Table S4. Complete list of refereces for table 2

Function Specific process	id	Unigene annotation	Arabidopsis AGI	Arabidopsis_thaliana_proteins most similar description	Arab Gene Name	Arab Gene Symbol	Hormone signaling	Sugar signaling/partioning	Hormone and secondary metabolite biosynthesis regulation	Cell wall and cytoesqueleton related	Cell polarity	References
k-means9												
Cytoskeleton organization and biogenesis												
Microtubule stability and organization	PPN077E06	Microtubule-associated protein	AT3G04630	protein with KLEEK protein-protein interaction domain	WVD2-LIKE 1	WDL1				Negative regulator of microtubule structure and stability		[1]
Protein degradation												
Ubiquitin ligase E3 complex/SFC-culin	PPN032H05	Cullin	AT4G02570	cullin family protein	AUXIN RESISTANT 6 ;CULLIN 1	AXR6/CUL1	AUX nuclear signaling					[2-4]
RNA transcription regulation												
MYB-family	PPN055C11	Sucrose responsive element binding protein	AT5G67300	myb family transcription factor	ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 44	MYBR1/MYB44	ABA, AUX, ET	Sucrose responsive element binding protein				[5-8]
Signal transduction pathway												
G-protein coupled receptor protein signaling pathway/G-protein complex	PPN065B10	Guanine nucleotide binding protein (G-protein), alpha subunit family protein	AT1G31930	extra-large guanine nucleotide binding protein, putative / G-protein	EXTRA-LARGE GTP-BINDING PROTEIN 3	XLG3	ABA, AUX, ET	sugar sensitivity				[9, 10]
Phosphorylation cascades/MAPK	PP1009F07	Trichoderma-induced protein kinase	AT3G45640	mitogen-activated protein kinase	MITOGEN-ACTIVATED PROTEIN KINASE 3	MPK3	positive regulation of ACS type I		positive regulation of ACS type I	pectin induced		[11-14]
Phosphorylation cascades/MAPKKK	PPN071C11	protein kinase family protein / ankyrin repeat family protein	AT1G14000	protein kinase family protein / ankyrin repeat family protein	VH1-INTERACTING KINASE	VIK	AUX and BR singaling	sugar partioning and homeostasis		vascular formation,		[15, 16]
Phosphorylation cascades/PP2A	PPN014G07	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	AT3G25800	serine/threonine protein phosphatase 2A 65 KDa regulatory subunit A	PROTEIN PHOSPHATASE 2A SUBUNIT A2	PDF1/PP2AA2	Regulates PIN subcellular distribution				cell polarity	[17, 18]
Trafficking machinery and membrane dynamics												
CME;Vesicle coat/ clathrin coated vesicles	PP1003H08	Putative Clathrin coat assembly protein AP50	AT5G46630	clathrin adaptor complexes medium subunit family protein	ADAPTOR PROTEIN-2 MU-ADAPTIN	AP2M	AUX signaling;regulates cellular auxin levels by controlling the abundance and distribution of PIN proteins at the plasma membrane			regulates cellulose synthesis controlling the abundance and distribution of active CESA complexes at the plasma membrane	Cell polarity regulation	[19, 20]
Fatty acid biosyntheis	PPN026B01	Carboxyl transferase alpha subunit	AT2G38040	acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family	ACETYL CO-ENZYME A CARBOXYLASE CARBOXYLTRANSFERASE ALPHA SUBUNIT	CAC3			fatty acid biosynthesis			[21]
Glycerolipid biosynthesis	PPN008G03	Digalactosyldiacylglycerol synthase 1, chloroplast precursor	AT3G11670	digalactosyldiacylglycerol synthase 1	DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1	DGD1			digalactosyl diacylglycerol biosynthesis		polar targeting of proteins to the plasma membrane;Lipid microdomains	[22-25]
Glycerolipid metabolism	PPN065F12	phosphatidic acid phosphatase-related / PAP2-related	AT3G50920	phosphatidic acid phosphatase-related / PAP2-related	LIPID PHOSPHATE PHOSPHATASE EPSILON 1	LPPEPSILON1			diacylglycerol biosynthesis			[26]
Phospholipid biosynthesis	PPN008H07	Putative phospholipid cytidylyltransferase	AT2G38670	ethanolamine-phosphate cytidylyltransferase	PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1	PECT1			phosphoethanolamine biosynthesis		polar targeting of proteins to the plasma membrane;Lipid microdomains	[23-25, 27]
