Transfer Sinfur Induced2.8021.181.60.00.002ALG25800Genetic 3:8588 <td>AT1G13420</td> <td>GeneID:837902</td> <td>Sulfotransferase family protein</td> <td>Sulfur-metabolism</td> <td>12743</td> <td>8940</td> <td>-1,43</td> <td>69,9</td> <td>0,03</td>	AT1G13420	GeneID:837902	Sulfotransferase family protein	Sulfur-metabolism	12743	8940	-1,43	69,9	0,03
AlfS00500     SenetD X83384     Sintur netabolism     16134     900     -1,22     1,11     0.01       AlfSC125400     GenetD X81083     Sintur nodoced     6002     11177     1,1,1     0.016       AlfSC125400     GenetD X81083     Sintur nodoced     15376     9057     1,1,2     80,0     0.012       AlfSC12700     GenetD X81557     VCCITATIVE STOAKCE PROTTIN L     Sulfur induced     2265     90,05     1,1,37     11,17,0     0.001       AlfSC24700     GenetD X81557     VCCITATIVE STOAKCE PROTTIN L     Sulfur induced     2267     94,221     1,61     161.0     0.001       AlfSC24700     GenetD X81547     VCCITATIVE STOAKCE PROTTIN L     Sulfur induced     2202     1,81     11,60     0.013       AlfSC24800     GenetD X81548     AlfColas Lampurotin     RECOX     2312     238     -1,11     81,60     0.042       AlfSC24800     GenetD X81548     AlfColas Lampurotin     RECOX     2121     238     -1,11     84,60     0.042       AlfSC24800     GeneD X81548     AlfColas Lampurotin	At5g43780	GeneID:834400	APS4	Sulfur-metabolism	3554	1932	-1,84	54,3	0,003
AT26.25.90     Genel D 31.03     imilar to ACC oxidase     Suffa-induced     6020     11.71     1.7.1     1.7.10     0.0.03       ATGL2207     Genel D 283556     VECTATVE STORAGE PROTEIN 2     Suffa-induced     15335     9957     1.6.1     0.0.25     0.0.013       ATGL2207     Genel D 28356     VECTATVE STORAGE PROTEIN 2     Suffa-induced     2057     3.0.025     11.37     11.0.0     0.0.013       Atg22707     Genel D 38356     VECTATVE STORAGE PROTEIN 2     Suffa-induced     2054     1.6.1     1.6.1     0.0.013       Atg2808     Genel D 38492     Midra for AGC 2001     2053     3.5.7     1.1.8     11.0.0     0.0.013       Atg2808     Genel D 38494     Midra for AGC 2001     3.5.1     3.5.7     1.1.8     8.6.5     0.0.013       Atg28030     Genel D 38494     Midra for AGC 2001     3.5.1     3.5.1     3.6.0     0.0.013       Atg28030     Genel D 38494     Midra for AGC 2001     3.6.0     0.0.013     3.6.0     0.0.013     3.6.0     0.0.013     3.6.0     0.0.013     3.6.0     0.0.01	AT5G04590	GeneID:830336	SiR	Sulfur-metabolism	16134	5008	-3,22	31,1	0
ATAG12470     GreentD-286827     GreentD-286827     GreentD-286827     GreentD-2862847     GreentD-2862844     GreentD-2862846     GreentD-2862844     GreentD-2862844     GreentD-2862846     GreentD-2862847     GreentD-2862847     GreentD-2862847     GreentD-2862847 <td>AT2G25450</td> <td>GeneID:817083</td> <td>similar to ACC oxidase</td> <td>Sulfur-induced</td> <td>6902</td> <td>11797</td> <td>1,71</td> <td>171,0</td> <td>0,036</td>	AT2G25450	GeneID:817083	similar to ACC oxidase	Sulfur-induced	6902	11797	1,71	171,0	0,036
ALG012/0     Genetic Association     choregates recorded hypothetic and synchronization of synchronizatio synchronization of synchronization of synchroniz	AT4G12470	GeneID:826859	lipid transfer protein family protein	Sulfur-induced	3877	3121	-1,24	80,6	0,014
Adg2470     Serello 33247     VECKTATV STORAGE PROTEIN 3     Juliar-induced     20/5     30/25     11.37     1137,0     0.001       Adg24780     Serello 33140     VECKTATV STORAGE PROTEIN 3     Juliar-induced     20.01     8.88     88.60     0.001       Adg2780     Serello 31474     MyOrdea family protein     REDOX     22.81     4.420     1.16     11.0     0.001       Adg2180     Serello 31474     MyOrdea family protein     REDOX     20.01     3.121     9.05     0.007       Adg21810     Serello 31474     MATH domain-containing protein     REDOX     1312     2.161     8.82     0.002       Adg26600     Serello 31458     Hordeain     REDOX     2120     1.81     8.92     0.023       Adg26600     Serello 31568     ghorine-rich protein     REDOX     2100     3.11     8.92     0.024       Adg26001     Serello 31568     ghorine-rich protein     REDOX     3108     2.202     7.8     0.012       Adg26001     Serello 31570     Serello 31570     Serello 31570     3.132	ATCG01270	GeneID:6686170	chloroplast encoded hypothetical prot	Sulfur-induced	15336	9567	-1,6	62,5	0,042
Abg24780     Schelo 32430     Viesk ALIVE 3 DMALE PHOTEIN     Subtrimuted     2104     13885     6,99     6980     0.001       Abg24780     Schelo 319400     Unitaredoxin     R EOX     2887     4421     1,18     1180     0.042       Abg23800     Schelo 319404     MHH domain containing protein     R EOX     2887     3421     1,14     1140     0.033       Abg23800     Schelo 318440     MH domain containing protein     R EOX     1753     1587     1,1     999     0.047       Abg24500     Genelo 328430     Thorestoxin     REDOX     2156     1562     -1,17     885     0.038       Abg26600     Genelo 328430     Thorestoxin     REDOX     2163     1813     0.012       Abg26000     Genelo 32840     Abgr07     REDOX     3430     2900     -1,18     847     0.083       Abg26000     Genelo 32804     Abgr07     REDOX     3430     1318     -1,20     77.5     0.013       Abg26000     Genelo 32810     Abgr07     REDOX     3428 <td>At5g24770</td> <td>GenelD:832546</td> <td>VEGETATIVE STORAGE PROTEIN 2</td> <td>Sulfur-induced</td> <td>2675</td> <td>30425</td> <td>11,37</td> <td>1137,0</td> <td>0,001</td>	At5g24770	GenelD:832546	VEGETATIVE STORAGE PROTEIN 2	Sulfur-induced	2675	30425	11,37	1137,0	0,001
