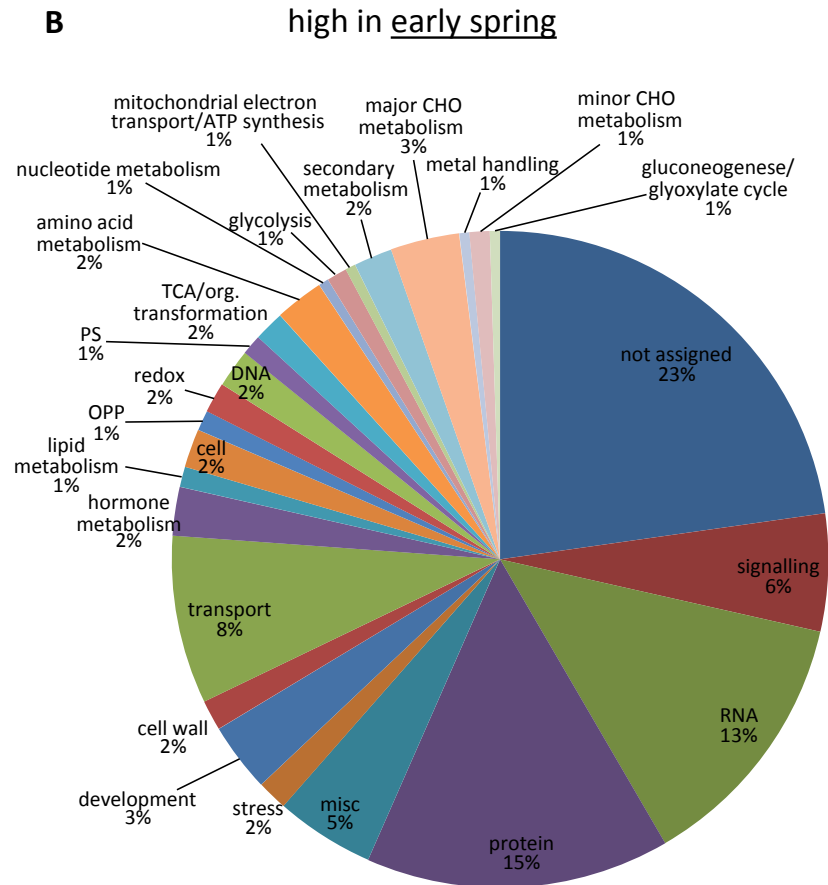
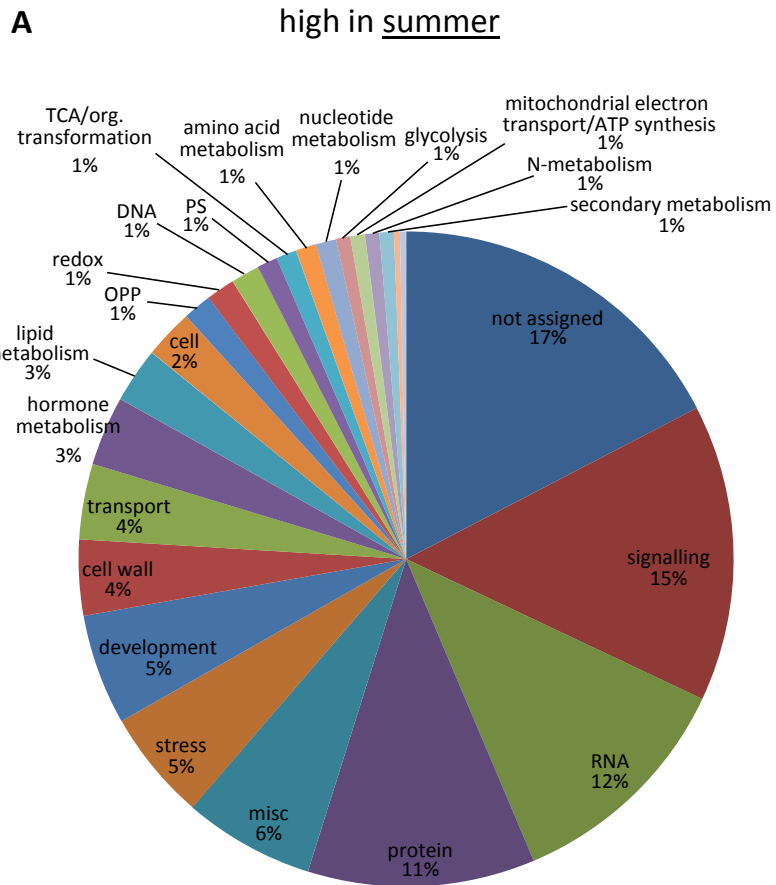
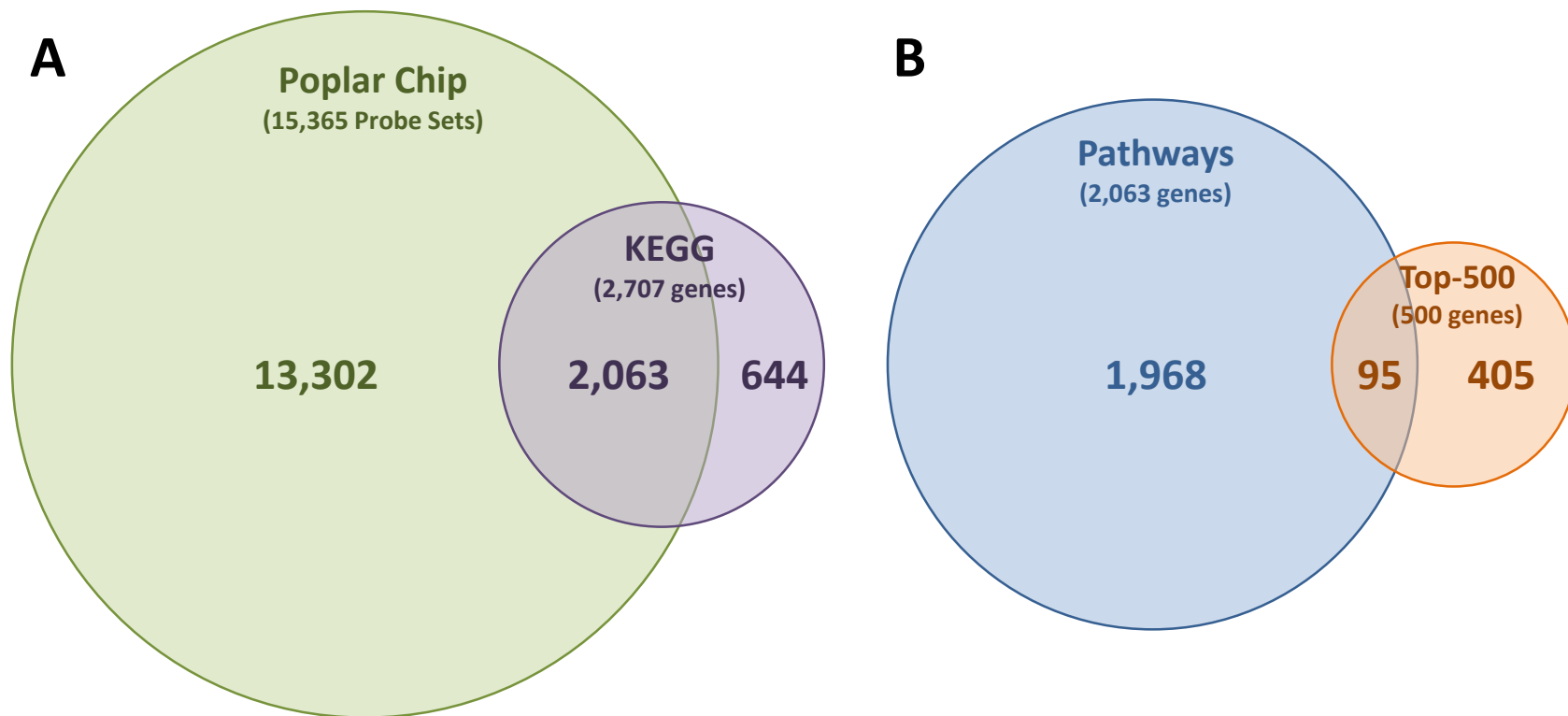


**Supplemental Figure S1.** Wood anatomy. A, Light micrograph of a cross section of mature wood used in this study. Ray parenchyma cells (R) appear blue-stained. In addition vessels (V) and fibers (F) occur. B, Light micrograph of a radial section of the same wood. C, Light micrograph of a tangential section of the same wood. No axial parenchyma cells were detectable in all three planes.

