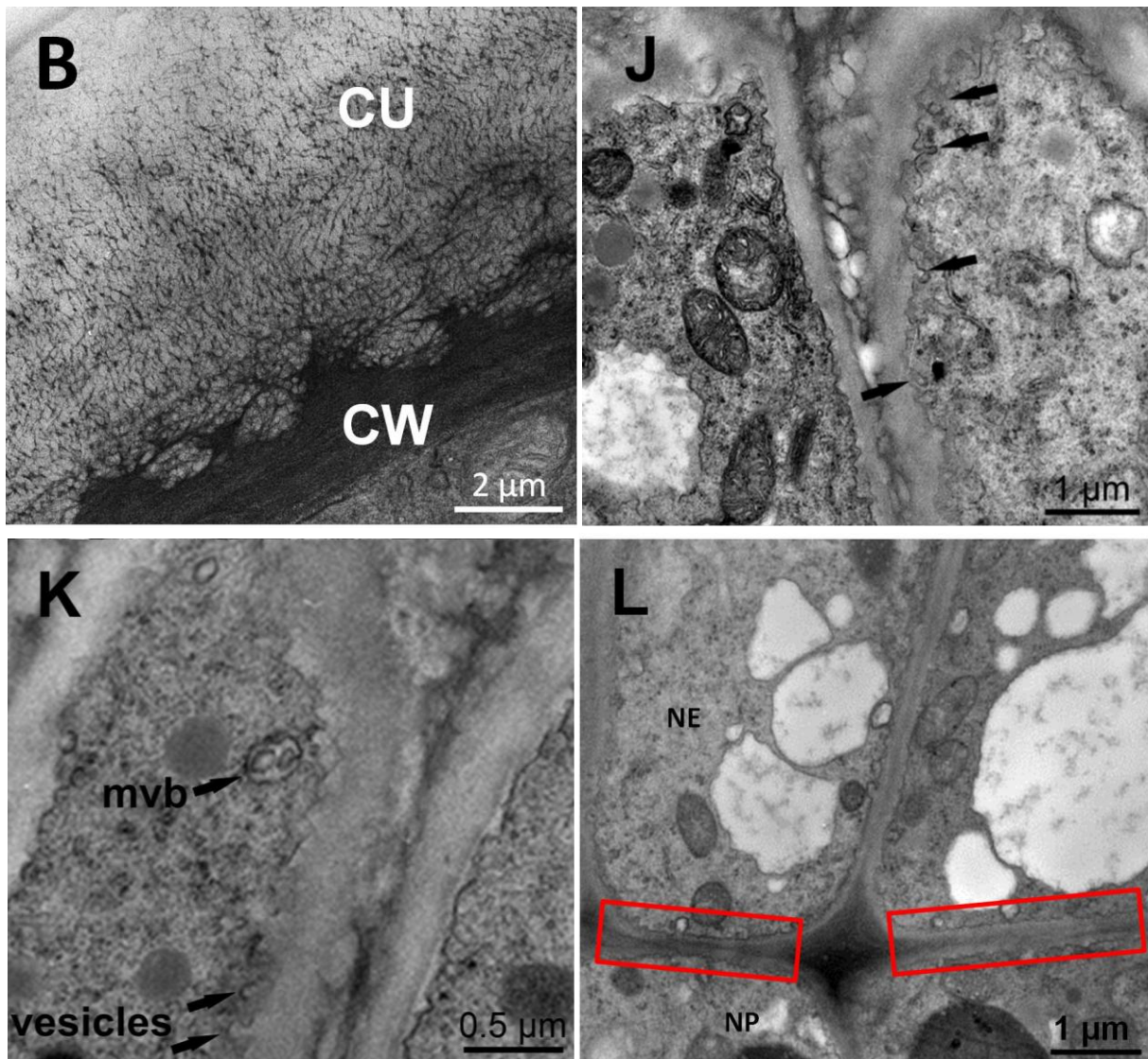


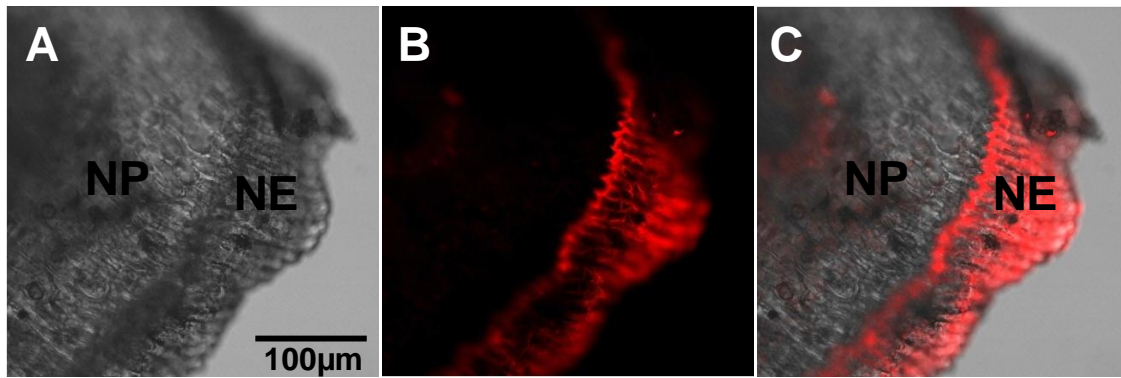
Supplemental Figures



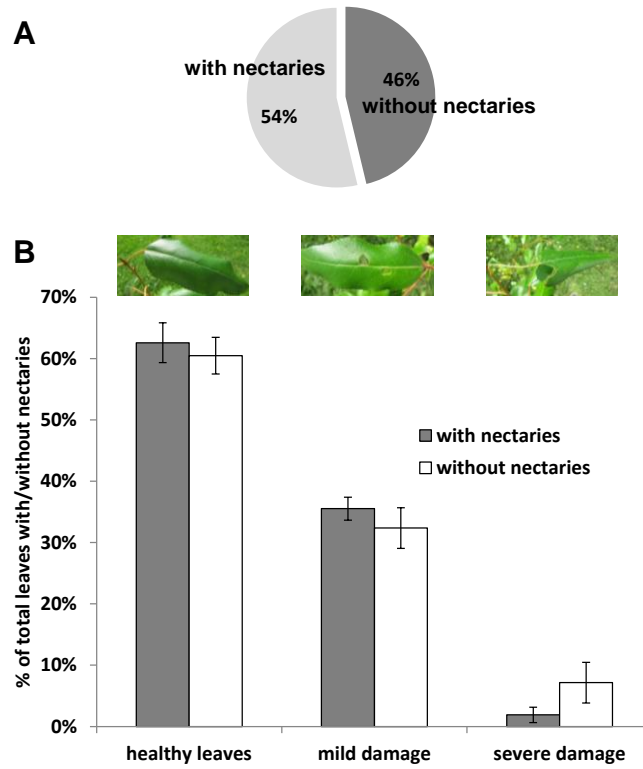
Supplemental Figure S1. Enlarged TEM images of *Ptt* and *Ptr* nectaries. Selected enlargements of Figure 2. **(B)**, numerous micro-channels in *Ptr* nectary cuticula. **(J)**, secretory cells in *Ptt* nectary. Black arrows denote vesicles connected to the plasma membrane. In the apoplastic space between the cells, numerous secreted vesicles are visible. **(K)**, vesicles and a multivesicular body in *Ptt* secretory cells. **(L)**, lack of symplastic connections between *Ptt* secretory cell (NE) and adjacent parenchymatic cells (NP).



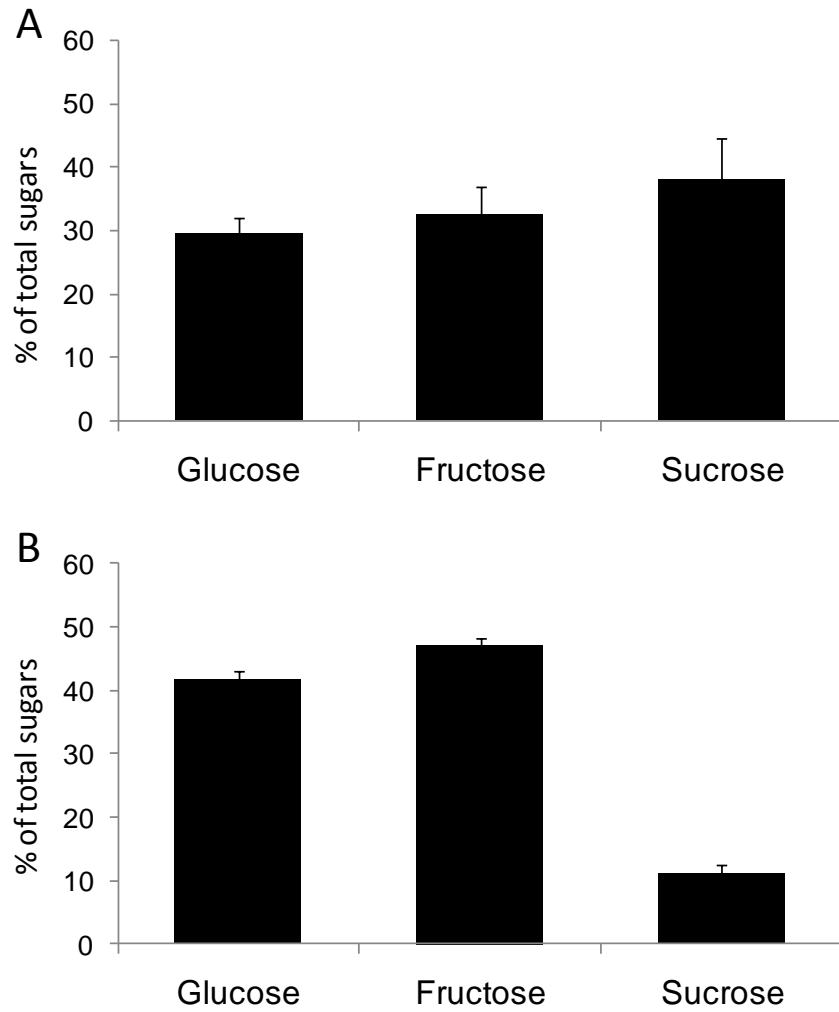
Supplemental Figure S2. *Ptt* nectaries stained with Sudan III. Secretory cells are not covered by a cuticle. Note: A lid of parenchyma cells covers the secretory cells and protects them from the environment.



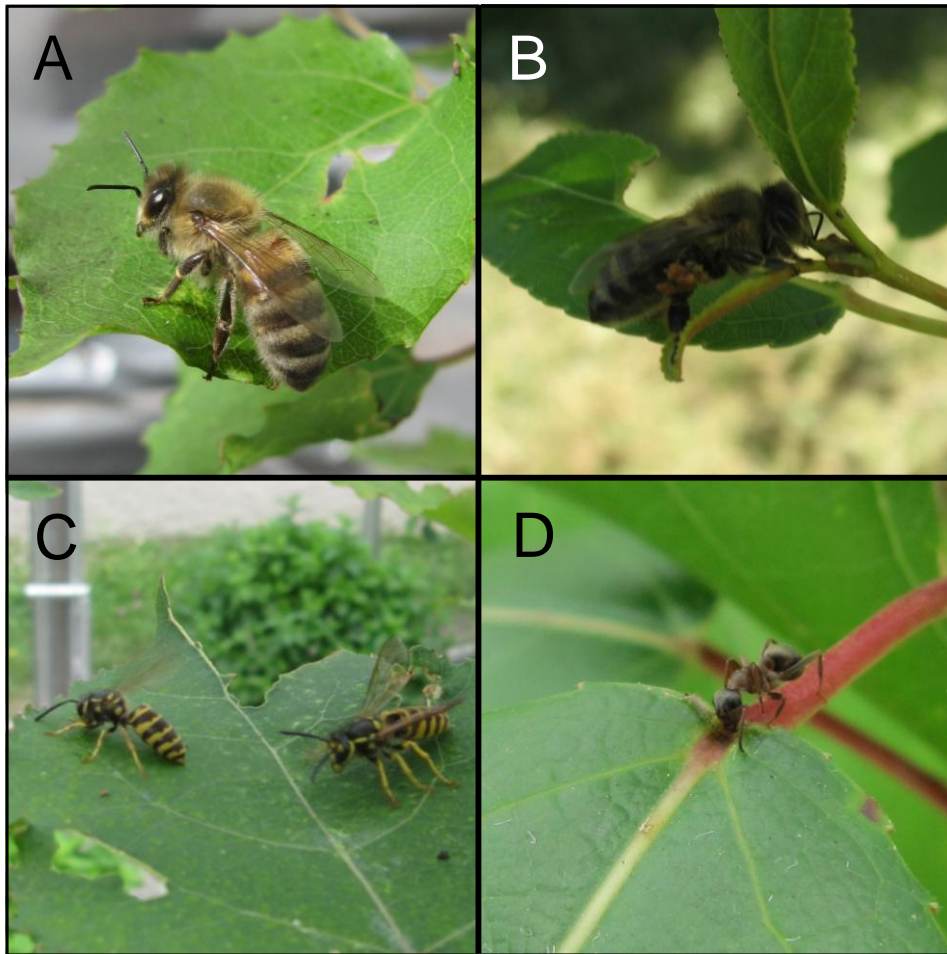
Supplemental Figure S3. Fluorescence microscopy of *Ptt* nectary longitudinal-sections stained with FM 4-64. **(A)**, bright field microscopy. **(B)**, nectaries labeled with FM 4-64. **(C)**, merge of both images. The dye is internalized in the secretory cells only and is unable to cross the apoplastic space to the neighboring cells. NE= nectary epidermis; NP= nectary parenchyma.



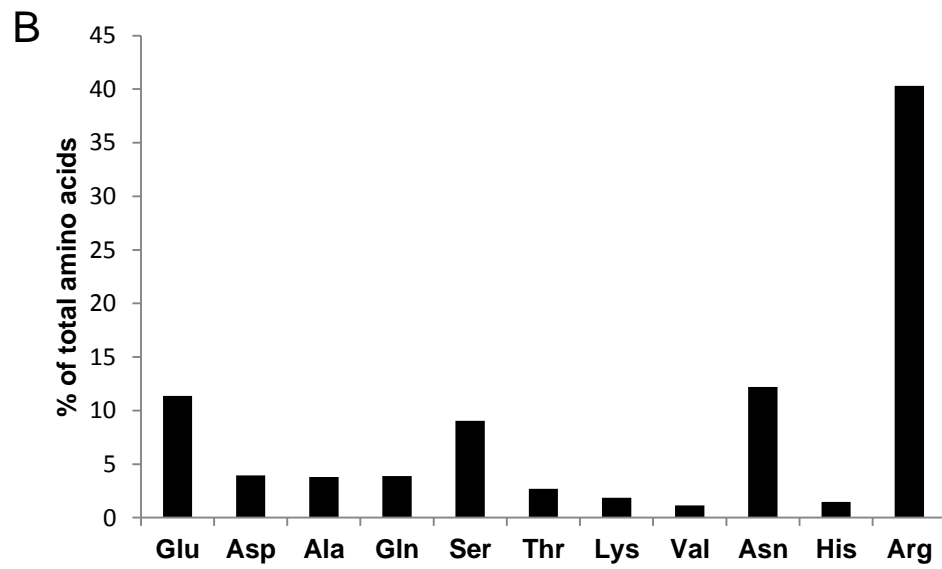
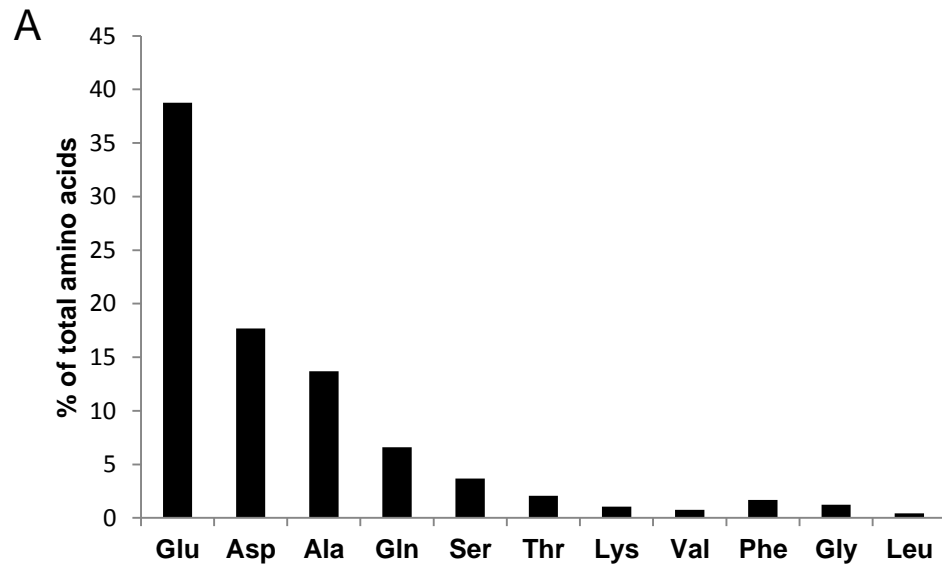
Supplemental Figure S4. *Ptr* nectaries density and effectiveness against herbivore attack. **(A)**, conserved percentage of *Ptr* leaves with and without nectaries. **(B)**, Severe damage by herbivores was reduced when leaves were equipped with nectaries. Mean \pm SE, n=6 branches (380 leaves).



