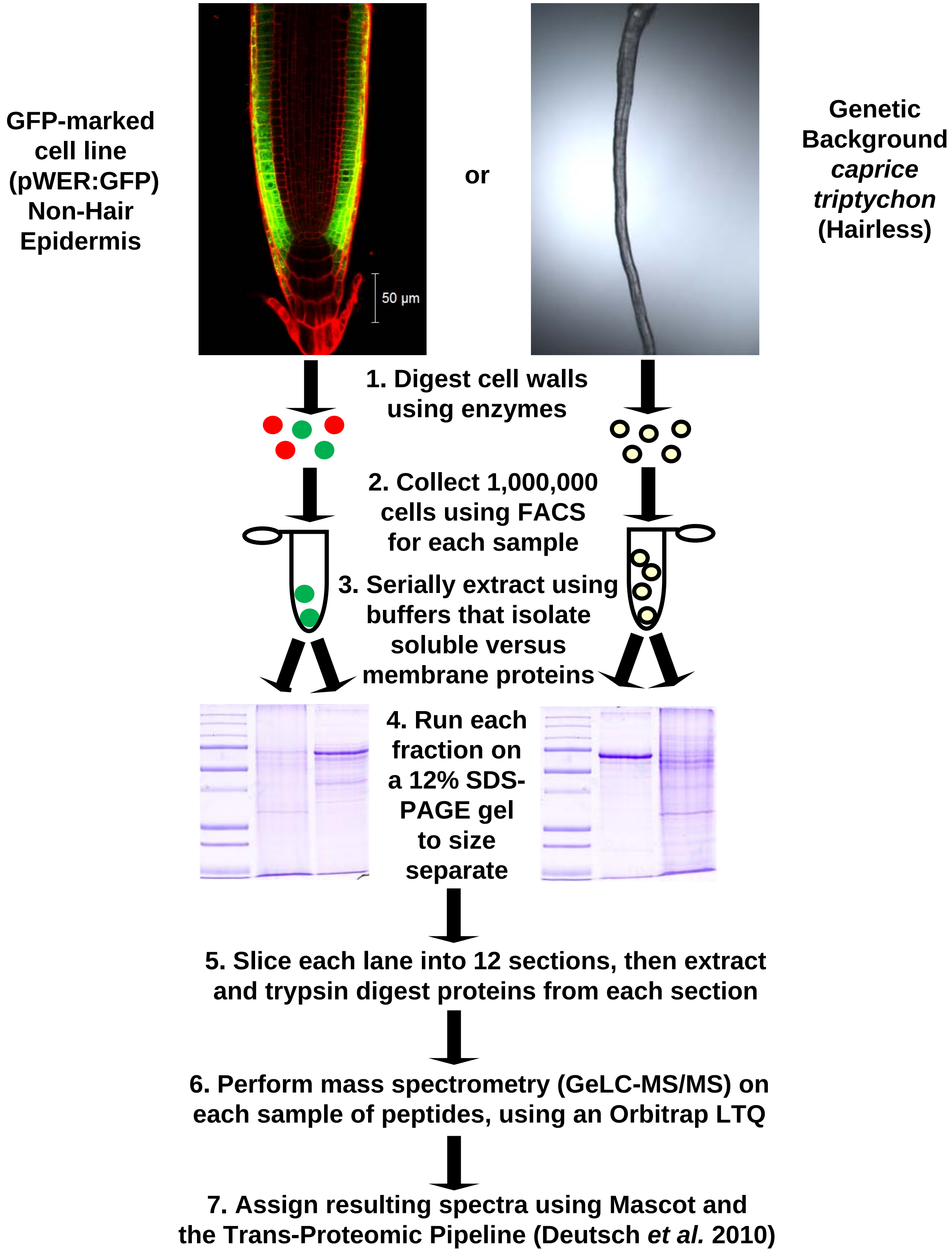
Supplementary Figure S1.
GeLC-MS/MS Proteomics Approach of this Study



GFP-marked
cell line
(pWER:GFP)
Non-Hair
Epidermis

or

Genetic
Background
caprice
triptychon
(Hairless)

1. Digest cell walls using enzymes

2. Collect 1,000,000 cells using FACS for each sample

3. Serially extract using buffers that isolate soluble versus membrane proteins

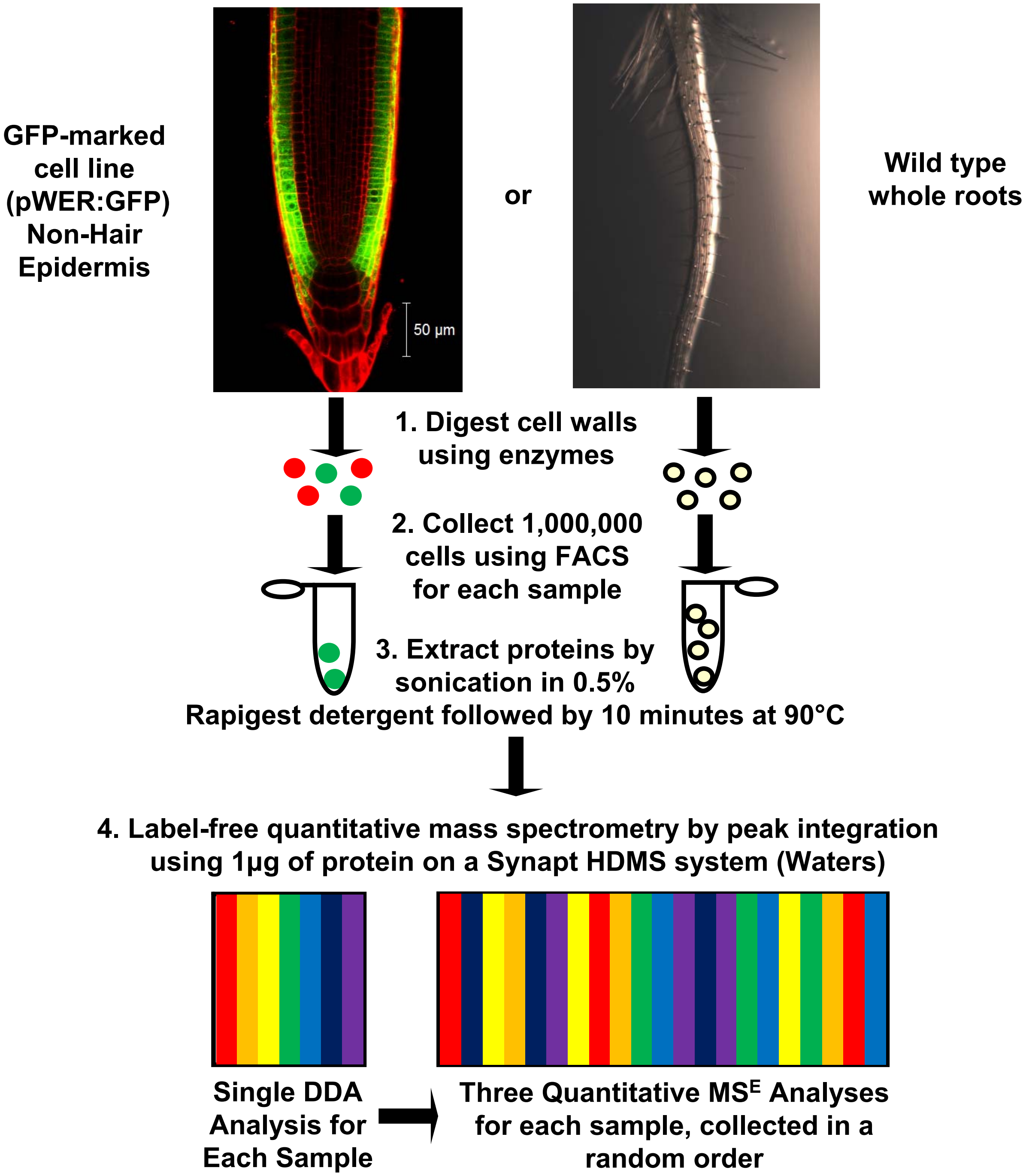
4. Run each fraction on a 12% SDS-PAGE gel to size separate

5. Slice each lane into 12 sections, then extract and trypsin digest proteins from each section

6. Perform mass spectrometry (GeLC-MS/MS) on each sample of peptides, using an Orbitrap LTQ

7. Assign resulting spectra using Mascot and the Trans-Proteomic Pipeline (Deutsch *et al.* 2010)

Supplementary Figure S2.
Peak-Integration Proteomics Approach of this Study



GFP-marked
cell line
(pWER:GFP)
Non-Hair
Epidermis

or

Wild type
whole roots

1. Digest cell walls using enzymes

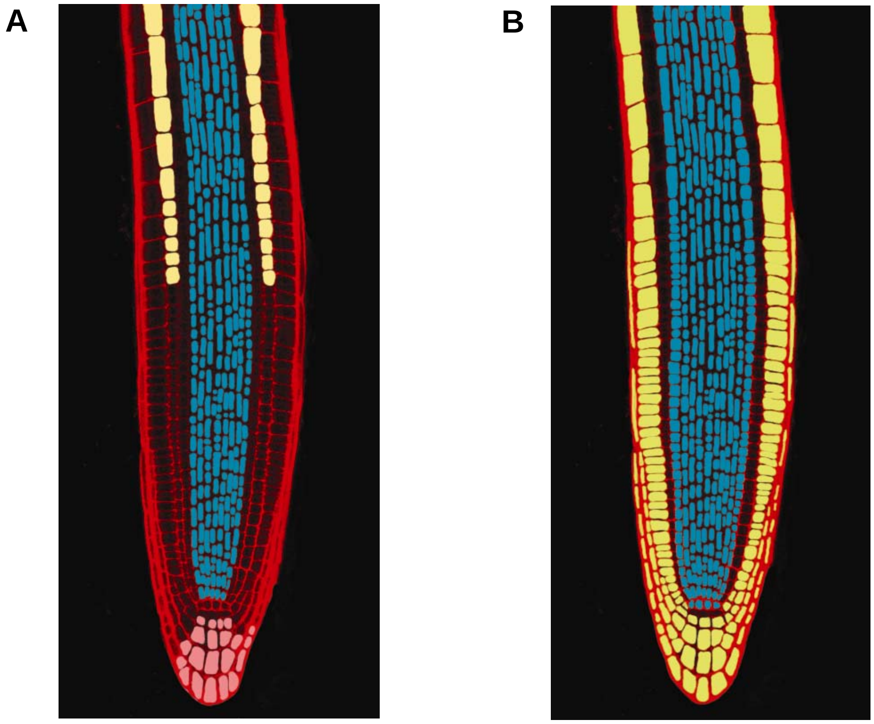
2. Collect 1,000,000 cells using FACS for each sample

3. Extract proteins by sonication in 0.5% Rapigest detergent followed by 10 minutes at 90°C

4. Label-free quantitative mass spectrometry by peak integration using 1μg of protein on a Synapt HDMS system (Waters)

Single DDA Analysis for Each Sample

Three Quantitative MS^E Analyses for each sample, collected in a random order



Supplementary Figure S3. Cell-type localization of PINFORMED auxin transporters and members of the TAILLESS complex.

(A) Schematic depicting the localization of PINFORMED (PIN) auxin transporters. Light yellow, blue, and pink cells correspond to cortex, vascular, and columella cells, respectively, where PIN2, PIN1, and PIN3, respectively were detected by shotgun proteomics. A single unique peptide was identified for PIN2 in the cortex. Localizations of PIN1, PIN2, and PIN3 proteins from FACS coupled with shotgun proteomics agree with published localizations.

(B) Schematic depicting the differential localization of members of the TAILLESS complex based on the root cellular proteome. Blue cells display the localization of alpha, beta, delta, epsilon, eta, and gamma subunits in the endodermal, quiescent, and vascular cells. Yellow cells display the complementary localization of the theta subunit in non-hair epidermal and columella cells.

Description of Spatial Clusters:

Spatial Clusters were obtained based on the identification of the 1,995 proteins from the Root Cellular Proteome, which was generated from GeLC-MS/MS proteomic profiling of six root cell populations that were isolated by FACS.

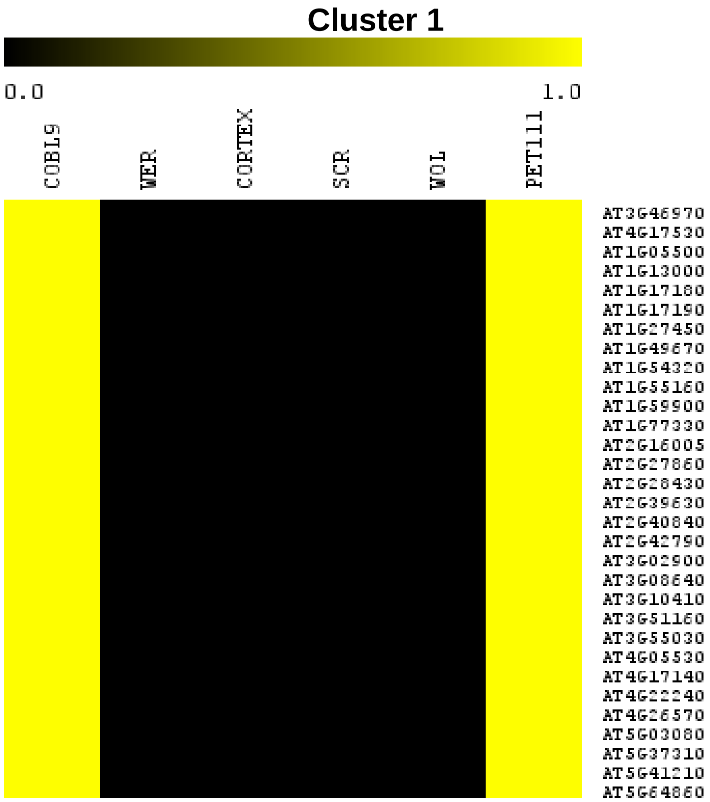
The first table is a summary of all of the binary clusters from this data and is titled “Summary of Spatial Clusters”.

Each binary spatial cluster is then shown. The data for Clusters 1-30 is provided in this document (Supplementary Figure S4), and the data for Clusters 31-60 is presented in Supplementary Figure S5. For each cluster, only unique proteins with two or more unique, high-confidence peptides are shown. A protein meeting this stringent criteria is given the value “1”, and this designation indicates the protein was detected. On the y-axis are all of the loci that were detected and belong to the given spatial cluster. Yellow denotes presence (value “1”), while black denotes absence (value “0”) of a protein in one of the following cell populations given on the x-axis of each cluster: COBL9 (Root Hairs), WER (Non-Hair Epidermis), CORTEX (Cortex), SCR (Endodermis/Quiescent Center), WOL (Vasculature), PET111 (Columella).

After the image of each spatial cluster, three tables are presented containing the following information:
(1) Loci that correspond to the proteins in that spatial cluster
(2) Gene ontology categories associated with these loci and corresponding p-value enrichment
(3) Loci corresponding to enriched gene ontology categories

Summary of Spatial Clusters

Cluster #	#proteins in cluster	Ratio of Total Proteins	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
1	31	0.0155	1					1
2	14	0.0070	1	1		1	1	
3	4	0.0020				1	1	1
4	4	0.0010		1		1		
5	266	0.1333	1	1	1	1	1	1
6	208	0.1043					1	
7	87	0.0436						1
8	42	0.0211	1	1	1		1	
9	36	0.0180	1	1	1	1	1	
10	31	0.0155	1	1			1	
11	24	0.0120	1	1				1
12	21	0.0105	1	1			1	1
13	21	0.0105	1			1	1	1
14	17	0.0085			1		1	
15	12	0.0060	1		1			1
16	8	0.0040		1	1		1	
17	8	0.0040			1	1	1	
18	6	0.0030			1		1	1
19	4	0.0020			1	1		1
20	3	0.0015		1		1	1	
21	2	0.0010		1	1	1	1	
22	2	0.0010	1	1		1		
23	148	0.0742	1				1	
24	91	0.0456	1	1	1		1	1
25	66	0.0331			1			
26	48	0.0241	1		1	1	1	1
27	48	0.0241	1		1		1	1
28	42	0.0211	1			1	1	
29	40	0.0201	1		1	1	1	
30	31	0.0155	1		1			
31	9	0.0045		1			1	
32	4	0.0020	1	1	1	1		1
33	238	0.1193	1					
34	56	0.0281		1				
35	11	0.0055		1				1
36	6	0.0030			1	1		
37	6	0.0030	1	1	1			1
38	6	0.0030				1		1
39	4	0.0020		1	1	1	1	1
40	3	0.0015	1		1	1		1
41	1	0.0005		1	1			1
42	28	0.0140				1	1	
43	26	0.0130	1	1				
44	5	0.0025	1		1	1		
45	2	0.0010	1	1	1	1		
46	1	0.0005		1		1	1	1
47	57	0.0286	1		1		1	
48	14	0.0070	1			1		
49	8	0.0040			1			1
50	8	0.0040	1	1	1			
51	22	0.0110	1				1	1
52	8	0.0040	1	1		1		1
53	5	0.0025		1	1			
54	2	0.0010	1			1		1
55	55	0.0276				1		
56	3	0.0015		1		1		1
57	20	0.0100	1	1		1	1	1
58	3	0.0015		1			1	1
59	16	0.0080					1	1
60	3	0.0015		1	1		1	1
Sum	**1995**							



Cluster 1
AT1G05500
AT1G13000
AT1G17180
AT1G17190
AT1G27450
AT1G49670
AT1G54320
AT1G55160
AT1G59900
AT1G77330
AT2G16005
AT2G27860
AT2G28430
AT2G39630
AT2G40840
AT2G42790
AT3G02900
AT3G08640
AT3G10410
AT3G46970
AT3G51160
AT3G55030
AT4G05530
AT4G17140
AT4G17530
AT4G22240
AT4G26570
AT5G03080
AT5G37310
AT5G41210
AT5G64860

Cluster 1 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004134	4-alpha-glucanotransferase activity	2	31	2.14E-06
GO:0005777	peroxisome	4	31	2.08E-05
GO:0009407	toxin catabolic process	3	31	3.01E-05
GO:0004364	glutathione transferase activity	3	31	3.73E-05
GO:0005983	starch catabolic process	2	31	1.64E-04
GO:0000025	maltose catabolic process	1	31	0.001486454
GO:0005976	polysaccharide metabolic process	1	31	0.001486454
GO:0009635	response to herbicide	1	31	0.001486454
GO:0042351	'de novo' GDP-L-fucose biosynthetic process	1	31	0.001486454
GO:0005829	cytosol	3	31	0.001972938
GO:0000023	maltose metabolic process	1	31	0.002968631
GO:0004645	phosphorylase activity	1	31	0.002968631
GO:0008444	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity	1	31	0.002968631
GO:0008446	GDP-mannose 4,6-dehydratase activity	1	31	0.002968631
GO:0010297	heteroglycan binding	1	31	0.002968631
GO:0017169	CDP-alcohol phosphatidyltransferase activity	1	31	0.002968631
GO:0005773	vacuole	4	31	0.00355759
GO:0046686	response to cadmium ion	3	31	0.00726192
GO:0003999	adenine phosphoribosyltransferase activity	1	31	0.007389592
GO:0004108	citrate (SI)-synthase activity	1	31	0.007389592
GO:0006168	adenine salvage	1	31	0.007389592
GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	1	31	0.008854752
GO:0005513	detection of calcium ion	1	31	0.010315679
GO:0006099	tricarboxylic acid cycle	1	31	0.014673155
GO:0009536	plastid	2	31	0.014996436
GO:0005739	mitochondrion	4	31	0.021030147
GO:0005737	cytoplasm	3	31	0.021183187
GO:0008654	phospholipid biosynthetic process	1	31	0.033122087
GO:0005792	microsome	1	31	0.034512405
GO:0006635	fatty acid beta-oxidation	1	31	0.034512405
GO:0016491	oxidoreductase activity	2	31	0.03974036
GO:0009505	plant-type cell wall	2	31	0.043344372
GO:0006486	protein amino acid glycosylation	1	31	0.044130994
GO:0016757	transferase activity, transferring glycosyl groups	2	31	0.062163769
GO:0007264	small GTPase mediated signal transduction	1	31	0.084401491
GO:0009941	chloroplast envelope	2	31	0.087073253
GO:0009826	unidimensional cell growth	1	31	0.104935291
GO:0009058	biosynthetic process	1	31	0.109613019
GO:0015031	protein transport	1	31	0.109613019
GO:0008150	biological_process	11	31	0.131914317
GO:0005886	plasma membrane	4	31	0.135798129
GO:0009507	chloroplast	5	31	0.136863239
GO:0003674	molecular_function	9	31	0.14124941
GO:0008152	metabolic process	2	31	0.151686486
GO:0005794	Golgi apparatus	1	31	0.158386534
GO:0009414	response to water deprivation	1	31	0.166346613
GO:0016020	membrane	3	31	0.185092935
GO:0005509	calcium ion binding	1	31	0.189009512
GO:0005525	GTP binding	1	31	0.202277795
GO:0009409	response to cold	1	31	0.213240362
GO:0006979	response to oxidative stress	1	31	0.216515556
GO:0016021	integral to membrane	1	31	0.259764834
GO:0005783	endoplasmic reticulum	1	31	0.268714086

Cluster 1 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006508	proteolysis	1	31	0.307611521
GO:0003824	catalytic activity	1	31	0.321801347
GO:0005622	intracellular	1	31	0.329031298

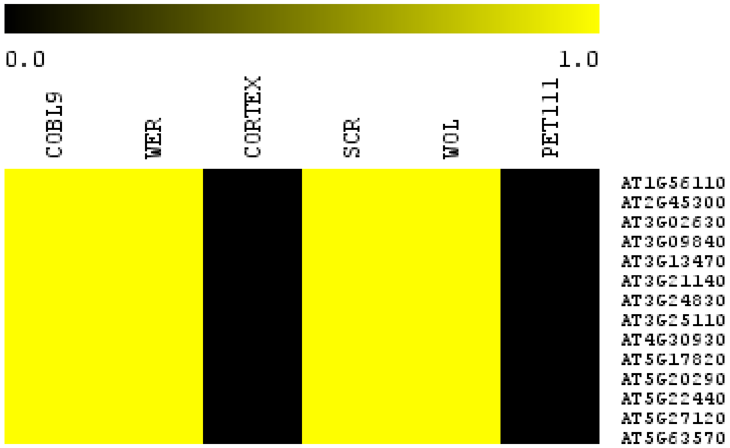
Cluster 1

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000023	1	AT2G40840					
GO:0000025	1	AT2G40840					
GO:0003674	9	AT1G05500	AT1G13000	AT1G55160	AT1G77330	AT2G16005	AT2G28430
		AT3G02900	AT3G08640	AT4G17140			
GO:0003824	1	AT5G03080					
GO:0003999	1	AT1G27450					
GO:0004108	1	AT2G42790					
GO:0004134	2	AT2G40840	AT5G64860				
GO:0004364	3	AT1G17180	AT1G17190	AT5G41210			
GO:0004645	1	AT3G46970					
GO:0004739	1	AT1G59900					
GO:0005509	1	AT4G26570					
GO:0005513	1	AT4G26570					
GO:0005525	1	AT4G17530					
GO:0005622	1	AT3G51160					
GO:0005737	3	AT1G17180	AT1G17190	AT5G41210			
GO:0005739	4	AT1G49670	AT1G55160	AT1G59900	AT3G08640		
GO:0005773	4	AT3G10410	AT4G17140	AT4G17530	AT4G26570		
GO:0005777	4	AT1G49670	AT2G42790	AT4G05530	AT5G41210		
GO:0005783	1	AT2G39630					
GO:0005792	1	AT3G55030					
GO:0005794	1	AT5G37310					
GO:0005829	3	AT1G27450	AT2G40840	AT3G46970			
GO:0005886	4	AT1G05500	AT1G27450	AT4G17530	AT4G26570		
GO:0005976	1	AT2G40840					
GO:0005983	2	AT2G40840	AT5G64860				
GO:0006099	1	AT2G42790					
GO:0006168	1	AT1G27450					
GO:0006486	1	AT2G39630					
GO:0006508	1	AT3G10410					
GO:0006635	1	AT2G42790					
GO:0006979	1	AT1G49670					
GO:0007264	1	AT4G17530					
GO:0008150	11	AT1G05500	AT1G13000	AT1G54320	AT1G55160	AT1G77330	AT2G16005
		AT2G28430	AT3G02900	AT3G08640	AT4G17140	AT5G03080	
GO:0008152	2	AT1G49670	AT1G59900				
GO:0008444	1	AT3G55030					
GO:0008446	1	AT3G51160					
GO:0008654	1	AT3G55030					
GO:0009058	1	AT2G39630					
GO:0009407	3	AT1G17180	AT1G17190	AT5G41210			
GO:0009409	1	AT1G17190					
GO:0009414	1	AT3G46970					
GO:0009505	2	AT1G27450	AT5G37310				
GO:0009507	5	AT1G27450	AT3G02900	AT3G08640	AT3G46970	AT5G64860	
GO:0009536	2	AT1G55160	AT3G08640				
GO:0009635	1	AT1G17190					
GO:0009826	1	AT3G51160					
GO:0009941	2	AT3G08640	AT3G55030				
GO:0010297	1	AT2G40840					
GO:0015031	1	AT4G17530					

Cluster 1 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)		
GO:0016020	3	AT1G54320	AT4G17530	AT5G03080
GO:0016021	1	AT5G37310		
GO:0016491	2	AT1G49670	AT4G05530	
GO:0016757	2	AT2G39630	AT3G46970	
GO:0017169	1	AT3G55030		
GO:0042351	1	AT3G51160		
GO:0046686	3	AT1G27450	AT1G59900	AT3G46970

Cluster 2



Cluster 2
AT1G56110
AT2G45300
AT3G02630
AT3G09840
AT3G13470
AT3G21140
AT3G24830
AT3G25110
AT4G30930
AT5G17820
AT5G20290
AT5G22440
AT5G27120
AT5G63570

Cluster 2 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022626	cytosolic ribosome	5	14	5.79E-08
GO:0005730	nucleolus	5	14	3.36E-07
GO:0003735	structural constituent of ribosome	4	14	2.94E-05
GO:0006412	translation	4	14	3.46E-05
GO:0005618	cell wall	4	14	3.79E-05
GO:0005840	ribosome	3	14	2.23E-04
GO:0006633	fatty acid biosynthetic process	2	14	4.41E-04
GO:0000741	karyogamy	1	14	6.71E-04
GO:0016297	acyl-[acyl-carrier-protein] hydrolase activity	1	14	0.001341767
GO:0042286	glutamate-1-semialdehyde 2,1-aminomutase activity	1	14	0.001341767
GO:0009570	chloroplast stroma	3	14	0.001464654
GO:0022625	cytosolic large ribosomal subunit	2	14	0.001957586

Cluster 2 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0042802	identical protein binding	1	14	0.002680189
GO:0045300	acyl-[acyl-carrier-protein] desaturase activity	1	14	0.003348147
GO:0000036	acyl carrier activity	1	14	6.01E-03
GO:0044267	cellular protein metabolic process	1	14	0.007338407
GO:0010181	FMN binding	1	14	0.008000542
GO:0006779	porphyrin biosynthetic process	1	14	0.009322325
GO:0005635	nuclear envelope	1	14	0.011298796
GO:0009507	chloroplast	5	14	0.01215598
GO:0051301	cell division	1	14	0.013267837
GO:0009567	double fertilization forming a zygote and endosperm	1	14	0.013922536
GO:0005819	spindle	1	14	0.014576413
GO:0016310	phosphorylation	1	14	0.014576413
GO:0009846	pollen germination	1	14	0.016533115
GO:0009553	embryo sac development	1	14	0.017833483
GO:0015934	large ribosomal subunit	1	14	0.022359031
GO:0009941	chloroplast envelope	2	14	0.023070357
GO:0009524	phragmoplast	1	14	0.024286337
GO:0009860	pollen tube growth	1	14	0.026844723
GO:0009555	pollen development	1	14	0.034442451
GO:0004601	peroxidase activity	1	14	4.25E-02
GO:0016020	membrane	3	14	0.046086677
GO:0022627	cytosolic small ribosomal subunit	1	14	0.051117931
GO:0042254	ribosome biogenesis	1	14	0.058942862
GO:0051082	unfolded protein binding	1	14	0.06310211
GO:0009416	response to light stimulus	1	14	0.067223733
GO:0016887	ATPase activity	1	14	0.071307963
GO:0005739	mitochondrion	2	14	0.078809008
GO:0006979	response to oxidative stress	1	14	0.114355257
GO:0006457	protein folding	1	14	0.120588075
GO:0009505	plant-type cell wall	1	14	0.137703646
GO:0048046	apoplast	1	14	0.139175791
GO:0046686	response to cadmium ion	1	14	0.156835983
GO:0005886	plasma membrane	2	14	0.214272038
GO:0005737	cytoplasm	1	14	0.21804863
GO:0005634	nucleus	2	14	0.218872119
GO:0005524	ATP binding	1	14	0.28263921
GO:0005515	protein binding	1	14	3.73E-01

Cluster 2

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**				
GO:0000036	1	AT3G25110				
GO:0000741	1	AT4G30930				
GO:0003735	4	AT3G24830	AT4G30930	AT5G20290	AT5G22440	
GO:0004601	1	AT5G17820				
GO:0005515	1	AT3G13470				
GO:0005524	1	AT3G13470				
GO:0005618	4	AT1G56110	AT3G09840	AT5G17820	AT5G20290	
GO:0005634	2	AT3G09840	AT3G13470			
GO:0005635	1	AT3G09840				
GO:0005730	5	AT1G56110	AT3G09840	AT3G13470	AT5G20290	AT5G22440
GO:0005737	1	AT3G09840				
GO:0005739	2	AT3G13470	AT4G30930			
GO:0005819	1	AT3G09840				
GO:0005840	3	AT4G30930	AT5G20290	AT5G22440		
GO:0005886	2	AT3G09840	AT5G20290			
GO:0006412	4	AT3G24830	AT4G30930	AT5G20290	AT5G22440	

Cluster 2 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)				
GO:0006457	1	AT3G13470				
GO:0006633	2	AT3G02630	AT3G25110			
GO:0006779	1	AT5G63570				
GO:0006979	1	AT5G17820				
GO:0009416	1	AT5G63570				
GO:0009505	1	AT5G17820				
GO:0009507	5	AT3G02630	AT3G13470	AT3G21140	AT5G20290	AT5G63570
GO:0009524	1	AT3G09840				
GO:0009553	1	AT4G30930				
GO:0009555	1	AT4G30930				
GO:0009567	1	AT4G30930				
GO:0009570	3	AT3G02630	AT3G13470	AT5G63570		
GO:0009846	1	AT3G09840				
GO:0009860	1	AT3G09840				
GO:0009941	2	AT3G13470	AT5G63570			
GO:0010181	1	AT3G21140				
GO:0015934	1	AT3G24830				
GO:0016020	3	AT3G24830	AT5G17820	AT5G20290		
GO:0016297	1	AT3G25110				
GO:0016310	1	AT3G09840				
GO:0016887	1	AT3G09840				
GO:0022625	2	AT3G24830	AT5G22440			
GO:0022626	5	AT3G09840	AT3G13470	AT3G24830	AT5G20290	AT5G22440
GO:0022627	1	AT5G20290				
GO:0042254	1	AT5G20290				
GO:0042286	1	AT5G63570				
GO:0042802	1	AT3G09840				
GO:0044267	1	AT3G13470				
GO:0045300	1	AT3G02630				
GO:0046686	1	AT3G09840				
GO:0048046	1	AT5G63570				
GO:0051082	1	AT3G13470				
GO:0051301	1	AT3G09840				

Cluster 3

Cluster 3
AT1G08480
AT1G16700
AT4G22330
AT5G18380

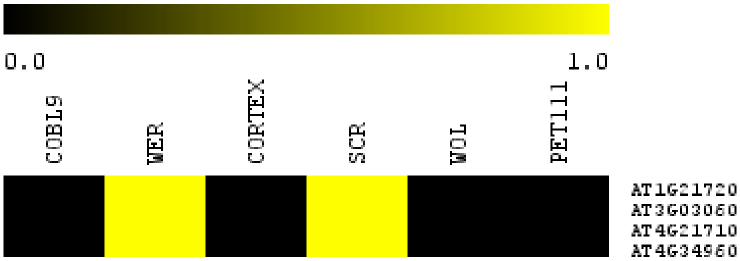
Cluster 3 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006672	ceramide metabolic process	1	4	1.92E-04
GO:0009536	plastid	1	4	0.024474187
GO:0005783	endoplasmic reticulum	1	4	0.048921054
GO:0003824	catalytic activity	1	4	0.067265162

Cluster 3 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005773	vacuole	1	4	0.079678425
GO:0005739	mitochondrion	1	4	0.131791079
GO:0016020	membrane	1	4	0.209989764
GO:0005886	plasma membrane	1	4	0.249279127

Cluster 3

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0003824	1	AT4G22330
GO:0005739	1	AT1G08480
GO:0005773	1	AT1G08480
GO:0005783	1	AT4G22330
GO:0005886	1	AT1G08480
GO:0006672	1	AT4G22330
GO:0009536	1	AT1G08480
GO:0016020	1	AT4G22330

Cluster 4



Cluster 4

AT1G21720
AT3G03060
AT4G21710
AT4G34960

Cluster 4 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016591	DNA-directed RNA polymerase II, holoenzyme	1	4	3.84E-04
GO:0005839	proteasome core complex	1	4	0.003825535
GO:0003899	DNA-directed RNA polymerase activity	1	4	0.008576504
GO:0008233	peptidase activity	1	4	0.008765829
GO:0006350	transcription	1	4	0.009144315
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	4	0.010278457
GO:0016887	ATPase activity	1	4	0.021511727
GO:0005794	Golgi apparatus	1	4	0.024104638
GO:0006511	ubiquitin-dependent protein catabolic process	1	4	0.035460181
GO:0006457	protein folding	1	4	0.037995705
GO:0009505	plant-type cell wall	1	4	0.044109724
GO:0009793	embryonic development ending in seed dormancy	1	4	0.051400566
GO:0005618	cell wall	1	4	0.055627004
GO:0003677	DNA binding	1	4	0.177307869
GO:0005886	plasma membrane	1	4	0.249279127

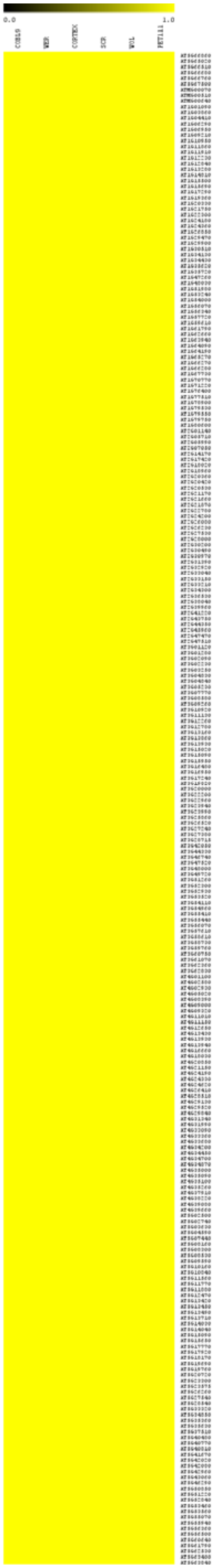
Cluster 4

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0003677	1	AT4G21710
GO:0003755	1	AT4G34960

Cluster 4 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0003899	1	AT4G21710
GO:0005618	1	AT3G03060
GO:0005794	1	AT4G34960
GO:0005839	1	AT1G21720
GO:0005886	1	AT1G21720
GO:0006350	1	AT4G21710
GO:0006457	1	AT4G34960
GO:0006511	1	AT1G21720
GO:0008233	1	AT1G21720
GO:0009505	1	AT3G03060
GO:0009793	1	AT4G21710
GO:0016591	1	AT4G21710
GO:0016887	1	AT3G03060

Cluster 5



Cluster 5

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Cluster 5

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ATMG00640

Cluster 5 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	109	263	2.63E-86
GO:0009507	chloroplast	117	263	4.42E-43
GO:0046686	response to cadmium ion	49	263	7.47E-42
GO:0005886	plasma membrane	99	263	9.14E-42
GO:0005773	vacuole	49	263	6.22E-32
GO:0009651	response to salt stress	41	263	4.31E-31
GO:0016020	membrane	74	263	1.88E-28
GO:0005783	endoplasmic reticulum	36	263	1.09E-26
GO:0009941	chloroplast envelope	38	263	1.15E-23
GO:0009570	chloroplast stroma	37	263	2.51E-23
GO:0009536	plastid	25	263	1.19E-22
GO:0005618	cell wall	26	263	1.31E-14
GO:0045271	respiratory chain complex I	12	263	1.72E-14
GO:0048046	apoplast	23	263	4.93E-14
GO:0005524	ATP binding	34	263	6.05E-13
GO:0003756	protein disulfide isomerase activity	7	263	2.73E-10
GO:0022626	cytosolic ribosome	15	263	3.07E-09
GO:0009409	response to cold	15	263	1.51E-08
GO:0006979	response to oxidative stress	15	263	2.00E-08
GO:0005743	mitochondrial inner membrane	10	263	3.21E-08
GO:0016615	malate dehydrogenase activity	5	263	3.68E-08
GO:0005741	mitochondrial outer membrane	6	263	4.10E-08
GO:0046961	proton-transporting ATPase activity, rotational mechanism	6	263	4.10E-08
GO:0000325	plant-type vacuole	7	263	4.28E-08
GO:0005759	mitochondrial matrix	7	263	5.57E-08
GO:0005750	mitochondrial respiratory chain complex III	5	263	5.50E-07
GO:0005774	vacuolar membrane	7	263	5.81E-07
GO:0009853	photorespiration	6	263	1.36E-06
GO:0008308	voltage-gated anion channel activity	4	263	1.65E-06
GO:0005730	nucleolus	14	263	1.76E-06
GO:0006633	fatty acid biosynthetic process	7	263	1.80E-06

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010319	stromule	6	263	2.05E-06
GO:0031966	mitochondrial membrane	5	263	3.00E-06
GO:0004148	dihydrolipoyl dehydrogenase activity	3	263	7.83E-06
GO:0004576	oligosaccharyl transferase activity	3	263	7.83E-06
GO:0004742	dihydrolipoyllysine-residue acetyltransferase activity	3	263	1.93E-05
GO:0005740	mitochondrial envelope	4	263	2.18E-05
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	4	263	2.94E-05
GO:0005794	Golgi apparatus	9	263	3.11E-05
GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	3	263	3.82E-05
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	3	263	3.82E-05
GO:0009505	plant-type cell wall	12	263	4.17E-05
GO:0006820	anion transport	4	263	5.00E-05
GO:0009579	thylakoid	10	263	5.12E-05
GO:0008152	metabolic process	19	263	6.32E-05
GO:0007005	mitochondrion organization	3	263	6.60E-05
GO:0008137	NADH dehydrogenase (ubiquinone) activity	3	263	6.60E-05
GO:0005777	peroxisome	8	263	7.13E-05
GO:0004353	glutamate dehydrogenase [NAD(P)+] activity	2	263	1.58E-04
GO:0004579	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	2	263	1.58E-04
GO:0004801	transaldolase activity	2	263	1.58E-04
GO:0004807	triose-phosphate isomerase activity	2	263	1.58E-04
GO:0045153	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity	2	263	1.58E-04
GO:0009793	embryonic development ending in seed dormancy	12	263	1.77E-04
GO:0006096	glycolysis	5	263	1.84E-04
GO:0006457	protein folding	10	263	2.18E-04
GO:0042742	defense response to bacterium	8	263	2.53E-04
GO:0015992	proton transport	4	263	2.81E-04
GO:0004618	phosphoglycerate kinase activity	2	263	4.69E-04
GO:0004776	succinate-CoA ligase (GDP-forming) activity	2	263	4.69E-04
GO:0010168	ER body	2	263	4.69E-04
GO:0015865	purine nucleotide transport	2	263	4.69E-04
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	3	263	6.29E-04
GO:0015986	ATP synthesis coupled proton transport	3	263	6.29E-04
GO:0018119	peptidyl-cysteine S-nitrosylation	3	263	6.29E-04
GO:0005471	ATP:ADP antiporter activity	2	263	9.27E-04
GO:0005746	mitochondrial respiratory chain	2	263	9.27E-04
GO:0006121	mitochondrial electron transport, succinate to ubiquinone	2	263	9.27E-04
GO:0006537	glutamate biosynthetic process	2	263	9.27E-04
GO:0017077	oxidative phosphorylation uncoupler activity	2	263	9.27E-04
GO:0000104	succinate dehydrogenase activity	2	263	9.27E-04
GO:0005829	cytosol	8	263	0.001221153
GO:0003989	acetyl-CoA carboxylase activity	2	263	0.001525621
GO:0004550	nucleoside diphosphate kinase activity	2	263	0.001525621
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	2	263	0.001525621
GO:0009082	branched chain family amino acid biosynthetic process	2	263	0.001525621
GO:0007030	Golgi organization	2	263	0.002259785
GO:0005789	endoplasmic reticulum membrane	3	263	0.002405861
GO:0004069	L-aspartate:2-oxoglutarate aminotransferase activity	2	263	0.003124094
GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	2	263	0.00411331

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005758	mitochondrial intermembrane space	2	263	0.00411331
GO:0016688	L-ascorbate peroxidase activity	2	263	0.00411331
GO:0004124	cysteine synthase activity	2	263	0.00522233
GO:0004332	fructose-bisphosphate aldolase activity	2	263	0.00522233
GO:0009790	embryonic development	3	263	0.006271659
GO:0019344	cysteine biosynthetic process	2	263	0.006446181
GO:0005544	calcium-dependent phospholipid binding	2	263	0.007780017
GO:0005507	copper ion binding	5	263	0.008823277
GO:0009416	response to light stimulus	5	263	0.009140701
GO:0009658	chloroplast organization	3	263	0.009355468
GO:0009705	plant-type vacuole membrane	3	263	0.010779232
GO:0003824	catalytic activity	10	263	0.011917932
GO:0006098	pentose-phosphate shunt	2	263	0.01239485
GO:0000221	vacuolar proton-transporting V-type ATPase, V1 domain	1	263	0.012610885
GO:0000327	lytic vacuole within protein storage vacuole	1	263	0.012610885
GO:0003842	1-pyrroline-5-carboxylate dehydrogenase activity	1	263	0.012610885
GO:0003867	4-aminobutyrate transaminase activity	1	263	0.012610885
GO:0003992	N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity	1	263	0.012610885
GO:0004019	adenylosuccinate synthase activity	1	263	0.012610885
GO:0004046	aminoacylase activity	1	263	0.012610885
GO:0004073	aspartate-semialdehyde dehydrogenase activity	1	263	0.012610885
GO:0004086	carbamoyl-phosphate synthase activity	1	263	0.012610885
GO:0004152	dihydroorotate dehydrogenase activity	1	263	0.012610885
GO:0004314	[acyl-carrier-protein] S-malonyltransferase activity	1	263	0.012610885
GO:0004316	3-oxoacyl-[acyl-carrier-protein] reductase activity	1	263	0.012610885
GO:0004318	enoyl-[acyl-carrier-protein] reductase (NADH) activity	1	263	0.012610885
GO:0004352	glutamate dehydrogenase activity	1	263	0.012610885
GO:0004455	ketol-acid reductoisomerase activity	1	263	0.012610885
GO:0004846	urate oxidase activity	1	263	0.012610885
GO:0005835	fatty acid synthase complex	1	263	0.012610885
GO:0006144	purine base metabolic process	1	263	0.012610885
GO:0006167	AMP biosynthetic process	1	263	0.012610885
GO:0006496	protein amino acid terminal N-glycosylation	1	263	0.012610885
GO:0006560	proline metabolic process	1	263	0.012610885
GO:0006721	terpenoid metabolic process	1	263	0.012610885
GO:0008240	tripeptidyl-peptidase activity	1	263	0.012610885
GO:0008250	oligosaccharyltransferase complex	1	263	0.012610885
GO:0009099	valine biosynthetic process	1	263	0.012610885
GO:0009317	acetyl-CoA carboxylase complex	1	263	0.012610885
GO:0010006	toc complex	1	263	0.012610885
GO:0010033	response to organic substance	1	263	0.012610885
GO:0010111	glyoxysome organization	1	263	0.012610885
GO:0010133	proline catabolic process to glutamate	1	263	0.012610885
GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	1	263	0.012610885
GO:0010285	L,L-diaminopimelate aminotransferase activity	1	263	0.012610885
GO:0015774	polysaccharide transport	1	263	0.012610885
GO:0015926	glucosidase activity	1	263	0.012610885
GO:0015928	fucosidase activity	1	263	0.012610885
GO:0016002	sulfite reductase activity	1	263	0.012610885
GO:0016018	cyclosporin A binding	1	263	0.012610885

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016040	glutamate synthase (NADH) activity	1	263	0.012610885
GO:0016631	enoyl-[acyl-carrier-protein] reductase activity	1	263	0.012610885
GO:0016710	trans-cinnamate 4-monooxygenase activity	1	263	0.012610885
GO:0016871	cycloartenol synthase activity	1	263	0.012610885
GO:0018279	protein amino acid N-linked glycosylation via asparagine	1	263	0.012610885
GO:0019320	hexose catabolic process	1	263	0.012610885
GO:0019484	beta-alanine catabolic process	1	263	0.012610885
GO:0019676	ammonia assimilation cycle	1	263	0.012610885
GO:0022900	electron transport chain	1	263	0.012610885
GO:0034387	4-aminobutyrate:pyruvate transaminase activity	1	263	0.012610885
GO:0048569	post-embryonic organ development	1	263	0.012610885
GO:0050311	sulfite reductase (ferredoxin) activity	1	263	0.012610885
GO:0051131	chaperone-mediated protein complex assembly	1	263	0.012610885
GO:0004089	carbonate dehydratase activity	2	263	0.014122644
GO:0019575	sucrose catabolic process, using beta-fructofuranosidase	2	263	0.014122644
GO:0048868	pollen tube development	2	263	0.014122644
GO:0050662	coenzyme binding	2	263	0.014122644
GO:0009826	unidimensional cell growth	4	263	0.014524935
GO:0005488	binding	11	263	0.014658811
GO:0003746	translation elongation factor activity	2	263	0.015938025
GO:0005778	peroxisomal membrane	2	263	0.017836862
GO:0006520	amino acid metabolic process	2	263	0.017836862
GO:0006807	nitrogen compound metabolic process	2	263	0.019815133
GO:0009615	response to virus	2	263	0.019815133
GO:0009695	jasmonic acid biosynthetic process	2	263	0.019815133
GO:0010051	xylem and phloem pattern formation	2	263	0.019815133
GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	1	263	0.024904895
GO:0003838	sterol 24-C-methyltransferase activity	1	263	0.024904895
GO:0003962	cystathionine gamma-synthase activity	1	263	0.024904895
GO:0004013	adenosylhomocysteinase activity	1	263	0.024904895
GO:0004075	biotin carboxylase activity	1	263	0.024904895
GO:0004128	cytochrome-b5 reductase activity	1	263	0.024904895
GO:0004347	glucose-6-phosphate isomerase activity	1	263	0.024904895
GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	1	263	0.024904895
GO:0004795	threonine synthase activity	1	263	0.024904895
GO:0006540	glutamate decarboxylation to succinate	1	263	0.024904895
GO:0008422	beta-glucosidase activity	1	263	0.024904895
GO:0009097	isoleucine biosynthetic process	1	263	0.024904895
GO:0009220	pyrimidine ribonucleotide biosynthetic process	1	263	0.024904895
GO:0009450	gamma-aminobutyric acid catabolic process	1	263	0.024904895
GO:0009865	pollen tube adhesion	1	263	0.024904895
GO:0010501	RNA secondary structure unwinding	1	263	0.024904895
GO:0015157	oligosaccharide transmembrane transporter activity	1	263	0.024904895
GO:0016041	glutamate synthase (ferredoxin) activity	1	263	0.024904895
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	1	263	0.024904895
GO:0019171	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity	1	263	0.024904895
GO:0019419	sulfate reduction	1	263	0.024904895
GO:0019773	proteasome core complex, alpha-subunit complex	1	263	0.024904895
GO:0030104	water homeostasis	1	263	0.024904895
GO:0031998	regulation of fatty acid beta-oxidation	1	263	0.024904895

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045281	succinate dehydrogenase complex	1	263	0.024904895
GO:0045703	ketoreductase activity	1	263	0.024904895
GO:0046423	allene-oxide cyclase activity	1	263	0.024904895
GO:0048598	embryonic morphogenesis	1	263	0.024904895
GO:0009617	response to bacterium	3	263	0.025918317
GO:0016126	sterol biosynthetic process	2	263	0.028445855
GO:0051082	unfolded protein binding	4	263	0.029124341
GO:0006810	transport	8	263	0.02960601
GO:0010119	regulation of stomatal movement	2	263	0.030764669
GO:0016036	cellular response to phosphate starvation	2	263	0.035571451
GO:0005509	calcium ion binding	5	263	0.036311796
GO:0001671	ATPase activator activity	1	263	0.036887979
GO:0003983	UTP:glucose-1-phosphate uridylyltransferase activity	1	263	0.036887979
GO:0003988	acetyl-CoA C-acyltransferase activity	1	263	0.036887979
GO:0003994	aconitate hydratase activity	1	263	0.036887979
GO:0004047	aminomethyltransferase activity	1	263	0.036887979
GO:0004096	catalase activity	1	263	0.036887979
GO:0004312	fatty-acid synthase activity	1	263	0.036887979
GO:0004634	phosphopyruvate hydratase activity	1	263	0.036887979
GO:0004802	transketolase activity	1	263	0.036887979
GO:0005749	mitochondrial respiratory chain complex II	1	263	0.036887979
GO:0006015	5-phosphoribose 1-diphosphate biosynthetic process	1	263	0.036887979
GO:0006090	pyruvate metabolic process	1	263	0.036887979
GO:0006406	mRNA export from nucleus	1	263	0.036887979
GO:0006465	signal peptide processing	1	263	0.036887979
GO:0009052	pentose-phosphate shunt, non-oxidative branch	1	263	0.036887979
GO:0009088	threonine biosynthetic process	1	263	0.036887979
GO:0009678	hydrogen-translocating pyrophosphatase activity	1	263	0.036887979
GO:0009920	cell plate formation involved in plant-type cell wall biogenesis	1	263	0.036887979
GO:0010008	endosome membrane	1	263	0.036887979
GO:0010255	glucose mediated signaling	1	263	0.036887979
GO:0015036	disulfide oxidoreductase activity	1	263	0.036887979
GO:0015217	ADP transmembrane transporter activity	1	263	0.036887979
GO:0015866	ADP transport	1	263	0.036887979
GO:0015867	ATP transport	1	263	0.036887979
GO:0016651	oxidoreductase activity, acting on NADH or NADPH	1	263	0.036887979
GO:0019395	fatty acid oxidation	1	263	0.036887979
GO:0031314	extrinsic to mitochondrial inner membrane	1	263	0.036887979
GO:0031359	integral to chloroplast outer membrane	1	263	0.036887979
GO:0032508	DNA duplex unwinding	1	263	0.036887979
GO:0042732	D-xylose metabolic process	1	263	0.036887979
GO:0043067	regulation of programmed cell death	1	263	0.036887979
GO:0048040	UDP-glucuronate decarboxylase activity	1	263	0.036887979
GO:0015250	water channel activity	2	263	0.043156186
GO:0000326	protein storage vacuole	1	263	0.048565988
GO:0004017	adenylate kinase activity	1	263	0.048565988
GO:0004473	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	1	263	0.048565988
GO:0005347	ATP transmembrane transporter activity	1	263	0.048565988
GO:0005753	mitochondrial proton-transporting ATP synthase complex	1	263	0.048565988
GO:0005779	integral to peroxisomal membrane	1	263	0.048565988

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005960	glycine cleavage complex	1	263	0.048565988
GO:0006207	'de novo' pyrimidine base biosynthetic process	1	263	0.048565988
GO:0006346	methylation-dependent chromatin silencing	1	263	0.048565988
GO:0006833	water transport	1	263	0.048565988
GO:0006954	inflammatory response	1	263	0.048565988
GO:0008453	alanine-glyoxylate transaminase activity	1	263	0.048565988
GO:0009060	aerobic respiration	1	263	0.048565988
GO:0009955	adaxial/abaxial pattern formation	1	263	0.048565988
GO:0016656	monodehydroascorbate reductase (NADH) activity	1	263	0.048565988
GO:0031897	Tic complex	1	263	0.048565988
GO:0006486	protein amino acid glycosylation	2	263	0.051117872
GO:0009535	chloroplast thylakoid membrane	6	263	0.056432993
GO:0003924	GTPase activity	2	263	0.059381182
GO:0004108	citrate (SI)-synthase activity	1	263	0.059944675
GO:0004340	glucokinase activity	1	263	0.059944675
GO:0004375	glycine dehydrogenase (decarboxylating) activity	1	263	0.059944675
GO:0004396	hexokinase activity	1	263	0.059944675
GO:0004449	isocitrate dehydrogenase (NAD+) activity	1	263	0.059944675
GO:0005985	sucrose metabolic process	1	263	0.059944675
GO:0006694	steroid biosynthetic process	1	263	0.059944675
GO:0008865	fructokinase activity	1	263	0.059944675
GO:0009152	purine ribonucleotide biosynthetic process	1	263	0.059944675
GO:0009648	photoperiodism	1	263	0.059944675
GO:0010183	pollen tube guidance	1	263	0.059944675
GO:0016485	protein processing	1	263	0.059944675
GO:0019464	glycine decarboxylation via glycine cleavage system	1	263	0.059944675
GO:0022621	shoot system development	1	263	0.059944675
GO:0042744	hydrogen peroxide catabolic process	1	263	0.059944675
GO:0044262	cellular carbohydrate metabolic process	1	263	0.059944675
GO:0009414	response to water deprivation	4	263	0.064410243
GO:0009926	auxin polar transport	2	263	0.065023346
GO:0006508	proteolysis	7	263	0.070710448
GO:0003878	ATP citrate synthase activity	1	263	0.071029696
GO:0004029	aldehyde dehydrogenase (NAD) activity	1	263	0.071029696
GO:0004470	malic enzyme activity	1	263	0.071029696
GO:0009086	methionine biosynthetic process	1	263	0.071029696
GO:0016652	oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	1	263	0.071029696
GO:0045037	protein import into chloroplast stroma	1	263	0.071029696
GO:0009860	pollen tube growth	2	263	0.079459339
GO:0000911	cytokinesis by cell plate formation	1	263	0.081826614
GO:0003954	NADH dehydrogenase activity	1	263	0.081826614
GO:0004356	glutamate-ammonia ligase activity	1	263	0.081826614
GO:0005742	mitochondrial outer membrane translocase complex	1	263	0.081826614
GO:0006995	cellular response to nitrogen starvation	1	263	0.081826614
GO:0008553	hydrogen-exporting ATPase activity, phosphorylative mechanism	1	263	0.081826614
GO:0009610	response to symbiotic fungus	1	263	0.081826614
GO:0009970	cellular response to sulfate starvation	1	263	0.081826614
GO:0006839	mitochondrial transport	2	263	0.082386095
GO:0009408	response to heat	3	263	0.084648801

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	2	263	0.085321391
GO:0016491	oxidoreductase activity	5	263	0.090759012
GO:0005982	starch metabolic process	1	263	0.092340899
GO:0006526	arginine biosynthetic process	1	263	0.092340899
GO:0008135	translation factor activity, nucleic acid binding	1	263	0.092340899
GO:0009646	response to absence of light	1	263	0.092340899
GO:0009901	anther dehiscence	1	263	0.092340899
GO:0016441	posttranscriptional gene silencing	1	263	0.092340899
GO:0019430	removal of superoxide radicals	1	263	0.092340899
GO:0019658	glucose catabolic process to lactate and acetate	1	263	0.092340899
GO:0042128	nitrate assimilation	1	263	0.092340899
GO:0045454	cell redox homeostasis	2	263	0.094160153
GO:0004784	superoxide dismutase activity	1	263	0.102577929
GO:0009089	lysine biosynthetic process via diaminopimelate	1	263	0.102577929
GO:0009986	cell surface	1	263	0.102577929
GO:0016559	peroxisome fission	1	263	0.102577929
GO:0030276	clathrin binding	1	263	0.102577929
GO:0042651	thylakoid membrane	1	263	0.102577929
GO:0045036	protein targeting to chloroplast	1	263	0.102577929
GO:0003690	double-stranded DNA binding	1	263	0.112542992
GO:0004743	pyruvate kinase activity	1	263	0.112542992
GO:0006014	D-ribose metabolic process	1	263	0.112542992
GO:0006099	tricarboxylic acid cycle	1	263	0.112542992
GO:0006108	malate metabolic process	1	263	0.112542992
GO:0012501	programmed cell death	1	263	0.112542992
GO:0016132	brassinosteroid biosynthetic process	1	263	0.112542992
GO:0019253	reductive pentose-phosphate cycle	1	263	0.112542992
GO:0019745	pentacyclic triterpenoid biosynthetic process	1	263	0.112542992
GO:0009555	pollen development	2	263	0.114762205
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	2	263	0.117680849
GO:0016887	ATPase activity	3	263	0.118007226
GO:0009699	phenylpropanoid biosynthetic process	1	263	0.122241288
GO:0009750	response to fructose stimulus	1	263	0.122241288
GO:0044267	cellular protein metabolic process	1	263	0.122241288
GO:0006970	response to osmotic stress	2	263	0.126370855
GO:0003697	single-stranded DNA binding	1	263	0.131677929
GO:0006730	one-carbon compound metabolic process	1	263	0.131677929
GO:0007389	pattern specification process	1	263	0.131677929
GO:0009306	protein secretion	1	263	0.131677929
GO:0009862	systemic acquired resistance, salicylic acid mediated signaling pathway	1	263	0.131677929
GO:0010075	regulation of meristem growth	1	263	0.131677929
GO:0019654	acetate fermentation	1	263	0.131677929
GO:0045309	protein phosphorylated amino acid binding	1	263	0.131677929
GO:0006800	oxygen and reactive oxygen species metabolic process	1	263	0.140857941
GO:0009737	response to abscisic acid stimulus	4	263	0.141506133
GO:0007031	peroxisome organization	1	263	0.149786267
GO:0010091	trichome branching	1	263	0.149786267
GO:0042023	DNA endoreduplication	1	263	0.149786267
GO:0042335	cuticle development	1	263	0.149786267
GO:0045087	innate immune response	1	263	0.149786267

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005737	cytoplasm	6	263	0.157277256
GO:0005874	microtubule	1	263	0.158467766
GO:0009561	megagametogenesis	1	263	0.158467766
GO:0009825	multidimensional cell growth	1	263	0.158467766
GO:0006626	protein targeting to mitochondrion	1	263	0.166907214
GO:0009504	cell plate	1	263	0.166907214
GO:0010027	thylakoid membrane organization	1	263	0.166907214
GO:0005516	calmodulin binding	3	263	0.171732168
GO:0009934	regulation of meristem organization	1	263	0.175109307
GO:0020037	heme binding	1	263	0.175109307
GO:0016021	integral to membrane	4	263	0.178805656
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	3	263	0.18275261
GO:0008483	transaminase activity	1	263	0.183078662
GO:0009225	nucleotide-sugar metabolic process	1	263	0.183078662
GO:0009749	response to glucose stimulus	1	263	0.183078662
GO:0046872	metal ion binding	2	263	0.184749739
GO:0005986	sucrose biosynthetic process	1	263	0.190819818
GO:0005839	proteasome core complex	1	263	0.198337237
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	1	263	0.198337237
GO:0051301	cell division	1	263	0.198337237
GO:0009567	double fertilization forming a zygote and endosperm	1	263	0.205635305
GO:0009742	brassinosteroid mediated signaling	1	263	0.205635305
GO:0010154	fruit development	1	263	0.205635305
GO:0010182	sugar mediated signaling	1	263	0.205635305
GO:0030244	cellulose biosynthetic process	1	263	0.205635305
GO:0005819	spindle	1	263	0.212718334
GO:0006414	translational elongation	1	263	0.212718334
GO:0006461	protein complex assembly	1	263	0.219590561
GO:0016049	cell growth	1	263	0.219590561
GO:0005792	microsome	1	263	0.226256153
GO:0006635	fatty acid beta-oxidation	1	263	0.226256153
GO:0009832	plant-type cell wall biogenesis	1	263	0.226256153
GO:0010228	vegetative to reproductive phase transition	1	263	0.226256153
GO:0048316	seed development	1	263	0.232719205
GO:0009611	response to wounding	2	263	0.238626976
GO:0009664	plant-type cell wall organization	1	263	0.238983742
GO:0009911	positive regulation of flower development	1	263	0.238983742
GO:0009553	embryo sac development	1	263	0.245053721
GO:0008219	cell death	1	263	0.262134862
GO:0009809	lignin biosynthetic process	1	263	0.262134862
GO:0009706	chloroplast inner membrane	1	263	0.267464832
GO:0007623	circadian rhythm	1	263	0.272619032
GO:0015934	large ribosomal subunit	1	263	0.282414319
GO:0003993	acid phosphatase activity	1	263	0.291548516
GO:0009524	phragmoplast	1	263	0.295876129
GO:0009744	response to sucrose stimulus	1	263	0.295876129
GO:0009845	seed germination	1	263	0.295876129
GO:0015979	photosynthesis	1	263	0.311665611
GO:0042803	protein homodimerization activity	1	263	0.311665611
GO:0007568	aging	1	263	0.32516973
GO:0008233	peptidase activity	1	263	0.328210828
GO:0016051	carbohydrate biosynthetic process	1	263	0.331123605

Cluster 5 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010287	plastoglobule	1	263	0.3339108
GO:0016829	lyase activity	1	263	0.336575103
GO:0008415	acyltransferase activity	1	263	0.357017955
GO:0046658	anchored to plasma membrane	1	263	0.358494953
GO:0004601	peroxidase activity	1	263	0.365453923
GO:0009055	electron carrier activity	1	263	0.370209883
GO:0016192	vesicle-mediated transport	1	263	0.3706885
GO:0030246	carbohydrate binding	1	263	0.370830512

Cluster 5

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000104	2	AT3G27380	AT5G66760				
GO:0000221	1	AT1G12840					
GO:0000275	1	AT5G13450					
GO:0000325	7	AT1G12840	AT1G15690	AT1G78900	AT3G42050	AT3G58730	AT4G11150
		AT4G39080					
GO:0000326	1	AT1G21750					
GO:0000327	1	AT1G21750					
GO:0000911	1	AT5G42080					
GO:0001671	1	AT3G42050					
GO:0003690	1	AT2G21660					
GO:0003697	1	AT2G21660					
GO:0003746	2	AT1G56070	AT4G02930				
GO:0003755	2	AT3G56070	AT4G34870				
GO:0003756	7	AT1G21750	AT1G35620	AT1G77510	AT2G32920	AT2G47470	AT3G54960
		AT5G60640					
GO:0003824	10	AT2G20360	AT2G30200	AT3G12260	AT3G19820	AT3G23940	AT3G52930
		AT3G53520	AT4G33360	AT4G34700	AT5G11560		
GO:0003838	1	AT5G13710					
GO:0003842	1	AT5G62530					
GO:0003867	1	AT3G22200					
GO:0003878	1	AT2G44350					
GO:0003924	2	AT1G59610	AT5G42080				
GO:0003954	1	AT5G37510					
GO:0003962	1	AT3G01120					
GO:0003983	1	AT3G03250					
GO:0003988	1	AT2G33150					
GO:0003989	2	AT2G38040	AT5G35360				
GO:0003992	1	AT1G80600					
GO:0003993	1	AT5G34850					
GO:0003994	1	AT2G05710					
GO:0004013	1	AT4G13940					
GO:0004017	1	AT5G63400					
GO:0004019	1	AT3G57610					
GO:0004028	3	AT2G14170	AT3G48000	AT5G62530			
GO:0004029	1	AT3G48000					
GO:0004046	1	AT4G38220					
GO:0004047	1	AT1G11860					
GO:0004069	2	AT2G30970	AT4G31990				
GO:0004073	1	AT1G14810					
GO:0004075	1	AT5G35360					
GO:0004086	1	AT1G29900					
GO:0004089	2	AT1G47260	AT5G66510				
GO:0004096	1	AT4G35090					