Arge/sed     SenelD-31930     Full protein     REOX     2416     4420     1,61     161.0     0.024       Alge/sed     SenelD-319324     MATH domain-containing protein     REOX     2032     2332     1,14     1110     0.034       Alge/sed     SenelD-319324     MATH domain-containing protein     REOX     2032     2332     1,14     1140     0.03       Alge/sed     GenelD-3193340     Thimase     REOX     2112     1557     1,1     88,5     0.033       Alge/sed     GenelD-329436     Thimase     REDOX     2112     1502     -1,17     88,5     0.038       Alge/sed     GenelD-329436     Clutaredoxin     REDOX     7185     1612     -1,18     84,7     0.013       Alge/sed     GenelD-329310     Alge/sed     GenelD-319301     Cin finger family protein     REDOX     19326     1-123     84,3     0.013       Alge/sed     GenelD-321561     Alge/sed     6124     44,4     64,0     0.022       Alge/sed     GenelD-31932     Alge/sed     <	At5g24780	GenelD:832547	VEGETATIVE STORAGE PROTEIN 1	Sulfur-Induced	2104	18883	8,98	898,0	0,001
Arg.2030     CentlD 31494     InyBroads family protein     FEDX     2881     3421     1.18     1180     0.002       Arg.20380     CentD 31494     MATH domain-containing protein     KEDX     2012     2212     1.14     1140     0.03       Arg.20380     CentD 38495     Initrace     REDOX     3112     2681     -1,16     66.2     0.025       Arg.20380     CentD 38495     Initrace     REDOX     2170     15502     -1,17     65.5     0.038       Arg.20380     CentD 38495     Giutathone Reductase1     REDOX     2180     67.6     7.123     81.3     0.012       Arg.20380     CentD 38496     Giutathone Reductase1     REDOX     4340     2000     -1,18     84.7     0.033       Arg.20380     CentD 38545     Giutathone Reductase1     REDOX     4340     7.3     0.014       Arg.20380     CentD 38556     Giutathone Reductase1     REDOX     4340     7.3     0.041       Arg.20380     CentD 38376     Giutathone Reductase1     REDOX     12743	At2g47880	GenelD:819400	Giutaredoxin	REDOX	2618	4220	1,61	161,0	0,032
Arightsom     Omnet Database     Divert Database <thdivert database<="" th="">     Divert Database<td>At2g03980</td><td>GenelD:814924</td><td>nydrolase family protein</td><td>REDOX</td><td>2887</td><td>3421</td><td>1,18</td><td>118,0</td><td>0,034</td></thdivert>	At2g03980	GenelD:814924	nydrolase family protein	REDOX	2887	3421	1,18	118,0	0,034
Angle 2.10     Deriv Datassen     pace regulation of the constraint of	At/g22150	GenelD:817849	main domain-containing protein	REDOX	2032	1597	1,14	114,0	0,03
Alg. 2008/00     SameD 3294/20     This medioxim     REDOX     1.17     8.5     0.055       Alg. 2660     SameD 3294/61     Glutarelowin     REDOX     7168     6124     -1.17     8.5     0.058       Alg. 2660     SameD 3294/21     Glutarelowin     REDOX     7168     6124     -1.17     8.5     0.058       Alg. 2660     SameD 3294/21     Glutarelowin     REDOX     716     6124     -1.17     8.5     0.029       Alg. 2660     SameD 32056     Jprimerich protein     REDOX     1982     61055     -1.23     8.13     0.012       Alg. 2530     Genel 38373     Zxp. Pr 8     REDOX     44286     3135     -1.37     73.0     0.04       Alg. 2530     Genel 38375     Zxp. Pr 8     REDOX     1274     1486     67.6     0.022       Alg. 2540     Genel 38373     Zxp. Pr 8     REDOX     1274     177.6     -1.6     6.25     0.022       Alg. 2540     Genel 38379     Pl 1     REDOX     1274     177.6     -1.6 <t< td=""><td>At+2g/3570</td><td>GenelD:818959</td><td>chitinase</td><td>REDOX</td><td>3112</td><td>2681</td><td>-1,1</td><td>86.2</td><td>0,047</td></t<>	At+2g/3570	GenelD:818959	chitinase	REDOX	3112	2681	-1,1	86.2	0,047
Algosol     Constraint	At1g03680	GenelD:839436	Thioredoxin	REDOX	21720	18502	-1,10	80,2	0,023
Alsgis330   GenelD336423   Glutaredoxin   REDOX   3430   2900   -1,18   84,7   0,03     Alzgis380   GenelD31506   plyciner(thr protein   REDOX   19426   16057   -1,22   81,1   0,012     Alzgis380   GenelD31507   AtGyr7   REDOX   4006   3118   -1,29   77,5   0,018     Aldgis180   GenelD33157   AtGyr7   REDOX   4410   7139   -1,32   77,6   0,004     Alzgis530   GenelD33057   2Cy5 Prx A   REDOX   12743   8940   -1,43   69,9   0,003     Alzgis530   GenelD32553   Thioredoxin   REDOX   12743   8940   -1,48   67,6   0,022     Alzgis520   GenelD32553   Thioredoxin   REDOX   2742   1716   -6,6   6,5   0,022     Alzgis520   GenelD32553   Thioredoxin   REDOX   1244   1717   -1,6   6,5   0,022     Alzgis520   GenelD32559   PR2   REDOX   1248   10710   -1,73   5,6   0,002     Alzgis520   GenelD3127	At3g54660	GenelD:824631	Glutathione Reductase I	REDOX	7168	6124	-1.17	85,5	0.039
Ar2g05380   Genel 3815086   eytener-tch protein   BEOX   19826   16677   1-123   81.1   0.012     Ar2g25580   Genel 381507   inc finger family protein   REDX   4400   3118   1-129   77.5   0.013     Ar2g05200   Genel 382501   2-Cy Fix 8   REDOX   42866   31255   1.37   73.0   0.004     Ar2g01300   Genel 382566   dihydroligoyd dehydrogenase   REDOX   12438   8940   1.443   6.09,9   0.033     Ar3g11630   Genel 382567   Thioredoxin   REDOX   33458   22366   1.44   6.04,9   0.002     Ar3g125205   Genel 324597   Thioredoxin   REDOX   2742   1716   1.6   6.6,5   0.022     Ar3g125205   Genel 324591   DX1   REDOX   2742   1716   1.6   6.6,5   0.022     Ar3g12520   Genel 324391   PR1   REDOX   2742   1716   1.6   6.0,25   0.002     Ar3g12520   Genel 32439   PR2   REDOX   2742   1716   1.6   0.023     Ar3g25205	At5g63030	GeneID:836423	Glutaredoxin	REDOX	3430	2900	-1,18	84,7	0,03