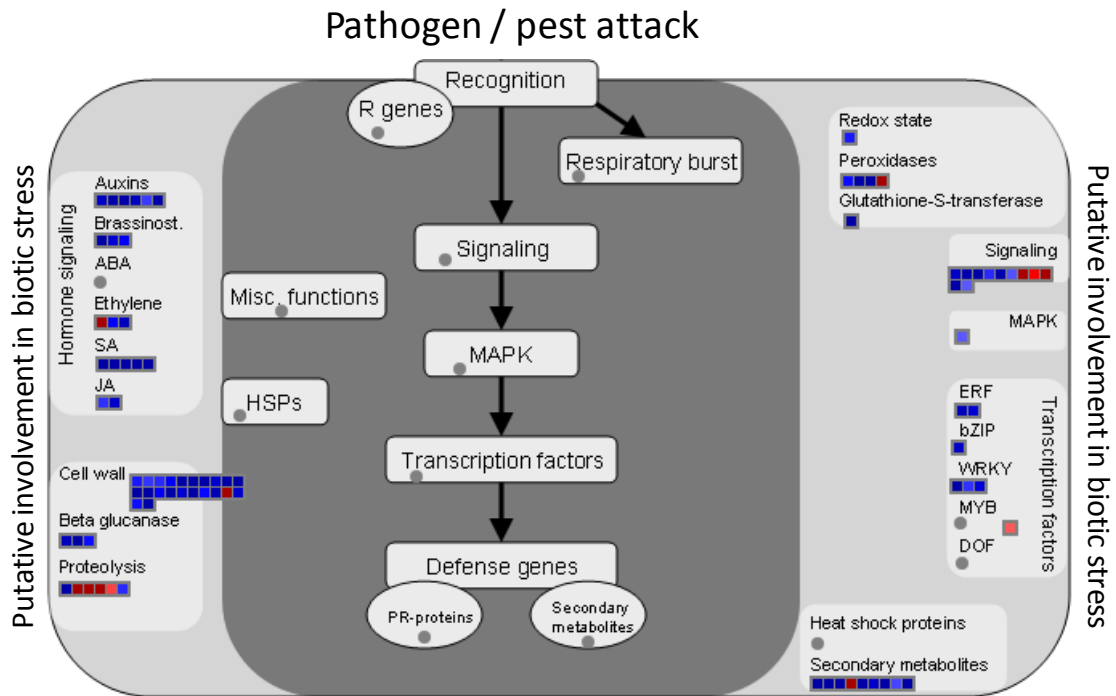
Supplemental Figure S5. Sugar content in nectars of *Populus tremula* x *P. tremuloides* (A) and *Populus trichocarpa* (B). Ratios were constant within the single species but differed between both poplar ecotypes. (Mean \pm SD, n=5).



Supplemental Figure S6. Visitors attracted by extrafloral *Ptt* and *Ptr* nectaries. **(A)**, honey bee at *Ptt*. **(B)**, honey bee at *Ptr*. **(C)**, wasps at *Ptt*. **(D)**, ant at *Ptr*.



Supplemental Figure S7. The most abundant amino acids in leaves of *Ptt* (**A**) and *Ptr* (**B**). Proline was not detectable in leaf extracts.



Supplemental Figure S8. MapMan gene-clusters involved in biotic stress responses. According to MapMan analyses of the 500 most differentially expressed genes. Genes of both, cell wall and hormone related classes, are possibly involved in biotic stress mechanisms. Further candidates belong to transcription factors of the ERF and WRKY group, and to proteins related to signaling, secondary metabolites and redox-state. Blue clusters represent up-regulated, red clusters down-regulated genes.