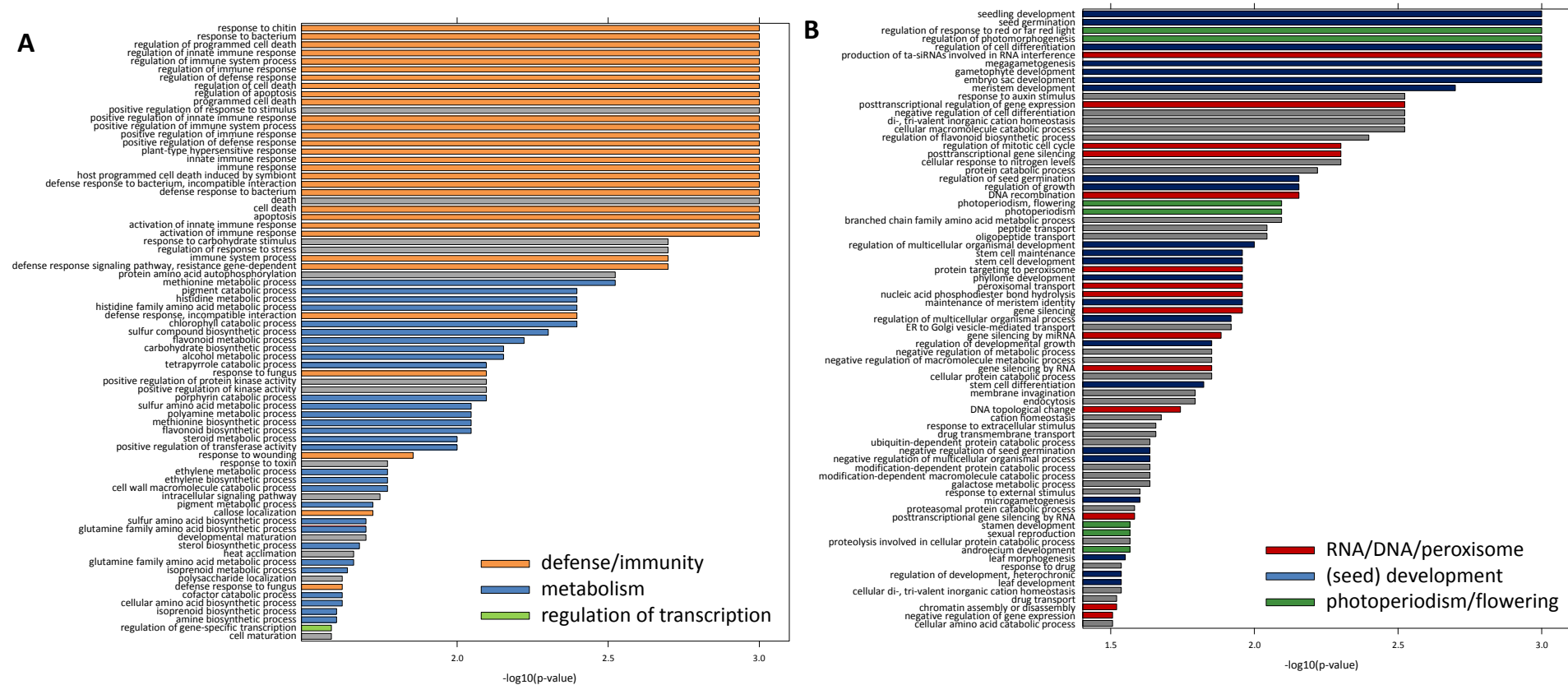


**Supplemental Figure S2.** Clustering of *Populus x canadensis* differently expressed genes in rays (summer vs. early spring).