Ar2g2950     SenelD 21707     Inc finger family protein     BDOX     4009     3118     -1.29     77.5     0.018       Aldg31570     GenelD 232316     AlGpA7     BDOX     42866     31255     -1.37     7.5.0     0.010       Alf261480     GenelD 232316     ditydrolpoyl dehydrogenase     REDOX     12743     8940     -1.43     66.9     0.033       Alf261480     GenelD 232355     Thioredxin     REDOX     12743     8940     -1.43     66.9     0.032       Alf262500     GenelD 232103     C/cy. Pr. A     REDOX     12743     144     67.6     0.022       Alf262501     GenelD 231093     PR1     REDOX     12742     1716     -1.6     6.25     0.022       Alf262503     GenelD 2310937     Upid transfer protein     REDOX     1284     10710     -1.73     0.75     0.022       Alf262503     GenelD 2310937     Upid transfer protein     REDOX     6112     3441     -1.78     0.75     0.024       Alf262503     GenelD 231204     Alf511/2	At2g05380	GeneID:815086	glycine-rich protein	REDOX	19826	16057	-1,23	81,3	0,012
Ardg1807     GenelD 28393.6     AGpx7     REDOX     9410     7139     1.32     75,8     0,017       Al5g06290     GenelD 283576     2/cys Px A     REDOX     42866     31255     1.37     7.30     0,004       Al72G14680     GenelD 283556     2/cys Px A     REDOX     12743     8940     -1.43     69.9     0.033       Al72G14580     GenelD 2820535     Z/cys Px A     REDOX     13455     127.43     -1.44     6.06.9     0.022       Al72G2520     GenelD 282033     Thioredoxin     REDOX     2742     1716     -1.6     6.62.5     0.022       Al2g5250     GenelD 812937     Upt transfer protein     REDOX     1844     1010     -1.73     57.8     0.002       Al2g24290     GenelD 812937     Lipt transfer protein     REDOX     1844     1010     -1.73     57.65     0.002       Al2g2490     GenelD 812937     Lipt transfer protein     REDOX     1848     1010     -1.73     0.002     Al2g2490     GenelD 81492     0.012     Al2g24     1.55	At2g29580	GenelD:817507	zinc finger family protein	REDOX	4009	3118	-1,29	77,5	0,018
Atsgbc2vv     GenelD 320517     2-Cyc Px R     REDX     42866     31255     -1.37     (7.9)     (0.004       AT2641580     GenelD 320351     Z/Cyc Px A     REDOX     31345     2328     -1.44     (9.9)     (0.03)       At2011630     GenelD 320352     Thoredoxin     REDOX     31345     2328     -1.44     (9.0)     (0.02)       At201203     GenelD 321353     Thoredoxin     REDOX     2124     1716     -1.65     (0.02)     (0.02)       At2245401     GenelD 321394     REDX     611     3444     -1.78     (0.02)     (0.01)       At2244200     GenelD 31394     ATGS US     GSUT Tansfer     41864     (0.71)     (0.02)     (0.02)       At2242500     GenelD 31794     ATGS F2     GSUT Tansfer     31325     (3.13)     (3.13)     (0.02)       At2262500     GenelD 38294     H11.1     pathogens-related     6112     13274     2.17     (0.02)       At262500     GenelD 382955     TH2.1     pathogens-related     6197     1.19     (0.	At4g31870	GenelD:829316	AtGpx7	REDOX	9410	7139	-1,32	75,8	0,017
AT2641800     GenelD.818766     dihydrolipoyl dehydrogenase     REDOX     12743     8940     -1,43     66,99     0.03       At3g11530     GenelD.823653     Thioredoxin     REDOX     33458     22286     -1,44     67,6     0.022       At4g03520     GenelD.822119     OX1     REDOX     2742     1716     -1,6     62,5     0.022       AT264160     GenelD.832493     PR1     REDOX     2742     1716     -1,6     62,5     0.022       At3g25200     GenelD.832493     PR2     REDOX     6142     3441     107,10     -1,73     65,6     0.002       At2g42490     GenelD.83744     ATGST US     GSH-Transfer     3718     273     -1,29     77.5     0.024       At2g2508     GenelD.83704     buttwe glutathione pervidase/Gor GSH-Transfer     3738     15340     -2,17     61,6     0.002       At2g25080     GenelD.83704     DHTA gener Selated     6112     1324     -1,15     64,5     0.021       At2g25080     GenelD.83705     TH1.1     path	At5g06290	GenelD:830517	2-Cys Prx B	REDOX	42866	31255	-1,37	73,0	0,004
At3g1130   Genelb:32033   2-Cyc Ptr A   REDOX   33458   2226   1,44   69,4   0,022     At4g03520   Genelb:32119   OX10   REDOX   1955   1324   1,48   67,6   0,022     At2g1401   Genelb:315949   PR1   REDOX   2742   1716   -1,6   6,2,5   0,022     At3g15200   Genelb:28493   PR2   REDOX   18444   10710   1,73   57,8   0,004     At2g24900   Genelb:31949   AtG5TUS   GSH-Transfer   4869   7458   1,53   0,003     At2g2030   Genelb:317440   AtG5T US   GSH-Transfer   13950   9001   -1,55   64,5   0,002     At2g2030   Genelb:31540   patatry glutathione peroxidas AtSp   GSH-Transfer   13950   9001   -1,55   64,5   0,002     At4g02520   Genelb:31542   patatry glutathione peroxidas AtSp   GSH-Transfer   13950   9001   -1,55   64,6   0,002     At205200   Genelb:31504   AtF0510   GPR3   pathogens-related   6112   13274   2,17   2,17   0,002<	AT2G41680	GenelD:818766	dihydrolipoyl dehydrogenase	REDOX	12743	8940	-1,43	69,9	0,03