Supplemental Tables

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.6940.1.S1_at | XP_002306379 | BU829342 | --- | --- | 7,9 | 1,05E-05 |
| PtpAffx.48329.2.S1_at | XP_002327914 | BU872043 | AT1G19715.2 | Symbols: jacalin lectin family protein chr1:6816934-6819244 REVERSE | 7,3 | 2,58E-05 |
| PtpAffx.24159.1.A1_at | XP_002322164 | CA923426 | AT5G14740.2 | Symbols: CA2, CA18, BETA CA2 CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding chr5:4760536-4762382 FORWARD | 7,0 | 2,73E-05 |
| Ptp.1362.1.S1_at | XP_002315497 | CK089988 | --- | --- | 6,7 | 1,30E-05 |
| PtpAffx.212900.1.S1_at | XP_002321730 | pmrna25246 | AT5G50790.1 | Symbols: nodulin MtN3 family protein chr5:20656461-20657827 REVERSE | 6,7 | 2,04E-05 |
| Ptp.6948.1.S1_at | XP_002336545 | CV243899 | --- | --- | 6,5 | 1,30E-05 |
| PtpAffx.24159.1.A1_x_at | XP_002322164 | CA923426 | AT5G14740.2 | Symbols: CA2, CA18, BETA CA2 CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding chr5:4760536-4762382 FORWARD | 6,4 | 2,50E-05 |
| PtpAffx.162311.1.S1_at | XP_002330499 | BP933945 | AT2G19800.1 | Symbols: MIOX2 MIOX2 (MYO-INOSITOL OXYGENASE 2); inositol oxygenase chr2:8531106-8533354 REVERSE | 6,2 | 2,81E-05 |
| PtpAffx.7903.2.A1_s_at | XP_002303728 | DN486357 | AT4G20320.2 | Symbols: CTP synthase/ catalytic chr4:10974980-10978998 FORWARD | 6,1 | 6,56E-05 |
| PtpAffx.32362.1.S1_at | XP_002301652 | CV242633 | AT1G65890.1 | Symbols: AAE12 AAE12 (ACYL ACTIVATING ENZYME 12); catalytic chr1:24512598-24514611 REVERSE | 6,0 | 1,05E-05 |
| Ptp.6610.1.S1_at | XP_002306379 | CK115218 | --- | --- | 5,8 | 1,98E-05 |
| Ptp.6649.1.S1_at | XP_002331012 | DN500314 | --- | --- | 5,5 | 3,59E-05 |
| Ptp.6792.1.S1_at | XP_002327894 | CA928793 | --- | --- | 5,5 | 2,81E-05 |
| Ptp.6649.1.S1_s_at | XP_002331012 | DN500314 | --- | --- | 5,4 | 2,50E-05 |
| PtpAffx.34213.1.S1_at | XP_002328991 | CV269008 | AT5G05340.1 | Symbols: peroxidase, putative chr5:1579142-1580819 REVERSE | 5,3 | 1,59E-05 |
| PtpAffx.5103.1.S1_s_at | XP_002328980 | CN520258 | AT4G24340.1 | Symbols: phosphorylase family protein chr4:12607475-12609148 FORWARD | 5,3 | 2,82E-05 |
| Ptp.2750.1.S1_s_at | XP_002310820 | BU825949 | AT4G36470.1 | Symbols: S-adenosyl-L-methionine:carboxyl methyltransferase family protein chr4:17215128-17216475 REVERSE | 5,3 | 2,27E-05 |
| PtpAffx.249.50.S1_x_at | --- | CV269222 | --- | --- | 5,1 | 1,94E-05 |
| Ptp.4045.1.S1_at | XP_002325384 | CV276911 | AT4G24340.1 | Symbols: phosphorylase family protein chr4:12607475-12609148 FORWARD | 5,0 | 3,50E-05 |
| PtpAffx.20875.1.A1_at | XP_002302055 | BP935619 | AT1G04380.1 | Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:1177142-1178384 REVERSE | 4,9 | 1,05E-05 |
| Ptp.1111.1.A1_s_at | XP_002310820 | CV263317 | AT1G19640.1 | Symbols: JMT JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase chr1:6789166-6791708 REVERSE | 4,9 | 3,44E-05 |
| PtpAffx.161412.1.S1_at | XP_002305084 | CN192923 | AT4G18550.1 | Symbols: lipase class 3 family protein chr4:10225006-10226862 REVERSE | 4,9 | 3,85E-05 |
| Ptp.5901.1.S1_at | XP_002323069 | BU826487 | AT5G59310.1 | Symbols: LTP4 LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding chr5:23925296-23925772 REVERSE | 4,8 | 2,52E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.3217.1.S1_at | --- | BU835684 | --- | --- | 4,7 | 1,30E-05 |
| PtpAffx.215154.1.S1_at | XP_002334262 | pmrna29192 | AT5G04370.2 | Symbols: NAMT1 NAMT1; S-adenosylmethionine-dependent methyltransferase chr5:1231856-1233888 FORWARD | 4,7 | 6,94E-05 |
| Ptp.7607.1.S1_s_at | XP_002297866 | BU813493 | AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) chr5:4219001-4220502 FORWARD | 4,6 | 3,85E-05 |
| Ptp.7607.1.S1_at | XP_002297866 | BU813493 | AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) chr5:4219001-4220502 FORWARD | 4,6 | 4,16E-05 |
| Ptp.6592.1.A1_s_at | XP_002333986 | CK319937 | AT1G04220.1 | Symbols: KCS2 KCS2 (3-KETOACYL-COA SYNTHASE 2); fatty acid elongase chr1:1119853-1122483 REVERSE | 4,6 | 2,58E-05 |
| PtpAffx.207743.1.S1_at | XP_002311205 | pmrna15396 | AT2G39980.1 | Symbols: transferase family protein chr2:16688437-16689885 REVERSE | 4,6 | 1,05E-05 |
| PtpAffx.249.270.S1_s_at | XP_002325727 | BP929963 | AT5G25610.1 | Symbols: RD22 RD22; nutrient reservoir chr5:8914498-8916684 REVERSE | 4,5 | 5,36E-05 |
| PtpAffx.221813.1.S1_at | XP_002335942 | pmrna38875 | AT5G38020.1 | Symbols: S-adenosyl-L-methionine:carboxyl methyltransferase family protein chr5:15165953-15167612 REVERSE | 4,5 | 4,31E-05 |
| PtpAffx.43288.1.A1_at | XP_002305084 | CV278131 | AT2G31100.1 | Symbols: triacylglycerol lipase chr2:13256738-13258174 REVERSE | 4,5 | 3,26E-05 |
| PtpAffx.2893.1.S1_at | XP_002313827 | BU811220 | --- | --- | 4,5 | 2,58E-05 |
| PtpAffx.216301.1.S1_s_at | XP_002330589 | pmrna30987 | AT1G55740.1 | Symbols: AtSIP1 AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds chr1:20835507-20838707 REVERSE | 4,4 | 4,08E-05 |
| Ptp.4116.1.S1_at | XP_002328109 | CV283544 | AT1G52340.1 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase chr1:19489997-19491527 REVERSE | 4,3 | 3,26E-05 |
| Ptp.370.1.S1_at | XP_002318864 | CK088667 | AT5G62200.1 | Symbols: embryo-specific protein-related chr5:24984463-24985674 REVERSE | 4,3 | 1,30E-05 |
| PtpAffx.216301.1.S1_at | XP_002330589 | pmrna30987 | AT1G55740.1 | Symbols: AtSIP1 AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds chr1:20835507-20838707 REVERSE | 4,3 | 5,66E-05 |
| PtpAffx.202177.1.S1_at | XP_002301307 | pmrna4350 | AT2G45580.1 | Symbols: CYP76C3 CYP76C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr2:18782388-18784286 REVERSE | 4,2 | 2,52E-05 |
| PtpAffx.13272.2.S1_a_at | XP_002319968 | CV282462 | AT5G58390.1 | Symbols: peroxidase, putative chr5:23599755-23601244 REVERSE | 4,2 | 1,30E-05 |
| Ptp.4116.1.S1_s_at | XP_002328109 | CV283544 | AT1G52340.1 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase chr1:19489997-19491527 REVERSE | 4,2 | 3,35E-05 |
| PtpAffx.99518.1.S1_at | XP_002320578 | CV243431 | AT4G21680.1 | Symbols: proton-dependent oligopeptide transport (POT) family protein chr4:11517540-11519576 REVERSE | 4,2 | 3,92E-05 |
| PtpAffx.212292.1.S1_at | XP_002325480 | pmrna24100 | AT3G05550.1 | Symbols: hypoxia-responsive family protein chr3:1612860-1613748 FORWARD | 4,2 | 1,98E-05 |
| PtpAffx.1030.1.S1_s_at | XP_002319588 | CV270748 | AT3G05000.1 | Symbols: transport protein particle (TRAPP) component Bet3 family protein chr3:1387444-1388697 REVERSE | 4,1 | 2,50E-05 |
| PtpAffx.153093.1.A1_at | XP_002299025 | CV270507 | AT5G44440.1 | Symbols: FAD-binding domain-containing protein chr5:17910694-17912295 REVERSE | 4,1 | 3,26E-05 |
| Ptp.7364.1.S1_a_at | XP_002322082 | CA929119 | AT1G15125.1 | Symbols: S-adenosylmethionine-dependent methyltransferase/ methyltransferase chr1:5204625-5205912 FORWARD | 4,0 | 2,58E-05 |
| PtpAffx.210014.1.S1_at | XP_002316954 | pmrna19744 | AT5G54510.1 | Symbols: GH3.6, DFL1 DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase chr5:22131321-22133564 REVERSE | 4,0 | 3,26E-05 |
| PtpAffx.212905.1.S1_s_at | XP_002321734 | pmrna25253 | AT5G13180.1 | Symbols: ANAC083 ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor chr5:4196643-4197577 FORWARD | 4,0 | 3,81E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.118874.1.A1_at | XP_002274332 | DN486553 | AT1G12740.1 | Symbols: CYP87A2 CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:4342462-4344569 FORWARD | 3,9 | 8,16E-05 |
| PtpAffx.132383.1.A1_s_at | XP_002326321 | CV268088 | AT4G33220.1 | Symbols: PME44, ATPME44 enzyme inhibitor/ pectinesterase chr4:16022506-16026130 FORWARD | 3,9 | 2,58E-05 |
| Ptp.6749.1.S1_at | XP_002306793 | BU834129 | AT1G19670.1 | Symbols: ATCLH1, COR11, ATHCOR1 ATCLH1 (ARABIDOPSIS THALIANA CORONATINE-INDUCED PROTEIN 1); chlorophyllase chr1:6803796-6804923 REVERSE | 3,9 | 3,26E-05 |
| PtpAffx.107876.1.A1_at | XP_002306073 | CV262541 | AT5G39220.1 | Symbols: hydrolase, alpha/beta fold family protein chr5:15705913-15708039 FORWARD | 3,9 | 1,74E-05 |
| PtpAffx.2120.3.S1_at | XP_002325686 | CF232315 | AT4G10270.1 | Symbols: wound-responsive family protein chr4:6374805-6375077 FORWARD | 3,9 | 5,83E-05 |
| Ptp.110.1.S1_at | XP_002319409 | AY435100.1 | AT2G40610.1 | Symbols: ATEXPA8, EXP8, ATEXP8, ATHEXP ALPHA 1.11 ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8) chr2:16949121-16950472 REVERSE | 3,9 | 3,26E-05 |
| PtpAffx.26968.3.S1_a_at | XP_002300055 | CV275318 | --- | --- | 3,9 | 7,38E-05 |
| PtpAffx.140294.1.A1_at | XP_002327628 | CV266675 | AT1G52340.1 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase chr1:19489997-19491527 REVERSE | 3,8 | 5,69E-05 |
| Ptp.6863.1.S1_at | XP_002299588 | CV276110 | --- | --- | 3,8 | 3,89E-05 |
| Ptp.1552.1.S1_s_at | XP_002302727 | DN487944 | AT4G02280.1 | Symbols: SUS3, ATSUS3 SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups chr4:995166-998719 FORWARD | 3,7 | 2,82E-05 |
| Ptp.6836.1.S1_at | XP_002322274 | CK094329 | AT5G13080.1 | Symbols: WRKY75, ATWRKY75 WRKY75; transcription factor chr5:4149928-4151019 REVERSE | 3,7 | 3,89E-05 |
| PtpAffx.1169.1.A1_a_at | --- | CV245093 | --- | --- | 3,7 | 3,72E-05 |
| PtpAffx.18783.1.A1_at | XP_002307053 | CV233908 | AT1G77380.1 | Symbols: AAP3, ATAAP3 AAP3; amino acid transmembrane transporter chr1:29075201-29077252 REVERSE | 3,7 | 2,58E-05 |
| Ptp.5757.1.S1_x_at | XP_002321858 | CV282029 | AT5G62200.1 | Symbols: embryo-specific protein-related chr5:24984463-24985674 REVERSE | 3,7 | 5,66E-05 |
| PtpAffx.2271.1.S1_s_at | XP_002325077 | CA933996 | AT4G11650.1 | Symbols: ATOSM34 ATOSM34 (osmotin 34) chr4:7025127-7026113 REVERSE | 3,6 | 3,26E-05 |
| PtpAffx.133632.2.A1_s_at | XP_002301305 | CV268745 | AT2G45560.1 | Symbols: CYP76C1 CYP76C1; electron carrier/ heme binding / iron ion binding / monooxygenase chr2:18776391-18778354 REVERSE | 3,6 | 2,58E-05 |
| PtpAffx.1501.2.S1_at | XP_002327186 | CX178645 | AT5G10600.1 | Symbols: CYP81K2 CYP81K2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr5:3351227-3352777 FORWARD | 3,6 | 2,66E-05 |
| Ptp.3503.1.A1_at | XP_002320154 | CV261037 | AT1G01490.2 | Symbols: heavy-metal-associated domain-containing protein chr1:180401-182066 REVERSE | 3,6 | 8,25E-05 |
| PtpAffx.35610.1.A1_at | XP_002306849 | CV257792 | AT1G06180.1 | Symbols: ATMYB13, ATMYBLFGN ATMYB13 (MYB DOMAIN PROTEIN 13); DNA binding / transcription factor chr1:1889510-1891089 FORWARD | 3,6 | 3,55E-05 |
| PtpAffx.143356.1.S1_s_at | XP_002324280 | CN522188 | AT5G11420.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unkn | 3,6 | 2,58E-05 |
| PtpAffx.210585.1.S1_at | XP_002318660 | pmrna20757 | AT5G63090.4 | Symbols: LOB LOB (LATERAL ORGAN BOUNDARIES) chr5:25308723-25309283 REVERSE | 3,6 | 2,04E-05 |
| PtpAffx.5304.1.A1_at | XP_002302924 | CV268322 | --- | --- | 3,6 | 3,44E-05 |
| Ptp.3871.1.S1_at | XP_002303256 | CA926586 | AT1G80160.1 | Symbols: lactoylglutathione lyase family protein / glyoxalase I family protein chr1:30151101-30151930 FORWARD | 3,6 | 3,26E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.4350.1.S1_at | XP_002311914 | CV266975 | AT1G17745.1 | Symbols: PGDH PGDH (3-PHOSPHOGLYCERATE DEHYDROGENASE); phosphoglycerate dehydrogenase chr1:6101157-6104979 FORWARD | 3,5 | 2,82E-05 |
| PtpAffx.47790.1.S1_at | XP_002311426 | CV283685 | AT1G68760.1 | Symbols: ATNUDT1, ATNUDX1 ATNUDX1 (ARABIDOPSIS THALIANA NUDIX HYDROLASE 1); dihydroneopterin triphosphate pyrophosphohydrolase/ hydrolase chr1:25829090-25829607 FORWARD | 3,5 | 1,98E-05 |
| Ptp.6223.1.S1_s_at | XP_002306765 | BU809597 | AT2G43020.1 | Symbols: ATPAO2 ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase chr2:17891945-17894440 FORWARD | 3,5 | 5,55E-05 |
| PtpAffx.48080.1.A1_at | XP_002319186 | CV272435 | AT5G15120.1 | Symbols: unknown protein chr5:4898814-4900351 FORWARD | 3,5 | 2,58E-05 |
| Ptp.5192.1.S1_at | XP_002315717 | CV231953 | AT3G04580.2 | Symbols: EIN4 EIN4 (ETHYLENE INSENSITIVE 4); ethylene binding / glycogen synthase kinase 3/ protein histidine kinase/ receptor chr3:1235576-1237965 REVERSE | 3,5 | 2,58E-05 |
| PtpAffx.24142.1.A1_at | XP_002306765 | CV262024 | AT3G59050.1 | Symbols: ATPAO3 ATPAO3 (Polyamine oxidase 3); polyamine oxidase chr3:21824932-21827173 REVERSE | 3,5 | 4,32E-05 |
| Ptp.2700.1.S1_at | XP_002325925 | BP934428 | AT1G26770.2 | Symbols: ATEXPA10, AT-EXP10, ATEXP10, ATHEXP ALPHA 1.1, EXP10 ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall chr1:9259775-9260792 FORWARD | 3,5 | 2,82E-05 |
| PtpAffx.2120.2.S1_a_at | XP_002325686 | CK097107 | AT4G10270.1 | Symbols: wound-responsive family protein chr4:6374805-6375077 FORWARD | 3,5 | 2,58E-05 |
| PtpAffx.201938.1.S1_at | XP_002302312 | pmrna3865 | AT1G22460.1 | Symbols: unknown protein chr1:7927530-7930351 REVERSE | 3,5 | 2,58E-05 |
| Ptp.7691.1.A1_s_at | XP_002318815 | DN488518 | AT5G52300.2 | Symbols: RD29B, LTI65 LTI65 (LOW-TEMPERATURE-INDUCED 65) chr5:21237205-21239404 FORWARD | 3,4 | 3,85E-05 |
| Ptp.3810.1.S1_at | XP_002331808 | CV253278 | AT1G78780.2 | Symbols: pathogenesis-related family protein chr1:29621447-29622431 REVERSE | 3,4 | 2,57E-05 |
| PtpAffx.211340.1.S1_at | XP_002319398 | pmrna22231 | AT5G54510.1 | Symbols: GH3.6, DFL1 DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase chr5:22131321-22133564 REVERSE | 3,4 | 4,94E-05 |
| PtpAffx.101017.1.A1_s_at | XP_002263759 | CV283101 | AT1G61680.1 | Symbols: TPS14, ATTPS14 TPS14 (TERPENE SYNTHASE 14); S-linalool synthase chr1:22772455-22774687 REVERSE | 3,4 | 5,78E-05 |
| PtpAffx.27712.1.S1_at | XP_002281225 | CK096276 | AT1G19250.1 | Symbols: FMO1 FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase chr1:6650656-6653053 REVERSE | 3,4 | 3,68E-05 |
| Ptp.5205.1.S1_at | XP_002324280 | BU888886 | AT5G11420.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unkn | 3,4 | 2,58E-05 |
| PtpAffx.209745.1.S1_at | XP_002270176 | pmrna19233 | AT1G61680.1 | Symbols: TPS14, ATTPS14 TPS14 (TERPENE SYNTHASE 14); S-linalool synthase chr1:22772455-22774687 REVERSE | 3,4 | 3,85E-05 |
| PtpAffx.205584.1.S1_at | XP_002307478 | pmrna11033 | AT1G43800.1 | Symbols: acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative chr1:16577662-16579549 FORWARD | 3,4 | 3,72E-05 |
| PtpAffx.26590.3.A1_a_at | XP_002304653 | CV264615 | AT5G13220.1 | Symbols: JAZ10, TIFY9, JAS1 JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) chr5:4219001-4220502 FORWARD | 3,4 | 2,92E-05 |
| PtpAffx.80486.1.A1_at | XP_002299662 | DN484699 | AT5G22860.1 | Symbols: serine carboxypeptidase S28 family protein chr5:7639511-7642945 REVERSE | 3,3 | 5,36E-05 |
| Ptp.1084.1.A1_at | XP_002313864 | CV281908 | AT3G19320.1 | Symbols: leucine-rich repeat family protein chr3:6696395-6698073 REVERSE | 3,3 | 6,56E-05 |
| PtpAffx.119413.1.A1_at | XP_002331196 | CV255249 | AT1G72520.1 | Symbols: lipoxigenase, putative chr1:27308611-27312589 FORWARD | 3,3 | 3,85E-05 |
| Ptp.1970.1.S1_s_at | XP_002301370 | CV230945 | AT3G61490.2 | Symbols: glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein chr3:22758439-22760137 FORWARD | 3,3 | 4,41E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.2848.2.A1_at | XP_002323565 | CV265624 | AT4G00430.1 | Symbols: TMP-C, PIP1;4, PIP1E PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel chr4:186143-187531 REVERSE | 3,3 | 7,14E-05 |
| Ptp.2607.1.S1_x_at | XP_002325043 | CV245762 | AT5G38410.1 | Symbols: ribulose biphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B) chr5:15377501-15378306 REVERSE | 3,3 | 4,31E-05 |
| PtpAffx.26968.1.S1_at | --- | DN502877 | --- | --- | 3,3 | 3,72E-05 |
| Ptp.6129.1.S1_at | XP_002315949 | BU885829 | AT1G68620.1 | Symbols: hydrolase chr1:25766018-25767028 FORWARD | 3,3 | 2,58E-05 |
| PtpAffx.28667.1.S1_at | XP_002332223 | BU824663 | AT4G37300.1 | Symbols: MEE59 MEE59 (maternal effect embryo arrest 59) chr4:17554805-17555498 FORWARD | 3,3 | 2,82E-05 |
| PtpAffx.2562.2.S1_s_at | XP_002320584 | DN492157 | AT1G02190.1 | Symbols: CER1 protein, putative chr1:415154-417796 FORWARD | 3,2 | 7,14E-05 |
| Ptp.559.1.S1_s_at | XP_002311499 | CV227910 | --- | --- | 3,2 | 3,89E-05 |
| PtpAffx.10196.3.A1_a_at | XP_002309049 | DN484733 | AT5G02540.1 | Symbols: short-chain dehydrogenase/reductase (SDR) family protein chr5:568609-570720 FORWARD | 3,2 | 4,28E-05 |
| Ptp.476.1.S1_s_at | XP_002299934 | CK087241 | AT3G08030.2 | Symbols: unknown protein chr3:2564517-2565819 FORWARD | 3,2 | 5,78E-05 |
| PtpAffx.217339.1.S1_s_at | XP_002310763 | pmrna32557 | AT2G23540.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr2:10024366-10026058 FORWARD | 3,2 | 3,52E-05 |
| PtpAffx.9887.2.S1_at | XP_002334409 | CV244429 | AT5G36160.1 | Symbols: aminotransferase-related chr5:14233261-14235129 REVERSE | 3,2 | 2,81E-05 |
| PtpAffx.10261.1.S1_a_at | XP_002323172 | CV258795 | --- | --- | 3,2 | 2,58E-05 |
| Ptp.7580.1.S1_at | XP_002328113 | DN484736 | AT5G06270.1 | Symbols: unknown protein chr5:1912895-1913263 FORWARD | 3,2 | 4,31E-05 |
| PtpAffx.118982.1.S1_at | XP_002331196 | CA930199 | AT1G72520.1 | Symbols: lipoxygenase, putative chr1:27308611-27312589 FORWARD | 3,2 | 8,44E-05 |
| PtpAffx.11536.1.A1_at | XP_002329630 | CV262158 | AT5G57480.1 | Symbols: AAA-type ATPase family protein chr5:23279406-23280968 REVERSE | 3,2 | 2,04E-05 |
| PtpAffx.123412.1.S1_s_at | NP_197138 | CN517487 | AT5G16340.1 | Symbols: AMP-binding protein, putative chr5:5349255-5350907 REVERSE | 3,2 | 3,72E-05 |
| PtpAffx.2848.1.S1_a_at | XP_002309126 | CV243610 | AT4G00430.1 | Symbols: TMP-C, PIP1;4, PIP1E PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel chr4:186143-187531 REVERSE | 3,2 | 7,96E-05 |
| PtpAffx.59348.1.S1_at | XP_002304118 | CA928346 | AT1G19180.1 | Symbols: JAZ1, TIFY10A JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding chr1:6622312-6623271 FORWARD | 3,2 | 2,04E-05 |
| Ptp.2084.1.S1_s_at | XP_002307094 | CV239353 | AT2G22170.1 | Symbols: lipid-associated family protein chr2:9427010-9427742 REVERSE | 3,1 | 2,82E-05 |
| PtpAffx.3541.1.S1_at | XP_002327150 | CN550182 | AT5G42930.1 | Symbols: triacylglycerol lipase chr5:17210738-17214152 REVERSE | 3,1 | 6,21E-05 |
| PtpAffx.154444.1.S1_s_at | XP_002299934 | CN520792 | AT3G08030.1 | Symbols: unknown protein chr3:2564191-2565819 FORWARD | 3,1 | 4,23E-05 |
| PtpAffx.86439.1.S1_s_at | XP_002301370 | CX176311 | AT3G61490.2 | Symbols: glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein chr3:22758439-22760137 FORWARD | 3,1 | 5,55E-05 |
| PtpAffx.3558.1.S1_a_at | XP_002319581 | AB120627.1 | AT4G08850.1 | Symbols: kinase chr4:5636693-5640496 REVERSE | 3,1 | 2,81E-05 |
| PtpAffx.22848.1.S1_at | XP_002304925 | BU891589 | AT1G11600.1 | Symbols: CYP77B1 CYP77B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:3902090-3903622 FORWARD | 3,1 | 4,32E-05 |
| PtpAffx.5915.1.A1_at | XP_002307391 | CV239595 | AT1G78070.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat- | 3,1 | 7,24E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|--|--------------------|------------------------|
| Ptp.3600.1.S1_s_at | XP_002322822 | AF273256.1 | AT4G37970.1 | Symbols: ATCAD6, CAD6 CAD6 (CINNAMYL ALCOHOL DEHYDROGENASE 6); binding / catalytic/ oxidoreductase/ zinc ion binding chr4:17849672-17852145 FORWARD | 3,1 | 3,27E-05 |
| PtpAffx.46665.2.S1_at | XP_002300707 | DN492397 | AT1G75750.1 | Symbols: GASA1 GASA1 (GAST1 PROTEIN HOMOLOG 1) chr1:28441813-28442284 REVERSE | 3,1 | 5,55E-05 |
| Ptp.476.1.S1_at | XP_002299934 | CK087241 | AT3G08030.2 | Symbols: unknown protein chr3:2564517-2565819 FORWARD | 3,1 | 3,44E-05 |
| PtpAffx.5903.1.A1_x_at | XP_002301752 | CN519614 | AT4G14130.1 | Symbols: XTR7 XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase chr4:8137161-8138196 REVERSE | 3,1 | 2,58E-05 |
| PtpAffx.211131.1.S1_s_at | XP_002319755 | pmrna21869 | AT5G12080.3 | Symbols: MSL10 MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel chr5:3898182-3900923 REVERSE | 3,1 | 6,21E-05 |
| PtpAffx.91597.1.S1_at | XP_002320732 | DN496124 | --- | --- | 3,1 | 6,02E-05 |
| PtpAffx.126071.1.S1_s_at | XP_002317431 | CX187314 | AT4G33070.1 | Symbols: pyruvate decarboxylase, putative chr4:15952519-15954676 REVERSE | 3,1 | 2,50E-05 |
| PtpAffx.215669.1.S1_at | XP_002329915 | pmrna30006 | --- | --- | 3,1 | 6,53E-05 |