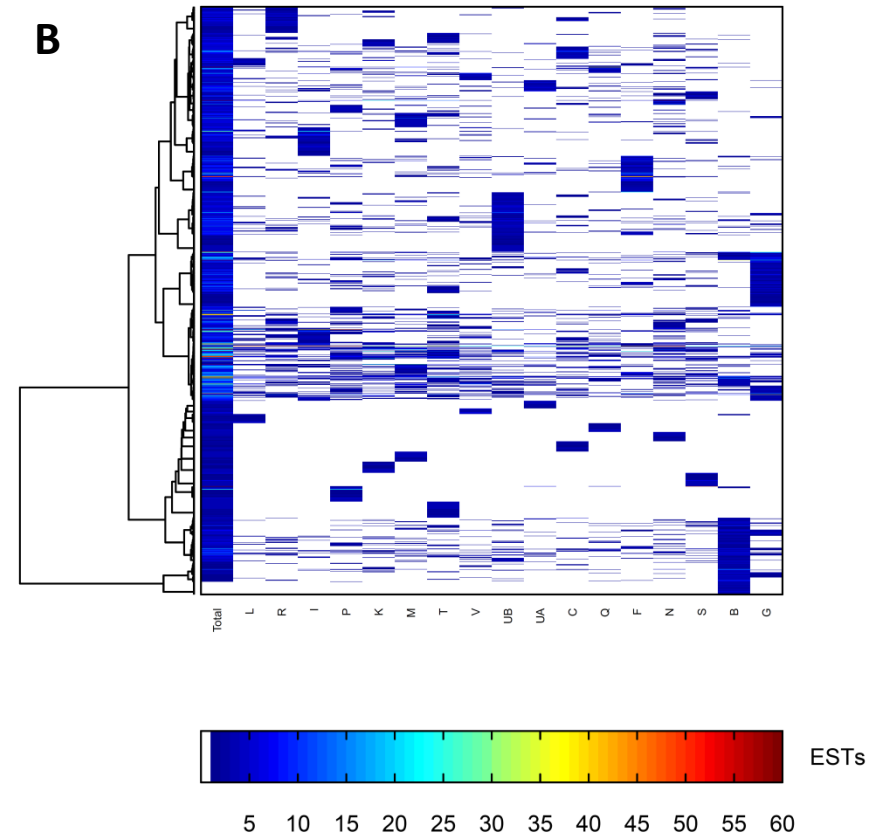
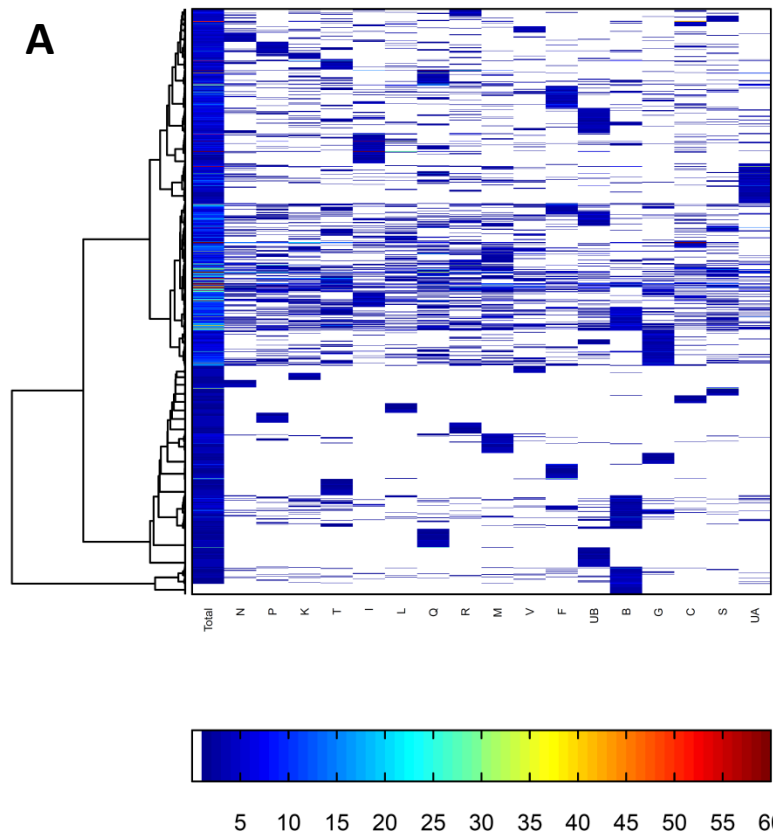
The 500 most significantly regulated mapped genes were imported into MapMan 3.5.1 and classified accordingly. Clusters revealed seasonal function of wood rays. A, Genes up-regulated in summer. B, Genes up-regulated in early spring.



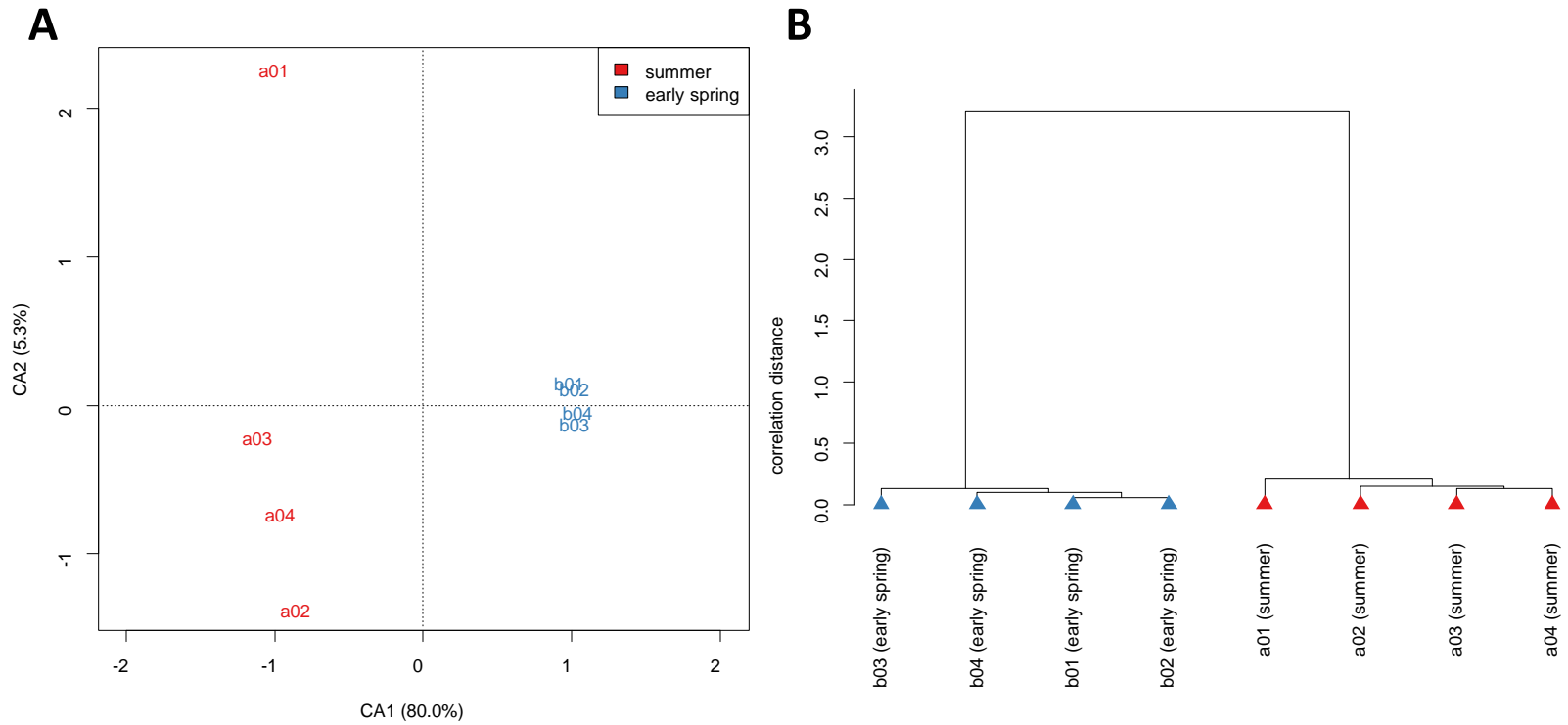
**Supplemental Figure S3.** KEGG pathway coverage. A, Of the 2,707 genes annotated in the 115 KEGG-pathways, 2,063 (76.2 %) genes representing 101 pathways were found within the 15,365 mapped genes on the chip. In turn only 13.4 % of the mapped chip genes are covered by KEGG pathways. B, The 2,063 KEGG pathway genes shown in A, to be represented on the poplar chip covered only 19 % of the 500 most significantly regulated genes.