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004108	1	AT2G44350					
GO:0004124	2	AT2G43750	AT3G59760				
GO:0004128	1	AT5G17770					
GO:0004148	3	AT1G48030	AT3G16950	AT3G17240			
GO:0004152	1	AT5G23300					
GO:0004312	1	AT5G46290					
GO:0004314	1	AT2G30200					
GO:0004316	1	AT1G24360					
GO:0004318	1	AT2G05990					
GO:0004332	2	AT2G01140	AT3G52930				
GO:0004340	1	AT4G29130					
GO:0004347	1	AT4G24620					
GO:0004352	1	AT5G07440					
GO:0004353	2	AT5G07440	AT5G18170				
GO:0004356	1	AT5G35630					
GO:0004375	1	AT2G26080					
GO:0004396	1	AT4G29130					
GO:0004449	1	AT4G35260					
GO:0004455	1	AT3G58610					
GO:0004470	1	AT1G79750					
GO:0004473	1	AT1G79750					
GO:0004550	2	AT4G09320	AT4G11010				
GO:0004553	3	AT1G62660	AT3G09260	AT5G63840			
GO:0004576	3	AT1G34130	AT1G76400	AT5G19690			
GO:0004579	2	AT4G21150	AT5G66680				
GO:0004591	1	AT3G55410					
GO:0004601	1	AT1G35720					
GO:0004616	2	AT1G64190	AT5G41670				
GO:0004618	2	AT1G79550	AT3G12780				
GO:0004634	1	AT2G36530					
GO:0004739	3	AT1G01090	AT1G24180	AT5G50850			
GO:0004742	3	AT1G34430	AT3G13930	AT3G25860			
GO:0004743	1	AT3G22960					
GO:0004776	2	AT2G20420	AT5G08300				
GO:0004784	1	AT3G10920					
GO:0004795	1	AT4G29840					
GO:0004801	2	AT1G12230	AT5G13420				
GO:0004802	1	AT3G60750					
GO:0004807	2	AT2G21170	AT3G55440				
GO:0004846	1	AT2G26230					
GO:0005347	1	AT4G01100					
GO:0005471	2	AT3G08580	AT5G13490				
GO:0005488	11	AT2G20360	AT2G30200	AT3G04830	AT3G08580	AT3G42050	AT3G54110
		AT4G01100	AT4G33360	AT5G13490	AT5G14040	AT5G19760	
GO:0005507	5	AT1G35720	AT1G56070	AT2G36530	AT3G09260	AT4G13940	
GO:0005509	5	AT1G09210	AT1G35720	AT1G56340	AT5G61790	AT5G65020	
GO:0005516	3	AT3G19820	AT5G20720	AT5G56360			
GO:0005524	34	AT1G22300	AT1G29900	AT1G35720	AT1G48030	AT1G51980	AT1G63940
		AT1G78900	AT2G05710	AT2G20420	AT2G26080	AT2G28000	AT2G33210
		AT2G44350	AT3G07770	AT3G13860	AT3G17240	AT3G23990	AT3G42050
		AT3G48000	AT3G59760	AT4G02930	AT4G09320	AT4G11010	AT4G16660
		AT4G24190	AT4G29130	AT4G34200	AT4G37910	AT5G02500	AT5G07440
		AT5G09590	AT5G18170	AT5G56500	AT5G66760		
GO:0005544	2	AT1G35720	AT5G65020				
GO:0005618	26	AT1G03860	AT1G35720	AT1G53240	AT1G78900	AT2G05710	AT2G33040
		AT2G44350	AT3G02090	AT3G05230	AT3G07770	AT3G08580	AT3G12780
		AT3G52930	AT3G55440	AT3G58610	AT4G02930	AT4G37910	AT5G02500
		AT5G08300	AT5G09590	AT5G10160	AT5G14040	AT5G15090	AT5G19760
		AT5G66760	AT5G67500				

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005730	14	AT1G56070	AT2G21870	AT2G33040	AT2G33150	AT3G02090	AT3G08580
		AT3G16950	AT3G52300	AT3G52930	AT5G02500	AT5G15090	AT5G40770
		AT5G50850	AT5G66680				
GO:0005737	6	AT1G22300	AT2G21660	AT2G33040	AT2G36530	AT3G12780	AT4G20850
GO:0005739	109	AT1G03860	AT1G09210	AT1G11860	AT1G14810	AT1G15690	AT1G22300
		AT1G24180	AT1G35720	AT1G47260	AT1G48030	AT1G51980	AT1G53240
		AT1G56340	AT1G63940	AT2G01140	AT2G05710	AT2G14170	AT2G20360
		AT2G20420	AT2G21170	AT2G21870	AT2G26080	AT2G28000	AT2G30970
		AT2G33040	AT2G33150	AT2G33210	AT2G36530	AT2G43750	AT2G44350
		AT3G01280	AT3G02090	AT3G07770	AT3G08580	AT3G10920	AT3G12260
		AT3G12780	AT3G13160	AT3G13860	AT3G13930	AT3G15020	AT3G15090
		AT3G16480	AT3G17240	AT3G20000	AT3G22200	AT3G23990	AT3G27240
		AT3G27380	AT3G44330	AT3G46740	AT3G47520	AT3G48000	AT3G52300
		AT3G52930	AT3G54110	AT3G55410	AT3G55440	AT3G58610	AT3G59760
		AT3G61070	AT4G01100	AT4G02580	AT4G02930	AT4G05020	AT4G08390
		AT4G11010	AT4G21150	AT4G24190	AT4G29130	AT4G34200	AT4G35000
		AT4G35090	AT4G35260	AT4G37910	AT4G39660	AT5G07440	AT5G08300
		AT5G08530	AT5G09590	AT5G11770	AT5G12470	AT5G13420	AT5G13450
		AT5G13490	AT5G14040	AT5G15090	AT5G18170	AT5G19760	AT5G20720
		AT5G23300	AT5G27540	AT5G35630	AT5G37510	AT5G40770	AT5G40810
		AT5G41670	AT5G42960	AT5G50850	AT5G52840	AT5G55070	AT5G56500
		AT5G60640	AT5G61790	AT5G62530	AT5G63400	AT5G66510	AT5G66760
		AT5G67500					
GO:0005740	4	AT2G36530	AT3G08580	AT3G52930	AT5G13490		
GO:0005741	6	AT3G01280	AT3G02090	AT3G16480	AT3G20000	AT5G15090	AT5G67500
GO:0005742	1	AT3G20000					
GO:0005743	10	AT3G02090	AT3G08580	AT3G16480	AT3G20000	AT3G54110	AT4G01100
		AT4G11010	AT5G13490	AT5G14040	AT5G19760		
GO:0005746	2	AT3G27240	AT5G40810				
GO:0005749	1	AT5G66760					
GO:0005750	5	AT1G51980	AT3G02090	AT3G16480	AT3G27240	AT5G40810	
GO:0005753	1	AT4G11150					
GO:0005758	2	AT3G02090	AT3G16480				
GO:0005759	7	AT1G48030	AT3G02090	AT3G16480	AT3G17240	AT3G23990	AT4G37910
		AT5G09590					
GO:0005773	49	AT1G03860	AT1G04410	AT1G09210	AT1G11910	AT1G12840	AT1G15690
		AT1G21750	AT1G35720	AT1G59610	AT1G62660	AT1G78900	AT2G07050
		AT2G18960	AT2G24200	AT2G32920	AT2G45960	AT3G01280	AT3G08580
		AT3G09260	AT3G19820	AT3G26520	AT3G27240	AT3G42050	AT3G44330
		AT3G51260	AT3G55440	AT3G58730	AT4G09320	AT4G11150	AT4G12650
		AT4G13940	AT4G20850	AT4G24190	AT4G29130	AT4G33360	AT4G35000
		AT4G38220	AT4G39080	AT5G11560	AT5G13710	AT5G15090	AT5G34850
		AT5G40770	AT5G40810	AT5G42080	AT5G43060	AT5G53560	AT5G61790
		AT5G66680					
GO:0005774	7	AT1G12840	AT1G15690	AT1G78900	AT3G42050	AT3G58730	AT4G11150
		AT4G39080					
GO:0005777	8	AT2G21660	AT2G22780	AT2G26230	AT2G33150	AT3G09260	AT3G15950
		AT4G35000	AT4G35090				
GO:0005778	2	AT3G61070	AT4G35000				
GO:0005779	1	AT3G61070					
GO:0005783	36	AT1G09210	AT1G19360	AT1G20330	AT1G21750	AT1G34130	AT1G35620
		AT1G56340	AT1G61790	AT1G64090	AT1G65270	AT1G67730	AT1G70770
		AT1G76400	AT1G77510	AT2G30490	AT2G32920	AT2G47470	AT3G05230
		AT3G44330	AT3G54960	AT3G62360	AT4G21150	AT4G24190	AT4G24330
		AT4G29520	AT4G31340	AT4G33360	AT5G11560	AT5G17770	AT5G19690
		AT5G53560	AT5G55940	AT5G60640	AT5G61790	AT5G63840	AT5G66680
GO:0005789	3	AT4G21150	AT5G53560	AT5G66680			
GO:0005792	1	AT5G61790					

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005794	9	AT1G10950	AT1G26850	AT1G29470	AT2G34300	AT3G49720	AT3G53520
		AT4G12650	AT4G18030	AT5G10840			
GO:0005819	1	AT3G51260					
GO:0005829	8	AT1G35720	AT1G79550	AT3G23990	AT3G55440	AT3G56070	AT4G34870
		AT5G02500	AT5G03630				
GO:0005835	1	AT2G05990					
GO:0005839	1	AT3G51260					
GO:0005874	1	AT5G42080					
GO:0005886	99	AT1G03860	AT1G04410	AT1G12840	AT1G13280	AT1G15690	AT1G22300
		AT1G34130	AT1G34430	AT1G35620	AT1G35720	AT1G51980	AT1G56070
		AT1G56340	AT1G59610	AT1G61790	AT1G65270	AT1G70770	AT1G77510
		AT1G78900	AT1G79550	AT2G05710	AT2G18960	AT2G30490	AT2G31390
		AT2G32920	AT2G33150	AT2G33210	AT2G36530	AT2G45960	AT2G47470
		AT3G01280	AT3G02090	AT3G03250	AT3G04840	AT3G08580	AT3G13860
		AT3G16480	AT3G19820	AT3G20000	AT3G22200	AT3G23990	AT3G26520
		AT3G27240	AT3G42050	AT3G44330	AT3G46740	AT3G47520	AT3G49720
		AT3G51260	AT3G52300	AT3G52930	AT3G54110	AT3G54960	AT3G55440
		AT3G58730	AT3G62360	AT4G01100	AT4G09320	AT4G11150	AT4G12650
		AT4G13940	AT4G16660	AT4G18030	AT4G20850	AT4G21150	AT4G24190
		AT4G29130	AT4G29520	AT4G31340	AT4G33090	AT4G33360	AT4G34700
		AT4G34870	AT4G35000	AT4G37910	AT4G39080	AT4G39660	AT5G02500
		AT5G07440	AT5G09590	AT5G10840	AT5G11560	AT5G13450	AT5G13490
		AT5G14030	AT5G14040	AT5G15090	AT5G17770	AT5G19690	AT5G19760
		AT5G40770	AT5G42080	AT5G50850	AT5G53560	AT5G60640	AT5G61790
		AT5G63400	AT5G66680	AT5G67500			
GO:0005960	1	AT2G26080					
GO:0005982	1	AT4G24620					
GO:0005985	1	AT3G03250					
GO:0005986	1	AT2G31390					
GO:0006014	1	AT2G31390					
GO:0006015	1	AT1G12230					
GO:0006086	2	AT3G16950	AT3G25860				
GO:0006090	1	AT3G13930					
GO:0006096	5	AT1G79550	AT3G12780	AT3G22960	AT3G55410	AT3G55440	
GO:0006098	2	AT2G01140	AT3G52930				
GO:0006099	1	AT2G44350					
GO:0006108	1	AT1G79750					
GO:0006120	3	AT4G02580	AT5G08530	AT5G11770			
GO:0006121	2	AT3G27380	AT5G66760				
GO:0006144	1	AT2G26230					
GO:0006167	1	AT3G57610					
GO:0006207	1	AT5G23300					
GO:0006346	1	AT4G13940					
GO:0006406	1	AT2G21660					
GO:0006414	1	AT4G02930					
GO:0006457	10	AT2G28000	AT3G07770	AT3G56070	AT4G24190	AT4G34870	AT4G37910
		AT5G02500	AT5G09590	AT5G56500	AT5G61790		
GO:0006461	1	AT4G34450					
GO:0006465	1	AT3G05230					
GO:0006486	2	AT1G34130	AT1G76400				
GO:0006496	1	AT4G21150					
GO:0006508	7	AT1G11910	AT1G51980	AT2G24200	AT3G02090	AT3G16480	AT4G20850
		AT4G38220					
GO:0006520	2	AT1G14810	AT4G38220				
GO:0006526	1	AT1G29900					
GO:0006537	2	AT2G41220	AT5G53460				
GO:0006540	1	AT3G22200					
GO:0006560	1	AT5G62530					
GO:0006626	1	AT3G20000					

Cluster 5 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0006633	7	AT1G24360	AT1G79750	AT2G05990	AT2G30200	AT2G38040	AT5G10160
		AT5G35360					
GO:0006635	1	AT2G33150					
GO:0006694	1	AT3G19820					
GO:0006721	1	AT4G33360					
GO:0006730	1	AT4G13940					
GO:0006800	1	AT5G62530					
GO:0006807	2	AT2G41220	AT5G18170				
GO:0006810	8	AT2G45960	AT3G08580	AT3G26520	AT3G54110	AT4G01100	AT5G13490
		AT5G14040	AT5G19760				
GO:0006820	4	AT3G01280	AT3G20000	AT5G15090	AT5G67500		
GO:0006833	1	AT2G45960					
GO:0006839	2	AT4G01100	AT5G19760				
GO:0006954	1	AT2G33210					
GO:0006970	2	AT1G35720	AT2G21660				
GO:0006979	15	AT1G09210	AT1G35720	AT1G56340	AT2G01140	AT2G05710	AT2G14170
		AT3G22200	AT4G02580	AT4G08390	AT4G11010	AT4G35000	AT4G35090
		AT5G37510	AT5G55070	AT5G60640			
GO:0006995	1	AT4G35090					
GO:0007005	3	AT3G23990	AT5G27540	AT5G40770			
GO:0007030	2	AT1G78900	AT4G11150				
GO:0007031	1	AT3G61070					
GO:0007389	1	AT1G20330					
GO:0007568	1	AT5G35630					
GO:0007623	1	AT2G21660					
GO:0008135	1	AT1G56070					
GO:0008137	3	AT4G02580	AT5G08530	AT5G11770			
GO:0008152	19	AT1G01090	AT1G12230	AT1G24180	AT1G24360	AT2G20420	AT2G30200
		AT2G41220	AT3G03250	AT3G13930	AT3G15090	AT3G23940	AT3G25860
		AT3G55410	AT3G55440	AT4G13430	AT4G35260	AT5G08300	AT5G46290
		AT5G55070					
GO:0008219	1	AT4G35090					
GO:0008233	1	AT3G51260					
GO:0008240	1	AT4G20850					
GO:0008250	1	AT5G66680					
GO:0008308	4	AT3G01280	AT3G20000	AT5G15090	AT5G67500		
GO:0008415	1	AT5G55070					
GO:0008422	1	AT3G09260					
GO:0008453	1	AT4G39660					
GO:0008483	1	AT4G33680					
GO:0008553	1	AT2G18960					
GO:0008757	1	AT1G20330					
GO:0008865	1	AT4G29130					
GO:0009052	1	AT1G12230					
GO:0009055	1	AT3G27380					
GO:0009060	1	AT4G01100					
GO:0009082	2	AT3G23940	AT3G58610				
GO:0009086	1	AT3G01120					
GO:0009088	1	AT4G29840					
GO:0009089	1	AT4G33680					
GO:0009097	1	AT3G23940					
GO:0009099	1	AT3G23940					
GO:0009152	1	AT3G57610					
GO:0009220	1	AT5G23300					
GO:0009225	1	AT3G53520					
GO:0009306	1	AT4G24190					
GO:0009317	1	AT2G38040					
GO:0009408	3	AT3G23990	AT5G02500	AT5G09590			

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009409	15	AT1G53240	AT1G56070	AT1G63940	AT2G21660	AT2G36530	AT3G12780
		AT3G47520	AT4G11150	AT4G21150	AT4G24190	AT4G31990	AT4G35090
		AT5G02500	AT5G04590	AT5G20720			
GO:0009414	4	AT1G15690	AT2G18960	AT2G45960	AT4G24190		
GO:0009416	5	AT1G48030	AT2G30490	AT2G36530	AT3G19820	AT4G35090	
GO:0009450	1	AT3G22200					
GO:0009504	1	AT5G42080					
GO:0009505	12	AT1G21750	AT1G35620	AT2G30490	AT2G47470	AT3G62360	AT4G18030
		AT4G21150	AT5G10840	AT5G17770	AT5G34850	AT5G61790	AT5G66680
GO:0009507	117	AT1G01090	AT1G03860	AT1G04410	AT1G06950	AT1G11860	AT1G12230
		AT1G12840	AT1G13280	AT1G14810	AT1G15690	AT1G21750	AT1G24360
		AT1G29900	AT1G30510	AT1G34430	AT1G35720	AT1G47260	AT1G51980
		AT1G53240	AT1G56070	AT1G56340	AT1G61790	AT1G63940	AT1G64190
		AT1G77510	AT1G78900	AT1G79750	AT1G80600	AT2G01140	AT2G05710
		AT2G05990	AT2G21170	AT2G21660	AT2G21870	AT2G22780	AT2G26080
		AT2G28000	AT2G30200	AT2G33040	AT2G33150	AT2G33210	AT2G36530
		AT2G38040	AT2G41220	AT2G43750	AT2G44350	AT2G45960	AT3G01120
		AT3G01280	AT3G02090	AT3G04840	AT3G08580	AT3G12780	AT3G13930
		AT3G16950	AT3G17240	AT3G22960	AT3G23940	AT3G25860	AT3G26520
		AT3G42050	AT3G46740	AT3G47520	AT3G48000	AT3G51260	AT3G52300
		AT3G52930	AT3G54110	AT3G54960	AT3G55440	AT3G57610	AT3G58610
		AT3G59760	AT3G60750	AT4G08390	AT4G09320	AT4G13430	AT4G16660
		AT4G20850	AT4G24190	AT4G24620	AT4G29840	AT4G31990	AT4G33680
		AT4G34200	AT4G34450	AT4G34870	AT4G35000	AT4G35090	AT4G39080
		AT5G04590	AT5G09590	AT5G10160	AT5G12470	AT5G13420	AT5G13450
		AT5G13490	AT5G14040	AT5G15090	AT5G19760	AT5G20720	AT5G26260
		AT5G35360	AT5G35630	AT5G37510	AT5G41670	AT5G42960	AT5G46290
		AT5G52840	AT5G53460	AT5G56500	AT5G60640	AT5G61790	AT5G62530
		AT5G63840	AT5G67500				
GO:0009524	1	AT3G51260					
GO:0009535	6	AT3G49720	AT3G52300	AT5G20720	AT5G35630	AT5G42080	AT5G53560
GO:0009536	25	AT1G01090	AT1G03860	AT1G47260	AT1G51980	AT2G21870	AT2G43750
		AT3G01280	AT3G16480	AT3G20000	AT3G46740	AT3G52300	AT4G01100
		AT4G11010	AT4G24620	AT4G29130	AT4G31990	AT5G04590	AT5G12470
		AT5G13490	AT5G14040	AT5G15090	AT5G23300	AT5G42960	AT5G53460
		AT5G63400					
GO:0009553	1	AT2G47470					
GO:0009555	2	AT1G78900	AT2G07050				
GO:0009561	1	AT4G34200					
GO:0009567	1	AT2G47470					
GO:0009570	37	AT1G04410	AT1G14810	AT1G22300	AT1G24360	AT1G29900	AT1G35720
		AT1G63940	AT1G80600	AT2G05990	AT2G21170	AT2G28000	AT2G30200
		AT2G38040	AT2G43750	AT3G12780	AT3G16950	AT3G22960	AT3G23940
		AT3G25860	AT3G47520	AT3G55440	AT3G57610	AT3G58610	AT3G60750
		AT4G08390	AT4G13430	AT4G24620	AT4G31990	AT4G33680	AT5G04590
		AT5G13420	AT5G20720	AT5G35360	AT5G35630	AT5G46290	AT5G53460
		AT5G56500					
GO:0009579	10	AT1G21750	AT1G35720	AT2G05990	AT2G21170	AT2G28000	AT3G12780
		AT3G52300	AT5G20720	AT5G35630	AT5G65020		
GO:0009610	1	AT3G09260					
GO:0009611	2	AT2G30490	AT2G33150				
GO:0009615	2	AT5G02500	AT5G09590				
GO:0009617	3	AT3G01280	AT5G15090	AT5G67500			
GO:0009646	1	AT5G18170					
GO:0009648	1	AT4G35090					

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009651	41	AT1G04410	AT1G09210	AT1G11910	AT1G15690	AT1G21750	AT1G24180
		AT1G47260	AT1G51980	AT1G53240	AT1G56340	AT1G64190	AT1G77510
		AT1G78900	AT2G05710	AT2G20360	AT2G21660	AT2G36530	AT2G45960
		AT3G03250	AT3G09260	AT3G10920	AT3G15950	AT3G26520	AT3G52300
		AT3G52930	AT3G55440	AT3G60750	AT4G09320	AT4G11150	AT4G24190
		AT4G37910	AT5G03630	AT5G04590	AT5G07440	AT5G09590	AT5G18170
		AT5G19690	AT5G35630	AT5G40770	AT5G43060	AT5G62530	
GO:0009658	3	AT1G06950	AT2G28000	AT3G46740			
GO:0009664	1	AT5G66680					
GO:0009678	1	AT1G15690					
GO:0009695	2	AT1G13280	AT2G33150				
GO:0009699	1	AT2G30490					
GO:0009705	3	AT1G15690	AT4G11150	AT4G39080			
GO:0009706	1	AT5G12470					
GO:0009737	4	AT1G35720	AT2G05710	AT2G18960	AT2G36530		
GO:0009742	1	AT1G22300					
GO:0009744	1	AT5G41670					
GO:0009749	1	AT5G41670					
GO:0009750	1	AT5G41670					
GO:0009790	3	AT1G21750	AT2G28000	AT5G27540			
GO:0009793	12	AT1G34430	AT1G79750	AT2G47470	AT3G10920	AT4G11150	AT4G13940
		AT5G13710	AT5G27540	AT5G37510	AT5G40480	AT5G42080	AT5G55940
GO:0009809	1	AT1G12840					
GO:0009825	1	AT1G20330					
GO:0009826	4	AT1G12840	AT3G19820	AT5G63840	AT5G66680		
GO:0009832	1	AT4G11150					
GO:0009845	1	AT1G79750					
GO:0009853	6	AT1G47260	AT3G54110	AT4G34700	AT5G37510	AT5G52840	AT5G66510
GO:0009860	2	AT3G22200	AT5G27540				
GO:0009862	1	AT4G33680					
GO:0009865	1	AT3G22200					
GO:0009901	1	AT1G47260					
GO:0009911	1	AT4G24620					
GO:0009920	1	AT5G42080					
GO:0009926	2	AT1G15690	AT4G33090				
GO:0009934	1	AT4G24190					
GO:0009941	38	AT1G01090	AT1G06950	AT1G11860	AT1G15690	AT1G24360	AT1G34430
		AT1G78900	AT2G05990	AT2G21170	AT2G26080	AT2G28000	AT2G38040
		AT2G41220	AT2G43750	AT3G01280	AT3G08580	AT3G12780	AT3G13930
		AT3G16950	AT3G25860	AT3G46740	AT3G47520	AT3G58610	AT3G60750
		AT4G24620	AT4G31990	AT4G35000	AT5G04590	AT5G12470	AT5G13490
		AT5G15090	AT5G19760	AT5G20720	AT5G35360	AT5G35630	AT5G42960
		AT5G46290	AT5G67500				
GO:0009955	1	AT2G27530					
GO:0009970	1	AT4G35090					
GO:0009986	1	AT5G65020					
GO:0010006	1	AT3G46740					
GO:0010008	1	AT1G15690					
GO:0010027	1	AT2G07050					
GO:0010033	1	AT3G22200					
GO:0010051	2	AT1G20330	AT5G42080				
GO:0010075	1	AT4G24190					
GO:0010091	1	AT5G42080					
GO:0010111	1	AT2G33150					
GO:0010119	2	AT2G18960	AT2G21660				
GO:0010133	1	AT5G62530					
GO:0010154	1	AT3G22200					
GO:0010168	2	AT3G09260	AT3G15950				
GO:0010182	1	AT4G29130					

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0010183	1	AT3G22200					
GO:0010228	1	AT2G21660					
GO:0010248	1	AT1G15690					
GO:0010255	1	AT4G29130					
GO:0010285	1	AT4G33680					
GO:0010287	1	AT2G01140					
GO:0010319	6	AT1G63940	AT3G12780	AT3G47520	AT4G31990	AT4G35090	AT5G04590
GO:0010501	1	AT2G21660					
GO:0012501	1	AT4G29130					
GO:0015036	1	AT4G05020					
GO:0015157	1	AT1G61790					
GO:0015217	1	AT4G01100					
GO:0015250	2	AT2G45960	AT3G26520				
GO:0015450	2	AT3G20000	AT3G46740				
GO:0015774	1	AT5G65020					
GO:0015865	2	AT3G08580	AT5G13490				
GO:0015866	1	AT4G01100					
GO:0015867	1	AT4G01100					
GO:0015926	1	AT5G63840					
GO:0015928	1	AT3G09260					
GO:0015934	1	AT2G27530					
GO:0015979	1	AT3G54110					
GO:0015986	3	AT2G33040	AT4G11150	AT5G13450			
GO:0015992	4	AT1G78900	AT2G18960	AT2G33040	AT4G39080		
GO:0016002	1	AT5G04590					
GO:0016018	1	AT3G56070					
GO:0016020	74	AT1G04410	AT1G06950	AT1G10950	AT1G11860	AT1G15690	AT1G21750
		AT1G26850	AT1G29900	AT1G34130	AT1G35720	AT1G47260	AT1G51980
		AT1G56070	AT1G64190	AT1G67730	AT1G70770	AT1G76400	AT1G78900
		AT1G79550	AT2G18960	AT2G20360	AT2G21870	AT2G28000	AT2G30490
		AT2G33040	AT2G33150	AT2G36530	AT2G38040	AT2G45960	AT3G02090
		AT3G08580	AT3G09260	AT3G12260	AT3G12780	AT3G13160	AT3G15020
		AT3G15950	AT3G19820	AT3G25860	AT3G26520	AT3G27240	AT3G46740
		AT3G47520	AT3G49720	AT3G53520	AT3G58730	AT4G01100	AT4G08390
		AT4G13940	AT4G20850	AT4G21150	AT4G24190	AT4G29130	AT4G34200
		AT4G34450	AT4G39080	AT4G39660	AT5G02500	AT5G04590	AT5G10160
		AT5G13450	AT5G13490	AT5G14040	AT5G15090	AT5G19690	AT5G35630
		AT5G40770	AT5G40810	AT5G46290	AT5G52840	AT5G56500	AT5G61790
		AT5G66680	AT5G67500				
GO:0016021	4	AT1G10950	AT3G19820	AT4G12650	AT5G10840		
GO:0016036	2	AT3G03250	AT4G35090				
GO:0016040	1	AT5G53460					
GO:0016041	1	AT2G41220					
GO:0016049	1	AT5G40770					
GO:0016051	1	AT1G12840					
GO:0016126	2	AT1G20330	AT5G13710				
GO:0016132	1	AT3G19820					
GO:0016192	1	AT4G34450					
GO:0016441	1	AT4G13940					
GO:0016485	1	AT3G44330					
GO:0016491	5	AT1G30510	AT1G67730	AT2G05990	AT5G07440	AT5G18170	
GO:0016559	1	AT3G61070					
GO:0016615	5	AT1G04410	AT1G53240	AT2G22780	AT3G15020	AT3G47520	
GO:0016620	1	AT1G14810					
GO:0016631	1	AT2G05990					
GO:0016651	1	AT5G52840					
GO:0016652	1	AT1G79750					
GO:0016656	1	AT5G03630					
GO:0016688	2	AT4G08390	AT4G35000				

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0016710	1	AT2G30490					
GO:0016829	1	AT4G13430					
GO:0016871	1	AT2G07050					
GO:0016887	3	AT1G15690	AT2G18960	AT4G39080			
GO:0017077	2	AT3G54110	AT5G19760				
GO:0018119	3	AT1G53240	AT3G12780	AT3G55440			
GO:0018279	1	AT5G66680					
GO:0019171	1	AT5G10160					
GO:0019253	1	AT2G21170					
GO:0019320	1	AT4G29130					
GO:0019344	2	AT2G43750	AT3G59760				
GO:0019395	1	AT2G33150					
GO:0019419	1	AT5G04590					
GO:0019430	1	AT3G10920					
GO:0019464	1	AT2G26080					
GO:0019484	1	AT3G22200					
GO:0019575	2	AT1G62660	AT2G31390				
GO:0019654	1	AT2G31390					
GO:0019658	1	AT1G12230					
GO:0019676	1	AT5G35630					
GO:0019745	1	AT2G07050					
GO:0019773	1	AT3G51260					
GO:0020037	1	AT5G53560					
GO:0022621	1	AT3G22200					
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		AT5G02500	AT5G35630	AT5G55070			
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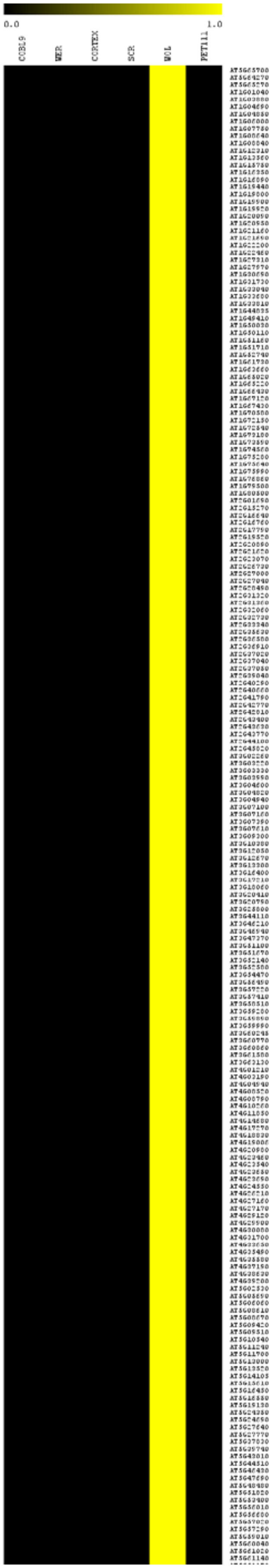
GO:0030104	1	AT3G26520					
GO:0030244	1	AT5G63840					
GO:0030246	1	AT3G62360					
GO:0030276	1	AT4G34450					
GO:0031314	1	AT4G05020					
GO:0031359	1	AT3G46740					
GO:0031897	1	AT1G06950					
GO:0031966	5	AT1G47260	AT4G34700	AT5G37510	AT5G52840	AT5G66510	
GO:0031998	1	AT2G22780					
GO:0032508	1	AT2G21660					
GO:0034387	1	AT3G22200					
GO:0042023	1	AT1G20330					
GO:0042128	1	AT5G53460					
GO:0042335	1	AT1G67730					
GO:0042651	1	AT1G30510					
GO:0042732	1	AT3G53520					
GO:0042742	8	AT1G53240	AT1G80600	AT3G10920	AT3G15020	AT3G26520	AT4G11150
		AT5G15090	AT5G50850				
GO:0042744	1	AT4G35090					
GO:0042803	1	AT1G35720					
GO:0043067	1	AT1G21750					
GO:0044262	1	AT3G55440					
GO:0044267	1	AT5G56500					
GO:0045036	1	AT3G46740					
GO:0045037	1	AT1G06950					
GO:0045087	1	AT2G21660					
GO:0045153	2	AT3G27240	AT5G40810				
GO:0045271	12	AT1G03860	AT1G47260	AT2G20360	AT3G12260	AT4G02580	AT4G34700
		AT5G08530	AT5G11770	AT5G37510	AT5G40770	AT5G52840	AT5G66510
GO:0045281	1	AT3G27380					
GO:0045309	1	AT1G22300					

Cluster 5 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0045454	2	AT1G35620 AT4G35090
GO:0045703	1	AT1G67730
GO:0046423	1	AT1G13280
GO:0046658	1	AT2G45960
GO:0046686	49	AT1G04410 AT1G11860 AT1G35720 AT1G48030 AT1G53240 AT1G56340 AT1G63940 AT1G77510 AT2G01140 AT2G05710 AT2G20420 AT2G21660 AT2G24200 AT2G30970 AT2G36530 AT2G43750 AT2G44350 AT2G47470 AT3G12780 AT3G13860 AT3G17240 AT3G22200 AT3G22960 AT3G23990 AT3G48000 AT3G52930 AT3G55440 AT3G56070 AT3G57610 AT3G58610 AT3G60750 AT4G09320 AT4G13430 AT4G24190 AT4G31990 AT4G37910 AT4G39660 AT5G02500 AT5G03630 AT5G07440 AT5G08300 AT5G09590 AT5G13420 AT5G18170 AT5G20720 AT5G41670 AT5G53460 AT5G63400 AT5G63840
GO:0046872	2	AT3G10920 AT5G08300
GO:0046933	4	AT1G78900 AT2G33040 AT3G52300 AT5G13450
GO:0046961	6	AT1G12840 AT2G33040 AT3G42050 AT3G52300 AT3G58730 AT4G11150
GO:0048040	1	AT3G53520
GO:0048046	23	AT1G04410 AT1G11860 AT1G35720 AT1G48030 AT1G79550 AT2G21170 AT2G28000 AT2G36530 AT2G43750 AT3G12780 AT3G15020 AT3G47520 AT3G52930 AT3G55440 AT3G57610 AT3G58610 AT4G09320 AT4G31990 AT4G34870 AT5G02500 AT5G04590 AT5G20720 AT5G35630
GO:0048316	1	AT1G21750
GO:0048569	1	AT2G27530
GO:0048598	1	AT3G46740
GO:0048868	2	AT2G47470 AT3G59760
GO:0050311	1	AT5G04590
GO:0050662	2	AT2G20360 AT4G33360
GO:0051082	4	AT2G28000 AT3G13860 AT5G56500 AT5G61790
GO:0051131	1	AT3G23990
GO:0051301	1	AT5G40770

Cluster 6



Cluster 6

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AT5G65700

Cluster 6
AT1G75990
AT1G76860
AT1G79500
AT1G80500

Cluster 6 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005886	plasma membrane	46	208	1.30E-10
GO:0005730	nucleolus	14	208	1.09E-07
GO:0003735	structural constituent of ribosome	14	208	8.96E-07
GO:0022627	cytosolic small ribosomal subunit	8	208	1.24E-06
GO:0022626	cytosolic ribosome	10	208	6.15E-06
GO:0006412	translation	13	208	7.48E-06
GO:0005635	nuclear envelope	4	208	2.01E-05
GO:0006606	protein import into nucleus	3	208	5.21E-05
GO:0008540	proteasome regulatory particle, base subcomplex	3	208	5.21E-05
GO:0005840	ribosome	9	208	8.31E-05
GO:0045735	nutrient reservoir activity	5	208	1.54E-04
GO:0006177	GMP biosynthetic process	2	208	2.94E-04
GO:0008026	ATP-dependent helicase activity	5	208	5.29E-04
GO:0004781	sulfate adenylyltransferase (ATP) activity	2	208	5.82E-04
GO:0006913	nucleocytoplasmic transport	3	208	6.88E-04
GO:0048589	developmental growth	2	208	9.61E-04
GO:0000910	cytokinesis	3	208	0.001088727
GO:0005737	cytoplasm	11	208	0.002479565
GO:0022625	cytosolic large ribosomal subunit	5	208	0.002789866
GO:0009941	chloroplast envelope	10	208	0.002869342
GO:0030276	clathrin binding	2	208	0.00332469
GO:0006014	D-ribose metabolic process	2	208	0.004114794
GO:0009926	auxin polar transport	3	208	0.005038795
GO:0009733	response to auxin stimulus	7	208	0.005240254
GO:0009640	photomorphogenesis	3	208	0.005429401
GO:0000103	sulfate assimilation	2	208	0.005916336
GO:0000148	1,3-beta-glucan synthase complex	2	208	0.005916336
GO:0003843	1,3-beta-glucan synthase activity	2	208	0.005916336
GO:0006075	1,3-beta-glucan biosynthetic process	2	208	0.005916336
GO:0019654	acetate fermentation	2	208	0.005916336
GO:0019575	sucrose catabolic process, using beta-fructofuranosidase	2	208	0.009136011
GO:0000072	M phase specific microtubule process	1	208	0.009973627
GO:0003922	GMP synthase (glutamine-hydrolyzing) activity	1	208	0.009973627
GO:0004170	dUTP diphosphatase activity	1	208	0.009973627
GO:0005201	extracellular matrix structural constituent	1	208	0.009973627
GO:0006436	tryptophanyl-tRNA aminoacylation	1	208	0.009973627
GO:0009394	2'-deoxyribonucleotide metabolic process	1	208	0.009973627
GO:0009528	plastid inner membrane	1	208	0.009973627
GO:0010064	embryonic shoot morphogenesis	1	208	0.009973627
GO:0017168	5-oxoprolinase (ATP-hydrolysing) activity	1	208	0.009973627
GO:0019107	myristoyltransferase activity	1	208	0.009973627
GO:0030981	cortical microtubule cytoskeleton	1	208	0.009973627
GO:0032153	cell division site	1	208	0.009973627
GO:0032454	histone demethylase activity (H3-K9 specific)	1	208	0.009973627
GO:0042284	sphingolipid delta-4 desaturase activity	1	208	0.009973627
GO:0043224	nuclear SCF ubiquitin ligase complex	1	208	0.009973627

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0043254	regulation of protein complex assembly	1	208	0.009973627
GO:0045014	negative regulation of transcription by glucose	1	208	0.009973627
GO:0048227	plasma membrane to endosome transport	1	208	0.009973627
GO:0048281	inflorescence morphogenesis	1	208	0.009973627
GO:0048283	indeterminate inflorescence morphogenesis	1	208	0.009973627
GO:0000226	microtubule cytoskeleton organization	2	208	0.010337946
GO:0005783	endoplasmic reticulum	7	208	0.012061162
GO:0006888	ER to Golgi vesicle-mediated transport	2	208	0.012921568
GO:0008536	Ran GTPase binding	2	208	0.012921568
GO:0010051	xylem and phloem pattern formation	2	208	0.012921568
GO:0009555	pollen development	3	208	0.013971379
GO:0005986	sucrose biosynthetic process	2	208	0.014298978
GO:0048443	stamen development	2	208	0.014298978
GO:0046686	response to cadmium ion	7	208	0.014901001
GO:0000166	nucleotide binding	6	208	0.015999951
GO:0009707	chloroplast outer membrane	2	208	0.018748861
GO:0030163	protein catabolic process	2	208	0.018748861
GO:0003938	IMP dehydrogenase activity	1	208	0.019749255
GO:0003975	UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase activity	1	208	0.019749255
GO:0004379	glycylpeptide N-tetradecanoyltransferase activity	1	208	0.019749255
GO:0005080	protein kinase C binding	1	208	0.019749255
GO:0005098	RAN GTPase activator activity	1	208	0.019749255
GO:0008676	3-deoxy-8-phosphooctulonate synthase activity	1	208	0.019749255
GO:0009590	detection of gravity	1	208	0.019749255
GO:0010306	rhamnogalacturonan II biosynthetic process	1	208	0.019749255
GO:0010317	pyrophosphate-dependent phosphofructokinase complex, alpha-subunit complex	1	208	0.019749255
GO:0010359	regulation of anion channel activity	1	208	0.019749255
GO:0010445	nuclear dicing body	1	208	0.019749255
GO:0010480	microsporocyte differentiation	1	208	0.019749255
GO:0016303	1-phosphatidylinositol-3-kinase activity	1	208	0.019749255
GO:0017151	DEAD/H-box RNA helicase binding	1	208	0.019749255
GO:0030198	extracellular matrix organization	1	208	0.019749255
GO:0031119	tRNA pseudouridine synthesis	1	208	0.019749255
GO:0032776	DNA methylation on cytosine	1	208	0.019749255
GO:0033169	histone H3-K9 demethylation	1	208	0.019749255
GO:0047958	glycine:2-oxoglutarate aminotransferase activity	1	208	0.019749255
GO:0048455	stamen formation	1	208	0.019749255
GO:0052543	callose deposition in cell wall	1	208	0.019749255
GO:0006461	protein complex assembly	2	208	0.020331418
GO:0010119	regulation of stomatal movement	2	208	0.020331418
GO:0005488	binding	9	208	0.020393216
GO:0016887	ATPase activity	4	208	0.021693097
GO:0006886	intracellular protein transport	4	208	0.022821847
GO:0006418	tRNA aminoacylation for protein translation	2	208	0.023633949
GO:0009816	defense response to bacterium, incompatible interaction	2	208	0.023633949
GO:0015992	proton transport	2	208	0.025350238
GO:0006810	transport	7	208	0.026348541
GO:0003743	translation initiation factor activity	3	208	0.027586625
GO:0008565	protein transporter activity	3	208	0.028519595
GO:0009507	chloroplast	30	208	0.028861089

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0000049	tRNA binding	1	208	0.029329818
GO:0000257	nitrilase activity	1	208	0.029329818
GO:0001671	ATPase activator activity	1	208	0.029329818
GO:0003923	GPI-anchor transamidase activity	1	208	0.029329818
GO:0004021	L-alanine:2-oxoglutarate aminotransferase activity	1	208	0.029329818
GO:0004614	phosphoglucomutase activity	1	208	0.029329818
GO:0005267	potassium channel activity	1	208	0.029329818
GO:0005663	DNA replication factor C complex	1	208	0.029329818
GO:0005719	nuclear euchromatin	1	208	0.029329818
GO:0006471	protein amino acid ADP-ribosylation	1	208	0.029329818
GO:0008361	regulation of cell size	1	208	0.029329818
GO:0008428	ribonuclease inhibitor activity	1	208	0.029329818
GO:0009920	cell plate formation involved in plant-type cell wall biogenesis	1	208	0.029329818
GO:0009925	basal plasma membrane	1	208	0.029329818
GO:0010098	suspensor development	1	208	0.029329818
GO:0010338	leaf formation	1	208	0.029329818
GO:0010599	RNA interference, production of lsiRNA	1	208	0.029329818
GO:0030572	phosphatidyltransferase activity	1	208	0.029329818
GO:0031048	chromatin silencing by small RNA	1	208	0.029329818
GO:0035279	gene silencing by miRNA, mRNA cleavage	1	208	0.029329818
GO:0042325	regulation of phosphorylation	1	208	0.029329818
GO:0045548	phenylalanine ammonia-lyase activity	1	208	0.029329818
GO:0051252	regulation of RNA metabolic process	1	208	0.029329818
GO:0051788	response to misfolded protein	1	208	0.029329818
GO:0006511	ubiquitin-dependent protein catabolic process	5	208	0.029881239
GO:0004683	calmodulin-dependent protein kinase activity	2	208	0.034511724
GO:0009706	chloroplast inner membrane	2	208	0.034511724
GO:0010319	stromule	2	208	0.034511724
GO:0001653	peptide receptor activity	1	208	0.03871821
GO:0005093	RAB GDP-dissociation inhibitor activity	1	208	0.03871821
GO:0006751	glutathione catabolic process	1	208	0.03871821
GO:0010329	auxin efflux transmembrane transporter activity	1	208	0.03871821
GO:0016579	protein deubiquitination	1	208	0.03871821
GO:0031053	primary microRNA processing	1	208	0.03871821
GO:0035196	gene silencing by miRNA, production of miRNAs	1	208	0.03871821
GO:0035198	miRNA binding	1	208	0.03871821
GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	1	208	0.03871821
GO:0043481	anthocyanin accumulation in tissues in response to UV light	1	208	0.03871821
GO:0047334	diphosphate-fructose-6-phosphate 1-phosphotransferase activity	1	208	0.03871821
GO:0048229	gametophyte development	1	208	0.03871821
GO:0051258	protein polymerization	1	208	0.03871821
GO:0016564	transcription repressor activity	2	208	0.040413185
GO:0006869	lipid transport	3	208	0.040704525
GO:0009744	response to sucrose stimulus	2	208	0.046567088
GO:0048367	shoot development	2	208	0.046567088
GO:0003883	CTP synthase activity	1	208	0.04791729
GO:0004040	amidase activity	1	208	0.04791729
GO:0005801	cis-Golgi network	1	208	0.04791729
GO:0008134	transcription factor binding	1	208	0.04791729
GO:0009113	purine base biosynthetic process	1	208	0.04791729

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010358	leaf shaping	1	208	0.04791729
GO:0016485	protein processing	1	208	0.04791729
GO:0030117	membrane coat	1	208	0.04791729
GO:0032012	regulation of ARF protein signal transduction	1	208	0.04791729
GO:0045177	apical part of cell	1	208	0.04791729
GO:0048437	floral organ development	1	208	0.04791729
GO:0005215	transporter activity	5	208	0.049034902
GO:0016491	oxidoreductase activity	5	208	0.05027965
GO:0042254	ribosome biogenesis	3	208	0.052058885
GO:0009860	pollen tube growth	2	208	0.055098779
GO:0000502	proteasome complex	1	208	0.056929877
GO:0003950	NAD+ ADP-ribosyltransferase activity	1	208	0.056929877
GO:0004003	ATP-dependent DNA helicase activity	1	208	0.056929877
GO:0005319	lipid transporter activity	1	208	0.056929877
GO:0006164	purine nucleotide biosynthetic process	1	208	0.056929877
GO:0006541	glutamine metabolic process	1	208	0.056929877
GO:0009081	branched chain family amino acid metabolic process	1	208	0.056929877
GO:0009527	plastid outer membrane	1	208	0.056929877
GO:0009880	embryonic pattern specification	1	208	0.056929877
GO:0010011	auxin binding	1	208	0.056929877
GO:0010268	brassinosteroid homeostasis	1	208	0.056929877
GO:0030176	integral to endoplasmic reticulum membrane	1	208	0.056929877
GO:0042147	retrograde transport, endosome to Golgi	1	208	0.056929877
GO:0042393	histone binding	1	208	0.056929877
GO:0045037	protein import into chloroplast stroma	1	208	0.056929877
GO:0045038	protein import into chloroplast thylakoid membrane	1	208	0.056929877
GO:0048528	post-embryonic root development	1	208	0.056929877
GO:0051555	flavonol biosynthetic process	1	208	0.056929877
GO:0016020	membrane	17	208	0.060769552
GO:0000902	cell morphogenesis	1	208	0.065758755
GO:0005085	guanyl-nucleotide exchange factor activity	1	208	0.065758755
GO:0006342	chromatin silencing	1	208	0.065758755
GO:0009616	virus induced gene silencing	1	208	0.065758755
GO:0015030	Cajal body	1	208	0.065758755
GO:0016469	proton-transporting two-sector ATPase complex	1	208	0.065758755
GO:0048653	anther development	1	208	0.065758755
GO:0048829	root cap development	1	208	0.065758755
GO:0000175	3'-5'-exoribonuclease activity	1	208	0.074406669
GO:0004525	ribonuclease III activity	1	208	0.074406669
GO:0006446	regulation of translational initiation	1	208	0.074406669
GO:0008142	oxysterol binding	1	208	0.074406669
GO:0008202	steroid metabolic process	1	208	0.074406669
GO:0009628	response to abiotic stimulus	1	208	0.074406669
GO:0009646	response to absence of light	1	208	0.074406669
GO:0010207	photosystem II assembly	1	208	0.074406669
GO:0030422	RNA interference, production of siRNA	1	208	0.074406669
GO:0040007	growth	1	208	0.074406669
GO:0051087	chaperone binding	1	208	0.074406669
GO:0005773	vacuole	7	208	0.078678573
GO:0006979	response to oxidative stress	4	208	0.082393204
GO:0002237	response to molecule of bacterial origin	1	208	0.08287633
GO:0004124	cysteine synthase activity	1	208	0.08287633

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006974	response to DNA damage stimulus	1	208	0.08287633
GO:0007186	G-protein coupled receptor protein signaling pathway	1	208	0.08287633
GO:0010102	lateral root morphogenesis	1	208	0.08287633
GO:0016070	RNA metabolic process	1	208	0.08287633
GO:0016559	peroxisome fission	1	208	0.08287633
GO:0045036	protein targeting to chloroplast	1	208	0.08287633
GO:0005634	nucleus	19	208	0.085092335
GO:0009793	embryonic development ending in seed dormancy	5	208	0.086030057
GO:0003824	catalytic activity	6	208	0.087760987
GO:0003725	double-stranded RNA binding	1	208	0.091170412
GO:0004721	phosphoprotein phosphatase activity	1	208	0.091170412
GO:0009574	preprophase band	1	208	0.091170412
GO:0010152	pollen maturation	1	208	0.091170412
GO:0016132	brassinosteroid biosynthetic process	1	208	0.091170412
GO:0019252	starch biosynthetic process	1	208	0.091170412
GO:0019344	cysteine biosynthetic process	1	208	0.091170412
GO:0030127	COPII vesicle coat	1	208	0.091170412
GO:0006396	RNA processing	2	208	0.093785914
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	3	208	0.096741294
GO:0004713	protein tyrosine kinase activity	1	208	0.099291555
GO:0008541	proteasome regulatory particle, lid subcomplex	1	208	0.099291555
GO:0009699	phenylpropanoid biosynthetic process	1	208	0.099291555
GO:0009750	response to fructose stimulus	1	208	0.099291555
GO:0010267	RNA interference, production of ta-siRNAs	1	208	0.099291555
GO:0010311	lateral root formation	1	208	0.099291555
GO:0015935	small ribosomal subunit	1	208	0.099291555
GO:0030125	clathrin vesicle coat	1	208	0.099291555
GO:0005618	cell wall	5	208	0.102727543
GO:0042742	defense response to bacterium	3	208	0.104677732
GO:0001522	pseudouridine synthesis	1	208	0.107242363
GO:0004630	phospholipase D activity	1	208	0.107242363
GO:0007389	pattern specification process	1	208	0.107242363
GO:0009534	chloroplast thylakoid	1	208	0.107242363
GO:0009958	positive gravitropism	1	208	0.107242363
GO:0010072	primary shoot apical meristem specification	1	208	0.107242363
GO:0010075	regulation of meristem growth	1	208	0.107242363
GO:0005388	calcium-transporting ATPase activity	1	208	0.115025405
GO:0048767	root hair elongation	1	208	0.115025405
GO:0000038	very-long-chain fatty acid metabolic process	1	208	0.115025405
GO:0048364	root development	2	208	0.11699749
GO:0005740	mitochondrial envelope	1	208	0.122643218
GO:0006098	pentose-phosphate shunt	1	208	0.122643218
GO:0006306	DNA methylation	1	208	0.122643218
GO:0008601	protein phosphatase type 2A regulator activity	1	208	0.122643218
GO:0009117	nucleotide metabolic process	1	208	0.122643218
GO:0042335	cuticle development	1	208	0.122643218
GO:0005516	calmodulin binding	3	208	0.125530629
GO:0009908	flower development	2	208	0.126148197
GO:0006468	protein amino acid phosphorylation	9	208	0.126806972
GO:0008152	metabolic process	7	208	0.127677956
GO:0016301	kinase activity	9	208	0.129585557

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005874	microtubule	1	208	0.130098303
GO:0009269	response to desiccation	1	208	0.130098303
GO:0009807	lignan biosynthetic process	1	208	0.130098303
GO:0009982	pseudouridine synthase activity	1	208	0.130098303
GO:0010029	regulation of seed germination	1	208	0.130098303
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	1	208	0.130098303
GO:0048366	leaf development	2	208	0.132924188
GO:0016192	vesicle-mediated transport	2	208	0.135163392
GO:0006626	protein targeting to mitochondrion	1	208	0.13739313
GO:0009504	cell plate	1	208	0.13739313
GO:0009532	plastid stroma	1	208	0.13739313
GO:0010027	thylakoid membrane organization	1	208	0.13739313
GO:0005576	extracellular region	2	208	0.139609609
GO:0009826	unidimensional cell growth	2	208	0.141815677
GO:0000271	polysaccharide biosynthetic process	1	208	0.144530136
GO:0005778	peroxisomal membrane	1	208	0.144530136
GO:0009630	gravitropism	1	208	0.144530136
GO:0009934	regulation of meristem organization	1	208	0.144530136
GO:0046961	proton-transporting ATPase activity, rotational mechanism	1	208	0.144530136
GO:0005524	ATP binding	7	208	0.145391208
GO:0009058	biosynthetic process	2	208	0.150515996
GO:0015031	protein transport	2	208	0.150515996
GO:0006807	nitrogen compound metabolic process	1	208	0.151511724
GO:0008033	tRNA processing	1	208	0.151511724
GO:0009556	microsporogenesis	1	208	0.151511724
GO:0009749	response to glucose stimulus	1	208	0.151511724
GO:0010017	red or far red light signaling pathway	1	208	0.151511724
GO:0005829	cytosol	3	208	0.152428169
GO:0005622	intracellular	5	208	0.153425798
GO:0004674	protein serine/threonine kinase activity	3	208	0.15472602
GO:0005525	GTP binding	3	208	0.15586426
GO:0008289	lipid binding	2	208	0.156899664
GO:0007010	cytoskeleton organization	1	208	0.165018105
GO:0051301	cell division	1	208	0.165018105
GO:0006397	mRNA processing	1	208	0.171547547
GO:0009831	plant-type cell wall modification during multidimensional cell growth	1	208	0.171547547
GO:0010182	sugar mediated signaling	1	208	0.171547547
GO:0005819	spindle	1	208	0.177930872
GO:0006414	translational elongation	1	208	0.177930872
GO:0004812	aminoacyl-tRNA ligase activity	1	208	0.184170328
GO:0008654	phospholipid biosynthetic process	1	208	0.184170328
GO:0010150	leaf senescence	1	208	0.184170328
GO:0009737	response to abscisic acid stimulus	3	208	0.186252854
GO:0010228	vegetative to reproductive phase transition	1	208	0.190268133
GO:0006499	N-terminal protein myristoylation	4	208	0.190423161
GO:0009570	chloroplast stroma	4	208	0.192383583
GO:0004888	transmembrane receptor activity	2	208	0.195694111
GO:0009637	response to blue light	1	208	0.196226477
GO:0009846	pollen germination	1	208	0.196226477
GO:0016071	mRNA metabolic process	1	208	0.196226477

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0030154	cell differentiation	1	208	0.196226477
GO:0000145	exocyst	1	208	0.202047517
GO:0003682	chromatin binding	1	208	0.202047517
GO:0005732	small nucleolar ribonucleoprotein complex	1	208	0.202047517
GO:0006364	rRNA processing	1	208	0.202047517
GO:0008283	cell proliferation	1	208	0.202047517
GO:0009909	regulation of flower development	1	208	0.202047517
GO:0009911	positive regulation of flower development	1	208	0.202047517
GO:0005777	peroxisome	2	208	0.204234749
GO:0048046	apoplast	3	208	0.211704539
GO:0008017	microtubule binding	1	208	0.21328618
GO:0009535	chloroplast thylakoid membrane	3	208	0.215178789
GO:0009853	photorespiration	1	208	0.218707979
GO:0009639	response to red or far red light	1	208	0.224000825
GO:0009828	plant-type cell wall loosening	1	208	0.224000825
GO:0016757	transferase activity, transferring glycosyl groups	3	208	0.226765562
GO:0010224	response to UV-B	1	208	0.234207707
GO:0035091	phosphoinositide binding	1	208	0.239125698
GO:0003924	GTPase activity	1	208	0.243922647
GO:0010583	response to cyclopentenone	1	208	0.243922647
GO:0006629	lipid metabolic process	2	208	0.249636076
GO:0009658	chloroplast organization	1	208	0.253161042
GO:0009524	phragmoplast	1	208	0.257606232
GO:0009845	seed germination	1	208	0.257606232
GO:0006260	DNA replication	1	208	0.261937874
GO:0009738	abscisic acid mediated signaling	1	208	0.261937874
GO:0004842	ubiquitin-protein ligase activity	2	208	0.272471955
GO:0019825	oxygen binding	2	208	0.272887554
GO:0042803	protein homodimerization activity	1	208	0.274269477
GO:0006813	potassium ion transport	1	208	0.278164775
GO:0009735	response to cytokinin stimulus	1	208	0.28195533
GO:0003899	DNA-directed RNA polymerase activity	1	208	0.28922895
GO:0006633	fatty acid biosynthetic process	1	208	0.296103581
GO:0006350	transcription	1	208	0.299395316
GO:0006334	nucleosome assembly	1	208	0.305695514
GO:0003779	actin binding	1	208	0.308707067
GO:0009624	response to nematode	1	208	0.31162828
GO:0005834	heterotrimeric G-protein complex	1	208	0.314460646
GO:0050832	defense response to fungus	1	208	0.314460646
GO:0006413	translational initiation	1	208	0.319864705
GO:0008415	acyltransferase activity	1	208	0.329670071
GO:0016567	protein ubiquitination	1	208	0.331920599
GO:0046658	anchored to plasma membrane	1	208	0.331920599
GO:0007264	small GTPase mediated signal transduction	1	208	0.336190088
GO:0017111	nucleoside-triphosphatase activity	1	208	0.342034872
GO:0004601	peroxidase activity	1	208	0.343839012
GO:0006812	cation transport	1	208	0.343839012
GO:0009055	electron carrier activity	1	208	0.355851537
GO:0006281	DNA repair	1	208	0.358224343
GO:0006950	response to stress	1	208	0.366116843
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	208	0.367299031

Cluster 6 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0008194	UDP-glycosyltransferase activity	1	208	0.367817815
GO:0030528	transcription regulator activity	1	208	0.368289589
GO:0009408	response to heat	1	208	0.369973712

Cluster 6

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000038	1	AT1G19440					
GO:0000049	1	AT2G40660					
GO:0000072	1	AT3G63130					
GO:0000103	2	AT1G19920	AT4G14680				
GO:0000145	1	AT3G10380					
GO:0000148	2	AT3G07160	AT5G13000				
GO:0000166	6	AT1G67120	AT2G33340	AT2G43770	AT3G18060	AT4G04940	AT5G11240
GO:0000175	1	AT3G46210					
GO:0000226	2	AT1G20090	AT2G35630				
GO:0000257	1	AT4G08790					
GO:0000271	1	AT3G57220					
GO:0000502	1	AT4G38630					
GO:0000902	1	AT1G20090					
GO:0000910	3	AT1G01040	AT2G35630	AT3G63130			
GO:0001522	1	AT3G04820					
GO:0001653	1	AT4G38630					
GO:0001671	1	AT3G12050					
GO:0002237	1	AT4G03190					
GO:0003682	1	AT1G74560					
GO:0003725	1	AT1G01040					
GO:0003735	14	AT1G67430	AT2G32060	AT3G47370	AT3G52580	AT3G60245	AT3G60770
		AT4G31700	AT4G35490	AT4G39200	AT5G09510	AT5G27770	AT5G39740
		AT5G57290	AT5G61170				
GO:0003743	3	AT1G21160	AT1G65220	AT4G20980			
GO:0003779	1	AT3G57410					
GO:0003824	6	AT1G19440	AT1G50110	AT1G75280	AT2G43400	AT3G03990	AT4G29120
GO:0003843	2	AT3G07160	AT5G13000				
GO:0003883	1	AT3G12670					
GO:0003899	1	AT5G60040					
GO:0003922	1	AT1G63660					
GO:0003923	1	AT5G19130					
GO:0003924	1	AT4G33650					
GO:0003938	1	AT1G16350					
GO:0003950	1	AT2G31320					
GO:0003975	1	AT3G57220					
GO:0004003	1	AT1G08840					
GO:0004021	1	AT1G70580					
GO:0004040	1	AT5G09420					
GO:0004124	1	AT3G04940					
GO:0004170	1	AT3G46940					
GO:0004379	1	AT5G57020					
GO:0004525	1	AT1G01040					
GO:0004601	1	AT2G39040					
GO:0004614	1	AT5G51820					
GO:0004630	1	AT4G11850					
GO:0004674	3	AT1G75640	AT2G26730	AT5G65700			
GO:0004683	2	AT3G20410	AT4G23650				
GO:0004713	1	AT5G59010					
GO:0004721	1	AT2G42810					

Cluster 6 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004781	2	AT1G19920	AT4G14680				
GO:0004812	1	AT3G04600					
GO:0004842	2	AT3G02260	AT4G03190				
GO:0004888	2	AT2G16640	AT5G44510				
GO:0005080	1	AT3G56490					
GO:0005085	1	AT3G60860					
GO:0005093	1	AT2G44100					
GO:0005098	1	AT3G63130					
GO:0005201	1	AT3G07390					
GO:0005215	5	AT1G30690	AT1G72150	AT1G73590	AT3G07100	AT3G51670	
GO:0005267	1	AT1G04690					
GO:0005319	1	AT1G19800					
GO:0005388	1	AT4G29900					
GO:0005488	9	AT1G75280	AT2G01690	AT2G32730	AT3G02260	AT3G52140	AT4G17270
		AT4G23540	AT5G59010	AT5G64270			
GO:0005516	3	AT1G51710	AT2G36910	AT4G29900			
GO:0005524	7	AT1G67120	AT1G75640	AT2G26730	AT3G04600	AT5G44510	AT5G59010
		AT5G65700					
GO:0005525	3	AT1G20090	AT4G33650	AT5G65270			
GO:0005576	2	AT3G03220	AT3G07390				
GO:0005618	5	AT2G33340	AT3G44110	AT3G47370	AT3G60770	AT5G43010	
GO:0005622	5	AT1G04850	AT1G27310	AT1G27970	AT1G80500	AT3G60860	
GO:0005634	19	AT1G01040	AT1G12310	AT1G15750	AT1G20090	AT1G27310	AT1G27970
		AT1G74560	AT1G76860	AT2G31320	AT2G32060	AT2G40290	AT2G42810
		AT2G43630	AT4G03190	AT4G30080	AT4G38630	AT5G43010	AT5G60040
		AT5G62190					
GO:0005635	4	AT1G27310	AT1G27970	AT2G42810	AT3G63130		
GO:0005663	1	AT1G21690					
GO:0005719	1	AT2G27040					
GO:0005730	14	AT1G20090	AT1G21690	AT1G61730	AT1G67430	AT2G27040	AT3G44110
		AT3G47370	AT3G58510	AT3G60770	AT4G31700	AT5G09510	AT5G27770
		AT5G39740	AT5G62190				
GO:0005732	1	AT1G76860					
GO:0005737	11	AT1G20090	AT1G27310	AT1G63660	AT1G73590	AT1G74560	AT1G79500
		AT2G37040	AT2G42810	AT3G12050	AT3G59990	AT5G37830	
GO:0005740	1	AT2G43400					
GO:0005773	7	AT1G52740	AT1G67430	AT1G72150	AT4G23650	AT5G11700	AT5G39740
		AT5G61170					
GO:0005777	2	AT1G70580	AT3G58510				
GO:0005778	1	AT2G42770					
GO:0005783	7	AT1G22200	AT1G65020	AT2G16760	AT2G31360	AT3G03330	AT3G57220
		AT5G19130					
GO:0005801	1	AT1G51160					
GO:0005819	1	AT2G35630					
GO:0005829	3	AT3G04600	AT4G33650	AT5G57020			
GO:0005834	1	AT2G43770					
GO:0005840	9	AT1G67430	AT3G60245	AT4G35490	AT4G39200	AT5G27770	AT5G39740
		AT5G57020	AT5G57290	AT5G61170			
GO:0005874	1	AT2G35630					
GO:0005886	46	AT1G04690	AT1G12310	AT1G20090	AT1G27970	AT1G30690	AT1G65020
		AT1G72150	AT1G73180	AT1G73590	AT1G75280	AT1G75640	AT1G75990
		AT2G01690	AT2G26730	AT2G36910	AT2G37050	AT2G45820	AT3G03330
		AT3G07160	AT3G07390	AT3G10380	AT3G17210	AT3G20410	AT3G25800
		AT3G44110	AT3G51670	AT3G52140	AT3G56490	AT3G57220	AT3G58510
		AT3G63130	AT4G11850	AT4G17270	AT4G23460	AT4G23650	AT4G29900
		AT4G31700	AT4G37190	AT5G09510	AT5G13000	AT5G27770	AT5G39740
		AT5G59010	AT5G62670	AT5G65270	AT5G65700		
GO:0005986	2	AT1G66430	AT4G10260				
GO:0006014	2	AT1G66430	AT4G10260				