Atdg0320     Genelb.32563     Thoredoxin     REDOX     19556     13243     1.48     67.6     0.022       At3G2520     Genelb.321949     PK1     REDOX     2742     1716     1.6     6.62,5     0.022       At3g57200     Genelb.324893     PK2     REDOX     18484     10710     1.73     7.78     0.004       At2g229450     Genelb.317494     ATGST U     GSH-Transfer     4869     7458     1.53     153,0     0.035       At2g22940     Genelb.817494     ATGST U     GSH-Transfer     3718     273     1.29     7.7     0.024       At2g25080     Genelb.81744     ATGST F2     GSH-Transfer     33328     15340     -2.17     46.1     0.009       At1601670     Genelb.83554     Chorophyliae     pathogens-related     6112     13244     2.17     2.17     0.002       At1601070     Genelb.83554     CHR3     pathogens-related     6112     13244     2.17     1.01     0.013       ATG60500     Genelb.831550     VPR3     pathogens	At3g11630	GenelD:820335	2-Cys Prx A	REDOX	33458	23286	-1,44	69,4	0,027
AT3G25250     GenelD:322119     OXI     REDOX     2742     1716     -1.6     66.25     0.022       AT3G257260     GenelD:324893     PR1     REDOX     1746     -1.6     66.25     0.022       AT3g57260     GenelD:324893     PR2     REDOX     6112     3441     -1.73     57.8     0.004       AT2g244200     GenelD:314924     ATGST US     GSH-Transfer     4889     7458     1.53     0.013     0.015       AT2g242930     GenelD:314822     putative glutathione s-transferace     GSH-Transfer     3738     2873     -1.29     77.5     0.0024       At4g02520     GenelD:314822     putative glutathione peroxidase At6p     GSH-Transfer     33328     15340     -2,17     46.1     0.009       AT101670     GenelD:327931     ATGST F2     GSH-Transfer     33328     15340     -2,17     46.1     0.002       AT2606050     GenelD:343524     HI1.1     pathogens-related     6112     3327     -2,17     46.1     0.003       AT2606050     GenelD:343558	At4g03520	GenelD:825653	Thioredoxin	REDOX	19556	13243	-1,48	67,6	0,022
At2g1610     GenelD:345949     PR1     REDOX     2742     1716     -1.6     62.5     0.022       At3g57260     GenelD:34939     PR2     REDOX     18484     10731     -1.78     56.2     0.004       At3g57260     GenelD:34794     ATGST U5     GSH-Transfer     4869     7458     1.53     153.0     0.032       At2g29500     GenelD:34794     putative glutathione stransfers     GSH-Transfer     31395     9001     -1.55     64.5     0.021       At2g2500     GenelD:34754     putative glutathione peroxidase AtGp     GSH-Transfer     33328     153.40     -2.17     46.1     0.002       At1265070     GenelD:38554     Chorophylase     pathogens-related     612     3328     1.36     136.0     0.038       At1265070     GenelD:83558     TH2.1     pathogens-related     2697     2.32     1.22     0.001       At127220     GenelD:8358     TH2.1     pathogens-related     2697     2.342     -1.15     87.0     0.038       At1625870     GenelD:83155	AT3G25250	GenelD:822119	OXI1	REDOX	2742	1716	-1,6	62,5	0,022
AlageS2400     GenelD:8248933     PR2     REDOX     18484     10710     -1,73     57.8     0,004       Al2geA290     GenelD:817931     Lipid transfer protein     REDOX     6112     3441     -1,78     55.6     0,004       Al2ge2930     GenelD:817944     ATGST US     GSH-Transfer     3718     2873     -1,29     77,5     0,024       Al4g02520     GenelD:817946     putative glutathione Stransferse     GSH-Transfer     33326     15340     -2,17     66,1     0,009       Al4g02520     GenelD:838554     Chlorophyllase     pathogens-related     6112     13274     2,17     21,00     0,002       Al1G19670     GenelD:838554     Chlorophyllase     pathogens-related     6112     13274     2,17     21,00     0,003       Al1G6100     GenelD:831556     OPR3     pathogens-related     2692     3296     1,22     122,0     0,011       Al1G6100     GenelD:831556     AVRPHB SUSCEPTIBL 1     pathogens-related     2697     2342     -1,15     87,0     0,032 <td< td=""><td>At2g14610</td><td>GenelD:815949</td><td>PR1</td><td>REDOX</td><td>2742</td><td>1716</td><td>-1,6</td><td>62,5</td><td>0,022</td></td<>	At2g14610	GenelD:815949	PR1	REDOX	2742	1716	-1,6	62,5	0,022
Ar224290   Genel0:81937   Lipid transfer protein   HEUX   0.112   3441   -1,78   356,2   0.004     Ar2229450   Genel0:817494   ATGST U5   GSH-Transfer   4869   7458   1,53   15,0   0,023     Ar2220450   Genel0:817046   putative glutathione peroxidase AtGp/GSH-Transfer   13950   9001   1,55   64,5   0.021     Ar42p0250   Genel0:81791   ATGST F2   GSH-Transfer   13320   9001   1,55   64,5   0.002     Ar12619670   Genel0:838554   Chlorophyllase   pathogens-related   6112   13274   2,17   217,0   0,002     Ar1266100   Genel0:842924   TH1.1   pathogens-related   2692   3296   1,22   122,0   0,011     Ar12606005   Genel0:84358   TH12.1   pathogens-related   2697   2342   1,15   87,0   0,038     Ar1269270   Genel0:84358   TH12.1   pathogens-related   2107   1576   1,4   71,4   0,024     Ar1369870   Genel0:84328   TPH binding cassette transporter   pathogens-related   2697   2342	At3g57260	GenelD:824893	PR2	REDOX	18484	10710	-1,73	57,8	0,004