trans-Golgi network transport vesicle/ COPI vesicles	PPN002C04	ARF GTPase-activating domain-containing protein	AT5G13300	ARF GTPase-activating domain-containing protein	VASCULAR NETWORK DEFECTIVE 3;SCARFACE	VAN3/SFC	AUX transport regulation;required for either normal PIN1 cycling or for PID-directed efflux machinery relocation			regulates formation of plant vascular networks	Cell polarity regulation	[28, 29]
Transport												
carbohydrate transport	PP1003F09	Integral membrane protein,	AT1G75220	vacuolar glucose exporter	ERD6-LIKE 6	ERDL6		sugar partioning and homeostasis				[30]

Cl-channel	PPN078A03	Cl-channel, voltage gated; IMP dehydrogenase related 1	AT5G33280	chloride channel-like protein	CHLORIDE CHANNEL G	CLCG					
Na/K antiporter	PPN064A01	Na+/H+ antiporter	AT2G01980	sodium proton exchanger,	SALT OVERLY SENSITIVE 1	SOS1					[31-33]
nitrate transport	PPN024D02	Nitrate transporter NRT1-2	AT1G18880	proton-dependent oligopeptide transport family protein	NITRATE TRANSPORTER 1.9	NRT1.9					
oligopepetide transport	PPN005F03	Oligopeptide transporter 7	AT4G10770	oligopeptide transporter OPT family protein	OLIGOPEPTIDE TRANSPORTER 7	OPT7					
	PPN064F08	POT family, putative	AT1G59740	proton-dependent oligopeptide transport (POT) family protein		NRT1/NPF4.3					
Unknown transporter	PPN066F09	Putative integral membrane protein	AT5G19980	Golgi-localized nucleotide-sugar transporter	GOLGI NUCLEOTIDE SUGAR TRANSPORTER 4	GONST4		sugar partioning and homeostasis		is probably involved in the provision of GDP-Fuc and GDP-l-Gal sugars into the Golgi for cell wall polysaccharide synthesis such as RG-II and XyG	[34-36]
Unknown function											
Unknown interferon protein	PPN065A05	interferon-related developmental regulator family protein	AT1G27760	interferon-related developmental regulator family protein	SALT-TOLERANCE 32	SAT32	ABA				[37]
Unkown Zinc finger RING-like	PP1003D02	ubiquitin ligase	AT3G23280	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein	XB3 ORTHOLOG 5 IN ARABIDOPSIS THALIANA	XBAT35	ET regualtion,ABA, AUX	glucose			[38, 39]
k-means2											
Aminoacid metabolism											
Alanine and Aspartate metabolism	PPN065C10	Putative aspartate aminotransferase	AT1G80360	methionine-specific aminotransferase	REVERSAL OF SAV3 PHENOTYPE 1	VAS1			Negative regulation of Trp-IAA and ET biosynthesis		[40]
	PPN080E12	Putative aspartate aminotransferase	AT1G80360	methionine-specific aminotransferase	REVERSAL OF SAV3 PHENOTYPE 1	VAS1			Negative regulation of Trp-IAA and ET biosynthesis		[40]
Cell wall related											
cellulose biosynthesis	PPN046D09	Cellulose synthase-like protein CslG	AT1G55850	cellulose synthase family protein	CELLULOSE SYNTHASE LIKE E1	CSLE1				SCW biosynthesis;hemicellulose biosynthesis	[41]
Hemicellulose biosynthesis	PPN036E12	Glycosyltransferase	AT4G36890	glycosyl transferase family 43 protein	IRREGULAR XYLEM 14	IRX14				SCW biosynthesis;hemicellulose glucuronoxylan biosyntheis (SCW)	[42]
Hemicellulose degradation	PP1002E04	Alpha-L-arabinofuranosidase / beta-D-xylosidase	AT5G49360	bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase	BETA-XYLOSIDASE 1	BXL1				Pectin metabolism;trim b-xylan and a-arabinan side groups from the RG I.	[43]
Pectin degradation	PPN041B11	Polygalacturonase-inhibiting protein	AT5G06860	polygalacturonase inhibiting protein 1	POLYGALACTURONASE INHIBITING PROTEIN 1	PGIP1				inhibition of degradation of the polygalacturonan	
	PPN047G10	Polygalacturonase-like protein	AT4G23500	Pectin lyase-like superfamily protein							
pectin methyl-esterification	PP1004E01	Putative pectinesterase	AT2G26440	pectinesterase family protein,							
	PPN001F02	pectinacetylesterase family protein	AT5G23870	pectinacetylesterase family protein							
	PPN066B05	Ripening-related protein-like	AT5G51520	invertase/pectin methylesterase inhibitor family protein..							