Cluster 6 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0006075	2	AT3G07160	AT5G13000				
GO:0006098	1	AT4G29120					
GO:0006164	1	AT1G63660					
GO:0006177	2	AT1G16350	AT1G63660				
GO:0006260	1	AT1G08840					
GO:0006281	1	AT2G31320					
GO:0006306	1	AT2G27040					
GO:0006334	1	AT1G74560					
GO:0006342	1	AT2G27040					
GO:0006350	1	AT5G60040					
GO:0006364	1	AT4G04940					
GO:0006396	2	AT1G01040	AT3G46210				
GO:0006397	1	AT5G64270					
GO:0006412	13	AT1G67430	AT2G32060	AT2G40290	AT3G47370	AT3G52580	AT3G60245
		AT3G60770	AT4G31700	AT4G39200	AT5G09510	AT5G27770	AT5G39740
		AT5G61170					
GO:0006413	1	AT4G20980					
GO:0006414	1	AT5G57290					
GO:0006418	2	AT2G40660	AT3G04600				
GO:0006436	1	AT3G04600					
GO:0006446	1	AT1G65220					
GO:0006461	2	AT1G31730	AT4G23460				
GO:0006468	9	AT1G72540	AT1G75640	AT2G23070	AT2G26730	AT2G37050	AT3G20410
		AT4G23650	AT5G59010	AT5G65700			
GO:0006471	1	AT2G31320					
GO:0006499	4	AT3G20410	AT4G23650	AT5G57020	AT5G59010		
GO:0006511	5	AT1G75990	AT2G32730	AT4G03190	AT4G38630	AT5G43010	
GO:0006541	1	AT1G63660					
GO:0006606	3	AT1G27310	AT1G27970	AT3G63130			
GO:0006626	1	AT5G09420					
GO:0006629	2	AT2G31360	AT3G61580				
GO:0006633	1	AT2G31360					
GO:0006751	1	AT5G37830					
GO:0006807	1	AT4G08790					
GO:0006810	7	AT1G30690	AT1G51160	AT1G72150	AT1G80500	AT3G07100	AT3G51670
		AT5G62670					
GO:0006812	1	AT5G62670					
GO:0006813	1	AT1G04690					
GO:0006869	3	AT1G19800	AT4G27160	AT4G27170			
GO:0006886	4	AT1G31730	AT2G17790	AT4G23460	AT4G24550		
GO:0006888	2	AT1G51160	AT1G80500				
GO:0006913	3	AT1G27310	AT1G27970	AT2G42810			
GO:0006950	1	AT2G21620					
GO:0006974	1	AT4G38630					
GO:0006979	4	AT1G75280	AT2G31320	AT2G37040	AT2G39040		
GO:0007010	1	AT3G57410					
GO:0007169	3	AT1G75640	AT2G26730	AT5G65700			
GO:0007186	1	AT2G20890					
GO:0007264	1	AT5G65270					
GO:0007389	1	AT4G30080					
GO:0008017	1	AT2G35630					
GO:0008026	5	AT1G01040	AT3G58510	AT5G08610	AT5G61140	AT5G62190	
GO:0008033	1	AT1G63660					
GO:0008134	1	AT1G67120					
GO:0008142	1	AT3G09300					
GO:0008152	7	AT1G50110	AT1G79500	AT3G03330	AT3G20790	AT4G29120	AT5G06060
		AT5G62670					
GO:0008194	1	AT1G06000					
GO:0008202	1	AT3G09300					

Cluster 6 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0008283	1	AT1G74560					
GO:0008289	2	AT4G27160	AT4G27170				
GO:0008361	1	AT2G36910					
GO:0008415	1	AT1G19440					
GO:0008428	1	AT5G16450					
GO:0008536	2	AT1G27310	AT1G27970				
GO:0008540	3	AT2G32730	AT4G38630	AT5G43010			
GO:0008541	1	AT1G75990					
GO:0008565	3	AT1G27310	AT1G27970	AT4G24550			
GO:0008601	1	AT3G25800					
GO:0008654	1	AT1G13560					
GO:0008676	1	AT1G79500					
GO:0009055	1	AT2G43400					
GO:0009058	2	AT1G63660	AT4G01210				
GO:0009081	1	AT1G50110					
GO:0009113	1	AT1G63660					
GO:0009117	1	AT1G63660					
GO:0009269	1	AT2G21620					
GO:0009394	1	AT3G46940					
GO:0009408	1	AT4G38630					
GO:0009504	1	AT3G63130					
GO:0009507	30	AT1G08640	AT1G08840	AT1G19800	AT1G19920	AT1G33810	AT1G50030
		AT1G61730	AT1G66430	AT1G70580	AT1G72150	AT1G72540	AT2G20890
		AT2G23070	AT2G33340	AT2G37020	AT2G42770	AT2G43630	AT3G52140
		AT3G60770	AT3G63130	AT4G14680	AT4G20980	AT4G31700	AT4G33650
		AT5G08610	AT5G10540	AT5G24690	AT5G44510	AT5G51820	AT5G64270
GO:0009524	1	AT2G35630					
GO:0009527	1	AT2G20890					
GO:0009528	1	AT2G20890					
GO:0009532	1	AT2G20890					
GO:0009534	1	AT2G20890					
GO:0009535	3	AT1G33810	AT2G20890	AT2G43630			
GO:0009555	3	AT3G07160	AT3G07610	AT4G38630			
GO:0009556	1	AT3G07160					
GO:0009570	4	AT1G66430	AT1G70580	AT2G20890	AT5G51820		
GO:0009574	1	AT2G35630					
GO:0009590	1	AT5G51820					
GO:0009616	1	AT1G01040					
GO:0009624	1	AT2G36910					
GO:0009628	1	AT2G31320					
GO:0009630	1	AT1G73590					
GO:0009637	1	AT2G36910					
GO:0009639	1	AT2G36910					
GO:0009640	3	AT1G73590	AT2G36910	AT3G02260			
GO:0009646	1	AT2G43400					
GO:0009658	1	AT4G33650					
GO:0009699	1	AT2G37040					
GO:0009706	2	AT1G19800	AT5G24690				
GO:0009707	2	AT1G19800	AT2G16640				
GO:0009733	7	AT1G15750	AT2G36910	AT3G02260	AT3G07390	AT4G03190	AT4G30080
		AT4G38630					
GO:0009735	1	AT4G38630					
GO:0009737	3	AT1G03880	AT2G31320	AT4G38630			
GO:0009738	1	AT4G23650					
GO:0009744	2	AT1G20950	AT4G38630				
GO:0009749	1	AT1G20950					
GO:0009750	1	AT1G20950					
GO:0009793	5	AT1G08840	AT1G21690	AT1G50030	AT3G12670	AT4G11850	
GO:0009807	1	AT4G23690					

Cluster 6 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009816	2	AT2G27040	AT4G11850				
GO:0009826	2	AT3G03220	AT5G05690				
GO:0009828	1	AT3G03220					
GO:0009831	1	AT3G03220					
GO:0009845	1	AT1G03880					
GO:0009846	1	AT3G10380					
GO:0009853	1	AT1G70580					
GO:0009860	2	AT1G20090	AT3G10380				
GO:0009880	1	AT1G01040					
GO:0009908	2	AT1G01040	AT3G07610				
GO:0009909	1	AT1G52740					
GO:0009911	1	AT5G05690					
GO:0009920	1	AT2G35630					
GO:0009925	1	AT1G73590					
GO:0009926	3	AT1G73590	AT2G36910	AT3G02260			
GO:0009934	1	AT5G65700					
GO:0009941	10	AT1G08640	AT1G19800	AT1G33810	AT1G67120	AT2G20890	AT2G42770
		AT2G43630	AT4G33650	AT5G24690	AT5G51820		
GO:0009958	1	AT2G36910					
GO:0009982	1	AT3G04820					
GO:0010011	1	AT4G03190					
GO:0010017	1	AT2G42810					
GO:0010027	1	AT2G20890					
GO:0010029	1	AT4G38630					
GO:0010051	2	AT1G15750	AT1G73590				
GO:0010064	1	AT5G57020					
GO:0010072	1	AT1G15750					
GO:0010075	1	AT5G65700					
GO:0010098	1	AT1G01040					
GO:0010102	1	AT3G07390					
GO:0010119	2	AT1G20090	AT4G23650				
GO:0010150	1	AT4G38630					
GO:0010152	1	AT4G03190					
GO:0010182	1	AT2G20890					
GO:0010207	1	AT2G20890					
GO:0010224	1	AT5G05690					
GO:0010228	1	AT1G01040					
GO:0010267	1	AT1G01040					
GO:0010268	1	AT5G05690					
GO:0010306	1	AT1G79500					
GO:0010311	1	AT1G74560					
GO:0010317	1	AT1G20950					
GO:0010319	2	AT2G20890	AT5G51820				
GO:0010329	1	AT2G36910					
GO:0010338	1	AT1G73590					
GO:0010358	1	AT1G73590					
GO:0010359	1	AT4G23650					
GO:0010445	1	AT1G01040					
GO:0010480	1	AT5G65700					
GO:0010583	1	AT1G73590					
GO:0010599	1	AT1G01040					
GO:0015030	1	AT2G27040					
GO:0015031	2	AT2G44100	AT5G65270				
GO:0015935	1	AT3G47370					
GO:0015992	2	AT4G26210	AT5G62670				
GO:0016020	17	AT1G04690	AT1G13560	AT1G67430	AT1G72150	AT1G73590	AT1G75990
		AT2G16640	AT2G31360	AT3G02260	AT3G47370	AT3G61580	AT4G31700
		AT4G33650	AT4G38630	AT5G27770	AT5G62670	AT5G65270	
GO:0016070	1	AT5G62190					

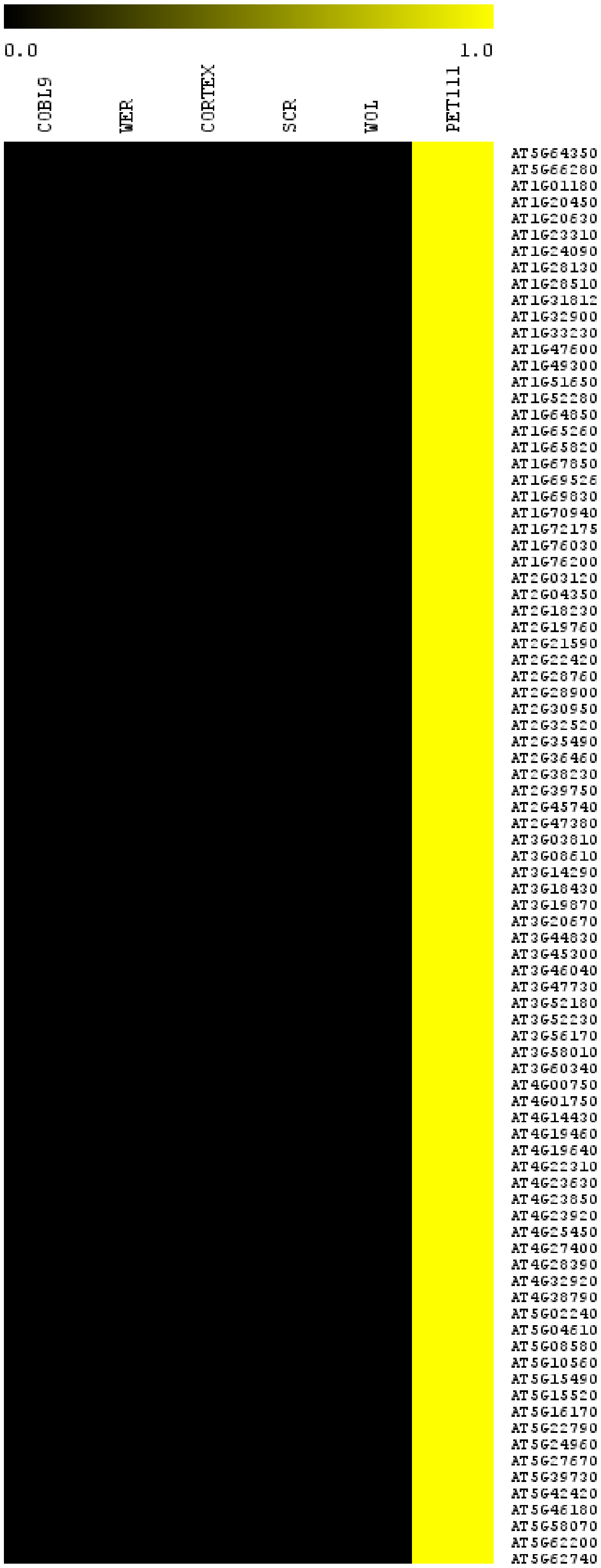
Cluster 6 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0016071	1	AT1G76860					
GO:0016132	1	AT5G05690					
GO:0016192	2	AT1G31730	AT4G23460				
GO:0016301	9	AT1G66430	AT1G72540	AT1G75640	AT2G23070	AT2G37050	AT3G20410
		AT4G10260	AT4G23650	AT5G65700			
GO:0016303	1	AT1G50030					
GO:0016469	1	AT4G26210					
GO:0016485	1	AT3G59990					
GO:0016491	5	AT2G31360	AT3G03330	AT3G20790	AT3G61580	AT5G06060	
GO:0016559	1	AT4G33650					
GO:0016564	2	AT1G15750	AT1G75280				
GO:0016567	1	AT2G33340					
GO:0016579	1	AT1G51710					
GO:0016757	3	AT1G06000	AT4G01210	AT5G13000			
GO:0016887	4	AT1G21690	AT1G67120	AT5G43010	AT5G62670		
GO:0017111	1	AT1G67120					
GO:0017151	1	AT5G62190					
GO:0017168	1	AT5G37830					
GO:0019107	1	AT5G57020					
GO:0019252	1	AT5G51820					
GO:0019344	1	AT3G04940					
GO:0019575	2	AT1G66430	AT4G10260				
GO:0019654	2	AT1G66430	AT4G10260				
GO:0019825	2	AT2G27000	AT5G05690				
GO:0022625	5	AT1G67430	AT3G60245	AT4G35490	AT5G27770	AT5G39740	
GO:0022626	10	AT1G67430	AT2G32060	AT3G47370	AT3G60770	AT4G31700	AT4G39200
		AT5G09510	AT5G39740	AT5G57290	AT5G61170		
GO:0022627	8	AT2G32060	AT3G47370	AT3G52580	AT3G60770	AT4G31700	AT4G39200
		AT5G09510	AT5G61170				
GO:0030117	1	AT1G31730					
GO:0030125	1	AT4G24550					
GO:0030127	1	AT3G07100					
GO:0030154	1	AT1G74560					
GO:0030163	2	AT1G75990	AT4G38630				
GO:0030176	1	AT2G42810					
GO:0030198	1	AT3G07390					
GO:0030276	2	AT1G31730	AT4G23460				
GO:0030422	1	AT1G01040					
GO:0030528	1	AT1G61730					
GO:0030572	1	AT1G13560					
GO:0030981	1	AT2G35630					
GO:0031048	1	AT2G27040					
GO:0031053	1	AT1G01040					
GO:0031119	1	AT3G04820					
GO:0032012	1	AT3G60860					
GO:0032153	1	AT3G63130					
GO:0032454	1	AT3G07610					
GO:0032776	1	AT3G07610					
GO:0033169	1	AT3G07610					
GO:0035091	1	AT4G33650					
GO:0035196	1	AT1G01040					
GO:0035198	1	AT4G30080					
GO:0035279	1	AT1G01040					
GO:0040007	1	AT5G57020					
GO:0042147	1	AT2G17790					
GO:0042254	3	AT3G60245	AT4G35490	AT5G39740			
GO:0042284	1	AT3G61580					
GO:0042325	1	AT3G25800					
GO:0042335	1	AT1G19440					

Cluster 6 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0042393	1	AT1G74560					
GO:0042626	1	AT2G36910					
GO:0042742	3	AT1G52740	AT3G17210	AT5G44510			
GO:0042803	1	AT1G15750					
GO:0043161	1	AT4G38630					
GO:0043224	1	AT4G03190					
GO:0043254	1	AT1G67120					
GO:0043481	1	AT2G36910					
GO:0045014	1	AT4G03190					
GO:0045036	1	AT2G16640					
GO:0045037	1	AT2G20890					
GO:0045038	1	AT2G20890					
GO:0045177	1	AT1G73590					
GO:0045548	1	AT2G37040					
GO:0045735	5	AT1G03880	AT1G07750	AT2G28490	AT4G27160	AT4G27170	
GO:0046658	1	AT3G07390					
GO:0046686	7	AT1G74560	AT1G75280	AT2G42810	AT3G12670	AT3G25800	AT4G08790
		AT5G10540					
GO:0046933	1	AT4G26210					
GO:0046961	1	AT4G26210					
GO:0047334	1	AT1G20950					
GO:0047958	1	AT1G70580					
GO:0048046	3	AT1G72150	AT5G10540	AT5G51820			
GO:0048227	1	AT2G44100					
GO:0048229	1	AT5G65700					
GO:0048281	1	AT4G29900					
GO:0048283	1	AT3G02260					
GO:0048364	2	AT1G73590	AT3G02260				
GO:0048366	2	AT3G07610	AT4G38630				
GO:0048367	2	AT1G73590	AT4G29900				
GO:0048437	1	AT5G65700					
GO:0048443	2	AT2G36910	AT4G03190				
GO:0048455	1	AT4G38630					
GO:0048528	1	AT4G38630					
GO:0048589	2	AT3G07160	AT4G03190				
GO:0048653	1	AT5G65700					
GO:0048767	1	AT4G38630					
GO:0048829	1	AT4G30080					
GO:0050832	1	AT3G17210					
GO:0051087	1	AT3G12050					
GO:0051252	1	AT5G16450					
GO:0051258	1	AT4G37190					
GO:0051301	1	AT4G30080					
GO:0051555	1	AT1G06000					
GO:0051788	1	AT4G38630					
GO:0052543	1	AT3G07160					

Cluster 7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Cluster 7

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AT5G64350
AT5G66280

Cluster 7 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005773	vacuole	11	87	2.00E-06
GO:0005739	mitochondrion	13	87	1.40E-05
GO:0009941	chloroplast envelope	8	87	1.33E-04
GO:0005886	plasma membrane	17	87	3.17E-04
GO:0015629	actin cytoskeleton	2	87	9.12E-04
GO:0005777	peroxisome	4	87	0.001102895
GO:0009225	nucleotide-sugar metabolic process	2	87	0.002465571
GO:0009535	chloroplast thylakoid membrane	5	87	0.003221857
GO:0003824	catalytic activity	6	87	0.003622847
GO:0004587	ornithine-oxo-acid transaminase activity	1	87	0.004171661
GO:0008470	isovaleryl-CoA dehydrogenase activity	1	87	0.004171661
GO:0009606	tropism	1	87	0.004171661
GO:0010170	glucose-1-phosphate adenylyltransferase complex	1	87	0.004171661
GO:0012506	vesicle membrane	1	87	0.004171661
GO:0016328	lateral plasma membrane	1	87	0.004171661
GO:0031210	phosphatidylcholine binding	1	87	0.004171661
GO:0005783	endoplasmic reticulum	5	87	0.004204992
GO:0015031	protein transport	3	87	0.004662127
GO:0016020	membrane	12	87	0.005807738
GO:0009409	response to cold	4	87	0.006812963
GO:0006754	ATP biosynthetic process	1	87	0.008308916
GO:0008154	actin polymerization or depolymerization	1	87	0.008308916
GO:0008446	GDP-mannose 4,6-dehydratase activity	1	87	0.008308916

Cluster 7 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009250	glucan biosynthetic process	1	87	0.008308916
GO:0047958	glycine:2-oxoglutarate aminotransferase activity	1	87	0.008308916
GO:0045271	respiratory chain complex I	2	87	0.009930159
GO:0005215	transporter activity	4	87	0.011939347
GO:0004021	L-alanine:2-oxoglutarate aminotransferase activity	1	87	0.012411973
GO:0004096	catalase activity	1	87	0.012411973
GO:0004165	dodecenoyl-CoA delta-isomerase activity	1	87	0.012411973
GO:0004523	ribonuclease H activity	1	87	0.012411973
GO:0006561	proline biosynthetic process	1	87	0.012411973
GO:0015865	purine nucleotide transport	1	87	0.012411973
GO:0048766	root hair initiation	1	87	0.012411973
GO:0031977	thylakoid lumen	2	87	0.014285648
GO:0006633	fatty acid biosynthetic process	2	87	0.015471601
GO:0010287	plastoglobule	2	87	0.016078331
GO:0003978	UDP-glucose 4-epimerase activity	1	87	0.016481044
GO:0003979	UDP-glucose 6-dehydrogenase activity	1	87	0.016481044
GO:0005471	ATP:ADP antiporter activity	1	87	0.016481044
GO:0005779	integral to peroxisomal membrane	1	87	0.016481044
GO:0006552	leucine catabolic process	1	87	0.016481044
GO:0009062	fatty acid catabolic process	1	87	0.016481044
GO:0010082	regulation of root meristem growth	1	87	0.016481044
GO:0010279	indole-3-acetic acid amido synthetase activity	1	87	0.016481044
GO:0006334	nucleosome assembly	2	87	0.017318579
GO:0003779	actin binding	2	87	0.017951816
GO:0016462	pyrophosphatase activity	1	87	0.020516334
GO:0000062	acyl-CoA binding	1	87	0.020516334
GO:0004607	phosphatidylcholine-sterol O-acyltransferase activity	1	87	0.024518053
GO:0008878	glucose-1-phosphate adenylyltransferase activity	1	87	0.024518053
GO:0009044	xylan 1,4-beta-xylosidase activity	1	87	0.024518053
GO:0009527	plastid outer membrane	1	87	0.024518053
GO:0010205	photoinhibition	1	87	0.024518053
GO:0010304	PSII associated light-harvesting complex II catabolic process	1	87	0.024518053
GO:0045037	protein import into chloroplast stroma	1	87	0.024518053
GO:0005509	calcium ion binding	3	87	0.024867218
GO:0007264	small GTPase mediated signal transduction	2	87	0.025452264
GO:0022626	cytosolic ribosome	3	87	0.027503954
GO:0009507	chloroplast	15	87	0.027947013
GO:0004427	inorganic diphosphatase activity	1	87	0.028486405
GO:0004467	long-chain-fatty-acid-CoA ligase activity	1	87	0.028486405
GO:0006995	cellular response to nitrogen starvation	1	87	0.028486405
GO:0008474	palmitoyl-(protein) hydrolase activity	1	87	0.028486405
GO:0009970	cellular response to sulfate starvation	1	87	0.028486405
GO:0030247	polysaccharide binding	1	87	0.028486405
GO:0009579	thylakoid	3	87	0.028670178
GO:0005525	GTP binding	3	87	0.030660689
GO:0004129	cytochrome-c oxidase activity	1	87	0.032421595
GO:0004556	alpha-amylase activity	1	87	0.032421595
GO:0005982	starch metabolic process	1	87	0.032421595
GO:0004332	fructose-bisphosphate aldolase activity	1	87	0.036323827
GO:0009415	response to water	1	87	0.036323827
GO:0009986	cell surface	1	87	0.036323827
GO:0016559	peroxisome fission	1	87	0.036323827

Cluster 7 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022627	cytosolic small ribosomal subunit	2	87	0.039508169
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	1	87	0.040193304
GO:0019252	starch biosynthetic process	1	87	0.040193304
GO:0050826	response to freezing	1	87	0.040193304
GO:0009058	biosynthetic process	2	87	0.042026177
GO:0006499	N-terminal protein myristoylation	4	87	0.042216889
GO:0009737	response to abscisic acid stimulus	3	87	0.043728214
GO:0010197	polar nucleus fusion	1	87	0.044030227
GO:0010252	auxin homeostasis	1	87	0.044030227
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	2	87	0.045448749
GO:0007389	pattern specification process	1	87	0.047834796
GO:0009534	chloroplast thylakoid	1	87	0.047834796
GO:0009672	auxin:hydrogen symporter activity	1	87	0.047834796
GO:0042546	cell wall biogenesis	1	87	0.047834796
GO:0005983	starch catabolic process	1	87	0.051607211
GO:0048767	root hair elongation	1	87	0.051607211
GO:0006098	pentose-phosphate shunt	1	87	0.05534767
GO:0007031	peroxisome organization	1	87	0.05534767
GO:0044237	cellular metabolic process	1	87	0.05534767
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	1	87	0.05905637
GO:0048868	pollen tube development	1	87	0.05905637
GO:0050662	coenzyme binding	1	87	0.05905637
GO:0005730	nucleolus	3	87	0.059931641
GO:0009508	plastid chromosome	1	87	0.062733508
GO:0010027	thylakoid membrane organization	1	87	0.062733508
GO:0009416	response to light stimulus	2	87	0.063467978
GO:0005778	peroxisomal membrane	1	87	0.066379277
GO:0009630	gravitropism	1	87	0.066379277
GO:0046983	protein dimerization activity	1	87	0.066379277
GO:0009631	cold acclimation	1	87	0.069993874
GO:0009749	response to glucose stimulus	1	87	0.069993874
GO:0005839	proteasome core complex	1	87	0.077130316
GO:0007010	cytoskeleton organization	1	87	0.077130316
GO:0005528	FK506 binding	1	87	0.084144366
GO:0005819	spindle	1	87	0.084144366
GO:0009707	chloroplast outer membrane	1	87	0.084144366
GO:0009536	plastid	2	87	0.085382806
GO:0009651	response to salt stress	3	87	0.08730815
GO:0004518	nuclease activity	1	87	0.087605967
GO:0009295	nucleoid	1	87	0.094439263
GO:0009846	pollen germination	1	87	0.094439263
GO:0016036	cellular response to phosphate starvation	1	87	0.094439263
GO:0005618	cell wall	3	87	0.095061828
GO:0006810	transport	3	87	0.103943616
GO:0005759	mitochondrial matrix	1	87	0.107751418
GO:0009853	photorespiration	1	87	0.107751418
GO:0009706	chloroplast inner membrane	1	87	0.11423321
GO:0042542	response to hydrogen peroxide	1	87	0.117431168
GO:0008152	metabolic process	4	87	0.120231474
GO:0009570	chloroplast stroma	3	87	0.123164952

Cluster 7 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005829	cytosol	2	87	0.125986488
GO:0009926	auxin polar transport	1	87	0.129940908
GO:0000786	nucleosome	1	87	0.132998702
GO:0009524	phragmoplast	1	87	0.132998702
GO:0009744	response to sucrose stimulus	1	87	0.132998702
GO:0042538	hyperosmotic salinity response	1	87	0.132998702
GO:0006470	protein amino acid dephosphorylation	1	87	0.142007735
GO:0006979	response to oxidative stress	2	87	0.144659838
GO:0005198	structural molecule activity	1	87	0.144956536
GO:0006839	mitochondrial transport	1	87	0.147878516
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	1	87	0.150773846
GO:0004364	glutathione transferase activity	1	87	0.153642693
GO:0005737	cytoplasm	3	87	0.158911764
GO:0008168	methyltransferase activity	1	87	0.159301608
GO:0008233	peptidase activity	1	87	0.159301608
GO:0006464	protein modification process	1	87	0.162092008
GO:0005488	binding	3	87	0.16764531
GO:0009555	pollen development	1	87	0.178297928
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	87	0.180911009
GO:0048046	apoplast	2	87	0.186388441
GO:0004601	peroxidase activity	1	87	0.210386628
GO:0046686	response to cadmium ion	2	87	0.212942056
GO:0048364	root development	1	87	0.214972243
GO:0003735	structural constituent of ribosome	2	87	0.216797404
GO:0009543	chloroplast thylakoid lumen	1	87	0.217231137
GO:0006412	translation	2	87	0.224118866
GO:0016757	transferase activity, transferring glycosyl groups	2	87	0.224705427
GO:0005743	mitochondrial inner membrane	1	87	0.230318849
GO:0009826	unidimensional cell growth	1	87	0.238610963
GO:0006869	lipid transport	1	87	0.246567079
GO:0006950	response to stress	1	87	0.250421867
GO:0009408	response to heat	1	87	0.266784344
GO:0009611	response to wounding	1	87	0.287722431
GO:0009753	response to jasmonic acid stimulus	1	87	0.296376515
GO:0016887	ATPase activity	1	87	0.297759612
GO:0005794	Golgi apparatus	1	87	0.315427882
GO:0009414	response to water deprivation	1	87	0.324176005
GO:0006629	lipid metabolic process	1	87	0.333831073
GO:0016787	hydrolase activity	1	87	0.33646357
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	1	87	0.344405025
GO:0005840	ribosome	1	87	0.359131327
GO:0006511	ubiquitin-dependent protein catabolic process	1	87	0.361679637
GO:0006457	protein folding	1	87	0.36629976
GO:0031225	anchored to membrane	1	87	0.366562434
GO:0009733	response to auxin stimulus	1	87	0.369762843

Cluster 7

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000062	1	AT1G31812	
GO:0000786	1	AT3G20670	
GO:0003735	2	AT3G46040	AT5G15520
GO:0003755	1	AT5G64350	

Cluster 7 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0003779	2	AT1G20450	AT2G19760				
GO:0003824	6	AT2G28760	AT2G36460	AT4G14430	AT4G23850	AT5G02240	AT5G04610
GO:0003978	1	AT4G23920					
GO:0003979	1	AT5G15490					
GO:0004021	1	AT1G23310					
GO:0004096	1	AT1G20630					
GO:0004129	1	AT2G47380					
GO:0004165	1	AT4G14430					
GO:0004332	1	AT2G36460					
GO:0004364	1	AT1G65820					
GO:0004427	1	AT2G18230					
GO:0004467	1	AT2G04350					
GO:0004518	1	AT3G56170					
GO:0004523	1	AT1G24090					
GO:0004553	1	AT5G10560					
GO:0004556	1	AT1G69830					
GO:0004587	1	AT5G46180					
GO:0004601	1	AT2G22420					
GO:0004607	1	AT3G44830					
GO:0005198	1	AT2G35490					
GO:0005215	4	AT1G70940	AT3G47730	AT4G25450	AT5G58070		
GO:0005471	1	AT4G28390					
GO:0005488	3	AT3G19870	AT4G28390	AT5G02240			
GO:0005509	3	AT1G64850	AT3G18430	AT5G08580			
GO:0005525	3	AT1G49300	AT1G52280	AT4G19640			
GO:0005528	1	AT5G64350					
GO:0005618	3	AT1G20630	AT2G19760	AT5G15490			
GO:0005730	3	AT2G19760	AT5G15520	AT5G27670			
GO:0005737	3	AT1G20450	AT1G28130	AT2G19760			
GO:0005739	13	AT1G20630	AT1G51650	AT2G36460	AT2G45740	AT2G47380	AT3G08610
		AT3G45300	AT3G47730	AT4G22310	AT4G28390	AT5G22790	AT5G46180
		AT5G58070					
GO:0005743	1	AT4G28390					
GO:0005759	1	AT3G45300					
GO:0005773	11	AT1G23310	AT1G52280	AT1G65820	AT2G28900	AT3G18430	AT3G60340
		AT4G23630	AT4G32920	AT5G10560	AT5G58070	AT5G62740	
GO:0005777	4	AT1G20630	AT1G23310	AT2G45740	AT4G14430		
GO:0005778	1	AT2G45740					
GO:0005779	1	AT2G45740					
GO:0005783	5	AT1G65820	AT2G03120	AT2G04350	AT4G23630	AT5G58070	
GO:0005794	1	AT4G00750					
GO:0005819	1	AT2G19760					
GO:0005829	2	AT1G31812	AT4G23920				
GO:0005839	1	AT3G14290					
GO:0005840	1	AT5G15520					
GO:0005886	17	AT1G31812	AT1G49300	AT1G52280	AT1G70940	AT2G19760	AT2G28760
		AT2G36460	AT4G19640	AT4G23630	AT4G23850	AT5G02240	AT5G08580
		AT5G10560	AT5G39730	AT5G58070	AT5G62200	AT5G62740	
GO:0005982	1	AT3G52180					
GO:0005983	1	AT1G69830					
GO:0006098	1	AT2G36460					
GO:0006334	2	AT3G20670	AT5G27670				
GO:0006412	2	AT3G46040	AT5G15520				
GO:0006457	1	AT5G64350					
GO:0006464	1	AT3G60340					
GO:0006470	1	AT3G52180					
GO:0006499	4	AT3G03810	AT3G18430	AT3G56170	AT5G62740		
GO:0006511	1	AT3G14290					
GO:0006552	1	AT3G45300					

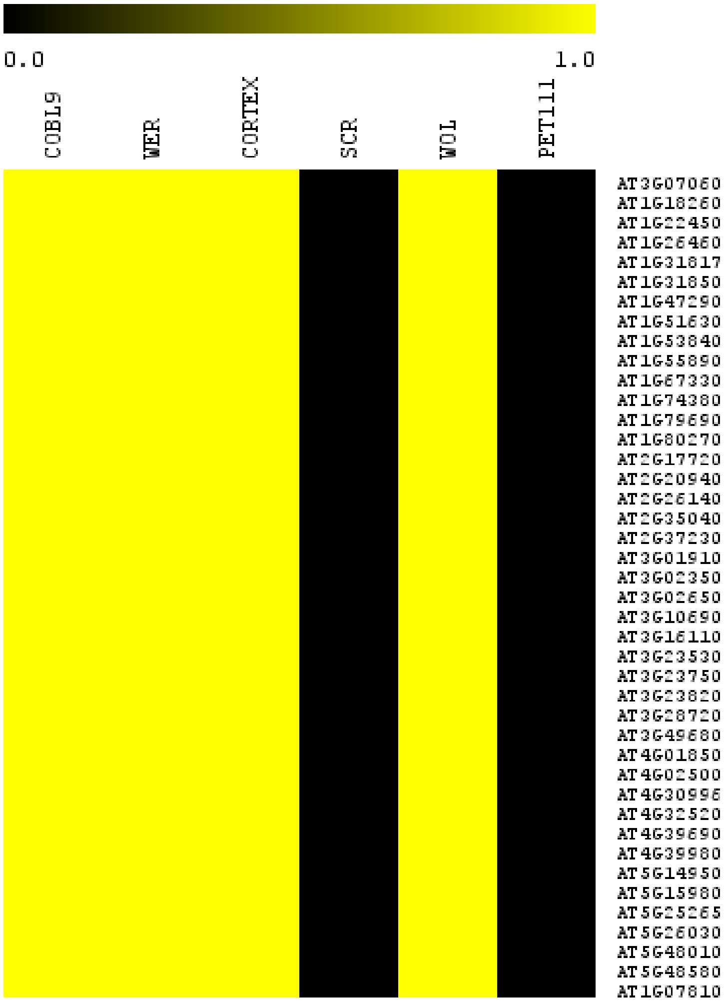
Cluster 7 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0006561	1	AT5G46180					
GO:0006629	1	AT3G44830					
GO:0006633	2	AT2G04350	AT4G23850				
GO:0006754	1	AT1G51650					
GO:0006810	3	AT4G25450	AT4G28390	AT5G58070			
GO:0006839	1	AT4G28390					
GO:0006869	1	AT1G31812					
GO:0006950	1	AT1G20450					
GO:0006979	2	AT1G49300	AT2G22420				
GO:0006995	1	AT1G20630					
GO:0007010	1	AT2G19760					
GO:0007031	1	AT2G45740					
GO:0007264	2	AT1G52280	AT4G19640				
GO:0007389	1	AT1G70940					
GO:0008138	1	AT3G52180					
GO:0008152	4	AT1G69526	AT2G18230	AT4G14430	AT5G02240		
GO:0008154	1	AT2G19760					
GO:0008168	1	AT1G69526					
GO:0008233	1	AT3G14290					
GO:0008446	1	AT5G66280					
GO:0008470	1	AT3G45300					
GO:0008474	1	AT3G60340					
GO:0008878	1	AT2G21590					
GO:0009044	1	AT5G10560					
GO:0009058	2	AT1G32900	AT4G19460				
GO:0009062	1	AT4G14430					
GO:0009225	2	AT2G28760	AT5G66280				
GO:0009250	1	AT1G32900					
GO:0009295	1	AT1G65260					
GO:0009408	1	AT5G58070					
GO:0009409	4	AT1G20450	AT1G31812	AT2G28900	AT5G58070		
GO:0009414	1	AT1G20450					
GO:0009415	1	AT1G20450					
GO:0009416	2	AT1G20630	AT5G58070				
GO:0009507	15	AT1G23310	AT1G32900	AT1G65260	AT1G69526	AT1G69830	AT2G28900
		AT2G30950	AT2G32520	AT2G35490	AT2G45740	AT3G03810	AT3G52180
		AT3G52230	AT3G58010	AT4G25450			
GO:0009508	1	AT1G65260					
GO:0009524	1	AT2G19760					
GO:0009527	1	AT2G28900					
GO:0009534	1	AT1G65260					
GO:0009535	5	AT1G65260	AT2G30950	AT2G35490	AT3G52230	AT3G58010	
GO:0009536	2	AT4G28390	AT5G22790				
GO:0009543	1	AT5G64350					
GO:0009555	1	AT2G03120					
GO:0009570	3	AT1G65260	AT1G69830	AT3G52180			
GO:0009579	3	AT2G30950	AT2G35490	AT3G58010			
GO:0009606	1	AT1G70940					
GO:0009611	1	AT2G28900					
GO:0009630	1	AT1G70940					
GO:0009631	1	AT1G20450					
GO:0009651	3	AT1G49300	AT2G36460	AT5G39730			
GO:0009672	1	AT1G70940					
GO:0009706	1	AT5G22790					
GO:0009707	1	AT3G52230					
GO:0009733	1	AT1G28130					
GO:0009737	3	AT1G20450	AT1G20630	AT5G02240			
GO:0009744	1	AT2G28900					
GO:0009749	1	AT2G28900					
GO:0009753	1	AT2G28900					

Cluster 7 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009826	1	AT2G19760					
GO:0009846	1	AT2G03120					
GO:0009853	1	AT1G23310					
GO:0009926	1	AT1G70940					
GO:0009941	8	AT1G20630	AT1G65260	AT2G28900	AT2G30950	AT3G52230	AT4G25450
		AT4G28390	AT5G22790				
GO:0009970	1	AT1G20630					
GO:0009986	1	AT1G70940					
GO:0010027	1	AT2G30950					
GO:0010082	1	AT1G70940					
GO:0010170	1	AT2G21590					
GO:0010197	1	AT3G03810					
GO:0010205	1	AT2G30950					
GO:0010252	1	AT1G28130					
GO:0010279	1	AT1G28130					
GO:0010287	2	AT2G35490	AT3G58010				
GO:0010304	1	AT2G30950					
GO:0012506	1	AT1G70940					
GO:0015031	3	AT1G52280	AT2G28900	AT4G19640			
GO:0015450	1	AT2G28900					
GO:0015629	2	AT1G20450	AT2G19760				
GO:0015865	1	AT4G28390					
GO:0016020	12	AT1G20450	AT1G23310	AT1G65260	AT1G65820	AT2G18230	AT2G30950
		AT2G36460	AT4G25450	AT4G28390	AT5G15520	AT5G42420	AT5G62740
GO:0016036	1	AT1G20630					
GO:0016328	1	AT1G70940					
GO:0016462	1	AT2G18230					
GO:0016559	1	AT2G45740					
GO:0016757	2	AT1G32900	AT4G19460				
GO:0016787	1	AT2G32520					
GO:0016887	1	AT2G30950					
GO:0019252	1	AT2G21590					
GO:0022626	3	AT1G20630	AT3G14290	AT3G46040			
GO:0022627	2	AT3G46040	AT5G15520				
GO:0030247	1	AT3G52180					
GO:0031210	1	AT1G31812					
GO:0031225	1	AT5G62200					
GO:0031977	2	AT2G30950	AT3G58010				
GO:0042538	1	AT5G46180					
GO:0042542	1	AT1G20630					
GO:0042546	1	AT4G23920					
GO:0042626	2	AT3G47730	AT4G25450				
GO:0044237	1	AT5G02240					
GO:0045037	1	AT2G28900					
GO:0045271	2	AT1G76200	AT3G08610				
GO:0046686	2	AT1G20630	AT2G36460				
GO:0046933	1	AT1G51650					
GO:0046983	1	AT4G23920					
GO:0047958	1	AT1G23310					
GO:0048046	2	AT1G23310	AT5G02240				
GO:0048364	1	AT1G70940					
GO:0048766	1	AT1G70940					
GO:0048767	1	AT1G70940					
GO:0048868	1	AT3G03810					
GO:0050662	1	AT5G02240					
GO:0050826	1	AT1G31812					

Cluster 8



Cluster 8

AT1G07810
AT1G18260
AT1G22450
AT1G26460
AT1G31817
AT1G31850
AT1G47290
AT1G51630
AT1G53840
AT1G55890
AT1G67330
AT1G74380
AT1G79690
AT1G80270
AT2G17720
AT2G20940
AT2G26140
AT2G35040
AT2G37230
AT3G01910
AT3G02350
AT3G02650

Cluster 8 (con.)

AT3G07060
AT3G10690
AT3G16110
AT3G23530
AT3G23750
AT3G23820
AT3G28720
AT3G49680
AT4G01850
AT4G02500
AT4G30996
AT4G32520
AT4G39690
AT4G39980
AT5G14950
AT5G15980
AT5G25265
AT5G26030
AT5G48010
AT5G48580

Cluster 8 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	11	42	2.17E-07
GO:0033843	xyloglucan 6-xylosyltransferase activity	2	42	1.19E-05
GO:0005794	Golgi apparatus	4	42	1.21E-04
GO:0048767	root hair elongation	2	42	3.02E-04
GO:0003937	IMP cyclohydrolase activity	1	42	0.002013906
GO:0004643	phosphoribosylaminoimidazolecarboxamide formyltransferase activity	1	42	0.002013906
GO:0008482	sulfite oxidase activity	1	42	0.002013906
GO:0010477	response to sulfur dioxide	1	42	0.002013906
GO:0051746	thalianol synthase activity	1	42	0.002013906
GO:0009536	plastid	3	42	0.002140663
GO:0009423	chorismate biosynthetic process	1	42	0.004019892
GO:0010263	tricyclic triterpenoid biosynthetic process	1	42	0.004019892
GO:0033014	tetrapyrrole biosynthetic process	1	42	0.004019892
GO:0047012	sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity	1	42	0.004019892
GO:0003824	catalytic activity	4	42	0.00556488
GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	1	42	0.006017983
GO:0004325	ferrochelatase activity	1	42	0.006017983
GO:0035252	UDP-xylosyltransferase activity	1	42	0.006017983
GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogenase activity	1	42	0.0080082
GO:0004084	branched-chain-amino-acid transaminase activity	1	42	0.0080082
GO:0004478	methionine adenosyltransferase activity	1	42	0.0080082
GO:0006268	DNA unwinding during replication	1	42	0.0080082
GO:0006556	S-adenosylmethionine biosynthetic process	1	42	0.0080082
GO:0015994	chlorophyll metabolic process	1	42	0.0080082
GO:0004372	glycine hydroxymethyltransferase activity	1	42	0.009990566
GO:0006544	glycine metabolic process	1	42	0.009990566
GO:0006563	L-serine metabolic process	1	42	0.009990566

Cluster 8 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006694	steroid biosynthetic process	1	42	0.009990566
GO:0009969	xyloglucan biosynthetic process	1	42	0.009990566
GO:0050378	UDP-glucuronate 4-epimerase activity	1	42	0.009990566
GO:0016740	transferase activity	2	42	0.010768598
GO:0006164	purine nucleotide biosynthetic process	1	42	0.011965105
GO:0009081	branched chain family amino acid metabolic process	1	42	0.011965105
GO:0004559	alpha-mannosidase activity	1	42	0.013931838
GO:0006783	heme biosynthetic process	1	42	0.013931838
GO:0004129	cytochrome-c oxidase activity	1	42	0.015890788
GO:0016757	transferase activity, transferring glycosyl groups	3	42	0.018858869
GO:0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	1	42	0.019785428
GO:0019745	pentacyclic triterpenoid biosynthetic process	1	42	0.019785428
GO:0055114	oxidation reduction	1	42	0.019785428
GO:0000139	Golgi membrane	1	42	0.013931838
GO:0006487	protein amino acid N-linked glycosylation	1	42	0.023649205
GO:0006259	DNA metabolic process	1	42	0.025569576
GO:0006790	sulfur metabolic process	1	42	0.025569576
GO:0009073	aromatic amino acid family biosynthetic process	1	42	0.025569576
GO:0006265	DNA topological change	1	42	0.027482297
GO:0003756	protein disulfide isomerase activity	1	42	0.029387391
GO:0000271	polysaccharide biosynthetic process	1	42	0.033174786
GO:0009225	nucleotide-sugar metabolic process	1	42	0.035057131
GO:0008299	isoprenoid biosynthetic process	1	42	0.036931937
GO:0005528	FK506 binding	1	42	0.042511338
GO:0030163	protein catabolic process	1	42	0.042511338
GO:0047262	polygalacturonate 4-alpha-galacturonosyltransferase activity	1	42	0.046193641
GO:0009295	nucleoid	1	42	0.048023669
GO:0010319	stromule	1	42	0.058849446
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	1	42	0.078021199
GO:0005783	endoplasmic reticulum	2	42	0.083321631
GO:0045454	cell redox homeostasis	1	42	0.084780394
GO:0016051	carbohydrate biosynthetic process	1	42	0.086452772
GO:0009507	chloroplast	7	42	0.09367506
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	42	0.097966575
GO:0009617	response to bacterium	1	42	0.097966575
GO:0016758	transferase activity, transferring hexosyl groups	1	42	0.104396143
GO:0042545	cell wall modification	1	42	0.107570604
GO:0030599	pectinesterase activity	1	42	0.120003308
GO:0048364	root development	1	42	0.120003308
GO:0009543	chloroplast thylakoid lumen	1	42	0.121527888
GO:0005576	extracellular region	1	42	0.13495924
GO:0022627	cytosolic small ribosomal subunit	1	42	0.137873962
GO:0016020	membrane	4	42	0.152269755
GO:0005773	vacuole	2	42	0.164724739
GO:0005507	copper ion binding	1	42	0.173531489
GO:0009611	response to wounding	1	42	0.174822445
GO:0005777	peroxisome	1	42	0.179928484
GO:0016887	ATPase activity	1	42	0.18369782
GO:0016787	hydrolase activity	1	42	0.224018356

Cluster 8 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004672	protein kinase activity	1	42	0.233348882
GO:0009579	thylakoid	1	42	0.245166266
GO:0005829	cytosol	1	42	0.247068197
GO:0009409	response to cold	1	42	0.261609258
GO:0006979	response to oxidative stress	1	42	0.265061428
GO:0006457	protein folding	1	42	0.274992972
GO:0005730	nucleolus	1	42	0.299846969
GO:0009505	plant-type cell wall	1	42	0.299846969
GO:0009535	chloroplast thylakoid membrane	1	42	0.306286109
GO:0016021	integral to membrane	1	42	0.308144483
GO:0009793	embryonic development ending in seed dormancy	1	42	0.323926992
GO:0003735	structural constituent of ribosome	1	42	0.326459742
GO:0009651	response to salt stress	1	42	0.328909517
GO:0006412	translation	1	42	0.332202398
GO:0005618	cell wall	1	42	0.335339001
GO:0006508	proteolysis	1	42	0.348466385
GO:0006499	N-terminal protein myristoylation	1	42	0.351699381
GO:0009570	chloroplast stroma	1	42	0.353802311
GO:0009941	chloroplast envelope	1	42	0.3581322
GO:0005488	binding	1	42	0.370353424

Cluster 8

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0000139	1	AT1G74380
GO:0000271	1	AT4G02500
GO:0003735	1	AT1G31817
GO:0003755	1	AT5G48580
GO:0003756	1	AT3G16110
GO:0003824	4	AT3G10690 AT3G23820 AT3G49680 AT5G48010
GO:0003849	1	AT4G39980
GO:0003854	1	AT1G47290
GO:0003937	1	AT2G35040
GO:0004084	1	AT3G49680
GO:0004129	1	AT1G22450
GO:0004325	1	AT5G26030
GO:0004372	1	AT4G32520
GO:0004478	1	AT4G01850
GO:0004559	1	AT5G14950
GO:0004643	1	AT2G35040
GO:0004672	1	AT3G23750
GO:0005488	1	AT1G18260
GO:0005507	1	AT4G01850
GO:0005528	1	AT5G48580
GO:0005576	1	AT1G53840
GO:0005618	1	AT4G01850
GO:0005730	1	AT4G01850
GO:0005739	11	AT1G22450 AT1G26460 AT1G55890 AT2G20940 AT2G26140 AT3G01910 AT3G10690 AT4G02500 AT4G39690 AT5G15980 AT5G26030
GO:0005773	2	AT1G79690 AT5G48580
GO:0005777	1	AT3G01910
GO:0005783	2	AT1G18260 AT3G16110
GO:0005794	4	AT1G31850 AT1G74380 AT3G02350 AT5G14950
GO:0005829	1	AT1G79690
GO:0006164	1	AT2G35040

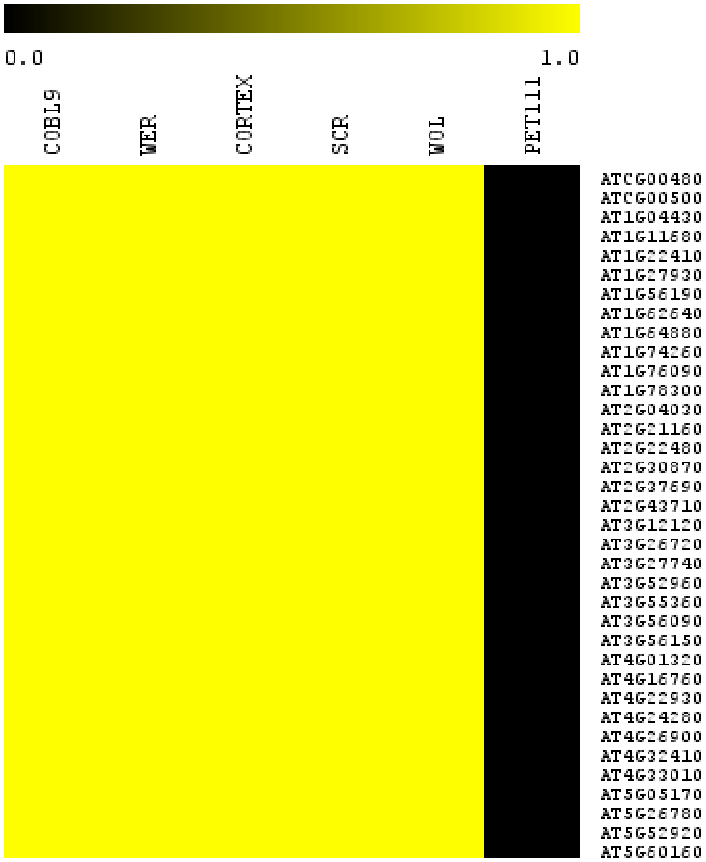
Cluster 8 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0006259	1	AT3G10690
GO:0006265	1	AT3G10690
GO:0006268	1	AT3G10690
GO:0006412	1	AT1G31817
GO:0006457	1	AT5G48580
GO:0006487	1	AT5G14950
GO:0006499	1	AT1G74380
GO:0006508	1	AT2G26140
GO:0006544	1	AT4G32520
GO:0006556	1	AT4G01850
GO:0006563	1	AT4G32520
GO:0006694	1	AT1G47290
GO:0006783	1	AT5G26030
GO:0006790	1	AT3G01910
GO:0006979	1	AT5G26030
GO:0008299	1	AT1G79690
GO:0008482	1	AT3G01910
GO:0009073	1	AT4G39980
GO:0009081	1	AT3G49680
GO:0009225	1	AT3G23820
GO:0009295	1	AT3G10690
GO:0009409	1	AT2G35040
GO:0009423	1	AT4G39980
GO:0009505	1	AT1G53840
GO:0009507	7	AT1G22450 AT2G35040 AT3G10690 AT3G49680 AT4G32520 AT4G39980 AT5G26030
GO:0009535	1	AT1G22450
GO:0009536	3	AT2G20940 AT2G26140 AT5G26030
GO:0009543	1	AT5G48580
GO:0009570	1	AT2G35040
GO:0009579	1	AT1G22450
GO:0009611	1	AT4G39980
GO:0009617	1	AT4G39980
GO:0009651	1	AT1G22450
GO:0009793	1	AT3G07060
GO:0009941	1	AT1G80270
GO:0009969	1	AT4G02500
GO:0010263	1	AT5G48010
GO:0010319	1	AT2G35040
GO:0010477	1	AT3G01910
GO:0015994	1	AT3G01910
GO:0016020	4	AT1G18260 AT1G47290 AT1G53840 AT2G26140
GO:0016021	1	AT4G02500
GO:0016051	1	AT3G02350
GO:0016706	1	AT2G17720
GO:0016740	2	AT1G74380 AT4G02500
GO:0016757	3	AT1G74380 AT3G02350 AT4G02500
GO:0016758	1	AT3G02350
GO:0016787	1	AT1G79690
GO:0016887	1	AT2G26140
GO:0018401	1	AT2G17720
GO:0019745	1	AT5G48010
GO:0022627	1	AT1G31817
GO:0030163	1	AT2G26140
GO:0030599	1	AT1G53840
GO:0033014	1	AT5G26030
GO:0033843	2	AT1G74380 AT4G02500
GO:0035252	1	AT4G02500
GO:0042545	1	AT1G53840

Cluster 8 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0045454	1	AT3G16110	
GO:0047012	1	AT1G47290	
GO:0047262	1	AT3G02350	
GO:0048364	1	AT5G48010	
GO:0048767	2	AT1G74380	AT4G02500
GO:0050378	1	AT3G23820	
GO:0051746	1	AT5G48010	
GO:0055114	1	AT1G22450	

Cluster 9



Cluster 9

AT1G04430
AT1G11680
AT1G22410
AT1G27930
AT1G56190
AT1G62640
AT1G64880
AT1G74260
AT1G76090
AT1G78300
AT2G04030
AT2G21160
AT2G22480
AT2G30870
AT2G37690
AT2G43710
AT3G12120

Cluster 9 (con.)

AT3G26720
AT3G27740
AT3G52960
AT3G55360
AT3G56090
AT3G56150
AT4G01320
AT4G16760
AT4G22930
AT4G24280
AT4G26900
AT4G32410
AT4G33010
AT5G05170
AT5G26780
AT5G52920
AT5G60160
ATCG00480
ATCG00500

Cluster 9 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009570	chloroplast stroma	8	34	7.49E-08
GO:0009507	chloroplast	15	34	1.05E-06
GO:0005783	endoplasmic reticulum	6	34	3.77E-06
GO:0046686	response to cadmium ion	6	34	4.95E-06
GO:0006207	'de novo' pyrimidine base biosynthetic process	2	34	1.54E-05
GO:0009833	primary cell wall biogenesis	2	34	1.54E-05
GO:0005886	plasma membrane	11	34	3.55E-05
GO:0006096	glycolysis	3	34	4.60E-05
GO:0005794	Golgi apparatus	4	34	5.25E-05
GO:0005773	vacuole	6	34	6.60E-05
GO:0005739	mitochondrion	7	34	1.78E-04
GO:0030244	cellulose biosynthetic process	2	34	5.26E-04
GO:0016126	sterol biosynthetic process	2	34	5.78E-04
GO:0016759	cellulose synthase activity	2	34	0.001459095
GO:0000107	imidazoleglycerol-phosphate synthase activity	1	34	0.001630304
GO:0004088	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	1	34	0.001630304
GO:0004151	dihydroorotase activity	1	34	0.001630304
GO:0004642	phosphoribosylformylglycinamidine synthase activity	1	34	0.001630304
GO:0004768	stearoyl-CoA 9-desaturase activity	1	34	0.001630304
GO:0008398	sterol 14-demethylase activity	1	34	0.001630304
GO:0010157	response to chlorate	1	34	0.001630304
GO:0016720	delta12-fatty acid dehydrogenase activity	1	34	0.001630304
GO:0019166	trans-2-enoyl-CoA reductase (NADPH) activity	1	34	0.001630304
GO:0019856	pyrimidine base biosynthetic process	1	34	0.001630304
GO:0009579	thylakoid	3	34	0.002481602
GO:0006633	fatty acid biosynthetic process	2	34	0.0026024
GO:0009941	chloroplast envelope	4	34	0.002657234
GO:0003838	sterol 24-C-methyltransferase activity	1	34	0.003255449
GO:0003865	3-oxo-5-alpha-steroid 4-dehydrogenase activity	1	34	0.003255449
GO:0004315	3-oxoacyl-[acyl-carrier-protein] synthase activity	1	34	0.003255449
GO:0009923	fatty acid elongase complex	1	34	0.003255449

Cluster 9 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045485	omega-6 fatty acid desaturase activity	1	34	0.003255449
GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	1	34	0.004875446
GO:0004618	phosphoglycerate kinase activity	1	34	0.004875446
GO:0006013	mannose metabolic process	1	34	0.004875446
GO:0055072	iron ion homeostasis	1	34	0.004875446
GO:0001676	long-chain fatty acid metabolic process	1	34	0.006490307
GO:0005960	glycine cleavage complex	1	34	0.006490307
GO:0006665	sphingolipid metabolic process	1	34	0.006490307
GO:0008199	ferric iron binding	1	34	0.006490307
GO:0003997	acyl-CoA oxidase activity	1	34	0.008100044
GO:0004372	glycine hydroxymethyltransferase activity	1	34	0.008100044
GO:0004375	glycine dehydrogenase (decarboxylating) activity	1	34	0.008100044
GO:0006544	glycine metabolic process	1	34	0.008100044
GO:0006563	L-serine metabolic process	1	34	0.008100044
GO:0006636	unsaturated fatty acid biosynthetic process	1	34	0.008100044
GO:0009704	de-etiolation	1	34	0.008100044
GO:0019464	glycine decarboxylation via glycine cleavage system	1	34	0.008100044
GO:0045300	acyl-[acyl-carrier-protein] desaturase activity	1	34	0.008100044
GO:0006541	glutamine metabolic process	1	34	0.009704669
GO:0006546	glycine catabolic process	1	34	0.009704669
GO:0008610	lipid biosynthetic process	1	34	0.009704669
GO:0009922	fatty acid elongase activity	1	34	0.009704669
GO:0000105	histidine biosynthetic process	1	34	0.011304193
GO:0003872	6-phosphofructokinase activity	1	34	0.011304193
GO:0004559	alpha-mannosidase activity	1	34	0.011304193
GO:0005945	6-phosphofructokinase complex	1	34	0.011304193
GO:0043295	glutathione binding	1	34	0.011304193
GO:0055046	microgametogenesis	1	34	0.011304193
GO:0006526	arginine biosynthetic process	1	34	0.012898628
GO:0000302	response to reactive oxygen species	1	34	0.014487986
GO:0005852	eukaryotic translation initiation factor 3 complex	1	34	0.014487986
GO:0006826	iron ion transport	1	34	0.014487986
GO:0006879	cellular iron ion homeostasis	1	34	0.014487986
GO:0010039	response to iron ion	1	34	0.014487986
GO:0004743	pyruvate kinase activity	1	34	0.016072279
GO:0010025	wax biosynthetic process	1	34	0.016072279
GO:0016209	antioxidant activity	1	34	0.017651518
GO:0042742	defense response to bacterium	2	34	0.018758721
GO:0045309	protein phosphorylated amino acid binding	1	34	0.019225716
GO:0009414	response to water deprivation	2	34	0.019265355
GO:0006631	fatty acid metabolic process	1	34	0.020794883
GO:0009073	aromatic amino acid family biosynthetic process	1	34	0.020794883
GO:0009863	salicylic acid mediated signaling pathway	1	34	0.020794883
GO:0051607	defense response to virus	1	34	0.020794883
GO:0018119	peptidyl-cysteine S-nitrosylation	1	34	0.022359031
GO:0009532	plastid stroma	1	34	0.025472318
GO:0006807	nitrogen compound metabolic process	1	34	0.028565668
GO:0009695	jasmonic acid biosynthetic process	1	34	0.028565668
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	1	34	0.031639175
GO:0009742	brassinosteroid mediated signaling	1	34	0.033168516
GO:0005789	endoplasmic reticulum membrane	1	34	0.03469293
GO:0009867	jasmonic acid mediated signaling pathway	1	34	0.036212429

Cluster 9 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006635	fatty acid beta-oxidation	1	34	0.037727024
GO:0009832	plant-type cell wall biogenesis	1	34	0.037727024
GO:0006457	protein folding	2	34	0.039111975
GO:0048316	seed development	1	34	0.039236727
GO:0009505	plant-type cell wall	2	34	0.050534959
GO:0048046	apoplast	2	34	0.051578773
GO:0042538	hyperosmotic salinity response	1	34	0.05697566
GO:0005524	ATP binding	3	34	0.062657235
GO:0009407	toxin catabolic process	1	34	0.062735794
GO:0015979	photosynthesis	1	34	0.062735794
GO:0009793	embryonic development ending in seed dormancy	2	34	0.065197381
GO:0004364	glutathione transferase activity	1	34	0.067006479
GO:0016757	transferase activity, transferring glycosyl groups	2	34	0.071855045
GO:0006413	translational initiation	1	34	0.082308314
GO:0006952	defense response	2	34	0.082770791
GO:0006508	proteolysis	2	34	0.086954303
GO:0003743	translation initiation factor activity	1	34	0.10228972
GO:0009908	flower development	1	34	0.104878453
GO:0048366	leaf development	1	34	0.108728784
GO:0009058	biosynthetic process	1	34	0.118806045
GO:0009408	response to heat	1	34	0.13221811
GO:0005507	copper ion binding	1	34	0.146277098
GO:0009611	response to wounding	1	34	0.147422231
GO:0005777	peroxisome	1	34	0.15196262
GO:0006629	lipid metabolic process	1	34	0.189036885
GO:0016020	membrane	3	34	0.202080402
GO:0005840	ribosome	1	34	0.224217231
GO:0009409	response to cold	1	34	0.227631989
GO:0019825	oxygen binding	1	34	0.230993851
GO:0009535	chloroplast thylakoid membrane	1	34	0.272788922
GO:0003735	structural constituent of ribosome	1	34	0.29485927
GO:0009651	response to salt stress	1	34	0.297651226
GO:0006412	translation	1	34	0.30145248
GO:0005975	carbohydrate metabolic process	1	34	0.302515796
GO:0005618	cell wall	1	34	0.305130367
GO:0003824	catalytic activity	1	34	0.334510642
GO:0005622	intracellular	1	34	0.34107388
GO:0005737	cytoplasm	1	34	0.351329878

Cluster 9

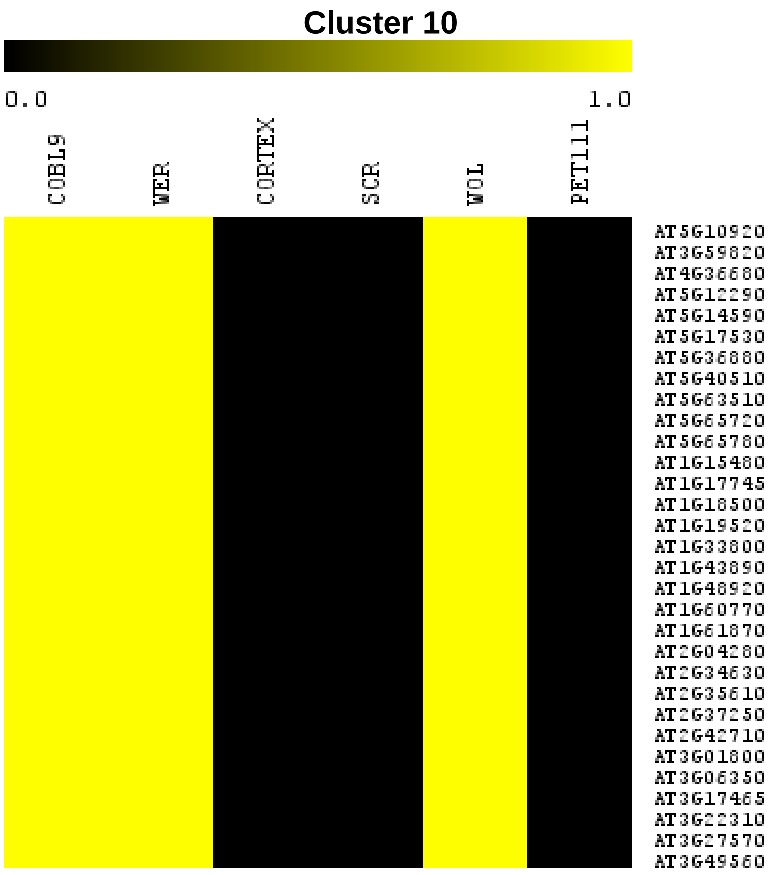
GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000105	1	AT4G26900
GO:0000107	1	AT4G26900
GO:0000302	1	AT3G56090
GO:0001676	1	AT4G16760
GO:0003735	1	AT1G64880
GO:0003743	1	AT3G56150
GO:0003824	1	AT1G74260
GO:0003838	1	AT1G76090
GO:0003849	1	AT1G22410
GO:0003865	1	AT3G55360
GO:0003872	1	AT2G22480
GO:0003997	1	AT4G16760
GO:0004088	1	AT3G27740

Cluster 9 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004151	1	AT4G22930					
GO:0004315	1	AT1G62640					
GO:0004364	1	AT2G30870					
GO:0004372	1	AT5G26780					
GO:0004375	1	AT4G33010					
GO:0004559	1	AT3G26720					
GO:0004618	1	AT1G56190					
GO:0004642	1	AT1G74260					
GO:0004743	1	AT5G52920					
GO:0004768	1	AT2G43710					
GO:0005507	1	AT2G30870					
GO:0005524	3	AT1G74260	AT2G04030	AT4G24280			
GO:0005618	1	AT2G30870					
GO:0005622	1	AT1G64880					
GO:0005737	1	AT2G30870					
GO:0005739	7	AT1G56190	AT1G74260	AT2G04030	AT4G24280	AT4G33010	AT5G26780
		AT5G52920					
GO:0005773	6	AT1G78300	AT2G21160	AT2G30870	AT3G26720	AT4G01320	AT5G60160
GO:0005777	1	AT4G16760					
GO:0005783	6	AT1G11680	AT1G76090	AT2G21160	AT3G12120	AT3G55360	AT4G01320
GO:0005789	1	AT3G55360					
GO:0005794	4	AT1G04430	AT1G64880	AT4G32410	AT5G05170		
GO:0005840	1	AT1G64880					
GO:0005852	1	AT3G56150					
GO:0005886	11	AT1G04430	AT1G11680	AT1G78300	AT2G04030	AT2G21160	AT2G30870
		AT3G26720	AT3G55360	AT4G32410	AT5G05170	AT5G60160	
GO:0005945	1	AT2G22480					
GO:0005960	1	AT4G33010					
GO:0005975	1	AT3G26720					
GO:0006013	1	AT3G26720					
GO:0006096	3	AT1G56190	AT2G22480	AT5G52920			
GO:0006207	2	AT3G27740	AT4G22930				
GO:0006412	1	AT1G64880					
GO:0006413	1	AT3G56150					
GO:0006457	2	AT2G04030	AT4G24280				
GO:0006508	2	AT4G01320	AT5G60160				
GO:0006526	1	AT3G27740					
GO:0006541	1	AT3G27740					
GO:0006544	1	AT5G26780					
GO:0006546	1	AT4G33010					
GO:0006563	1	AT5G26780					
GO:0006629	1	AT3G12120					
GO:0006631	1	AT2G43710					
GO:0006633	2	AT1G62640	AT5G52920				
GO:0006635	1	AT4G16760					
GO:0006636	1	AT2G43710					
GO:0006665	1	AT3G55360					
GO:0006807	1	AT3G27740					
GO:0006826	1	AT3G56090					
GO:0006879	1	AT3G56090					
GO:0006952	2	AT2G43710	AT5G05170				
GO:0008199	1	AT3G56090					
GO:0008398	1	AT1G11680					
GO:0008610	1	AT2G43710					
GO:0008757	1	AT1G76090					
GO:0009058	1	AT3G27740					
GO:0009073	1	AT1G22410					
GO:0009407	1	AT2G30870					
GO:0009408	1	AT2G04030					

Cluster 9 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009409	1	AT4G24280					
GO:0009414	2	AT2G04030	AT2G30870				
GO:0009505	2	AT3G26720	AT3G52960				
GO:0009507	15	AT1G56190	AT1G62640	AT1G74260	AT2G04030	AT2G22480	AT2G30870
		AT2G43710	AT3G27740	AT3G52960	AT3G56090	AT4G22930	AT4G24280
		AT4G26900	AT4G33010	AT5G52920			
GO:0009532	1	AT4G24280					
GO:0009535	1	AT2G21160					
GO:0009570	8	AT1G56190	AT1G74260	AT2G04030	AT2G43710	AT3G27740	AT3G52960
		AT4G24280	AT5G52920				
GO:0009579	3	AT1G56190	AT3G52960	AT4G24280			
GO:0009611	1	AT4G16760					
GO:0009651	1	AT2G04030					
GO:0009695	1	AT2G43710					
GO:0009704	1	AT2G04030					
GO:0009742	1	AT1G78300					
GO:0009793	2	AT1G11680	AT2G04030				
GO:0009832	1	AT4G32410					
GO:0009833	2	AT4G32410	AT5G05170				
GO:0009863	1	AT2G43710					
GO:0009867	1	AT2G43710					
GO:0009908	1	AT3G56090					
GO:0009922	1	AT3G55360					
GO:0009923	1	AT3G55360					
GO:0009941	4	AT2G04030	AT3G56090	AT4G24280	AT4G33010		
GO:0010025	1	AT3G55360					
GO:0010039	1	AT3G56090					
GO:0010157	1	AT2G04030					
GO:0015979	1	AT3G56090					
GO:0016020	3	AT1G22410	AT1G56190	AT3G56090			
GO:0016126	2	AT1G11680	AT1G76090				
GO:0016209	1	AT3G52960					
GO:0016720	1	AT3G12120					
GO:0016757	2	AT4G32410	AT5G05170				
GO:0016759	2	AT4G32410	AT5G05170				
GO:0018119	1	AT3G52960					
GO:0019166	1	AT3G55360					
GO:0019464	1	AT4G33010					
GO:0019825	1	AT1G11680					
GO:0019856	1	AT4G22930					
GO:0030244	2	AT4G32410	AT5G05170				
GO:0042538	1	AT4G32410					
GO:0042742	2	AT2G43710	AT3G52960				
GO:0043295	1	AT2G30870					
GO:0045300	1	AT2G43710					
GO:0045309	1	AT1G78300					
GO:0045485	1	AT3G12120					
GO:0046686	6	AT1G56190	AT2G30870	AT4G16760	AT4G24280	AT5G52920	AT5G60160
GO:0048046	2	AT2G30870	AT4G33010				
GO:0048316	1	AT5G52920					
GO:0048366	1	AT3G56090					
GO:0051607	1	AT2G43710					
GO:0055046	1	AT1G74260					
GO:0055072	1	AT3G56090					



Cluster 10

Cluster 10

AT1G15480
AT1G17745
AT1G18500
AT1G19520
AT1G33800
AT1G43890
AT1G48920
AT1G60770
AT1G61870
AT2G04280
AT2G34630
AT2G35610
AT2G37250
AT2G42710
AT3G01800
AT3G06350
AT3G17465
AT3G22310
AT3G27570
AT3G49560
AT3G59820
AT4G36680
AT5G10920
AT5G12290
AT5G14590
AT5G17530
AT5G36880

Cluster 10 (con.)