Ard22930   GenelD:817434   Ard51 OS   GM-Hallslef   44869   7488   1.53   15.0   0.033     Ard202930   GenelD:8120   putative glutathione 5-transferac   GSH-Transfer   3718   2873   -1,29   77.5   0.023     Ard202520   GenelD:827931   ArGST F2   GSH-Transfer   33228   15340   -2,17   46.1   0.009     AT1619670   GenelD:83554   Chlorophyllase   pathogens-related   6112   13274   2,17   217,0   0,002     Ar1266100   GenelD:83554   Chlorophyllase   pathogens-related   2692   3296   1,22   122,0   0,011     Ar1262050   GenelD:843558   TH11.1   pathogens-related   2692   3296   1,22   122,0   0,031     Ar1272060   GenelD:843558   TH21   pathogens-related   2697   2342   1,15   87,0   0.038     Ar1618600   GenelD:821625   ETHYLENE-INSENSTIVE3   pathogens-related   2697   2342   1,15   87,0   0.038     Ar1645800   GenelD:821625   ETHYLENE-INSENSTIVE3   pathogens-related   2697	At2g44290	GenelD:819037	Lipid transfer protein	CSU Transfer	6112	3441	-1,/8	56,2	0,004
Ar2g02930   GenelD:814822   putative glutatinone 5-transfer   37.8   28.73   -1.29   77.5   0.024     Ar2g25080   GenelD:817046   putative glutatinone 5-transfer   33328   15340   -2.17   46.1   0.009     Attag02520   GenelD:838554   Chlorophyllase   pathogens-related   6112   132.74   2.17   21.70   0.002     At1G19670   GenelD:842924   TH1.1   pathogens-related   6370   5138   1,36   136.0   0.038     AT2G06050   GenelD:843558   TH2.1   pathogens-related   2692   3296   1,22   122.0   0.011     AT2G06050   GenelD:843558   TH2.1   pathogens-related   2697   3422   -1,15   87.0   0.038     AT2G05070   GenelD:843558   TH2.1   pathogens-related   2177   1576   -1,4   71,4   0.024     AT1659870   GenelD:84281   ATP PH0 matograssette transporter   pathogens-related   2177   15576   -1,4   71,4   0.024     AT3620770   GenelD:827395   RPP4   pathogens-related   6297   4170   -1,51 <td>At2g29450</td> <td>GenelD:817494</td> <td></td> <td>GSH-Transfer</td> <td>4809</td> <td>7458</td> <td>1,53</td> <td>153,0</td> <td>0,035</td>	At2g29450	GenelD:817494		GSH-Transfer	4809	7458	1,53	153,0	0,035
Actg2:0000     GenelD:827931     ATGST F2     GSH-Transfer     13328     15340     -2,17     46,1     0,024       Artg0:2520     GenelD:827931     ATGST F2     GSH-Transfer     33328     15340     -2,17     46,1     0,002       Artg0:2520     GenelD:838554     Chlorophyllase     pathogens-related     3790     5138     1,36     136,0     0,038       AT2G06050     GenelD:84358     THI1.1     pathogens-related     2692     3296     1,22     0,011       At1g72260     GenelD:84358     THI2.1     pathogens-related     2697     2342     -1,15     87,0     0,038       AT1g7250     GenelD:831155     AVRPPHB SUSCEPTIBLE 1     pathogens-related     2697     2342     -1,15     87,0     0,038       AT16258070     GenelD:821255     THYLENE-INSENSITIVE3     pathogens-related     2177     15576     -1,4     71,4     0,024       AT3620770     GenelD:821625     ETHYLENE-INSENSITIVE3     pathogens-related     2697     4170     -1,51     66,2     0,007       AT4616860 </td <td>AL2802930</td> <td>GenelD:814822</td> <td>putative glutathione perovidase AtCox</td> <td>GSH-Transfer</td> <td>12050</td> <td>2873</td> <td>-1,29</td> <td>//,5</td> <td>0,024</td>	AL2802930	GenelD:814822	putative glutathione perovidase AtCox	GSH-Transfer	12050	2873	-1,29	//,5	0,024
ATIG19670     Genel D:838554     Chlorophyllase     pathogens-related     6112     13274     2,17     217,0     0.002       ATIG19670     Genel D:838554     Chlorophyllase     pathogens-related     3790     5138     1,36     136,0     0,038       ATIG19670     Genel D:838554     Chlorophyllase     pathogens-related     2692     3296     1,22     122,0     0,011       ATI205050     Genel D:831550     OPR3     pathogens-related     2692     3296     1,22     122,0     0,011       ATI205070     Genel D:831555     AVRPPHB SUSCEPTIBLE 1     pathogens-related     2697     2342     -1,15     87,0     0,038       ATI3659870     Genel D:842281     ATP binding cassette transporter     pathogens-related     21777     15576     -1,4     71,4     0,022       ATI3619600     Genel D:821625     ETHYLENE-INSENSITIVE3     pathogens-related     21977     4150     66,2     0,007       ATI3616800     Genel D:823573     RPP4     pathogens-related     6297     4170     -1,51     66,2     0,002	At2g23080	GenelD:827931	ATGST F2	GSH-Transfer	33328	15340	-1,55	46.1	0,021
Arlag6100     Gene Disad2924     TH11.1     pathogens-related     372     1.367     1.367     1.360     0.002       Arlag6100     Gene Disad2924     TH11.1     pathogens-related     3730     5138     1.36     136,0     0.038       Arlag6100     Gene Disad2924     TH12.1     pathogens-related     1486     1767     1.19     119,0     0.031       Arlag5100     Gene Disad2924     TH12.1     pathogens-related     1486     1767     1.19     119,0     0.031       Arlag513160     Gene Disad2251     ATP Phinding cassette transporter     pathogens-related     2697     2342     -1,15     87,0     0.038       ArlaG6000     Gene Disa21625     ETHYLENE-INSENSITIVE3     pathogens-related     21777     15576     -1,4     71,4     0.002       ArlaG6800     Gene Disa27305     RPP4     pathogens-related     7455     4951     -1,51     66,2     0.002       ArlaG6800     Gene Disa32573     RPP10     pathogens-related     16675     10827     -1,51     66,2     0.0025 <t< td=""><td>AT1G19670</td><td>GenelD:838554</td><td>Chlorophyllase</td><td>pathogens-related</td><td>6112</td><td>13274</td><td>2 17</td><td>217.0</td><td>0.002</td></t<>	AT1G19670	GenelD:838554	Chlorophyllase	pathogens-related	6112	13274	2 17	217.0	0.002