**Supplemental Figure S4.** GO enrichment analysis of biological processes (competitive test). In total 1,075 pathways have been analyzed. All significant pathways (after multiple testing correction) are represented by the negative decadic logarithm of the enrichment p-value (i.e. longer bars represent more significant pathways). Coloring depicts the higher level cellular process of each pathway. A, Pathways up-regulated in summer. B, Pathways up-regulated in early spring.



**Supplemental Figure S5:** Comparison of rays with other seasonal array analyses. Digital northern heat map generated using the PopGenIE eNorthern tool showing the frequency of occurrence of genes up-regulated in dormant rays (A) and in active rays (B) within the expressed sequence tag (EST) libraries represented at PopulusDB (Sterky *et al.*, 2004; <http://www.populus.db.umu.se/>). A + B = cambial zone, UB = active cambium, dormant UA = cambium, G = tension wood, X = wood cell death, C = young leaves, I = senescing leaves, L = cold-stressed leaves, Q = dormant buds, P = petioles, Y = virusfungal-infected leaves, F = floral buds, M = female catkins, V = male catkins, K = apical shoot, T = shoot meristem, N = bark, R = roots, S = imbibed seeds (according to Sterky *et al.* 2004)



**Supplemental Figure S6.** Exploratory array analysis by hierarchical clustering and correspondence analysis (CA). Summer and early spring samples are clearly separated. A, CA (top 5% of the genes with maximal variance). B, Hierarchical Clustering (top 5% of the genes with maximal variance).

