**Table 2S:**

Overview of transcripts that are at least two-fold down- or up-regulated in both replicate experiments with DTT.

*control*: RMA normalised intensity value for the control incubation. *DTT*: RMA normalised intensity value for the DTT treated tissue. *call*: the present (P) or absent (P) call as defined by the MAS5 analyses software.
*ratio*: DTT to control ratio of the normalised intensity values. *Log2[ratio]*: log2 transformed value of the ratio. The *average log2[ratio]* and its *p-value* are calculated using the AffylmGUI software package from Bioconductor.

| ATH1 code | replica 1 | | | | | | replica 2 | | | | | | average | | annotation Tigre5 |
| | control | call | DTT | call | ratio | log2[ratio] | control | call | DTT | call | ratio | log2[ratio] | log2[ratio] | p-value | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 266743_at | 702 | P | 97 | M | 0.14 | **-2.85** | 551 | P | 78 | A | 0.14 | **-2.82** | -2.8357 | 0.000 | At2g02990: ribonuclease 1 (RNS1) |
| 261177_at | 1007 | P | 131 | P | 0.13 | **-2.94** | 378 | P | 116 | P | 0.31 | **-1.71** | -2.3240 | 0.017 | At1g04770: male sterility MS5 family protein |
| 267645_at | 1063 | P | 151 | P | 0.14 | **-2.82** | 722 | P | 216 | P | 0.30 | **-1.74** | -2.2782 | 0.003 | At2g32860: glycosyl hydrolase family 1 protein |
| 245151_at | 962 | P | 335 | P | 0.35 | **-1.52** | 538 | P | 122 | P | 0.23 | **-2.15** | -1.8326 | 0.053 | At2g47550: pectinesterase family protein |
| 245317_at | 2922 | P | 1186 | P | 0.41 | **-1.30** | 870 | P | 210 | P | 0.24 | **-2.05** | -1.6744 | 0.228 | At4g15610: integral membrane family protein |
| 249752_at | 398 | P | 101 | P | 0.25 | **-1.98** | 427 | P | 185 | P | 0.43 | **-1.21** | -1.5911 | 0.013 | At5g24660: expressed protein |
| 260438_at | 366 | P | 134 | P | 0.37 | **-1.45** | 234 | P | 79 | P | 0.34 | **-1.56** | -1.5048 | 0.022 | At1g68290: bifunctional nuclease, putative |
| 255261_s_at | 1884 | P | 610 | P | 0.32 | **-1.63** | 1394 | P | 554 | P | 0.40 | **-1.33** | -1.4789 | 0.003 | At4g05110: equilibrative nucleoside transporter, putative (ENT6); At4g05120: equilibrative nucleoside |
| 246944_at | 1565 | P | 699 | P | 0.45 | **-1.16** | 963 | P | 286 | P | 0.30 | **-1.75** | -1.4578 | 0.068 | At5g25450: ubiquinol-cytochrome C reductase complex 14 kDa protein, putative |
| 260528_at | 329 | P | 128 | P | 0.39 | **-1.37** | 273 | P | 101 | P | 0.37 | **-1.44** | -1.4018 | 0.003 | At2g47260: WRKY family transcription factor |
| 250448_at | 589 | P | 167 | P | 0.28 | **-1.82** | 396 | P | 193 | P | 0.49 | **-1.04** | -1.4253 | 0.007 | At5g10820: integral membrane transporter family protein |
| 255284_at | 608 | P | 195 | P | 0.32 | **-1.64** | 571 | P | 270 | P | 0.47 | **-1.08** | -1.3595 | 0.004 | At4g04610: 5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19) |
| 256177_at | 683 | P | 247 | P | 0.36 | **-1.46** | 559 | P | 243 | P | 0.44 | **-1.20** | -1.3314 | 0.002 | At1g15620: protein kinase family protein |
| 248812_at | 494 | P | 258 | P | 0.52 | **-0.93** | 542 | P | 151 | P | 0.28 | **-1.84** | -1.3893 | 0.015 | At5g47330: palmitoyl protein thioesterase family protein |
| 247730_at | 197 | P | 93 | A | 0.47 | **-1.08** | 238 | P | 79 | A | 0.33 | **-1.59** | -1.3351 | 0.002 | At5g59580: UDP-glucoronosyl/UDP-glucosyl transferase family protein |
| 259375_at | 2149 | P | 499 | P | 0.23 | **-2.11** | 3385 | P | 1952 | P | 0.58 | **-0.79** | -1.4505 | 0.148 | At3g16370: GDSL-motif lipase/hydrolase family protein |
| 252437_at | 1115 | P | 538 | P | 0.48 | **-1.05** | 628 | P | 219 | P | 0.35 | **-1.52** | -1.2877 | 0.102 | At3g47380: invertase/pectin methylesterase inhibitor family protein |
| 266089_at | 2242 | P | 1045 | P | 0.47 | **-1.10** | 1280 | P | 498 | P | 0.39 | **-1.36** | -1.2323 | 0.083 | At2g38010: ceramidase family protein |
| 246463_at | 1475 | P | 595 | P | 0.40 | **-1.31** | 1172 | P | 567 | P | 0.48 | **-1.05** | -1.1793 | 0.003 | At5g16970: NADP-dependent oxidoreductase, putative (P1) |
| 251895_at | 3057 | P | 1391 | P | 0.45 | **-1.14** | 1573 | P | 684 | P | 0.43 | **-1.20** | -1.1692 | 0.104 | At3g54420: class IV chitinase (CHIV) |
| 252984_at | 386 | P | 160 | A | 0.42 | **-1.27** | 253 | P | 124 | A | 0.49 | **-1.03** | -1.1466 | 0.020 | At4g37990: mannitol dehydrogenase, putative (ELI3-2) |
| 260386_at | 343 | P | 176 | A | 0.51 | **-0.96** | 263 | P | 107 | A | 0.41 | **-1.30** | -1.1290 | 0.030 | At1g74010: strictosidine synthase family protein |
| 264749_at | 209 | P | 91 | P | 0.44 | **-1.19** | 251 | P | 123 | P | 0.49 | **-1.03** | -1.1108 | 0.009 | At1g22830: pentatricopeptide (PPR) repeat-containing protein |
| 245181_at | 220 | P | 109 | P | 0.50 | **-1.01** | 120 | P | 53 | P | 0.44 | **-1.17** | -1.0911 | 0.111 | At5g12420: expressed protein |
| 250365_at | 96 | P | 39 | P | 0.41 | **-1.30** | 222 | P | 119 | P | 0.54 | **-0.90** | -1.1004 | 0.231 | At5g11410: protein kinase family protein |
| 265411_at | 339 | P | 157 | P | 0.46 | **-1.11** | 341 | P | 165 | P | 0.48 | **-1.05** | -1.0801 | 0.001 | At2g16630: proline-rich family protein |
| 257093_at | 263 | P | 131 | P | 0.50 | **-1.01** | 253 | P | 116 | P | 0.46 | **-1.13** | -1.0706 | 0.002 | At3g20570: plastocyanin-like domain-containing protein |
| 249283_at | 2521 | P | 1259 | P | 0.50 | **-1.00** | 1839 | P | 846 | P | 0.46 | **-1.12** | -1.0610 | 0.028 | At5g41800: amino acid transporter family protein |
| 260551_at | 744 | P | 341 | P | 0.46 | **-1.13** | 694 | P | 357 | P | 0.51 | **-0.96** | -1.0439 | 0.001 | At2g43510: trypsin inhibitor, putative |