AT2G06050     GeneID:815160     OPR3     pathogens-related     2692     3296     1,22     122,0     0,011       At1g72260     GeneID:843558     THI2.1     pathogens-related     1486     1767     1,19     119,0     0,031       AT5G13160     GeneID:843558     THI2.1     pathogens-related     2697     2342     -1,15     87,0     0,038       AT1G59870     GeneID:821625     CTMYLENE-INSENSTIVE3     pathogens-related     21777     15576     -1,4     71,4     0,024       AT3G20770     GeneID:821625     CTMYLENE-INSENSTIVE3     pathogens-related     9919     G722     -1,48     67,6     0,007       AT4G16860     GeneID:821637     RPP4     pathogens-related     7455     4951     -1,51     66,2     0,009       AT4G16860     GeneID:823573     RPP4     pathogens-related     6297     4170     -1,51     66,2     0,025       AT4G16850     GeneID:823432     RPS     pathogens-related     16675     10827     -1,54     64,9     0,012       AT1675040	At1g66100	GenelD:842924	THI1.1	pathogens-related	3790	5138	1,36	136.0	0.038
Attg72260     GeneID:843558     THI2.1     pathogens-related     1486     1767     1,19     119,0     0,031       AT5G13160     GeneID:831155     AVRPPH8 SUSCEPTIBLE 1     pathogens-related     2697     2342     -1,15     87,0     0,038       AT1G59870     GeneID:831155     AVRPPH8 SUSCEPTIBLE 1     pathogens-related     21777     15576     -1,4     71,4     0,024       AT1G59870     GeneID:821635     ETHVEINE-INSENSITIVE3     pathogens-related     21777     15576     -1,4     71,4     0,024       AT3620770     GeneID:821635     ETHVEINE-INSENSITIVE3     pathogens-related     7455     4951     -1,51     66,2     0,009       AT3640480     GeneID:823573     RPP4     pathogens-related     6297     4170     -1,51     66,2     0,022       AT4616950     GeneID:823733     RPP5     pathogens-related     16675     10827     -1,54     64,9     0,012       AT1675040     GeneID:831935     glutamate dehydrogenase     amino acid synthesis     3356     2820     -1,19     84,0     0	AT2G06050	GenelD:815160	OPR3	pathogens-related	2692	3296	1,22	122,0	0,011
AT5G13160     GeneID:831155     AVRPPHB SUSCEPTIBLE 1     pathogens-related     2697     2342     -1,15     87,0     0,038       AT1G59370     GeneID:822281     ATP binding cassette transporter     pathogens-related     21777     15576     -1,4     71,4     0,024       AT3G20770     GeneID:8221625     ETHYLENE-INSENSITIVE3     pathogens-related     9919     6722     -1,48     67,6     0,007       AT4G15860     GeneID:827395     RPP4     pathogens-related     7455     4951     -1,51     66,2     0,009       AT3G44800     GeneID:827373     RPP4     pathogens-related     6297     4170     -1,51     66,2     0,025       AT4G15800     GeneID:823573     RPP4     pathogens-related     16675     10827     -1,54     64,9     0,012       AT1G75040     GeneID:83492     PR5     pathogens-related     6586     4134     -1,59     62,9     0,006       At5g15170     GeneID:830457     ASA1     amino acid synthesis     3356     2820     -1,19     84,0     0,022	At1g72260	GenelD:843558	THI2.1	pathogens-related	1486	1767	1,19	119,0	0,031
AT1659870GenelD:842281ATP binding cassette transporterpathogens-related217711576-1.4<1.7.40.024AT3620770GenelD:821625ETHYLEN-INSENSITIVE3pathogens-related991966722-1.4.866.6.60.007AT4616860GenelD:827305RPP4pathogens-related62924170-1.5.166.6.20.0025AT3644480GenelD:827303RPP10pathogens-related62924170-1.5.166.6.20.0025AT4616950GenelD:827403RPP5pathogens-related6166510827-1.5.166.20.0025AT4616950GenelD:831935glutamat edhydrogenaseamino acid synthesis33562820-1.1984.00.022At4g39540GenelD:831035shikmate kinase - like proteinamino acid synthesis33662922-1.657.9.40.033AT3644300GenelD:831375gibberellin-regulated (GASA4)Hormon induced/related277837781.3.6136.00.012AT3644300GenelD:831375gibberellin-regulated (GASA4)Hormon induced/related277837781.3.6136.00.012AT3644300GenelD:82355NT1Auxin-Biosynthese558642931.2.4124.00.022AT3644300GenelD:833375gibberellin-regulated (GASA4)Hormon induced/related277837781.3.6136.00.012AT3644300GenelD:82356NT1Auxin-Biosynthese558642931.2.412	AT5G13160	GenelD:831155	AVRPPHB SUSCEPTIBLE 1	pathogens-related	2697	2342	-1,15	87,0	0,038
AT3G20770GenelD:821625FTHYLENE-INSENSITIVE3pathogens-related9919 $6722$ $1.48$ $667.6$ $0,007$ AT4G16860GenelD:827305RPP4pathogens-related $7455$ $44951$ $-1,51$ $66.2$ $0,009$ AT3G44040GenelD:823733RPP10pathogens-related $6297$ $4170$ $-1,51$ $66.2$ $0,002$ AT4G16950GenelD:824703RPP5pathogens-related $16675$ $01827$ $-1,54$ $66.49$ $0,012$ AT1G75040GenelD:831935glutamate dehydrogenaseamino acid synthesis $3356$ $2282$ $-1,19$ $84.0$ $0.022$ At5g50570GenelD:831075Jutamate dehydrogenaseamino acid synthesis $3366$ $2922$ $-1,26$ $0.026$ $0.008$ At4g39540GenelD:831075Jithiase - like proteinamino acid synthesis $3686$ $2922$ $-1,26$ $0.79.4$ $0.033$ AT3G44300GenelD:831375gibberellin-regulated (GASA4)Hormon induced/related $2778$ $3778$ $1,36$ $136.0$ $0.012$ AT3G4206GenelD:823556NT1Auxin-Biosynthese $5752$ $9348$ $1,24$ $124.0$ $0.022$ AT4G4560GenelD:827103auxin induced gene (IAA1)Hormon induced/related $3725$ $2836$ $-1,31$ $76.3$ $0.033$	AT1G59870	GeneID:842281	ATP binding cassette transporter	pathogens-related	21777	15576	-1,4	71,4	0,024