AT5G40510
AT5G63510
AT5G65720
AT5G65780

Cluster 10 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	12	31	4.06E-10
GO:0009507	chloroplast	11	31	2.74E-04
GO:0048367	shoot development	2	31	0.001356397
GO:0000478	endonucleolytic cleavages during rRNA processing	1	31	0.001486454
GO:0003855	3-dehydroquinate dehydratase activity	1	31	0.001486454
GO:0004056	argininosuccinate lyase activity	1	31	0.001486454
GO:0004764	shikimate 5-dehydrogenase activity	1	31	0.001486454
GO:0009570	chloroplast stroma	4	31	0.001625979
GO:0003987	acetate-CoA ligase activity	1	31	0.002968631
GO:0004617	phosphoglycerate dehydrogenase activity	1	31	0.002968631
GO:0031071	cysteine desulfurase activity	1	31	0.002968631
GO:0048364	root development	2	31	0.00444309
GO:0004161	dimethylallyltranstransferase activity	1	31	0.004446541
GO:0004450	isocitrate dehydrogenase (NADP+) activity	1	31	0.004446541
GO:0016868	intramolecular transferase activity, phosphotransferases	1	31	0.004446541
GO:0042450	arginine biosynthetic process via ornithine	1	31	0.004446541
GO:0050665	hydrogen peroxide biosynthetic process	1	31	0.004446541
GO:0003852	2-isopropylmalate synthase activity	1	31	0.005920192
GO:0004017	adenylate kinase activity	1	31	0.005920192
GO:0004084	branched-chain-amino-acid transaminase activity	1	31	0.005920192
GO:0006564	L-serine biosynthetic process	1	31	0.005920192
GO:0009098	leucine biosynthetic process	1	31	0.005920192
GO:0019201	nucleotide kinase activity	1	31	0.005920192
GO:0050661	NADP or NADPH binding	1	31	0.005920192
GO:0015031	protein transport	2	31	0.006499735
GO:0008652	amino acid biosynthetic process	1	31	0.007389592
GO:0006412	translation	3	31	0.008559136
GO:0009081	branched chain family amino acid metabolic process	1	31	0.008854752
GO:0016208	AMP binding	1	31	0.010315679
GO:0019375	galactolipid biosynthetic process	1	31	0.010315679
GO:0006526	arginine biosynthetic process	1	31	0.011772382
GO:0009536	plastid	2	31	0.014996436
GO:0003824	catalytic activity	3	31	0.015141447
GO:0010588	cotyledon vascular tissue pattern formation	1	31	0.016117241
GO:0004089	carbonate dehydratase activity	1	31	0.021851791
GO:0005741	mitochondrial outer membrane	1	31	0.024694111
GO:0010305	leaf vascular tissue pattern formation	1	31	0.024694111
GO:0016226	iron-sulfur cluster assembly	1	31	0.024694111
GO:0008483	transaminase activity	1	31	0.026109063
GO:0031966	mitochondrial membrane	1	31	0.027519887
GO:0005840	ribosome	2	31	0.027915355
GO:0005744	mitochondrial inner membrane presequence translocase complex	1	31	0.028926594
GO:0006364	rRNA processing	1	31	0.037280823
GO:0008152	metabolic process	3	31	0.040222226
GO:0009853	photorespiration	1	31	0.041403033

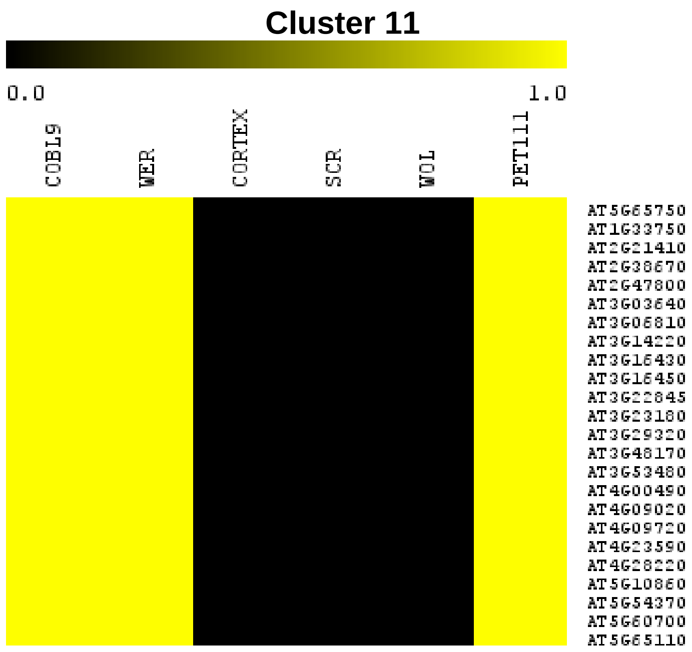
Cluster 10 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009790	embryonic development	1	31	0.044130994
GO:0015934	large ribosomal subunit	1	31	0.048192837
GO:0045271	respiratory chain complex I	1	31	0.052218765
GO:0003735	structural constituent of ribosome	2	31	0.057884344
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	1	31	0.060163778
GO:0007264	small GTPase mediated signal transduction	1	31	0.084401491
GO:0048366	leaf development	1	31	0.100199532
GO:0005488	binding	2	31	0.112587457
GO:0042254	ribosome biogenesis	1	31	0.121056689
GO:0005794	Golgi apparatus	1	31	0.158386534
GO:0016020	membrane	3	31	0.185092935
GO:0005509	calcium ion binding	1	31	0.189009512
GO:0006355	regulation of transcription, DNA-dependent	2	31	0.197253253
GO:0005525	GTP binding	1	31	0.202277795
GO:0005730	nucleolus	1	31	0.251019391
GO:0009793	embryonic development ending in seed dormancy	1	31	0.277191974
GO:0009651	response to salt stress	1	31	0.282967286
GO:0005975	carbohydrate metabolic process	1	31	0.287970339
GO:0003676	nucleic acid binding	1	31	0.306682031
GO:0009941	chloroplast envelope	1	31	0.321801347
GO:0005737	cytoplasm	1	31	0.340672641
GO:0005524	ATP binding	1	31	0.373204805

Cluster 10

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000478	1	AT1G48920					
GO:0003676	1	AT1G48920					
GO:0003735	2	AT2G42710	AT3G17465				
GO:0003824	3	AT3G06350	AT5G36880	AT5G65780			
GO:0003852	1	AT1G18500					
GO:0003855	1	AT3G06350					
GO:0003987	1	AT5G36880					
GO:0004017	1	AT2G37250					
GO:0004056	1	AT5G10920					
GO:0004084	1	AT5G65780					
GO:0004089	1	AT5G63510					
GO:0004161	1	AT2G34630					
GO:0004450	1	AT5G14590					
GO:0004617	1	AT1G17745					
GO:0004764	1	AT3G06350					
GO:0005488	2	AT1G60770	AT3G06350				
GO:0005509	1	AT3G59820					
GO:0005524	1	AT5G65720					
GO:0005525	1	AT1G43890					
GO:0005730	1	AT1G48920					
GO:0005737	1	AT2G37250					
GO:0005739	12	AT1G60770	AT1G61870	AT3G01800	AT3G17465	AT3G49560	AT3G59820
		AT4G36680	AT5G12290	AT5G14590	AT5G63510	AT5G65720	AT5G65780
GO:0005741	1	AT5G12290					
GO:0005744	1	AT3G49560					
GO:0005794	1	AT2G35610					
GO:0005840	2	AT2G42710	AT3G17465				
GO:0005975	1	AT5G17530					

Cluster 10 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0006355	2	AT1G19520	AT1G43890				
GO:0006364	1	AT1G48920					
GO:0006412	3	AT2G42710	AT3G01800	AT3G17465			
GO:0006526	1	AT5G10920					
GO:0006564	1	AT1G17745					
GO:0007264	1	AT1G43890					
GO:0008152	3	AT5G14590	AT5G36880	AT5G65780			
GO:0008483	1	AT5G65720					
GO:0008652	1	AT2G37250					
GO:0009081	1	AT5G65780					
GO:0009098	1	AT1G18500					
GO:0009507	11	AT1G17745	AT1G18500	AT2G34630	AT2G37250	AT3G06350	AT3G49560
		AT5G10920	AT5G14590	AT5G17530	AT5G36880	AT5G65780	
GO:0009536	2	AT2G34630	AT3G49560				
GO:0009570	4	AT2G37250	AT3G06350	AT5G10920	AT5G36880		
GO:0009651	1	AT5G63510					
GO:0009790	1	AT2G34630					
GO:0009793	1	AT3G06350					
GO:0009853	1	AT5G63510					
GO:0009941	1	AT3G49560					
GO:0010305	1	AT1G48920					
GO:0010588	1	AT1G48920					
GO:0015031	2	AT1G43890	AT3G49560				
GO:0015450	1	AT3G49560					
GO:0015934	1	AT2G42710					
GO:0016020	3	AT1G61870	AT3G49560	AT5G63510			
GO:0016208	1	AT5G36880					
GO:0016226	1	AT5G65720					
GO:0016868	1	AT5G17530					
GO:0019201	1	AT2G37250					
GO:0019375	1	AT5G12290					
GO:0031071	1	AT5G65720					
GO:0031966	1	AT5G63510					
GO:0042254	1	AT1G48920					
GO:0042450	1	AT5G10920					
GO:0045271	1	AT5G63510					
GO:0048364	2	AT1G48920	AT2G37250				
GO:0048366	1	AT1G48920					
GO:0048367	2	AT1G48920	AT2G37250				
GO:0050661	1	AT3G06350					
GO:0050665	1	AT5G12290					



Cluster 11

AT1G33750
AT2G21410
AT2G38670
AT2G47800
AT3G03640
AT3G06810
AT3G14220
AT3G16430
AT3G16450
AT3G22845
AT3G23180
AT3G29320
AT3G48170
AT3G53480
AT4G00490
AT4G09020
AT4G09720
AT4G23590
AT4G28220
AT5G10860
AT5G54370
AT5G60700
AT5G65110
AT5G65750

Cluster 11 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0000325	plant-type vacuole	2	24	4.67E-04
GO:0005774	vacuolar membrane	2	24	9.51E-04
GO:0003995	acyl-CoA dehydrogenase activity	1	24	0.001150803
GO:0004306	ethanolamine-phosphate cytidylyltransferase activity	1	24	0.001150803
GO:0006646	phosphatidylethanolamine biosynthetic process	1	24	0.001150803
GO:0009569	chloroplast starch grain	1	24	0.001150803
GO:0006855	multidrug transport	2	24	0.001200722
GO:0005773	vacuole	4	24	0.001394632
GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	1	24	0.002299068
GO:0004645	phosphorylase activity	1	24	0.002299068
GO:0019285	glycine betaine biosynthetic process from choline	1	24	0.002299068
GO:0008517	folic acid transporter activity	1	24	0.003444798
GO:0015036	disulfide oxidoreductase activity	1	24	0.003444798
GO:0019156	isoamylase activity	1	24	0.003444798
GO:0031314	extrinsic to mitochondrial inner membrane	1	24	0.003444798
GO:0009058	biosynthetic process	2	24	0.003964584
GO:0005975	carbohydrate metabolic process	3	24	0.004334075
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	2	24	0.004339927
GO:0001676	long-chain fatty acid metabolic process	1	24	0.004587998
GO:0000272	polysaccharide catabolic process	1	24	0.005728671
GO:0003997	acyl-CoA oxidase activity	1	24	0.005728671
GO:0005777	peroxisome	2	24	0.006904417
GO:0003954	NADH dehydrogenase activity	1	24	0.008002455
GO:0004556	alpha-amylase activity	1	24	0.009135573
GO:0005739	mitochondrion	4	24	0.009228822
GO:0009414	response to water deprivation	2	24	0.010110124
GO:0016161	beta-amylase activity	1	24	0.010266181
GO:0009266	response to temperature stimulus	1	24	0.012519881
GO:0005983	starch catabolic process	1	24	0.014763587
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	24	0.015881702
GO:0008483	transaminase activity	1	24	0.020329335
GO:0010118	stomatal movement	1	24	0.020329335
GO:0000287	magnesium ion binding	1	24	0.026926736
GO:0006635	fatty acid beta-oxidation	1	24	0.026926736
GO:0015992	proton transport	1	24	0.029106249
GO:0009705	plant-type vacuole membrane	1	24	0.04197948
GO:0016829	lyase activity	1	24	0.053477012
GO:0009570	chloroplast stroma	2	24	0.054519
GO:0009624	response to nematode	1	24	0.056563108
GO:0007264	small GTPase mediated signal transduction	1	24	0.066698537
GO:0005886	plasma membrane	4	24	0.082172093
GO:0015031	protein transport	1	24	0.087237669
GO:0004091	carboxylesterase activity	1	24	0.104059853
GO:0008152	metabolic process	2	24	0.108807748
GO:0009611	response to wounding	1	24	0.109510535
GO:0016887	ATPase activity	1	24	0.11577228
GO:0009536	plastid	1	24	0.129697167
GO:0006629	lipid metabolic process	1	24	0.143094005
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	1	24	0.153599566
GO:0009507	chloroplast	4	24	0.155799678
GO:0005525	GTP binding	1	24	0.166073957

Cluster 11 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009409	response to cold	1	24	0.175847745
GO:0016491	oxidoreductase activity	1	24	0.202625701
GO:0046686	response to cadmium ion	1	24	0.235183418
GO:0009651	response to salt stress	1	24	0.241499194
GO:0016757	transferase activity, transferring glycosyl groups	1	24	0.245972133
GO:0006810	transport	1	24	0.257762225
GO:0006355	regulation of transcription, DNA-dependent	1	24	0.368510249

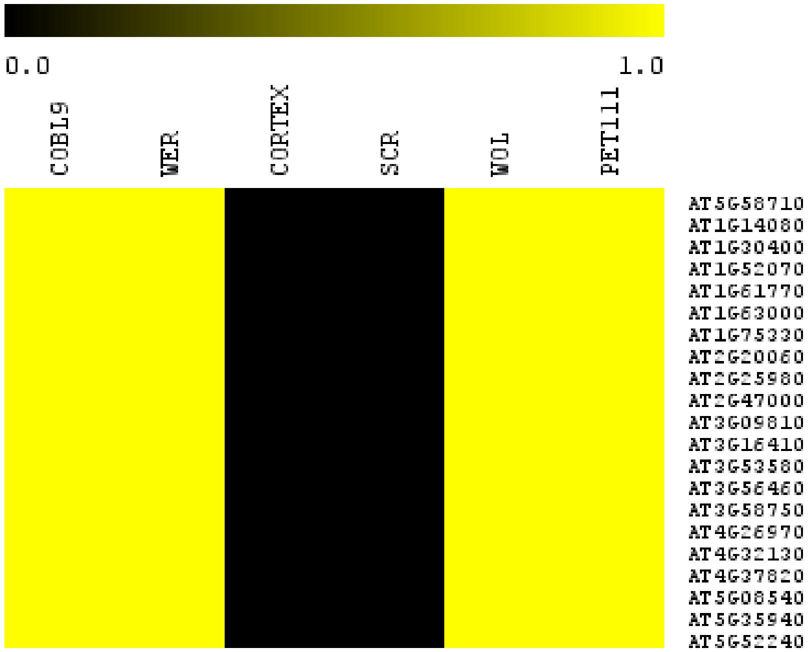
Cluster 11

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**			
GO:0000272	1	AT4G00490			
GO:0000287	1	AT1G33750			
GO:0000325	2	AT2G21410	AT2G47800		
GO:0001676	1	AT5G65110			
GO:0003954	1	AT4G28220			
GO:0003995	1	AT3G06810			
GO:0003997	1	AT5G65110			
GO:0004028	1	AT3G48170			
GO:0004091	1	AT3G14220			
GO:0004306	1	AT2G38670			
GO:0004553	1	AT3G03640			
GO:0004556	1	AT4G09020			
GO:0004591	1	AT5G65750			
GO:0004645	1	AT3G29320			
GO:0005525	1	AT4G09720			
GO:0005739	4	AT2G21410	AT2G38670	AT5G10860	AT5G65750
GO:0005773	4	AT2G21410	AT2G47800	AT3G14220	AT3G22845
GO:0005774	2	AT2G21410	AT2G47800		
GO:0005777	2	AT3G48170	AT5G65110		
GO:0005886	4	AT2G21410	AT2G47800	AT3G53480	AT4G09720
GO:0005975	3	AT3G03640	AT4G00490	AT4G09020	
GO:0005983	1	AT4G09020			
GO:0006355	1	AT4G09720			
GO:0006629	1	AT3G14220			
GO:0006635	1	AT5G65110			
GO:0006646	1	AT2G38670			
GO:0006810	1	AT3G22845			
GO:0006855	2	AT2G47800	AT3G53480		
GO:0007264	1	AT4G09720			
GO:0008152	2	AT1G33750	AT3G48170		
GO:0008483	1	AT4G23590			
GO:0008517	1	AT2G47800			
GO:0009058	2	AT2G38670	AT4G23590		
GO:0009266	1	AT3G29320			
GO:0009409	1	AT3G16450			
GO:0009414	2	AT2G47800	AT3G29320		
GO:0009507	4	AT2G21410	AT3G29320	AT4G00490	AT4G09020
GO:0009536	1	AT3G29320			
GO:0009569	1	AT4G09020			
GO:0009570	2	AT3G29320	AT4G09020		
GO:0009611	1	AT2G47800			
GO:0009624	1	AT2G47800			
GO:0009651	1	AT5G10860			
GO:0009705	1	AT2G21410			

Cluster 11 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0010118	1	AT2G47800	
GO:0015031	1	AT4G09720	
GO:0015036	1	AT4G28220	
GO:0015992	1	AT2G21410	
GO:0016161	1	AT4G00490	
GO:0016491	1	AT3G06810	
GO:0016757	1	AT3G29320	
GO:0016829	1	AT1G33750	
GO:0016887	1	AT2G21410	
GO:0019156	1	AT4G09020	
GO:0019285	1	AT3G48170	
GO:0031314	1	AT4G28220	
GO:0042626	2	AT2G47800	AT3G53480
GO:0046686	1	AT5G65750	

Cluster 12



Cluster 12

AT1G14080
AT1G30400
AT1G52070
AT1G61770
AT1G63000
AT1G75330
AT2G20060
AT2G25980
AT2G47000
AT3G09810
AT3G16410
AT3G53580
AT3G56460
AT3G58750
AT4G26970
AT4G32130
AT4G37820

Cluster 12 (con.)

AT5G08540
AT5G35940
AT5G52240
AT5G58710

Cluster 12 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0008559	xenobiotic-transporting ATPase activity	2	21	9.66E-07
GO:0008830	dTDP-4-dehydrorhamnose 3,5-epimerase activity	1	21	0.001006953
GO:0008831	dTDP-4-dehydrorhamnose reductase activity	1	21	0.001006953
GO:0008837	diaminopimelate epimerase activity	1	21	0.001006953
GO:0005496	steroid binding	1	21	0.002011974
GO:0010315	auxin efflux	1	21	0.002011974
GO:0010489	UDP-4-keto-6-deoxy-glucose-3,5-epimerase activity	1	21	0.002011974
GO:0010490	UDP-4-keto-rhamnose-4-keto-reductase activity	1	21	0.002011974
GO:0016743	carboxyl- or carbamoyltransferase activity	1	21	0.002011974
GO:0030308	negative regulation of cell growth	1	21	0.002011974
GO:0003994	aconitate hydratase activity	1	21	0.003015067
GO:0019305	dTDP-rhamnose biosynthetic process	1	21	0.003015067
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	2	21	0.003342869
GO:0010253	UDP-rhamnose biosynthetic process	1	21	0.004016233
GO:0004108	citrate (SI)-synthase activity	1	21	0.005015476
GO:0004449	isocitrate dehydrogenase (NAD+) activity	1	21	0.005015476
GO:0005625	soluble fraction	1	21	0.005015476
GO:0010540	basipetal auxin transport	1	21	0.006012798
GO:0009089	lysine biosynthetic process via diaminopimelate	1	21	0.008993265
GO:0006099	tricarboxylic acid cycle	1	21	0.009982929
GO:0008417	fucosyltransferase activity	1	21	0.009982929
GO:0042546	cell wall biogenesis	1	21	0.011956538
GO:0048767	root hair elongation	1	21	0.012940487
GO:0016597	amino acid binding	1	21	0.015880945
GO:0006457	protein folding	2	21	0.016618408
GO:0006520	amino acid metabolic process	1	21	0.01685731
GO:0009630	gravitropism	1	21	0.01685731
GO:0006635	fatty acid beta-oxidation	1	21	0.023639101
GO:0005783	endoplasmic reticulum	2	21	0.026539472
GO:0000325	plant-type vacuole	1	21	0.027473182
GO:0015934	large ribosomal subunit	1	21	0.033168516
GO:0009926	auxin polar transport	1	21	0.035052166
GO:0005774	vacuolar membrane	1	21	0.038797397
GO:0009735	response to cytokinin stimulus	1	21	0.041587089
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	21	0.051676093
GO:0009507	chloroplast	5	21	0.053794279
GO:0005886	plasma membrane	4	21	0.059421517
GO:0008152	metabolic process	2	21	0.089787188
GO:0051082	unfolded protein binding	1	21	0.091549839
GO:0005507	copper ion binding	1	21	0.096483036
GO:0031072	heat shock protein binding	1	21	0.097299375
GO:0005777	peroxisome	1	21	0.100548078
GO:0005794	Golgi apparatus	1	21	0.11406079
GO:0005739	mitochondrion	2	21	0.139876451
GO:0009733	response to auxin stimulus	1	21	0.180625826
GO:0009535	chloroplast thylakoid membrane	1	21	0.196752999

Cluster 12 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0046686	response to cadmium ion	1	21	0.214217213
GO:0003735	structural constituent of ribosome	1	21	0.217567324
GO:0006412	translation	1	21	0.224128119
GO:0016757	transferase activity, transferring glycosyl groups	1	21	0.224666538
GO:0016020	membrane	2	21	0.244978296
GO:0009570	chloroplast stroma	1	21	0.253313139
GO:0009941	chloroplast envelope	1	21	0.260658257
GO:0005773	vacuole	1	21	0.290570085
GO:0008270	zinc ion binding	1	21	0.35914802

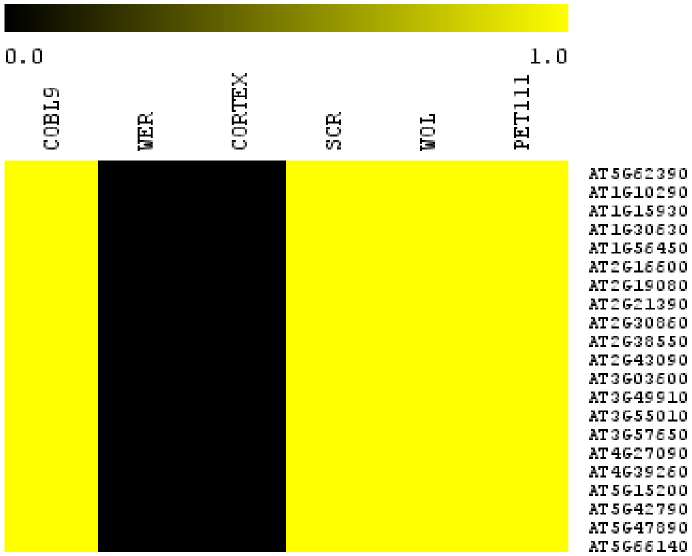
Cluster 12 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**				
GO:0000325	1	AT1G30400				
GO:0003735	1	AT2G20060				
GO:0003755	1	AT5G58710				
GO:0003994	1	AT4G26970				
GO:0004108	1	AT3G58750				
GO:0004449	1	AT3G09810				
GO:0005496	1	AT5G52240				
GO:0005507	1	AT4G26970				
GO:0005625	1	AT1G63000				
GO:0005739	2	AT3G09810	AT4G26970			
GO:0005773	1	AT1G30400				
GO:0005774	1	AT1G30400				
GO:0005777	1	AT3G58750				
GO:0005783	2	AT1G61770	AT5G52240			
GO:0005794	1	AT4G37820				
GO:0005886	4	AT1G30400	AT1G63000	AT2G47000	AT5G52240	
GO:0006099	1	AT3G58750				
GO:0006412	1	AT2G20060				
GO:0006457	2	AT1G61770	AT5G58710			
GO:0006520	1	AT1G75330				
GO:0006635	1	AT3G58750				
GO:0008152	2	AT3G09810	AT3G56460			
GO:0008270	1	AT3G56460				
GO:0008417	1	AT1G14080				
GO:0008559	2	AT1G30400	AT2G47000			
GO:0008830	1	AT1G63000				
GO:0008831	1	AT1G63000				
GO:0008837	1	AT3G53580				
GO:0009089	1	AT3G53580				
GO:0009507	5	AT1G75330	AT3G53580	AT4G26970	AT5G08540	AT5G58710
GO:0009535	1	AT5G08540				
GO:0009570	1	AT1G75330				
GO:0009630	1	AT2G47000				
GO:0009733	1	AT2G47000				
GO:0009735	1	AT2G47000				
GO:0009926	1	AT2G47000				
GO:0009941	1	AT5G08540				
GO:0010253	1	AT1G63000				
GO:0010315	1	AT2G47000				
GO:0010489	1	AT1G63000				
GO:0010490	1	AT1G63000				
GO:0010540	1	AT2G47000				

Cluster 12 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0015934	1	AT2G20060	
GO:0016020	2	AT1G14080	AT2G47000
GO:0016597	1	AT1G75330	
GO:0016743	1	AT1G75330	
GO:0016757	1	AT1G14080	
GO:0019305	1	AT1G63000	
GO:0030308	1	AT5G52240	
GO:0031072	1	AT1G61770	
GO:0042546	1	AT1G14080	
GO:0042626	2	AT1G30400	AT2G47000
GO:0046686	1	AT4G26970	
GO:0048767	1	AT2G47000	
GO:0051082	1	AT1G61770	

Cluster 13



Cluster 13

AT1G10290
AT1G15930
AT1G30630
AT1G56450
AT2G16600
AT2G19080
AT2G21390
AT2G30860
AT2G38550
AT2G43090
AT3G03600
AT3G49910
AT3G55010
AT3G57650
AT4G27090
AT4G39260
AT5G15200
AT5G42790
AT5G47890
AT5G62390
AT5G66140

Cluster 13 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022626	cytosolic ribosome	5	21	5.57E-07
GO:0005839	proteasome core complex	3	21	9.88E-07
GO:0005886	plasma membrane	10	21	1.49E-06
GO:0003735	structural constituent of ribosome	5	21	7.42E-06
GO:0006412	translation	5	21	9.05E-06
GO:0008233	peptidase activity	3	21	1.29E-05
GO:0009507	chloroplast	10	21	2.97E-05
GO:0005730	nucleolus	4	21	8.17E-05
GO:0009651	response to salt stress	4	21	1.71E-04
GO:0006511	ubiquitin-dependent protein catabolic process	3	21	8.42E-04
GO:0004641	phosphoribosylformylglycinamidine cyclo-ligase activity	1	21	0.001006953
GO:0016655	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	1	21	0.002011974
GO:0019773	proteasome core complex, alpha-subunit complex	1	21	0.002011974
GO:0005783	endoplasmic reticulum	3	21	0.002148839
GO:0022627	cytosolic small ribosomal subunit	2	21	0.002841847
GO:0022625	cytosolic large ribosomal subunit	2	21	0.004370869
GO:0005763	mitochondrial small ribosomal subunit	1	21	0.005015476
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	1	21	0.005015476
GO:0006896	Golgi to vacuole transport	1	21	0.005015476
GO:0016836	hydro-lyase activity	1	21	0.005015476
GO:0005739	mitochondrion	4	21	0.005815456
GO:0006164	purine nucleotide biosynthetic process	1	21	0.006012798
GO:0030126	COPI vesicle coat	1	21	0.006012798
GO:0000502	proteasome complex	1	21	0.006012798
GO:0003841	1-acylglycerol-3-phosphate O-acyltransferase activity	1	21	0.007008202
GO:0043295	glutathione binding	1	21	0.007008202
GO:0009536	plastid	2	21	0.007203187
GO:0005773	vacuole	3	21	0.008625029
GO:0004602	glutathione peroxidase activity	1	21	0.008993265
GO:0045087	innate immune response	1	21	0.013922536
GO:0009409	response to cold	2	21	0.014317136
GO:0006626	protein targeting to mitochondrion	1	21	0.015880945
GO:0005741	mitochondrial outer membrane	1	21	0.01685731
GO:0006888	ER to Golgi vesicle-mediated transport	1	21	0.017831785
GO:0030163	protein catabolic process	1	21	0.021710843
GO:0046686	response to cadmium ion	2	21	0.028863784
GO:0009706	chloroplast inner membrane	1	21	0.03032919
GO:0016020	membrane	4	21	0.032593145
GO:0003924	GTPase activity	1	21	0.033168516
GO:0015934	large ribosomal subunit	1	21	0.033168516
GO:0005618	cell wall	2	21	0.033515255
GO:0045271	respiratory chain complex I	1	21	0.035991229
GO:0009407	toxin catabolic process	1	21	0.039729122
GO:0004364	glutathione transferase activity	1	21	0.042513337
GO:0009570	chloroplast stroma	2	21	0.04365762
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	21	0.051676093
GO:0008565	protein transporter activity	1	21	0.066841995
GO:0005743	mitochondrial inner membrane	1	21	0.070336337
GO:0042254	ribosome biogenesis	1	21	0.085717768
GO:0008152	metabolic process	2	21	0.089787188
GO:0005507	copper ion binding	1	21	0.096483036

Cluster 13 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005777	peroxisome	1	21	0.100548078
GO:0005794	Golgi apparatus	1	21	0.11406079
GO:0042742	defense response to bacterium	1	21	0.118717657
GO:0005516	calmodulin binding	1	21	0.130854656
GO:0009579	thylakoid	1	21	0.145461745
GO:0005829	cytosol	1	21	0.146888592
GO:0005840	ribosome	1	21	0.155322448
GO:0006457	protein folding	1	21	0.168901963
GO:0005215	transporter activity	1	21	0.181899925
GO:0007165	signal transduction	1	21	0.185688384
GO:0048046	apoplast	1	21	0.192503263
GO:0003723	RNA binding	1	21	0.223588428
GO:0006952	defense response	1	21	0.2397356
GO:0009941	chloroplast envelope	1	21	0.260658257
GO:0005737	cytoplasm	1	21	0.283333597
GO:0005524	ATP binding	1	21	0.34268671

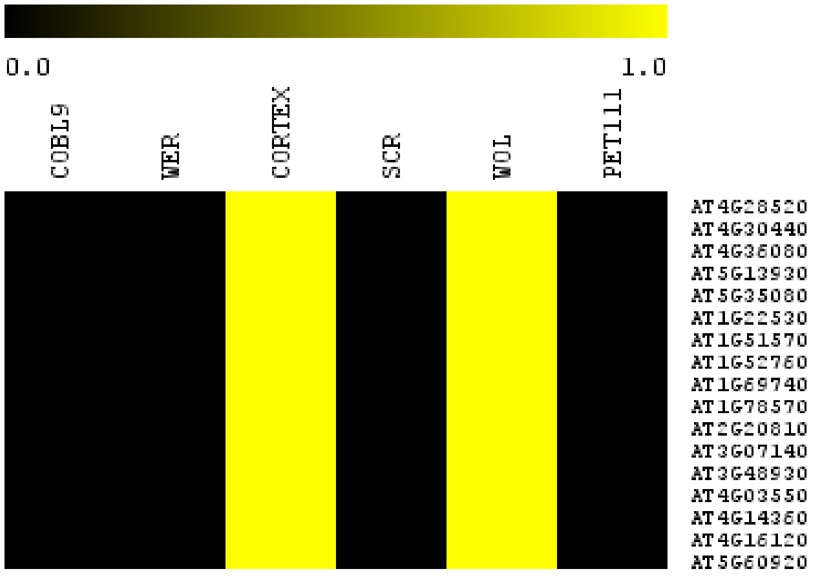
Cluster 13

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000502	1	AT5G42790					
GO:0003723	1	AT4G39260					
GO:0003735	5	AT1G15930	AT3G03600	AT3G49910	AT4G27090	AT5G15200	
GO:0003755	1	AT2G16600					
GO:0003841	1	AT3G57650					
GO:0003924	1	AT1G10290					
GO:0004364	1	AT2G30860					
GO:0004602	1	AT2G30860					
GO:0004641	1	AT3G55010					
GO:0005215	1	AT2G21390					
GO:0005507	1	AT2G30860					
GO:0005516	1	AT5G62390					
GO:0005524	1	AT3G55010					
GO:0005618	2	AT4G39260	AT5G15200				
GO:0005730	4	AT3G49910	AT4G27090	AT4G39260	AT5G15200		
GO:0005737	1	AT2G30860					
GO:0005739	4	AT2G19080	AT2G38550	AT3G55010	AT5G47890		
GO:0005741	1	AT2G19080					
GO:0005743	1	AT2G19080					
GO:0005763	1	AT3G03600					
GO:0005773	3	AT2G30860	AT4G27090	AT5G66140			
GO:0005777	1	AT4G39260					
GO:0005783	3	AT3G57650	AT4G27090	AT5G62390			
GO:0005794	1	AT1G10290					
GO:0005829	1	AT2G16600					
GO:0005839	3	AT1G56450	AT5G42790	AT5G66140			
GO:0005840	1	AT4G27090					
GO:0005886	10	AT1G10290	AT1G30630	AT2G16600	AT2G30860	AT3G49910	AT4G27090
		AT4G39260	AT5G15200	AT5G42790	AT5G62390		
GO:0006164	1	AT3G55010					
GO:0006412	5	AT1G15930	AT3G03600	AT3G49910	AT4G27090	AT5G15200	
GO:0006457	1	AT2G16600					
GO:0006511	3	AT1G56450	AT5G42790	AT5G66140			
GO:0006626	1	AT2G19080					
GO:0006888	1	AT2G21390					

Cluster 13 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0006890	1	AT1G30630					
GO:0006896	1	AT1G10290					
GO:0006952	1	AT2G30860					
GO:0007165	1	AT2G16600					
GO:0008152	2	AT2G43090	AT3G57650				
GO:0008233	3	AT1G56450	AT5G42790	AT5G66140			
GO:0008565	1	AT1G30630					
GO:0009407	1	AT2G30860					
GO:0009409	2	AT3G49910	AT4G39260				
GO:0009507	10	AT2G16600	AT2G30860	AT2G38550	AT2G43090	AT3G49910	AT3G55010
		AT4G27090	AT4G39260	AT5G15200	AT5G66140		
GO:0009536	2	AT2G19080	AT2G38550				
GO:0009570	2	AT2G30860	AT2G43090				
GO:0009579	1	AT2G30860					
GO:0009651	4	AT1G15930	AT1G56450	AT2G43090	AT4G39260		
GO:0009706	1	AT2G38550					
GO:0009941	1	AT2G38550					
GO:0015934	1	AT3G49910					
GO:0016020	4	AT1G10290	AT2G21390	AT3G49910	AT5G15200		
GO:0016655	1	AT5G47890					
GO:0016836	1	AT2G43090					
GO:0019773	1	AT5G66140					
GO:0022625	2	AT3G49910	AT4G27090				
GO:0022626	5	AT1G15930	AT1G56450	AT3G49910	AT4G27090	AT5G15200	
GO:0022627	2	AT1G15930	AT5G15200				
GO:0030126	1	AT2G21390					
GO:0030163	1	AT5G42790					
GO:0042254	1	AT4G27090					
GO:0042742	1	AT2G30860					
GO:0043295	1	AT2G30860					
GO:0045087	1	AT4G39260					
GO:0045271	1	AT5G47890					
GO:0046686	2	AT1G15930	AT1G56450				
GO:0048046	1	AT2G30860					

Cluster 14



Cluster 14
AT1G22530
AT1G51570
AT1G52760
AT1G69740
AT1G78570
AT2G20810
AT3G07140
AT3G48930
AT4G03550
AT4G14360
AT4G16120
AT4G28520
AT4G30440
AT4G36080
AT5G13930
AT5G35080
AT5G60920

Cluster 14 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009225	nucleotide-sugar metabolic process	2	17	9.46E-05
GO:0009715	chalcone biosynthetic process	1	17	8.15E-04
GO:0009930	longitudinal side of cell surface	1	17	8.15E-04
GO:0016210	naringenin-chalcone synthase activity	1	17	8.15E-04
GO:0042735	protein body	1	17	8.15E-04
GO:0046658	anchored to plasma membrane	2	17	0.001061677
GO:0005783	endoplasmic reticulum	3	17	0.001155695
GO:0004655	porphobilinogen synthase activity	1	17	0.001629054
GO:0009629	response to gravity	1	17	0.001629054
GO:0010315	auxin efflux	1	17	0.001629054
GO:0050377	UDP-glucose 4,6-dehydratase activity	1	17	0.001629054
GO:0003923	GPI-anchor transamidase activity	1	17	0.002441706
GO:0009897	external side of plasma membrane	1	17	0.002441706
GO:0010280	UDP-L-rhamnose synthase activity	1	17	0.002441706
GO:0003824	catalytic activity	3	17	0.002937773
GO:0010215	cellulose microfibril organization	1	17	0.003253109
GO:0010253	UDP-rhamnose biosynthetic process	1	17	0.003253109
GO:0052542	callose deposition during defense response	1	17	0.003253109
GO:0005625	soluble fraction	1	17	0.004063266
GO:0050378	UDP-glucuronate 4-epimerase activity	1	17	0.004063266
GO:0005794	Golgi apparatus	2	17	0.004641499
GO:0051555	flavonol biosynthetic process	1	17	0.004872178
GO:0031540	regulation of anthocyanin biosynthetic process	1	17	0.005679845
GO:0000148	1,3-beta-glucan synthase complex	1	17	0.009699568
GO:0003843	1,3-beta-glucan synthase activity	1	17	0.009699568
GO:0006075	1,3-beta-glucan biosynthetic process	1	17	0.009699568
GO:0009863	salicylic acid mediated signaling pathway	1	17	0.010499799
GO:0009870	defense response signaling pathway, resistance gene-dependent	1	17	0.010499799
GO:0031225	anchored to membrane	2	17	0.011292096
GO:0006779	porphyrin biosynthetic process	1	17	0.011298796
GO:0009825	multidimensional cell growth	1	17	0.012096559

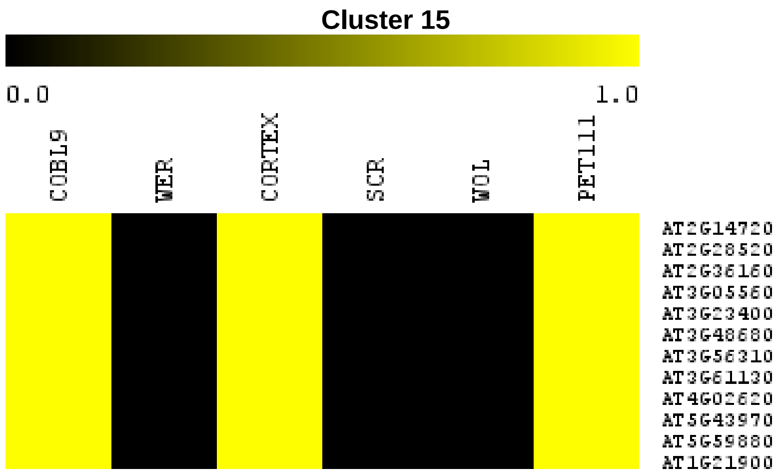
Cluster 14 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0052544	callose deposition in cell wall during defense response	1	17	0.01289309
GO:0000162	tryptophan biosynthetic process	1	17	0.015275303
GO:0047262	polygalacturonate 4-alpha-galacturonosyltransferase activity	1	17	0.019221143
GO:0009793	embryonic development ending in seed dormancy	2	17	0.019844722
GO:0009813	flavonoid biosynthetic process	1	17	0.020790929
GO:0016757	transferase activity, transferring glycosyl groups	2	17	0.022199382
GO:0009620	response to fungus	1	17	0.022355845
GO:0005618	cell wall	2	17	0.023005946
GO:0010224	response to UV-B	1	17	0.025471109
GO:0009926	auxin polar transport	1	17	0.028567021
GO:0009965	leaf morphogenesis	1	17	0.029337985
GO:0009705	plant-type vacuole membrane	1	17	0.030107746
GO:0016051	carbohydrate biosynthetic process	1	17	0.036981675
GO:0045735	nutrient reservoir activity	1	17	0.040758814
GO:0016758	transferase activity, transferring hexosyl groups	1	17	0.045252339
GO:0022627	cytosolic small ribosomal subunit	1	17	0.061368544
GO:0009611	response to wounding	1	17	0.08038956
GO:0009753	response to jasmonic acid stimulus	1	17	0.084505279
GO:0042742	defense response to bacterium	1	17	0.09859819
GO:0005886	plasma membrane	3	17	0.108412229
GO:0022626	cytosolic ribosome	1	17	0.1197847
GO:0006979	response to oxidative stress	1	17	0.135076857
GO:0009737	response to abscisic acid stimulus	1	17	0.142777205
GO:0005215	transporter activity	1	17	0.15372846
GO:0009505	plant-type cell wall	1	17	0.16157143
GO:0003735	structural constituent of ribosome	1	17	0.186028391
GO:0009651	response to salt stress	1	17	0.188568416
GO:0006412	translation	1	17	0.192086321
GO:0006810	transport	1	17	0.203336094
GO:0006499	N-terminal protein myristoylation	1	17	0.216405877
GO:0009570	chloroplast stroma	1	17	0.219568361
GO:0009507	chloroplast	2	17	0.287354079
GO:0005739	mitochondrion	1	17	0.343822974
GO:0005515	protein binding	1	17	0.379145853

Cluster 14

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0000148	1	AT4G03550		
GO:0000162	1	AT1G51570		
GO:0003735	1	AT3G48930		
GO:0003824	3	AT1G52760	AT1G78570	AT4G30440
GO:0003843	1	AT4G03550		
GO:0003923	1	AT3G07140		
GO:0004655	1	AT1G69740		
GO:0005215	1	AT1G22530		
GO:0005515	1	AT5G35080		
GO:0005618	2	AT1G51570	AT3G48930	
GO:0005625	1	AT1G78570		
GO:0005739	1	AT2G20810		
GO:0005783	3	AT1G51570	AT3G07140	AT5G13930
GO:0005794	2	AT4G14360	AT4G16120	
GO:0005886	3	AT1G22530	AT4G03550	AT5G60920
GO:0006075	1	AT4G03550		

Cluster 14 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0006412	1	AT3G48930	
GO:0006499	1	AT4G14360	
GO:0006779	1	AT1G69740	
GO:0006810	1	AT1G22530	
GO:0006979	1	AT5G13930	
GO:0009225	2	AT1G78570	AT4G30440
GO:0009505	1	AT5G60920	
GO:0009507	2	AT1G22530	AT1G69740
GO:0009570	1	AT1G69740	
GO:0009611	1	AT5G13930	
GO:0009620	1	AT4G03550	
GO:0009629	1	AT5G13930	
GO:0009651	1	AT5G60920	
GO:0009705	1	AT5G13930	
GO:0009715	1	AT5G13930	
GO:0009737	1	AT4G28520	
GO:0009753	1	AT5G13930	
GO:0009793	2	AT3G48930	AT4G28520
GO:0009813	1	AT5G13930	
GO:0009825	1	AT5G60920	
GO:0009863	1	AT4G03550	
GO:0009870	1	AT4G03550	
GO:0009897	1	AT5G60920	
GO:0009926	1	AT5G13930	
GO:0009930	1	AT5G60920	
GO:0009965	1	AT4G03550	
GO:0010215	1	AT5G60920	
GO:0010224	1	AT5G13930	
GO:0010253	1	AT1G78570	
GO:0010280	1	AT1G78570	
GO:0010315	1	AT1G78570	
GO:0016051	1	AT2G20810	
GO:0016210	1	AT5G13930	
GO:0016757	2	AT2G20810	AT4G03550
GO:0016758	1	AT2G20810	
GO:0022626	1	AT3G48930	
GO:0022627	1	AT3G48930	
GO:0031225	2	AT4G16120	AT5G60920
GO:0031540	1	AT5G13930	
GO:0042735	1	AT4G28520	
GO:0042742	1	AT4G03550	
GO:0045735	1	AT4G28520	
GO:0046658	2	AT4G16120	AT5G60920
GO:0047262	1	AT2G20810	
GO:0050377	1	AT1G78570	
GO:0050378	1	AT4G30440	
GO:0051555	1	AT1G78570	
GO:0052542	1	AT4G03550	
GO:0052544	1	AT4G03550	



Cluster 15
AT1G21900
AT2G14720
AT2G28520
AT2G36160
AT3G05560
AT3G23400
AT3G48680
AT3G56310
AT3G61130
AT4G02620
AT5G43970
AT5G59880

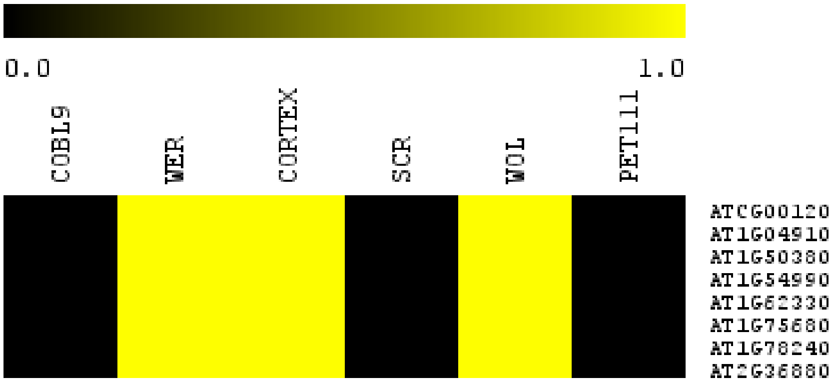
Cluster 15 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0003735	structural constituent of ribosome	2	12	0.010644001
GO:0005886	plasma membrane	7	12	1.09E-05
GO:0005773	vacuole	3	12	0.001728795
GO:0004557	alpha-galactosidase activity	1	12	0.002297966
GO:0005742	mitochondrial outer membrane translocase complex	1	12	0.004015079
GO:0005739	mitochondrion	3	12	0.007845499
GO:0005198	structural molecule activity	1	12	0.023098336
GO:0003779	actin binding	1	12	0.028580558
GO:0005794	Golgi apparatus	1	12	0.068863939
GO:0005840	ribosome	1	12	0.096088636
GO:0005730	nucleolus	1	12	0.120762461
GO:0005622	intracellular	1	12	0.182044909
GO:0005634	nucleus	1	12	0.384040506

Cluster 15 **GO Identifier**	**#Loci**	**Associated Loci (Left to Right)**	
GO:0003735	2	AT2G36160	AT3G05560
GO:0003779	1	AT5G59880	
GO:0004557	1	AT3G56310	
GO:0005198	1	AT3G23400	
GO:0005622	1	AT5G59880	
GO:0005634	1	AT3G23400	
GO:0005730	1	AT3G05560	

Cluster 15 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)				
GO:0005739	3	AT3G48680	AT5G43970	AT5G59880		
GO:0005742	1	AT5G43970				
GO:0005773	3	AT2G28520	AT3G56310	AT4G02620		
GO:0005794	1	AT3G61130				
GO:0005840	1	AT3G05560				
GO:0005886	7	AT2G36160	AT3G05560	AT3G23400	AT3G48680	AT4G02620
		AT5G43970	AT5G59880			
GO:0005975	1	AT3G56310				
GO:0005990	1	AT3G56310				
GO:0006412	2	AT2G36160	AT3G05560			
GO:0006626	1	AT5G43970				
GO:0006810	1	AT3G23400				
GO:0006886	1	AT1G21900				
GO:0006979	1	AT5G59880				
GO:0008152	1	AT3G56310				
GO:0008320	1	AT1G21900				
GO:0008415	1	AT3G48680				
GO:0009507	4	AT2G36160	AT3G23400	AT3G48680	AT5G59880	
GO:0009535	1	AT3G23400				
GO:0009536	1	AT5G43970				
GO:0009579	1	AT3G23400				
GO:0009853	1	AT3G48680				
GO:0010287	1	AT3G23400				
GO:0010289	1	AT3G61130				
GO:0012510	1	AT2G28520				
GO:0015450	1	AT5G43970				
GO:0015986	1	AT4G02620				
GO:0016020	3	AT1G21900	AT2G36160	AT3G23400		
GO:0016051	1	AT3G61130				
GO:0016740	1	AT3G48680				
GO:0016757	1	AT3G61130				
GO:0016887	1	AT2G28520				
GO:0022625	1	AT3G05560				
GO:0022626	2	AT2G36160	AT3G05560			
GO:0022627	1	AT2G36160				
GO:0031966	1	AT3G48680				
GO:0031977	1	AT3G23400				
GO:0045271	1	AT3G48680				
GO:0046686	1	AT5G59880				
GO:0046933	1	AT4G02620				

Cluster 16



Cluster 16
AT1G04910
AT1G50380
AT1G54990
AT1G62330
AT1G75680
AT1G78240
AT2G36880
ATCG00120

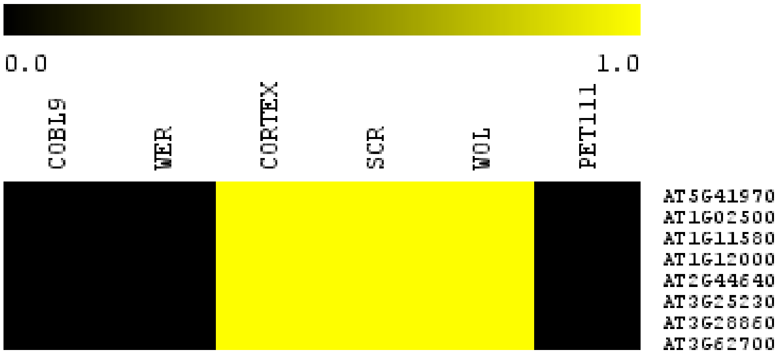
Cluster 16 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005794	Golgi apparatus	2	7	7.62E-04
GO:0010289	homogalacturonan biosynthetic process	1	7	0.001006373
GO:0004478	methionine adenosyltransferase activity	1	7	0.001341445
GO:0006556	S-adenosylmethionine biosynthetic process	1	7	0.001341445
GO:0009612	response to mechanical stimulus	1	7	0.002679803
GO:0008236	serine-type peptidase activity	1	7	0.010645374
GO:0009926	auxin polar transport	1	7	0.011962248
GO:0048367	shoot development	1	7	0.012290989
GO:0005886	plasma membrane	3	7	0.01283583
GO:0009735	response to cytokinin stimulus	1	7	0.014259436
GO:0008168	methyltransferase activity	1	7	0.015241091
GO:0048364	root development	1	7	0.022387749
GO:0005507	copper ion binding	1	7	0.034517469
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	1	7	0.050987635
GO:0009733	response to auxin stimulus	1	7	0.069899735
GO:0005783	endoplasmic reticulum	1	7	0.082400828
GO:0005975	carbohydrate metabolic process	1	7	0.091774451
GO:0006508	proteolysis	1	7	0.102609263
GO:0003674	molecular_function	3	7	0.178292796
GO:0005739	mitochondrion	1	7	0.206075695
GO:0005575	cellular_component	2	7	0.311759034

Cluster 16

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0003674	3	AT1G04910	AT1G54990	AT1G62330
GO:0004478	1	AT2G36880		
GO:0004553	1	AT1G75680		
GO:0005507	1	AT2G36880		
GO:0005575	2	AT1G50380	AT1G62330	
GO:0005739	1	AT1G54990		
GO:0005783	1	AT1G54990		
GO:0005794	2	AT1G04910	AT1G78240	
GO:0005886	3	AT1G54990	AT1G75680	AT2G36880
GO:0005975	1	AT1G75680		
GO:0006508	1	AT1G50380		
GO:0006556	1	AT2G36880		
GO:0008168	1	AT1G78240		
GO:0008236	1	AT1G50380		
GO:0009612	1	AT1G54990		
GO:0009733	1	AT1G54990		
GO:0009735	1	AT1G78240		
GO:0009926	1	AT1G54990		
GO:0010289	1	AT1G78240		
GO:0048364	1	AT1G78240		

Cluster 16 (con.)		
GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0048367	1	AT1G78240

Cluster 17



Cluster 17
AT1G02500
AT1G11580
AT1G12000
AT2G44640
AT3G25230
AT3G28860
AT3G62700
AT5G41970

Cluster 17 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0046686	response to cadmium ion	3	8	1.23E-04
GO:0005886	plasma membrane	5	8	1.42E-04
GO:0005618	cell wall	3	8	1.58E-04
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	2	8	4.70E-04
GO:0010318	pyrophosphate-dependent phosphofructokinase complex, beta-subunit complex	1	8	7.67E-04
GO:0010541	acropetal auxin transport	1	8	7.67E-04
GO:0008361	regulation of cell size	1	8	0.001150031
GO:0004478	methionine adenosyltransferase activity	1	8	0.00153286
GO:0006556	S-adenosylmethionine biosynthetic process	1	8	0.00153286
GO:0010329	auxin efflux transmembrane transporter activity	1	8	0.00153286
GO:0043481	anthocyanin accumulation in tissues in response to UV light	1	8	0.00153286
GO:0047334	diphosphate-fructose-6-phosphate 1-phosphotransferase activity	1	8	0.00153286
GO:0010540	basipetal auxin transport	1	8	0.002297746
GO:0009958	positive gravitropism	1	8	0.00458624
GO:0009693	ethylene biosynthetic process	1	8	0.00648627
GO:0048443	stamen development	1	8	0.007244491
GO:0005528	FK506 binding	1	8	0.008379906
GO:0048527	lateral root development	1	8	0.008379906
GO:0009637	response to blue light	1	8	0.009513024
GO:0000325	plant-type vacuole	1	8	0.010643849
GO:0009639	response to red or far red light	1	8	0.011396459

Cluster 17 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010218	response to far red light	1	8	0.012898628
GO:0009926	auxin polar transport	1	8	0.013648189
GO:0009640	photomorphogenesis	1	8	0.014022589
GO:0005774	vacuolar membrane	1	8	0.015144268
GO:0006096	glycolysis	1	8	0.016263668
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	8	0.020348685
GO:0042545	cell wall modification	1	8	0.022564031
GO:0030599	pectinesterase activity	1	8	0.025503772
GO:0048364	root development	1	8	0.025503772
GO:0005739	mitochondrion	2	8	0.03036572
GO:0009611	response to wounding	1	8	0.03960677
GO:0009536	plastid	1	8	0.047748157
GO:0005516	calmodulin binding	1	8	0.054722882
GO:0016020	membrane	2	8	0.077133288
GO:0009733	response to auxin stimulus	1	8	0.079038583
GO:0009505	plant-type cell wall	1	8	0.084276101
GO:0009651	response to salt stress	1	8	0.100576089
GO:0006810	transport	1	8	0.109887706
GO:0009941	chloroplast envelope	1	8	0.125256373
GO:0005773	vacuole	1	8	0.146267346
GO:0009507	chloroplast	1	8	0.390264817

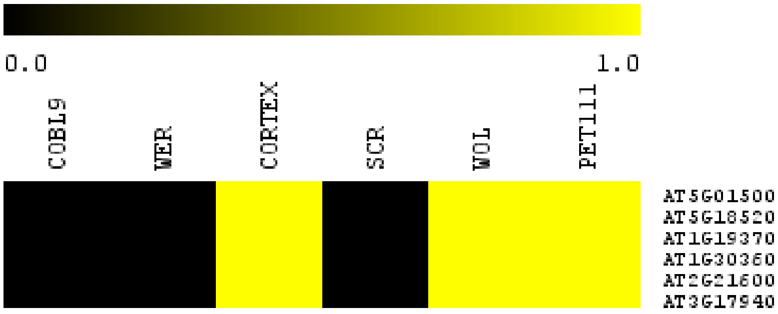
Cluster 17

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**				
GO:0000325	1	AT3G62700				
GO:0003755	1	AT3G25230				
GO:0004478	1	AT1G02500				
GO:0005516	1	AT3G25230				
GO:0005528	1	AT3G25230				
GO:0005618	3	AT1G02500	AT1G11580	AT1G12000		
GO:0005739	2	AT2G44640	AT5G41970			
GO:0005773	1	AT3G62700				
GO:0005774	1	AT3G62700				
GO:0005886	5	AT1G02500	AT1G11580	AT2G44640	AT3G28860	AT3G62700
GO:0006096	1	AT1G12000				
GO:0006556	1	AT1G02500				
GO:0006810	1	AT3G62700				
GO:0008361	1	AT3G28860				
GO:0009505	1	AT1G11580				
GO:0009507	1	AT2G44640				
GO:0009536	1	AT2G44640				
GO:0009611	1	AT3G25230				
GO:0009637	1	AT3G28860				
GO:0009639	1	AT3G28860				
GO:0009640	1	AT3G28860				
GO:0009651	1	AT1G02500				
GO:0009693	1	AT1G02500				
GO:0009733	1	AT3G28860				
GO:0009926	1	AT3G28860				
GO:0009941	1	AT2G44640				
GO:0009958	1	AT3G28860				
GO:0010218	1	AT3G28860				
GO:0010318	1	AT1G12000				
GO:0010329	1	AT3G28860				

Cluster 17 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0010540	1	AT3G28860		
GO:0010541	1	AT3G28860		
GO:0016020	2	AT1G02500	AT1G12000	
GO:0030599	1	AT1G11580		
GO:0042545	1	AT1G11580		
GO:0042626	2	AT3G28860	AT3G62700	
GO:0043481	1	AT3G28860		
GO:0046686	3	AT1G02500	AT1G12000	AT3G25230
GO:0047334	1	AT1G12000		
GO:0048364	1	AT3G28860		
GO:0048443	1	AT3G28860		
GO:0048527	1	AT3G28860		