## Larisch et al., Supplemental Table S1

Summer / early spring fold changes of transcripts related to metabolites mentioned in Table 1 and Table 2

FC in blue = up-regulated in early spring, FC in red = up-regulated in summer

N-assimilation
fatty acid metabolism
cryo-protection
starch and sucrose metabolism

Probe.Set	Description	AGI	logFC	FC	P.Value	adj.P.Val
PtpAffx.141421.1.S1_at	ATSP51F   ATSP51F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups	AT5G20280	-3.003	0.125	7.847E-04	5.603E-03
PtpAffx.23657.1.S1_s_at	SUS3, ATUS3   SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	AT4G02280	-2.847	0.139	4.805E-04	3.919E-03
PtpAffx.44916.2.A1_at	SNF4, ATSNF4   SNF4 (HOMOLOG OF YEAST SUCROSE NONFERMENTING 4); protein kinase activator	AT1G09020	-2.460	0.182	9.117E-06	2.784E-04
PtpAffx.208804.1.S1_at	SUT2, ATUC3, SUC3, ATUT2   SUT2 (SUCROSE TRANSPORTER 2); sucrose transmembrane transporter	AT2G02860	-1.495	0.355	2.318E-03	1.272E-02
PtpAffx.163121.1.S1_at	AtcwiNV2   AtcwiNV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds	AT3G52600	-7.892	0.004	6.112E-11	4.695E-07
PtpAffx.103096.1.S1_at	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	AT4G34860	-3.867	0.069	1.489E-06	9.097E-05
Ptp.5816.1.S1_at	invertase/pectin methyltransferase inhibitor family protein	AT5G62360	-4.950	0.032	3.770E-05	6.857E-04
PtpAffx.8465.1.S1_at	invertase/pectin methyltransferase inhibitor family protein	AT1G62760	-2.009	0.249	2.092E-03	1.174E-02
PtpAffx.93131.1.S1_at	ATAMY3, AMY3   AMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	AT1G69830	-3.846	0.070	1.929E-08	1.098E-05
PtpAffx.212918.1.S1_s_at	ATPU1, ATLDA, PU1   ATLDA (LIMIT DEXTRINASE); alpha-amylase/ limit dextrinase/ pullulanase	AT5G04360	-2.937	0.131	4.804E-07	4.853E-05
Ptp.5279.1.S1_at	CT-BMY, BAM3, BMY8   CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase	AT4G17090	-4.665	0.039	8.718E-07	6.598E-05
PtpAffx.3761.4.S1_at	BMY3, BAM9   BMY3; beta-amylase/ catalytic/ cation binding	AT5G18670	-2.405	0.189	1.205E-04	1.485E-03
PtpAffx.26085.1.S1_at	LACS7, ATLACS7   LACS7 (LONG-CHAIN ACYL-COA SYNTHETASE 7); long-chain-fatty-acid-CoA ligase/ protein binding	AT5G27600	-2.883	0.136	2.099E-04	2.185E-03
PtpAffx.13681.1.S1_s_at	long-chain-fatty-acid-CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)	AT2G04350	-1.462	0.363	1.400E-02	4.841E-02
PtpAffx.13681.1.S1_s_at	long-chain-fatty-acid-CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)	AT2G04350	-1.462	0.363	1.400E-02	4.841E-02
PtpAffx.161.1.A1_at	ACX2, ATACX2   ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	AT5G65110	-1.032	0.489	6.777E-03	2.810E-02
PtpAffx.161.1.A1_at	ACX2, ATACX2   ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	AT5G65110	-1.032	0.489	6.777E-03	2.810E-02
PtpAffx.208467.1.S1_at	IBR3   IBR3 (IBA-RESPONSE 3); acyl-CoA dehydrogenase/ oxidoreductase	AT3G06810	-2.357	0.195	2.119E-04	2.196E-03
Ptp.3421.2.S1_s_at	AIM1   AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase	AT4G29010	-3.031	0.122	2.274E-06	1.205E-04