UDP-L-arabinose, UDP-galacturonate and UDP-xylose Biosynthesis	PPN062D06	UDP-arabinose 4-epimerase 1	AT1G30620	NAD-dependent epimerase/dehydratase family protein	UDP-D-XYLOSE 4-EPIMERASE 1 ;MURUS 4	UXE1/MUR4		Sugar signaling		arabionoglactan biosynthesis	[44-47]
Protein degradation											

protease	PP1004E07	Putative serine protease	AT5G67360	cucumisin-like serine protease	subtilisin-like serine protease 1.7	SBT1.7/ARA12			indirectly affects the pectin methylation status of mucilage and/or the primary cell wall		[48]
	PPN009E02	Cysteine protease 14	AT4G35350	cysteine endopeptidase	XYLEM CYSTEINE PEPTIDASE 1	XCP1			SCW biosynthesis;postive regulation of thacheray element differentialion		[49]
RNA transcription regulation											
LUG-family	PP1003C09	STY-L protein	AT2G32700	WD-40 repeat family protein	MUCILAGE-MODIFIED 1 ;LEUNIG_HOMOLOG	MUM1/LUH			control mucilage production and extrusion		[50-52]
	PPN076D05	Transcriptional corepressor LEUNIG	AT4G32551	WD-40 repeat family protein (LEUNIG)	LEUNIG	LUG	AUX signaling regulator		control mucilage production and extrusion		[50-54].
NAC-family	PPN054B06	No apical meristem (NAM) protein-like	AT4G28500	no apical meristem (NAM) family protein	NAC DOMAIN CONTAINING PROTEIN 73 ;SECONDARY WALL-ASSOCIATED NAC DOMAIN PROTEIN 2	anac073/SND2			SCW biosynthesis;postive regulator of lignin, cellulose and hemicellulose biosyntehsis		[55, 56].
WRKY-family	PPN059A06	WRKY 13	AT2G37260	WRKY family transcription factor	TRANSPARENT TESTA GLABRA 2 ;WRKY family transcription factor 44	TTG2/WRKY44		anthocyanin /proanthocyanin polimerization regulation	mucilage production regulation,		[57]
Secondary metabolism											
Anthocyanin metabolism	PPN007E12	Anthocyanidin 3-O-glucosyltransferase	AT3G50740	UDPG:coniferyl alcohol glucosyltransferase	UDP-GLUCOSYL TRANSFERASE 72E1	UGT72E1			SCW biosynthesis;lignin biosynthesis		[58]
Carotenoid metabolism	PP1005H08	Zeaxanthin epoxidase, chloroplast precursor	AT5G67030	zeaxanthin epoxidase	ABA DEFICIENT 1 ;LOW EXPRESSION OF OSMOTIC STRESS-RESPONSIVE GENES 6 ;NON-PHOTOCHEMICAL QUENCHING 2 ;ARABIDOPSIS THALIANA ZEAXANTHIN EPOXIDASE ;ZEAXANTHIN EPOXIDASE ;IMPAIRED IN BABA-INDUCED STERILITY 3 ;ARABIDOPSIS THALIANA ABA DEFICIENT 1	ABA1/LOS6/ZEP	ABA biosynthesis		mucilage production regulation		[59, 60]
ET biosynthesis	PPN004H06	1-aminocyclopropane-1-carboxylate synthase 1	AT3G61510	1-aminocyclopropane-1-carboxylate synthase	ACC SYNTHASE 1	ACS1		ET biosynthesis			[61]
Phenylpropanoid metabolism	PPN025B05	Cinnamoyl CoA reductase	AT1G15950	cinnamoyl-CoA reductase	CINNAMOYL COA REDUCTASE 1 ; IRREGULAR XYLEM 4	CCR1/IRX4			SCW biosynthesis;lignin biosythesis		[62]
	PPN053B11	Cinnamyl alcohol dehydrogenase	AT4G37980	Cinnamyl alcohol dehydrogenase	ELICITOR-ACTIVATED GENE 3-1 ;CINNAMYL-ALCOHOL DEHYDROGENASE 7	ELI3-1/CAD7			SCW biosynthesis;lignin biosythesis		[63]
Sterol metabolism	PPN012F12	delta(14)-sterol reductase	AT3G52940	delta(14)-sterol reductase	FACKEL ; HYDRA 2	FK/HYD2	AUX and ET crosstalk;regulate auxin transporters localization in plasma membrane microdomains lipid microdomain formation and in the secretion machinery.		cellulose, callose and lignin, vascular development	polar targeting of proteins to the plasma membrane;Lipid microdomains	[64-67]
	PPN063B12	Helix-turn-helix, AraC type	AT4G37760	squalene monooxygenase	SQUALENE EPOXIDASE 3	SQE3					
Terpene metabolism	PPN068G10	Beta-amyrin synthase	AT1G78950	beta-amyrin synthase	BETA-AMYRIN SYNTHASE	BAS					

Signal transduction pathway												