Cluster 18



Cluster 18

AT1G19370
AT1G30360
AT2G21600
AT3G17940
AT5G01500
AT5G18520

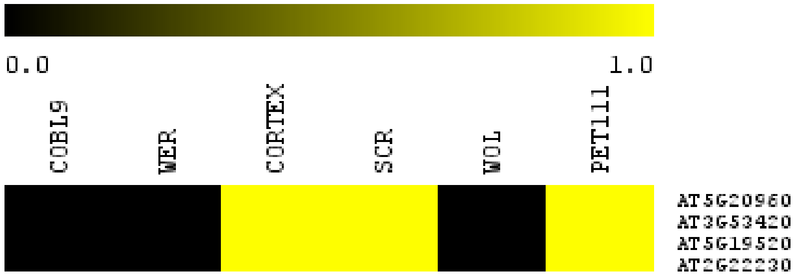
Cluster 18 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004034	aldose 1-epimerase activity	1	6	0.003157127
GO:0005347	ATP transmembrane transporter activity	1	6	0.001149976
GO:0005488	binding	1	6	0.114504149
GO:0009507	chloroplast	2	6	0.117237127
GO:0009941	chloroplast envelope	2	6	0.004385178
GO:0005801	cis-Golgi network	1	6	0.001437125
GO:0012505	endomembrane system	1	6	0.36903943
GO:0005783	endoplasmic reticulum	2	6	0.00229346
GO:0006012	galactose metabolic process	1	6	0.003729361
GO:0005794	Golgi apparatus	1	6	0.035717836
GO:0016021	integral to membrane	1	6	0.067986567
GO:0016020	membrane	1	6	0.275969005
GO:0005743	mitochondrial inner membrane	1	6	0.021197393
GO:0005739	mitochondrion	1	6	0.183391785
GO:0005886	plasma membrane	1	6	0.316486099
GO:0009536	plastid	1	6	0.036258427
GO:0009526	plastid envelope	1	6	0.001149976
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	1	6	0.001437125

Cluster 18 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0042651	thylakoid membrane	1	6	0.002584344
GO:0006810	transport	1	6	0.084988653
GO:0005215	transporter activity	1	6	0.061071892
GO:0005773	vacuole	1	6	0.114504149

Cluster 18

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0004034	1	AT3G17940	
GO:0005215	1	AT5G01500	
GO:0005347	1	AT5G01500	
GO:0005488	1	AT5G01500	
GO:0005739	1	AT5G01500	
GO:0005743	1	AT5G01500	
GO:0005773	1	AT1G30360	
GO:0005783	2	AT1G19370	AT2G21600
GO:0005794	1	AT2G21600	
GO:0005801	1	AT2G21600	
GO:0005886	1	AT1G30360	
GO:0006012	1	AT3G17940	
GO:0006810	1	AT5G01500	
GO:0006890	1	AT2G21600	
GO:0009507	2	AT1G30360	AT5G01500
GO:0009526	1	AT5G01500	
GO:0009536	1	AT5G01500	
GO:0009941	2	AT1G30360	AT5G01500
GO:0012505	1	AT5G18520	
GO:0016020	1	AT1G30360	
GO:0016021	1	AT5G18520	
GO:0042651	1	AT5G01500	

Cluster 19



Cluster19

AT2G22230
AT3G53420
AT5G19520
AT5G20960

Cluster 19 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0008381	mechanically-gated ion channel activity	1	4	3.84E-04
GO:0019171	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity	1	4	3.84E-04
GO:0050302	indole-3-acetaldehyde oxidase activity	1	4	3.84E-04
GO:0050982	detection of mechanical stimulus	1	4	3.84E-04
GO:0004031	aldehyde oxidase activity	1	4	5.75E-04
GO:0006833	water transport	1	4	7.67E-04
GO:0009851	auxin biosynthetic process	1	4	0.00153286
GO:0015250	water channel activity	1	4	0.005349581
GO:0006633	fatty acid biosynthetic process	1	4	0.0089551
GO:0016020	membrane	2	4	0.021528308
GO:0009414	response to water deprivation	1	4	0.025581533
GO:0005886	plasma membrane	2	4	0.032511279
GO:0009651	response to salt stress	1	4	0.053165286
GO:0005618	cell wall	1	4	0.055627004
GO:0006810	transport	1	4	0.058427724
GO:0009507	chloroplast	2	4	0.059481381
GO:0005773	vacuole	1	4	0.079678425

Cluster 19

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0004031	1	AT5G20960	
GO:0005618	1	AT2G22230	
GO:0005773	1	AT3G53420	
GO:0005886	2	AT3G53420	AT5G19520
GO:0006633	1	AT2G22230	
GO:0006810	1	AT3G53420	
GO:0006833	1	AT3G53420	
GO:0008381	1	AT5G19520	
GO:0009414	1	AT3G53420	
GO:0009507	2	AT2G22230	AT3G53420
GO:0009651	1	AT3G53420	
GO:0009851	1	AT5G20960	
GO:0015250	1	AT3G53420	
GO:0016020	2	AT3G53420	AT5G19520
GO:0019171	1	AT2G22230	
GO:0050302	1	AT5G20960	
GO:0050982	1	AT5G19520	

Cluster 20

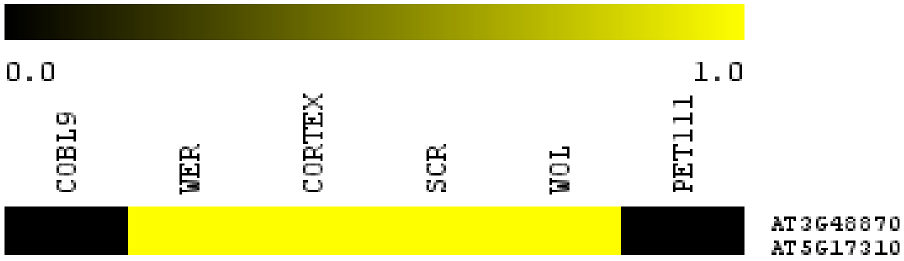
Cluster 20
AT1G09620
AT2G45290
AT3G18130

Cluster 20 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004802	transketolase activity	1	3	4.31E-04
GO:0004812	aminoacyl-tRNA ligase activity	1	3	0.003301582
GO:0006418	tRNA aminoacylation for protein translation	1	3	0.003587987
GO:0048367	shoot development	1	3	0.005304104
GO:0005834	heterotrimeric G-protein complex	1	3	0.007586096
GO:0048364	root development	1	3	0.009719072
GO:0000166	nucleotide binding	1	3	0.030710135
GO:0005730	nucleolus	1	3	0.033462623
GO:0009507	chloroplast	2	3	0.03349462
GO:0046686	response to cadmium ion	1	3	0.038935069
GO:0009570	chloroplast stroma	1	3	0.049213621
GO:0005524	ATP binding	1	3	0.084606448

Cluster 20

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000166	1	AT3G18130	
GO:0004802	1	AT2G45290	
GO:0004812	1	AT1G09620	
GO:0005524	1	AT1G09620	
GO:0005730	1	AT3G18130	
GO:0005834	1	AT3G18130	
GO:0006418	1	AT1G09620	
GO:0009507	2	AT1G09620	AT2G45290
GO:0009570	1	AT2G45290	
GO:0046686	1	AT2G45290	
GO:0048364	1	AT3G18130	
GO:0048367	1	AT3G18130	

Cluster 21



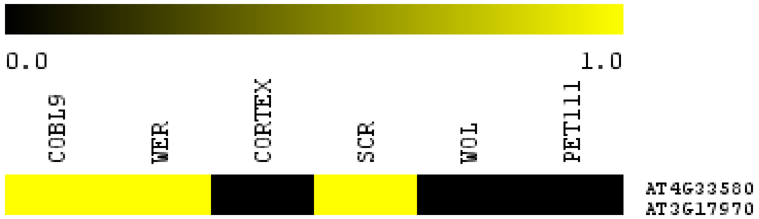
Cluster 21
AT3G48870
AT5G17310

Cluster 21 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0003983	UTP:glucose-1-phosphate uridylyltransferase activity	1	2	2.88E-04
GO:0046686	response to cadmium ion	1	2	0.02630615
GO:0009651	response to salt stress	1	2	0.027332421
GO:0008152	metabolic process	1	2	0.052083059
GO:0005886	plasma membrane	1	2	0.147255393

Cluster 21

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0003983	1	AT5G17310
GO:0005886	1	AT5G17310
GO:0008152	1	AT5G17310
GO:0009651	1	AT5G17310
GO:0046686	1	AT5G17310

Cluster 22



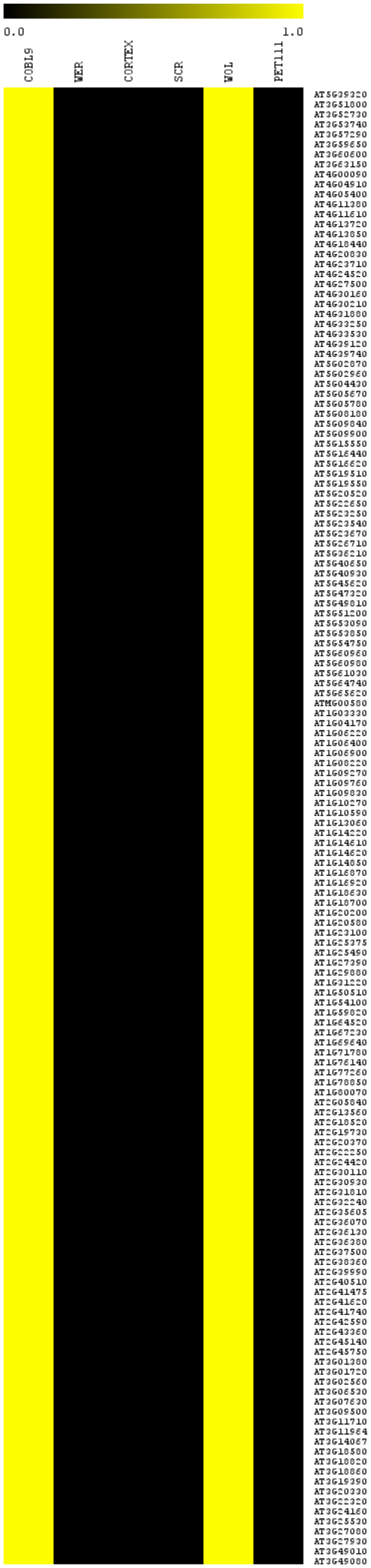
Cluster 22
AT3G17970
AT4G33580

Cluster 22 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016884	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	1	2	9.59E-05
GO:0015976	carbon utilization	1	2	5.75E-04
GO:0004089	carbonate dehydratase activity	1	2	0.001437538
GO:0009507	chloroplast	2	2	0.012574049
GO:0005488	binding	1	2	0.041583373
GO:0008270	zinc ion binding	1	2	0.066578273

Cluster 22

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0004089	1	AT4G33580	
GO:0005488	1	AT3G17970	
GO:0008270	1	AT4G33580	
GO:0009507	2	AT3G17970	AT4G33580
GO:0015976	1	AT4G33580	
GO:0016884	1	AT3G17970	

Cluster 23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1.0
COBL9
WER
CORTEX
SCR
WOL
PET111
AT5G39320
AT3G51800
AT3G52730
AT3G53740
AT3G57290
AT3G59650
AT3G60600
AT3G63150
AT4G00090
AT4G04910
AT4G05400
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AT4G30160
AT4G30210
AT4G31880
AT4G33250
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AT3G27930
AT3G49010
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Cluster 23

AT1G03330
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AT5G54750
AT5G60960
AT5G60980
AT5G61030
AT5G64740
AT5G65620
ATMG00580

Cluster 23 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0008541	proteasome regulatory particle, lid subcomplex	6	147	4.94E-11
GO:0005783	endoplasmic reticulum	15	147	5.83E-10
GO:0005886	plasma membrane	35	147	2.58E-09
GO:0005730	nucleolus	12	147	1.13E-07
GO:0006626	protein targeting to mitochondrion	4	147	3.97E-06
GO:0005744	mitochondrial inner membrane presequence translocase complex	4	147	1.03E-05
GO:0005742	mitochondrial outer membrane translocase complex	3	147	1.17E-05

Cluster 23 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	17	147	2.26E-05
GO:0005852	eukaryotic translation initiation factor 3 complex	3	147	2.76E-05
GO:0006412	translation	10	147	4.05E-05
GO:0003958	NADPH-hemoprotein reductase activity	2	147	4.93E-05
GO:0006511	ubiquitin-dependent protein catabolic process	7	147	3.44E-04
GO:0022625	cytosolic large ribosomal subunit	5	147	6.38E-04
GO:0004069	L-aspartate:2-oxoglutarate aminotransferase activity	2	147	0.001000775
GO:0022626	cytosolic ribosome	6	147	0.001016913
GO:0003743	translation initiation factor activity	4	147	0.001378602
GO:0009640	photomorphogenesis	3	147	0.002106128
GO:0009698	phenylpropanoid metabolic process	2	147	0.00254891
GO:0003735	structural constituent of ribosome	7	147	0.00313795
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	3	147	0.003208669
GO:0009507	chloroplast	27	147	0.003245621
GO:0042254	ribosome biogenesis	4	147	0.003745125
GO:0003723	RNA binding	7	147	0.003808517
GO:0016597	amino acid binding	2	147	0.005370481
GO:0005741	mitochondrial outer membrane	2	147	0.006044194
GO:0006913	nucleocytoplasmic transport	2	147	0.006752403
GO:0003858	3-hydroxybutyrate dehydrogenase activity	1	147	0.007048669
GO:0004070	aspartate carbamoyltransferase activity	1	147	0.007048669
GO:0004076	biotin synthase activity	1	147	0.007048669
GO:0004358	glutamate N-acetyltransferase activity	1	147	0.007048669
GO:0004637	phosphoribosylamine-glycine ligase activity	1	147	0.007048669
GO:0004644	phosphoribosylglycinamide formyltransferase activity	1	147	0.007048669
GO:0004824	lysine-tRNA ligase activity	1	147	0.007048669
GO:0006430	lysyl-tRNA aminoacylation	1	147	0.007048669
GO:0009240	isopentenyl diphosphate biosynthetic process	1	147	0.007048669
GO:0010256	endomembrane organization	1	147	0.007048669
GO:0010330	cellulose synthase complex	1	147	0.007048669
GO:0019866	organelle inner membrane	1	147	0.007048669
GO:0030581	intracellular protein transport in host	1	147	0.007048669
GO:0042353	fucose biosynthetic process	1	147	0.007048669
GO:0046500	S-adenosylmethionine metabolic process	1	147	0.007048669
GO:0046512	sphingosine biosynthetic process	1	147	0.007048669
GO:0046719	regulation of viral protein levels in host cell	1	147	0.007048669
GO:0048194	Golgi vesicle budding	1	147	0.007048669
GO:0006508	proteolysis	7	147	0.007320884
GO:0005737	cytoplasm	8	147	0.00732732
GO:0007010	cytoskeleton organization	2	147	0.008269037
GO:0005773	vacuole	8	147	0.009165095
GO:0030163	protein catabolic process	2	147	0.00991396
GO:0005794	Golgi apparatus	4	147	0.010741474
GO:0005643	nuclear pore	2	147	0.010782572
GO:0000398	nuclear mRNA splicing, via spliceosome	2	147	0.012608286
GO:0006418	tRNA aminoacylation for protein translation	2	147	0.012608286
GO:0016071	mRNA metabolic process	2	147	0.012608286
GO:0005732	small nucleolar ribonucleoprotein complex	2	147	0.013563895
GO:0000170	sphingosine hydroxylase activity	1	147	0.013998643
GO:0004452	isopentenyl-diphosphate delta-isomerase activity	1	147	0.013998643
GO:0004758	serine C-palmitoyltransferase activity	1	147	0.013998643

Cluster 23 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004818	glutamate-tRNA ligase activity	1	147	0.013998643
GO:0004820	glycine-tRNA ligase activity	1	147	0.013998643
GO:0004839	ubiquitin activating enzyme activity	1	147	0.013998643
GO:0005487	nucleocytoplasmic transporter activity	1	147	0.013998643
GO:0005548	phospholipid transporter activity	1	147	0.013998643
GO:0005853	eukaryotic translation elongation factor 1 complex	1	147	0.013998643
GO:0006426	glycyl-tRNA aminoacylation	1	147	0.013998643
GO:0006997	nucleus organization	1	147	0.013998643
GO:0009220	pyrimidine ribonucleotide biosynthetic process	1	147	0.013998643
GO:0010155	regulation of proton transport	1	147	0.013998643
GO:0015462	protein-transmembrane transporting ATPase activity	1	147	0.013998643
GO:0016743	carboxyl- or carbamoyltransferase activity	1	147	0.013998643
GO:0030173	integral to Golgi membrane	1	147	0.013998643
GO:0045281	succinate dehydrogenase complex	1	147	0.013998643
GO:0046520	sphingoid biosynthetic process	1	147	0.013998643
GO:0005743	mitochondrial inner membrane	3	147	0.014056439
GO:0003984	acetolactate synthase activity	1	147	0.020850949
GO:0004776	succinate-CoA ligase (GDP-forming) activity	1	147	0.020850949
GO:0005047	signal recognition particle binding	1	147	0.020850949
GO:0009102	biotin biosynthetic process	1	147	0.020850949
GO:0009647	skotomorphogenesis	1	147	0.020850949
GO:0030148	sphingolipid biosynthetic process	1	147	0.020850949
GO:0051788	response to misfolded protein	1	147	0.020850949
GO:0000104	succinate dehydrogenase activity	1	147	0.027606608
GO:0000326	protein storage vacuole	1	147	0.027606608
GO:0003727	single-stranded RNA binding	1	147	0.027606608
GO:0003979	UDP-glucose 6-dehydrogenase activity	1	147	0.027606608
GO:0006121	mitochondrial electron transport, succinate to ubiquinone	1	147	0.027606608
GO:0008864	formyltetrahydrofolate deformylase activity	1	147	0.027606608
GO:0009833	primary cell wall biogenesis	1	147	0.027606608
GO:0016742	hydroxymethyl-, formyl- and related transferase activity	1	147	0.027606608
GO:0031897	Tic complex	1	147	0.027606608
GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	1	147	0.027606608
GO:0005840	ribosome	4	147	0.031563865
GO:0005763	mitochondrial small ribosomal subunit	1	147	0.034266631
GO:0006424	glutamyl-tRNA aminoacylation	1	147	0.034266631
GO:0009082	branched chain family amino acid biosynthetic process	1	147	0.034266631
GO:0009113	purine base biosynthetic process	1	147	0.034266631
GO:0009152	purine ribonucleotide biosynthetic process	1	147	0.034266631
GO:0009969	xyloglucan biosynthetic process	1	147	0.034266631
GO:0016462	pyrophosphatase activity	1	147	0.034266631
GO:0046907	intracellular transport	1	147	0.034266631
GO:0016020	membrane	14	147	0.0388827
GO:0006886	intracellular protein transport	3	147	0.03966244
GO:0000502	proteasome complex	1	147	0.040832019
GO:0004470	malic enzyme activity	1	147	0.040832019
GO:0004664	prephenate dehydratase activity	1	147	0.040832019
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	1	147	0.040832019
GO:0006164	purine nucleotide biosynthetic process	1	147	0.040832019
GO:0009094	L-phenylalanine biosynthetic process	1	147	0.040832019
GO:0016652	oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	1	147	0.040832019

Cluster 23 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045037	protein import into chloroplast stroma	1	147	0.040832019
GO:0047769	arogenate dehydratase activity	1	147	0.040832019
GO:0048528	post-embryonic root development	1	147	0.040832019
GO:0005618	cell wall	5	147	0.043023368
GO:0003779	actin binding	2	147	0.044680713
GO:0015030	Cajal body	1	147	0.047303764
GO:0031540	regulation of anthocyanin biosynthetic process	1	147	0.047303764
GO:0000166	nucleotide binding	4	147	0.049361996
GO:0006413	translational initiation	2	147	0.050604051
GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	1	147	0.053682849
GO:0006446	regulation of translational initiation	1	147	0.053682849
GO:0006506	GPI anchor biosynthetic process	1	147	0.053682849
GO:0006526	arginine biosynthetic process	1	147	0.053682849
GO:0008135	translation factor activity, nucleic acid binding	1	147	0.053682849
GO:0010005	cortical microtubule, transverse to long axis	1	147	0.053682849
GO:0008121	ubiquinol-cytochrome-c reductase activity	1	147	0.059970247
GO:0008441	3'(2'),5'-bisphosphate nucleotidase activity	1	147	0.059970247
GO:0030276	clathrin binding	1	147	0.059970247
GO:0043622	cortical microtubule organization	1	147	0.059970247
GO:0007264	small GTPase mediated signal transduction	2	147	0.06135929
GO:0003690	double-stranded DNA binding	1	147	0.066166923
GO:0004521	endoribonuclease activity	1	147	0.066166923
GO:0006108	malate metabolic process	1	147	0.066166923
GO:0048364	root development	2	147	0.070877003
GO:0005634	nucleus	15	147	0.074621587
GO:0009908	flower development	2	147	0.077330608
GO:0005524	ATP binding	7	147	0.078070027
GO:0003697	single-stranded DNA binding	1	147	0.078291924
GO:0005802	trans-Golgi network	1	147	0.078291924
GO:0009789	positive regulation of abscisic acid mediated signaling	1	147	0.078291924
GO:0045309	protein phosphorylated amino acid binding	1	147	0.078291924
GO:0009055	electron carrier activity	2	147	0.080581205
GO:0016192	vesicle-mediated transport	2	147	0.083844009
GO:0005654	nucleoplasm	1	147	0.084222135
GO:0006790	sulfur metabolic process	1	147	0.084222135
GO:0008180	signalosome	1	147	0.084222135
GO:0009863	salicylic acid mediated signaling pathway	1	147	0.084222135
GO:0009793	embryonic development ending in seed dormancy	4	147	0.087125064
GO:0005829	cytosol	3	147	0.088228619
GO:0000159	protein phosphatase type 2A complex	1	147	0.090065394
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	147	0.090065394
GO:0004407	histone deacetylase activity	1	147	0.090065394
GO:0005740	mitochondrial envelope	1	147	0.090065394
GO:0005750	mitochondrial respiratory chain complex III	1	147	0.090065394
GO:0008601	protein phosphatase type 2A regulator activity	1	147	0.090065394
GO:0022627	cytosolic small ribosomal subunit	2	147	0.090395854
GO:0005525	GTP binding	3	147	0.091026166
GO:0009651	response to salt stress	4	147	0.093615704
GO:0015031	protein transport	2	147	0.095322961
GO:0004437	inositol or phosphatidylinositol phosphatase activity	1	147	0.095822622
GO:0009269	response to desiccation	1	147	0.095822622
GO:0003746	translation elongation factor activity	1	147	0.101494733

Cluster 23 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009944	polarity specification of adaxial/abaxial axis	1	147	0.101494733
GO:0006979	response to oxidative stress	3	147	0.106908312
GO:0006520	amino acid metabolic process	1	147	0.10708263
GO:0006807	nitrogen compound metabolic process	1	147	0.112587207
GO:0006888	ER to Golgi vesicle-mediated transport	1	147	0.112587207
GO:0015662	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	1	147	0.112587207
GO:0008299	isoprenoid biosynthetic process	1	147	0.118009354
GO:0006457	protein folding	3	147	0.11801709
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	1	147	0.123349947
GO:0051301	cell division	1	147	0.123349947
GO:0006397	mRNA processing	1	147	0.128609859
GO:0015079	potassium ion transmembrane transporter activity	1	147	0.128609859
GO:0030244	cellulose biosynthetic process	1	147	0.128609859
GO:0005789	endoplasmic reticulum membrane	1	147	0.133789952
GO:0006414	translational elongation	1	147	0.133789952
GO:0009570	chloroplast stroma	4	147	0.134326247
GO:0004812	aminoacyl-tRNA ligase activity	1	147	0.138891079
GO:0006461	protein complex assembly	1	147	0.138891079
GO:0010119	regulation of stomatal movement	1	147	0.138891079
GO:0016049	cell growth	1	147	0.138891079
GO:0048825	cotyledon development	1	147	0.138891079
GO:0009832	plant-type cell wall biogenesis	1	147	0.143914088
GO:0008380	RNA splicing	1	147	0.148859818
GO:0009294	DNA mediated transformation	1	147	0.148859818
GO:0048046	apoplast	3	147	0.15050596
GO:0015995	chlorophyll biosynthetic process	1	147	0.153729099
GO:0006352	transcription initiation	1	147	0.158522755
GO:0016481	negative regulation of transcription	1	147	0.158522755
GO:0007275	multicellular organismal development	2	147	0.164619705
GO:0009536	plastid	2	147	0.168925026
GO:0009706	chloroplast inner membrane	1	147	0.176957314
GO:0009790	embryonic development	1	147	0.176957314
GO:0008236	serine-type peptidase activity	1	147	0.18138492
GO:0003924	GTPase activity	1	147	0.190028362
GO:0010583	response to cyclopentenone	1	147	0.190028362
GO:0015934	large ribosomal subunit	1	147	0.190028362
GO:0016759	cellulose synthase activity	1	147	0.194245733
GO:0009658	chloroplast organization	1	147	0.198394547
GO:0009926	auxin polar transport	1	147	0.198394547
GO:0009845	seed germination	1	147	0.202475553
GO:0009965	leaf morphogenesis	1	147	0.202475553
GO:0048367	shoot development	1	147	0.202475553
GO:0009738	abscisic acid mediated signaling	1	147	0.206489493
GO:0005509	calcium ion binding	2	147	0.207557623
GO:0005198	structural molecule activity	1	147	0.218136234
GO:0003824	catalytic activity	3	147	0.220822517
GO:0006813	potassium ion transport	1	147	0.221889191
GO:0009735	response to cytokinin stimulus	1	147	0.225578688
GO:0003899	DNA-directed RNA polymerase activity	1	147	0.2327701
GO:0009409	response to cold	2	147	0.235539685
GO:0008233	peptidase activity	1	147	0.236273396

Cluster 23 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006350	transcription	1	147	0.243098575
GO:0051707	response to other organism	1	147	0.246421801
GO:0009737	response to abscisic acid stimulus	2	147	0.248568793
GO:0005834	heterotrimeric G-protein complex	1	147	0.259134313
GO:0009555	pollen development	1	147	0.259134313
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	147	0.262170575
GO:0009505	plant-type cell wall	2	147	0.265656198
GO:0006970	response to osmotic stress	1	147	0.270949002
GO:0046686	response to cadmium ion	2	147	0.273397644
GO:0006396	RNA processing	1	147	0.273767087
GO:0016567	protein ubiquitination	1	147	0.279244826
GO:0017111	nucleoside-triphosphatase activity	1	147	0.292042637
GO:0008565	protein transporter activity	1	147	0.305791355
GO:0048366	leaf development	1	147	0.314037224
GO:0009826	unidimensional cell growth	1	147	0.321586346
GO:0046872	metal ion binding	1	147	0.321586346
GO:0016740	transferase activity	1	147	0.323368557
GO:0009058	biosynthetic process	1	147	0.328470885
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	147	0.334721763
GO:0009408	response to heat	1	147	0.344224829
GO:0009723	response to ethylene stimulus	1	147	0.349964028
GO:0031072	heat shock protein binding	1	147	0.357472367
GO:0042742	defense response to bacterium	1	147	0.369918678

Cluster 23

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000104	1	AT5G40650
GO:0000159	1	AT1G25490
GO:0000166	4	AT3G18860 AT4G00090 AT4G04910 AT5G15550
GO:0000170	1	AT1G69640
GO:0000326	1	AT3G60600
GO:0000398	2	AT1G09760 AT1G80070
GO:0000502	1	AT1G64520
GO:0003690	1	AT4G13850
GO:0003697	1	AT4G13850
GO:0003723	7	AT1G18630 AT3G11964 AT4G13850 AT5G08180 AT5G47320 AT5G60980 AT5G61030
GO:0003727	1	AT5G04430
GO:0003735	7	AT2G19730 AT3G02560 AT3G09500 AT3G49010 AT3G49080 AT3G53740 AT5G02870
GO:0003743	4	AT1G04170 AT2G39990 AT3G57290 AT4G33250
GO:0003746	1	AT5G19510
GO:0003755	1	AT2G36130
GO:0003779	2	AT2G41740 AT4G30160
GO:0003824	3	AT1G25375 AT1G69640 AT2G20370
GO:0003858	1	AT3G25530
GO:0003899	1	AT3G22320
GO:0003924	1	AT3G63150
GO:0003958	2	AT4G24520 AT4G30210
GO:0003979	1	AT5G39320
GO:0003984	1	AT2G31810
GO:0004028	1	AT1G54100
GO:0004069	2	AT2G22250 AT5G19550

Cluster 23 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004070	1	AT3G20330					
GO:0004076	1	AT2G43360					
GO:0004358	1	AT2G37500					
GO:0004407	1	AT5G22650					
GO:0004437	1	AT4G39120					
GO:0004452	1	AT5G16440					
GO:0004470	1	AT2G13560					
GO:0004521	1	AT1G14220					
GO:0004616	1	AT3G25530					
GO:0004637	1	AT1G09830					
GO:0004644	1	AT1G31220					
GO:0004664	1	AT3G07630					
GO:0004758	1	AT5G23670					
GO:0004776	1	AT5G23250					
GO:0004812	1	AT1G14610					
GO:0004818	1	AT5G26710					
GO:0004820	1	AT1G29880					
GO:0004824	1	AT3G11710					
GO:0004839	1	AT2G30110					
GO:0005047	1	AT5G05670					
GO:0005198	1	AT2G45140					
GO:0005487	1	AT1G14850					
GO:0005509	2	AT2G42590	AT3G63150				
GO:0005524	7	AT1G14610	AT1G23100	AT2G13560	AT3G11710	AT4G04910	AT4G13850
		AT5G61030					
GO:0005525	3	AT1G06400	AT1G16920	AT3G18820			
GO:0005548	1	AT1G59820					
GO:0005618	5	AT1G25490	AT2G19730	AT3G49010	AT5G19550	AT5G22650	
GO:0005634	15	AT1G03330	AT1G09270	AT1G09760	AT1G10270	AT1G20580	AT1G64520
		AT1G67230	AT2G35605	AT2G39990	AT2G42590	AT3G18820	AT3G22320
		AT3G57290	AT5G09900	AT5G23540			
GO:0005643	2	AT1G09270	AT1G14850				
GO:0005654	1	AT1G09760					
GO:0005730	12	AT1G09760	AT1G14850	AT1G20580	AT2G41620	AT3G09500	AT3G11964
		AT3G49010	AT3G51800	AT5G02870	AT5G08180	AT5G15550	AT5G22650
GO:0005732	2	AT1G03330	AT1G20580				
GO:0005737	8	AT1G09270	AT1G09760	AT2G39990	AT2G42590	AT3G11710	AT3G57290
		AT5G09900	AT5G26710				
GO:0005739	17	AT1G14610	AT1G18630	AT1G23100	AT1G27390	AT1G29880	AT2G13560
		AT2G36070	AT3G27080	AT3G52730	AT3G59650	AT3G63150	AT4G13850
		AT4G20830	AT5G09840	AT5G23250	AT5G40650	AT5G61030	
GO:0005740	1	AT3G52730					
GO:0005741	2	AT1G27390	AT3G27080				
GO:0005742	3	AT1G27390	AT3G27080	AT5G40930			
GO:0005743	3	AT1G27390	AT2G36070	AT3G27080			
GO:0005744	4	AT1G27390	AT2G36070	AT3G27080	AT5G40930		
GO:0005750	1	AT3G52730					
GO:0005763	1	AT5G47320					
GO:0005773	8	AT1G16920	AT3G06530	AT3G14067	AT4G04910	AT4G20830	AT4G23710
		AT5G02870	AT5G23670				
GO:0005783	15	AT1G18700	AT1G69640	AT1G71780	AT2G24420	AT2G38360	AT2G45140
		AT3G01380	AT3G24160	AT3G60600	AT4G24520	AT4G27500	AT4G30210
		AT5G05670	AT5G20520	AT5G23670			
GO:0005789	1	AT3G60600					
GO:0005794	4	AT1G59820	AT1G69640	AT2G20370	AT5G64740		
GO:0005802	1	AT1G16920					
GO:0005829	3	AT3G25530	AT5G16440	AT5G19550			
GO:0005834	1	AT5G15550					
GO:0005840	4	AT2G19730	AT3G09500	AT3G49010	AT3G53740		

Cluster 23 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005852	3	AT2G39990	AT3G57290	AT4G33250			
GO:0005853	1	AT5G19510					
GO:0005886	35	AT1G06400	AT1G10590	AT1G14850	AT1G16920	AT1G20200	AT1G25490
		AT1G59820	AT2G19730	AT2G24420	AT2G30110	AT2G30930	AT2G36380
		AT2G42590	AT2G45140	AT3G11964	AT3G14067	AT3G18820	AT3G24160
		AT3G49010	AT3G51800	AT3G53740	AT3G57290	AT3G60600	AT4G11380
		AT4G20830	AT4G23710	AT4G27500	AT4G33530	AT5G02870	AT5G05670
		AT5G19550	AT5G20520	AT5G22650	AT5G40930	AT5G64740	
GO:0006108	1	AT2G13560					
GO:0006121	1	AT5G40650					
GO:0006122	1	AT3G52730					
GO:0006164	1	AT1G09830					
GO:0006350	1	AT3G22320					
GO:0006352	1	AT3G57290					
GO:0006396	1	AT3G11964					
GO:0006397	1	AT3G11964					
GO:0006412	10	AT2G19730	AT3G02560	AT3G09500	AT3G49010	AT3G49080	AT3G53740
		AT3G57290	AT5G02870	AT5G26710	AT5G47320		
GO:0006413	2	AT2G39990	AT4G33250				
GO:0006414	1	AT5G19510					
GO:0006418	2	AT1G14610	AT5G26710				
GO:0006424	1	AT5G26710					
GO:0006426	1	AT1G29880					
GO:0006430	1	AT3G11710					
GO:0006446	1	AT4G33250					
GO:0006457	3	AT1G18700	AT1G23100	AT2G36130			
GO:0006461	1	AT4G11380					
GO:0006506	1	AT3G01380					
GO:0006508	7	AT1G06900	AT1G76140	AT3G14067	AT3G19390	AT3G51800	AT5G36210
		AT5G65620					
GO:0006511	7	AT1G20200	AT1G64520	AT2G30110	AT5G05780	AT5G09900	AT5G23540
		AT5G45620					
GO:0006520	1	AT3G20330					
GO:0006526	1	AT2G37500					
GO:0006626	4	AT1G27390	AT2G36070	AT3G27080	AT5G40930		
GO:0006790	1	AT4G39120					
GO:0006807	1	AT5G19550					
GO:0006813	1	AT4G33530					
GO:0006886	3	AT1G09270	AT1G16920	AT4G11380			
GO:0006888	1	AT5G54750					
GO:0006913	2	AT1G14850	AT5G60980				
GO:0006970	1	AT4G13850					
GO:0006979	3	AT3G25530	AT4G20830	AT4G24520			
GO:0006997	1	AT1G67230					
GO:0007010	2	AT2G41740	AT4G30160				
GO:0007264	2	AT1G06400	AT3G18820				
GO:0007275	2	AT5G09900	AT5G53090				
GO:0008121	1	AT3G52730					
GO:0008135	1	AT1G04170					
GO:0008180	1	AT3G57290					
GO:0008233	1	AT1G64520					
GO:0008236	1	AT5G36210					
GO:0008299	1	AT5G16440					
GO:0008380	1	AT5G04430					
GO:0008441	1	AT4G39120					
GO:0008541	6	AT1G20200	AT1G64520	AT5G05780	AT5G09900	AT5G23540	AT5G45620
GO:0008565	1	AT1G09270					
GO:0008601	1	AT1G25490					
GO:0008757	1	AT5G49810					

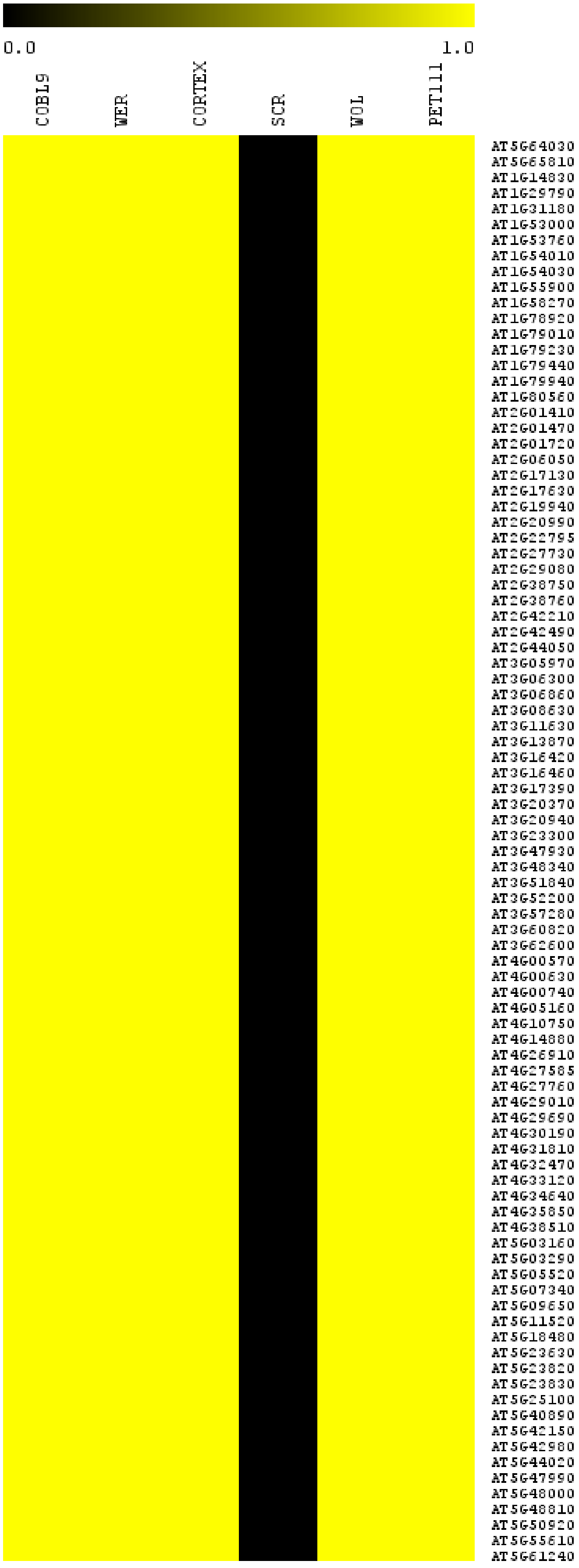
Cluster 23 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0008864	1	AT1G31220					
GO:0009055	2	AT4G20830	AT5G40650				
GO:0009058	1	AT1G31220					
GO:0009082	1	AT2G31810					
GO:0009094	1	AT3G07630					
GO:0009102	1	AT2G43360					
GO:0009113	1	AT1G09830					
GO:0009152	1	AT1G31220					
GO:0009220	1	AT3G20330					
GO:0009240	1	AT5G16440					
GO:0009269	1	AT1G54100					
GO:0009294	1	AT5G22650					
GO:0009408	1	AT1G64520					
GO:0009409	2	AT1G09760	AT4G13850				
GO:0009505	2	AT3G14067	AT4G20830				
GO:0009507	27	AT1G09760	AT1G09830	AT1G14610	AT1G14850	AT1G31220	AT1G76140
		AT1G80070	AT2G13560	AT2G19730	AT2G22250	AT2G30930	AT2G31810
		AT2G37500	AT3G02560	AT3G06530	AT3G07630	AT3G20330	AT4G30210
		AT4G31880	AT4G39120	AT5G02870	AT5G16440	AT5G16620	AT5G36210
		AT5G51200	AT5G53850	AT5G65620			
GO:0009536	2	AT1G27390	AT5G16440				
GO:0009555	1	AT5G23670					
GO:0009570	4	AT2G42590	AT3G20330	AT5G53850	AT5G65620		
GO:0009640	3	AT1G69640	AT3G57290	AT5G23670			
GO:0009647	1	AT1G64520					
GO:0009651	4	AT1G54100	AT2G13560	AT3G57290	AT5G23540		
GO:0009658	1	AT5G16620					
GO:0009698	2	AT4G24520	AT4G30210				
GO:0009706	1	AT5G16620					
GO:0009723	1	AT1G25490					
GO:0009735	1	AT1G64520					
GO:0009737	2	AT1G54100	AT3G63150				
GO:0009738	1	AT1G25490					
GO:0009789	1	AT1G25490					
GO:0009790	1	AT1G10270					
GO:0009793	4	AT1G14610	AT1G20200	AT2G22250	AT5G09900		
GO:0009826	1	AT2G20370					
GO:0009832	1	AT5G64740					
GO:0009833	1	AT5G64740					
GO:0009845	1	AT4G13850					
GO:0009863	1	AT2G20370					
GO:0009908	2	AT1G64520	AT3G57290				
GO:0009926	1	AT1G25490					
GO:0009944	1	AT5G22650					
GO:0009965	1	AT5G05780					
GO:0009969	1	AT2G20370					
GO:0010005	1	AT5G64740					
GO:0010119	1	AT1G25490					
GO:0010155	1	AT4G27500					
GO:0010256	1	AT2G20370					
GO:0010330	1	AT5G64740					
GO:0010583	1	AT5G64740					
GO:0015030	1	AT1G09760					
GO:0015031	2	AT1G06400	AT3G18820				
GO:0015079	1	AT4G33530					
GO:0015450	3	AT1G27390	AT3G27080	AT5G40930			
GO:0015462	1	AT2G36070					
GO:0015662	1	AT1G59820					
GO:0015934	1	AT5G02870					

Cluster 23 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0015995	1	AT5G16440					
GO:0016020	14	AT1G80070	AT2G18520	AT2G20370	AT2G30930	AT2G39990	AT3G02560
		AT3G24160	AT3G49010	AT3G52730	AT3G53740	AT5G02870	AT5G16620
		AT5G23670	AT5G64740				
GO:0016049	1	AT5G64740					
GO:0016071	2	AT1G03330	AT1G20580				
GO:0016192	2	AT2G38360	AT4G11380				
GO:0016462	1	AT4G13720					
GO:0016481	1	AT5G22650					
GO:0016567	1	AT2G30110					
GO:0016597	2	AT2G31810	AT3G20330				
GO:0016652	1	AT2G13560					
GO:0016740	1	AT3G01380					
GO:0016742	1	AT1G31220					
GO:0016743	1	AT3G20330					
GO:0016759	1	AT5G64740					
GO:0017111	1	AT4G04910					
GO:0019866	1	AT5G20520					
GO:0022625	5	AT2G19730	AT3G09500	AT3G49010	AT3G53740	AT5G02870	
GO:0022626	6	AT1G27390	AT2G19730	AT3G02560	AT3G49010	AT3G53740	AT5G02870
GO:0022627	2	AT3G02560	AT3G49080				
GO:0030148	1	AT5G23670					
GO:0030163	2	AT1G64520	AT5G23540				
GO:0030173	1	AT2G20370					
GO:0030244	1	AT5G64740					
GO:0030276	1	AT4G11380					
GO:0030581	1	AT1G09270					
GO:0031072	1	AT1G18700					
GO:0031540	1	AT1G64520					
GO:0031897	1	AT5G16620					
GO:0042254	4	AT2G19730	AT3G09500	AT3G49010	AT5G08180		
GO:0042353	1	AT2G20370					
GO:0042626	1	AT2G36380					
GO:0042742	1	AT5G19510					
GO:0043161	1	AT1G64520					
GO:0043622	1	AT5G64740					
GO:0045037	1	AT5G16620					
GO:0045281	1	AT5G40650					
GO:0045309	1	AT2G42590					
GO:0046500	1	AT5G49810					
GO:0046512	1	AT5G23670					
GO:0046520	1	AT1G69640					
GO:0046686	2	AT1G29880	AT2G30110				
GO:0046719	1	AT5G04430					
GO:0046872	1	AT1G27390					
GO:0046907	1	AT3G60600					
GO:0047769	1	AT3G07630					
GO:0048046	3	AT3G14067	AT4G20830	AT5G19510			
GO:0048194	1	AT1G59820					
GO:0048364	2	AT1G59820	AT5G20520				
GO:0048366	1	AT1G64520					
GO:0048367	1	AT1G59820					
GO:0048528	1	AT1G64520					
GO:0048825	1	AT1G64520					
GO:0051301	1	AT1G10270					
GO:0051707	1	AT2G30110					
GO:0051788	1	AT1G64520					

Cluster 24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Cluster 24

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AT5G65810

Cluster 24 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	24	91	1.46E-14
GO:0005783	endoplasmic reticulum	11	91	2.01E-08
GO:0009536	plastid	8	91	9.56E-08
GO:0016020	membrane	21	91	1.69E-07
GO:0005777	peroxisome	7	91	5.31E-07
GO:0005794	Golgi apparatus	7	91	1.38E-06
GO:0005886	plasma membrane	22	91	1.55E-06
GO:0006635	fatty acid beta-oxidation	4	91	3.31E-06
GO:0009507	chloroplast	23	91	8.74E-05
GO:0004300	enoyl-CoA hydratase activity	2	91	1.86E-04
GO:0004449	isocitrate dehydrogenase (NAD+) activity	2	91	1.86E-04
GO:0030176	integral to endoplasmic reticulum membrane	2	91	2.78E-04
GO:0005788	endoplasmic reticulum lumen	2	91	5.14E-04
GO:0005773	vacuole	8	91	5.73E-04
GO:0009986	cell surface	2	91	6.58E-04
GO:0009570	chloroplast stroma	7	91	7.55E-04
GO:0010152	pollen maturation	2	91	8.19E-04
GO:0009941	chloroplast envelope	7	91	9.65E-04
GO:0005544	calcium-dependent phospholipid binding	2	91	9.97E-04
GO:0008152	metabolic process	8	91	0.002300053
GO:0006888	ER to Golgi vesicle-mediated transport	2	91	0.002690572
GO:0009695	jasmonic acid biosynthetic process	2	91	0.002690572
GO:0005789	endoplasmic reticulum membrane	2	91	0.003993272
GO:0000906	6,7-dimethyl-8-ribityllumazine synthase activity	1	91	0.004363462
GO:0003857	3-hydroxyacyl-CoA dehydrogenase activity	1	91	0.004363462

Cluster 24 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0003862	3-isopropylmalate dehydrogenase activity	1	91	0.004363462
GO:0004777	succinate-semialdehyde dehydrogenase activity	1	91	0.004363462
GO:0006555	methionine metabolic process	1	91	0.004363462
GO:0009103	lipopolysaccharide biosynthetic process	1	91	0.004363462
GO:0015988	energy coupled proton transport, against electrochemical gradient	1	91	0.004363462
GO:0016633	galactonolactone dehydrogenase activity	1	91	0.004363462
GO:0016783	sulfurtransferase activity	1	91	0.004363462
GO:0016830	carbon-carbon lyase activity	1	91	0.004363462
GO:0019648	formaldehyde assimilation via xylulose monophosphate cycle	1	91	0.004363462
GO:0046459	short-chain fatty acid metabolic process	1	91	0.004363462
GO:0015992	proton transport	2	91	0.00552284
GO:0005618	cell wall	5	91	0.008427217
GO:0051082	unfolded protein binding	3	91	0.008614777
GO:0000266	mitochondrial fission	1	91	0.008689261
GO:0004310	farnesyl-diphosphate farnesyltransferase activity	1	91	0.008689261
GO:0004321	fatty-acyl-CoA synthase activity	1	91	0.008689261
GO:0004648	O-phospho-L-serine:2-oxoglutarate aminotransferase activity	1	91	0.008689261
GO:0004656	procollagen-proline 4-dioxygenase activity	1	91	0.008689261
GO:0004792	thiosulfate sulfurtransferase activity	1	91	0.008689261
GO:0006535	cysteine biosynthetic process from serine	1	91	0.008689261
GO:0006540	glutamate decarboxylation to succinate	1	91	0.008689261
GO:0009450	gamma-aminobutyric acid catabolic process	1	91	0.008689261
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	1	91	0.008689261
GO:0016629	12-oxophytodienoate reductase activity	1	91	0.008689261
GO:0016784	3-mercaptopyruvate sulfurtransferase activity	1	91	0.008689261
GO:0019829	cation-transporting ATPase activity	1	91	0.008689261
GO:0006457	protein folding	4	91	0.010256087
GO:0031072	heat shock protein binding	3	91	0.010264617
GO:0045271	respiratory chain complex I	2	91	0.010796726
GO:0016887	ATPase activity	3	91	0.01207096
GO:0005938	cell cortex	1	91	0.012977638
GO:0006090	pyruvate metabolic process	1	91	0.012977638
GO:0009678	hydrogen-translocating pyrophosphatase activity	1	91	0.012977638
GO:0051920	peroxiredoxin activity	1	91	0.012977638
GO:0007275	multicellular organismal development	3	91	0.015834804
GO:0005730	nucleolus	4	91	0.016528161
GO:0001676	long-chain fatty acid metabolic process	1	91	0.017228833
GO:0003860	3-hydroxyisobutyryl-CoA hydrolase activity	1	91	0.017228833
GO:0004478	methionine adenosyltransferase activity	1	91	0.017228833
GO:0004576	oligosaccharyl transferase activity	1	91	0.017228833
GO:0006556	S-adenosylmethionine biosynthetic process	1	91	0.017228833
GO:0006725	cellular aromatic compound metabolic process	1	91	0.017228833
GO:0006885	regulation of pH	1	91	0.017228833
GO:0009098	leucine biosynthetic process	1	91	0.017228833
GO:0019642	anaerobic glycolysis	1	91	0.017228833
GO:0031897	Tic complex	1	91	0.017228833
GO:0042742	defense response to bacterium	3	91	0.018076859
GO:0003997	acyl-CoA oxidase activity	1	91	0.021443085

Cluster 24 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004742	dihydrolipoyllysine-residue acetyltransferase activity	1	91	0.021443085
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	1	91	0.021443085
GO:0016462	pyrophosphatase activity	1	91	0.021443085
GO:0004470	malic enzyme activity	1	91	0.02562063
GO:0005253	anion channel activity	1	91	0.02562063
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	1	91	0.02562063
GO:0006821	chloride transport	1	91	0.02562063
GO:0009527	plastid outer membrane	1	91	0.02562063
GO:0010073	meristem maintenance	1	91	0.02562063
GO:0010188	response to microbial phytotoxin	1	91	0.02562063
GO:0016652	oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	1	91	0.02562063
GO:0019650	glucose catabolic process to butanediol	1	91	0.02562063
GO:0045037	protein import into chloroplast stroma	1	91	0.02562063
GO:0046686	response to cadmium ion	4	91	0.026070846
GO:0005509	calcium ion binding	3	91	0.027649105
GO:0004069	L-aspartate:2-oxoglutarate aminotransferase activity	1	91	0.029761704
GO:0004427	inorganic diphosphatase activity	1	91	0.029761704
GO:0004467	long-chain-fatty-acid-CoA ligase activity	1	91	0.029761704
GO:0005247	voltage-gated chloride channel activity	1	91	0.029761704
GO:0007005	mitochondrion organization	1	91	0.029761704
GO:0008553	hydrogen-exporting ATPase activity, phosphorylative mechanism	1	91	0.029761704
GO:0010380	regulation of chlorophyll biosynthetic process	1	91	0.029761704
GO:0006812	cation transport	2	91	0.03070788
GO:0048364	root development	2	91	0.032333272
GO:0015386	potassium:hydrogen antiporter activity	1	91	0.033866541
GO:0004124	cysteine synthase activity	1	91	0.037935376
GO:0006094	gluconeogenesis	1	91	0.037935376
GO:0006875	cellular metal ion homeostasis	1	91	0.037935376
GO:0008121	ubiquinol-cytochrome-c reductase activity	1	91	0.037935376
GO:0009932	cell tip growth	1	91	0.037935376
GO:0015035	protein disulfide oxidoreductase activity	1	91	0.037935376
GO:0009409	response to cold	3	91	0.039917828
GO:0006108	malate metabolic process	1	91	0.041968438
GO:0009231	riboflavin biosynthetic process	1	91	0.041968438
GO:0010053	root epidermal cell differentiation	1	91	0.041968438
GO:0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	1	91	0.041968438
GO:0019253	reductive pentose-phosphate cycle	1	91	0.041968438
GO:0019853	L-ascorbic acid biosynthetic process	1	91	0.041968438
GO:0051287	NAD or NADH binding	1	91	0.041968438
GO:0016209	antioxidant activity	1	91	0.04596596
GO:0010167	response to nitrate	1	91	0.049928169
GO:0016671	oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor	1	91	0.049928169
GO:0019654	acetate fermentation	1	91	0.049928169
GO:0006800	oxygen and reactive oxygen species metabolic process	1	91	0.053855294
GO:0016207	4-coumarate-CoA ligase activity	1	91	0.053855294
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	91	0.057747562
GO:0005750	mitochondrial respiratory chain complex III	1	91	0.057747562
GO:0009117	nucleotide metabolic process	1	91	0.057747562
GO:0015986	ATP synthesis coupled proton transport	1	91	0.057747562

Cluster 24 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016779	nucleotidyltransferase activity	1	91	0.061605197
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	1	91	0.061605197
GO:0009504	cell plate	1	91	0.065428425
GO:0009532	plastid stroma	1	91	0.065428425
GO:0005507	copper ion binding	2	91	0.067094575
GO:0006520	amino acid metabolic process	1	91	0.069217466
GO:0020037	heme binding	1	91	0.069217466
GO:0006807	nitrogen compound metabolic process	1	91	0.072972544
GO:0008483	transaminase activity	1	91	0.072972544
GO:0010193	response to ozone	1	91	0.076693878
GO:0031966	mitochondrial membrane	1	91	0.076693878
GO:0005744	mitochondrial inner membrane presequence translocase complex	1	91	0.080381687
GO:0005839	proteasome core complex	1	91	0.080381687
GO:0004872	receptor activity	1	91	0.084036189
GO:0015079	potassium ion transmembrane transporter activity	1	91	0.084036189
GO:0016126	sterol biosynthetic process	1	91	0.087657601
GO:0030163	protein catabolic process	1	91	0.087657601
GO:0009867	jasmonic acid mediated signaling pathway	1	91	0.091246138
GO:0010150	leaf senescence	1	91	0.091246138
GO:0009832	plant-type cell wall biogenesis	1	91	0.094802013
GO:0009846	pollen germination	1	91	0.09832544
GO:0030036	actin cytoskeleton organization	1	91	0.09832544
GO:0009620	response to fungus	1	91	0.108703142
GO:0005759	mitochondrial matrix	1	91	0.11209888
GO:0009853	photorespiration	1	91	0.11209888
GO:0009809	lignin biosynthetic process	1	91	0.115463216
GO:0006486	protein amino acid glycosylation	1	91	0.118796356
GO:0009706	chloroplast inner membrane	1	91	0.118796356
GO:0010319	stromule	1	91	0.118796356
GO:0042542	response to hydrogen peroxide	1	91	0.122098504
GO:0003924	GTPase activity	1	91	0.128610637
GO:0009579	thylakoid	2	91	0.131482239
GO:0005829	cytosol	2	91	0.133447563
GO:0003993	acid phosphatase activity	1	91	0.135001227
GO:0009658	chloroplast organization	1	91	0.135001227
GO:0005525	GTP binding	2	91	0.136381243
GO:0009845	seed germination	1	91	0.138151443
GO:0016298	lipase activity	1	91	0.14127187
GO:0019825	oxygen binding	2	91	0.152632481
GO:0005524	ATP binding	4	91	0.153029954
GO:0006813	potassium ion transport	1	91	0.153459601
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	1	91	0.153459601
GO:0006096	glycolysis	1	91	0.156434008
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	1	91	0.156434008
GO:0007568	aging	1	91	0.162297132
GO:0008233	peptidase activity	1	91	0.165186227

Cluster 24 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045454	cell redox homeostasis	1	91	0.165186227
GO:0016491	oxidoreductase activity	2	91	0.182731953
GO:0050832	defense response to fungus	1	91	0.184634574
GO:0048046	apoplast	2	91	0.194794276
GO:0006970	response to osmotic stress	1	91	0.195154806
GO:0009535	chloroplast thylakoid membrane	2	91	0.200143219
GO:0008415	acyltransferase activity	1	91	0.200257819
GO:0009793	embryonic development ending in seed dormancy	2	91	0.221577971
GO:0009908	flower development	1	91	0.230980914
GO:0009055	electron carrier activity	1	91	0.235345375
GO:0005743	mitochondrial inner membrane	1	91	0.237492692
GO:0015031	protein transport	1	91	0.253854059
GO:0006950	response to stress	1	91	0.257723069
GO:0009408	response to heat	1	91	0.274085012
GO:0004091	carboxylesterase activity	1	91	0.28567315
GO:0009416	response to light stimulus	1	91	0.294853267
GO:0009611	response to wounding	1	91	0.294853267
GO:0006629	lipid metabolic process	1	91	0.339528849
GO:0016787	hydrolase activity	1	91	0.342007186
GO:0006511	ubiquitin-dependent protein catabolic process	1	91	0.36472322
GO:0009737	response to abscisic acid stimulus	1	91	0.368570465
GO:0000166	nucleotide binding	1	91	0.370301683

Cluster 24

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000166	1	AT2G01470	
GO:0000266	1	AT1G14830	
GO:0000906	1	AT2G44050	
GO:0001676	1	AT3G05970	
GO:0003857	1	AT3G06860	
GO:0003860	1	AT4G31810	
GO:0003862	1	AT1G80560	
GO:0003924	1	AT1G14830	
GO:0003993	1	AT5G44020	
GO:0003997	1	AT3G51840	
GO:0004028	1	AT1G79440	
GO:0004069	1	AT5G11520	
GO:0004091	1	AT1G54030	
GO:0004124	1	AT4G14880	
GO:0004300	2	AT3G06860	AT4G29010
GO:0004310	1	AT4G34640	
GO:0004321	1	AT4G05160	
GO:0004427	1	AT5G09650	
GO:0004449	2	AT2G17130	AT5G03290
GO:0004467	1	AT3G05970	
GO:0004470	1	AT4G00570	
GO:0004478	1	AT3G17390	
GO:0004576	1	AT2G01720	
GO:0004648	1	AT2G17630	
GO:0004656	1	AT3G06300	
GO:0004742	1	AT3G52200	
GO:0004777	1	AT1G79440	
GO:0004792	1	AT1G79230	
GO:0004872	1	AT5G55610	

Cluster 24 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0005247	1	AT5G40890					
GO:0005253	1	AT5G40890					
GO:0005507	2	AT2G42490	AT3G16460				
GO:0005509	3	AT2G38750	AT2G38760	AT5G07340			
GO:0005524	4	AT3G52200	AT4G00570	AT5G03290	AT5G50920		
GO:0005525	2	AT1G14830	AT3G13870				
GO:0005544	2	AT2G38750	AT2G38760				
GO:0005618	5	AT3G06860	AT3G17390	AT4G29010	AT5G42980	AT5G50920	
GO:0005730	4	AT2G19940	AT2G27730	AT3G06860	AT3G17390		
GO:0005739	24	AT1G53000	AT1G53760	AT1G55900	AT1G79230	AT1G79440	AT1G79940
		AT2G17130	AT2G27730	AT2G29080	AT2G42210	AT3G47930	AT3G52200
		AT4G00570	AT4G10750	AT4G26910	AT4G31810	AT4G32470	AT4G35850
		AT5G03290	AT5G05520	AT5G42150	AT5G42980	AT5G50920	AT5G55610
GO:0005743	1	AT1G55900					
GO:0005744	1	AT2G42210					
GO:0005750	1	AT4G32470					
GO:0005759	1	AT1G79440					
GO:0005773	8	AT1G54030	AT1G78920	AT2G27730	AT2G38760	AT4G38510	AT5G23820
		AT5G42980	AT5G44020				
GO:0005777	7	AT2G06050	AT3G06860	AT3G51840	AT4G05160	AT4G14880	AT4G29010
		AT5G11520					
GO:0005783	11	AT1G79940	AT2G01470	AT2G01720	AT3G13870	AT4G34640	AT5G03160
		AT5G07340	AT5G23630	AT5G47990	AT5G48000	AT5G48810	
GO:0005788	2	AT3G62600	AT5G03160				
GO:0005789	2	AT4G34640	AT5G48810				
GO:0005794	7	AT1G29790	AT1G78920	AT3G23300	AT4G00740	AT5G25100	AT5G61240
		AT5G64030					
GO:0005829	2	AT4G14880	AT5G42980				
GO:0005839	1	AT3G60820					
GO:0005886	22	AT1G14830	AT1G29790	AT1G53760	AT1G79940	AT2G01410	AT2G01470
		AT2G01720	AT3G13870	AT3G17390	AT3G23300	AT3G60820	AT3G62600
		AT4G14880	AT4G30190	AT4G32470	AT4G34640	AT4G38510	AT5G03160
		AT5G07340	AT5G23630	AT5G25100	AT5G42980		
GO:0005938	1	AT1G14830					
GO:0006086	1	AT3G52200					
GO:0006090	1	AT3G52200					
GO:0006094	1	AT4G10750					
GO:0006096	1	AT4G10750					
GO:0006108	1	AT4G00570					
GO:0006122	1	AT4G32470					
GO:0006457	4	AT1G79940	AT3G62600	AT5G03160	AT5G07340		
GO:0006486	1	AT2G01720					
GO:0006511	1	AT3G60820					
GO:0006520	1	AT2G19940					
GO:0006535	1	AT4G14880					
GO:0006540	1	AT1G79440					
GO:0006555	1	AT3G17390					
GO:0006556	1	AT3G17390					
GO:0006629	1	AT1G54030					
GO:0006635	4	AT3G06860	AT3G51840	AT4G29010	AT4G31810		
GO:0006725	1	AT4G10750					
GO:0006800	1	AT1G79440					
GO:0006807	1	AT5G11520					
GO:0006812	2	AT4G00630	AT4G30190				
GO:0006813	1	AT4G00630					
GO:0006821	1	AT5G40890					
GO:0006875	1	AT5G23630					
GO:0006885	1	AT4G00630					
GO:0006888	2	AT2G01470	AT3G13870				

Cluster 24 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0006950	1	AT1G79440					
GO:0006970	1	AT2G38750					
GO:0007005	1	AT1G14830					
GO:0007275	3	AT4G27760	AT4G29010	AT5G55610			
GO:0007568	1	AT1G79230					
GO:0008121	1	AT4G32470					
GO:0008152	8	AT1G80560	AT2G17130	AT3G52200	AT4G00630	AT4G26910	AT4G30190
		AT5G03290	AT5G09650				
GO:0008233	1	AT3G60820					
GO:0008415	1	AT4G26910					
GO:0008483	1	AT2G17630					
GO:0008553	1	AT4G30190					
GO:0009055	1	AT5G42150					
GO:0009098	1	AT1G80560					
GO:0009103	1	AT1G53000					
GO:0009117	1	AT4G29690					
GO:0009231	1	AT2G44050					
GO:0009408	1	AT1G79440					
GO:0009409	3	AT3G11630	AT3G16460	AT3G17390			
GO:0009416	1	AT1G79440					
GO:0009450	1	AT1G79440					
GO:0009504	1	AT1G14830					
GO:0009507	23	AT1G79230	AT1G79440	AT1G80560	AT2G17630	AT2G19940	AT2G42210
		AT2G44050	AT3G08630	AT3G11630	AT3G57280	AT3G60820	AT4G00570
		AT4G00630	AT4G10750	AT4G14880	AT4G29010	AT5G03290	AT5G07340
		AT5G09650	AT5G42980	AT5G44020	AT5G50920	AT5G55610	
GO:0009527	1	AT2G42210					
GO:0009532	1	AT5G50920					
GO:0009535	2	AT2G29080	AT5G50920				
GO:0009536	8	AT1G53000	AT1G53760	AT1G80560	AT3G47930	AT4G32470	AT5G05520
		AT5G11520	AT5G55610				
GO:0009570	7	AT1G80560	AT2G19940	AT2G44050	AT3G11630	AT5G09650	AT5G42980
		AT5G50920					
GO:0009579	2	AT3G11630	AT5G09650				
GO:0009611	1	AT2G06050					
GO:0009620	1	AT2G06050					
GO:0009658	1	AT5G50920					
GO:0009678	1	AT1G78920					
GO:0009695	2	AT2G06050	AT4G05160				
GO:0009706	1	AT3G57280					
GO:0009737	1	AT2G38750					
GO:0009793	2	AT1G55900	AT3G51840				
GO:0009809	1	AT3G17390					
GO:0009832	1	AT3G13870					
GO:0009845	1	AT4G29010					
GO:0009846	1	AT5G23630					
GO:0009853	1	AT2G27730					
GO:0009867	1	AT2G44050					
GO:0009908	1	AT4G29010					
GO:0009932	1	AT3G13870					
GO:0009941	7	AT1G80560	AT3G11630	AT3G57280	AT4G00630	AT4G38510	AT5G09650
		AT5G50920					
GO:0009986	2	AT2G38750	AT2G38760				
GO:0010053	1	AT3G13870					
GO:0010073	1	AT4G27760					
GO:0010150	1	AT5G11520					
GO:0010152	2	AT1G14830	AT5G23630				
GO:0010167	1	AT5G40890					
GO:0010188	1	AT5G42980					