AT4G16860     GeneID:827395     RPP4     pathogens-related     7455     44951     -1,51     66,2     0,009       AT3G44480     GeneID:823573     RPP10     pathogens-related     6297     4170     -1,51     66,2     0,009       AT3G44480     GeneID:823573     RPP10     pathogens-related     16675     10827     -1,51     66,9     0,002       AT1G75040     GeneID:824342     PR5     pathogens-related     16675     10827     -1,59     62,9     0,006       At5g18170     GeneID:834942     PR5     pathogens-related     6586     4134     -1,59     62,9     0,006       At5g18170     GeneID:830457     ASA1     amino acid synthesis     3356     2820     -1,12     84,0     0,022       At4g39504     GeneID:830455     ASA1     amino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3G44310     GeneID:823555     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT3G44310     GeneID:823556	AT3G20770	GenelD:821625	ETHYLENE-INSENSITIVE3	pathogens-related	9919	6722	-1,48	67,6	0,007
AT364480     GeneID:823573     RPP10     pathogen-related     6297     4170     -1,51     66,2     0,025       AT4616950     GeneID:824703     RPP5     pathogens-related     16675     10827     -1,51     66,2     0,025       AT4616950     GeneID:824703     RPP5     pathogens-related     16675     10827     -1,54     64,9     0,012       AT1675040     GeneID:834935     glutamate dehydrogenase     amino acid synthesis     3356     2820     -1,19     84,0     0,022       At5g05730     GeneID:830457     ASA1     amino acid synthesis     3456     2820     -1,12     82,0     0,033       At4g39504     GeneID:830457     ASA1     amino acid synthesis     3666     2922     -1,26     79,4     0,033       At3G94300     GeneID:830455     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT3G44310     GeneID:823556     NT1     Auxin-Biosynthese     7552     9348     1,24     124,0     0,022       AT4624620	AT4G16860	GeneID:827395	RPP4	pathogens-related	7455	4951	-1,51	66,2	0,009
AT4G16950     GeneID:827403     RPP5     pathogens-related     16675     10827     -1,54     66,9     0,012       AT1G75040     GeneID:834842     PR5     pathogens-related     6586     4134     -1,59     62,9     0,006       At5g18170     GeneID:834842     PR5     amino acid synthesis     3356     2820     -1,19     84,0     0,022       At5g05730     GeneID:830457     ASA1     amino acid synthesis     3482     3420     -1,22     82,0     0,033       At4g39540     GeneID:830108     shikimate kinase - like protein     amino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3G44300     GeneID:831375     gibberellin-regulated (GASA4)     Hormon induced/related     2778     3778     1,36     136,0     0,011       AT4624200     GeneID:823556     NIT1     Auxin-Biosynthese     752     3378     1,26     136,0     0,012       AT4624200     GeneID:823556     NIT1     Auxin-Biosynthesis     5388     4293     -1,26     77,4     0,022	AT3G44480	GeneID:823573	RPP10	pathogens-related	6297	4170	-1,51	66,2	0,025
AT1675040     GeneID:843842     PR5     pathogens-related     6586     4134     -1,59     62,9     0,006       At5g18170     GeneID:831935     glutamate dehydrogenase     amino acid synthesis     3356     2820     -1,19     84,0     0,022       At5g05700     GeneID:830185     Shikimate kinase - like protein     amino acid synthesis     3486     2822     -1,22     82,0     0,033       At4g39540     GeneID:830185     shikimate kinase - like protein     amino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3G44300     GeneID:830155     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT3G44310     GeneID:823556     NT1     Auxin-Biosynthese     752     3778     1,36     136,0     0,012       AT4624204     GeneID:823556     NT1     Auxin-Biosynthese     752     9348     1,24     124,0     0,022       AT4624204     GeneID:823556     NT1     Auxin-Biosynthesis     5388     4293     -1,26     79,4     0,022 <	AT4G16950	GeneID:827403	RPP5	pathogens-related	16675	10827	-1,54	64,9	0,012
Atsg18170     GeneID:831935     [glutamate dehydrogenase     amino acid synthesis     3356     2820     -1,19     84,0     0,022       Atsg05703     GeneID:830457     ASA1     amino acid synthesis,     4182     3420     -1,22     82,0     0,033       Atsg05704     GeneID:830457     ASA1     amino acid synthesis,     4182     3420     -1,22     82,0     0,033       At4g39540     GeneID:830455     nitrilase - like protein     amino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3644300     GeneID:833555     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT3644310     GeneID:823556     NT1     Auxin-Biosynthese     752     9348     1,24     124,0     0,022       AT4624200     GeneID:823556     NT1     Auxin-Biosynthesis     5388     4293     1,26     79,4     0,022       AT4614504     GeneID:823556     Phosphoglucose isomerase     Asc-biosynthesis     5388     4293     1,26     79,4     0,022	AT1G75040	GeneID:843842	PR5	pathogens-related	6586	4134	-1,59	62,9	0,006
Atsgup /su     GenelD:83045 /     ASA1     amino acid synthesis,     4182     3420     -1,22     82,0     0,033       At4g39540     GenelD:830108     shikmate kinase - like protein     amino acid synthesis     3686     2922     -1,26     79,4     0,033       At4g39540     GenelD:830158     shikmate kinase - like protein     amino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3G44300     GenelD:823555     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT3G44310     GenelD:823556     NT1     Auxin-Biosynthese     752     3778     1,36     136,0     0,012       AT462420     GenelD:823556     NT1     Auxin-Biosynthese     7552     9348     1,24     124,0     0,022       AT4614506     GenelD:827103     auxin induced gene (IAA1)     Hormon induced/related     3725     2836     -1,31     76,3     0,033	At5g18170	GenelD:831935	giutamate dehydrogenase	amino acid synthesis	3356	2820	-1,19	84,0	0,022