ABA signaling/ Ca signal transducer	PPN069F09	Putative serine/threonine protein kinase PK11-C1	AT4G33950	similar to abscisic acid-activated protein kinase	OPEN STOMATA 1 ;SUCROSE NONFERMENTING 1-RELATED PROTEIN KINASE 2-6	OST1//SRK2E/SNRK2-6	ABA	Sucrose metabolism regulation				[68-71]
ABA signaling/ABF phosphorylation	PPN010B11	Serine-threonine protein kinase, putative	AT1G78290	serine/threonine protein kinase	SNF1-RELATED PROTEIN KINASE 2.8 ;SNF1-RELATED PROTEIN KINASE 2C	SNRK2.8/SRK2C	ABA	sucrose signaling				[72, 73]
Phosphorylation cascades/metabolic switch	PPN054E02	AKIN beta3	AT2G28060	5'-AMP-activated protein kinase beta-2 subunit protein		KINβ3	ABA	sucrose signaling				[72-75]
Trafficking machinery and membrane dynamics												
ER to Golgi	PP1003D05	Root hair defective 3	AT3G13870	root hair defective 3	GOLGI MUTANT 8 ;ROOT HAIR DEFECTIVE 3	RHD3/GOM8	AUX, ET			required for cell wall biosynthesis and actin organization	Cell polarity regulation	[76, 77]
sphingolipid metabolism	PPN021D05	similar to alkaline ceramidase	AT1G07380	ceramidase family protein					Ceramide biosynthesis/degradation		polar targeting of proteins to the plasma membrane;Lipid microdomains	[66, 67, 78, 79]
	PPN031D01	similar to alkaline ceramidase	AT1G07380	ceramidase family protein					Ceramide biosynthesis/degradation		polar targeting of proteins to the plasma membrane;Lipid microdomains	[66, 67, 78, 79]
Transport												
AUX efflux to the apoplast	PPN070B12	Multidrug resistance protein 11	AT3G28860	ATP-binding cassette (ABC) transporters	MULTIDRUG RESISTANCE PROTEIN 11 ;P-GLYCOPROTEIN 19 ATP-BINDING CASSETTE B19	PGP19/MDR11/ABCB19	AUX transport					[80-83]
AUX transport into ER	PP1004E09	Auxin Efflux Carrier family protein.	AT2G17500	Endoplasmic reticulum auxin efflux carrier family protein	PILS5	PILS5	AUX transport					[84, 85]
	PPN075H08	Auxin Efflux Carrier family protein.	AT5G01990	Endoplasmic reticulum auxin efflux carrier family protein	PILS6	PILS6	AUX transport					[84, 85]
carbohydrate transport	PPN046B03	Sorbitol transporter	AT3G18830	plasma membrane-localized polyol/cyclitol/monosaccharide-H+-symporter	ARABIDOPSIS THALIANA POLYOL/MONOSACCHARIDE TRANSPORTER 5 ;POLYOL/MONOSACCHARIDE TRANSPORTER 5 ;POLYOL TRANSPORTER 5	PMT5/PLT5		sugar partioning and homeostasis				
Cooper transport	PPN040A04	Copper transport protein-like	AT5G59040	copper transporter family protein	COPPER TRANSPORTER 3	COPT3						
ion transporter activity	PPN016B02	Senescence-associated	AT2G17840	senescence/dehydration-associated protein-related	EARLY-RESPONSIVE TO DEHYDRATION 7	ERD7						
metal-ion transport	PP1005G08	Metal tolerance protein C2	AT3G12100	cation efflux family protein / metal tolerance protein	METAL TRANSPORT PROTEIN 5	MTP5						
	PPN007G12	Metal transporter Nramp3	AT2G23150	NRAMP metal ion transporter 3	NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 3	ATNRAMP3						
oligopepetide transport	PPN029A02	Putative peptide transporter	AT3G01350	proton-dependent oligopeptide transport family protein								
k-means1												
Energy production												
plasma membrane ATP production	PPN027C11	Plasma membrane proton ATPase	AT1G17260	proton-exporting ATPase 10	AUTOINHIBITED H-ATPASE ISOFORM 10	AHA10			proanthocyanidin transport and polymerization			[86, 87]
RNA transcription regulation												
b-HLH family	PPN080F10	Prf interactor 30137	AT2G27230	similar to basic helix-loop-helix(bHLH)-domain protein	LONESOME HIGHWAY	LHW	AUX signaling			Vascular establisment, maintenance, cell number and pattern		[88]
HB-family	PPN069A12	BEL1-like homeodomain transcription factor	AT2G35940	BEL1-like homeobox 4 protein	BEL1-LIKE HOMEODOMAIN 1	BLH1						[89, 90]
Signal transduction pathway												