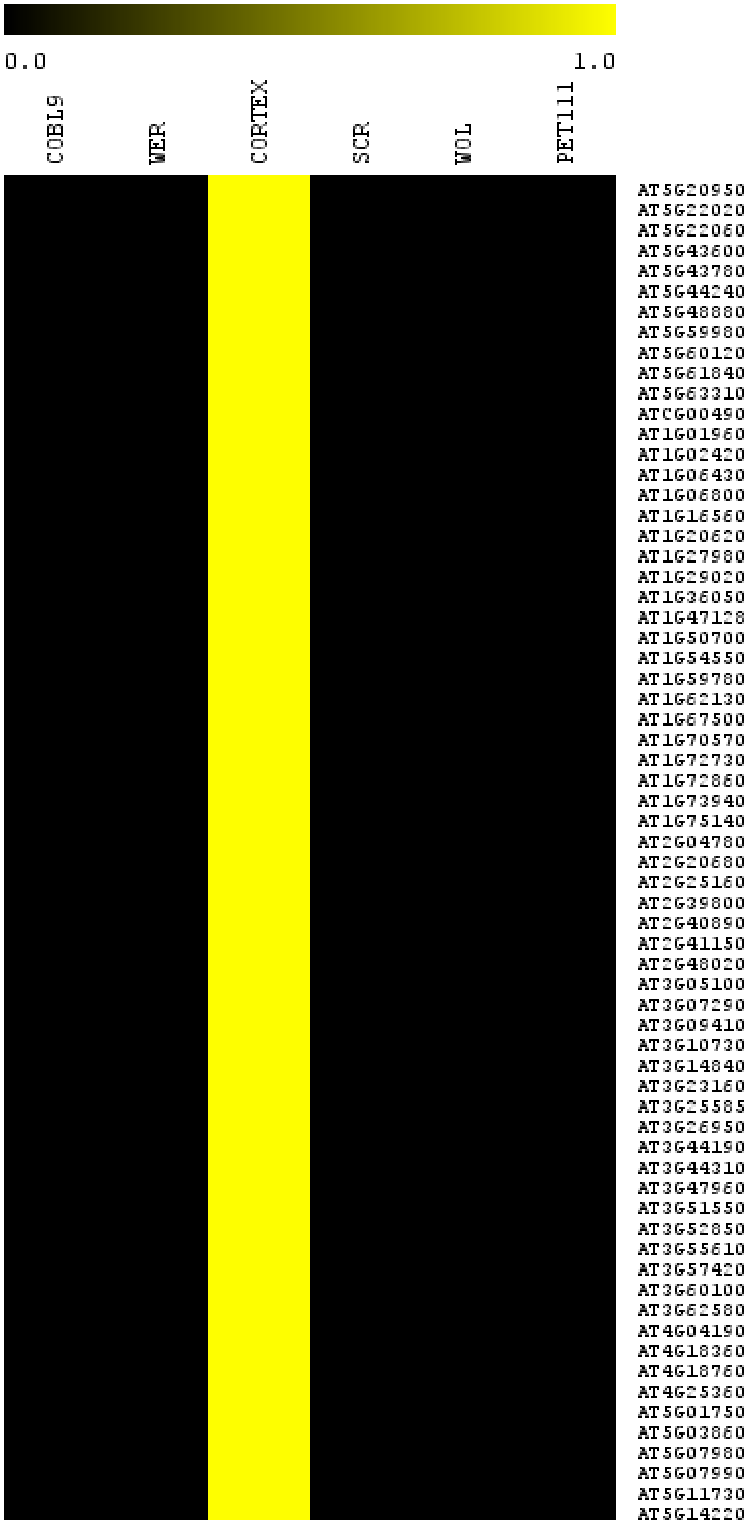
Cluster 24 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0010193	1	AT2G06050					
GO:0010319	1	AT3G11630					
GO:0010380	1	AT5G50920					
GO:0015031	1	AT2G42210					
GO:0015035	1	AT5G42150					
GO:0015079	1	AT4G00630					
GO:0015386	1	AT4G00630					
GO:0015450	1	AT2G42210					
GO:0015986	1	AT4G38510					
GO:0015988	1	AT4G38510					
GO:0015992	2	AT1G78920	AT4G30190				
GO:0016020	21	AT1G14830	AT1G53760	AT2G01470	AT2G19940	AT2G42210	AT3G05970
		AT3G16460	AT3G17390	AT3G20370	AT4G00630	AT4G14880	AT4G26910
		AT4G30190	AT4G32470	AT4G38510	AT5G07340	AT5G09650	AT5G11520
		AT5G42980	AT5G44020	AT5G55610			
GO:0016126	1	AT4G34640					
GO:0016207	1	AT4G05160					
GO:0016209	1	AT3G11630					
GO:0016298	1	AT1G54030					
GO:0016462	1	AT5G09650					
GO:0016491	2	AT3G51840	AT4G27760				
GO:0016620	1	AT2G19940					
GO:0016629	1	AT2G06050					
GO:0016633	1	AT3G47930					
GO:0016652	1	AT4G00570					
GO:0016671	1	AT5G42980					
GO:0016706	1	AT3G06300					
GO:0016779	1	AT1G53000					
GO:0016783	1	AT1G79230					
GO:0016784	1	AT1G79230					
GO:0016787	1	AT4G29690					
GO:0016830	1	AT4G10750					
GO:0016887	3	AT2G29080	AT4G30190	AT5G50920			
GO:0018401	1	AT3G06300					
GO:0019253	1	AT4G10750					
GO:0019642	1	AT4G10750					
GO:0019648	1	AT4G10750					
GO:0019650	1	AT4G10750					
GO:0019654	1	AT4G10750					
GO:0019825	2	AT5G47990	AT5G48000				
GO:0019829	1	AT5G23630					
GO:0019853	1	AT3G47930					
GO:0020037	1	AT5G48810					
GO:0030036	1	AT3G13870					
GO:0030163	1	AT2G29080					
GO:0030176	2	AT1G79940	AT2G01470				
GO:0031072	3	AT1G79940	AT3G62600	AT5G03160			
GO:0031897	1	AT5G50920					
GO:0031966	1	AT2G27730					
GO:0042542	1	AT5G42980					
GO:0042742	3	AT3G11630	AT5G09650	AT5G48810			
GO:0045037	1	AT5G50920					
GO:0045271	2	AT2G27730	AT2G42210				
GO:0045454	1	AT5G42150					
GO:0046459	1	AT3G51840					
GO:0046686	4	AT2G17630	AT2G19940	AT4G14880	AT5G09650		
GO:0046933	1	AT4G38510					
GO:0048046	2	AT3G11630	AT4G14880				
GO:0048364	2	AT5G47990	AT5G48000				

Cluster 24 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)		
GO:0050832	1	AT5G42980		
GO:0051082	3	AT1G79940	AT3G62600	AT5G07340
GO:0051287	1	AT1G79440		
GO:0051920	1	AT3G11630		

Cluster 25



Cluster 25

AT1G01960
AT1G02420
AT1G06430
AT1G06800
AT1G16560
AT1G20620
AT1G27980
AT1G29020
AT1G36050
AT1G47128
AT1G50700
AT1G54550
AT1G59780
AT1G62130
AT1G67500
AT1G70570
AT1G72730
AT1G72860
AT1G73940
AT1G75140
AT2G04780
AT2G20680
AT2G25160
AT2G39800
AT2G40890
AT2G41150
AT2G48020
AT3G05100
AT3G07290
AT3G09410
AT3G10730
AT3G14840
AT3G23160
AT3G25585
AT3G26950
AT3G44190
AT3G44310
AT3G47960
AT3G51550
AT3G52850
AT3G55610
AT3G57420
AT3G60100
AT3G62580
AT4G04190
AT4G18360
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AT4G25360
AT5G01750
AT5G03860
AT5G07980
AT5G07990
AT5G11730
AT5G14220
AT5G20950
AT5G22020
AT5G22060
AT5G43600
AT5G43780
AT5G44240
AT5G48880
AT5G59980
AT5G60120
AT5G61840
AT5G63310
ATCG00490

Cluster 25 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009411	response to UV	3	65	2.26E-05
GO:0016020	membrane	11	65	0.001832108
GO:0009813	flavonoid biosynthetic process	2	65	0.002890829
GO:0004474	malate synthase activity	1	65	0.003116759
GO:0009940	amino-terminal vacuolar sorting propeptide binding	1	65	0.003116759
GO:0010483	pollen tube reception	1	65	0.003116759
GO:0016035	zeta DNA polymerase complex	1	65	0.003116759
GO:0016711	flavonoid 3'-monooxygenase activity	1	65	0.003116759
GO:0030149	sphingolipid catabolic process	1	65	0.003116759
GO:0043680	filiform apparatus	1	65	0.003116759
GO:0046409	p-coumarate 3-hydroxylase activity	1	65	0.003116759
GO:0005777	peroxisome	3	65	0.004643314
GO:0004048	anthranilate phosphoribosyltransferase activity	1	65	0.006214387
GO:0004729	protoporphyrinogen oxidase activity	1	65	0.006214387
GO:0006097	glyoxylate cycle	1	65	0.006214387
GO:0007034	vacuolar transport	1	65	0.006214387
GO:0008891	glycolate oxidase activity	1	65	0.006214387
GO:0005783	endoplasmic reticulum	4	65	0.007994995
GO:0005886	plasma membrane	11	65	0.008471668
GO:0000213	tRNA-intron endonuclease activity	1	65	0.009292971
GO:0003988	acetyl-CoA C-acyltransferase activity	1	65	0.009292971
GO:0004096	catalase activity	1	65	0.009292971
GO:0009805	coumarin biosynthetic process	1	65	0.009292971
GO:0019395	fatty acid oxidation	1	65	0.009292971
GO:0030572	phosphatidyltransferase activity	1	65	0.009292971
GO:0004781	sulfate adenylyltransferase (ATP) activity	1	65	0.012352598
GO:0016831	carboxy-lyase activity	1	65	0.012352598
GO:0004108	citrate (SI)-synthase activity	1	65	0.015393354
GO:0004550	nucleoside diphosphate kinase activity	1	65	0.015393354

Cluster 25 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006896	Golgi to vacuole transport	1	65	0.015393354
GO:0017119	Golgi transport complex	1	65	0.015393354
GO:0042744	hydrogen peroxide catabolic process	1	65	0.015393354
GO:0010304	PSII associated light-harvesting complex II catabolic process	1	65	0.018415324
GO:0005085	guanyl-nucleotide exchange factor activity	1	65	0.021418594
GO:0006995	cellular response to nitrogen starvation	1	65	0.021418594
GO:0009970	cellular response to sulfate starvation	1	65	0.021418594
GO:0009941	chloroplast envelope	4	65	0.022377523
GO:0010417	glucuronoxylan biosynthetic process	1	65	0.024403249
GO:0006099	tricarboxylic acid cycle	1	65	0.03031705
GO:0009699	phenylpropanoid biosynthetic process	1	65	0.033246365
GO:0015914	phospholipid transport	1	65	0.033246365
GO:0000103	sulfate assimilation	1	65	0.036157401
GO:0005802	trans-Golgi network	1	65	0.036157401
GO:0009585	red, far-red light phototransduction	1	65	0.039050241
GO:0006779	porphyrin biosynthetic process	1	65	0.04192497
GO:0016887	ATPase activity	2	65	0.043861081
GO:0009561	megagametogenesis	1	65	0.044781668
GO:0009834	secondary cell wall biogenesis	1	65	0.044781668
GO:0005635	nuclear envelope	1	65	0.050441304
GO:0005887	integral to plasma membrane	1	65	0.050441304
GO:0006520	amino acid metabolic process	1	65	0.050441304
GO:0006623	protein targeting to vacuole	1	65	0.050441304
GO:0009507	chloroplast	11	65	0.051240009
GO:0005794	Golgi apparatus	2	65	0.053040507
GO:0008033	tRNA processing	1	65	0.053244406
GO:0015662	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	1	65	0.053244406
GO:0005618	cell wall	3	65	0.053944826
GO:0000162	tryptophan biosynthetic process	1	65	0.056029805
GO:0003887	DNA-directed DNA polymerase activity	1	65	0.056029805
GO:0046777	protein amino acid autophosphorylation	1	65	0.056029805
GO:0005739	mitochondrion	5	65	0.059012425
GO:0005819	spindle	1	65	0.064280596
GO:0008654	phospholipid biosynthetic process	1	65	0.066995992
GO:0009734	auxin mediated signaling pathway	1	65	0.066995992
GO:0005792	microsome	1	65	0.069694087
GO:0016036	cellular response to phosphate starvation	1	65	0.072374962
GO:0004672	protein kinase activity	2	65	0.07386884
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	2	65	0.074582129
GO:0009579	thylakoid	2	65	0.082479924
GO:0005524	ATP binding	4	65	0.085325306
GO:0009809	lignin biosynthetic process	1	65	0.085523772
GO:0004683	calmodulin-dependent protein kinase activity	1	65	0.088102969
GO:0010224	response to UV-B	1	65	0.090665492
GO:0042542	response to hydrogen peroxide	1	65	0.090665492
GO:0004806	triacylglycerol lipase activity	1	65	0.095740824
GO:0019825	oxygen binding	2	65	0.098443729
GO:0009524	phragmoplast	1	65	0.103230677
GO:0008643	carbohydrate transport	1	65	0.10569476
GO:0004497	monooxygenase activity	1	65	0.108142701
GO:0005773	vacuole	3	65	0.110630464

Cluster 25 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006633	fatty acid biosynthetic process	1	65	0.12715402
GO:0009505	plant-type cell wall	2	65	0.131555494
GO:0048046	apoplast	2	65	0.133667068
GO:0005515	protein binding	5	65	0.149000392
GO:0006857	oligopeptide transport	1	65	0.153824663
GO:0046658	anchored to plasma membrane	1	65	0.15595044
GO:0005975	carbohydrate metabolic process	2	65	0.171749221
GO:0008026	ATP-dependent helicase activity	1	65	0.172438039
GO:0009055	electron carrier activity	1	65	0.18421279
GO:0006810	transport	2	65	0.184558109
GO:0006281	DNA repair	1	65	0.188027961
GO:0015144	carbohydrate transmembrane transporter activity	1	65	0.188027961
GO:0006952	defense response	2	65	0.188657615
GO:0005351	sugar:hydrogen symporter activity	1	65	0.191789122
GO:0009570	chloroplast stroma	2	65	0.204151046
GO:0004091	carboxylesterase activity	1	65	0.231322669
GO:0031224	intrinsic to membrane	1	65	0.235996738
GO:0004888	transmembrane receptor activity	1	65	0.239053678
GO:0009416	response to light stimulus	1	65	0.240564587
GO:0008152	metabolic process	2	65	0.270162548
GO:0009536	plastid	1	65	0.272217184
GO:0009414	response to water deprivation	1	65	0.279544474
GO:0006629	lipid metabolic process	1	65	0.290955133
GO:0005509	calcium ion binding	1	65	0.305328862
GO:0022626	cytosolic ribosome	1	65	0.31185084
GO:0009409	response to cold	1	65	0.328940122
GO:0006457	protein folding	1	65	0.339648499
GO:0031225	anchored to membrane	1	65	0.34025567
GO:0005215	transporter activity	1	65	0.35048923
GO:0016491	oxidoreductase activity	1	65	0.351428008
GO:0009535	chloroplast thylakoid membrane	1	65	0.360144099
GO:0016021	integral to membrane	1	65	0.36111492
GO:0046686	response to cadmium ion	1	65	0.367716977
GO:0009793	embryonic development ending in seed dormancy	1	65	0.367891887

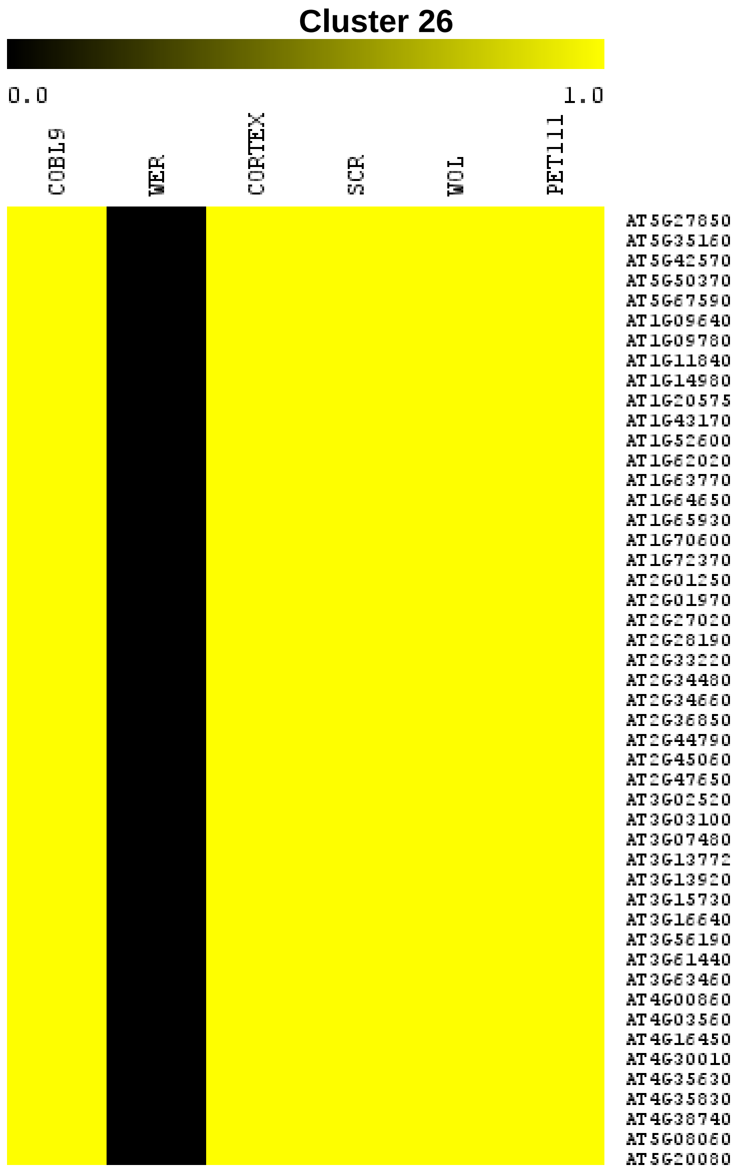
Cluster 25 **GO Identifier**	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000103	1	AT5G43780	
GO:0000162	1	AT1G70570	
GO:0000213	1	AT5G59980	
GO:0003887	1	AT1G67500	
GO:0003988	1	AT5G48880	
GO:0004048	1	AT1G70570	
GO:0004091	1	AT3G09410	
GO:0004096	1	AT1G20620	
GO:0004108	1	AT3G60100	
GO:0004474	1	AT5G03860	
GO:0004497	1	AT2G40890	
GO:0004550	1	AT5G63310	
GO:0004553	2	AT2G20680	AT5G20950
GO:0004672	2	AT3G14840	AT3G51550
GO:0004683	1	AT1G50700	
GO:0004729	1	AT5G14220	
GO:0004781	1	AT5G43780	

Cluster 25 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004806	1	AT1G06800					
GO:0004888	1	AT1G72860					
GO:0005085	1	AT1G01960					
GO:0005215	1	AT3G47960					
GO:0005351	1	AT2G48020					
GO:0005509	1	AT1G29020					
GO:0005515	5	AT1G59780	AT1G72860	AT3G14840	AT5G22060	AT5G63310	
GO:0005524	4	AT1G59780	AT1G72860	AT3G14840	AT5G63310		
GO:0005618	3	AT1G20620	AT3G57420	AT5G20950			
GO:0005635	1	AT3G10730					
GO:0005739	5	AT1G20620	AT2G40890	AT3G60100	AT5G14220	AT5G43780	
GO:0005773	3	AT1G20620	AT1G47128	AT2G48020			
GO:0005777	3	AT1G20620	AT4G18360	AT5G48880			
GO:0005783	4	AT1G27980	AT1G75140	AT2G40890	AT3G10730		
GO:0005792	1	AT2G40890					
GO:0005794	2	AT3G52850	AT5G61840				
GO:0005802	1	AT3G52850					
GO:0005819	1	AT3G10730					
GO:0005886	11	AT1G20620	AT1G36050	AT1G72730	AT2G04780	AT2G40890	AT2G48020
		AT3G14840	AT3G47960	AT3G51550	AT3G52850	AT5G22060	
GO:0005887	1	AT3G52850					
GO:0005975	2	AT2G20680	AT5G20950				
GO:0006097	1	AT5G03860					
GO:0006099	1	AT3G60100					
GO:0006281	1	AT1G67500					
GO:0006457	1	AT5G22060					
GO:0006520	1	AT1G27980					
GO:0006623	1	AT3G52850					
GO:0006629	1	AT1G06800					
GO:0006633	1	AT1G36050					
GO:0006779	1	AT5G14220					
GO:0006810	2	AT2G48020	AT5G44240				
GO:0006857	1	AT3G47960					
GO:0006896	1	AT3G52850					
GO:0006952	2	AT1G59780	AT1G72860				
GO:0006995	1	AT1G20620					
GO:0007034	1	AT3G52850					
GO:0008026	1	AT1G72730					
GO:0008033	1	AT5G59980					
GO:0008152	2	AT4G18360	AT5G44240				
GO:0008643	1	AT2G48020					
GO:0008654	1	AT3G25585					
GO:0008891	1	AT4G18360					
GO:0009055	1	AT3G44190					
GO:0009409	1	AT1G20620					
GO:0009411	3	AT1G67500	AT5G07990	AT5G63310			
GO:0009414	1	AT1G47128					
GO:0009416	1	AT1G20620					
GO:0009505	2	AT1G72730	AT5G20950				
GO:0009507	11	AT1G06430	AT1G06800	AT1G20620	AT1G47128	AT1G62130	AT1G70570
		AT2G48020	AT5G01750	AT5G14220	AT5G43780	AT5G63310	
GO:0009524	1	AT3G10730					
GO:0009535	1	AT1G06430					
GO:0009536	1	AT5G14220					
GO:0009561	1	AT1G01960					
GO:0009570	2	AT1G20620	AT5G63310				
GO:0009579	2	AT1G06430	AT5G63310				
GO:0009585	1	AT5G63310					
GO:0009699	1	AT2G40890					

Cluster 25 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0009734	1	AT5G63310					
GO:0009793	1	AT5G14220					
GO:0009805	1	AT2G40890					
GO:0009809	1	AT2G40890					
GO:0009813	2	AT2G40890	AT5G07990				
GO:0009834	1	AT5G61840					
GO:0009940	1	AT3G52850					
GO:0009941	4	AT1G06430	AT1G20620	AT5G14220	AT5G63310		
GO:0009970	1	AT1G20620					
GO:0010224	1	AT1G67500					
GO:0010304	1	AT1G06430					
GO:0010417	1	AT5G61840					
GO:0010483	1	AT3G51550					
GO:0015144	1	AT2G48020					
GO:0015662	1	AT5G44240					
GO:0015914	1	AT5G44240					
GO:0016020	11	AT1G06430	AT1G20620	AT1G27980	AT2G04780	AT2G48020	AT3G25585
		AT3G47960	AT3G51550	AT5G20950	AT5G44240	AT5G61840	
GO:0016021	1	AT5G44240					
GO:0016035	1	AT1G67500					
GO:0016036	1	AT1G20620					
GO:0016491	1	AT5G14220					
GO:0016711	1	AT5G07990					
GO:0016831	1	AT1G27980					
GO:0016887	2	AT1G06430	AT1G62130				
GO:0017119	1	AT3G52850					
GO:0019395	1	AT5G48880					
GO:0019825	2	AT2G25160	AT5G07990				
GO:0022626	1	AT1G20620					
GO:0030149	1	AT1G27980					
GO:0030572	1	AT3G25585					
GO:0031224	1	AT1G72860					
GO:0031225	1	AT2G04780					
GO:0042542	1	AT5G63310					
GO:0042744	1	AT1G20620					
GO:0043680	1	AT3G51550					
GO:0046409	1	AT2G40890					
GO:0046658	1	AT2G04780					
GO:0046686	1	AT1G20620					
GO:0046777	1	AT3G51550					
GO:0048046	2	AT1G20620	AT1G47128				



Cluster 26

AT1G09640
AT1G09780
AT1G11840
AT1G14980
AT1G20575
AT1G43170
AT1G52600
AT1G62020
AT1G63770
AT1G64650
AT1G65930
AT1G70600
AT1G72370
AT2G01250
AT2G01970
AT2G27020
AT2G28190
AT2G33220
AT2G34480
AT2G34660
AT2G36850
AT2G44790
AT2G45060
AT2G47650
AT3G02520
AT3G03100
AT3G07480
AT3G13772
AT3G13920
AT3G15730
AT3G16640
AT3G56190
AT3G61440
AT3G63460
AT4G00860
AT4G03560
AT4G16450
AT4G30010
AT4G35630
AT4G35830
AT4G38740
AT5G08060
AT5G20080
AT5G27850
AT5G35160
AT5G42570
AT5G50370
AT5G67590

Cluster 26 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005886	plasma membrane	24	48	1.83E-14
GO:0005739	mitochondrion	15	48	8.98E-11
GO:0046686	response to cadmium ion	9	48	1.18E-08
GO:0005773	vacuole	9	48	6.00E-07
GO:0048046	apoplast	7	48	1.17E-06
GO:0045271	respiratory chain complex I	4	48	1.52E-06
GO:0022626	cytosolic ribosome	5	48	3.80E-05
GO:0022625	cytosolic large ribosomal subunit	4	48	7.90E-05
GO:0016020	membrane	11	48	1.41E-04
GO:0009536	plastid	4	48	2.15E-04
GO:0003735	structural constituent of ribosome	5	48	4.34E-04
GO:0006412	translation	5	48	5.21E-04
GO:0031966	mitochondrial membrane	2	48	8.54E-04
GO:0010119	regulation of stomatal movement	2	48	0.001252881
GO:0000325	plant-type vacuole	2	48	0.001851315
GO:0009853	photorespiration	2	48	0.001984058
GO:0004582	dolichyl-phosphate beta-D-mannosyltransferase activity	1	48	0.002301606
GO:0004686	elongation factor-2 kinase activity	1	48	0.002301606
GO:0005245	voltage-gated calcium channel activity	1	48	0.002301606
GO:0030136	clathrin-coated vesicle	1	48	0.002301606
GO:0042256	mature ribosome assembly	1	48	0.002301606
GO:0050017	L-3-cyanoalanine synthase activity	1	48	0.002301606
GO:0015934	large ribosomal subunit	2	48	0.002711372
GO:0005794	Golgi apparatus	3	48	0.002979409
GO:0009845	seed germination	2	48	0.00319756
GO:0005774	vacuolar membrane	2	48	0.003720119
GO:0009651	response to salt stress	4	48	0.003834041
GO:0001558	regulation of cell growth	1	48	0.004592838
GO:0004128	cytochrome-b5 reductase activity	1	48	0.004592838
GO:0004648	O-phospho-L-serine:2-oxoglutarate aminotransferase activity	1	48	0.004592838
GO:0019499	cyanide metabolic process	1	48	0.004592838
GO:0046537	2,3-bisphosphoglycerate-independent phosphoglycerate mutase activity	1	48	0.004592838
GO:0051410	detoxification of nitrogen compound	1	48	0.004592838
GO:0008233	peptidase activity	2	48	0.004871211
GO:0003994	aconitate hydratase activity	1	48	0.00687373
GO:0004450	isocitrate dehydrogenase (NADP+) activity	1	48	0.00687373
GO:0005262	calcium channel activity	1	48	0.00687373
GO:0006970	response to osmotic stress	2	48	0.007330857
GO:0009570	chloroplast stroma	4	48	0.00753689
GO:0004017	adenylate kinase activity	1	48	0.009144315
GO:0006564	L-serine biosynthetic process	1	48	0.009144315
GO:0009507	chloroplast	11	48	0.009730916
GO:0048589	developmental growth	1	48	0.011404629
GO:0048768	root hair cell tip growth	1	48	0.011404629
GO:0030126	COPI vesicle coat	1	48	0.013654705
GO:0004462	lactoylglutathione lyase activity	1	48	0.015894577
GO:0008137	NADH dehydrogenase (ubiquinone) activity	1	48	0.015894577
GO:0016021	integral to membrane	3	48	0.01738258
GO:0019430	removal of superoxide radicals	1	48	0.018124279
GO:0046688	response to copper ion	1	48	0.018124279

Cluster 26 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0051087	chaperone binding	1	48	0.018124279
GO:0005783	endoplasmic reticulum	3	48	0.019852204
GO:0000302	response to reactive oxygen species	1	48	0.020343844
GO:0004124	cysteine synthase activity	1	48	0.020343844
GO:0004784	superoxide dismutase activity	1	48	0.020343844
GO:0010039	response to iron ion	1	48	0.020343844
GO:0019344	cysteine biosynthetic process	1	48	0.022553307
GO:0005507	copper ion binding	2	48	0.022930492
GO:0009061	anaerobic respiration	1	48	0.024752701
GO:0010252	auxin homeostasis	1	48	0.024752701
GO:0015935	small ribosomal subunit	1	48	0.024752701
GO:0000148	1,3-beta-glucan synthase complex	1	48	0.026942059
GO:0003843	1,3-beta-glucan synthase activity	1	48	0.026942059
GO:0004630	phospholipase D activity	1	48	0.026942059
GO:0006075	1,3-beta-glucan biosynthetic process	1	48	0.026942059
GO:0009789	positive regulation of abscisic acid mediated signaling	1	48	0.026942059
GO:0045309	protein phosphorylated amino acid binding	1	48	0.026942059
GO:0005618	cell wall	3	48	0.027345074
GO:0006631	fatty acid metabolic process	1	48	0.029121414
GO:0005740	mitochondrial envelope	1	48	0.031290801
GO:0006816	calcium ion transport	1	48	0.031290801
GO:0009117	nucleotide metabolic process	1	48	0.031290801
GO:0006915	apoptosis	1	48	0.033450252
GO:0005635	nuclear envelope	1	48	0.037739478
GO:0051536	iron-sulfur cluster binding	1	48	0.037739478
GO:0006888	ER to Golgi vesicle-mediated transport	1	48	0.039869319
GO:0009556	microsporogenesis	1	48	0.039869319
GO:0009631	cold acclimation	1	48	0.039869319
GO:0009695	jasmonic acid biosynthetic process	1	48	0.039869319
GO:0010193	response to ozone	1	48	0.041989355
GO:0005839	proteasome core complex	1	48	0.04409962
GO:0048527	lateral root development	1	48	0.048290966
GO:0009579	thylakoid	2	48	0.05134179
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1	48	0.05450551
GO:0005737	cytoplasm	3	48	0.057591262
GO:0005840	ribosome	2	48	0.058326215
GO:0009409	response to cold	2	48	0.060356485
GO:0006486	protein amino acid glycosylation	1	48	0.066676868
GO:0006457	protein folding	2	48	0.068605919
GO:0009860	pollen tube growth	1	48	0.086214851
GO:0005730	nucleolus	2	48	0.086617653
GO:0009505	plant-type cell wall	2	48	0.086617653
GO:0009555	pollen development	1	48	0.108464977
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	48	0.110261796
GO:0009617	response to bacterium	1	48	0.110261796
GO:0006413	translational initiation	1	48	0.11204993
GO:0046658	anchored to plasma membrane	1	48	0.120861348
GO:0008026	ATP-dependent helicase activity	1	48	0.134518584
GO:0048364	root development	1	48	0.134518584
GO:0003743	translation initiation factor activity	1	48	0.137849514
GO:0006508	proteolysis	2	48	0.13931069

Cluster 26 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009055	electron carrier activity	1	48	0.144412904
GO:0022627	cytosolic small ribosomal subunit	1	48	0.154015159
GO:0009941	chloroplast envelope	2	48	0.155973702
GO:0006950	response to stress	1	48	0.161798232
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	48	0.16485659
GO:0042254	ribosome biogenesis	1	48	0.173846323
GO:0009408	response to heat	1	48	0.175317862
GO:0009416	response to light stimulus	1	48	0.193768212
GO:0005777	peroxisome	1	48	0.19919654
GO:0005634	nucleus	4	48	0.204117981
GO:0006886	intracellular protein transport	1	48	0.205821531
GO:0042742	defense response to bacterium	1	48	0.228241272
GO:0005829	cytosol	1	48	0.268725412
GO:0006511	ubiquitin-dependent protein catabolic process	1	48	0.284932731
GO:0006979	response to oxidative stress	1	48	0.286623748
GO:0031225	anchored to membrane	1	48	0.297101232
GO:0005215	transporter activity	1	48	0.310876666
GO:0016491	oxidoreductase activity	1	48	0.312224865
GO:0007165	signal transduction	1	48	0.314864854
GO:0009793	embryonic development ending in seed dormancy	1	48	0.341503363
GO:0016757	transferase activity, transferring glycosyl groups	1	48	0.34886951
GO:0005975	carbohydrate metabolic process	1	48	0.349243879
GO:0006810	transport	1	48	0.356301346

Cluster 26

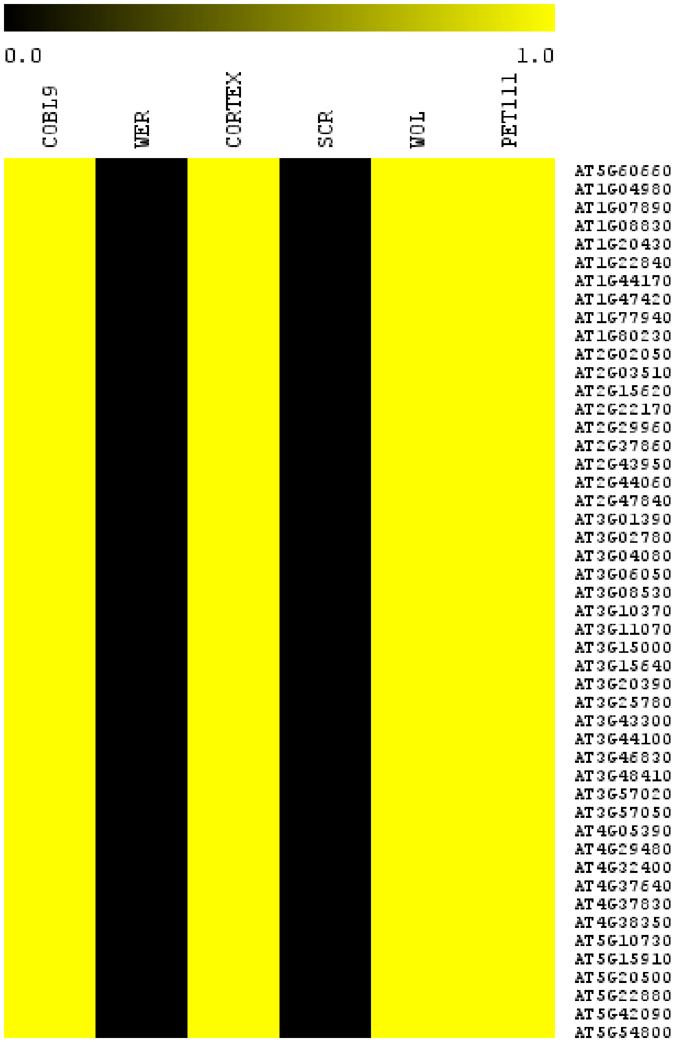
GO Identifier	**#Loci**	**Associated Loci (Left to Right)**				
GO:0000148	1	AT2G36850				
GO:0000302	1	AT4G00860				
GO:0000325	2	AT2G34660	AT4G03560			
GO:0001558	1	AT3G16640				
GO:0003735	5	AT1G43170	AT1G72370	AT2G01250	AT2G34480	AT5G27850
GO:0003743	1	AT3G13920				
GO:0003755	1	AT4G38740				
GO:0003843	1	AT2G36850				
GO:0003994	1	AT4G35830				
GO:0004017	1	AT5G50370				
GO:0004124	1	AT3G61440				
GO:0004128	1	AT5G20080				
GO:0004450	1	AT1G65930				
GO:0004462	1	AT1G11840				
GO:0004582	1	AT1G20575				
GO:0004630	1	AT3G15730				
GO:0004648	1	AT4G35630				
GO:0004686	1	AT1G20575				
GO:0004784	1	AT2G28190				
GO:0005215	1	AT1G62020				
GO:0005245	1	AT4G03560				
GO:0005262	1	AT4G03560				
GO:0005507	2	AT1G65930	AT2G44790			
GO:0005618	3	AT1G43170	AT2G01250	AT3G13920		
GO:0005634	4	AT1G72370	AT2G27020	AT3G15730	AT3G16640	
GO:0005635	1	AT3G02520				
GO:0005730	2	AT1G43170	AT3G13920			

Cluster 26 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0005737	3	AT1G72370	AT3G02520	AT3G16640			
GO:0005739	15	AT1G14980	AT2G33220	AT2G45060	AT3G03100	AT3G07480	AT3G15730
		AT3G61440	AT4G00860	AT4G16450	AT4G30010	AT4G35830	AT5G08060
		AT5G20080	AT5G50370	AT5G67590			
GO:0005740	1	AT1G09780					
GO:0005773	9	AT1G11840	AT1G43170	AT1G63770	AT2G01250	AT2G27020	AT2G34660
		AT4G03560	AT4G35830	AT5G27850			
GO:0005774	2	AT2G34660	AT4G03560				
GO:0005777	1	AT4G00860					
GO:0005783	3	AT1G20575	AT1G52600	AT5G42570			
GO:0005794	3	AT2G01970	AT3G13772	AT5G35160			
GO:0005829	1	AT4G38740					
GO:0005839	1	AT2G27020					
GO:0005840	2	AT1G43170	AT2G34480				
GO:0005886	24	AT1G09780	AT1G11840	AT1G43170	AT1G52600	AT1G62020	AT1G63770
		AT1G64650	AT1G65930	AT1G72370	AT2G01250	AT2G01970	AT2G27020
		AT2G34480	AT2G34660	AT2G36850	AT3G02520	AT3G13772	AT3G15730
		AT3G16640	AT4G03560	AT4G35830	AT4G38740	AT5G42570	AT5G50370
GO:0005975	1	AT1G11840					
GO:0006075	1	AT2G36850					
GO:0006139	1	AT5G50370					
GO:0006412	5	AT1G43170	AT1G72370	AT2G01250	AT2G34480	AT5G27850	
GO:0006413	1	AT3G13920					
GO:0006457	2	AT1G14980	AT4G38740				
GO:0006486	1	AT1G20575					
GO:0006508	2	AT1G52600	AT1G63770				
GO:0006511	1	AT2G27020					
GO:0006564	1	AT4G35630					
GO:0006631	1	AT3G15730					
GO:0006810	1	AT2G01970					
GO:0006816	1	AT4G03560					
GO:0006886	1	AT5G42570					
GO:0006888	1	AT1G62020					
GO:0006915	1	AT5G42570					
GO:0006950	1	AT2G28190					
GO:0006970	2	AT1G72370	AT5G67590				
GO:0006979	1	AT2G28190					
GO:0007165	1	AT4G38740					
GO:0008026	1	AT3G13920					
GO:0008137	1	AT5G67590					
GO:0008233	2	AT1G52600	AT2G27020				
GO:0009055	1	AT3G07480					
GO:0009061	1	AT5G50370					
GO:0009117	1	AT5G50370					
GO:0009408	1	AT1G14980					
GO:0009409	2	AT1G09780	AT2G27020				
GO:0009416	1	AT2G28190					
GO:0009505	2	AT2G01970	AT5G20080				
GO:0009507	11	AT1G09780	AT1G63770	AT1G72370	AT2G01250	AT2G28190	AT3G02520
		AT3G07480	AT3G15730	AT3G16640	AT3G61440	AT4G35630	
GO:0009536	4	AT2G33220	AT4G00860	AT4G30010	AT5G50370		
GO:0009555	1	AT2G36850					
GO:0009556	1	AT2G36850					
GO:0009570	4	AT1G63770	AT2G28190	AT3G02520	AT4G35630		
GO:0009579	2	AT2G28190	AT3G16640				
GO:0009617	1	AT4G00860					
GO:0009631	1	AT5G67590					
GO:0009651	4	AT1G65930	AT1G72370	AT4G35830	AT5G20080		
GO:0009695	1	AT4G03560					

Cluster 26

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009789	1	AT3G15730					
GO:0009793	1	AT1G43170					
GO:0009845	2	AT3G15730	AT4G03560				
GO:0009853	2	AT2G33220	AT4G16450				
GO:0009860	1	AT3G16640					
GO:0009941	2	AT1G11840	AT1G63770				
GO:0010039	1	AT2G28190					
GO:0010119	2	AT3G15730	AT4G03560				
GO:0010193	1	AT4G00860					
GO:0010252	1	AT3G16640					
GO:0015934	2	AT2G01250	AT5G27850				
GO:0015935	1	AT1G72370					
GO:0016020	11	AT1G43170	AT1G52600	AT1G62020	AT1G72370	AT2G01250	AT3G13920
		AT3G15730	AT3G63460	AT4G00860	AT4G16450	AT5G27850	
GO:0016021	3	AT2G01970	AT3G13772	AT5G35160			
GO:0016491	1	AT3G03100					
GO:0016757	1	AT2G36850					
GO:0019344	1	AT3G61440					
GO:0019430	1	AT2G28190					
GO:0019499	1	AT3G61440					
GO:0022625	4	AT1G43170	AT2G01250	AT2G34480	AT5G27850		
GO:0022626	5	AT1G43170	AT1G72370	AT2G01250	AT2G34480	AT5G27850	
GO:0022627	1	AT1G72370					
GO:0030126	1	AT1G62020					
GO:0030136	1	AT3G15730					
GO:0031225	1	AT2G44790					
GO:0031966	2	AT2G33220	AT4G16450				
GO:0042254	1	AT2G34480					
GO:0042256	1	AT1G72370					
GO:0042626	1	AT2G34660					
GO:0042742	1	AT3G16640					
GO:0045271	4	AT2G33220	AT3G03100	AT4G16450	AT5G67590		
GO:0045309	1	AT3G02520					
GO:0046537	1	AT1G09780					
GO:0046658	1	AT2G44790					
GO:0046686	9	AT1G09780	AT1G11840	AT1G63770	AT1G65930	AT2G27020	AT3G13920
		AT3G15730	AT3G16640	AT4G38740			
GO:0046688	1	AT2G28190					
GO:0048046	7	AT1G63770	AT1G65930	AT2G27020	AT2G28190	AT3G16640	AT4G35830
		AT4G38740					
GO:0048364	1	AT3G16640					
GO:0048527	1	AT3G16640					
GO:0048589	1	AT2G36850					
GO:0048768	1	AT3G16640					
GO:0050017	1	AT3G61440					
GO:0051087	1	AT1G14980					
GO:0051410	1	AT3G61440					
GO:0051536	1	AT3G07480					


Cluster 27

Cluster 27

AT1G04980
AT1G07890
AT1G08830
AT1G20430
AT1G22840
AT1G44170
AT1G47420
AT1G77940
AT1G80230
AT2G02050
AT2G03510
AT2G15620
AT2G22170
AT2G29960
AT2G37860
AT2G43950
AT2G44060
AT2G47840
AT3G01390
AT3G02780
AT3G04080
AT3G06050
AT3G08530
AT3G10370
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AT3G15640
AT3G20390
AT3G25780
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AT3G44100
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AT3G48410
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AT4G05390
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AT4G37830
AT4G38350
AT5G10730
AT5G15910
AT5G20500
AT5G22880
AT5G42090
AT5G54800
AT5G60660

Cluster 27 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	18	48	3.18E-14
GO:0009536	plastid	6	48	4.99E-07
GO:0004129	cytochrome-c oxidase activity	3	48	6.34E-07
GO:0005783	endoplasmic reticulum	5	48	3.18E-04
GO:0005773	vacuole	6	48	4.48E-04
GO:0005740	mitochondrial envelope	2	48	4.60E-04
GO:0044237	cellular metabolic process	2	48	4.60E-04
GO:0009269	response to desiccation	2	48	5.29E-04
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	2	48	5.29E-04
GO:0050662	coenzyme binding	2	48	5.29E-04
GO:0016020	membrane	10	48	6.02E-04
GO:0005829	cytosol	4	48	6.09E-04
GO:0004368	glycerol-3-phosphate dehydrogenase activity	1	48	0.002301606
GO:0006127	glycerophosphate shuttle	1	48	0.002301606
GO:0006862	nucleotide transport	1	48	0.002301606
GO:0015215	nucleotide transmembrane transporter activity	1	48	0.002301606
GO:0019279	methionine biosynthetic process from L-homoserine via cystathionine	1	48	0.002301606
GO:0047889	ferredoxin-nitrate reductase activity	1	48	0.002301606
GO:0050421	nitrite reductase (NO-forming) activity	1	48	0.002301606
GO:0005886	plasma membrane	10	48	0.002933328
GO:0046686	response to cadmium ion	4	48	0.003358253
GO:0009507	chloroplast	12	48	0.003779682
GO:0009651	response to salt stress	4	48	0.003834041
GO:0004121	cystathionine beta-lyase activity	1	48	0.004592838
GO:0004452	isopentenyl-diphosphate delta-isomerase activity	1	48	0.004592838
GO:0004551	nucleotide diphosphatase activity	1	48	0.004592838
GO:0005624	membrane fraction	1	48	0.004592838
GO:0008158	hedgehog receptor activity	1	48	0.004592838
GO:0015085	calcium ion transmembrane transporter activity	1	48	0.004592838
GO:0019563	glycerol catabolic process	1	48	0.004592838
GO:0046423	allene-oxide cyclase activity	1	48	0.004592838
GO:0015152	glucose-6-phosphate transmembrane transporter activity	1	48	0.00687373
GO:0015991	ATP hydrolysis coupled proton transport	1	48	0.00687373
GO:0005743	mitochondrial inner membrane	2	48	0.012248099
GO:0004029	aldehyde dehydrogenase (NAD) activity	1	48	0.013654705
GO:0005771	multivesicular body	1	48	0.013654705
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1	48	0.013654705
GO:0005085	guanyl-nucleotide exchange factor activity	1	48	0.015894577
GO:0008137	NADH dehydrogenase (ubiquinone) activity	1	48	0.015894577
GO:0016469	proton-transporting two-sector ATPase complex	1	48	0.015894577
GO:0016688	L-ascorbate peroxidase activity	1	48	0.018124279
GO:0019430	removal of superoxide radicals	1	48	0.018124279
GO:0046688	response to copper ion	1	48	0.018124279
GO:0000302	response to reactive oxygen species	1	48	0.020343844
GO:0004784	superoxide dismutase activity	1	48	0.020343844
GO:0010039	response to iron ion	1	48	0.020343844
GO:0042651	thylakoid membrane	1	48	0.020343844
GO:0004521	endoribonuclease activity	1	48	0.022553307
GO:0016209	antioxidant activity	1	48	0.024752701
GO:0009821	alkaloid biosynthetic process	1	48	0.026942059

Cluster 27 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005388	calcium-transporting ATPase activity	1	48	0.029121414
GO:0008794	arsenate reductase (glutaredoxin) activity	1	48	0.029121414
GO:0006810	transport	3	48	0.030825006
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	48	0.031290801
GO:0016844	strictosidine synthase activity	1	48	0.031290801
GO:0003756	protein disulfide isomerase activity	1	48	0.033450252
GO:0006071	glycerol metabolic process	1	48	0.033450252
GO:0042742	defense response to bacterium	2	48	0.034503898
GO:0005768	endosome	1	48	0.0355998
GO:0005795	Golgi stack	1	48	0.0355998
GO:0009504	cell plate	1	48	0.0355998
GO:0005216	ion channel activity	1	48	0.037739478
GO:0046961	proton-transporting ATPase activity, rotational mechanism	1	48	0.037739478
GO:0009695	jasmonic acid biosynthetic process	1	48	0.039869319
GO:0005516	calmodulin binding	2	48	0.041758085
GO:0008299	isoprenoid biosynthetic process	1	48	0.041989355
GO:0010193	response to ozone	1	48	0.041989355
GO:0031966	mitochondrial membrane	1	48	0.041989355
GO:0005789	endoplasmic reticulum membrane	1	48	0.048290966
GO:0009579	thylakoid	2	48	0.05134179
GO:0009846	pollen germination	1	48	0.05450551
GO:0008283	cell proliferation	1	48	0.056557827
GO:0015992	proton transport	1	48	0.056557827
GO:0015995	chlorophyll biosynthetic process	1	48	0.056557827
GO:0000325	plant-type vacuole	1	48	0.060633857
GO:0009620	response to fungus	1	48	0.060633857
GO:0015250	water channel activity	1	48	0.060633857
GO:0006979	response to oxidative stress	2	48	0.06240048
GO:0005759	mitochondrial matrix	1	48	0.062657633
GO:0009853	photorespiration	1	48	0.062657633
GO:0005488	binding	3	48	0.063008625
GO:0009706	chloroplast inner membrane	1	48	0.066676868
GO:0045271	respiratory chain complex I	1	48	0.078510298
GO:0005730	nucleolus	2	48	0.086617653
GO:0006839	mitochondrial transport	1	48	0.088118222
GO:0015297	antiporter activity	1	48	0.091897859
GO:0016021	integral to membrane	2	48	0.093600958
GO:0006334	nucleosome assembly	1	48	0.10302211
GO:0009624	response to nematode	1	48	0.106659442
GO:0009793	embryonic development ending in seed dormancy	2	48	0.108672259
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	48	0.110261796
GO:0005618	cell wall	2	48	0.121500526
GO:0007264	small GTPase mediated signal transduction	1	48	0.124326141
GO:0004601	peroxidase activity	1	48	0.131154531
GO:0006812	cation transport	1	48	0.131154531
GO:0009908	flower development	1	48	0.141147546
GO:0009055	electron carrier activity	1	48	0.144412904
GO:0048366	leaf development	1	48	0.1460334
GO:0009570	chloroplast stroma	2	48	0.14798441
GO:0046872	metal ion binding	1	48	0.152434812
GO:0003824	catalytic activity	2	48	0.155973702
GO:0009941	chloroplast envelope	2	48	0.155973702

Cluster 27 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0015031	protein transport	1	48	0.158708627
GO:0009408	response to heat	1	48	0.175317862
GO:0022625	cytosolic large ribosomal subunit	1	48	0.183988984
GO:0016887	ATPase activity	1	48	0.20319275
GO:0008152	metabolic process	2	48	0.232230778
GO:0016787	hydrolase activity	1	48	0.245288768
GO:0022626	cytosolic ribosome	1	48	0.263898005
GO:0005525	GTP binding	1	48	0.27155272
GO:0006457	protein folding	1	48	0.296326372
GO:0009737	response to abscisic acid stimulus	1	48	0.297101232
GO:0031225	anchored to membrane	1	48	0.297101232
GO:0005215	transporter activity	1	48	0.310876666
GO:0016491	oxidoreductase activity	1	48	0.312224865
GO:0009505	plant-type cell wall	1	48	0.319923105
GO:0048046	apoplast	1	48	0.32174515
GO:0009535	chloroplast thylakoid membrane	1	48	0.325841481
GO:0003735	structural constituent of ribosome	1	48	0.343670975
GO:0006412	translation	1	48	0.348491553
GO:0005622	intracellular	1	48	0.370000606
GO:0005737	cytoplasm	1	48	0.372084923

Cluster 27

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000302	1	AT1G07890					
GO:0000325	1	AT3G01390					
GO:0003735	1	AT1G77940					
GO:0003755	1	AT2G29960					
GO:0003756	1	AT1G04980					
GO:0003824	2	AT5G10730	AT5G15910				
GO:0004028	1	AT1G44170					
GO:0004029	1	AT1G44170					
GO:0004121	1	AT3G57050					
GO:0004129	3	AT1G80230	AT3G15640	AT4G37830			
GO:0004368	1	AT3G10370					
GO:0004452	1	AT3G02780					
GO:0004521	1	AT3G20390					
GO:0004551	1	AT3G04080					
GO:0004601	1	AT3G06050					
GO:0004784	1	AT1G08830					
GO:0005085	1	AT3G43300					
GO:0005215	1	AT4G32400					
GO:0005216	1	AT2G43950					
GO:0005388	1	AT4G37640					
GO:0005488	3	AT4G32400	AT5G10730	AT5G15910			
GO:0005516	2	AT3G04080	AT4G37640				
GO:0005525	1	AT3G46830					
GO:0005618	2	AT1G07890	AT3G44100				
GO:0005622	1	AT3G43300					
GO:0005624	1	AT2G29960					
GO:0005730	2	AT2G03510	AT5G22880				
GO:0005737	1	AT1G08830					
GO:0005739	18	AT1G20430	AT1G22840	AT1G47420	AT1G80230	AT2G02050	AT2G15620
		AT2G43950	AT2G47840	AT3G02780	AT3G06050	AT3G10370	AT3G15000
		AT3G15640	AT3G20390	AT4G29480	AT4G32400	AT4G37830	AT5G15910

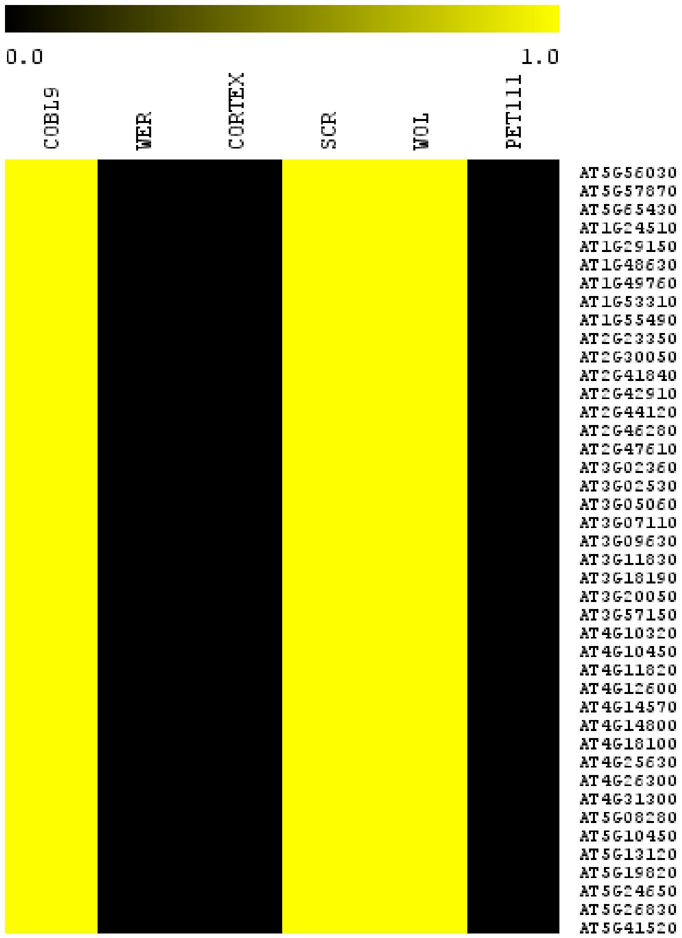
Cluster 27 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005740	2	AT1G80230	AT3G15640				
GO:0005743	2	AT3G10370	AT4G32400				
GO:0005759	1	AT3G06050					
GO:0005768	1	AT3G46830					
GO:0005771	1	AT2G29960					
GO:0005773	6	AT1G44170	AT3G01390	AT3G20390	AT3G44100	AT3G57020	AT4G38350
GO:0005783	5	AT1G44170	AT2G03510	AT2G29960	AT3G57020	AT4G37640	
GO:0005789	1	AT4G37640					
GO:0005795	1	AT2G29960					
GO:0005829	4	AT1G07890	AT1G08830	AT2G29960	AT3G02780		
GO:0005886	10	AT1G07890	AT1G22840	AT2G03510	AT2G44060	AT3G01390	AT3G25780
		AT3G46830	AT4G37640	AT4G38350	AT5G10730		
GO:0006071	1	AT3G10370					
GO:0006120	1	AT2G02050					
GO:0006127	1	AT3G10370					
GO:0006334	1	AT5G22880					
GO:0006412	1	AT1G77940					
GO:0006457	1	AT2G29960					
GO:0006810	3	AT4G32400	AT4G37640	AT5G60660			
GO:0006812	1	AT2G43950					
GO:0006839	1	AT4G32400					
GO:0006862	1	AT4G32400					
GO:0006979	2	AT1G08830	AT3G06050				
GO:0007264	1	AT3G46830					
GO:0008137	1	AT2G02050					
GO:0008152	2	AT5G10730	AT5G15910				
GO:0008158	1	AT4G38350					
GO:0008283	1	AT1G22840					
GO:0008299	1	AT3G02780					
GO:0008794	1	AT5G20500					
GO:0009055	1	AT1G22840					
GO:0009269	2	AT1G44170	AT2G44060				
GO:0009408	1	AT1G07890					
GO:0009504	1	AT3G46830					
GO:0009505	1	AT1G04980					
GO:0009507	12	AT1G07890	AT2G15620	AT2G22170	AT2G37860	AT2G43950	AT2G47840
		AT3G02780	AT3G20390	AT3G57050	AT4G05390	AT4G32400	AT5G54800
GO:0009535	1	AT3G15640					
GO:0009536	6	AT1G44170	AT2G43950	AT2G47840	AT3G20390	AT4G32400	AT5G15910
GO:0009570	2	AT1G07890	AT2G15620				
GO:0009579	2	AT2G22170	AT3G20390				
GO:0009620	1	AT3G25780					
GO:0009624	1	AT5G54800					
GO:0009651	4	AT1G07890	AT1G08830	AT1G44170	AT3G25780		
GO:0009695	1	AT3G25780					
GO:0009706	1	AT2G43950					
GO:0009737	1	AT1G44170					
GO:0009793	2	AT1G07890	AT2G44060				
GO:0009821	1	AT3G57020					
GO:0009846	1	AT3G04080					
GO:0009853	1	AT2G02050					
GO:0009908	1	AT3G02780					
GO:0009941	2	AT2G43950	AT2G47840				
GO:0010039	1	AT1G08830					
GO:0010193	1	AT1G08830					
GO:0015031	1	AT3G46830					
GO:0015085	1	AT4G37640					
GO:0015152	1	AT5G54800					
GO:0015215	1	AT4G32400					

Cluster 27 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0015250	1	AT5G60660					
GO:0015297	1	AT5G54800					
GO:0015991	1	AT3G01390					
GO:0015992	1	AT4G29480					
GO:0015995	1	AT3G02780					
GO:0016020	10	AT1G44170	AT2G15620	AT2G22170	AT2G37860	AT2G43950	AT2G44060
		AT3G25780	AT4G38350	AT5G54800	AT5G60660		
GO:0016021	2	AT5G42090	AT5G54800				
GO:0016209	1	AT3G06050					
GO:0016469	1	AT3G01390					
GO:0016491	1	AT4G05390					
GO:0016688	1	AT1G07890					
GO:0016787	1	AT3G48410					
GO:0016844	1	AT3G57020					
GO:0016887	1	AT3G04080					
GO:0019279	1	AT3G57050					
GO:0019430	1	AT1G08830					
GO:0019563	1	AT3G10370					
GO:0022625	1	AT1G77940					
GO:0022626	1	AT1G77940					
GO:0031225	1	AT3G44100					
GO:0031966	1	AT2G02050					
GO:0042651	1	AT4G05390					
GO:0042742	2	AT1G08830	AT3G43300				
GO:0044237	2	AT5G10730	AT5G15910				
GO:0045271	1	AT2G02050					
GO:0046423	1	AT3G25780					
GO:0046686	4	AT1G07890	AT2G44060	AT3G06050	AT3G20390		
GO:0046688	1	AT1G08830					
GO:0046872	1	AT3G15640					
GO:0046933	2	AT3G01390	AT4G29480				
GO:0046961	1	AT4G29480					
GO:0047889	1	AT2G15620					
GO:0048046	1	AT2G15620					
GO:0048366	1	AT2G37860					
GO:0050421	1	AT2G15620					
GO:0050662	2	AT5G10730	AT5G15910				

Cluster 28



Cluster 28

AT1G24510
AT1G29150
AT1G48630
AT1G49760
AT1G53310
AT1G55490
AT2G23350
AT2G30050
AT2G41840
AT2G42910
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AT3G02530
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AT4G11820
AT4G12600
AT4G14570
AT4G14800
AT4G18100
AT4G25630
AT4G26300
AT4G31300
AT5G08280
AT5G10450
AT5G13120
AT5G19820
AT5G24650
AT5G26830
AT5G41520
AT5G56030
AT5G57870
AT5G65430

Cluster 28 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022626	cytosolic ribosome	9	42	3.78E-11
GO:0005730	nucleolus	9	42	8.74E-10
GO:0051082	unfolded protein binding	6	42	4.65E-08
GO:0006412	translation	8	42	1.10E-07
GO:0046686	response to cadmium ion	7	42	1.18E-06
GO:0003735	structural constituent of ribosome	7	42	1.36E-06

Cluster 28 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022625	cytosolic large ribosomal subunit	5	42	1.65E-06
GO:0005618	cell wall	7	42	2.09E-06
GO:0005524	ATP binding	8	42	2.64E-05
GO:0015934	large ribosomal subunit	3	42	4.29E-05
GO:0006457	protein folding	5	42	5.09E-05
GO:0009507	chloroplast	14	42	9.25E-05
GO:0044267	cellular protein metabolic process	2	42	2.14E-04
GO:0005773	vacuole	6	42	2.17E-04
GO:0045309	protein phosphorylated amino acid binding	2	42	2.56E-04
GO:0003743	translation initiation factor activity	3	42	3.67E-04
GO:0005839	proteasome core complex	2	42	7.27E-04
GO:0009742	brassinosteroid mediated signaling	2	42	8.02E-04
GO:0005886	plasma membrane	10	42	0.001086318
GO:0005737	cytoplasm	5	42	0.001361365
GO:0005515	protein binding	8	42	0.001871039
GO:0004418	hydroxymethylbilane synthase activity	1	42	0.002013906
GO:0004421	hydroxymethylglutaryl-CoA synthase activity	1	42	0.002013906
GO:0003723	RNA binding	4	42	0.002573353
GO:0016020	membrane	8	42	0.003480614
GO:0008233	peptidase activity	2	42	0.003765704
GO:0001510	RNA methylation	1	42	0.004019892
GO:0004814	arginine-tRNA ligase activity	1	42	0.004019892
GO:0004829	threonine-tRNA ligase activity	1	42	0.004019892
GO:0006420	arginyl-tRNA aminoacylation	1	42	0.004019892
GO:0006435	threonyl-tRNA aminoacylation	1	42	0.004019892
GO:0006900	membrane budding	1	42	0.004019892
GO:0019287	isopentenyl diphosphate biosynthetic process, mevalonate pathway	1	42	0.004019892
GO:0030089	phycobilisome	1	42	0.004019892
GO:0030515	snoRNA binding	1	42	0.004019892
GO:0031119	tRNA pseudouridine synthesis	1	42	0.004019892
GO:0051085	chaperone mediated protein folding requiring cofactor	1	42	0.004019892
GO:0006511	ubiquitin-dependent protein catabolic process	3	42	0.006012115
GO:0003985	acetyl-CoA C-acetyltransferase activity	1	42	0.006017983
GO:0004749	ribose phosphate diphosphokinase activity	1	42	0.0080082
GO:0008964	phosphoenolpyruvate carboxylase activity	1	42	0.0080082
GO:0050821	protein stabilization	1	42	0.0080082
GO:0009165	nucleotide biosynthetic process	1	42	0.009990566
GO:0030529	ribonucleoprotein complex	1	42	0.009990566
GO:0022627	cytosolic small ribosomal subunit	2	42	0.010768598
GO:0048046	apoplast	3	42	0.011178647
GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	1	42	0.015890788
GO:0009651	response to salt stress	3	42	0.017636549
GO:0006099	tricarboxylic acid cycle	1	42	0.019785428
GO:0008541	proteasome regulatory particle, lid subcomplex	1	42	0.021721164
GO:0010286	heat acclimation	1	42	0.021721164
GO:0042742	defense response to bacterium	2	42	0.027361702
GO:0006779	porphyrin biosynthetic process	1	42	0.027482297
GO:0009414	response to water deprivation	2	42	0.028078956
GO:0009982	pseudouridine synthase activity	1	42	0.029387391
GO:0009941	chloroplast envelope	3	42	0.031799089