| ATH1 code | replica 1 | | | | | | replica 2 | | | | | | average | | annotation Tigre5 |
| | control | call | DTT | call | ratio | log2[ratio] | control | call | DTT | call | ratio | log2[ratio] | log2[ratio] | p-value | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 253228_at | 216 | P | 2242 | P | 10.39 | **3.38** | 261 | P | 1739 | P | 6.67 | **2.74** | 3.0580 | 0.000 | At4g34630: expressed protein |
| 247293_at | 71 | P | 746 | P | 10.54 | **3.40** | 64 | P | 258 | P | 4.06 | **2.02** | 2.7102 | 0.013 | At5g64510: expressed protein |
| 253687_at | 212 | P | 1969 | P | 9.27 | **3.21** | 210 | P | 803 | P | 3.82 | **1.93** | 2.5729 | 0.009 | At4g29520: expressed protein |
| 261485_at | 352 | P | 2427 | P | 6.89 | **2.78** | 261 | P | 1370 | P | 5.25 | **2.39** | 2.5889 | 0.003 | At1g14360: UDP-galactose/UDP-glucose transporter, putative |
| 247494_at | 950 | P | 6367 | P | 6.71 | **2.75** | 614 | P | 2236 | P | 3.64 | **1.86** | 2.3046 | 0.026 | At5g61790: calnexin 1 (CNX1) |
| 245956_s_at | 2004 | P | 12563 | P | 6.27 | **2.65** | 1457 | P | 4689 | P | 3.22 | **1.69** | 2.1676 | 0.024 | At5g42020: luminal binding protein 2 (BiP-2) (BP2); At5g28540: luminal binding protein 1 (BiP-1) (BP1) |
| 256911_at | 61 | A | 424 | P | 6.97 | **2.80** | 64 | P | 127 | P | 1.99 | **0.99** | 1.8973 | 0.053 | At3g24090: glucosamine--fructose-6-phosphate aminotransferase (isomerizing), putative / |
| 267483_at | 271 | P | 1451 | P | 5.35 | **2.42** | 167 | P | 585 | P | 3.50 | **1.81** | 2.1118 | 0.025 | At2g02810: UDP-galactose/UDP-glucose transporter |
| 250930_at | 136 | P | 779 | P | 5.71 | **2.51** | 141 | P | 374 | P | 2.66 | **1.41** | 1.9640 | 0.012 | At5g03160: DNAJ heat shock N-terminal domain-containing protein |
| 259757_at | 287 | P | 1374 | P | 4.79 | **2.26** | 136 | P | 287 | P | 2.11 | **1.08** | 1.6687 | 0.161 | At1g77510: protein disulfide isomerase, putative |
| 249944_at | 101 | P | 464 | P | 4.60 | **2.20** | 99 | P | 201 | P | 2.04 | **1.03** | 1.6147 | 0.031 | At5g22290: no apical meristem (NAM) family protein |
| 250625_at | 73 | P | 293 | P | 4.03 | **2.01** | 64 | P | 126 | P | 1.96 | **0.97** | 1.4929 | 0.041 | At5g07340: calnexin, putative |
| 251182_at | 1865 | P | 6013 | P | 3.22 | **1.69** | 819 | P | 2262 | P | 2.76 | **1.46** | 1.5767 | 0.096 | At3g62600: DNAJ heat shock family protein |
| 266869_at | 131 | P | 396 | P | 3.02 | **1.59** | 157 | P | 329 | P | 2.09 | **1.06** | 1.3286 | 0.003 | At2g44660: ALG6, ALG8 glycosyltransferase family protein |
| 248327_at | 401 | P | 860 | P | 2.14 | **1.10** | 553 | P | 1189 | P | 2.15 | **1.11** | 1.1030 | 0.019 | At5g52750: heavy-metal-associated domain-containing protein |