| PtpAffx.5103.1.S1_a_at | XP_002328980 | CN520258 | AT4G24340.1 | Symbols: phosphorylase family protein chr4:12607475-12609148 FORWARD | 3,1 | 2,58E-05 |
| Ptp.883.1.A1_at | XP_002321155 | CK090129 | AT2G04570.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr2:1594747-1596129 FORWARD | 3,1 | 5,13E-05 |
| Ptp.6832.1.S1_at | XP_002335751 | DN490346 | AT5G07010.1 | Symbols: ATST2A, ST2A ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase chr5:2174960-2176039 REVERSE | 3,0 | 6,08E-05 |
| PtpAffx.20066.1.S1_s_at | XP_002322154 | BP935166 | AT5G62890.3 | Symbols: permease, putative chr5:25243723-25247075 FORWARD | 3,0 | 3,35E-05 |
| PtpAffx.5036.2.A1_at | XP_002336590 | BU832900 | --- | --- | 3,0 | 2,58E-05 |
| PtpAffx.249.478.A1_s_at | XP_002329643 | CF235544 | AT5G03690.1 | Symbols: fructose-bisphosphate aldolase, putative chr5:963389-964982 REVERSE | 3,0 | 3,26E-05 |
| Ptp.1084.2.A1_a_at | XP_002313864 | DN502989 | AT1G49750.1 | Symbols: leucine-rich repeat family protein chr1:18411177-18412779 REVERSE | 3,0 | 7,14E-05 |
| PtpAffx.3558.4.S1_at | XP_002319056 | DN486119 | AT4G08850.1 | Symbols: kinase chr4:5636693-5640496 REVERSE | 3,0 | 2,58E-05 |
| Ptp.3610.1.S1_at | XP_002312542 | BU896004 | AT3G22740.1 | Symbols: HMT3 HMT3; homocysteine S-methyltransferase chr3:8033200-8035710 REVERSE | 3,0 | 2,82E-05 |
| PtpAffx.137562.1.S1_at | --- | BU824735 | --- | --- | 3,0 | 4,96E-05 |
| Ptp.1552.1.S1_x_at | XP_002302727 | DN487944 | AT4G02280.1 | Symbols: SUS3, ATSUS3 SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups chr4:995166-998719 FORWARD | 3,0 | 2,17E-05 |
| PtpAffx.10247.2.S1_at | XP_002323692 | CV261717 | AT5G44460.1 | Symbols: calcium-binding protein, putative chr5:17917286-17917831 FORWARD | 3,0 | 7,21E-05 |
| PtpAffx.53694.1.S1_at | XP_002320677 | BU887034 | --- | --- | 3,0 | 8,28E-05 |
| PtpAffx.42594.1.S1_at | XP_002325925 | CX658121 | AT2G40610.1 | Symbols: ATEXPA8, EXP8, ATEXP8, ATHEXP ALPHA 1.11 ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8) chr2:16949121-16950472 REVERSE | 3,0 | 3,26E-05 |
| PtpAffx.45922.1.A1_at | XP_002325514 | BU891817 | AT4G32480.1 | Symbols: unknown protein chr4:15676488-15677776 FORWARD | 2,9 | 2,81E-05 |
| Ptp.36.1.S1_s_at | XP_002321319 | CV252847 | AT1G02920.1 | Symbols: ATGSTF7, GST11, ATGSTF8, GSTF7 GSTF7; copper ion binding / glutathione binding / glutathione transferase chr1:658886-659705 REVERSE | 2,9 | 2,58E-05 |
| PtpAffx.7152.1.S1_at | XP_002305027 | AJ778792 | AT3G01350.1 | Symbols: proton-dependent oligopeptide transport (POT) family protein chr3:135024-137460 FORWARD | 2,9 | 6,48E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.1084.1.A1_a_at | XP_002313864 | CV281908 | AT3G19320.1 | Symbols: leucine-rich repeat family protein chr3:6696395-6698073 REVERSE | 2,9 | 7,77E-05 |
| Ptp.2465.1.S1_at | XP_002314053 | CK092035 | AT5G19440.1 | Symbols: cinnamyl-alcohol dehydrogenase, putative (CAD) chr5:6556493-6558123 FORWARD | 2,9 | 3,44E-05 |
| PtpAffx.2848.1.S1_at | XP_002309126 | CV243610 | AT4G00430.1 | Symbols: TMP-C, PIP1;4, PIP1E PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel chr4:186143-187531 REVERSE | 2,9 | 6,42E-05 |
| PtpAffx.1025.10.S1_a_at | XP_002313635 | CX186298 | AT5G17920.2 | Symbols: ATCIMS ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase chr5:5935771-5939195 FORWARD | 2,9 | 3,55E-05 |
| PtpAffx.249.62.S1_s_at | XP_002329661 | CV258788 | AT5G45670.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr5:18528600-18530164 FORWARD | 2,9 | 4,08E-05 |
| PtpAffx.5661.4.A1_a_at | XP_002318449 | BU874770 | AT1G64650.2 | Symbols: LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transpor | 2,9 | 8,24E-05 |
| PtpAffx.1208.2.A1_at | XP_002318920 | CK088565 | --- | --- | 2,9 | 3,85E-05 |
| PtpAffx.4106.1.A1_s_at | XP_002318737 | CV270184 | AT3G48610.1 | Symbols: phosphoesterase family protein chr3:18011653-18013959 REVERSE | 2,8 | 3,95E-05 |
| PtpAffx.6950.1.S1_at | XP_002318981 | CK107127 | AT4G15920.1 | Symbols: INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane | 2,8 | 7,32E-05 |
| Ptp.56.1.S1_at | XP_002313289 | CV266604 | AT3G12610.1 | Symbols: DRT100 DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100); nucleotide binding / protein binding chr3:4006661-4007779 REVERSE | 2,8 | 8,42E-05 |
| Ptp.4381.2.A1_a_at | XP_002303239 | CV268269 | AT2G40890.1 | Symbols: CYP98A3 CYP98A3 (cytochrome P450, family 98, subfamily A, polypeptide 3); monooxygenase/ p-coumarate 3-hydroxylase chr2:17058291-17060532 REVERSE | 2,8 | 7,24E-05 |
| PtpAffx.7740.2.A1_a_at | --- | DN492286 | --- | --- | 2,8 | 7,24E-05 |
| Ptp.578.1.A1_s_at | XP_002316313 | CV246372 | --- | --- | 2,8 | 8,05E-05 |
| Ptp.6414.1.S1_at | XP_002313651 | CV277660 | AT1G08250.1 | Symbols: ADT6 ADT6 (arogenate dehydratase 6); arogenate dehydratase/ prephenate dehydratase chr1:2588994-2590235 REVERSE | 2,8 | 2,82E-05 |
| PtpAffx.140839.1.A1_at | XP_002331862 | CV243252 | AT4G18170.1 | Symbols: WRKY28, ATWRKY28 WRKY28; transcription factor chr4:10061508-10062691 FORWARD | 2,8 | 3,26E-05 |
| PtpAffx.249.692.A1_s_at | XP_002329643 | DN491523 | AT5G03690.2 | Symbols: fructose-bisphosphate aldolase, putative chr5:963389-964982 REVERSE | 2,8 | 2,82E-05 |
| PtpAffx.9190.1.S1_s_at | --- | BI125264 | --- | --- | 2,8 | 4,41E-05 |
| PtpAffx.4106.2.S1_s_at | XP_002318737 | CF229894 | AT3G48610.1 | Symbols: phosphoesterase family protein chr3:18011653-18013959 REVERSE | 2,8 | 6,08E-05 |
| PtpAffx.4106.1.A1_at | XP_002318737 | CV270184 | AT3G48610.1 | Symbols: phosphoesterase family protein chr3:18011653-18013959 REVERSE | 2,8 | 6,76E-05 |
| Ptp.7834.1.S1_at | XP_002326230 | CV241427 | AT3G10050.1 | Symbols: OMR1 OMR1 (L-O-METHYLTHREONINE RESISTANT 1); L-threonine ammonia-lyase chr3:3099164-3101741 REVERSE | 2,8 | 8,12E-05 |
| Ptp.6722.1.S1_at | XP_002315514 | CF936619 | AT3G16660.1 | Symbols: unknown protein chr3:5676904-5677788 FORWARD | 2,8 | 3,85E-05 |
| PtpAffx.249.318.A1_s_at | XP_002326656 | CV130443 | AT4G16760.1 | Symbols: ACX1, ATACX1 ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase chr4:9424930-9428689 REVERSE | 2,8 | 8,24E-05 |
| PtpAffx.25137.1.A1_at | XP_002302312 | CV231296 | AT1G22460.1 | Symbols: unknown protein chr1:7927530-7930351 REVERSE | 2,8 | 6,01E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.43257.1.S1_s_at | XP_002314489 | CV281820 | AT4G04470.1 | Symbols: PMP22 PMP22 chr4:2227963-2229226 REVERSE | 2,8 | 2,82E-05 |
| PtpAffx.221793.1.S1_s_at | XP_002336658 | pmrna38847 | AT5G16530.1 | Symbols: PIN5 PIN5 (PIN-FORMED 5); auxin:hydrogen symporter/ transporter chr5:5400735-5402626 FORWARD | 2,8 | 4,40E-05 |
| Ptp.1445.1.S1_at | XP_002305449 | CK109893 | AT1G45130.1 | Symbols: BGAL5 BGAL5 (beta-galactosidase 5); beta-galactosidase/ catalytic/ cation binding chr1:17065447-17069110 FORWARD | 2,7 | 4,47E-05 |
| Ptp.3019.1.A1_at | --- | DN485673 | --- | --- | 2,7 | 3,36E-05 |
| PtpAffx.161118.1.S1_s_at | XP_002326656 | CK319174 | AT4G16760.1 | Symbols: ACX1, ATACX1 ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase chr4:9424930-9428689 REVERSE | 2,7 | 4,28E-05 |
| PtpAffx.4962.1.S1_at | XP_002322412 | CV267650 | AT5G51550.1 | Symbols: EXL3 EXL3 (EXORDIUM LIKE 3) chr5:20939793-20940806 REVERSE | 2,7 | 8,25E-05 |
| Ptp.2020.1.S1_s_at | XP_002318694 | CF227942 | AT4G24780.1 | Symbols: pectate lyase family protein chr4:12770631-12772227 REVERSE | 2,7 | 2,92E-05 |
| Ptp.4747.1.A1_s_at | XP_002282736 | CV267614 | AT4G34480.1 | Symbols: catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds chr4:16481147-16483988 REVERSE | 2,7 | 3,26E-05 |
| PtpAffx.10247.1.A1_a_at | XP_002326267 | CV257648 | AT4G20780.1 | Symbols: calcium-binding protein, putative chr4:11133309-11133884 REVERSE | 2,7 | 8,24E-05 |
| PtpAffx.122940.1.S1_s_at | XP_002322085 | CV271536 | AT3G18080.1 | Symbols: BGLU44 BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-gl | 2,7 | 5,10E-05 |
| PtpAffx.8917.1.S1_at | XP_002318456 | CK109849 | --- | --- | 2,7 | 8,25E-05 |
| PtpAffx.206701.1.S1_x_at | XP_002309524 | pmrna13302 | AT3G49690.1 | Symbols: RAX3, MYB84, ATMYB84 MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor chr3:18427941-18429100 FORWARD | 2,7 | 8,44E-05 |
| PtpAffx.38384.1.S1_at | XP_002310279 | CV236703 | AT4G36360.1 | Symbols: BGAL3 BGAL3 (beta-galactosidase 3); beta-galactosidase/ catalytic/ cation binding / sugar binding chr4:17176840-17181143 REVERSE | 2,7 | 3,35E-05 |
| PtpAffx.152696.1.S1_at | XP_002327150 | DN495940 | AT5G42930.1 | Symbols: triacylglycerol lipase chr5:17210738-17214152 REVERSE | 2,7 | 5,55E-05 |
| PtpAffx.33481.1.S1_at | XP_002311215 | CA823181 | AT3G19820.2 | Symbols: DWF1, DIM, EVE1, DIM1, CBB1 DWF1 (DWARF 1); calmodulin binding / catalytic chr3:6879835-6881616 REVERSE | 2,7 | 5,49E-05 |
| PtpAffx.48228.1.A1_at | XP_002321717 | CV246219 | --- | --- | 2,7 | 6,65E-05 |
| Ptp.621.2.S1_a_at | XP_002317711 | CV240743 | --- | --- | 2,7 | 7,44E-05 |
| PtpAffx.6302.1.S1_s_at | XP_002311914 | BU880308 | AT1G17745.1 | Symbols: PGDH PGDH (3-PHOSPHOGLYCERATE DEHYDROGENASE); phosphoglycerate dehydrogenase chr1:6101157-6104979 FORWARD | 2,7 | 8,24E-05 |
| Ptp.6656.1.S1_s_at | XP_002312253 | BU893810 | AT1G69530.4 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) chr1:26142034-26143200 FORWARD | 2,7 | 3,72E-05 |
| PtpAffx.58827.1.S1_at | XP_002323485 | CK089146 | AT2G36910.1 | Symbols: ATPGP1, PGP1, ABCB1 ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding chr2:15502162-15507050 FORWARD | 2,6 | 6,41E-05 |
| PtpAffx.128620.1.A1_at | XP_002311370 | CV260807 | AT3G05820.1 | Symbols: beta-fructofuranosidase/ catalytic chr3:1733119-1735757 REVERSE | 2,6 | 8,24E-05 |
| PtpAffx.70120.1.A1_at | XP_002315400 | CV271262 | --- | --- | 2,6 | 6,48E-05 |
| PtpAffx.43742.1.S1_at | XP_002304118 | DN494840 | --- | --- | 2,6 | 3,26E-05 |
| PtpAffx.45801.1.S1_at | XP_002315949 | CK094291 | AT5G16080.1 | Symbols: AtCXE17 AtCXE17 (Arabidopsis thaliana carboxyesterase 17); hydrolase chr5:5252533-5253567 REVERSE | 2,6 | 3,70E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.4066.1.S1_at | XP_002331183 | CV234488 | AT1G19180.1 | Symbols: JAZ1, TIFY10A JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding chr1:6622312-6623271 FORWARD | 2,6 | 3,89E-05 |
| PtpAffx.138857.1.A1_at | XP_002312905 | BP930260 | AT2G27690.1 | Symbols: CYP94C1 CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding chr2:11809373-11810860 FORWARD | 2,6 | 3,70E-05 |
| PtpAffx.9498.1.A1_at | XP_002282702 | CV259314 | AT1G77420.1 | Symbols: hydrolase, alpha/beta fold family protein chr1:29093641-29095442 FORWARD | 2,6 | 7,85E-05 |
| PtpAffx.9887.3.S1_at | XP_002328047 | BU810796 | AT2G20610.1 | Symbols: SUR1, HLS3, RTY, ALF1, RTY1 SUR1 (SUPERROOT 1); S-alkylthiohydroximate lyase/ carbon-sulfur lyase/ transaminase chr2:8878150-8880298 REVERSE | 2,6 | 4,85E-05 |
| PtpAffx.120846.1.A1_s_at | XP_002315043 | CV254082 | AT1G26770.2 | Symbols: ATEXPA10, AT-EXP10, ATEXP10, ATHEXP ALPHA 1.1, EXP10 ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall chr1:9259775-9260792 FORWARD | 2,6 | 2,82E-05 |
| PtpAffx.1232.1.A1_at | XP_002306655 | CV238234 | AT1G77280.1 | Symbols: protein kinase family protein chr1:29031468-29035882 REVERSE | 2,6 | 4,28E-05 |
| Ptp.5554.1.S1_s_at | XP_002325514 | CK096302 | AT4G32480.1 | Symbols: unknown protein chr4:15676488-15677776 FORWARD | 2,6 | 2,81E-05 |
| PtpAffx.32865.1.A1_at | XP_002333414 | CK097026 | --- | --- | 2,6 | 8,44E-05 |
| Ptp.5520.1.S1_at | XP_002301423 | CK099052 | AT3G61880.1 | Symbols: CYP78A9 CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding chr3:22906114-22907890 REVERSE | 2,6 | 3,85E-05 |
| Ptp.1854.1.S1_s_at | XP_002330395 | CK093573 | AT5G03610.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr5:915650-918326 FORWARD | 2,6 | 3,35E-05 |
| PtpAffx.205727.1.S1_s_at | XP_002307617 | pmrna11302 | AT1G03055.1 | Symbols: unknown protein chr1:710102-711763 REVERSE | 2,5 | 6,23E-05 |
| PtpAffx.224165.1.S1_at | XP_002299719 | pmrna42443 | AT1G52190.1 | Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:19434671-19438673 FORWARD | 2,5 | 4,37E-05 |
| PtpAffx.225828.1.S1_s_at | XP_002333832 | pmrna45440 | AT1G78950.1 | Symbols: beta-amyrin synthase, putative chr1:29684558-29688673 REVERSE | 2,5 | 3,26E-05 |
| PtpAffx.122940.1.S1_at | XP_002322085 | CV271536 | AT3G18080.1 | Symbols: BGLU44 BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-gl | 2,5 | 8,24E-05 |
| PtpAffx.1398.12.A1_a_at | XP_002301432 | CV276660 | AT4G00870.1 | Symbols: basic helix-loop-helix (bHLH) family protein chr4:362230-363639 REVERSE | 2,5 | 5,51E-05 |
| PtpAffx.39069.1.S1_at | XP_002319903 | CK097783 | --- | --- | 2,5 | 3,72E-05 |
| PtpAffx.200331.1.S1_at | XP_002299425 | pmrna659 | AT4G00870.1 | Symbols: basic helix-loop-helix (bHLH) family protein chr4:362230-363639 REVERSE | 2,5 | 3,55E-05 |
| PtpAffx.111515.1.S1_at | XP_002315797 | CV238264 | AT1G69780.1 | Symbols: ATHB13 ATHB13; DNA binding / sequence-specific DNA binding / transcription factor chr1:26259166-26260465 FORWARD | 2,5 | 8,44E-05 |
| PtpAffx.2448.1.S1_at | XP_002317165 | CF231252 | --- | --- | 2,5 | 8,00E-05 |
| Ptp.2188.1.S1_a_at | XP_002272395 | BU897683 | AT2G38800.1 | Symbols: calmodulin-binding protein-related chr2:16216999-16218837 FORWARD | 2,5 | 4,27E-05 |
| PtpAffx.17212.1.S1_at | XP_002320189 | CV225916 | AT4G01070.1 | Symbols: GT72B1, UGT72B1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups chr4:461858-463300 REVERSE | 2,5 | 4,31E-05 |
| PtpAffx.225305.1.S1_s_at | XP_002331218 | pmrna44559 | AT3G14240.1 | Symbols: subtilase family protein chr3:4741637-4743964 REVERSE | 2,5 | 3,72E-05 |
| Ptp.3586.1.S1_at | XP_002329171 | DN492909 | AT1G33440.1 | Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:12127712-12130327 REVERSE | 2,5 | 3,26E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.9887.2.S1_s_at | XP_002334409 | CV244429 | AT5G36160.1 | Symbols: aminotransferase-related chr5:14233261-14235129 REVERSE | 2,5 | 4,74E-05 |
| Ptp.5843.1.S1_s_at | XP_002329620 | CX173101 | AT3G18490.1 | Symbols: aspartyl protease family protein chr3:6349090-6350592 REVERSE | 2,5 | 4,74E-05 |
| Ptp.5511.2.A1_at | --- | CK088605 | --- | --- | 2,5 | 3,72E-05 |
| PtpAffx.3558.1.S1_x_at | XP_002319581 | AB120627.1 | AT4G08850.1 | Symbols: kinase chr4:5636693-5640496 REVERSE | 2,5 | 4,16E-05 |
| Ptp.5356.1.S1_s_at | XP_002322154 | CN517393 | AT5G62890.3 | Symbols: permease, putative chr5:25243723-25247075 FORWARD | 2,5 | 3,26E-05 |
| PtpAffx.5661.1.A1_x_at | XP_002318449 | CX657739 | AT4G27720.1 | Symbols: LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transpor | 2,4 | 6,41E-05 |
| PtpAffx.158132.1.A1_at | XP_002329857 | CV282478 | AT1G62810.1 | Symbols: copper amine oxidase, putative chr1:23258253-23261772 REVERSE | 2,4 | 3,55E-05 |
| Ptp.5144.1.S1_at | XP_002311301 | DN484561 | AT3G28960.1 | Symbols: amino acid transporter family protein chr3:10984245-10985767 REVERSE | 2,4 | 3,72E-05 |
| PtpAffx.47344.1.S1_at | XP_002328852 | CK097216 | AT1G31770.1 | Symbols: ABC transporter family protein chr1:11375252-11377644 REVERSE | 2,4 | 5,36E-05 |
| PtpAffx.162370.1.S1_at | XP_002311302 | CX659276 | AT2G02990.1 | Symbols: RNS1, ATRNS1 RNS1 (RIBONUCLEASE 1); endoribonuclease/ ribonuclease chr2:873714-874667 FORWARD | 2,4 | 4,23E-05 |
| PtpAffx.10759.1.S1_at | XP_002307111 | CV266358 | AT4G39700.1 | Symbols: heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related chr4:18424265-18424906 FORWARD | 2,4 | 4,85E-05 |
| PtpAffx.9932.1.S1_at | XP_002304257 | BU811740 | AT3G14310.1 | Symbols: ATPME3 ATPME3; pectinesterase chr3:4772214-4775095 REVERSE | 2,4 | 8,24E-05 |
| PtpAffx.139092.1.S1_at | XP_002315916 | CF230457 | AT1G15080.1 | Symbols: ATPAP2, ATLPP2, LPP2 LPP2 (LIPID PHOSPHATE PHOSPHATASE 2); acid phosphatase/ phosphatidate phosphatase chr1:5188080-5189476 FORWARD | 2,4 | 7,44E-05 |
| PtpAffx.27102.1.A1_at | XP_002300235 | CV256143 | AT4G34200.1 | Symbols: EDA9 EDA9 (embryo sac development arrest 9); ATP binding chr4:16374041-16376561 REVERSE | 2,4 | 8,16E-05 |
| PtpAffx.9312.1.A1_at | XP_002309648 | CV283108 | AT5G25280.2 | Symbols: serine-rich protein-related chr5:8773882-8774544 FORWARD | 2,4 | 3,89E-05 |
| Ptp.6775.1.S1_at | XP_002310715 | CF230389 | AT4G36920.1 | Symbols: AP2, FLO2, FL1 AP2 (APETALA 2); transcription factor chr4:17400998-17403140 FORWARD | 2,4 | 6,42E-05 |
| PtpAffx.20066.2.S1_a_at | XP_002318639 | CK090955 | AT5G62890.3 | Symbols: permease, putative chr5:25243723-25247075 FORWARD | 2,4 | 3,72E-05 |
| PtpAffx.224379.1.S1_s_at | XP_002304995 | pmrna42854 | --- | --- | 2,4 | 7,24E-05 |
| PtpAffx.27897.1.A1_at | XP_002306561 | CV261331 | AT2G22430.1 | Symbols: ATHB6 ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor chr2:9526470-9527612 REVERSE | 2,4 | 3,72E-05 |
| PtpAffx.218193.1.S1_s_at | XP_002334812 | pmrna33741 | AT3G07320.1 | Symbols: glycosyl hydrolase family 17 protein chr3:2332324-2333925 REVERSE | 2,4 | 4,23E-05 |
| PtpAffx.2712.1.S1_at | XP_002313971 | CV261324 | AT1G07090.1 | Symbols: LSH6 LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) chr1:2174202-2174792 REVERSE | 2,4 | 8,05E-05 |
| PtpAffx.8849.1.S1_at | XP_002302353 | CV272213 | AT5G65640.1 | Symbols: bHLH093 bHLH093 (beta HLH protein 93); DNA binding / transcription factor chr5:26237137-26238904 FORWARD | 2,4 | 8,33E-05 |
| PtpAffx.204337.1.S1_at | XP_002306218 | pmrna8534 | AT1G29440.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to auxin stimulus; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Auxin responsive SAUR protein (InterPro:IPR003676); BEST Ara | 2,4 | 3,89E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.125952.1.S1_s_at | XP_002330395 | BI121036 | AT5G03610.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr5:915650-918326 FORWARD | 2,4 | 4,47E-05 |
| PtpAffx.201465.1.S1_s_at | XP_002300561 | pmrna2882 | AT4G20880.1 | Symbols: ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) chr4:11179389-11180606 REVERSE | 2,4 | 7,37E-05 |
| PtpAffx.57928.1.S1_s_at | XP_002311045 | CK319492 | AT3G52990.1 | Symbols: pyruvate kinase, putative chr3:19649046-19652237 FORWARD | 2,4 | 4,79E-05 |
| Ptp.2105.1.S1_s_at | XP_002323655 | CK089279 | AT3G08860.1 | Symbols: alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative chr3:2696754-2699087 REVERSE | 2,4 | 4,40E-05 |
| PtpAffx.208166.1.S1_at | XP_002311637 | pmrna16238 | AT4G14746.1 | Symbols: INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; CONTAINS InterPro DOMAIN/s: EGF (InterPro:IPR006210); Has 201 Blast hits to 179 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 168; Fungi - 0; Plants - 31 | 2,4 | 4,17E-05 |
| PtpAffx.10261.1.S1_at | XP_002323172 | CV258795 | --- | --- | 2,4 | 3,61E-05 |
| PtpAffx.160624.1.A1_s_at | XP_002316215 | CV226412 | AT3G11210.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr3:3511101-3512899 REVERSE | 2,4 | 3,76E-05 |
| PtpAffx.126167.1.S1_at | XP_002317480 | CX659711 | AT5G57850.1 | Symbols: aminotransferase class IV family protein chr5:23435548-23437287 REVERSE | 2,3 | 7,17E-05 |
| PtpAffx.25167.1.A1_s_at | XP_002306615 | CV237921 | AT1G77690.1 | Symbols: LAX3 LAX3 (LIKE AUX1 3); amino acid transmembrane transporter/ auxin influx transmembrane transporter/ transporter chr1:29201232-29203317 REVERSE | 2,3 | 8,24E-05 |
| PtpAffx.26773.2.A1_at | --- | CF232644 | --- | --- | 2,3 | 4,18E-05 |
| Ptp.6199.1.S1_at | XP_002301992 | DN495158 | AT1G19870.1 | Symbols: iqd32 iqd32 (IQ-domain 32); calmodulin binding chr1:6895400-6898539 REVERSE | 2,3 | 4,23E-05 |
| PtpAffx.3745.2.S1_at | XP_002299240 | CA934783 | AT3G20820.1 | Symbols: leucine-rich repeat family protein chr3:7280930-7282027 FORWARD | 2,3 | 7,14E-05 |
| PtpAffx.19564.1.S1_s_at | XP_002302351 | CN524106 | AT5G65670.2 | Symbols: IAA9 IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor chr5:26254463-26256134 FORWARD | 2,3 | 3,26E-05 |
| PtpAffx.16882.2.S1_at | XP_002299626 | CX658941 | AT3G15540.1 | Symbols: IAA19, MSG2 IAA19 (INDOLE-3-ACETIC ACID INDUCIBLE 19); transcription factor chr3:5264100-5265378 FORWARD | 2,3 | 4,99E-05 |