Cluster 28 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005744	mitochondrial inner membrane presequence translocase complex	1	42	0.038799226
GO:0009627	systemic acquired resistance	1	42	0.040659019
GO:0016310	phosphorylation	1	42	0.042511338
GO:0030163	protein catabolic process	1	42	0.042511338
GO:0006364	rRNA processing	1	42	0.049846309
GO:0015995	chlorophyll biosynthetic process	1	42	0.049846309
GO:0008219	cell death	1	42	0.057063422
GO:0010319	stromule	1	42	0.058849446
GO:0008236	serine-type peptidase activity	1	42	0.06062821
GO:0000166	nucleotide binding	2	42	0.061726323
GO:0048367	shoot development	1	42	0.069413874
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	1	42	0.079721491
GO:0031977	thylakoid lumen	1	42	0.083101068
GO:0016829	lyase activity	1	42	0.089776765
GO:0009793	embryonic development ending in seed dormancy	2	42	0.089893841
GO:0005834	heterotrimeric G-protein complex	1	42	0.096342266
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	42	0.097966575
GO:0006413	translational initiation	1	42	0.099584097
GO:0048364	root development	1	42	0.120003308
GO:0009543	chloroplast thylakoid lumen	1	42	0.121527888
GO:0009570	chloroplast stroma	2	42	0.125130269
GO:0009908	flower development	1	42	0.126062752
GO:0048366	leaf development	1	42	0.130539698
GO:0005739	mitochondrion	3	42	0.133030538
GO:0015031	protein transport	1	42	0.14219896
GO:0042254	ribosome biogenesis	1	42	0.156213583
GO:0009408	response to heat	1	42	0.157581497
GO:0005777	peroxisome	1	42	0.179928484
GO:0005634	nucleus	4	42	0.195975351
GO:0009579	thylakoid	1	42	0.245166266
GO:0005829	cytosol	1	42	0.247068197
GO:0005840	ribosome	1	42	0.258084766
GO:0009409	response to cold	1	42	0.261609258
GO:0009505	plant-type cell wall	1	42	0.299846969
GO:0009535	chloroplast thylakoid membrane	1	42	0.306286109
GO:0006952	defense response	1	42	0.344589024
GO:0006508	proteolysis	1	42	0.348466385

Cluster 28

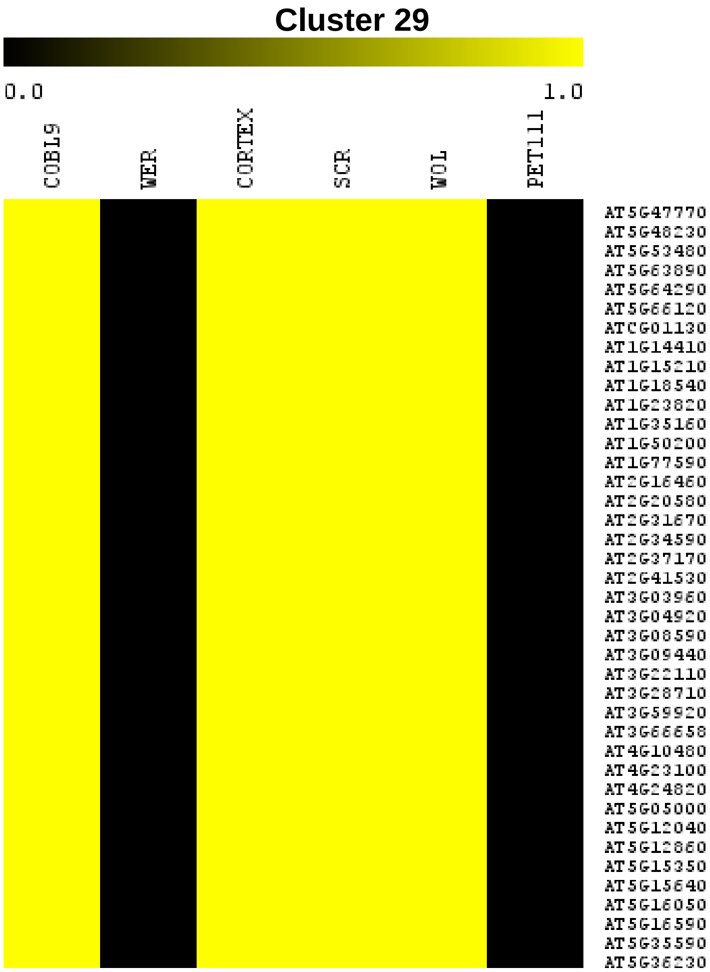
GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000166	2	AT1G48630 AT2G30050
GO:0001510	1	AT4G25630
GO:0003723	4	AT1G49760 AT2G23350 AT4G12600 AT5G57870
GO:0003735	7	AT2G41840 AT2G44120 AT2G47610 AT3G07110 AT3G09630 AT4G10450 AT5G41520
GO:0003743	3	AT1G49760 AT2G23350 AT5G57870
GO:0003755	1	AT5G13120
GO:0003985	1	AT4G11820
GO:0004418	1	AT5G08280
GO:0004421	1	AT4G11820
GO:0004616	1	AT3G02360

Cluster 28 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004749	1	AT2G42910					
GO:0004814	1	AT4G26300					
GO:0004829	1	AT5G26830					
GO:0005515	8	AT1G24510	AT1G55490	AT3G02530	AT3G11830	AT3G18190	AT3G20050
		AT5G10450	AT5G65430				
GO:0005524	8	AT1G24510	AT1G55490	AT3G02530	AT3G11830	AT3G18190	AT3G20050
		AT4G26300	AT5G56030				
GO:0005618	7	AT3G09630	AT5G10450	AT5G19820	AT5G26830	AT5G41520	AT5G56030
		AT5G65430					
GO:0005634	4	AT1G29150	AT5G10450	AT5G57870	AT5G65430		
GO:0005730	9	AT2G30050	AT2G41840	AT2G44120	AT2G47610	AT3G05060	AT3G07110
		AT3G09630	AT3G57150	AT4G25630			
GO:0005737	5	AT2G42910	AT3G02530	AT5G10450	AT5G57870	AT5G65430	
GO:0005739	3	AT4G26300	AT5G26830	AT5G56030			
GO:0005744	1	AT5G24650					
GO:0005773	6	AT2G44120	AT3G09630	AT4G14570	AT4G14800	AT4G31300	AT5G24650
GO:0005777	1	AT3G02360					
GO:0005829	1	AT5G10450					
GO:0005834	1	AT2G30050					
GO:0005839	2	AT4G14800	AT4G31300				
GO:0005840	1	AT3G09630					
GO:0005886	10	AT1G24510	AT1G55490	AT2G42910	AT2G47610	AT3G09630	AT4G31300
		AT5G10450	AT5G24650	AT5G26830	AT5G65430		
GO:0006099	1	AT1G53310					
GO:0006364	1	AT4G25630					
GO:0006412	8	AT2G41840	AT2G44120	AT2G47610	AT3G07110	AT3G09630	AT4G10450
		AT5G41520	AT5G57870				
GO:0006413	1	AT5G57870					
GO:0006420	1	AT4G26300					
GO:0006435	1	AT5G26830					
GO:0006457	5	AT1G24510	AT1G55490	AT3G20050	AT5G13120	AT5G56030	
GO:0006508	1	AT4G14570					
GO:0006511	3	AT1G29150	AT4G14800	AT4G31300			
GO:0006779	1	AT5G08280					
GO:0006900	1	AT2G30050					
GO:0006952	1	AT5G56030					
GO:0008219	1	AT1G55490					
GO:0008233	2	AT4G14800	AT4G31300				
GO:0008236	1	AT4G14570					
GO:0008541	1	AT1G29150					
GO:0008964	1	AT1G53310					
GO:0009165	1	AT2G42910					
GO:0009408	1	AT5G56030					
GO:0009409	1	AT1G55490					
GO:0009414	2	AT1G53310	AT5G56030				
GO:0009505	1	AT5G65430					
GO:0009507	14	AT1G55490	AT2G44120	AT2G47610	AT3G07110	AT3G09630	AT4G14570
		AT4G26300	AT5G08280	AT5G10450	AT5G13120	AT5G24650	AT5G26830
		AT5G41520	AT5G65430				
GO:0009535	1	AT5G13120					
GO:0009543	1	AT5G13120					
GO:0009570	2	AT1G55490	AT5G08280				
GO:0009579	1	AT5G13120					
GO:0009627	1	AT1G55490					
GO:0009651	3	AT3G02360	AT4G31300	AT5G56030			
GO:0009742	2	AT5G10450	AT5G65430				
GO:0009793	2	AT4G26300	AT5G19820				
GO:0009908	1	AT5G56030					
GO:0009941	3	AT1G55490	AT5G08280	AT5G24650			

Cluster 28

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0009982	1	AT3G57150					
GO:0010286	1	AT5G56030					
GO:0010319	1	AT1G55490					
GO:0015031	1	AT5G24650					
GO:0015450	1	AT5G24650					
GO:0015934	3	AT2G44120	AT3G07110	AT4G10450			
GO:0015995	1	AT5G08280					
GO:0016020	8	AT1G55490	AT2G41840	AT2G44120	AT3G02530	AT3G05060	AT3G07110
		AT3G09630	AT5G26830				
GO:0016310	1	AT5G10450					
GO:0016829	1	AT5G19820					
GO:0019287	1	AT4G11820					
GO:0022625	5	AT2G44120	AT2G47610	AT3G07110	AT3G09630	AT4G10450	
GO:0022626	9	AT1G48630	AT1G55490	AT2G41840	AT2G44120	AT2G47610	AT3G07110
		AT3G09630	AT4G10450	AT5G41520			
GO:0022627	2	AT2G41840	AT5G41520				
GO:0030089	1	AT5G19820					
GO:0030163	1	AT1G29150					
GO:0030515	1	AT4G25630					
GO:0030529	1	AT4G12600					
GO:0031119	1	AT3G57150					
GO:0031977	1	AT5G13120					
GO:0042254	1	AT4G12600					
GO:0042742	2	AT5G08280	AT5G10450				
GO:0044267	2	AT1G24510	AT3G20050				
GO:0045309	2	AT5G10450	AT5G65430				
GO:0046686	7	AT1G29150	AT1G49760	AT2G23350	AT3G02530	AT3G11830	AT3G18190
		AT5G10450					
GO:0048046	3	AT1G53310	AT1G55490	AT5G08280			
GO:0048364	1	AT1G48630					
GO:0048366	1	AT5G56030					
GO:0048367	1	AT1G48630					
GO:0050821	1	AT5G56030					
GO:0051082	6	AT1G24510	AT1G55490	AT3G02530	AT3G11830	AT3G18190	AT3G20050
GO:0051085	1	AT1G55490					



Cluster 29

AT1G14410
AT1G15210
AT1G18540
AT1G23820
AT1G35160
AT1G50200
AT1G77590
AT2G16460
AT2G20580
AT2G31670
AT2G34590
AT2G37170
AT2G41530
AT3G03960
AT3G04920
AT3G08590
AT3G09440
AT3G22110
AT3G28710
AT3G59920
AT3G66658
AT4G10480
AT4G23100
AT4G24820
AT5G05000
AT5G12040
AT5G12860
AT5G15350
AT5G15640
AT5G16050
AT5G16590
AT5G35590
AT5G36230
AT5G47770
AT5G48230
AT5G53480
AT5G63890
AT5G64290
AT5G66120
ATCG01130

Cluster 29 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009507	chloroplast	17	39	2.53E-07
GO:0046686	response to cadmium ion	7	39	7.02E-07
GO:0015367	oxoglutarate:malate antiporter activity	2	39	1.02E-05
GO:0015743	malate transport	2	39	3.39E-05
GO:0016020	membrane	10	39	1.06E-04
GO:0005886	plasma membrane	11	39	1.37E-04
GO:0022626	cytosolic ribosome	4	39	2.48E-04
GO:0005739	mitochondrion	7	39	4.21E-04
GO:0009941	chloroplast envelope	5	39	5.40E-04
GO:0030163	protein catabolic process	2	39	7.60E-04
GO:0009536	plastid	3	39	0.001735716
GO:0003856	3-dehydroquinate synthase activity	1	39	0.001870055
GO:0004357	glutamate-cysteine ligase activity	1	39	0.001870055
GO:0004399	histidinol dehydrogenase activity	1	39	0.001870055
GO:0004813	alanine-tRNA ligase activity	1	39	0.001870055
GO:0006419	alanyl-tRNA aminoacylation	1	39	0.001870055
GO:0016876	ligase activity, forming aminoacyl-tRNA and related compounds	1	39	0.001870055
GO:0018738	S-formylglutathione hydrolase activity	1	39	0.001870055
GO:0019750	chloroplast transport	1	39	0.001870055
GO:0032211	negative regulation of telomere maintenance via telomerase	1	39	0.001870055
GO:0009570	chloroplast stroma	4	39	0.003711306
GO:0004337	geranyltranstransferase activity	1	39	0.003733295
GO:0005697	telomerase holoenzyme complex	1	39	0.003733295
GO:0006750	glutathione biosynthetic process	1	39	0.003733295
GO:0009700	indole phytoalexin biosynthetic process	1	39	0.003733295
GO:0045337	farnesyl diphosphate biosynthetic process	1	39	0.003733295
GO:0046537	2,3-bisphosphoglycerate-independent phosphoglycerate mutase activity	1	39	0.003733295
GO:0009624	response to nematode	2	39	0.004134124
GO:0005524	ATP binding	5	39	0.00490599
GO:0006511	ubiquitin-dependent protein catabolic process	3	39	0.004917472
GO:0003985	acetyl-CoA C-acetyltransferase activity	1	39	0.005589738
GO:0004161	dimethylallyltranstransferase activity	1	39	0.005589738
GO:0004766	spermidine synthase activity	1	39	0.005589738
GO:0004802	transketolase activity	1	39	0.005589738
GO:0008295	spermidine biosynthetic process	1	39	0.005589738
GO:0005093	RAB GDP-dissociation inhibitor activity	1	39	0.007439402
GO:0042162	telomeric DNA binding	1	39	0.007439402
GO:0048046	apoplast	3	39	0.009211473
GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	1	39	0.009282305
GO:0002213	defense response to insect	1	39	0.011118465
GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	1	39	0.011118465
GO:0009408	response to heat	2	39	0.012644968
GO:0004467	long-chain-fatty-acid-CoA ligase activity	1	39	0.0129479
GO:0009610	response to symbiotic fungus	1	39	0.0129479
GO:0006446	regulation of translational initiation	1	39	0.014770628
GO:0008540	proteasome regulatory particle, base subcomplex	1	39	0.014770628
GO:0045036	protein targeting to chloroplast	1	39	0.016586667
GO:0005777	peroxisome	2	39	0.017133571
GO:0008541	proteasome regulatory particle, lid subcomplex	1	39	0.02019875

Cluster 29 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0044267	cellular protein metabolic process	1	39	0.02019875
GO:0045309	protein phosphorylated amino acid binding	1	39	0.021994828
GO:0000059	protein import into nucleus, docking	1	39	0.023784289
GO:0006631	fatty acid metabolic process	1	39	0.023784289
GO:0009073	aromatic amino acid family biosynthetic process	1	39	0.023784289
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	39	0.02556715
GO:0048868	pollen tube development	1	39	0.027343427
GO:0009508	plastid chromosome	1	39	0.02911314
GO:0052544	callose deposition in cell wall during defense response	1	39	0.02911314
GO:0005635	nuclear envelope	1	39	0.030876306
GO:0006807	nitrogen compound metabolic process	1	39	0.032632941
GO:0009411	response to UV	1	39	0.032632941
GO:0010193	response to ozone	1	39	0.034383064
GO:0019761	glucosinolate biosynthetic process	1	39	0.034383064
GO:0005839	proteasome core complex	1	39	0.036126692
GO:0009707	chloroplast outer membrane	1	39	0.039594532
GO:0005773	vacuole	3	39	0.040352863
GO:0005643	nuclear pore	1	39	0.041318779
GO:0005840	ribosome	2	39	0.041467152
GO:0009295	nucleoid	1	39	0.044748014
GO:0009816	defense response to bacterium, incompatible interaction	1	39	0.044748014
GO:0006457	protein folding	2	39	0.049203175
GO:0016788	hydrolase activity, acting on ester bonds	1	39	0.054882875
GO:0006839	mitochondrial transport	1	39	0.072878059
GO:0005783	endoplasmic reticulum	2	39	0.074497173
GO:0006855	multidrug transport	1	39	0.077656704
GO:0008233	peptidase activity	1	39	0.079237452
GO:0006633	fatty acid biosynthetic process	1	39	0.080812162
GO:0003735	structural constituent of ribosome	2	39	0.082707883
GO:0006412	translation	2	39	0.087936908
GO:0009555	pollen development	1	39	0.090134511
GO:0050832	defense response to fungus	1	39	0.090134511
GO:0005618	cell wall	2	39	0.090997636
GO:0051726	regulation of cell cycle	1	39	0.096230685
GO:0046658	anchored to plasma membrane	1	39	0.100741215
GO:0003743	translation initiation factor activity	1	39	0.115400811
GO:0008565	protein transporter activity	1	39	0.116835399
GO:0009908	flower development	1	39	0.118264346
GO:0005743	mitochondrial inner membrane	1	39	0.12251749
GO:0046872	metal ion binding	1	39	0.128110296
GO:0022627	cytosolic small ribosomal subunit	1	39	0.129494661
GO:0015031	protein transport	1	39	0.133614792
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	39	0.139031943
GO:0005737	cytoplasm	2	39	0.143323703
GO:0042254	ribosome biogenesis	1	39	0.146995986
GO:0005488	binding	2	39	0.151172997
GO:0022625	cytosolic large ribosomal subunit	1	39	0.156045949
GO:0051082	unfolded protein binding	1	39	0.156045949
GO:0005507	copper ion binding	1	39	0.163599721
GO:0009753	response to jasmonic acid stimulus	1	39	0.172179569

Cluster 29 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1	39	0.189742029
GO:0042742	defense response to bacterium	1	39	0.196460889
GO:0005829	cytosol	1	39	0.235168883
GO:0004674	protein serine/threonine kinase activity	1	39	0.237030008
GO:0005525	GTP binding	1	39	0.237954219
GO:0031225	anchored to membrane	1	39	0.263772531
GO:0005730	nucleolus	1	39	0.288160691
GO:0009505	plant-type cell wall	1	39	0.288160691
GO:0009793	embryonic development ending in seed dormancy	1	39	0.313170388
GO:0006810	transport	1	39	0.332525229
GO:0006952	defense response	1	39	0.335444077
GO:0003676	nucleic acid binding	1	39	0.339003474
GO:0006499	N-terminal protein myristoylation	1	39	0.343420557
GO:0005622	intracellular	1	39	0.356108996

Cluster 29

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**						
GO:0000059	1	AT5G53480						
GO:0002213	1	AT4G23100						
GO:0003676	1	AT1G50200						
GO:0003735	2	AT1G18540	AT3G04920					
GO:0003743	1	AT5G36230						
GO:0003856	1	AT5G66120						
GO:0003985	1	AT5G48230						
GO:0004028	1	AT3G66658						
GO:0004161	1	AT5G47770						
GO:0004337	1	AT5G47770						
GO:0004357	1	AT4G23100						
GO:0004399	1	AT5G63890						
GO:0004467	1	AT1G77590						
GO:0004674	1	AT5G16590						
GO:0004739	1	AT2G34590						
GO:0004766	1	AT1G23820						
GO:0004802	1	AT2G34590						
GO:0004813	1	AT1G50200						
GO:0005093	1	AT3G59920						
GO:0005488	2	AT2G20580	AT5G15640					
GO:0005507	1	AT5G15350						
GO:0005524	5	AT1G50200	AT3G03960	AT3G09440	AT5G16050	AT5G16590		
GO:0005525	1	AT5G05000						
GO:0005618	2	AT3G09440	AT5G16050					
GO:0005622	1	AT1G18540						
GO:0005635	1	AT5G16050						
GO:0005643	1	AT5G53480						
GO:0005697	1	AT1G14410						
GO:0005730	1	AT3G04920						
GO:0005737	2	AT5G16050	AT5G53480					
GO:0005739	7	AT1G50200	AT1G77590	AT2G16460	AT5G05000	AT5G12860	AT5G15640	AT5G16050
GO:0005743	1	AT5G15640						
GO:0005773	3	AT3G09440	AT3G22110	AT5G15350				
GO:0005777	2	AT2G31670	AT5G48230					
GO:0005783	2	AT1G18540	AT3G66658					

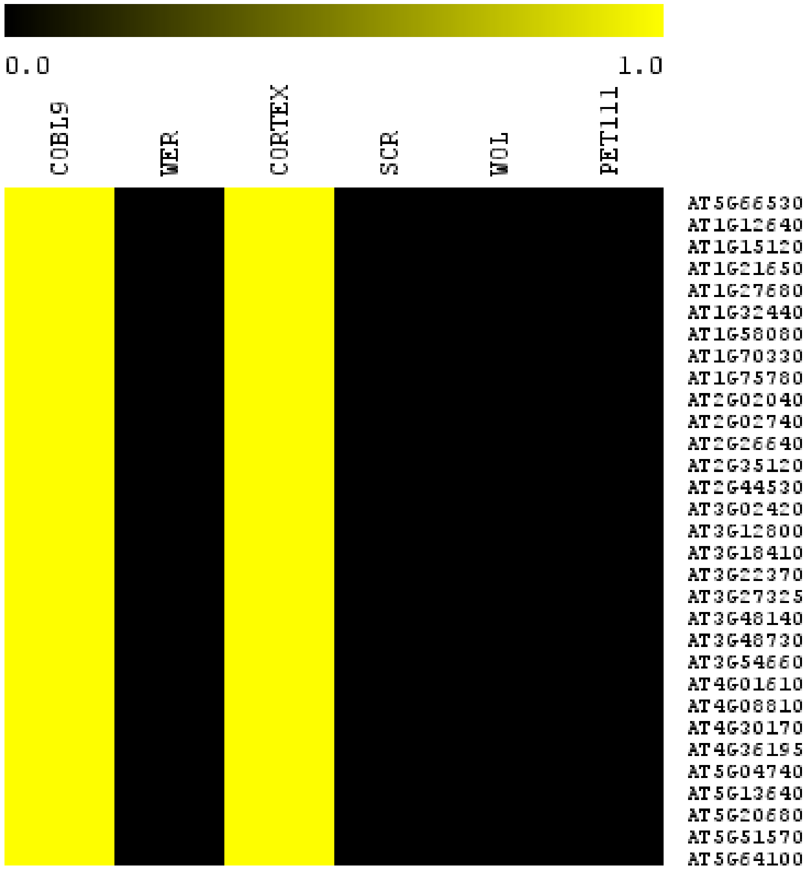
Cluster 29 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005829	1	AT3G09440					
GO:0005839	1	AT3G22110					
GO:0005840	2	AT1G18540	AT3G04920				
GO:0005886	11	AT1G15210	AT1G18540	AT2G16460	AT2G20580	AT3G04920	AT3G09440
		AT4G24820	AT5G15350	AT5G16050	AT5G16590	AT5G48230	
GO:0006412	2	AT1G18540	AT3G04920				
GO:0006419	1	AT1G50200					
GO:0006446	1	AT5G36230					
GO:0006457	2	AT3G03960	AT3G09440				
GO:0006499	1	AT5G12860					
GO:0006511	3	AT2G20580	AT3G22110	AT4G24820			
GO:0006631	1	AT1G77590					
GO:0006633	1	AT1G77590					
GO:0006750	1	AT4G23100					
GO:0006807	1	AT5G12040					
GO:0006810	1	AT5G15640					
GO:0006839	1	AT5G15640					
GO:0006855	1	AT1G15210					
GO:0006952	1	AT1G14410					
GO:0007169	1	AT5G16590					
GO:0008233	1	AT3G22110					
GO:0008295	1	AT1G23820					
GO:0008540	1	AT2G20580					
GO:0008541	1	AT4G24820					
GO:0008565	1	AT5G53480					
GO:0009073	1	AT5G66120					
GO:0009295	1	AT1G14410					
GO:0009408	2	AT3G09440	AT4G23100				
GO:0009411	1	AT5G63890					
GO:0009505	1	AT5G16590					
GO:0009507	17	AT1G14410	AT1G15210	AT1G18540	AT1G50200	AT1G77590	AT2G31670
		AT2G34590	AT3G04920	AT3G09440	AT4G23100	AT5G05000	AT5G12040
		AT5G12860	AT5G53480	AT5G63890	AT5G64290	AT5G66120	
GO:0009508	1	AT1G14410					
GO:0009536	3	AT1G77590	AT5G05000	AT5G12860			
GO:0009555	1	AT5G63890					
GO:0009570	4	AT2G31670	AT4G23100	AT5G16050	AT5G63890		
GO:0009610	1	AT5G16590					
GO:0009624	2	AT5G12860	AT5G64290				
GO:0009700	1	AT4G23100					
GO:0009707	1	AT5G05000					
GO:0009753	1	AT4G23100					
GO:0009793	1	AT5G48230					
GO:0009816	1	AT4G23100					
GO:0009908	1	AT4G23100					
GO:0009941	5	AT1G77590	AT2G34590	AT5G05000	AT5G12860	AT5G64290	
GO:0010193	1	AT4G23100					
GO:0015031	1	AT3G59920					
GO:0015367	2	AT5G12860	AT5G64290				
GO:0015743	2	AT5G12860	AT5G64290				
GO:0016020	10	AT1G15210	AT1G18540	AT1G77590	AT3G03960	AT3G04920	AT4G24820
		AT5G12860	AT5G16590	AT5G36230	AT5G64290		
GO:0016788	1	AT2G41530					
GO:0016810	1	AT5G12040					
GO:0016876	1	AT1G50200					
GO:0018738	1	AT2G41530					
GO:0019750	1	AT5G05000					
GO:0019761	1	AT4G23100					
GO:0022625	1	AT1G18540					

Cluster 29 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0022626	4	AT1G18540	AT3G04920	AT3G09440	AT3G22110		
GO:0022627	1	AT3G04920					
GO:0030163	2	AT2G20580	AT4G24820				
GO:0031225	1	AT5G15350					
GO:0032211	1	AT1G14410					
GO:0042162	1	AT1G14410					
GO:0042254	1	AT3G04920					
GO:0042626	1	AT1G15210					
GO:0042742	1	AT4G23100					
GO:0044267	1	AT3G03960					
GO:0045036	1	AT5G05000					
GO:0045309	1	AT5G16050					
GO:0045337	1	AT5G47770					
GO:0046537	1	AT3G08590					
GO:0046658	1	AT5G15350					
GO:0046686	7	AT1G50200	AT2G41530	AT3G08590	AT3G09440	AT3G22110	AT4G23100
		AT5G16050					
GO:0046872	1	AT2G16460					
GO:0048046	3	AT2G41530	AT3G08590	AT3G09440			
GO:0048868	1	AT2G34590					
GO:0050832	1	AT4G23100					
GO:0051082	1	AT3G03960					
GO:0051726	1	AT2G20580					
GO:0052544	1	AT4G23100					

Cluster 30



Cluster 30

AT1G12640
AT1G15120
AT1G21650
AT1G27680
AT1G32440
AT1G58080
AT1G70330
AT1G75780
AT2G02040
AT2G02740
AT2G26640
AT2G35120
AT2G44530
AT3G02420
AT3G12800
AT3G18410
AT3G22370
AT3G27325
AT3G48140
AT3G48730
AT3G54660
AT4G01610
AT4G08810
AT4G30170
AT4G36195
AT5G04740
AT5G13640
AT5G20680
AT5G51570
AT5G64100
AT5G66530

Cluster 30 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009570	chloroplast stroma	5	31	1.50E-04
GO:0005773	vacuole	5	31	4.14E-04
GO:0010174	nucleoside transmembrane transporter activity, against a concentration gradient	1	31	0.001486454
GO:0015197	peptide transporter activity	1	31	0.001486454
GO:0015334	high affinity oligopeptide transporter activity	1	31	0.001486454
GO:0015833	peptide transport	1	31	0.001486454
GO:0003879	ATP phosphoribosyltransferase activity	1	31	0.002968631
GO:0004362	glutathione-disulfide reductase activity	1	31	0.002968631
GO:0006749	glutathione metabolic process	1	31	0.002968631
GO:0042286	glutamate-1-semialdehyde 2,1-aminomutase activity	1	31	0.002968631
GO:0045333	cellular respiration	1	31	0.002968631
GO:0008415	acyltransferase activity	2	31	0.003379379
GO:0004601	peroxidase activity	2	31	0.004195379
GO:0006505	GPI anchor metabolic process	1	31	0.004446541
GO:0042937	tripeptide transporter activity	1	31	0.004446541
GO:0042939	tripeptide transport	1	31	0.004446541

Cluster 30 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004749	ribose phosphate diphosphokinase activity	1	31	0.005920192
GO:0005960	glycine cleavage complex	1	31	0.005920192
GO:0042936	dipeptide transporter activity	1	31	0.005920192
GO:0042938	dipeptide transport	1	31	0.005920192
GO:0004375	glycine dehydrogenase (decarboxylating) activity	1	31	0.007389592
GO:0009165	nucleotide biosynthetic process	1	31	0.007389592
GO:0004607	phosphatidylcholine-sterol O-acyltransferase activity	1	31	0.008854752
GO:0005337	nucleoside transmembrane transporter activity	1	31	0.008854752
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	1	31	0.008854752
GO:0006546	glycine catabolic process	1	31	0.008854752
GO:0008878	glucose-1-phosphate adenylyltransferase activity	1	31	0.008854752
GO:0009916	alternative oxidase activity	1	31	0.008854752
GO:0000105	histidine biosynthetic process	1	31	0.010315679
GO:0009416	response to light stimulus	2	31	0.010474261
GO:0006886	intracellular protein transport	2	31	0.012165262
GO:0009507	chloroplast	8	31	0.01276041
GO:0008121	ubiquinol-cytochrome-c reductase activity	1	31	0.013224871
GO:0004743	pyruvate kinase activity	1	31	0.014673155
GO:0019252	starch biosynthetic process	1	31	0.014673155
GO:0055114	oxidation reduction	1	31	0.014673155
GO:0003824	catalytic activity	3	31	0.015141447
GO:0004034	aldose 1-epimerase activity	1	31	0.016117241
GO:0015112	nitrate transmembrane transporter activity	1	31	0.016117241
GO:0006012	galactose metabolic process	1	31	0.018992857
GO:0005750	mitochondrial respiratory chain complex III	1	31	0.020424405
GO:0006779	porphyrin biosynthetic process	1	31	0.020424405
GO:0005739	mitochondrion	4	31	0.021030147
GO:0009508	plastid chromosome	1	31	0.023275023
GO:0016597	amino acid binding	1	31	0.023275023
GO:0005886	plasma membrane	6	31	0.023980792
GO:0009409	response to cold	2	31	0.028982421
GO:0006979	response to oxidative stress	2	31	0.030062861
GO:0010150	leaf senescence	1	31	0.033122087
GO:0009295	nucleoid	1	31	0.035898647
GO:0000325	plant-type vacuole	1	31	0.040033007
GO:0016788	hydrolase activity, acting on ester bonds	1	31	0.044130994
GO:0005524	ATP binding	3	31	0.051549046
GO:0005783	endoplasmic reticulum	2	31	0.051753698
GO:0005774	vacuolar membrane	1	31	0.056209003
GO:0005198	structural molecule activity	1	31	0.05753119
GO:0006096	glycolysis	1	31	0.060163778
GO:0006633	fatty acid biosynthetic process	1	31	0.065382032
GO:0009826	unidimensional cell growth	1	31	0.104935291
GO:0006950	response to stress	1	31	0.111930276
GO:0005777	peroxisome	1	31	0.140773345
GO:0008152	metabolic process	2	31	0.151686486
GO:0009536	plastid	1	31	0.160395992
GO:0006629	lipid metabolic process	1	31	0.176008496
GO:0016020	membrane	3	31	0.185092935
GO:0005215	transporter activity	1	31	0.241117538
GO:0016491	oxidoreductase activity	1	31	0.242563381
GO:0048046	apoplast	1	31	0.253075467

Cluster 30 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009535	chloroplast thylakoid membrane	1	31	0.257784351
GO:0005618	cell wall	1	31	0.290671562
GO:0006810	transport	1	31	0.298948489
GO:0006952	defense response	1	31	0.30239758
GO:0006508	proteolysis	1	31	0.307611521
GO:0006499	N-terminal protein myristoylation	1	31	0.312137664
GO:0009941	chloroplast envelope	1	31	0.321801347
GO:0005488	binding	1	31	0.34613426

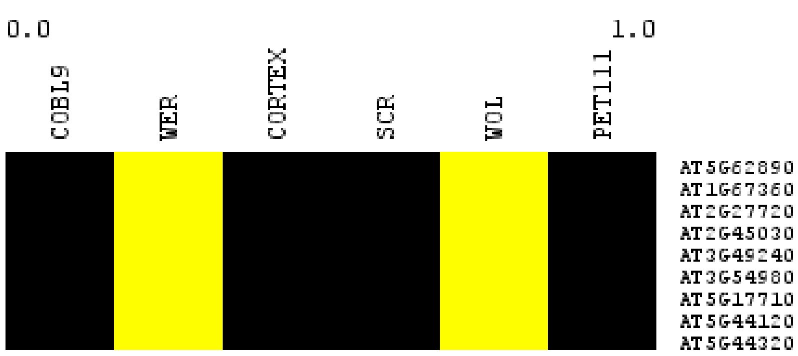
Cluster 30

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000105	1	AT1G58080					
GO:0000325	1	AT2G02040					
GO:0003824	3	AT2G26640	AT3G12800	AT3G27325			
GO:0003879	1	AT1G58080					
GO:0004034	1	AT5G66530					
GO:0004362	1	AT3G54660					
GO:0004375	1	AT2G35120					
GO:0004601	2	AT4G30170	AT5G64100				
GO:0004607	1	AT5G13640					
GO:0004743	1	AT1G32440					
GO:0004749	1	AT2G44530					
GO:0005198	1	AT1G75780					
GO:0005215	1	AT2G02040					
GO:0005337	1	AT1G70330					
GO:0005488	1	AT3G12800					
GO:0005524	3	AT1G21650	AT2G35120	AT3G54660			
GO:0005618	1	AT5G64100					
GO:0005739	4	AT1G15120	AT2G35120	AT3G22370	AT3G54660		
GO:0005750	1	AT1G15120					
GO:0005773	5	AT1G75780	AT2G02040	AT4G01610	AT5G13640	AT5G51570	
GO:0005774	1	AT2G02040					
GO:0005777	1	AT3G12800					
GO:0005783	2	AT3G27325	AT5G13640				
GO:0005886	6	AT1G12640	AT1G70330	AT2G02040	AT3G12800	AT3G27325	AT5G51570
GO:0005960	1	AT2G35120					
GO:0006012	1	AT5G66530					
GO:0006096	1	AT1G32440					
GO:0006122	1	AT1G15120					
GO:0006499	1	AT5G51570					
GO:0006505	1	AT3G27325					
GO:0006508	1	AT4G01610					
GO:0006546	1	AT2G35120					
GO:0006629	1	AT5G13640					
GO:0006633	1	AT1G32440					
GO:0006749	1	AT3G54660					
GO:0006779	1	AT3G48730					
GO:0006810	1	AT1G70330					
GO:0006886	2	AT1G21650	AT3G27325				
GO:0006950	1	AT3G22370					
GO:0006952	1	AT2G02740					
GO:0006979	2	AT4G30170	AT5G64100				
GO:0008121	1	AT1G15120					
GO:0008152	2	AT3G12800	AT5G04740				
GO:0008415	2	AT1G12640	AT2G26640				

Cluster 30 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0008878	1	AT1G27680					
GO:0009165	1	AT2G44530					
GO:0009295	1	AT2G02740					
GO:0009409	2	AT2G26640	AT3G22370				
GO:0009416	2	AT1G75780	AT2G26640				
GO:0009507	8	AT1G32440	AT1G58080	AT2G02740	AT2G44530	AT3G48730	AT3G54660
		AT5G04740	AT5G66530				
GO:0009508	1	AT2G02740					
GO:0009535	1	AT5G04740					
GO:0009536	1	AT3G22370					
GO:0009570	5	AT1G32440	AT3G48730	AT3G54660	AT5G04740	AT5G66530	
GO:0009826	1	AT1G75780					
GO:0009916	1	AT3G22370					
GO:0009941	1	AT3G48730					
GO:0010150	1	AT3G48140					
GO:0010174	1	AT1G70330					
GO:0015112	1	AT2G02040					
GO:0015197	1	AT2G02040					
GO:0015334	1	AT2G02040					
GO:0015833	1	AT2G02040					
GO:0016020	3	AT1G12640	AT1G21650	AT3G02420			
GO:0016491	1	AT3G12800					
GO:0016597	1	AT5G04740					
GO:0016788	1	AT3G27325					
GO:0019252	1	AT1G27680					
GO:0042286	1	AT3G48730					
GO:0042936	1	AT2G02040					
GO:0042937	1	AT2G02040					
GO:0042938	1	AT2G02040					
GO:0042939	1	AT2G02040					
GO:0045333	1	AT3G22370					
GO:0048046	1	AT5G66530					
GO:0055114	1	AT3G22370					

Cluster 31



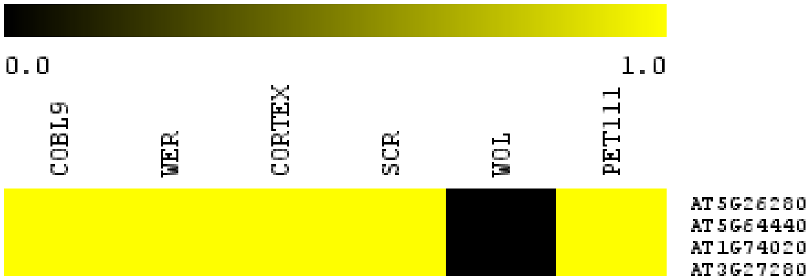
Cluster 31
AT1G67360
AT2G27720
AT2G45030
AT3G49240
AT3G54980
AT5G17710
AT5G44120
AT5G44320
AT5G62890

Cluster 31 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0000774	adenyl-nucleotide exchange factor activity	1	9	0.00129366
GO:0051087	chaperone binding	1	9	0.003443148
GO:0009793	embryonic development ending in seed dormancy	2	9	0.005846459
GO:0022857	transmembrane transporter activity	1	9	0.006438578
GO:0006414	translational elongation	1	9	0.009417898
GO:0005773	vacuole	2	9	0.013955281
GO:0042803	protein homodimerization activity	1	9	0.017423865
GO:0045735	nutrient reservoir activity	1	9	0.022005287
GO:0006413	translational initiation	1	9	0.02324798
GO:0003743	translation initiation factor activity	1	9	0.029418037
GO:0022626	cytosolic ribosome	1	9	0.06760475
GO:0009579	thylakoid	1	9	0.068739397
GO:0005840	ribosome	1	9	0.07399833
GO:0009409	response to cold	1	9	0.075490004
GO:0006457	protein folding	1	9	0.081408638
GO:0009737	response to abscisic acid stimulus	1	9	0.081776008
GO:0016020	membrane	2	9	0.09283015
GO:0003735	structural constituent of ribosome	1	9	0.109867922
GO:0005618	cell wall	1	9	0.116354759
GO:0006810	transport	1	9	0.121737915
GO:0009570	chloroplast stroma	1	9	0.133263417
GO:0009507	chloroplast	2	9	0.196957651
GO:0005524	ATP binding	1	9	0.211517571
GO:0005739	mitochondrion	1	9	0.245792749
GO:0005515	protein binding	1	9	0.322438886
GO:0005634	nucleus	1	9	0.372122789
GO:0012505	endomembrane system	1	9	0.389818186

Cluster 31

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000774	1	AT5G17710	
GO:0003735	1	AT2G27720	
GO:0003743	1	AT5G44320	
GO:0005515	1	AT5G17710	
GO:0005524	1	AT3G49240	
GO:0005618	1	AT5G62890	
GO:0005634	1	AT2G27720	
GO:0005739	1	AT3G49240	
GO:0005773	2	AT1G67360	AT5G62890
GO:0005840	1	AT2G27720	
GO:0006413	1	AT5G44320	
GO:0006414	1	AT2G27720	
GO:0006457	1	AT5G17710	
GO:0006810	1	AT5G62890	
GO:0009409	1	AT2G27720	
GO:0009507	2	AT3G49240	AT5G17710
GO:0009570	1	AT5G17710	
GO:0009579	1	AT5G17710	
GO:0009737	1	AT5G44120	
GO:0009793	2	AT3G49240	AT5G17710
GO:0012505	1	AT5G44120	
GO:0016020	2	AT2G27720	AT5G62890
GO:0022626	1	AT2G27720	
GO:0022857	1	AT5G62890	
GO:0042803	1	AT5G17710	
GO:0045735	1	AT5G44120	
GO:0051087	1	AT5G17710	

Cluster 32



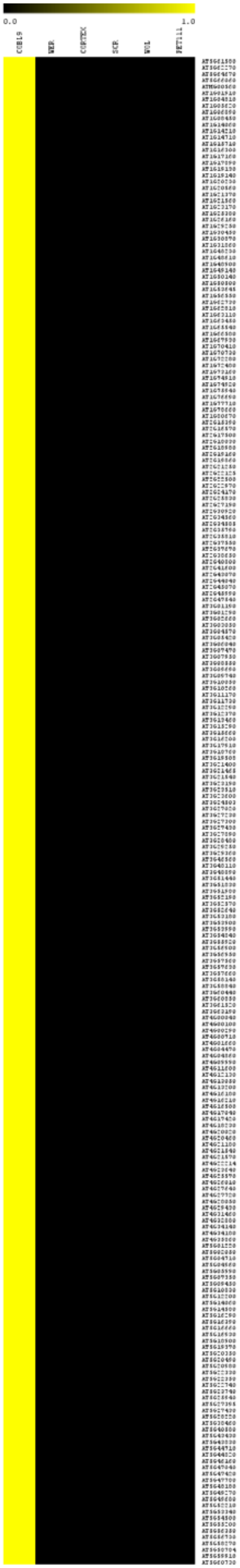
Cluster 32
AT1G74020
AT3G27280
AT5G26280
AT5G64440

Cluster 32 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005773	vacuole	3	4	3.73E-05
GO:0047412	N-(long-chain-acyl)ethanolamine deacylase activity	1	4	1.92E-04
GO:0004040	amidase activity	1	4	9.58E-04
GO:0005886	plasma membrane	3	4	0.001883287
GO:0016844	strictosidine synthase activity	1	4	0.002680189
GO:0045271	respiratory chain complex I	1	4	0.007059929
GO:0006950	response to stress	1	4	0.016106822
GO:0009611	response to wounding	1	4	0.020211282
GO:0009753	response to jasmonic acid stimulus	1	4	0.021326112
GO:0042742	defense response to bacterium	1	4	0.025212634
GO:0009505	plant-type cell wall	1	4	0.044109724
GO:0005783	endoplasmic reticulum	1	4	0.048921054
GO:0005739	mitochondrion	1	4	0.131791079
GO:0016020	membrane	1	4	0.209989764
GO:0009507	chloroplast	1	4	0.314011489

Cluster 32

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0004040	1	AT5G64440		
GO:0005739	1	AT3G27280		
GO:0005773	3	AT1G74020	AT3G27280	AT5G64440
GO:0005783	1	AT5G64440		
GO:0005886	3	AT1G74020	AT3G27280	AT5G64440
GO:0006950	1	AT3G27280		
GO:0009505	1	AT3G27280		
GO:0009507	1	AT3G27280		
GO:0009611	1	AT1G74020		
GO:0009753	1	AT1G74020		
GO:0016020	1	AT5G26280		
GO:0016844	1	AT1G74020		
GO:0042742	1	AT5G64440		
GO:0045271	1	AT3G27280		
GO:0047412	1	AT5G64440		

Cluster 33



Cluster 33

AT1G01910
AT1G04810
AT1G05620
AT1G06890
AT1G08450
AT1G14060
AT1G14210
AT1G14710
AT1G15710
AT1G16300
AT1G17160
AT1G17890
AT1G19130
AT1G19140
AT1G20230
AT1G20560
AT1G21370
AT1G21560
AT1G23170
AT1G25380
AT1G26160
AT1G29250
AT1G30450
AT1G30870
AT1G31860
AT1G48230
AT1G48610
AT1G48900
AT1G49140
AT1G50140
AT1G50500
AT1G53645
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AT1G65540
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AT1G75940
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AT1G77710
AT1G78660
AT1G80670
AT2G15390
AT2G16570
AT2G17500
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AT2G40800
AT2G41600
AT2G43070
AT2G44040
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AT2G45990
AT2G47540
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AT3G04570
AT3G05420
AT3G06040
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AT3G23600
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AT3G27300
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AT3G28480
AT3G29250
AT3G29360
AT3G46560
AT3G48110
AT3G48890
AT3G51440
AT3G51830
AT3G51980
AT3G52190
AT3G52570
AT3G52640
AT3G53180
AT3G53900
AT3G53990
AT3G54840
AT4G00040
AT4G00100
AT4G00290
AT4G00710
AT4G01660
AT4G04470
AT4G04860
AT4G09990
AT4G11600
AT4G12130
AT4G13050
AT4G13200
AT4G16180
AT4G16210
AT4G16500
AT4G17040
AT4G17420
AT4G18230
AT4G20020
AT4G20460
AT4G21180
AT4G21540
AT4G21570
AT4G22214
AT4G23640
AT4G25570
AT4G26010
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AT4G34140
AT4G34180
AT4G35860
AT5G01220
AT5G02050
AT5G04710
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AT5G05990
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AT5G16390
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AT5G49270
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AT5G55200
AT5G56350
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AT5G58270
AT5G58784
AT5G59910
AT5G60730
AT5G61580
AT5G62270

Cluster 33
(con.)

AT3G55920
AT3G56900
AT3G56950
AT3G57560
AT3G57630
AT3G57660
AT3G58140
AT3G58840
AT3G60440
AT3G60850
AT3G61520
AT3G63190
AT5G64670
AT5G66060
ATMG00560

Cluster 33 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	23	237	1.64E-05
GO:0009932	cell tip growth	3	237	1.14E-04
GO:0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	3	237	1.61E-04
GO:0006412	translation	11	237	4.49E-04
GO:0005794	Golgi apparatus	7	237	5.51E-04
GO:0005783	endoplasmic reticulum	10	237	7.09E-04
GO:0003735	structural constituent of ribosome	10	237	0.001161272
GO:0006744	ubiquinone biosynthetic process	2	237	0.001843583
GO:0016036	cellular response to phosphate starvation	3	237	0.002600203
GO:0005759	mitochondrial matrix	3	237	0.003948399
GO:0016757	transferase activity, transferring glycosyl groups	9	237	0.004904106
GO:0004601	peroxidase activity	4	237	0.005834007
GO:0009699	phenylpropanoid biosynthetic process	2	237	0.006387293
GO:0005773	vacuole	11	237	0.007903408
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	2	237	0.010214625
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	3	237	0.01070978
GO:0000035	acyl binding	1	237	0.011364181
GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	1	237	0.011364181
GO:0003991	acetylglutamate kinase activity	1	237	0.011364181
GO:0004157	dihydropyrimidinase activity	1	237	0.011364181
GO:0004395	hexaprenyldihydroxybenzoate methyltransferase activity	1	237	0.011364181
GO:0004635	phosphoribosyl-AMP cyclohydrolase activity	1	237	0.011364181
GO:0004636	phosphoribosyl-ATP diphosphatase activity	1	237	0.011364181
GO:0004794	L-threonine ammonia-lyase activity	1	237	0.011364181
GO:0006566	threonine metabolic process	1	237	0.011364181
GO:0008535	respiratory chain complex IV assembly	1	237	0.011364181
GO:0008691	3-hydroxybutyryl-CoA dehydrogenase activity	1	237	0.011364181
GO:0008705	methionine synthase activity	1	237	0.011364181
GO:0008752	FMN reductase activity	1	237	0.011364181
GO:0009399	nitrogen fixation	1	237	0.011364181
GO:0010009	external side of endosome membrane	1	237	0.011364181
GO:0010420	polyprenyldihydroxybenzoate methyltransferase activity	1	237	0.011364181
GO:0016417	S-acyltransferase activity	1	237	0.011364181
GO:0040014	regulation of multicellular organism growth	1	237	0.011364181

Cluster 33 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0042350	GDP-L-fucose biosynthetic process	1	237	0.011364181
GO:0045022	early endosome to late endosome transport	1	237	0.011364181
GO:0046510	UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity	1	237	0.011364181
GO:0050269	coniferyl-aldehyde dehydrogenase activity	1	237	0.011364181
GO:0009536	plastid	5	237	0.012791724
GO:0005840	ribosome	6	237	0.013698279
GO:0006820	anion transport	2	237	0.014755184
GO:0005886	plasma membrane	27	237	0.015383636
GO:0005839	proteasome core complex	2	237	0.019924246
GO:0004665	prephenate dehydrogenase (NADP+) activity	1	237	0.022471151
GO:0004820	glycine-tRNA ligase activity	1	237	0.022471151
GO:0006402	mRNA catabolic process	1	237	0.022471151
GO:0006426	glycyl-tRNA aminoacylation	1	237	0.022471151
GO:0006571	tyrosine biosynthetic process	1	237	0.022471151
GO:0009097	isoleucine biosynthetic process	1	237	0.022471151
GO:0009374	biotin binding	1	237	0.022471151
GO:0009747	hexokinase-dependent signaling	1	237	0.022471151
GO:0016655	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	1	237	0.022471151
GO:0019285	glycine betaine biosynthetic process from choline	1	237	0.022471151
GO:0045597	positive regulation of cell differentiation	1	237	0.022471151
GO:0046506	sulfolipid biosynthetic process	1	237	0.022471151
GO:0046900	tetrahydrofolylpolyglutamate metabolic process	1	237	0.022471151
GO:0047262	polygalacturonate 4-alpha-galacturonosyltransferase activity	2	237	0.02765864
GO:0007264	small GTPase mediated signal transduction	3	237	0.028138876
GO:0009507	chloroplast	33	237	0.032838734
GO:0003984	acetolactate synthase activity	1	237	0.033325256
GO:0004044	amidophosphoribosyltransferase activity	1	237	0.033325256
GO:0004047	aminomethyltransferase activity	1	237	0.033325256
GO:0004614	phosphoglucomutase activity	1	237	0.033325256
GO:0004826	phenylalanine-tRNA ligase activity	1	237	0.033325256
GO:0005769	early endosome	1	237	0.033325256
GO:0006432	phenylalanyl-tRNA aminoacylation	1	237	0.033325256
GO:0006465	signal peptide processing	1	237	0.033325256
GO:0006612	protein targeting to membrane	1	237	0.033325256
GO:0008805	carbon-monoxide oxygenase activity	1	237	0.033325256
GO:0015074	DNA integration	1	237	0.033325256
GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	1	237	0.033325256
GO:0016853	isomerase activity	1	237	0.033325256
GO:0030742	GTP-dependent protein binding	1	237	0.033325256
GO:0042450	arginine biosynthetic process via ornithine	1	237	0.033325256
GO:0045995	regulation of embryonic development	1	237	0.033325256
GO:0051753	mannan synthase activity	1	237	0.033325256
GO:0005525	GTP binding	5	237	0.034747981
GO:0003824	catalytic activity	8	237	0.035335458
GO:0008565	protein transporter activity	3	237	0.038405585
GO:0005743	mitochondrial inner membrane	3	237	0.043364475
GO:0003979	UDP-glucose 6-dehydrogenase activity	1	237	0.043930781
GO:0005746	mitochondrial respiratory chain	1	237	0.043930781
GO:0006552	leucine catabolic process	1	237	0.043930781

Cluster 33 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006617	SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	1	237	0.043930781
GO:0009247	glycolipid biosynthetic process	1	237	0.043930781
GO:0010288	response to lead ion	1	237	0.043930781
GO:0022627	cytosolic small ribosomal subunit	3	237	0.049858161
GO:0015031	protein transport	3	237	0.053894255
GO:0000062	acyl-CoA binding	1	237	0.054291944
GO:0003989	acetyl-CoA carboxylase activity	1	237	0.054291944
GO:0004340	glucokinase activity	1	237	0.054291944
GO:0004396	hexokinase activity	1	237	0.054291944
GO:0006467	protein thiol-disulfide exchange	1	237	0.054291944
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	1	237	0.054291944
GO:0008312	7S RNA binding	1	237	0.054291944
GO:0008865	fructokinase activity	1	237	0.054291944
GO:0009082	branched chain family amino acid biosynthetic process	1	237	0.054291944
GO:0009113	purine base biosynthetic process	1	237	0.054291944
GO:0009396	folic acid and derivative biosynthetic process	1	237	0.054291944
GO:0016485	protein processing	1	237	0.054291944
GO:0017004	cytochrome complex assembly	1	237	0.054291944
GO:0019303	D-ribose catabolic process	1	237	0.054291944
GO:0019762	glucosinolate catabolic process	1	237	0.054291944
GO:0030234	enzyme regulator activity	1	237	0.054291944
GO:0004029	aldehyde dehydrogenase (NAD) activity	1	237	0.064412899
GO:0004345	glucose-6-phosphate dehydrogenase activity	1	237	0.064412899
GO:0004845	uracil phosphoribosyltransferase activity	1	237	0.064412899
GO:0006006	glucose metabolic process	1	237	0.064412899
GO:0006546	glycine catabolic process	1	237	0.064412899
GO:0009086	methionine biosynthetic process	1	237	0.064412899
GO:0009116	nucleoside metabolic process	1	237	0.064412899
GO:0015976	carbon utilization	1	237	0.064412899
GO:0030176	integral to endoplasmic reticulum membrane	1	237	0.064412899
GO:0046914	transition metal ion binding	1	237	0.064412899
GO:0009651	response to salt stress	6	237	0.064932138
GO:0006839	mitochondrial transport	2	237	0.070339331
GO:0006096	glycolysis	2	237	0.072937573
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	2	237	0.072937573
GO:0000105	histidine biosynthetic process	1	237	0.074297741
GO:0000911	cytokinesis by cell plate formation	1	237	0.074297741
GO:0003872	6-phosphofructokinase activity	1	237	0.074297741
GO:0004356	glutamate-ammonia ligase activity	1	237	0.074297741
GO:0005945	6-phosphofructokinase complex	1	237	0.074297741
GO:0015996	chlorophyll catabolic process	1	237	0.074297741
GO:0016208	AMP binding	1	237	0.074297741
GO:0019408	dolichol biosynthetic process	1	237	0.074297741
GO:0045547	dehydrodolichyl diphosphate synthase activity	1	237	0.074297741
GO:0008233	peptidase activity	2	237	0.080799359
GO:0006633	fatty acid biosynthetic process	2	237	0.083437404
GO:0016051	carbohydrate biosynthetic process	2	237	0.083437404
GO:0000175	3'-5'-exoribonuclease activity	1	237	0.083950501
GO:0004439	phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity	1	237	0.083950501
GO:0005758	mitochondrial intermembrane space	1	237	0.083950501

Cluster 33 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005788	endoplasmic reticulum lumen	1	237	0.083950501
GO:0006506	GPI anchor biosynthetic process	1	237	0.083950501
GO:0006526	arginine biosynthetic process	1	237	0.083950501
GO:0006817	phosphate transport	1	237	0.083950501
GO:0008284	positive regulation of cell proliferation	1	237	0.083950501
GO:0008540	proteasome regulatory particle, base subcomplex	1	237	0.083950501
GO:0009051	pentose-phosphate shunt, oxidative branch	1	237	0.083950501
GO:0010014	meristem initiation	1	237	0.083950501
GO:0016020	membrane	17	237	0.089648457
GO:0016021	integral to membrane	5	237	0.090923376
GO:0000036	acyl carrier activity	1	237	0.09337515
GO:0003729	mRNA binding	1	237	0.09337515
GO:0004602	glutathione peroxidase activity	1	237	0.09337515
GO:0005786	signal recognition particle, endoplasmic reticulum targeting	1	237	0.09337515
GO:0005777	peroxisome	3	237	0.094722455
GO:0016887	ATPase activity	3	237	0.099250077
GO:0005834	heterotrimeric G-protein complex	2	237	0.099353793
GO:0006499	N-terminal protein myristoylation	6	237	0.101844207
GO:0004521	endoribonuclease activity	1	237	0.102575599
GO:0004743	pyruvate kinase activity	1	237	0.102575599
GO:0006014	D-ribose metabolic process	1	237	0.102575599
GO:0008417	fucosyltransferase activity	1	237	0.102575599
GO:0010053	root epidermal cell differentiation	1	237	0.102575599
GO:0012501	programmed cell death	1	237	0.102575599
GO:0048765	root hair cell differentiation	1	237	0.102575599
GO:0055114	oxidation reduction	1	237	0.102575599
GO:0005524	ATP binding	9	237	0.105971309
GO:0009570	chloroplast stroma	6	237	0.106148019
GO:0006979	response to oxidative stress	4	237	0.106880394
GO:0008113	peptide-methionine-(S)-S-oxide reductase activity	1	237	0.111555701
GO:0010089	xylem histogenesis	1	237	0.111555701
GO:0019538	protein metabolic process	1	237	0.111555701
GO:0032312	regulation of ARF GTPase activity	1	237	0.111555701
GO:0048507	meristem development	1	237	0.111555701
GO:0006457	protein folding	4	237	0.119098349
GO:0009672	auxin:hydrogen symporter activity	1	237	0.120319248
GO:0009821	alkaloid biosynthetic process	1	237	0.120319248
GO:0010072	primary shoot apical meristem specification	1	237	0.120319248
GO:0010181	FMN binding	1	237	0.120319248
GO:0016671	oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor	1	237	0.120319248
GO:0042546	cell wall biogenesis	1	237	0.120319248
GO:0000059	protein import into nucleus, docking	1	237	0.128869979
GO:0006631	fatty acid metabolic process	1	237	0.128869979
GO:0005618	cell wall	5	237	0.130158966
GO:0005740	mitochondrial envelope	1	237	0.137211574
GO:0016844	strictosidine synthase activity	1	237	0.137211574
GO:0005215	transporter activity	4	237	0.138333341
GO:0005737	cytoplasm	6	237	0.142586898
GO:0004089	carbonate dehydratase activity	1	237	0.145347657
GO:0016779	nucleotidyltransferase activity	1	237	0.145347657
GO:0008152	metabolic process	7	237	0.147053862
GO:0016787	hydrolase activity	3	237	0.14986076

Cluster 33 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005730	nucleolus	4	237	0.150610182
GO:0006626	protein targeting to mitochondrion	1	237	0.153281798
GO:0009532	plastid stroma	1	237	0.153281798
GO:0015198	oligopeptide transporter activity	1	237	0.153281798
GO:0016597	amino acid binding	1	237	0.153281798
GO:0009055	electron carrier activity	2	237	0.153388453
GO:0000271	polysaccharide biosynthetic process	1	237	0.161017512
GO:0005778	peroxisomal membrane	1	237	0.161017512
GO:0010090	trichome morphogenesis	1	237	0.161017512
GO:0020037	heme binding	1	237	0.161017512
GO:0009826	unidimensional cell growth	2	237	0.165295715
GO:0009941	chloroplast envelope	5	237	0.165965595
GO:0006888	ER to Golgi vesicle-mediated transport	1	237	0.168558262
GO:0009225	nucleotide-sugar metabolic process	1	237	0.168558262
GO:0009749	response to glucose stimulus	1	237	0.168558262
GO:0009058	biosynthetic process	2	237	0.174449206
GO:0005829	cytosol	3	237	0.177954447
GO:0046686	response to cadmium ion	4	237	0.178519245
GO:0009793	embryonic development ending in seed dormancy	4	237	0.179065055
GO:0005744	mitochondrial inner membrane presequence translocase complex	1	237	0.183068455
GO:0008514	organic anion transmembrane transporter activity	1	237	0.183068455
GO:0009742	brassinosteroid mediated signaling	1	237	0.190044563
GO:0009831	plant-type cell wall modification during multidimensional cell growth	1	237	0.190044563
GO:0010182	sugar mediated signaling	1	237	0.190044563
GO:0015079	potassium ion transmembrane transporter activity	1	237	0.190044563
GO:0030244	cellulose biosynthetic process	1	237	0.190044563
GO:0006810	transport	4	237	0.194495808
GO:0006511	ubiquitin-dependent protein catabolic process	3	237	0.195760746
GO:0009817	defense response to fungus, incompatible interaction	1	237	0.196839036
GO:0030163	protein catabolic process	1	237	0.196839036
GO:0006508	proteolysis	4	237	0.197454873
GO:0004812	aminoacyl-tRNA ligase activity	1	237	0.20345508
GO:0005643	nuclear pore	1	237	0.20345508
GO:0009832	plant-type cell wall biogenesis	1	237	0.209895854
GO:0000166	nucleotide binding	3	237	0.215352177
GO:0006418	tRNA aminoacylation for protein translation	1	237	0.216164466
GO:0005507	copper ion binding	2	237	0.219564182
GO:0006364	rRNA processing	1	237	0.222263978
GO:0009505	plant-type cell wall	3	237	0.22331609
GO:0009535	chloroplast thylakoid membrane	3	237	0.225518357
GO:0050660	FAD binding	1	237	0.228197404
GO:0006886	intracellular protein transport	2	237	0.234824373
GO:0006486	protein amino acid glycosylation	1	237	0.250328926
GO:0008236	serine-type peptidase activity	1	237	0.25547554
GO:0042742	defense response to bacterium	2	237	0.25551777
GO:0003924	GTPase activity	1	237	0.265324623
GO:0010583	response to cyclopentenone	1	237	0.265324623
GO:0015934	large ribosomal subunit	1	237	0.265324623
GO:0016759	cellulose synthase activity	1	237	0.270032459
GO:0005509	calcium ion binding	2	237	0.271088735
GO:0022626	cytosolic ribosome	2	237	0.27270635

Cluster 33 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009579	thylakoid	2	237	0.273099639
GO:0003993	acid phosphatase activity	1	237	0.274599331
GO:0009926	auxin polar transport	1	237	0.274599331
GO:0009965	leaf morphogenesis	1	237	0.279027821
GO:0006813	potassium ion transport	1	237	0.299182047
GO:0003899	DNA-directed RNA polymerase activity	1	237	0.30977057
GO:0007568	aging	1	237	0.30977057
GO:0008168	methyltransferase activity	1	237	0.313063278
GO:0045454	cell redox homeostasis	1	237	0.313063278
GO:0006464	protein modification process	1	237	0.316241288
GO:0006350	transcription	1	237	0.31930677
GO:0010287	plastoglobule	1	237	0.31930677
GO:0006334	nucleosome assembly	1	237	0.325108652
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	237	0.335453771
GO:0006970	response to osmotic stress	1	237	0.342173644
GO:0006396	RNA processing	1	237	0.344225844
GO:0016758	transferase activity, transferring hexosyl groups	1	237	0.344225844
GO:0006857	oligopeptide transport	1	237	0.346187221
GO:0008415	acyltransferase activity	1	237	0.346187221
GO:0042545	cell wall modification	1	237	0.348059565
GO:0030599	pectinesterase activity	1	237	0.36003856
GO:0009543	chloroplast thylakoid lumen	1	237	0.361185525
GO:0004871	signal transducer activity	1	237	0.367868395
GO:0030246	carbohydrate binding	1	237	0.367868395
GO:0046872	metal ion binding	1	237	0.368898228
GO:0006869	lipid transport	1	237	0.37026285
GO:0006950	response to stress	1	237	0.37061741
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	237	0.370766105

Cluster 33

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000035	1	AT5G20350
GO:0000036	1	AT4G13050
GO:0000059	1	AT4G27640
GO:0000062	1	AT3G05420
GO:0000105	1	AT1G31860
GO:0000166	3	AT1G80670 AT3G21540 AT3G52190
GO:0000175	1	AT5G14580
GO:0000271	1	AT3G03050
GO:0000911	1	AT4G00100
GO:0003729	1	AT1G48900
GO:0003735	10	AT1G66580 AT3G06040 AT3G12370 AT3G18760 AT4G00100 AT4G29430 AT4G31460 AT5G23740 AT5G46160 AT5G64670
GO:0003755	1	AT3G55920
GO:0003824	8	AT1G17890 AT1G26160 AT1G63450 AT3G12290 AT3G57630 AT4G00040 AT4G16210 AT4G20460
GO:0003871	1	AT5G20980
GO:0003872	1	AT5G61580
GO:0003899	1	AT3G57660
GO:0003924	1	AT3G54840
GO:0003979	1	AT3G29360
GO:0003984	1	AT5G16290
GO:0003989	1	AT5G16390
GO:0003991	1	AT3G57560