PtpAffx.111009.1.S1_at	ECHIA, E-COAH-2   ECHIA (ENOYL-COA HYDRATASE/ISOMERASE A); catalytic	AT4G16210	-1.848	0.278	1.496E-05	3.903E-04
PtpAffx.111009.1.S1_at	ECHIA, E-COAH-2   ECHIA (ENOYL-COA HYDRATASE/ISOMERASE A); catalytic	AT4G16210	-1.848	0.278	1.496E-05	3.903E-04
Ptp.1540.1.S1_a_at	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	AT2G05710	-2.238	0.212	2.767E-05	5.675E-04
Ptp.1540.1.S1_a_at	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	AT2G05710	-2.238	0.212	2.767E-05	5.675E-04
PtpAffx.2015.1.S1_s_at	ICL   ICL (ISOCITRATE LYASE); catalytic/ isocitrate lyase	AT3G21720	-5.317	0.025	1.795E-07	3.030E-05
PtpAffx.2015.1.S1_s_at	ICL   ICL (ISOCITRATE LYASE); catalytic/ isocitrate lyase	AT3G21720	-5.317	0.025	1.795E-07	3.030E-05
Ptp.7022.1.S1_at	MLS   MLS (MALATE SYNTHASE); malate synthase	AT5G03860	-4.131	0.057	1.925E-05	4.515E-04
PtpAffx.52508.1.S1_x_at	PGK   PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase	AT1G79550	-2.049	0.242	8.882E-06	2.737E-04
PtpAffx.52508.1.S1_x_at	PGK   PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase	AT1G79550	-2.049	0.242	8.882E-06	2.737E-04
PtpAffx.18295.2.A1_s_at	GAPC, GAPC-1, GAPC1   GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1)	AT3G04120	-3.054	0.120	4.831E-04	3.936E-03
PtpAffx.18295.2.A1_s_at	GAPC, GAPC-1, GAPC1   GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1)	AT3G04120	-3.054	0.120	4.831E-04	3.936E-03
Ptp.6563.2.S1_at	fructose-bisphosphate aldolase, putative	AT2G36460	-1.072	0.476	4.237E-03	1.982E-02
Ptp.6081.1.S1_at	glucose-6-phosphate isomerase, cytosolic (PGIC)	AT5G42740	-1.080	0.473	3.493E-04	3.106E-03
PtpAffx.3724.1.A1_at	AtGolS2   AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups	AT1G56600	-4.194	0.055	2.825E-04	2.663E-03
PtpAffx.82184.1.S1_at	ATQC, QC, QCT   QC (GLUTAMINYL CYCLASE); catalytic/ glutaminyl-peptide cyclotransferase	AT4G25720	4.284	19.477	8.634E-07	6.567E-05
PtpAffx.116307.1.S1_at	glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase	AT3G24090	4.310	19.832	9.755E-06	2.911E-04
PtpAffx.2469.1.A1_at	ASN3   ASN3 (ASPARAGINE SYNTHETASE 3); asparagine synthase (glutamine-hydrolyzing)	AT5G10240	1.253	2.384	1.204E-03	7.729E-03
PtpAffx.249.322.1.S1_a_at	GS2, GLN2, ATGSL1   GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	AT5G35630	1.485	2.799	2.653E-02	7.947E-02
PtpAffx.25006.1.S1_at	NIR1, NIR, ATHNIR   NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming)	AT2G15620	5.936	61.222	4.128E-08	1.455E-05
Ptp.5714.1.S1_at	ATNRT2.5   ATNRT2.5 (nitrate transporter 2.5); nitrate transmembrane transporter	AT1G12940	4.120	17.385	4.779E-06	1.922E-04
Ptp.5930.1.S1_s_at	NIA1, GNR1, NR1   NIA1 (NITRATE REDUCTASE 1); nitrate reductase	AT1G77760	5.886	59.121	5.687E-06	2.116E-04
PtpAffx.205004.1.S1_at	CNX2   CNX2 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2); catalytic	AT2G31955	1.421	2.678	5.123E-04	4.089E-03
PtpAffx.102478.1.A1_at	NIA2, B29, NIA2-1, CHL3, NR, NR2, ATNR2   NIA2 (NITRATE REDUCTASE 2); nitrate reductase (NADH)/ nitrate reductase	AT1G37130	2.255	4.772	2.977E-03	1.528E-02