| PtpAffx.67431.1.S1_at | XP_002329196 | CV250464 | AT5G58300.2 | Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:23572821-23574871 FORWARD | 2,3 | 5,36E-05 |
| PtpAffx.160091.2.A1_a_at | XP_002330823 | CK089240 | AT5G24800.1 | Symbols: ATBZIP9, BZO2H2, BZIP9 BZIP9 (BASIC LEUCINE ZIPPER 9); DNA binding / protein heterodimerization/ transcription factor chr5:8515259-8516541 FORWARD | 2,3 | 4,85E-05 |
| PtpAffx.33300.1.A1_at | XP_002326909 | BP933461 | --- | --- | 2,3 | 8,16E-05 |
| Ptp.3600.1.S1_at | XP_002322822 | AF273256.1 | AT4G37970.1 | Symbols: ATCAD6, CAD6 CAD6 (CINNAMYL ALCOHOL DEHYDROGENASE 6); binding / catalytic/ oxidoreductase/ zinc ion binding chr4:17849672-17852145 FORWARD | 2,3 | 3,26E-05 |
| PtpAffx.115155.1.S1_at | XP_002303605 | CV230935 | AT4G23500.1 | Symbols: glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein chr4:12264640-12267074 FORWARD | 2,3 | 4,15E-05 |
| Ptp.138.1.S1_s_at | XP_002302351 | AJ306825.1 | AT5G65670.2 | Symbols: IAA9 IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor chr5:26254463-26256134 FORWARD | 2,3 | 4,40E-05 |
| PtpAffx.9932.3.S1_a_at | XP_002304257 | DN486441 | AT1G53830.1 | Symbols: ATPME2 ATPME2; pectinesterase chr1:20098562-20100745 FORWARD | 2,3 | 3,26E-05 |
| PtpAffx.28131.1.A1_s_at | XP_002317501 | CK096596 | AT4G27480.2 | Symbols: glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein chr4:13736835-13738317 REVERSE | 2,3 | 3,72E-05 |
| Ptp.7952.1.S1_at | --- | DN502508 | --- | --- | 2,3 | 7,14E-05 |
| PtpAffx.119736.1.S1_s_at | XP_002316078 | CX659087 | AT3G08900.1 | Symbols: RGP3, RGP RGP3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); transferase, transferring hexosyl groups chr3:2708347-2709714 REVERSE | 2,3 | 5,82E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.1701.1.S1_s_at | XP_002269182 | CK093047 | AT3G50760.1 | Symbols: GATL2 GATL2 (Galacturonosyltransferase-like 2); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups chr3:18868074-18869099 FORWARD | 2,3 | 3,99E-05 |
| Ptp.657.1.S1_at | XP_002301067 | CK088107 | AT1G22410.1 | Symbols: 2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative chr1:7912120-7914742 FORWARD | 2,3 | 3,52E-05 |
| PtpAffx.159492.1.A1_at | XP_002297962 | CV277474 | --- | --- | 2,3 | 5,20E-05 |
| Ptp.6778.1.S1_s_at | XP_002301752 | CN520892 | AT4G14130.1 | Symbols: XTR7 XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase chr4:8137161-8138196 REVERSE | 2,3 | 8,24E-05 |
| PtpAffx.1251.2.S1_at | XP_002301604 | BU869826 | AT3G21670.1 | Symbols: nitrate transporter (NTP3) chr3:7626942-7628954 REVERSE | 2,3 | 7,14E-05 |
| Ptp.2188.1.S1_s_at | XP_002272395 | BU897683 | AT2G38800.1 | Symbols: calmodulin-binding protein-related chr2:16216999-16218837 FORWARD | 2,3 | 7,02E-05 |
| PtpAffx.6163.1.S1_at | XP_002311294 | AJ778035 | AT3G19820.2 | Symbols: DWF1, DIM, EVE1, DIM1, CBB1 DWF1 (DWARF 1); calmodulin binding / catalytic chr3:6879835-6881616 REVERSE | 2,3 | 5,55E-05 |
| PtpAffx.35380.1.S1_a_at | XP_002318444 | CV256335 | AT4G27740.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Yippee-like protein (InterPro:IPR004910); BEST Arabidopsis thaliana protein match is: unkno | 2,3 | 8,38E-05 |
| PtpAffx.48461.1.A1_at | XP_002312220 | BP932360 | AT3G12710.1 | Symbols: methyladenine glycosylase family protein chr3:4040572-4041828 REVERSE | 2,3 | 7,14E-05 |
| PtpAffx.1262.1.S1_a_at | XP_002321377 | CV258856 | AT5G24400.1 | Symbols: emb2024 emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic chr5:8330532-8331784 REVERSE | 2,3 | 6,20E-05 |
| PtpAffx.23657.1.S1_s_at | XP_002302727 | BP928698 | AT4G02280.1 | Symbols: SUS3, ATSUS3 SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups chr4:995166-998719 FORWARD | 2,3 | 3,72E-05 |
| PtpAffx.21099.1.S1_s_at | XP_002306481 | CK094737 | --- | --- | 2,2 | 3,26E-05 |
| PtpAffx.11077.4.A1_s_at | XP_002320972 | CV276377 | AT4G01250.1 | Symbols: WRKY22, AtWRKY22 WRKY22; transcription factor chr4:522839-524129 REVERSE | 2,2 | 3,68E-05 |
| PtpAffx.3300.1.S1_s_at | XP_002302349 | CX184250 | AT4G37870.1 | Symbols: PCK1, PEPCK PCK1 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase/ purine nucleotide binding chr4:17802974-17806332 REVERSE | 2,2 | 8,16E-05 |
| Ptp.4742.2.S1_a_at | XP_002325401 | CF119365 | AT2G39050.1 | Symbols: hydroxyproline-rich glycoprotein family protein chr2:16303427-16305336 FORWARD | 2,2 | 4,08E-05 |
| PtpAffx.218194.1.S1_s_at | XP_002310016 | pmrna33742 | AT1G13080.1 | Symbols: CYP71B2 CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr1:4459212-4460807 FORWARD | 2,2 | 7,14E-05 |
| PtpAffx.48508.1.A1_s_at | --- | BP933832 | --- | --- | 2,2 | 4,74E-05 |
| PtpAffx.4558.1.S1_at | XP_002337594 | CF227976 | --- | --- | 2,2 | 8,01E-05 |
| PtpAffx.212640.1.S1_s_at | XP_002322035 | pmrna24737 | AT1G68800.1 | Symbols: BRC2, TCP12 TCP12 (TCP DOMAIN PROTEIN 12); transcription factor chr1:25847306-25848471 REVERSE | 2,2 | 7,46E-05 |
| Ptp.3850.1.S1_at | XP_002315876 | BU884767 | AT1G70850.3 | Symbols: MLP34 MLP34 (MLP-LIKE PROTEIN 34) chr1:26715429-26716744 REVERSE | 2,2 | 3,89E-05 |
| PtpAffx.67814.1.A1_at | XP_002318546 | BP936019 | AT1G68320.1 | Symbols: MYB62, AtMYB62, BW62B, BW62C MYB62 (myb domain protein 62); DNA binding / transcription factor chr1:25603842-25604884 FORWARD | 2,2 | 3,72E-05 |
| Ptp.2105.1.S1_at | XP_002323655 | CK089279 | AT3G08860.1 | Symbols: alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative chr3:2696754-2699087 REVERSE | 2,2 | 8,16E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.1931.1.A1_at | XP_002310262 | CK093159 | AT5G17730.1 | Symbols: AAA-type ATPase family protein chr5:5852498-5853999 REVERSE | 2,2 | 3,72E-05 |
| PtpAffx.8465.1.S1_at | XP_002304431 | DN497267 | AT1G62760.1 | Symbols: invertase/pectin methylesterase inhibitor family protein chr1:23237574-23238512 REVERSE | 2,2 | 5,80E-05 |
| Ptp.4358.1.S1_at | XP_002313132 | BU831393 | AT5G67210.1 | Symbols: unknown protein chr5:26819019-26819972 FORWARD | 2,2 | 4,83E-05 |
| Ptp.981.1.S1_at | XP_002313401 | CK089877 | AT5G58960.1 | Symbols: GIL1 GIL1 (GRAVITROPIC IN THE LIGHT) chr5:23805799-23808360 FORWARD | 2,2 | 8,24E-05 |
| PtpAffx.25035.1.A1_at | XP_002297660 | CV236410 | AT3G12120.2 | Symbols: FAD2 FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/omega-6 fatty acid desaturase chr3:3860592-3861743 REVERSE | 2,2 | 7,74E-05 |
| PtpAffx.85534.1.S1_at | XP_002309790 | CV228431 | AT1G06110.1 | Symbols: SKIP16 SKIP16 (SKP1/ASK-interacting protein 16); protein binding chr1:1853237-1854938 REVERSE | 2,2 | 4,18E-05 |
| PtpAffx.25650.2.S1_at | XP_002313691 | BU895759 | AT2G16990.2 | Symbols: tetracycline transporter chr2:7383194-7387783 FORWARD | 2,2 | 6,74E-05 |
| Ptp.3331.1.A1_at | XP_002324581 | CV261113 | AT2G12400.1 | Symbols: unknown protein chr2:5005144-5008140 REVERSE | 2,2 | 7,83E-05 |
| PtpAffx.18889.1.A1_at | XP_002299711 | CF235352 | --- | --- | 2,2 | 8,07E-05 |
| PtpAffx.45836.1.A1_at | --- | CK092162 | --- | --- | 2,2 | 5,55E-05 |
| Ptp.361.1.S1_at | XP_002311584 | CK088596 | AT5G62890.3 | Symbols: permease, putative chr5:25243723-25247075 FORWARD | 2,1 | 6,56E-05 |
| PtpAffx.19997.1.A1_at | XP_002303315 | CV245076 | AT3G16500.1 | Symbols: PAP1, IAA26 PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor chr3:5612801-5614208 REVERSE | 2,1 | 6,56E-05 |
| PtpAffx.88441.1.A1_at | XP_002324110 | CV266803 | AT5G39220.1 | Symbols: hydrolase, alpha/beta fold family protein chr5:15705913-15708039 FORWARD | 2,1 | 5,24E-05 |
| PtpAffx.29666.2.S1_at | XP_002316649 | CK090551 | AT1G11200.1 | Symbols: unknown protein chr1:3753896-3755459 FORWARD | 2,1 | 5,06E-05 |
| PtpAffx.144719.1.S1_at | XP_002323655 | BU874446 | AT3G08860.1 | Symbols: alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative chr3:2696754-2699087 REVERSE | 2,1 | 4,31E-05 |
| Ptp.7701.1.A1_at | XP_002329620 | CV265872 | AT3G18490.1 | Symbols: aspartyl protease family protein chr3:6349090-6350592 REVERSE | 2,1 | 4,31E-05 |
| PtpAffx.52959.1.S1_at | XP_002322933 | BU886267 | --- | --- | 2,1 | 3,89E-05 |
| Ptp.6496.1.A1_s_at | XP_002327435 | CV263678 | AT1G72960.1 | Symbols: root hair defective 3 GTP-binding (RHD3) family protein chr1:27446734-27450862 FORWARD | 2,1 | 8,24E-05 |
| PtpAffx.30187.2.S1_at | XP_002321699 | CX170990 | AT3G48530.1 | Symbols: KING1 KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1) chr3:17987559-17989592 FORWARD | 2,1 | 5,81E-05 |
| Ptp.1541.1.S1_at | XP_002329661 | CK109591 | AT5G45670.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr5:18528600-18530164 FORWARD | 2,1 | 8,33E-05 |
| PtpAffx.1262.1.S1_at | XP_002321377 | CV258856 | AT5G24400.1 | Symbols: emb2024 emb2024 (embryo defective 2024); 6-phosphogluconolactonase/catalytic chr5:8330532-8331784 REVERSE | 2,1 | 6,08E-05 |
| PtpAffx.4495.2.A1_at | XP_002314013 | CK087588 | AT5G23860.1 | Symbols: TUB8 TUB8; structural constituent of cytoskeleton chr5:8042962-8044528 FORWARD | 2,1 | 5,37E-05 |
| PtpAffx.200622.1.S1_x_at | XP_002299711 | pmma1214 | AT3G24600.1 | Symbols: INVOLVED IN: antigen processing and presentation; LOCATED IN: MHC class I protein complex, membrane; CONTAINS InterPro DOMAIN/s: MHC class I, alpha chain, C-terminal (InterPro:IPR010579), Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsi | 2,1 | 3,72E-05 |
| PtpAffx.155525.1.A1_at | XP_002312266 | CK092422 | AT1G69420.1 | Symbols: zinc finger (DHHC type) family protein chr1:26093690-26096736 FORWARD | 2,1 | 5,96E-05 |
| Ptp.5677.1.S1_at | XP_002318694 | AI165969 | AT4G24780.1 | Symbols: pectate lyase family protein chr4:12770631-12772227 REVERSE | 2,1 | 5,13E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.60647.1.S1_at | XP_002307300 | CV266317 | AT1G58440.1 | Symbols: XF1, SQE1 XF1; squalene monooxygenase chr1:21714094-21717246 REVERSE | 2,1 | 6,42E-05 |
| PtpAffx.79296.1.S1_s_at | XP_002327823 | CK092098 | AT4G36780.1 | Symbols: transcription regulator chr4:17332989-17334212 REVERSE | 2,1 | 8,44E-05 |
| PtpAffx.25650.3.S1_a_at | XP_002313691 | CV254559 | AT2G16990.2 | Symbols: tetracycline transporter chr2:7383194-7387783 FORWARD | 2,1 | 8,16E-05 |
| PtpAffx.214284.1.S1_at | XP_002324379 | pmrna27785 | AT4G31590.1 | Symbols: ATCSLC05, CSLC05, ATCSLC5 ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups chr4:15309889-15312336 REVERSE | 2,1 | 5,36E-05 |
| Ptp.1313.1.S1_at | XP_002328602 | CK092935 | AT3G06860.1 | Symbols: MFP2, ATMFP2 MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase chr3:2161926-2166009 FORWARD | 2,1 | 5,55E-05 |
| PtpAffx.49787.2.S1_a_at | XP_002305678 | CV271186 | AT5G08370.1 | Symbols: AtAGAL2 AtAGAL2 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 2); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds chr5:2691116-2693441 REVERSE | 2,1 | 6,41E-05 |
| PtpAffx.145807.1.S1_at | XP_002302732 | CX184416 | AT2G40940.1 | Symbols: ERS1, ERS ERS1 (ETHYLENE RESPONSE SENSOR 1); ethylene binding / protein histidine kinase/ receptor chr2:17084635-17086819 REVERSE | 2,0 | 6,43E-05 |
| PtpAffx.67207.1.S1_at | XP_002305859 | CK318571 | AT1G23170.1 | Symbols: unknown protein chr1:8212724-8215516 FORWARD | 2,0 | 7,96E-05 |
| PtpAffx.132618.1.S1_at | XP_002312905 | BP922442 | AT2G27690.1 | Symbols: CYP94C1 CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding chr2:11809373-11810860 FORWARD | 2,0 | 5,66E-05 |
| PtpAffx.141077.1.A1_at | XP_002323261 | CV233127 | AT3G57130.1 | Symbols: BOP1 BOP1 (BLADE ON PETIOLE 1); protein binding chr3:21147835-21150027 FORWARD | 2,0 | 8,24E-05 |
| PtpAffx.206631.1.S1_at | XP_002309457 | pmrna13163 | AT2G26290.1 | Symbols: ARSK1 ARSK1 (root-specific kinase 1); kinase chr2:11192237-11194259 REVERSE | 2,0 | 8,05E-05 |
| PtpAffx.25650.1.S1_a_at | XP_002313691 | CV257918 | AT5G42210.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Major facilitator superfamily MFS-1 (InterPro:IPR011701), Major facilitator superfamily, general s | 2,0 | 7,24E-05 |
| PtpAffx.93652.1.S1_s_at | XP_002321089 | CN517305 | AT3G16920.1 | Symbols: chitinase chr3:5776663-5777886 REVERSE | 2,0 | 5,51E-05 |
| Ptp.4102.2.A1_a_at | XP_002303510 | CV256358 | AT4G17260.1 | Symbols: L-lactate dehydrogenase, putative chr4:9674057-9675309 FORWARD | 2,0 | 5,55E-05 |
| PtpAffx.9932.2.A1_a_at | XP_002326621 | CA927911 | AT3G14310.1 | Symbols: ATPME3 ATPME3; pectinesterase chr3:4772214-4775095 REVERSE | 2,0 | 8,24E-05 |
| PtpAffx.37646.1.S1_s_at | XP_002304429 | CF232194 | AT1G62710.1 | Symbols: BETA-VPE, BETAVPE BETA-VPE (BETA VACUOLAR PROCESSING ENZYME); cysteine-type endopeptidase chr1:23224070-23226857 REVERSE | 2,0 | 5,55E-05 |
| PtpAffx.159420.1.A1_at | XP_002308862 | CV273595 | AT5G07050.1 | Symbols: LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 p | 2,0 | 4,72E-05 |
| PtpAffx.97214.1.A1_at | XP_002302687 | CK095550 | AT3G30340.1 | Symbols: nodulin MtN21 family protein chr3:11956626-11958969 FORWARD | 2,0 | 7,14E-05 |
| PtpAffx.19154.1.S1_at | XP_002327640 | CV237711 | AT5G42180.1 | Symbols: peroxidase 64 (PER64) (P64) (PRXR4) chr5:16852702-16854021 FORWARD | 2,0 | 5,66E-05 |
| PtpAffx.129645.1.S1_at | XP_002307654 | CA932058 | AT4G21150.1 | Symbols: HAP6 HAP6 (HAPLESS 6); dolichyl-diphosphooligosaccharide-protein glycotransferase chr4:11278646-11283599 FORWARD | 2,0 | 5,55E-05 |
| PtpAffx.157406.1.S1_at | XP_002331390 | CK102418 | AT5G58090.1 | Symbols: glycosyl hydrolase family 17 protein chr5:23505556-23507193 REVERSE | 2,0 | 4,74E-05 |
| PtpAffx.2332.1.S1_at | XP_002306881 | CV272022 | AT5G66460.1 | Symbols: (1-4)-beta-mannan endohydrolase, putative chr5:26538911-26540837 REVERSE | 2,0 | 7,21E-05 |
| PtpAffx.219727.1.S1_at | XP_002326320 | pmrna35741 | AT2G26440.1 | Symbols: pectinesterase family protein chr2:11247407-11249407 FORWARD | 2,0 | 8,16E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.109015.1.S1_at | XP_002330514 | AJ776323 | AT4G29680.1 | Symbols: type I phosphodiesterase/nucleotide pyrophosphatase family protein chr4:14538067-14539557 REVERSE | 1,9 | 7,14E-05 |
| PtpAffx.104298.1.S1_at | XP_002304086 | CN524432 | AT1G60500.1 | Symbols: dynamin family protein chr1:22291582-22293822 FORWARD | 1,9 | 8,44E-05 |
| Ptp.1280.1.S1_s_at | XP_002307765 | CV230458 | AT1G76160.1 | Symbols: sks5 sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase chr1:28578211-28581020 REVERSE | 1,9 | 6,67E-05 |
| PtpAffx.2551.1.S1_at | XP_002299325 | CV270107 | AT1G27990.1 | Symbols: unknown protein chr1:9752799-9753919 REVERSE | 1,9 | 6,22E-05 |
| PtpAffx.28188.1.A1_at | XP_002300663 | CK095830 | AT1G47670.1 | Symbols: amino acid transporter family protein chr1:17536834-17539486 REVERSE | 1,9 | 7,14E-05 |
| PtpAffx.3084.2.A1_a_at | XP_002328185 | CV244899 | AT1G08200.1 | Symbols: AXS2 AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase chr1:2574259-2576609 REVERSE | 1,9 | 5,78E-05 |
| PtpAffx.205046.1.S1_at | XP_002313512 | pmrna9995 | AT5G60640.1 | Symbols: ATPDIL1-4, PDI2, ATPDIL2 ATPDIL1-4 (PDI-LIKE 1-4); protein disulfide isomerase chr5:24371141-24373993 REVERSE | 1,9 | 8,12E-05 |
| Ptp.2081.1.A1_s_at | XP_002302195 | CV272057 | AT1G77120.1 | Symbols: ADH1, ADH, ATADH, ATADH1 ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase chr1:28975509-28977216 FORWARD | 1,9 | 6,72E-05 |
| PtpAffx.125797.1.A1_at | XP_002305790 | BP935651 | AT1G28280.1 | Symbols: VQ motif-containing protein chr1:9886652-9887395 REVERSE | 1,9 | 8,05E-05 |
| PtpAffx.215371.1.S1_at | XP_002329703 | pmrna29520 | AT5G16560.1 | Symbols: KAN, KAN1 KAN (KANADI); transcription factor chr5:5407365-5411092 REVERSE | 1,9 | 5,55E-05 |
| PtpAffx.30830.2.A1_a_at | XP_002312179 | CK097727 | AT1G09870.1 | Symbols: histidine acid phosphatase family protein chr1:3205817-3208444 FORWARD | 1,9 | 6,65E-05 |
| PtpAffx.209463.1.S1_s_at | XP_002316439 | pmrna18765 | AT1G16860.1 | Symbols: merozoite surface protein-related chr1:5768280-5770183 FORWARD | 1,9 | 5,55E-05 |
| PtpAffx.224524.1.S1_at | XP_002308642 | pmrna43143 | AT2G26640.1 | Symbols: KCS11 KCS11 (3-KETOACYL-COA SYNTHASE 11); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups chr2:11330094-11331623 FORWARD | 1,9 | 8,24E-05 |
| PtpAffx.68303.1.S1_at | XP_002317480 | CV131863 | AT5G57850.1 | Symbols: aminotransferase class IV family protein chr5:23435548-23437287 REVERSE | 1,9 | 6,74E-05 |
| Ptp.3480.1.S1_s_at | XP_002316095 | CV227643 | AT5G15490.1 | Symbols: UDP-glucose 6-dehydrogenase, putative chr5:5027872-5029314 REVERSE | 1,9 | 8,31E-05 |
| Ptp.5934.1.S1_s_at | XP_002301066 | CV245437 | AT4G08980.5 | Symbols: F-box family protein (FBW2) chr4:5758993-5760108 FORWARD | 1,9 | 6,48E-05 |
| PtpAffx.203360.1.S1_at | XP_002304615 | pmrna6689 | AT1G75820.1 | Symbols: CLV1, FAS3, FLO5 CLV1 (CLAVATA 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase chr1:28463631-28466652 REVERSE | 1,8 | 8,16E-05 |
| PtpAffx.145983.1.S1_at | XP_002307300 | BU878447 | AT4G37760.1 | Symbols: SQE3 SQE3 (squalene epoxidase 3); squalene monooxygenase chr4:17744085-17746426 FORWARD | 1,8 | 7,37E-05 |
| PtpAffx.200622.1.S1_at | XP_002299711 | pmrna1214 | AT3G24600.1 | Symbols: INVOLVED IN: antigen processing and presentation; LOCATED IN: MHC class I protein complex, membrane; CONTAINS InterPro DOMAIN/s: MHC class I, alpha chain, C-terminal (InterPro:IPR010579), Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsi | 1,8 | 7,24E-05 |
| Ptp.1142.1.S1_at | XP_002297946 | CK090292 | AT1G64670.1 | Symbols: BDG1 BDG1 (BODYGUARD1); hydrolase chr1:24030990-24033474 REVERSE | 1,8 | 8,24E-05 |
| PtpAffx.99667.1.S1_s_at | XP_002306893 | DN485593 | AT4G36360.1 | Symbols: BGAL3 BGAL3 (beta-galactosidase 3); beta-galactosidase/ catalytic/ cation binding / sugar binding chr4:17176840-17181143 REVERSE | 1,8 | 8,24E-05 |
| PtpAffx.94716.1.A1_at | XP_002328565 | CV262113 | AT1G55020.1 | Symbols: LOX1 LOX1; lipoxygenase chr1:20525798-20530143 FORWARD | 1,8 | 7,37E-05 |
| PtpAffx.74505.1.S1_at | XP_002314962 | CV240092 | AT5G49520.1 | Symbols: WRKY48, ATWRKY48 WRKY48; transcription factor chr5:20090890-20092867 FORWARD | 1,8 | 8,44E-05 |
| PtpAffx.7892.4.S1_a_at | XP_002304658 | CV258695 | --- | --- | 1,8 | 7,35E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.3084.5.A1_a_at | XP_002328185 | CV230306 | AT2G27860.1 | Symbols: AXS1 AXS1 (UDP-D-apiose/UDP-D-xylose synthase 1); NAD or NADH binding / UDP-glucuronate decarboxylase chr2:11864684-11866843 REVERSE | 1,8 | 8,25E-05 |
| PtpAffx.211657.1.S1_s_at | XP_002271695 | pmrna22842 | AT2G46870.1 | Symbols: NGA1 NGA1 (NGATHA1); transcription factor chr2:19261313-19262245 FORWARD | 1,8 | 8,42E-05 |
| PtpAffx.75622.1.A1_at | XP_002305508 | CV263084 | AT4G38640.1 | Symbols: choline transporter-related chr4:18059884-18062091 REVERSE | 1,8 | 8,24E-05 |
| PtpAffx.204496.1.S1_s_at | XP_002312924 | pmrna8823 | AT1G29440.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to auxin stimulus; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Auxin responsive SAUR protein (InterPro:IPR003676); BEST Ara | 1,8 | 6,48E-05 |
| PtpAffx.209657.1.S1_s_at | XP_002317166 | pmrna19057 | AT3G18670.1 | Symbols: ankyrin repeat family protein chr3:6424135-6426471 REVERSE | 1,8 | 6,42E-05 |
| Ptp.6328.2.S1_s_at | XP_002330612 | CK087416 | AT5G23860.1 | Symbols: TUB8 TUB8; structural constituent of cytoskeleton chr5:8042962-8044528 FORWARD | 1,7 | 8,44E-05 |
| PtpAffx.140928.1.A1_at | XP_002303740 | CV239658 | AT1G28130.2 | Symbols: GH3.17 GH3.17; indole-3-acetic acid amido synthetase chr1:9826379-9827883 FORWARD | 1,7 | 8,02E-05 |
| PtpAffx.12038.2.S1_at | XP_002325096 | CN523119 | AT5G57800.1 | Symbols: FLP1, YRE, CER3, WAX2 CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase chr5:23420589-23423832 FORWARD | 1,7 | 8,42E-05 |
| Ptp.5554.1.S1_at | XP_002325514 | CK096302 | AT4G32480.1 | Symbols: unknown protein chr4:15676488-15677776 FORWARD | 1,7 | 8,24E-05 |
| PtpAffx.30187.1.S1_at | XP_002321699 | CV264639 | AT3G48530.1 | Symbols: KING1 KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1) chr3:17987559-17989592 FORWARD | 1,7 | 8,33E-05 |
| PtpAffx.225407.1.S1_s_at | XP_002339676 | pmrna44733 | AT4G05200.1 | Symbols: protein kinase family protein chr4:2679793-2682309 REVERSE | 1,7 | 8,24E-05 |