AUX signaling/ AUX receptor E3 ubiquitin ligase SFC-TIR	PPN078E01	TRANSPORT INHIBITOR RESPONSE 1 protein	AT3G62980	E3 ubiquitin ligase SCF complex F-box subunit	TRANSPORT INHIBITOR RESPONSE 1	TIR1	AUX nuclear signaling					[2, 3]

AUX signaling/Nuclear signaling pathway	PPN078G01	Putative auxin-resistance protein	AT1G05180	auxin-resistance protein 1	AUXIN RESISTANT 1	AXR1	AUX nuclear signaling				[2-4]
Calcium signaling/ Calcium sensor-transducer	PPN027B08	Calcium-dependent protein kinase	AT3G57530	calcium-dependent protein kinase	CALCIUM-DEPENDENT PROTEIN KINASE 32	CPK32	ABA				[91]
Calcium signaling/Calcium signal transducer	PPN013H01	Serine/threonine kinase	AT5G58380	CBL-interacting protein kinase 10	CBL-INTERACTING PROTEIN KINASE 10 ;SNF1-RELATED PROTEIN KINASE 3.8 ;SOS3-INTERACTING PROTEIN 1 ;	CIPK10/SIP1/SNRK3.8	ABA				[92]
	PPN020F10	CBL-interacting protein kinase	AT4G30960	CBL-interacting protein kinase 6	CBL-INTERACTING PROTEIN KINASE 6 ;SOS3-INTERACTING PROTEIN 3 ;SNF1-RELATED PROTEIN KINASE 3.14	SNRK3.14/CIPK6/SIP3	ABA	sucrose signaling			[72, 73]
ET signaling	PPN057C10	Ethylene signaling protein	AT5G03280	ethylene-insensitive 2	ETHYLENE INSENSITIVE 2	EIN2	ABA;positive regulator of ET signaling		positive regulator of ACS type I and negative regulator of ACS type II	Vascular cel division regulation	[93-102]
ET signaling/ Culin E3 ubiquitin ligase	PPN020G10	Ethylene-overproduction protein 1	AT3G51770	tetratricopeptide repeat (TPR)-containing protein	ETHYLENE OVERPRODUCER 1	ETO1	repressor of ET biosynthesis (inhibits type II ACS)		repressor of ET biosynthesis (inhibits type II ACS)	vascular cell division	[102-104]
Phosphorylation cascades/MAPK	PPN020H02	Mitogen-activated protein kinase 4	AT4G01370	mitogen-activated protein kinase 4	MAP KINASE 4	MPK4				Negative regulator of microtubule structure and stability; negative regulate MAP65-1	[105]
Phosphorylation cascades/metabolic switch	PPN008G11	AKIN gamma	AT3G48530	CBS domain-containing protein	SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA	KING1	ABA	sucrose signaling			[72-75]
Phosphorylation cascades/PP2A	PPN037E11	Ser/thr protein phosphatase 2A regulatory subunit B' gamma isoform	AT4G15415	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B'gamma	B' regulatory subunit of PP2A	ATB'GAMMA			Yang Cycle regulation		[106]
Transport											
carbohydrate transport	PPN025D11	SLT1 protein	AT3G12570	HSP20-like chaperones superfamily protein	FYD	FYD		sugar partioning and homeostasis			
	PPN078G04	Putative membrane transporter	AT2G43330	Proton myo-inositol co-transporter	INOSITOL TRANSPORTER 1	INT1		sugar partioning and homeostasis			
Cooper transport	PPN025H09	Putative copper-transporting ATPase 3	AT1G63440	copper-exporting ATPase	HEAVY METAL ATPASE 5	HMA5					
ion channel	PPN023C11	MscS-Like mechanosensitive ion channel	AT5G10490	mechanosensitive ion channel domain-containing protein	MSCS-LIKE 2	MSL2					
Mg transport	PPN001H12	MRS2-5	AT2G03620	magnesium transporter CorA-like family protein	MAGNESIUM TRANSPORTER 3	MGT3					
oligopepetide transport	PPN015D04	Metal-nicotianamine transporter YSL6	AT3G27020	oligopeptide transporter OPT family protein	YELLOW STRIPE LIKE 6	YSL6					
	PPN028F10	Oligopeptide transporter OPT superfamily	AT5G55930	oligopeptide transporter OPT family protein	OLIGOPEPTIDE TRANSPORTER 1	OPT1					
	PPN035B10	Oligopeptide transporter 7	AT4G10770	oligopeptide transporter OPT family protein	OLIGOPEPTIDE TRANSPORTER 7	OPT7					
	PPN057F10	Oligopeptide transporter-like protein	AT3G54450	proton-dependent oligopeptide transport (POT) family protein							
k-means11											
Aminoacid metabolism											