Ardg3v3vu     Genelux3suus     Ishkimate kinase - like protein     Jamino acid synthesis     3686     2922     -1,26     79,4     0,033       AT3G44300     GenelDx823555     nitrilase     Auxin-Biosynthese     6014     9007     1,5     150,0     0,006       AT5G15230     GenelDx823555     gibberellin-regulated (GASA4)     Hormon induced/related     2778     3778     1,36     136,0     0,011       AT3G44310     GenelDx823556     NIT1     Auxin-Biosynthese     7552     9348     1,24     124,0     0,022       AT4G24520     GenelDx823556     NIT1     Auxin-Biosynthese     7552     9348     1,24     124,0     0,022       AT4G24520     GenelDx823564     Phosphoglucose isomerase     Asc-biosynthesis     5388     4293     -1,26     79,4     0,022       AT4G24504     GenelDx82703     auxin induced gene (IAA1)     Hormon induced/related     3725     2836     -1,31     76.3     0.033	At5g05730	GenelD:830457	ASA1	amino acid synthesis,	4182	3420	-1,22	82,0	0,033
AT3G44300     OetileUx23555     INTTIBSE     Auxin-BioSynthese     6014     9007     1,5     150,0     0,006       AT3G44300     GeneIDx831375     gibberellin-regulated (GASA4)     Hormon induced/related     2778     3778     1,36     136,0     0,011       AT3G44310     GeneIDx823556     NTT     Auxin-Biosynthese     7552     9348     1,24     124,0     0,022       AT4G24520     GeneIDx828564     Phosphoglucose isomerase     Asc-biosynthesis     5388     4293     -1,26     79,4     0,022       AT4G24500     GeneIDx82703     auxin induced gene (IAA1)     Hormon induced/related     3725     2836     -1,31     76.3     0.033	At4g39540	GenelD:830108	snikimate kinase - like protein	amino acid synthesis	3686	2922	-1,26	79,4	0,033
AT3G4310     GeneID:823556     NIT1     Auxin-Biosynthese     7752     9348     1,24     124,0     0,022       AT4G24520     GeneID:823556     NIT1     Auxin-Biosynthese     752     9348     1,24     124,0     0,022       AT4G24520     GeneID:828564     Phosphoglucose isomerase     Asc-biosynthesis     5388     4293     -1,26     79,4     0,022       AT4G14560     GeneID:827103     auxin induced gene (IAA1)     Hornon induced/related     3725     2836     -1,31     76.3     0.033	AT5C15330	GenelD:823555	niu nase	Auxin-Biosynthese	6U14	9007	1,5	150,0	0,006
AT462450     GeneID:828564     Phosphoglucose isomerase     Asc-biosynthesis     538     4293     -1,26     79,4     0,022       AT4614560     GeneID:828713     auxin induced gene (IAA1)     Hormon induced/related     3725     2836     -1,31     76.3     0.033	AT3G//210	GenelD:822556	NIT1		2//8	5//8	1,30	130,0	0,01
Art61450 GeneID:827103 auxin induced gene (IAA1) Hormon induced/related 3725 2836 -1,31 76.3 0.033	AT4624620	GeneID:828564	Phosphoglucose isomerase	Asc-hiosynthesis	5388	9548 4293	-1.26	124,0	0,022
	AT4G14560	GeneID:827103	auxin induced gene (IAA1)	Hormon induced/related	3725	2836	-1,31	76,3	0,033

## Supplemental Table 1: Significantly regulated transcripts in leaves of 7 week old *sir1-1* plants

The table represents significantly up- (white) and down-regulated (red) transcript levels in leaves of *sir1-1* in comparison to the wild type (Col-0). MIPS code (unique identifier of genes in *Arabidopsis thaliana*), NCBI GeneID (unique identifier of cDNAs), Identity, description (common name or function of gene product), Category (classification in metabolic network), median fitted data (raw data sets), Change (difference in transcript level in x-fold of wild type), Change in % of wild type (difference in transcript level in percent of wild type), P-value (indicator of statistical significance determined by M-CHiPS).

Supplemental Data. Khan et al. Plant Cell. (2010). 10.1105/tpc.110.074088

### Supplemental Methods: Processing of microarray data

Signal intensities were normalized by loglinear regression as described [1]. All hybridizations showed correlation coefficients higher than 0.8 between the two channels. The normalized data were used to compute P-values via the limma package [1]. In limma, a contrast matrix defines the comparisons of interest between samples in the experiment. We used a complete pairwise-comparisons contrast matrix to test differential expression across all samples.

Regression coefficients were estimated using a least squares linear model fitting procedure and tested for differential expression with moderated Student's t-statistic via the empirical Bayesian statistics described in the limma package. P-values computed for the *F-statistic* [2] were adjusted for multiple testing to control the FDR at 5% [3]. The adjusted p-values can serve to accept or reject the nullhypothesis based on a significance level. We selected genes showing intensity levels of more than 1000 in at least one of the conditions and also exhibit p-values smaller than 0.05.

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[3] Benjamini, Y. & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. J. R. Stat. Soc. Ser. B, 1995, **57**: 289–300