

Table S1. Screened key DEPs

Protein Description	Gene name	R3/R1	R4/R3
Plant Hormone			
Histidine-containing phosphotransfer protein 1	AHP1	0.5611	1.5958
Absciscic acid receptor PYR1	PYR1	0.6509	1.1888
Absciscic acid receptor PYR9	PYL9	2.6765	0.8963
Absciscic acid receptor PYL8	PYL8	2.1238	0.8772
Serine/threonine-protein kinase SRK2B	SRK2B	1.5381	0.9534
ABSCISIC ACID-INSENSITIVE 5-like protein 5	ABF2	2.2512	0.9011
REDOX state			
Putative respiratory burst oxidase homolog protein H	RBOHH	1.3905	2.1763
Rhodanese-like domain-containing protein 15	STR15	1.1015	2.0785
L-ascorbate peroxidase 2	APX2	2.3173	0.7459
Probable glutathione S-transferase	DHAR2	0.6495	1.8374
Superoxide dismutase [Cu-Zn] 2	SODCC.2	2.0041	0.9698
ATP sulfurylase 2	APS2	0.5183	0.7859
Iron-sulfur assembly protein IscA-like 1	At2g16710	1.5874	1.39
ATP sulfurylase 1	APS1	0.5153	0.9158
Catalase	CAT1	1.1907	1.7114
Superoxide dismutase [Fe] 2	FSD2	0.6827	0.6892
Copper chaperone for superoxide dismutase	CCS	1.3974	0.6586
Selenium-binding protein 2	SBP2	1.6917	1.3908
Frataxin	FH	1.3937	1.281
Glutathione hydrolase 3	GGT3	0.8574	0.7493

Puromycin-sensitive aminopeptidase	MPA1	1.0622	0.5792
Glutathione S-transferase L3	GSTL3	1.031	1.7687
Probable glutathione S-transferase	HSP26-A	1.6967	1.7482
Probable phospholipid hydroperoxide glutathione peroxidase 6	GPX6	1.8502	0.8935
Phosphoenolpyruvate carboxylase 4	PPC4	0.8299	1.8925
Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform	G6PDH	1.3513	1.1709
Inactive glucose-6-phosphate 1-dehydrogenase 4, chloroplastic	G6PD4	0.7129	0.8884
6-phosphogluconate dehydrogenase, decarboxylating 2	PGD2	1.2506	1.3556
Spermine synthase	SPMS	2.6394	0.8586
Ion channel			
Calcium-transporting ATPase 9	ACA9	0.5319	0.6051
Calcium-transporting ATPase	LCA1	0.5779	--
Plasma membrane ATPase 4	PMA4	0.368	0.8838
Cyclic nucleotide-gated ion channel 1	CNGC1	0.6078	0.9517
Cation-chloride cotransporter 1	CCC1	0.5679	0.7385
Aquaporin PIP2-7	PIP2-7	0.6062	1.3758
Aquaporin PIP1-1	PIP1-1	0.5014	1.6361
Sodium/proton antiporter 1	NHD1	0.5581	1.2936
Cytoskeleton			
Tubulin alpha chain	TUBA	0.644	0.788
LIM domain-containing protein WLIM2b	WLIM2B	0.5023	0.7093
Probable F-actin-capping protein subunit beta	At1g71790	0.6023	0.9675

Tubulin beta-1 chain	TUBB1	0.5376	0.6527
Myosin-8	XI-B	0.4928	0.9572
65-kDa microtubule-associated protein 6	MAP65-6	0.8981	0.6556
Actin-depolymerizing factor 6	ADF6	1.5217	0.6024
Kinesin-like protein KIN-13A	KIN13A	0.5297	0.8289
LIM domain-containing protein WLIM1	WLIM1	0.1169	0.6703
Tubulin beta-5 chain	TUBB5	0.6433	0.6466
Kinesin-like protein KIN-13B	KIN13B	0.49	--
F-actin-capping protein subunit alpha	At3g05520	0.5058	0.8297
Microtubule-associated protein RP/EB family member 1B	EB1B	0.6859	0.5256
65-kDa microtubule-associated protein 1	MAP65-1	0.5382	0.5485
Actin-depolymerizing factor 1	ADF1	0.8797	0.7094
Protein MOR1	MOR1	0.8406	0.7595
Cell wall			
Cellulose synthase A catalytic subunit 1	CESA1	0.2912	--
Cellulose synthase A catalytic subunit 3	CESA3	0.1919	--
Cellulose synthase A catalytic subunit 4	CESA4	0.1430	--
Probable glycosyltransferase STELLO1	STL1	0.4531	0.2396
Probable xyloglucan 6-xylosyltransferase 5	XXT5	0.6381	0.8683
Xyloglucan 6-xylosyltransferase 1	XXT1	0.8617	0.6481
Probable beta-1,4-xylosyltransferase IRX14H	IRX14H	0.1470	0.6732
Protein PECTIC ARABINO GALACTAN SYNTHESIS-	PAGR	0.6869	0.6151

---

RELATED

UDP-glucuronate 4-epimerase 1	GAE1	0.6279	0.6508
Protein trichome birefringence-like 39	TBL39	0.3172	0.9079
Protein trichome birefringence-like 38	TBL38	0.5921	0.7677
Protein trichome birefringence-like 36	TBL36	0.0829	--
Protein REDUCED WALL ACETYLTATION 2	RWA2	0.617	0.9341
Pectin acetylesterase 8	PAE8	0.9879	0.6295
Pectin acetylesterase 12	PAE12	1.2769	0.5451
Probable pectin methylesterase CGR2	CGR2	0.3377	1.0972
Laccase-7	LAC7	1.2410	5.3646
Peroxidase21	PER21	0.7680	2.2727
Peroxidase47	PER47	7.8685	1.3266
Peroxidase42	PER42	0.6130	0.6621
Peroxidase3	PER3	1.9856	0.3876
Glucose-1-phosphate adenylyltransferase small subunit 2	AGPP	2.6307	0.4312
Glucose-1-phosphate adenylyltransferase large subunit 1	AGPS1	1.102	0.6369
Protein MANNAN SYNTHESIS-RELATED 1	MSR1	0.5165	0.5443
Mannan endo-1,4-beta-mannosidase 7	MAN7	2.1778	0.9709
UDP-glucuronic acid decarboxylase 1	UXS1	0.7076	0.7585
UDP-glucuronic acid decarboxylase 2	UXS2	0.6148	1.1564
Probable arabinosyltransferase ARAD1	ARAD1	0.6285	1.072
UDP-N-acetylglucosamine diphosphorylase 2	GLCNAC-1PUT2	0.7766	0.1882

---

Probable pectin methyltransferase QUA2	QUA2	0.5844	1.1118
Protein CELLULOSE SYNTHASE INTERACTIVE 1	CSI1	0.3088	0.4690
Uclacyanin 1	UCC1	0.8461	0.2328
Exocyst complex component EXO70B1	EXO70B1	0.8349	0.7663

---