GABA biosynthesis	PPN044B12	Glutamate decarboxylase, putative	AT3G17760	glutamate decarboxylase, putative, similar to glutamate decarboxylase GB:Q07346 (Petunia x hybrid...	glutamate decarboxylase 5 (GAD5),	GAD5					[107]
Pyruvate and Reactive carbonyl species											
conversion of oxalacetate to PEP	PP1002C02	Phosphoenolpyruvate carboxykinase [ATP]	AT4G37870	phosphoenolpyruvate carboxykinase (ATP), putative / PEP carboxykinase, putative / PEPCK, putative...	PHOSPHOENOLPYRUVATE CARBOXYKINASE 1 , PHOSPHOENOLPYRUVATE CARBOXYKINASE ,	PEPCK;PCK1					
Pyruvate conversion to acetyl-CoA	PPN054C12	Pyruvate dehydrogenase	AT1G59900	pyruvate dehydrogenase E1 component alpha subunit	PYRUVATE DEHYDROGENASE COMPLEX E1 ALPHA SUBUNIT ;PYRUVATE DEHYDROGENASE COMPLEX E1 ALPHA	PDHE1-A					

					SUBUNIT					
	PPN059C05	Pyruvate dehydrogenase E1 beta subunit isoform 3	AT5G50850	pyruvate dehydrogenase E1 component beta subunit	MACCI-BOU ,	MAB1/PDHE1-				
pyruvate-lactate interconversions	PP1006E06	Aldehyde dehydrogenase, putative	AT1G44170	aldehyde dehydrogenase	ALDEHYDE DEHYDROGENASE 3H1 , ALDEHYDE DEHYDROGENASE 4	ALDH4;ALDH3H1	ABA			[108]
	PPN035E06	Aldehyde dehydrogenase	AT1G44170	aldehyde dehydrogenase	ALDEHYDE DEHYDROGENASE 3H1 , ALDEHYDE DEHYDROGENASE 4	ALDH4;ALDH3H1	ABA			[108]
	PPN038B05	Aldehyde dehydrogenase, putative	AT1G44170	aldehyde dehydrogenase	ALDEHYDE DEHYDROGENASE 3H1 , ALDEHYDE DEHYDROGENASE 4	ALDH4;ALDH3H1	ABA			[108]
k-means5										
Aminoacid metabolism										
cyanide detoxification	PPN075E10	Beta-cyanoalanine synthase 1	AT3G61440	encodes a cysteine synthase isomer	CYSTEINE SYNTHASE C1	CYSC1				[109]
methionine metabolism	PPN034A06	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 4	AT5G43850	acireductone dioxygenase [iron(II)-requiring] activity	acireductone dioxygenase 4	ARD4		Yang Cycle	associated to vascular tissue	[110, 111]
	PPN034C12	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3	AT4G14710	acireductone dioxygenase [iron(II)-requiring] activity	acireductone dioxygenase 2	ARD2		Yang Cycle	associated to vascular tissue	[110, 111]
	PPN072E05	Cystathionine gamma synthase	AT3G01120	cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS), identical t...	METHIONINE OVERACCUMULATION 1 (MTO1), CYSTATHIONINE GAMMA-SYNTHASE (CGS), A. THALIANA CYSTATHIONINE GAMMA-SYNTHASE 1 (ATCYS1), CYSTATHIONINE GAMMA-SYNTHASE 1 (CGS1),	MTO1;CGS1				[112]
Antioxidant system										
GLUTHATHIONE-GLUTAREDOXIN AND THIOREDOXIN REDOX HOMEOSTASIS	PPN039H11	Glutathione S-transferase	AT5G17220	glutathione S-transferase	TRANSPARENT TESTA 19 ;GLUTATHIONE S-TRANSFERASE PHI 12	TT19/GSTF12		proanthocyanin monomer transporter		[113, 114]
Cytoskeleton organization and biogenesis										
actin microfilament-actin depolimerization	PPN047E05	Actin depolymerizing factor 2	AT5G59880	actin-depolymerizing factor 3	ACTIN DEPOLYMERIZING FACTOR 3	ADF3				[115, 116]
Microtubule-Microtubule binding and stabilization	PPN073D05	MICROTUBULE-ASSOCIATED PROTEINS	AT5G55230	MICROTUBULE-ASSOCIATED PROTEINS	MICROTUBULE-ASSOCIATED PROTEINS 65-1	MAP65-1				[117, 118]
Microtubule-microtubule organization and formation	PPN075E12	Tubulin folding cofactor B	AT3G10220	tubulin folding cofactor B	EMBRYO DEFECTIVE 2804	EMB2804/TFC				[119]
RNA transcription regulation										
AP2/EREBP family	PPN054F05	AP2-related transcription factor	AT5G47220	ethylene response factor subfamily B-3 of ERF/AP2 transcription factor	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2	ERF2	ET signaling		vascular cell division	[102, 120]