| PtpAffx.94440.1.S1_s_at | XP_002302017 | CX170804 | AT1G59580.2 | Symbols: ATMPK2, MPK2 ATMPK2 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2); MAP kinase/ kinase/ protein kinase chr1:21884521-21885743 FORWARD | 1,6 | 8,24E-05 |
| PtpAffx.158774.2.S1_s_at | XP_002323447 | CN519385 | AT3G09600.2 | Symbols: myb family transcription factor chr3:2946459-2948200 FORWARD | -1,6 | 8,16E-05 |
| Ptp.881.1.A1_s_at | XP_002327750 | CV283317 | AT5G66190.1 | Symbols: ATLFNR1, FNR1 FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within th | -1,7 | 8,44E-05 |
| Ptp.3631.1.S1_at | XP_002319272 | BU895422 | AT1G11530.1 | Symbols: ATCXXS1 ATCXXS1 (C-terminal cysteine residue is changed to a serine 1); protein disulfide isomerase chr1:3874518-3875311 FORWARD | -1,7 | 8,24E-05 |
| PtpAffx.213335.1.S1_at | XP_002322717 | pmrna26084 | AT1G60080.1 | Symbols: 3' exoribonuclease family domain 1-containing protein chr1:22152605-22154339 REVERSE | -1,7 | 8,16E-05 |
| PtpAffx.201206.1.S1_at | XP_002298792 | pmrna2389 | AT1G17870.1 | Symbols: ATEGY3, EGY3 EGY3 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3) chr1:6150036-6152185 REVERSE | -1,7 | 8,44E-05 |
| Ptp.6131.1.S1_at | XP_002329895 | BU809772 | AT4G12300.1 | Symbols: CYP706A4 CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr4:7308016-7309692 REVERSE | -1,7 | 8,16E-05 |
| PtpAffx.216099.1.S1_at | XP_002330399 | pmrna30679 | --- | --- | -1,8 | 8,24E-05 |
| Ptp.4481.1.S1_a_at | XP_002307907 | DN489068 | AT4G16410.1 | Symbols: unknown protein chr4:9262019-9262576 REVERSE | -1,8 | 8,01E-05 |
| PtpAffx.249.322.S1_a_at | XP_002312733 | CX658313 | AT5G35630.3 | Symbols: GS2, GLN2, ATGSL1 GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase chr5:13831220-13833239 FORWARD | -1,8 | 6,42E-05 |
| PtpAffx.134976.1.S1_at | XP_002327829 | CV237603 | AT3G25810.1 | Symbols: myrcene/ocimene synthase, putative chr3:9430805-9433844 FORWARD | -1,8 | 7,84E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.200954.1.S1_at | XP_002298527 | pmrna1871 | AT2G16890.2 | Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:7316938-7319022 FORWARD | -1,8 | 6,41E-05 |
| PtpAffx.7188.1.A1_at | XP_002321607 | CK107538 | #NV | --- | -1,8 | 7,28E-05 |
| PtpAffx.748.1.S1_at | XP_002324301 | CV233419 | AT4G32260.1 | Symbols: ATP synthase family chr4:15573859-15574586 REVERSE | -1,9 | 7,35E-05 |
| PtpAffx.202994.1.S1_at | XP_002304253 | pmrna5925 | AT3G14260.1 | Symbols: unknown protein chr3:4747986-4748779 REVERSE | -1,9 | 7,84E-05 |
| PtpAffx.71037.1.S1_at | --- | DN493445 | --- | --- | -1,9 | 8,33E-05 |
| PtpAffx.63908.1.S1_at | XP_002304296 | AJ770045 | --- | --- | -1,9 | 6,02E-05 |
| PtpAffx.221475.1.S1_s_at | XP_002327516 | pmrna38376 | AT1G21210.1 | Symbols: WAK4 WAK4 (wall associated kinase 4); ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase chr1:7424653-7427041 FORWARD | -1,9 | 8,24E-05 |
| Ptp.7888.1.S1_at | --- | DN500883 | --- | --- | -2,0 | 7,14E-05 |
| PtpAffx.36424.1.A1_at | XP_002327350 | CX185295 | AT4G09350.1 | Symbols: DNAJ heat shock N-terminal domain-containing protein chr4:5931317-5932152 REVERSE | -2,0 | 8,05E-05 |
| PtpAffx.209887.1.S1_x_at | XP_002317395 | pmrna19474 | --- | --- | -2,0 | 7,14E-05 |
| PtpAffx.102817.1.S1_s_at | XP_002298321 | CV236374 | --- | --- | -2,0 | 8,16E-05 |
| PtpAffx.85113.1.A1_at | XP_002333230 | CX182523 | AT3G50770.1 | Symbols: calmodulin-related protein, putative chr3:18873987-18874604 FORWARD | -2,1 | 3,89E-05 |
| Ptp.5283.1.S1_s_at | XP_002330771 | CN518834 | AT5G19940.1 | Symbols: plastid-lipid associated protein PAP-related / fibrillin-related chr5:6739693-6740661 FORWARD | -2,1 | 6,41E-05 |
| PtpAffx.66546.1.S1_at | --- | BU833357 | --- | --- | -2,1 | 4,31E-05 |
| PtpAffx.9873.1.S1_at | XP_002308418 | CX180643 | AT4G30845.1 | Symbols: unknown protein chr4:15019895-15020319 FORWARD | -2,1 | 8,24E-05 |
| PtpAffx.692.23.S1_at | XP_002301832 | CN549957 | AT4G28750.1 | Symbols: PSAE-1 PSAE-1 (PSA E1 KNOCKOUT); catalytic chr4:14202951-14203888 REVERSE | -2,1 | 7,14E-05 |
| Ptp.1489.2.S1_s_at | XP_002306705 | CF229570 | --- | --- | -2,2 | 3,74E-05 |
| PtpAffx.56718.1.A1_at | XP_002312532 | CV130672 | AT4G14870.1 | Symbols: P-P-bond-hydrolysis-driven protein transmembrane transporter chr4:8517248-8517781 FORWARD | -2,2 | 6,41E-05 |
| Ptp.1440.1.A1_s_at | XP_002309787 | CV238767 | AT2G31350.1 | Symbols: GLX2-5 GLX2-5 (GLYOXALASE 2-5); hydroxyacylglutathione hydrolase/ iron ion binding / zinc ion binding chr2:13368451-13370802 FORWARD | -2,2 | 4,74E-05 |
| PtpAffx.14790.1.A1_s_at | XP_002324518 | CK091627 | AT2G24090.1 | Symbols: ribosomal protein L35 family protein chr2:10242038-10243416 FORWARD | -2,2 | 7,36E-05 |
| Ptp.1083.1.S1_at | XP_002315574 | CV237374 | AT2G33450.1 | Symbols: 50S ribosomal protein L28, chloroplast (CL28) chr2:14173620-14174380 FORWARD | -2,2 | 4,46E-05 |
| PtpAffx.90513.2.S1_at | XP_002333922 | CV267118 | AT3G07600.1 | Symbols: heavy-metal-associated domain-containing protein chr3:2424300-2424954 REVERSE | -2,2 | 5,51E-05 |
| PtpAffx.134284.1.A1_at | XP_002308699 | CV240771 | --- | --- | -2,3 | 3,89E-05 |
| Ptp.6103.1.S1_s_at | XP_002270634 | BU815369 | AT3G50685.1 | Symbols: unknown protein chr3:18834272-18834748 REVERSE | -2,3 | 8,24E-05 |
| PtpAffx.6372.1.S1_s_at | XP_002330306 | CV264952 | AT2G26500.1 | Symbols: cytochrome b6f complex subunit (petM), putative chr2:11270370-11270747 FORWARD | -2,3 | 8,24E-05 |
| Ptp.6219.1.S1_at | XP_002298321 | CV278182 | AT3G47070.1 | Symbols: unknown protein chr3:17337205-17337507 REVERSE | -2,3 | 6,76E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| Ptp.832.1.S1_at | XP_002323714 | CK089569 | AT2G43940.1 | Symbols: thiol methyltransferase, putative chr2:18196091-18197664 REVERSE | -2,3 | 3,72E-05 |
| PtpAffx.83213.1.A1_at | XP_002329276 | CV283434 | AT5G38510.2 | Symbols: rhomboid family protein chr5:15417839-15420002 REVERSE | -2,3 | 8,25E-05 |
| PtpAffx.47049.1.A1_s_at | XP_002324294 | BU895029 | AT3G47650.1 | Symbols: bundle-sheath defective protein 2 family / bsd2 family chr3:17569576-17570262 FORWARD | -2,3 | 5,66E-05 |
| PtpAffx.103575.1.S1_at | XP_002315986 | CK090377 | --- | --- | -2,3 | 8,44E-05 |
| PtpAffx.161923.1.A1_at | XP_002322732 | CK094056 | AT5G06690.1 | Symbols: WCRKC1 WCRKC1 (WCRKC THIOREDOXIN 1) chr5:2060651-2061956 REVERSE | -2,3 | 6,55E-05 |
| PtpAffx.503.2.S1_at | XP_002318638 | BU878067 | AT1G60010.1 | Symbols: unknown protein chr1:22095660-22096434 REVERSE | -2,3 | 3,27E-05 |
| PtpAffx.23940.2.S1_a_at | XP_002326159 | CV257731 | AT2G37240.1 | Symbols: INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like fold (InterPro:IPR012 | -2,3 | 3,26E-05 |
| Ptp.5326.1.S1_s_at | XP_002304324 | AJ768862 | AT5G66190.1 | Symbols: ATLFNR1, FNR1 FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within th | -2,3 | 5,81E-05 |
| Ptp.5374.1.A1_at | XP_002299183 | CV277637 | AT5G07020.1 | Symbols: proline-rich family protein chr5:2180669-2182284 REVERSE | -2,3 | 4,37E-05 |
| PtpAffx.9873.1.S1_s_at | XP_002308418 | CX180643 | AT4G30845.1 | Symbols: unknown protein chr4:15019895-15020319 FORWARD | -2,4 | 8,16E-05 |
| PtpAffx.216835.1.S1_s_at | XP_002331071 | pmrna31873 | AT5G55570.1 | Symbols: unknown protein chr5:22514587-22515260 REVERSE | -2,4 | 7,14E-05 |
| Ptp.5156.1.S1_at | XP_002324294 | BU815588 | AT3G47650.1 | Symbols: bundle-sheath defective protein 2 family / bsd2 family chr3:17569576-17570262 FORWARD | -2,4 | 5,55E-05 |
| Ptp.1460.1.S1_a_at | XP_002312755 | CV272979 | AT3G06390.1 | Symbols: integral membrane family protein chr3:1938913-1939707 REVERSE | -2,4 | 8,16E-05 |
| PtpAffx.130241.1.S1_s_at | XP_002310031 | BU886458 | AT5G64840.1 | Symbols: ATGCN5 ATGCN5 (A. THALIANA GENERAL CONTROL NON-REPRESSIBLE 5); transporter chr5:25916956-25919693 REVERSE | -2,4 | 3,26E-05 |
| PtpAffx.131515.1.S1_at | XP_002313220 | CV241310 | AT1G07010.3 | Symbols: calcineurin-like phosphoesterase family protein chr1:2152949-2154968 FORWARD | -2,4 | 6,08E-05 |
| PtpAffx.17245.1.S1_a_at | XP_002313030 | CF229356 | --- | --- | -2,4 | 3,59E-05 |
| Ptp.2908.1.A1_at | XP_002319231 | CN524682 | AT5G35970.1 | Symbols: DNA-binding protein, putative chr5:14119060-14123078 REVERSE | -2,4 | 5,66E-05 |
| Ptp.6123.1.S1_at | XP_002307402 | BU809142 | --- | --- | -2,5 | 2,82E-05 |
| PtpAffx.207002.1.S1_at | XP_002310476 | pmrna13874 | --- | --- | -2,5 | 8,16E-05 |
| Ptp.3941.1.S1_at | XP_002298632 | CV230881 | AT5G40950.1 | Symbols: RPL27 RPL27 (RIBOSOMAL PROTEIN LARGE SUBUNIT 27); structural constituent of ribosome chr5:16410866-16411845 FORWARD | -2,5 | 2,82E-05 |
| Ptp.4420.1.S1_s_at | XP_002263772 | CV236676 | AT4G10300.1 | Symbols: FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR011051), Protein of unknown function DUF861, c | -2,5 | 4,31E-05 |
| PtpAffx.133356.1.A1_at | XP_002325127 | CV280606 | AT4G30610.1 | Symbols: BRS1, SCPL24 BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase chr4:14944219-14948391 FORWARD | -2,5 | 4,29E-05 |
| PtpAffx.224107.1.S1_at | XP_002339728 | pmrna42345 | AT5G55570.1 | Symbols: unknown protein chr5:22514587-22515260 REVERSE | -2,5 | 3,89E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.200006.1.S1_at | XP_002297610 | pmrna8 | --- | --- | -2,5 | 3,89E-05 |
| PtpAffx.93558.1.A1_at | XP_002300646 | BP932992 | AT1G24420.1 | Symbols: transferase family protein chr1:8656687-8657997 FORWARD | -2,5 | 3,35E-05 |
| PtpAffx.59464.1.A1_at | XP_002326046 | AJ780287 | AT3G21340.1 | Symbols: leucine-rich repeat protein kinase, putative chr3:7511848-7515937 REVERSE | -2,5 | 5,55E-05 |
| PtpAffx.119000.1.S1_at | XP_002326072 | DN497277 | AT5G05280.1 | Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:1565509-1566039 REVERSE | -2,5 | 5,81E-05 |
| PtpAffx.146387.1.A1_at | XP_002320226 | CV279718 | --- | --- | -2,5 | 4,29E-05 |
| PtpAffx.53128.1.S1_at | XP_002331481 | CV238625 | AT3G44890.1 | Symbols: RPL9 RPL9 (RIBOSOMAL PROTEIN L9); structural constituent of ribosome chr3:16386505-16387963 FORWARD | -2,6 | 6,23E-05 |
| PtpAffx.156713.1.S1_at | XP_002302952 | DN497323 | --- | --- | -2,6 | 2,82E-05 |
| PtpAffx.216199.1.S1_at | XP_002329938 | pmrna30829 | AT3G57520.1 | Symbols: AtSIP2 AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds chr3:21288982-21292694 REVERSE | -2,6 | 2,82E-05 |
| PtpAffx.106035.1.S1_at | XP_002324690 | DN483857 | AT5G57150.1 | Symbols: basic helix-loop-helix (bHLH) family protein chr5:23152361-23154872 FORWARD | -2,6 | 3,85E-05 |
| Ptp.6638.1.S1_s_at | XP_002298222 | CV244428 | AT1G79850.1 | Symbols: RPS17, CS17, PRPS17 RPS17 (RIBOSOMAL PROTEIN S17); structural constituent of ribosome chr1:30041473-30041922 REVERSE | -2,6 | 8,16E-05 |
| Ptp.1447.1.S1_at | XP_002300713 | CV280897 | AT1G75690.1 | Symbols: chaperone protein dnaJ-related chr1:28422273-28423170 REVERSE | -2,6 | 8,24E-05 |
| PtpAffx.23940.3.S1_a_at | XP_002326159 | BI125225 | AT2G37240.1 | Symbols: INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like fold (InterPro:IPR012 | -2,6 | 3,26E-05 |
| Ptp.1041.1.S1_at | XP_002299424 | CK090202 | AT1G64680.1 | Symbols: unknown protein chr1:24036071-24037062 FORWARD | -2,6 | 6,86E-05 |
| PtpAffx.203864.1.S1_at | XP_002305104 | pmrna7631 | AT4G35160.1 | Symbols: O-methyltransferase family 2 protein chr4:16730989-16732808 REVERSE | -2,6 | 3,72E-05 |
| PtpAffx.119469.1.S1_at | XP_002317837 | BP931170 | AT1G05260.1 | Symbols: RCI3, RCI3A RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase chr1:1529827-1531271 FORWARD | -2,6 | 5,26E-05 |
| PtpAffx.211473.1.S1_at | XP_002320065 | pmrna22487 | AT5G37770.1 | Symbols: TCH2, CML24 TCH2 (TOUCH 2); calcium ion binding chr5:14999075-14999560 REVERSE | -2,7 | 6,07E-05 |
| PtpAffx.49589.1.S1_at | XP_002304996 | CV279163 | AT4G21445.1 | Symbols: unknown protein chr4:11424781-11425590 FORWARD | -2,7 | 5,78E-05 |
| PtpAffx.162338.1.S1_at | XP_002302507 | CN519765 | AT5G47060.1 | Symbols: senescence-associated protein-related chr5:19116843-19117639 FORWARD | -2,7 | 2,58E-05 |
| PtpAffx.42186.1.A1_at | XP_002327383 | BP936012 | AT4G32480.1 | Symbols: unknown protein chr4:15676488-15677776 FORWARD | -2,7 | 3,05E-05 |
| PtpAffx.4043.1.S1_at | XP_002319481 | CX658760 | AT1G56500.1 | Symbols: haloacid dehalogenase-like hydrolase family protein chr1:21159775-21167092 FORWARD | -2,7 | 6,77E-05 |
| PtpAffx.39050.2.S1_at | XP_002298402 | CK090154 | AT5G19855.1 | Symbols: unknown protein chr5:6712166-6713445 REVERSE | -2,7 | 8,28E-05 |
| Ptp.1460.1.S1_at | XP_002312755 | CV272979 | AT3G06390.1 | Symbols: integral membrane family protein chr3:1938913-1939707 REVERSE | -2,8 | 8,42E-05 |
| PtpAffx.16145.1.S1_at | XP_002312467 | CV276628 | AT2G01755.1 | Symbols: unknown protein chr2:332249-332770 REVERSE | -2,8 | 5,55E-05 |
| PtpAffx.207898.1.S1_at | XP_002311342 | pmrna15677 | AT5G61040.1 | Symbols: unknown protein chr5:24562431-24564395 REVERSE | -2,8 | 2,58E-05 |
| PtpAffx.99814.1.A1_at | XP_002317124 | CV271088 | AT1G62250.1 | Symbols: unknown protein chr1:22995615-22997003 REVERSE | -2,8 | 8,44E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|--|--------------------|------------------------|
| Ptp.6115.1.S1_at | XP_002319881 | DN496766 | AT5G05220.1 | Symbols: unknown protein chr5:1550273-1550821 FORWARD | -2,8 | 2,58E-05 |
| PtpAffx.88583.1.A1_at | XP_002274448 | CV262125 | AT4G36850.1 | Symbols: INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Cystinosin/ERS1p repeat (InterPro:IPR006603); BEST Arabidopsis thaliana protein match is: PQ-loop repeat family protein / transmembrane family protein | -2,8 | 5,15E-05 |
| PtpAffx.43322.5.A1_s_at | XP_002325947 | CV236644 | AT1G70170.1 | Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase/metallopeptidase chr1:26424005-26425141 FORWARD | -2,8 | 3,05E-05 |
| PtpAffx.5078.5.A1_at | XP_002308818 | CK114960 | --- | --- | -2,9 | 6,78E-05 |
| PtpAffx.206281.1.S1_at | XP_002308187 | pmrna12449 | AT1G52240.2 | Symbols: ATROPGEF11, ROPGEF11 ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor chr1:19458844-19459235 REVERSE | -2,9 | 7,14E-05 |
| Ptp.5133.1.S1_s_at | XP_002311693 | AJ767409 | AT2G05620.1 | Symbols: PGR5 PGR5 (proton gradient regulation 5); electron carrier chr2:2081204-2081687 REVERSE | -2,9 | 2,58E-05 |
| PtpAffx.151041.1.S1_s_at | XP_002305073 | AJ780822 | AT5G45890.1 | Symbols: SAG12 SAG12 (SENESCENCE-ASSOCIATED GENE 12); cysteine-type peptidase chr5:18613300-18614759 FORWARD | -2,9 | 6,65E-05 |
| PtpAffx.66254.1.S1_at | XP_002318873 | DN501858 | AT3G47800.1 | Symbols: aldose 1-epimerase family protein chr3:17634971-17636998 FORWARD | -2,9 | 5,89E-05 |
| Ptp.5233.1.S1_at | --- | CK089657 | --- | --- | -2,9 | 3,26E-05 |
| PtpAffx.79787.1.S1_at | XP_002328208 | DN493946 | --- | --- | -3,0 | 5,55E-05 |
| PtpAffx.204875.1.S1_s_at | XP_002314074 | pmrna9632 | AT5G19855.1 | Symbols: unknown protein chr5:6712166-6713445 REVERSE | -3,0 | 5,13E-05 |
| Ptp.6052.1.S1_s_at | NP_001130133 | BI122423 | AT1G17710.1 | Symbols: phosphatase chr1:6090763-6091975 REVERSE | -3,0 | 3,26E-05 |
| PtpAffx.208878.1.S1_at | XP_002314796 | pmrna17599 | AT1G23200.1 | Symbols: pectinesterase family protein chr1:8227236-8229400 FORWARD | -3,0 | 2,58E-05 |
| PtpAffx.98978.1.S1_at | --- | DN500537 | --- | --- | -3,0 | 2,81E-05 |
| PtpAffx.90356.2.A1_a_at | XP_002304436 | CV271797 | AT1G62850.3 | Symbols: translation release factor chr1:23272608-23274211 REVERSE | -3,0 | 4,85E-05 |
| PtpAffx.35031.1.S1_at | XP_002303984 | BU810466 | AT1G55480.1 | Symbols: binding / protein binding chr1:20713822-20715351 FORWARD | -3,0 | 3,26E-05 |
| PtpAffx.139964.1.A1_at | --- | CX658305 | --- | --- | -3,0 | 6,52E-05 |
| PtpAffx.211760.1.S1_s_at | XP_002321006 | pmrna23049 | AT3G62820.1 | Symbols: invertase/pectin methylesterase inhibitor family protein chr3:23229782-23230366 FORWARD | -3,1 | 5,13E-05 |
| PtpAffx.200647.1.S1_at | XP_002299733 | pmrna1258 | --- | --- | -3,1 | 2,58E-05 |
| PtpAffx.24009.1.A1_at | XP_002326631 | CV279164 | AT3G12750.1 | Symbols: ZIP1 ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transmembrane transporter chr3:4051950-4053156 REVERSE | -3,1 | 3,72E-05 |
| PtpAffx.214116.1.S1_at | XP_002324213 | pmrna27477 | AT5G25840.1 | Symbols: unknown protein chr5:9010909-9011430 REVERSE | -3,1 | 3,26E-05 |
| PtpAffx.150078.1.S1_s_at | XP_002319474 | BU880077 | AT1G09340.1 | Symbols: CRB, CSP41B CRB (CHLOROPLAST RNA BINDING); binding / catalytic/coenzyme binding chr1:3015473-3018035 FORWARD | -3,1 | 8,44E-05 |
| PtpAffx.28262.1.S1_at | XP_002304998 | CF234847 | AT4G27360.1 | Symbols: dynein light chain, putative chr4:13694032-13694517 FORWARD | -3,2 | 2,58E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.111903.2.S1_at | XP_002307561 | CV281410 | --- | --- | -3,2 | 2,22E-05 |
| PtpAffx.10948.1.S1_a_at | XP_002304545 | CV277589 | AT5G41761.1 | Symbols: unknown protein chr5:16711437-16711742 FORWARD | -3,2 | 2,58E-05 |
| PtpAffx.28501.2.S1_a_at | XP_002325917 | CK094696 | AT3G56290.1 | Symbols: unknown protein chr3:20878743-20879541 REVERSE | -3,2 | 5,81E-05 |
| Ptp.5354.1.S1_at | XP_002314698 | CV232039 | AT4G14890.1 | Symbols: ferredoxin family protein chr4:8520887-8521351 FORWARD | -3,3 | 5,07E-05 |
| PtpAffx.10889.1.S1_s_at | XP_002304136 | CV283550 | AT1G72610.1 | Symbols: GLP1, ATGER1, GER1 GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase chr1:27339302-27339928 REVERSE | -3,4 | 6,21E-05 |
| PtpAffx.99357.1.A1_s_at | XP_002331052 | BI069533 | AT2G12462.1 | Symbols: unknown protein chr2:5050583-5051585 REVERSE | -3,4 | 2,73E-05 |
| PtpAffx.10889.1.S1_at | XP_002304136 | CV283550 | AT1G72610.1 | Symbols: GLP1, ATGER1, GER1 GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase chr1:27339302-27339928 REVERSE | -3,4 | 7,45E-05 |
| PtpAffx.5177.1.S1_at | XP_002314367 | CV258464 | AT3G06840.1 | Symbols: unknown protein chr3:2156930-2157624 FORWARD | -3,5 | 2,58E-05 |
| Ptp.4827.1.S1_a_at | XP_002306836 | DN490862 | AT5G59540.1 | Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr5:23996293-23997576 REVERSE | -3,5 | 2,58E-05 |
| PtpAffx.206281.1.S1_x_at | XP_002308187 | pmrna12449 | AT1G52240.2 | Symbols: ATROPGEF11, ROPGEF11 ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor chr1:19458844-19459235 REVERSE | -3,5 | 5,75E-05 |
| PtpAffx.215329.1.S1_at | XP_002338056 | pmrna29449 | --- | --- | -3,5 | 4,28E-05 |
| PtpAffx.59823.1.S1_a_at | XP_002300278 | CK094119 | AT1G49975.1 | Symbols: unknown protein chr1:18504845-18505431 FORWARD | -3,5 | 4,40E-05 |
| PtpAffx.47743.1.S1_at | --- | BI126271 | --- | --- | -3,5 | 8,28E-05 |
| Ptp.1108.2.A1_at | XP_002328680 | CK090142 | AT1G73870.1 | Symbols: zinc finger (B-box type) family protein chr1:27779214-27780522 FORWARD | -3,6 | 6,41E-05 |
| Ptp.1108.1.A1_s_at | XP_002328680 | CV280255 | AT1G68520.1 | Symbols: zinc finger (B-box type) family protein chr1:25709331-25710749 REVERSE | -3,6 | 5,55E-05 |
| PtpAffx.89190.1.A1_at | XP_002304410 | CV234138 | AT3G47430.1 | Symbols: PEX11B PEX11B chr3:17480798-17481692 FORWARD | -3,7 | 7,24E-05 |
| PtpAffx.146348.1.A1_s_at | XP_002302358 | CV282108 | --- | --- | -3,8 | 3,26E-05 |
| Ptp.1108.1.A1_a_at | XP_002328680 | CV280255 | AT1G68520.1 | Symbols: zinc finger (B-box type) family protein chr1:25709331-25710749 REVERSE | -3,8 | 6,42E-05 |
| Ptp.7601.1.S1_s_at | --- | BU814226 | --- | --- | -3,8 | 1,94E-05 |
| PtpAffx.100112.1.A1_at | XP_002312665 | BP931069 | AT2G02580.1 | Symbols: CYP71B9 CYP71B9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding chr2:701985-703661 FORWARD | -3,9 | 7,46E-05 |
| Ptp.6981.1.S1_at | XP_002280193 | DN488994 | AT4G00165.2 | Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:69433-69819 REVERSE | -3,9 | 8,01E-05 |
| PtpAffx.133294.1.A1_at | XP_002310556 | CV283606 | --- | --- | -4,0 | 3,26E-05 |
| Ptp.857.1.S1_at | XP_002321835 | CK089982 | AT1G14890.1 | Symbols: enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor chr1:5137045-5137704 FORWARD | -4,0 | 8,05E-05 |
| PtpAffx.49413.1.S1_at | XP_002315690 | CX178932 | AT1G10657.2 | Symbols: unknown protein chr1:3530652-3531522 FORWARD | -4,1 | 3,72E-05 |
| PtpAffx.204108.1.S1_s_at | XP_002305342 | pmrna8104 | --- | --- | -4,4 | 7,25E-05 |
| PtpAffx.206280.1.S1_at | XP_002308186 | pmrna12448 | --- | --- | -4,5 | 2,50E-05 |