AUX/IAA family	PPN014H03	Auxin-induced protein AUX28	AT1G04250	auxin-responsive protein / indoleacetic acid-induced protein 17	INDOLE-3-ACETIC ACID INDUCIBLE 17 ;AUXIN RESISTANT 3	AXR3/IAA17	AUX and ABA nuclear signaling; negative regulator			[121]
	PPN057F01	AUX/IAA protein	AT4G29080	auxin-responsive protein / indoleacetic acid-induced protein 27	INDOLE-3-ACETIC ACID INDUCIBLE 27 ;PHYTOCHROME-ASSOCIATED PROTEIN 2	PAP2/IAA27	AUX nuclear signaling;negative regulator			[122, 123]
LIM-family	PPN009B01	Pollen-specific protein SF3, putative	AT1G10200	transcription factor LIM, putative	widely expressed LIM protein 1	WLIM1				[124]
	PPN069C01	Transcription factor lim1	AT1G10200	transcription factor LIM, putative	widely expressed LIM protein 1	WLIM1		Actin stabilizing protein	Actin stabilizing protein	[124]
MADS-box family	PP1006G03	MADS-box transcription factor	AT5G60910	agamous-like MADS box protein AGL8 / FRUITFULL	FRUITFULL ;AGAMOUS-LIKE 8	FUL/AGL8		positive regulatior of caroterne and anthocyanin biosynthesis,	negative regulation of lignin	[125-128]
	PPN042H02	MADS4	AT4G18960	floral homeotic protein AGAMOUS (AG), contains an ACG start codon	AGAMOUS	AG	ET up-regulation	postisitive carotene biosynthesis regulation;	negative regulation of lignin	[129-131]

				(Riechmann, Ito, and Meyerowitz...						biosynthesis		
RNA translation and protein assembly												
regulation of protein biosynthesis	PPN006H04	Translationally-controlled tumor protein homolog	AT3G16640	translationally controlled tumor family protein	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN	TCTP	AUX cytoplasmic signaling	Sugar signaling		Cell wall biosynthesis regulation		[132, 133]
Secondary metabolism												
Anthocyanin metabolism	PpLDOX (PpLDOX)	leucoanthocyanidin dioxygenase				PpLDOX			flavonoid/proanthocyanin biosynthesis			[134]
	PPN055C03	Anthocyanidin reductase	AT1G61720	dihydroflavonol 4-reductase	BANYULS	BAN			proanthocyanin biosynthess			[134]
Aspartate biosyntheis	PPN046D06	1-aminocyclopropane-1-carboxylate synthase	AT1G62960	aminotransferase with broad specificity for aspartate and aromatic amino acids	ACC SYNTHASE 10	ACS10						[135]
Carotenoid metabolism	PPN006A10	Phytoene synthase	AT5G17230	phytoene synthase	PHYTOENE SYNTHASE	PSY						
	PPN067A01	Capsanthin/capsorubin synthase, chloroplast precursor	AT3G10230	lycopene beta cyclase	LYCOPENE CYCLASE	LYC						
cyanide detoxification	PP1000E01	Cyanate hydratase	AT3G23490	cyanate lyase family	CYANASE	CYN						[136]
	PPN066B01	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein;	AT5G12040	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein								[109, 137]
Flavonoid metabolism	PPN050G05	Dihydroflavonol 4-reductase-like	AT5G58490	cinnamoyl-CoA reductase family					flavonoid/proanthocyanin biosynthesis			[138]
	PPN052H09	Chalcone synthase 2	AT5G13930	naringenin-chalcone synthase	CHALCONE SYNTHASE ;TRANSPARENT TESTA 4	CHS/TT4	negative regulation of auxin transport					[139, 140]
Signal transduction pathway												
Cytoplasmic TOR signaling	PPN076G10	protein LETHAL WITH SEC THIRTEEN 8-2	AT3G18140	transducin family protein / WD-40 repeat family protein	LETHAL WITH SEC THIRTEEN 8-1	LST8-1	AUX cytoplasmic signaling	Sugar signaling		Cell wall biosynthesis regulation		[133, 141]
ET signaling/ET signal transduction	PPN011G11	GTP-binding protein	AT3G46060	Ras-related protein/ small GTP-binding protein	RAB GTPASE HOMOLOG 8A	ARA3/RAB8A	ET signaling					[142]
Trafficking machinery and membrane dynamics												
CME;Early endosome;internalization and intracellular trafficking of PM proteins	PPN011F03	Clathrin_L-chain	AT2G40060	clathrin light chain	CLATHRIN LIGHT CHAIN 2	CLC2	AUX signaling;regulates cellular auxin levels by controlling the abundance and distribution of PIN proteins at the plasma membrane				Cell polarity regulation	[143]
CME;internalization and intracellular trafficking of PM proteins	PPN017G03	Calcium-binding EF-hand	AT3G01780	cytokinesis adaptor protein targeted to the cell plate		TPLATE	AUX signaling;regulates cellular auxin levels by controlling the abundance and distribution of PIN proteins at the plasma membrane			regulation of cellulose synthesis by controlling the abundance of active CESA complexes at the plasma membrane	Cell polarity regulation	[144, 145]
Endosomal sorting complex	PPN060A04	Putative endosomal Vps protein complex subunit	AT5G22950	SNF7 family protein	Vacuolar protein-sorting-associated protein 24	VPS24.1	required for internalize PIN1, PIN2, and AUX1 to the MVB/late for vacuolar degradation					[146]
Golgy to ER/ COPI vesicles	PPN044E10	ARF-like small GTPase 1	AT2G47170	ADP-ribosylation factor 1	ADP-ribosylation factor 1 AC1/bfa-visualized exocytic trafficking defective1	ARF1A1C/BEX1	Essential for recycling of PIN auxin transporters to the plasma membrane and for vacuolar targeting				cell polarity	[147]
Retromer complex;Late endosome to vacuole	PPN007G03	Sorting nexin-like protein	AT5G06140	phox (PX) domain-containing protein	SORTING NEXIN 1	SNX1	Regulates both the recycling vacuolar sorting receptors (VSR) from the TGN/EE to the ER and the balance between vacuolar degradation and recycling of PIN					[148, 149]

							proteins		
	PPN023B01	Ras-related protein Rab7	AT3G18820	Ras-related GTP-binding protein	RAB GTPASE HOMOLOG G3F	RABG3F/RAB7B			[150]
k-means8									
Aminoacid metabolism									
AUX biosynthesis	PPN058D11	Anthranilate synthase beta subunit	AT1G25220	anthranilate synthase beta subunit	ANTHRANILATE SYNTHASE BETA SUBUNIT 1	ASB1	AUX biosynthesis		[151]
RNA transcription regulation									
AUX/IAA family	PP1009D02	IAA16 protein	AT1G04250	auxin-responsive protein / indoleacetic acid-induced protein 17	INDOLE-3-ACETIC ACID INDUCIBLE 17 ;AUXIN RESISTANT 3	AXR3/IAA17	AUX and ABA nuclear signaling; negative regulator		[121]
	PPN060G07	AUX/IAA protein	AT1G04240	auxin-responsive protein / indoleacetic acid-induced protein 3	INDOLE-3-ACETIC ACID INDUCIBLE 3;SHORT HYPOCOTYL 2	IAA3/SHY2	AUX nuclear signaling;negative regulator		[152]
HD-ZIP family	PPN074H05	HB2 homeodomain protein	AT4G35550	homeobox-leucine zipper protein (HB-2) / HD-ZIP protein	WUSCHEL RELATED HOMEOBOX 13	HB-4/WOX13	AUX regulated	SCW biosynthesis;negative regulator lignin biosynthesis	[153, 154]
MYB-family	PPN067A04	MYB-like DNA-binding domain protein	AT4G38620	myb family transcription factor	MYB DOMAIN PROTEIN 4	MYB4		SCW biosynthesis;negative regulator lignin biosynthesis	[155]
Signal transduction pathway									
ET signaling/ET receptor	PPN054G06	Ethylene receptor	AT3G04580	Ethylene receptor, subfamily 2.	ETHYLENE INSENSITIVE 4	EIN4	ET signaling		[99, 156, 157]
Transport									
Cooper transport	PPN035H02	Copper-transporting ATPase RAN1	AT5G44790	copper-exporting ATPase / responsive-to-antagonist 1	RESPONSIVE-TO-ANTAGONIST 1 ;	RAN1	ET signaling; delivers cooper ion into the ET receptors;is required for both ET binding and the receptor functionality		[158]

Abreviatures: AUX:auxin; ET; ethylene; ABA: Abcisic acid; PM:plasma membrane;CW: cell wall; SCW: secondary cell wall; ER: endoplasmic reticulum; MVB/ LE:microvesicular body/ late endosome; TGN/ EE:trans-golgy network/ early endosome; VSR:vacuolar sorting receptors VN:vascular networks; PA: proanthocyanines; PIN; PIN formed auxin efflux carrier; RG:rhamnogalacturonan; XyG:xyloglucan

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