| Probe.Set.ID ^a | NCBI RefSeq ^b | Public ID ^c | AGI code ^d | Annotation ^e | logFC ^f | adj.P-val ^g |
|---------------------------|--------------------------|------------------------|-----------------------|---|--------------------|------------------------|
| PtpAffx.120370.1.S1_at | XP_002317294 | CX178829 | AT1G30260.1 | Symbols: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cytokinin stimulus; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: galactosyltransferase family protein (TA | -4,5 | 2,50E-05 |
| PtpAffx.7984.1.S1_s_at | XP_002326118 | CA926076 | AT5G20630.1 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 GER3 (GERMIN 3); oxalate oxidase chr5:6975315-6975950 REVERSE | -4,9 | 4,41E-05 |

Supplemental Table S1. List of 500 differentially expressed genes *Ptt* nectaries versus leaves. ^a Probe Set IDs (Affymetrix). ^b and ^c accession numbers of corresponding sequences at (www.ncbi.nlm.nih.gov/guide/) received from (http://www.plexdb.org/modules/PD_probeset/annotation.php?genechip=Poplar) with Affymetrix Probe Set IDs. ^d AGI code of the nearest Arabidopsis homolog according to ^c. ^e Annotation according to ^d. ^f logFC, log2 of fold change. ^g adj.P-val, adjusted P-value.

| Public ID ^a | AGI code ^b | Annotation ^c | qPCR logFC ^d | Array logFC ^e |
|------------------------|-----------------------|---|-------------------------|--------------------------|
| CV242633 | At1g65890 | AAE12 (acyl activating enzyme 12) | 6,4 | 6,0 |
| BU825949 | At4g36470 | carboxyl methyltransferase family protein | 4,3 | 5,3 |
| CV276911 | At4g24340 | phosphorylase family protein | 4,6 | 5,0 |
| CV283544 | At1g52340 | ABA2 (ABA deficient 2); alcohol dehydrogenase | 5,1 | 4,2 |
| AJ744954.1 | At1g51760 | IAR3 (IAA-alanine resistant 3) | -0,6 | 1,2 |
| XP_002326709 | At1g32450 | NRT1.5 (nitrate transporter 1.5) | 0,6 | 1,1 |
| CV246702 | At1g47670 | amino acid transporter family protein | 0,0 | 1,1 |
| AJ777538 | At2g42790 | CSY3 (citrate synthase 3) | 0,6 | 0,9 |
| CK093044 | At5g48930 | HCT (quinic acid hydroxycinnamoyl transferase) | 0,8 | 0,8 |
| XP_002315752 | At5g43860 | ATCLH2; chlorophyllase | -1,0 | 0,7 |
| CV249255 | At1g05260 | RCI3 (rare cold inducible gene 3) | -1,4 | -0,4 |
| CV242179 | At2g05620 | PGR5 (proton gradient regulation 5); electron carrier | -4,8 | -1,7 |
| CV283317 | At5g66190 | FNR1 (ferredoxin-NADP(+) oxidoreductase 1) | -4,7 | -1,7 |
| CA926076 | At5g20630 | GLP3, GER3 (germin 3) | -8,4 | -4,9 |

Supplemental Table S2. Validation of microarray data by qPCR. Fold changes (FC) of randomly selected transcripts from the arrays were verified by qPCR. ^a accession number of corresponding sequence at (www.ncbi.nlm.nih.gov/guide/) received from (http://www.plexdb.org/modules/PD_probeset/annotation.php?genechip=Poplar) with Affymetrix Probe Set IDs. ^b AGI code of the nearest Arabidopsis homolog according to ^a. ^c Annotation according to ^b. ^d and ^e log fold change in qPCR and arrays.

| Public ID ^a | | |
|------------------------|--------------------------------|--|
| GU385982 | PtACT2fwd PtACT2rev | 5'-CCCAGAAGTCCTCTT-3' 5'-ACTGAGCACAATGTTAC-3' |
| AJ744954.1 | PtILR1fwd PtILR1rev | 5'-TGGTAGGGGTAAGGAG-3' 5'-ATTTCTGCATAGCAA-3' |
| CK093044 | PtHCTfwd PtHCTrev | 5'-TATCTAAGGTCAGCCC-3' 5'-AATAGTTTCATGTGTTTCAG-3' |
| XP_002315752 | PtCLH2fwd PtCLH2rev | 5'-TCTCAGCACTAATTGG-3' 5'-ACAACGAAATAACTAGCC-3' |
| CV246702 | PtLysHisfwd PtLysHisrev | 5'-TTGACTAAGCTAAATCCG-3' 5'-CAAGCTCCACATATCTGT-3' |
| AJ777538 | PtCSY3fwd PtCSY3rev | 5'-GATTTTCATCGAGGGTG-3' 5'-AAGCCTATCCGCATC-3' |
| CV242179 | PtPGR5fwd PtPGR5rev | 5'-CGTCAAATAATCGGCA-3' 5'-TGGCCAACCTAATCAG-3' |
| CV283317 | PtLFNR1fwd PtLFNR1rev | 5'-CCACTATCATTATGCTTG-3' 5'-TCTTTAGTAATCCCACAG-3' |
| CA926076 | PtGLP3fwd PtGLP3rev | 5'-AAATTCGGAGGTGTAAT-3' 5'-CGTCATCGAGGAATGTTG-3' |
| CV283544 | PtSDRfwd PtSDRrev | 5'-GGCGCATTCTTAGGCACT-3' 5'-GGGGTCAAACAACGTAG-3' |
| XP_002326709 | PtPTR2fwd PtPTR2rev | 5'-GGCCTTGTGATAGCAATA-3' 5'-CTAGCGAGATAGATGTCA-3' |
| CV276911 | PtPIN288fwd PtPIN288rev | 5'-TGTATACTTCCGGGAACC-3' 5'-CGGAACAAGATATAAGGC-3' |
| BU825949 | PtSABfwd PtSABrev | 5'-GTCCACCAAGCGTGCTTA-3' 5'-CATGCACTTAGCAACATT-3' |
| CV242633 | PtACCL10fwd PtACCL10rev | 5'-GGCGAGGCAAGGGATTAG-3' 5'-TTGCAGTAAGCGATAAT-3' |
| CV249255 | PtRCI3fwd PtRCI3rev | 5'-CTCTAGATAGCGAATATG -3' 5'-TCTGATTGAAATAGACCT -3' |
| XP_002314626 | PtAla3(1)fwd PtAla3(1)rev | 5'-ATTCTATTTCTACCTCACG-3' 5'-CATACCCAGGTGATTC-3' |
| XP_002339708 | PtAla3(2)fwd PtAla3(2)rev | 5'-AATCTATTTCTACCTCACG-3' 5'-CTGCCCTAGTGTTGTC-3' |
| BU810775 | PtAla3(3)fwd PtAla3(3)rev | 5'-ATCCTAAATATCGTGATCT-3' 5'-ACAATACATGCGACTG-3' |
| CV275482 | PtArf1(1)fwd PtArf1(1)rev | 5'-GCTGTATGAGGGATTG-3' 5'-GGCTTTGCTATTTGAATAA-3' |
| CK088579 | PtArf1(2)fwd PtArf1(2)rev | 5'-CCACCATTCTACTATTG-3' 5'-CCCTGTCGTTGCTATC-3' |
| CV278073 | PtDAGfwd PtDAGrev | 5'-AGGGTGCCACTAAGC-3' 5'-CTTTGTATTCGGGGTC-3' |
| BU824735 | PtDyn(1)fwd PtDyn(1)rev | 5'-AAGTGTACACTACTACATTC-3' 5'-ACCATCATGTCTACC-3' |
| CK090501 | PtDyn(2)fwd PtDyn(2)rev | 5'-TGAAGACTCGTGGTAT-3' 5'-TTTGTTCCAAGGGTTCTA-3' |
| CK092620 | PtPEP12(1)fwd PtPEP12(1)rev | 5'-TCTGATCGCTAGTATGG-3' 5'-CATTTAGATTTACGGTT-3' |
| CF936851 | PtPEP12(2)fwd PtPEP12(2)rev | 5'-GGAAACGGCATATACT-3' 5'-GTTCTCTCTCCTCGATAA-3' |

| | | |
|--------------|---------------------------------|---|
| CV241725 | PtRabAfw PtRabArev | 5'-TTCTGGATGGGCAAAG-3' 5'-GGATCCTGGAAACCGT-3' |
| DN496417 | PtRabE/8(1)fw PtRabE/8(1)rev | 5'-TCACAACTGCTTATTATCG-3' 5'-TTGATCCCGTACTCAT-3' |
| BU893135 | PtRabE/8(2)fw PtRabE/8(2)rev | 5'-CAACTGCTTACTATCGC-3' 5'-CCTTGTGTCCGGTGTGTC-3' |
| CV277800 | PtRabF(1)fw PtRabF(1)rev | 5'-GGTTATGGCATTAGTAGC-3' 5'-GATTCACCCAGTAGA-3' |
| CX178052 | PtRabF(2)fw PtRabF(2)rev | 5'-TACCACAGCTTAGCTC-3' 5'-GCTGGCTGTACTTGA-3' |
| CV240653 | PtRabF(3)fw PtRabF(3)rev | 5'-GTCCAGTCTCGTATTG-3' 5'-ATACTCCTGGGCATAA-3' |
| XP_002306120 | PtSEC14fw PtSEC14rev | 5'-ATATCGCATCCCCTAA-3' 5'-CCAGTGAGCGAAAGA-3' |
| XP_002327686 | PtSNARE(1)fw PtSNARE(1)rev | 5'-CGAAGGATCGTATTGT-3' 5'-CCTTAATGTCGTAGAACT-3' |
| CK093245 | PtSNARE(2)fw PtSNARE(2)rev | 5'-AGGAACTCCGATTTATAG-3' 5'-ACCTGTCCTGTATCTC-3' |
| BP932273 | PtSNX1fw PtSNX1rev | 5'-GTAAGGCAGTAAACTCC-3' 5'-AAGAACGTGTTAGCATA-3' |
| CF120135 | PtVHA-a1fw PtVHA-a1rev | 5'-GTGATTACTCTCCTGAAG-3' 5'-CTGCGAGCTAAGATG-3' |

Supplemental Table S3. Primers used in qPCR.

^a accession number of the corresponding sequence at (www.ncbi.nlm.nih.gov/guide/).

Supplemental Protocols

Sudan III Staining

100µm longitudinal sections of extrafloral nectaries from *Ptt* were cut with a hand-microtome (Leica) and stained with Sudan III (0.3µg/ml, Sigma-Aldrich). Sections were examined with a Keyence VHX-100K digital microscope (Keyence Corporation).

FM4-64 Staining and confocal microscopy.

Complete nectaries from *Ptt* were immersed for 1 minute in a solution containing 5µl/ml Fm4-64 dye (Invitrogen) on ice. The nectaries were washed and subsequently cut into 100µm sections with a hand microtome (Leica). Sections were examined with confocal microscopy using a laser scanning microscope, Axioskop2 mot Plus (Zeiss), with an excitation at 558nm and an emission at 734nm.