Cluster 33 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0003993	1	AT2G27190					
GO:0004028	2	AT1G74920	AT3G24503				
GO:0004029	1	AT3G24503					
GO:0004044	1	AT2G16570					
GO:0004047	1	AT4G12130					
GO:0004089	1	AT1G70410					
GO:0004157	1	AT5G12200					
GO:0004340	1	AT2G19860					
GO:0004345	1	AT3G27300					
GO:0004356	1	AT3G53180					
GO:0004395	1	AT2G30920					
GO:0004396	1	AT2G19860					
GO:0004439	1	AT3G51830					
GO:0004521	1	AT1G14210					
GO:0004601	4	AT1G30870	AT2G18980	AT3G01190	AT4G26010		
GO:0004602	1	AT4G11600					
GO:0004614	1	AT1G70730					
GO:0004635	1	AT1G31860					
GO:0004636	1	AT1G31860					
GO:0004665	1	AT1G15710					
GO:0004743	1	AT5G56350					
GO:0004794	1	AT3G10050					
GO:0004812	1	AT3G02660					
GO:0004820	1	AT3G48110					
GO:0004826	1	AT3G58140					
GO:0004845	1	AT3G53900					
GO:0004871	1	AT2G37670					
GO:0005215	4	AT1G50500	AT3G56950	AT4G01660	AT5G58270		
GO:0005507	2	AT1G62810	AT3G29250				
GO:0005509	2	AT1G08450	AT1G65540				
GO:0005524	9	AT1G01910	AT2G19860	AT2G34560	AT3G02660	AT3G52570	AT3G58140
		AT5G47040	AT5G55200	AT5G60730			
GO:0005525	5	AT1G48900	AT3G11730	AT3G54840	AT4G35860	AT5G52210	
GO:0005618	5	AT1G74920	AT2G16570	AT4G16500	AT4G34180	AT5G27430	
GO:0005643	1	AT4G27640					
GO:0005730	4	AT3G21540	AT4G00100	AT5G22330	AT5G59910		
GO:0005737	6	AT3G08550	AT3G13460	AT3G23600	AT4G12130	AT4G27640	AT5G18900
GO:0005739	23	AT1G19140	AT1G50500	AT1G65540	AT2G19860	AT2G40800	AT3G01290
		AT3G02660	AT3G10260	AT3G15660	AT3G17910	AT3G46560	AT3G48110
		AT3G52570	AT3G58140	AT3G58840	AT4G11600	AT4G29430	AT5G25940
		AT5G27395	AT5G43430	AT5G55200	AT5G56730	AT5G58270	
GO:0005740	1	AT2G30920					
GO:0005743	3	AT1G25380	AT2G22500	AT3G46560			
GO:0005744	1	AT5G27395					
GO:0005746	1	AT4G01660					
GO:0005758	1	AT3G46560					
GO:0005759	3	AT2G41600	AT5G02050	AT5G05990			
GO:0005769	1	AT3G54840					
GO:0005773	11	AT1G66580	AT1G78660	AT2G34585	AT3G01290	AT3G07470	AT3G52640
		AT4G16500	AT4G25570	AT4G29430	AT5G04710	AT5G54500	
GO:0005777	3	AT1G74910	AT3G15290	AT4G16210			
GO:0005778	1	AT4G04470					
GO:0005783	10	AT1G08450	AT1G72280	AT3G03050	AT3G10260	AT3G23190	AT3G51440
		AT3G52190	AT3G56950	AT4G21180	AT5G47420		
GO:0005786	1	AT1G48900					
GO:0005788	1	AT1G75940					
GO:0005794	7	AT1G06890	AT1G72480	AT2G38650	AT3G03050	AT3G16200	AT3G27230
		AT3G28480					
GO:0005829	3	AT3G05420	AT3G27300	AT4G11600			
GO:0005834	2	AT2G37670	AT3G21540				

Cluster 33 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0005839	2	AT3G27430	AT5G40580				
GO:0005840	6	AT1G66580	AT3G12370	AT3G18760	AT4G31460	AT5G46160	AT5G64670
GO:0005886	27	AT1G04810	AT1G29250	AT1G63110	AT1G66580	AT1G70410	AT1G70730
		AT2G22125	AT2G34585	AT3G01290	AT3G03050	AT3G08550	AT3G09740
		AT3G11730	AT3G23600	AT3G27020	AT3G27890	AT3G28480	AT3G52190
		AT3G52640	AT3G55920	AT4G00710	AT4G11600	AT4G16180	AT4G21180
		AT4G23640	AT4G27720	AT5G54500			
GO:0005945	1	AT5G61580					
GO:0006006	1	AT3G27300					
GO:0006014	1	AT1G17160					
GO:0006096	2	AT5G56350	AT5G61580				
GO:0006334	1	AT5G59910					
GO:0006350	1	AT3G57660					
GO:0006364	1	AT3G21540					
GO:0006396	1	AT5G14580					
GO:0006402	1	AT5G14580					
GO:0006412	11	AT1G66580	AT3G06040	AT3G12370	AT3G18760	AT3G63190	AT4G00100
		AT4G29430	AT4G31460	AT5G23740	AT5G46160	AT5G64670	
GO:0006418	1	AT3G02660					
GO:0006426	1	AT3G48110					
GO:0006432	1	AT3G58140					
GO:0006457	4	AT1G08450	AT3G55920	AT4G21180	AT5G55200		
GO:0006464	1	AT2G18030					
GO:0006465	1	AT5G27430					
GO:0006467	1	AT1G72280					
GO:0006486	1	AT5G53340					
GO:0006499	6	AT1G14060	AT3G01290	AT3G21400	AT3G53180	AT3G54840	AT4G00710
GO:0006506	1	AT1G63110					
GO:0006508	4	AT2G22970	AT4G04860	AT5G04710	AT5G56730		
GO:0006511	3	AT1G04810	AT3G27430	AT5G40580			
GO:0006526	1	AT3G57560					
GO:0006546	1	AT4G12130					
GO:0006552	1	AT5G43430					
GO:0006566	1	AT3G10050					
GO:0006571	1	AT1G15710					
GO:0006612	1	AT3G09740					
GO:0006617	1	AT1G48900					
GO:0006626	1	AT3G46560					
GO:0006631	1	AT3G15290					
GO:0006633	2	AT4G13050	AT5G16390				
GO:0006744	2	AT1G19140	AT2G30920				
GO:0006810	4	AT1G25380	AT1G50500	AT2G22500	AT3G56950		
GO:0006813	1	AT4G23640					
GO:0006817	1	AT3G52190					
GO:0006820	2	AT1G01910	AT5G60730				
GO:0006839	2	AT1G25380	AT2G22500				
GO:0006857	1	AT3G27020					
GO:0006869	1	AT3G05420					
GO:0006886	2	AT3G09740	AT5G27395				
GO:0006888	1	AT3G52190					
GO:0006890	1	AT1G50500					
GO:0006950	1	AT3G53990					
GO:0006970	1	AT1G50500					
GO:0006979	4	AT1G30870	AT2G18980	AT3G01190	AT4G26010		
GO:0007264	3	AT3G11730	AT4G35860	AT5G52210			
GO:0007568	1	AT4G28050					
GO:0008113	1	AT2G18030					
GO:0008152	7	AT1G20560	AT1G74920	AT2G16570	AT3G15290	AT3G29250	AT4G16210
			AT5G10830				
GO:0008168	1	AT5G10830					

Cluster 33 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0008233	2	AT3G27430	AT5G40580				
GO:0008236	1	AT5G47040					
GO:0008284	1	AT4G32880					
GO:0008312	1	AT1G48900					
GO:0008415	1	AT4G00040					
GO:0008417	1	AT2G15390					
GO:0008514	1	AT1G48230					
GO:0008535	1	AT3G17910					
GO:0008540	1	AT1G04810					
GO:0008565	3	AT2G45070	AT3G09740	AT4G27640			
GO:0008691	1	AT3G15290					
GO:0008705	1	AT5G20980					
GO:0008752	1	AT3G27890					
GO:0008805	1	AT4G25570					
GO:0008865	1	AT2G19860					
GO:0009051	1	AT3G27300					
GO:0009055	2	AT1G72280	AT5G43430				
GO:0009058	2	AT1G73160	AT1G74910				
GO:0009082	1	AT5G16290					
GO:0009086	1	AT5G20980					
GO:0009097	1	AT3G10050					
GO:0009113	1	AT2G16570					
GO:0009116	1	AT3G53900					
GO:0009225	1	AT4G20460					
GO:0009247	1	AT5G01220					
GO:0009374	1	AT5G16390					
GO:0009396	1	AT3G12290					
GO:0009399	1	AT3G53180					
GO:0009505	3	AT2G22970	AT2G27190	AT5G04960			
GO:0009507	33	AT1G15710	AT1G17160	AT1G26160	AT1G31860	AT1G67930	AT2G25830
		AT2G45990	AT3G02660	AT3G10050	AT3G12290	AT3G27300	AT3G27890
		AT3G48110	AT3G53900	AT3G57560	AT3G58140	AT3G60440	AT3G63190
		AT4G11600	AT4G13050	AT4G13200	AT4G17040	AT4G25570	AT4G35860
		AT5G01220	AT5G16390	AT5G16660	AT5G19370	AT5G20980	AT5G22330
		AT5G56730	AT5G58270	AT5G61580			
GO:0009532	1	AT4G17040					
GO:0009535	3	AT3G48890	AT4G13200	AT5G16660			
GO:0009536	5	AT1G65540	AT2G19860	AT3G58840	AT5G56730	AT5G58270	
GO:0009543	1	AT3G08550					
GO:0009570	6	AT1G17160	AT2G45990	AT3G27890	AT3G48110	AT3G63190	AT4G17040
GO:0009579	2	AT3G63190	AT4G13200				
GO:0009651	6	AT1G14210	AT3G23600	AT3G27890	AT4G11600	AT4G34180	AT5G20350
GO:0009672	1	AT2G17500					
GO:0009699	2	AT3G24503	AT4G00040				
GO:0009742	1	AT4G00710					
GO:0009747	1	AT2G19860					
GO:0009749	1	AT3G08550					
GO:0009793	4	AT2G30920	AT3G02660	AT3G46560	AT3G48110		
GO:0009817	1	AT5G22330					
GO:0009821	1	AT3G51440					
GO:0009826	2	AT3G08550	AT4G23640				
GO:0009831	1	AT3G08550					
GO:0009832	1	AT3G03050					
GO:0009926	1	AT2G17500					
GO:0009932	3	AT4G23640	AT5G20350	AT5G49270			
GO:0009941	5	AT1G70410	AT4G17040	AT5G01220	AT5G16660	AT5G58270	
GO:0009965	1	AT4G00100					
GO:0010009	1	AT3G54840					
GO:0010014	1	AT4G32880					
GO:0010053	1	AT5G49270					

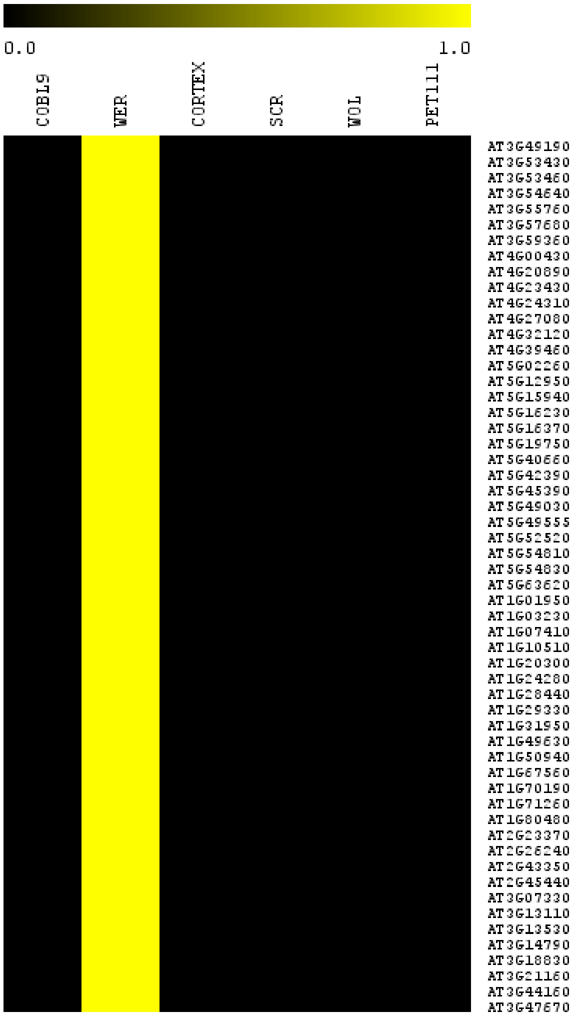
Cluster 33 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0010072	1	AT4G32880					
GO:0010089	1	AT4G32880					
GO:0010090	1	AT4G00100					
GO:0010181	1	AT5G54500					
GO:0010182	1	AT2G19860					
GO:0010287	1	AT4G13200					
GO:0010288	1	AT5G58270					
GO:0010420	1	AT2G30920					
GO:0010583	1	AT3G03050					
GO:0012501	1	AT2G19860					
GO:0015031	3	AT2G45070	AT3G11730	AT4G35860			
GO:0015074	1	AT2G25830					
GO:0015079	1	AT4G23640					
GO:0015198	1	AT3G27020					
GO:0015450	2	AT3G46560	AT5G27395				
GO:0015934	1	AT3G06040					
GO:0015976	1	AT1G70410					
GO:0015996	1	AT5G43430					
GO:0016020	17	AT1G01910	AT1G06890	AT1G63450	AT1G75940	AT2G15390	AT3G01290
		AT3G56950	AT3G57630	AT3G58140	AT4G00100	AT4G00710	AT4G23640
		AT5G16660	AT5G23740	AT5G53340	AT5G54500	AT5G60730	
GO:0016021	5	AT2G17500	AT2G24170	AT3G09740	AT4G25570	AT4G28050	
GO:0016036	3	AT2G27190	AT3G52190	AT5G01220			
GO:0016051	2	AT2G38650	AT5G47780				
GO:0016208	1	AT1G20560					
GO:0016417	1	AT5G20350					
GO:0016485	1	AT3G52640					
GO:0016597	1	AT5G16290					
GO:0016655	1	AT5G54500					
GO:0016671	1	AT1G72280					
GO:0016706	3	AT3G28480	AT5G18900	AT5G66060			
GO:0016747	1	AT4G00040					
GO:0016757	9	AT1G73160	AT2G15390	AT2G38650	AT3G03050	AT5G01220	AT5G22740
		AT5G38460	AT5G47780	AT5G53340			
GO:0016758	1	AT5G53340					
GO:0016759	1	AT3G03050					
GO:0016779	1	AT1G74910					
GO:0016787	3	AT1G05620	AT3G09690	AT3G23600			
GO:0016844	1	AT3G51440					
GO:0016853	1	AT5G19370					
GO:0016887	3	AT1G50140	AT2G34560	AT5G16930			
GO:0017004	1	AT4G01660					
GO:0018401	3	AT3G28480	AT5G18900	AT5G66060			
GO:0019285	1	AT1G74920					
GO:0019303	1	AT1G17160					
GO:0019408	1	AT5G58784					
GO:0019538	1	AT2G34560					
GO:0019762	1	AT5G48180					
GO:0020037	1	AT3G48890					
GO:0022626	2	AT1G66580	AT4G29430				
GO:0022627	3	AT4G00100	AT4G29430	AT5G23740			
GO:0030163	1	AT1G04810					
GO:0030176	1	AT4G21180					
GO:0030234	1	AT4G16500					
GO:0030244	1	AT3G08550					
GO:0030246	1	AT5G49270					
GO:0030599	1	AT5G04960					
GO:0030742	1	AT3G11730					
GO:0032312	1	AT2G37550					
GO:0040014	1	AT5G58270					

Cluster 33 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)			
GO:0042350	1	AT1G17890			
GO:0042450	1	AT3G57560			
GO:0042545	1	AT5G04960			
GO:0042546	1	AT2G15390			
GO:0042626	1	AT5G58270			
GO:0042742	2	AT3G27890	AT3G63190		
GO:0045022	1	AT3G54840			
GO:0045454	1	AT3G15660			
GO:0045547	1	AT5G58784			
GO:0045597	1	AT4G32880			
GO:0045995	1	AT3G48110			
GO:0046506	1	AT5G01220			
GO:0046510	1	AT5G01220			
GO:0046686	4	AT1G70730	AT3G27300	AT4G11600	AT5G58270
GO:0046872	1	AT3G15660			
GO:0046900	1	AT1G78660			
GO:0046914	1	AT3G48890			
GO:0047262	2	AT2G38650	AT5G47780		
GO:0048507	1	AT5G22330			
GO:0048765	1	AT5G49270			
GO:0050269	1	AT3G24503			
GO:0050660	1	AT1G72280			
GO:0051753	1	AT5G22740			
GO:0055114	1	AT5G54500			

Cluster 34



Cluster 34

AT1G01950
AT1G03230
AT1G07410
AT1G10510
AT1G20300
AT1G24280
AT1G28440
AT1G29330
AT1G31950
AT1G49630
AT1G50940
AT1G67560
AT1G70190
AT1G71260
AT1G80480
AT2G23370
AT2G26240
AT2G43350
AT2G45440
AT3G07330
AT3G13110
AT3G13530
AT3G14790
AT3G18830
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AT3G47670
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AT3G53430
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AT3G54640
AT3G55760
AT3G57680
AT3G59360
AT4G00430
AT4G20890
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AT4G39460
AT5G02260
AT5G12950
AT5G15940
AT5G16230
AT5G16370
AT5G19750
AT5G40660
AT5G42390
AT5G45390
AT5G49030
AT5G49555
AT5G52520
AT5G54810
AT5G54830
AT5G63620

Cluster 34 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005739	mitochondrion	12	56	6.36E-07
GO:0009507	chloroplast	19	56	4.44E-06
GO:0009570	chloroplast stroma	7	56	3.90E-05
GO:0004812	aminoacyl-tRNA ligase activity	2	56	0.001696729
GO:0006418	tRNA aminoacylation for protein translation	2	56	0.002001514
GO:0048481	ovule development	2	56	0.002329645
GO:0050660	FAD binding	2	56	0.002329645
GO:0000095	S-adenosylmethionine transmembrane transporter activity	1	56	0.002685207
GO:0005046	KDEL sequence binding	1	56	0.002685207
GO:0005365	myo-inositol transmembrane transporter activity	1	56	0.002685207
GO:0006621	protein retention in ER lumen	1	56	0.002685207
GO:0010109	regulation of photosynthesis	1	56	0.002685207
GO:0015148	D-xylose transmembrane transporter activity	1	56	0.002685207
GO:0015575	mannitol transmembrane transporter activity	1	56	0.002685207
GO:0015576	sorbitol transmembrane transporter activity	1	56	0.002685207
GO:0015591	D-ribose transmembrane transporter activity	1	56	0.002685207
GO:0015805	S-adenosylmethionine transport	1	56	0.002685207
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1	56	0.002685207
GO:0009658	chloroplast organization	2	56	0.004084833
GO:0005794	Golgi apparatus	3	56	0.004550286
GO:0004571	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	1	56	0.005356251
GO:0008840	dihydrodipicolinate synthase activity	1	56	0.005356251
GO:0015168	glycerol transmembrane transporter activity	1	56	0.005356251
GO:0051605	protein maturation via proteolysis	1	56	0.005356251
GO:0004834	tryptophan synthase activity	1	56	0.008013186
GO:0005354	galactose transmembrane transporter activity	1	56	0.008013186
GO:0010280	UDP-L-rhamnose synthase activity	1	56	0.008013186
GO:0009001	serine O-acetyltransferase activity	1	56	0.010656066
GO:0010253	UDP-rhamnose biosynthetic process	1	56	0.010656066
GO:0015145	monosaccharide transmembrane transporter activity	1	56	0.010656066
GO:0005355	glucose transmembrane transporter activity	1	56	0.013284948
GO:0005625	soluble fraction	1	56	0.013284948
GO:0005801	cis-Golgi network	1	56	0.013284948
GO:0015780	nucleotide-sugar transport	1	56	0.013284948
GO:0042631	cellular response to water deprivation	1	56	0.013284948

Cluster 34 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045300	acyl-[acyl-carrier-protein] desaturase activity	1	56	0.013284948
GO:0009941	chloroplast envelope	4	56	0.014243383
GO:0004345	glucose-6-phosphate dehydrogenase activity	1	56	0.015899884
GO:0006006	glucose metabolic process	1	56	0.015899884
GO:0000139	Golgi membrane	1	56	0.01850093
GO:0005338	nucleotide-sugar transmembrane transporter activity	1	56	0.01850093
GO:0009840	chloroplastic endopeptidase Clp complex	1	56	0.01850093
GO:0016165	lipoxygenase activity	1	56	0.01850093
GO:0015031	protein transport	2	56	0.019526495
GO:0009051	pentose-phosphate shunt, oxidative branch	1	56	0.021088139
GO:0040007	growth	1	56	0.021088139
GO:0045298	tubulin complex	1	56	0.021088139
GO:0004602	glutathione peroxidase activity	1	56	0.023661566
GO:0009089	lysine biosynthetic process via diaminopimelate	1	56	0.023661566
GO:0019344	cysteine biosynthetic process	1	56	0.026221264
GO:0016117	carotenoid biosynthetic process	1	56	0.036323834
GO:0048510	regulation of timing of transition from vegetative to reproductive phase	1	56	0.036323834
GO:0003756	protein disulfide isomerase activity	1	56	0.038815687
GO:0048868	pollen tube development	1	56	0.038815687
GO:0005768	endosome	1	56	0.04129413
GO:0008266	poly(U) binding	1	56	0.04129413
GO:0009504	cell plate	1	56	0.04129413
GO:0009508	plastid chromosome	1	56	0.04129413
GO:0009532	plastid stroma	1	56	0.04129413
GO:0052544	callose deposition in cell wall during defense response	1	56	0.04129413
GO:0009536	plastid	2	56	0.042567057
GO:0006810	transport	3	56	0.043709033
GO:0005778	peroxisomal membrane	1	56	0.043759214
GO:0008152	metabolic process	4	56	0.045840933
GO:0006913	nucleocytoplasmic transport	1	56	0.046210993
GO:0009225	nucleotide-sugar metabolic process	1	56	0.046210993
GO:0000162	tryptophan biosynthetic process	1	56	0.048649518
GO:0004872	receptor activity	1	56	0.053487016
GO:0009831	plant-type cell wall modification during multidimensional cell growth	1	56	0.053487016
GO:0000287	magnesium ion binding	1	56	0.060645154
GO:0009295	nucleoid	1	56	0.063005243
GO:0048316	seed development	1	56	0.063005243
GO:0009579	thylakoid	2	56	0.065691827
GO:0009553	embryo sac development	1	56	0.067686789
GO:0015250	water channel activity	1	56	0.070008348
GO:0009828	plant-type cell wall loosening	1	56	0.074613291
GO:0006486	protein amino acid glycosylation	1	56	0.076896774
GO:0008236	serine-type peptidase activity	1	56	0.079167665
GO:0042542	response to hydrogen peroxide	1	56	0.079167665
GO:0016020	membrane	6	56	0.08175283
GO:0015934	large ribosomal subunit	1	56	0.083671869
GO:0016759	cellulose synthase activity	1	56	0.085905281
GO:0008643	carbohydrate transport	1	56	0.092531346
GO:0009738	abscisic acid mediated signaling	1	56	0.092531346
GO:0004497	monooxygenase activity	1	56	0.094715474
GO:0005198	structural molecule activity	1	56	0.099047179

Cluster 34 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016491	oxidoreductase activity	2	56	0.1004172
GO:0006839	mitochondrial transport	1	56	0.101194852
GO:0046910	pectinesterase inhibitor activity	1	56	0.101194852
GO:0005875	microtubule associated complex	1	56	0.105454083
GO:0006633	fatty acid biosynthetic process	1	56	0.111753351
GO:0016829	lyase activity	1	56	0.115893696
GO:0016021	integral to membrane	2	56	0.116052898
GO:0046686	response to cadmium ion	2	56	0.132670713
GO:0016758	transferase activity, transferring hexosyl groups	1	56	0.133950291
GO:0003735	structural constituent of ribosome	2	56	0.13630355
GO:0003777	microtubule motor activity	1	56	0.141679422
GO:0007264	small GTPase mediated signal transduction	1	56	0.141679422
GO:0007242	intracellular signaling cascade	1	56	0.143583771
GO:0005524	ATP binding	3	56	0.148883531
GO:0048364	root development	1	56	0.152940135
GO:0009543	chloroplast thylakoid lumen	1	56	0.154778642
GO:0009055	electron carrier activity	1	56	0.163809751
GO:0005743	mitochondrial inner membrane	1	56	0.16558399
GO:0006508	proteolysis	2	56	0.167029409
GO:0015144	carbohydrate transmembrane transporter activity	1	56	0.16734767
GO:0005351	sugar:hydrogen symporter activity	1	56	0.170843518
GO:0009826	unidimensional cell growth	1	56	0.172575771
GO:0042254	ribosome biogenesis	1	56	0.195755272
GO:0022625	cytosolic large ribosomal subunit	1	56	0.206616656
GO:0006886	intracellular protein transport	1	56	0.229709188
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1	56	0.245520229
GO:0042742	defense response to bacterium	1	56	0.252963328
GO:0009414	response to water deprivation	1	56	0.255377746
GO:0005509	calcium ion binding	1	56	0.281866316
GO:0004674	protein serine/threonine kinase activity	1	56	0.295316033
GO:0005525	GTP binding	1	56	0.296223361
GO:0005840	ribosome	1	56	0.304080008
GO:0007165	signal transduction	1	56	0.33621264
GO:0009535	chloroplast thylakoid membrane	1	56	0.345505753
GO:0005783	endoplasmic reticulum	1	56	0.352785108
GO:0009793	embryonic development ending in seed dormancy	1	56	0.357767164
GO:0003723	RNA binding	1	56	0.362420375
GO:0006412	translation	1	56	0.362676122
GO:0016757	transferase activity, transferring glycosyl groups	1	56	0.362927861
GO:0006952	defense response	1	56	0.368568639
GO:0003824	catalytic activity	1	56	0.37169306

Cluster 34 GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000095	1	AT4G39460	
GO:0000139	1	AT3G59360	
GO:0000162	1	AT3G54640	
GO:0000287	1	AT1G31950	
GO:0003723	1	AT3G53460	
GO:0003735	2	AT1G70190	AT3G53430
GO:0003756	1	AT4G27080	
GO:0003777	1	AT1G01950	
GO:0003824	1	AT3G14790	

Cluster 34 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004345	1	AT1G24280					
GO:0004497	1	AT5G54830					
GO:0004571	1	AT3G21160					
GO:0004602	1	AT2G43350					
GO:0004674	1	AT1G28440					
GO:0004812	2	AT5G49030	AT5G52520				
GO:0004834	1	AT3G54640					
GO:0004872	1	AT1G29330					
GO:0005046	1	AT1G29330					
GO:0005198	1	AT4G20890					
GO:0005338	1	AT3G59360					
GO:0005351	1	AT3G18830					
GO:0005354	1	AT3G18830					
GO:0005355	1	AT3G18830					
GO:0005365	1	AT3G18830					
GO:0005509	1	AT3G21160					
GO:0005524	3	AT1G28440	AT5G49030	AT5G52520			
GO:0005525	1	AT1G07410					
GO:0005625	1	AT3G14790					
GO:0005739	12	AT1G10510	AT1G49630	AT1G50940	AT1G70190	AT1G71260	AT2G26240
		AT2G43350	AT3G13110	AT4G39460	AT5G42390	AT5G49555	AT5G52520
GO:0005743	1	AT4G39460					
GO:0005768	1	AT1G07410					
GO:0005778	1	AT5G19750					
GO:0005783	1	AT1G29330					
GO:0005794	3	AT1G29330	AT3G07330	AT3G21160			
GO:0005801	1	AT1G29330					
GO:0005840	1	AT3G53430					
GO:0005875	1	AT1G01950					
GO:0006006	1	AT1G24280					
GO:0006412	1	AT1G70190					
GO:0006418	2	AT5G49030	AT5G52520				
GO:0006486	1	AT4G32120					
GO:0006508	2	AT1G49630	AT5G42390				
GO:0006621	1	AT1G29330					
GO:0006633	1	AT5G16230					
GO:0006810	3	AT3G18830	AT4G00430	AT4G39460			
GO:0006839	1	AT4G39460					
GO:0006886	1	AT1G07410					
GO:0006913	1	AT1G07410					
GO:0006952	1	AT1G71260					
GO:0007165	1	AT1G07410					
GO:0007169	1	AT1G28440					
GO:0007242	1	AT3G57680					
GO:0007264	1	AT1G07410					
GO:0008152	4	AT1G31950	AT5G15940	AT5G54830	AT5G63620		
GO:0008236	1	AT3G57680					
GO:0008266	1	AT3G53460					
GO:0008643	1	AT3G18830					
GO:0008840	1	AT2G45440					
GO:0009001	1	AT3G13110					
GO:0009051	1	AT1G24280					
GO:0009055	1	AT1G50940					
GO:0009089	1	AT2G45440					
GO:0009225	1	AT3G14790					
GO:0009295	1	AT1G80480					
GO:0009414	1	AT4G00430					
GO:0009504	1	AT1G07410					

Cluster 34 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0009507	19	AT1G01950	AT1G10510	AT1G24280	AT1G49630	AT1G67560	AT1G80480
		AT2G45440	AT3G53460	AT3G54640	AT3G55760	AT4G20890	AT4G39460
		AT5G02260	AT5G16230	AT5G19750	AT5G42390	AT5G45390	AT5G49030
		AT5G52520					
GO:0009508	1	AT1G80480					
GO:0009532	1	AT5G45390					
GO:0009535	1	AT5G45390					
GO:0009536	2	AT1G10510	AT4G39460				
GO:0009543	1	AT3G57680					
GO:0009553	1	AT5G52520					
GO:0009570	7	AT1G80480	AT3G53460	AT3G54640	AT3G55760	AT5G42390	AT5G45390
		AT5G52520					
GO:0009579	2	AT3G53460	AT5G45390				
GO:0009658	2	AT4G39460	AT5G45390				
GO:0009738	1	AT2G43350					
GO:0009793	1	AT1G10510					
GO:0009826	1	AT5G02260					
GO:0009828	1	AT5G02260					
GO:0009831	1	AT5G02260					
GO:0009840	1	AT5G45390					
GO:0009941	4	AT1G10510	AT4G39460	AT5G19750	AT5G45390		
GO:0010109	1	AT5G52520					
GO:0010253	1	AT3G14790					
GO:0010280	1	AT3G14790					
GO:0015031	2	AT1G07410	AT1G29330				
GO:0015144	1	AT3G18830					
GO:0015145	1	AT3G18830					
GO:0015148	1	AT3G18830					
GO:0015168	1	AT3G18830					
GO:0015250	1	AT4G00430					
GO:0015575	1	AT3G18830					
GO:0015576	1	AT3G18830					
GO:0015591	1	AT3G18830					
GO:0015780	1	AT3G59360					
GO:0015805	1	AT4G39460					
GO:0015934	1	AT1G70190					
GO:0016020	6	AT1G31950	AT3G18830	AT3G53430	AT3G57680	AT4G00430	AT4G32120
GO:0016021	2	AT1G29330	AT3G59360				
GO:0016117	1	AT5G49555					
GO:0016165	1	AT1G67560					
GO:0016491	2	AT5G15940	AT5G49555				
GO:0016705	1	AT5G49555					
GO:0016757	1	AT3G07330					
GO:0016758	1	AT4G32120					
GO:0016759	1	AT3G07330					
GO:0016829	1	AT1G31950					
GO:0019344	1	AT3G13110					
GO:0022625	1	AT3G53430					
GO:0040007	1	AT1G67560					
GO:0042254	1	AT3G53430					
GO:0042542	1	AT2G43350					
GO:0042631	1	AT2G43350					
GO:0042742	1	AT3G54640					
GO:0045298	1	AT4G20890					
GO:0045300	1	AT5G16230					
GO:0046686	2	AT3G13110	AT4G20890				
GO:0046910	1	AT3G47670					
GO:0048316	1	AT5G52520					
GO:0048364	1	AT1G01950					
GO:0048481	2	AT5G49030	AT5G52520				

Cluster 34 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0048510	1	AT5G45390	
GO:0048868	1	AT3G07330	
GO:0050660	2	AT1G50940	AT5G49555
GO:0051605	1	AT1G49630	
GO:0052544	1	AT3G54640	

Cluster 35

Cluster 35
AT1G57620
AT2G43610
AT3G19430
AT3G60900
AT4G01690
AT4G18800
AT5G17190
AT5G23140
AT5G26570
AT5G57500
AT5G59290

Cluster 35 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0051752	phosphoglucan, water dikinase activity	1	11	5.27E-04
GO:0004729	protoporphyrinogen oxidase activity	1	11	0.001054397
GO:0019200	carbohydrate kinase activity	1	11	0.001580837
GO:0042732	D-xylose metabolic process	1	11	0.001580837
GO:0048040	UDP-glucuronate decarboxylase activity	1	11	0.001580837
GO:0008320	protein transmembrane transporter activity	1	11	0.003157127
GO:0009840	chloroplastic endopeptidase Clp complex	1	11	0.003681549
GO:0005982	starch metabolic process	1	11	0.004205466
GO:0005983	starch catabolic process	1	11	0.006817506
GO:0004568	chitinase activity	1	11	0.007338407
GO:0006779	porphyrin biosynthetic process	1	11	0.007338407
GO:0009532	plastid stroma	1	11	0.008378704
GO:0009225	nucleotide-sugar metabolic process	1	11	0.009416998
GO:0046777	protein amino acid autophosphorylation	1	11	0.009935394
GO:0016998	cell wall catabolic process	1	11	0.010970686
GO:0009570	chloroplast stroma	2	11	0.013557722
GO:0003824	catalytic activity	2	11	0.014709048

Cluster 35 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005759	mitochondrial matrix	1	11	0.015091909
GO:0006486	protein amino acid glycosylation	1	11	0.016117241
GO:0005199	structural constituent of cell wall	1	11	0.019690292
GO:0046658	anchored to plasma membrane	1	11	0.030762855
GO:0007264	small GTPase mediated signal transduction	1	11	0.031757717
GO:0015031	protein transport	1	11	0.042086841
GO:0005886	plasma membrane	3	11	0.04336576
GO:0006886	intracellular protein transport	1	11	0.057892154
GO:0009536	plastid	1	11	0.0644424
GO:0005829	cytosol	1	11	0.083549685
GO:0005525	GTP binding	1	11	0.084883701
GO:0031225	anchored to membrane	1	11	0.098001779
GO:0009535	chloroplast thylakoid membrane	1	11	0.11611196
GO:0016020	membrane	2	11	0.124265462
GO:0016757	transferase activity, transferring glycosyl groups	1	11	0.135781427
GO:0005975	carbohydrate metabolic process	1	11	0.136172333
GO:0009941	chloroplast envelope	1	11	0.163242531
GO:0012505	endomembrane system	2	11	0.233849117
GO:0009507	chloroplast	2	11	0.237219757
GO:0006355	regulation of transcription, DNA-dependent	1	11	0.264722213
GO:0005739	mitochondrion	1	11	0.278685183

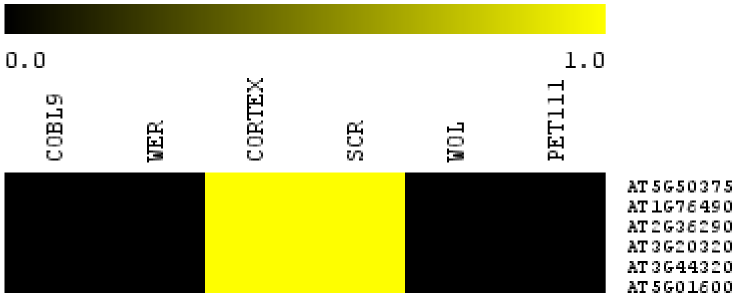
Cluster 35

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0003824	2	AT5G26570	AT5G59290	
GO:0004568	1	AT2G43610		
GO:0004729	1	AT4G01690		
GO:0005199	1	AT3G19430		
GO:0005525	1	AT4G18800		
GO:0005739	1	AT5G23140		
GO:0005759	1	AT5G23140		
GO:0005829	1	AT5G59290		
GO:0005886	3	AT2G43610	AT3G60900	AT4G18800
GO:0005975	1	AT5G26570		
GO:0005982	1	AT5G26570		
GO:0005983	1	AT5G26570		
GO:0006355	1	AT4G18800		
GO:0006486	1	AT5G57500		
GO:0006779	1	AT4G01690		
GO:0006886	1	AT1G57620		
GO:0007264	1	AT4G18800		
GO:0008320	1	AT1G57620		
GO:0009225	1	AT5G59290		
GO:0009507	2	AT4G01690	AT5G26570	
GO:0009532	1	AT5G23140		
GO:0009535	1	AT5G23140		
GO:0009536	1	AT5G26570		
GO:0009570	2	AT5G23140	AT5G26570	
GO:0009840	1	AT5G23140		
GO:0009941	1	AT4G01690		
GO:0012505	2	AT5G17190	AT5G57500	
GO:0015031	1	AT4G18800		
GO:0016020	2	AT1G57620	AT5G57500	
GO:0016757	1	AT5G57500		
GO:0016998	1	AT2G43610		

Cluster 35 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0019200	1	AT5G26570
GO:0031225	1	AT3G60900
GO:0042732	1	AT5G59290
GO:0046658	1	AT3G60900
GO:0046777	1	AT5G26570
GO:0048040	1	AT5G59290
GO:0051752	1	AT5G26570

Cluster 36



Cluster 36

AT1G76490
AT2G36290
AT3G20320
AT3G44320
AT5G01600
AT5G50375

Cluster 36 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016126	sterol biosynthetic process	2	6	1.59E-05
GO:0005783	endoplasmic reticulum	3	6	3.91E-05
GO:0006907	pinocytosis	1	6	2.88E-04
GO:0047793	cycloeucalenol cycloisomerase activity	1	6	2.88E-04
GO:0042282	hydroxymethylglutaryl-CoA reductase activity	1	6	5.75E-04
GO:0000257	nitrilase activity	1	6	8.63E-04
GO:0005543	phospholipid binding	1	6	8.63E-04
GO:0055072	iron ion homeostasis	1	6	8.63E-04
GO:0008199	ferric iron binding	1	6	0.001149976
GO:0019762	glucosinolate catabolic process	1	6	0.001437125
GO:0005319	lipid transporter activity	1	6	0.001724136
GO:0009970	cellular response to sulfate starvation	1	6	0.00201101
GO:0000302	response to reactive oxygen species	1	6	0.002584344
GO:0006826	iron ion transport	1	6	0.002584344
GO:0006879	cellular iron ion homeostasis	1	6	0.002584344
GO:0010039	response to iron ion	1	6	0.002584344
GO:0009958	positive gravitropism	1	6	0.003443313
GO:0016020	membrane	3	6	0.004294585
GO:0008299	isoprenoid biosynthetic process	1	6	0.005442762
GO:0000910	cytokinesis	1	6	0.006012798
GO:0005506	iron ion binding	1	6	0.007435487
GO:0009706	chloroplast inner membrane	1	6	0.008854752
GO:0042542	response to hydrogen peroxide	1	6	0.009138194
GO:0015979	photosynthesis	1	6	0.011683028
GO:0009617	response to bacterium	1	6	0.015339405

GO:0009908	flower development	1	6	0.020364192
GO:0048366	leaf development	1	6	0.021197393
GO:0016787	hydrolase activity	1	6	0.041367573
GO:0009579	thylakoid	1	6	0.046959023
GO:0009409	response to cold	1	6	0.051705575
GO:0009535	chloroplast thylakoid membrane	1	6	0.067222901
GO:0046686	response to cadmium ion	1	6	0.074807732
GO:0009570	chloroplast stroma	1	6	0.093512381
GO:0009941	chloroplast envelope	1	6	0.097358085
GO:0009507	chloroplast	2	6	0.117237127

Cluster 36

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0000257	1	AT3G44320		
GO:0000302	1	AT5G01600		
GO:0000910	1	AT5G50375		
GO:0005319	1	AT3G20320		
GO:0005506	1	AT5G01600		
GO:0005543	1	AT3G20320		
GO:0005783	3	AT1G76490	AT2G36290	AT5G50375
GO:0006826	1	AT5G01600		
GO:0006879	1	AT5G01600		
GO:0006907	1	AT5G50375		
GO:0008199	1	AT5G01600		
GO:0008299	1	AT1G76490		
GO:0009409	1	AT5G01600		
GO:0009507	2	AT3G20320	AT5G01600	
GO:0009535	1	AT5G01600		
GO:0009570	1	AT5G01600		
GO:0009579	1	AT5G01600		
GO:0009617	1	AT5G01600		
GO:0009706	1	AT3G20320		
GO:0009908	1	AT5G01600		
GO:0009941	1	AT3G20320		
GO:0009958	1	AT5G50375		
GO:0009970	1	AT3G44320		
GO:0010039	1	AT5G01600		
GO:0015979	1	AT5G01600		
GO:0016020	3	AT1G76490	AT3G20320	AT5G01600
GO:0016126	2	AT1G76490	AT5G50375	
GO:0016787	1	AT2G36290		
GO:0019762	1	AT3G44320		
GO:0042282	1	AT1G76490		
GO:0042542	1	AT5G01600		
GO:0046686	1	AT3G44320		
GO:0047793	1	AT5G50375		
GO:0048366	1	AT5G01600		
GO:0055072	1	AT5G01600		

Cluster 37

Cluster 37
AT1G27770
AT1G56330
AT2G24180
AT4G29680
AT5G41600
AT5G57655

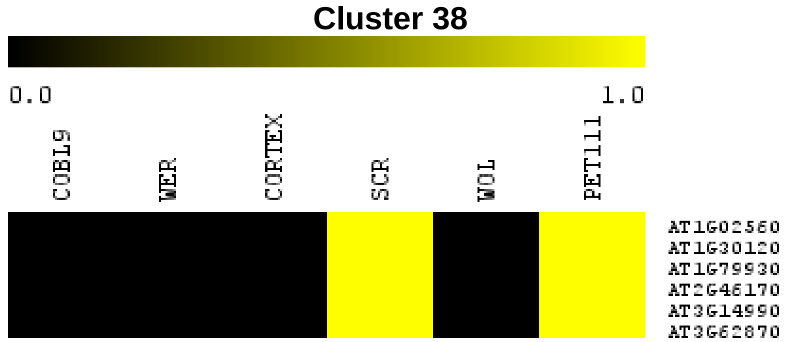
Cluster 37 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005783	endoplasmic reticulum	5	6	1.89E-09
GO:0005886	plasma membrane	5	6	1.80E-05
GO:0009045	xylose isomerase activity	1	6	2.88E-04
GO:0048221	rough ER to cis-Golgi vesicle-mediated transport	1	6	2.88E-04
GO:0000300	peripheral to membrane of membrane fraction	1	6	5.75E-04
GO:0005262	calcium channel activity	1	6	8.63E-04
GO:0005388	calcium-transporting ATPase activity	1	6	0.003729361
GO:0006816	calcium ion transport	1	6	0.004015271
GO:0009117	nucleotide metabolic process	1	6	0.004015271
GO:0005773	vacuole	2	6	0.006199877
GO:0015992	proton transport	1	6	0.007435487
GO:0009706	chloroplast inner membrane	1	6	0.008854752
GO:0006812	cation transport	1	6	0.01869414
GO:0016787	hydrolase activity	1	6	0.041367573
GO:0005516	calmodulin binding	1	6	0.041635151
GO:0005829	cytosol	1	6	0.047488516
GO:0005525	GTP binding	1	6	0.04828177
GO:0019825	oxygen binding	1	6	0.052754607
GO:0005975	carbohydrate metabolic process	1	6	0.079800598
GO:0006810	transport	1	6	0.084988653
GO:0008152	metabolic process	1	6	0.140210956
GO:0005739	mitochondrion	1	6	0.183391785
GO:0016020	membrane	1	6	0.275969005

Cluster 37

GO Identifier	#Loci	Associated Loci (Left to Right)				
GO:0000300	1	AT1G56330				
GO:0005262	1	AT1G27770				
GO:0005388	1	AT1G27770				
GO:0005516	1	AT1G27770				
GO:0005525	1	AT1G56330				
GO:0005739	1	AT2G24180				
GO:0005773	2	AT4G29680	AT5G57655			
GO:0005783	5	AT1G27770	AT1G56330	AT2G24180	AT5G41600	AT5G57655
GO:0005829	1	AT1G56330				
GO:0005886	5	AT1G27770	AT1G56330	AT2G24180	AT5G41600	AT5G57655
GO:0005975	1	AT5G57655				
GO:0006810	1	AT1G27770				
GO:0006812	1	AT1G27770				
GO:0006816	1	AT1G27770				
GO:0008152	1	AT1G27770				
GO:0009045	1	AT5G57655				
GO:0009117	1	AT4G29680				
GO:0009706	1	AT1G27770				
GO:0015992	1	AT1G27770				
GO:0016020	1	AT2G24180				

Cluster 37 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0016787	1	AT4G29680
GO:0019825	1	AT2G24180
GO:0048221	1	AT1G56330



Cluster 38
AT1G02560
AT1G30120
AT1G79930
AT2G46170
AT3G14990
AT3G62870

Cluster 38 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010240	plastid pyruvate dehydrogenase complex	1	6	2.88E-04
GO:0009228	thiamin biosynthetic process	1	6	0.001437125
GO:0004739	pyruvate dehydrogenase (acetyl-transferring) activity	1	6	0.001724136
GO:0009840	chloroplastic endopeptidase Clp complex	1	6	0.00201101
GO:0009534	chloroplast thylakoid	1	6	0.003443313
GO:0018119	peptidyl-cysteine S-nitrosylation	1	6	0.004015271
GO:0009941	chloroplast envelope	2	6	0.004385178
GO:0009532	plastid stroma	1	6	0.00458668
GO:0005886	plasma membrane	3	6	0.007971767
GO:0006633	fatty acid biosynthetic process	1	6	0.013373445
GO:0022625	cytosolic large ribosomal subunit	1	6	0.028093568
GO:0022626	cytosolic ribosome	1	6	0.0461638
GO:0009579	thylakoid	1	6	0.046959023
GO:0005783	endoplasmic reticulum	1	6	0.071535093
GO:0046686	response to cadmium ion	1	6	0.074807732
GO:0003735	structural constituent of ribosome	1	6	0.076310923
GO:0006412	translation	1	6	0.079303593
GO:0009570	chloroplast stroma	1	6	0.093512381
GO:0003824	catalytic activity	1	6	0.097358085
GO:0005773	vacuole	1	6	0.114504149
GO:0009507	chloroplast	2	6	0.117237127
GO:0016020	membrane	1	6	0.275969005

Cluster 38

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0003735	1	AT3G62870
GO:0003824	1	AT3G14990
GO:0004739	1	AT1G30120
GO:0005773	1	AT3G14990

Cluster 38 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0005783	1	AT2G46170		
GO:0005886	3	AT2G46170	AT3G14990	AT3G62870
GO:0006412	1	AT3G62870		
GO:0006633	1	AT1G30120		
GO:0009228	1	AT3G14990		
GO:0009507	2	AT1G02560	AT1G30120	
GO:0009532	1	AT1G02560		
GO:0009534	1	AT1G02560		
GO:0009570	1	AT1G02560		
GO:0009579	1	AT1G02560		
GO:0009840	1	AT1G02560		
GO:0009941	2	AT1G02560	AT1G30120	
GO:0010240	1	AT1G30120		
GO:0016020	1	AT3G62870		
GO:0018119	1	AT1G02560		
GO:0022625	1	AT3G62870		
GO:0022626	1	AT3G62870		
GO:0046686	1	AT3G14990		

Cluster 39

Cluster 39
AT3G22890
AT3G57010
AT3G63410
AT5G57490

Cluster 39 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0051741	2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity	1	4	1.92E-04
GO:0004781	sulfate adenylyltransferase (ATP) activity	1	4	7.67E-04
GO:0010236	plastoquinone biosynthetic process	1	4	7.67E-04
GO:0010189	vitamin E biosynthetic process	1	4	0.001341445
GO:0008308	voltage-gated anion channel activity	1	4	0.00153286
GO:0009821	alkaloid biosynthetic process	1	4	0.002297966
GO:0016844	strictosidine synthase activity	1	4	0.002680189
GO:0005741	mitochondrial outer membrane	1	4	0.003253109
GO:0006820	anion transport	1	4	0.003253109
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	1	4	0.003825535
GO:0009706	chloroplast inner membrane	1	4	0.005920192
GO:0008168	methyltransferase activity	1	4	0.008765829
GO:0009617	response to bacterium	1	4	0.010278457
GO:0005886	plasma membrane	2	4	0.032511279
GO:0005783	endoplasmic reticulum	1	4	0.048921054
GO:0046686	response to cadmium ion	1	4	0.051223803

Cluster 39 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009507	chloroplast	2	4	0.059481381
GO:0009570	chloroplast stroma	1	4	0.064507322
GO:0009941	chloroplast envelope	1	4	0.067265162
GO:0005739	mitochondrion	1	4	0.131791079
GO:0016020	membrane	1	4	0.209989764

Cluster 39

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0004781	1	AT3G22890	
GO:0005739	1	AT5G57490	
GO:0005741	1	AT5G57490	
GO:0005783	1	AT3G57010	
GO:0005886	2	AT3G22890	AT5G57490
GO:0006820	1	AT5G57490	
GO:0008168	1	AT3G63410	
GO:0008308	1	AT5G57490	
GO:0008757	1	AT3G63410	
GO:0009507	2	AT3G22890	AT3G63410
GO:0009570	1	AT3G22890	
GO:0009617	1	AT5G57490	
GO:0009706	1	AT3G63410	
GO:0009821	1	AT3G57010	
GO:0009941	1	AT3G63410	
GO:0010189	1	AT3G63410	
GO:0010236	1	AT3G63410	
GO:0016020	1	AT5G57490	
GO:0016844	1	AT3G57010	
GO:0046686	1	AT3G22890	
GO:0051741	1	AT3G63410	

Cluster 40

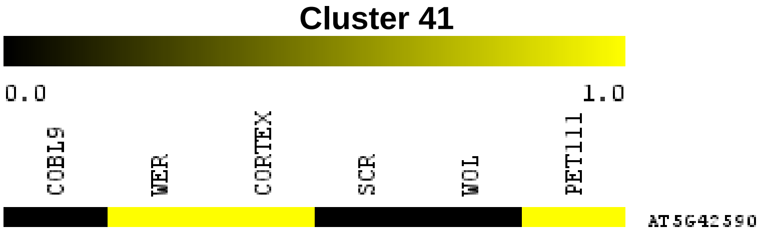
Cluster 40
AT1G19580
AT3G61430
AT5G59870

Cluster 40 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0006833	water transport	1	3	5.75E-04
GO:0004089	carbonate dehydratase activity	1	3	0.00215486
GO:0031966	mitochondrial membrane	1	3	0.002728441
GO:0005739	mitochondrion	2	3	0.003924047

Cluster 40 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0015250	water channel activity	1	3	0.004017388
GO:0009853	photorespiration	1	3	0.004160466
GO:0045271	respiratory chain complex I	1	3	0.005304104
GO:0006334	nucleosome assembly	1	3	0.007158759
GO:0009414	response to water deprivation	1	3	0.019311174
GO:0005730	nucleolus	1	3	0.033462623
GO:0009651	response to salt stress	1	3	0.040432401
GO:0006810	transport	1	3	0.044499424
GO:0009941	chloroplast envelope	1	3	0.051357705
GO:0005773	vacuole	1	3	0.061052959
GO:0003677	DNA binding	1	3	0.140273055
GO:0016020	membrane	1	3	0.168256477
GO:0005886	plasma membrane	1	3	0.203214985

Cluster 40

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0003677	1	AT5G59870	
GO:0004089	1	AT1G19580	
GO:0005730	1	AT5G59870	
GO:0005739	2	AT1G19580	AT3G61430
GO:0005773	1	AT3G61430	
GO:0005886	1	AT3G61430	
GO:0006334	1	AT5G59870	
GO:0006810	1	AT3G61430	
GO:0006833	1	AT3G61430	
GO:0009414	1	AT3G61430	
GO:0009651	1	AT3G61430	
GO:0009853	1	AT1G19580	
GO:0009941	1	AT3G61430	
GO:0015250	1	AT3G61430	
GO:0016020	1	AT3G61430	
GO:0031966	1	AT1G19580	
GO:0045271	1	AT1G19580	



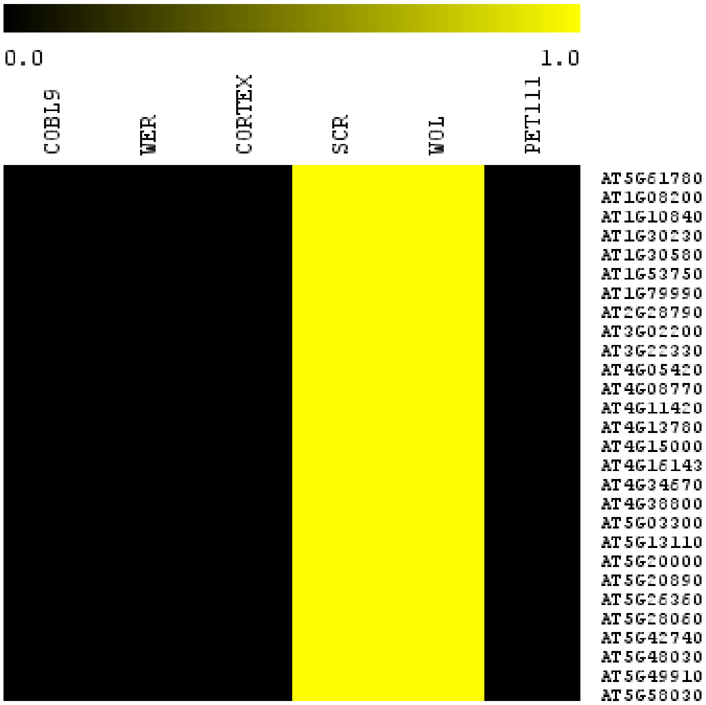
Cluster 41
AT5G42590

Cluster 41 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0019825	oxygen binding	1	1	0.009206425
GO:0009507	chloroplast	1	1	0.112155358

Cluster 41

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0009507	1	AT5G42590
GO:0019825	1	AT5G42590

Cluster 42



Cluster 42

AT1G08200
AT1G10840
AT1G30230
AT1G30580
AT1G53750
AT1G79990
AT2G28790
AT3G02200
AT3G22330
AT4G05420
AT4G08770
AT4G11420
AT4G13780
AT4G15000
AT4G16143
AT4G34670
AT4G38800
AT5G03300
AT5G13110
AT5G20000
AT5G20890
AT5G26360
AT5G28060
AT5G42740
AT5G48030
AT5G49910
AT5G58030
AT5G61780

Cluster 42 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0051082	unfolded protein binding	4	28	9.12E-06
GO:0046686	response to cadmium ion	5	28	2.95E-05
GO:0005852	eukaryotic translation initiation factor 3 complex	2	28	6.20E-05
GO:0044267	cellular protein metabolic process	2	28	9.45E-05
GO:0006457	protein folding	4	28	1.44E-04
GO:0000740	nuclear membrane fusion	1	28	0.001342604
GO:0004825	methionine-tRNA ligase activity	1	28	0.001342604
GO:0006431	methionyl-tRNA aminoacylation	1	28	0.001342604
GO:0010198	synergid death	1	28	0.001342604
GO:0016442	RNA-induced silencing complex	1	28	0.001342604
GO:0022626	cytosolic ribosome	3	28	0.00135614
GO:0006413	translational initiation	2	28	0.002415995
GO:0004001	adenosine kinase activity	1	28	0.002681731
GO:0004347	glucose-6-phosphate isomerase activity	1	28	0.002681731
GO:0006169	adenosine salvage	1	28	0.002681731
GO:0008930	methylthioadenosine nucleosidase activity	1	28	0.002681731
GO:0051085	chaperone mediated protein folding requiring cofactor	1	28	0.002681731
GO:0003743	translation initiation factor activity	2	28	0.003855989
GO:0008565	protein transporter activity	2	28	0.003962794
GO:0009558	cellularization of the embryo sac	1	28	0.004017388
GO:0022627	cytosolic small ribosomal subunit	2	28	0.004982744
GO:0003735	structural constituent of ribosome	3	28	0.005830912
GO:0006412	translation	3	28	0.006508853
GO:0005618	cell wall	3	28	0.006924046
GO:0004345	glucose-6-phosphate dehydrogenase activity	1	28	0.008003603
GO:0006006	glucose metabolic process	1	28	0.008003603
GO:0009116	nucleoside metabolic process	1	28	0.008003603
GO:0030126	COPI vesicle coat	1	28	0.008003603
GO:0006886	intracellular protein transport	2	28	0.010053373
GO:0006606	protein import into nucleus	1	28	0.010643849
GO:0009051	pentose-phosphate shunt, oxidative branch	1	28	0.010643849
GO:0006094	gluconeogenesis	1	28	0.011958821
GO:0010100	negative regulation of photomorphogenesis	1	28	0.011958821
GO:0010197	polar nucleus fusion	1	28	0.014578498
GO:0009532	plastid stroma	1	28	0.021068092
GO:0005840	ribosome	2	28	0.023297968
GO:0006888	ER to Golgi vesicle-mediated transport	1	28	0.023640224
GO:0004518	nuclease activity	1	28	0.030011734
GO:0006461	protein complex assembly	1	28	0.030011734
GO:0009553	embryo sac development	1	28	0.035048857
GO:0016481	negative regulation of transcription	1	28	0.035048857
GO:0005730	nucleolus	2	28	0.03646029
GO:0005524	ATP binding	3	28	0.041147205
GO:0005198	structural molecule activity	1	28	0.052264226
GO:0005515	protein binding	4	28	0.05407758
GO:0006096	glycolysis	1	28	0.05467158
GO:0051707	response to other organism	1	28	0.061816742
GO:0046658	anchored to plasma membrane	1	28	0.074620186
GO:0005622	intracellular	2	28	0.080578756
GO:0004601	peroxidase activity	1	28	0.081444753
GO:0016192	vesicle-mediated transport	1	28	0.092573656
GO:0042254	ribosome biogenesis	1	28	0.11080349
GO:0009408	response to heat	1	28	0.111849281

Cluster 42 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005886	plasma membrane	4	28	0.113462681
GO:0022625	cytosolic large ribosomal subunit	1	28	0.118063021
GO:0005507	copper ion binding	1	28	0.124173042
GO:0031072	heat shock protein binding	1	28	0.125181379
GO:0009579	thylakoid	1	28	0.183199042
GO:0005829	cytosol	1	28	0.184870745
GO:0005525	GTP binding	1	28	0.187359531
GO:0006979	response to oxidative stress	1	28	0.201043305
GO:0009505	plant-type cell wall	1	28	0.234647235
GO:0048046	apoplast	1	28	0.236672648
GO:0016020	membrane	2	28	0.277561831
GO:0003676	nucleic acid binding	1	28	0.290769747
GO:0009570	chloroplast stroma	1	28	0.299666635
GO:0003824	catalytic activity	1	28	0.30667329
GO:0009941	chloroplast envelope	1	28	0.30667329
GO:0005773	vacuole	1	28	0.333418954

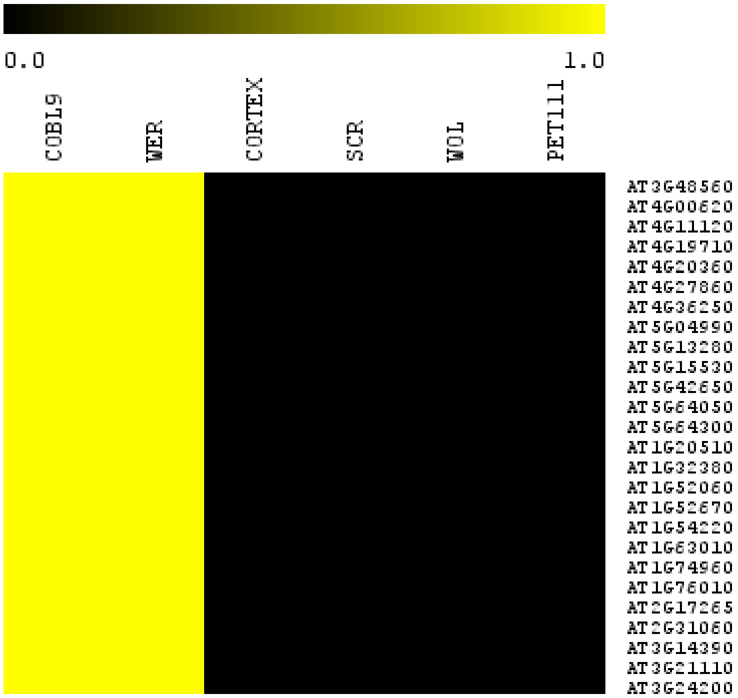
Cluster 42

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**			
GO:0000740	1	AT5G48030			
GO:0003676	1	AT5G61780			
GO:0003735	3	AT4G15000	AT4G34670	AT5G28060	
GO:0003743	2	AT1G10840	AT4G11420		
GO:0003824	1	AT4G38800			
GO:0004001	1	AT5G03300			
GO:0004345	1	AT5G13110			
GO:0004347	1	AT5G42740			
GO:0004518	1	AT5G61780			
GO:0004601	1	AT4G08770			
GO:0004825	1	AT4G13780			
GO:0005198	1	AT1G79990			
GO:0005507	1	AT5G03300			
GO:0005515	4	AT1G79990	AT4G05420	AT5G20890	AT5G26360
GO:0005524	3	AT5G20890	AT5G26360	AT5G49910	
GO:0005525	1	AT1G30580			
GO:0005618	3	AT4G34670	AT5G20890	AT5G28060	
GO:0005622	2	AT1G30580	AT4G15000		
GO:0005730	2	AT4G16143	AT4G34670		
GO:0005773	1	AT4G08770			
GO:0005829	1	AT4G13780			
GO:0005840	2	AT4G15000	AT5G28060		
GO:0005852	2	AT1G10840	AT4G11420		
GO:0005886	4	AT4G11420	AT4G34670	AT4G38800	AT5G03300
GO:0006006	1	AT5G13110			
GO:0006094	1	AT5G42740			
GO:0006096	1	AT5G42740			
GO:0006169	1	AT5G03300			
GO:0006412	3	AT4G15000	AT4G34670	AT5G28060	
GO:0006413	2	AT1G10840	AT4G11420		
GO:0006431	1	AT4G13780			
GO:0006457	4	AT5G20890	AT5G26360	AT5G48030	AT5G49910
GO:0006461	1	AT1G79990			
GO:0006606	1	AT4G16143			
GO:0006886	2	AT1G79990	AT4G16143		
GO:0006888	1	AT5G58030			

Cluster 42 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)				
GO:0006979	1	AT4G08770				
GO:0008565	2	AT1G79990	AT4G16143			
GO:0008930	1	AT4G38800				
GO:0009051	1	AT5G13110				
GO:0009116	1	AT4G38800				
GO:0009408	1	AT5G49910				
GO:0009505	1	AT2G28790				
GO:0009532	1	AT5G49910				
GO:0009553	1	AT5G48030				
GO:0009558	1	AT5G48030				
GO:0009570	1	AT5G49910				
GO:0009579	1	AT5G49910				
GO:0009941	1	AT5G49910				
GO:0010100	1	AT4G05420				
GO:0010197	1	AT5G48030				
GO:0010198	1	AT5G48030				
GO:0016020	2	AT4G34670	AT5G28060			
GO:0016192	1	AT1G79990				
GO:0016442	1	AT5G61780				
GO:0016481	1	AT4G05420				
GO:0022625	1	AT4G15000				
GO:0022626	3	AT4G15000	AT4G34670	AT5G28060		
GO:0022627	2	AT4G34670	AT5G28060			
GO:0030126	1	AT1G79990				
GO:0031072	1	AT5G48030				
GO:0042254	1	AT5G28060				
GO:0044267	2	AT5G20890	AT5G26360			
GO:0046658	1	AT5G20890				
GO:0046686	5	AT1G30580	AT4G13780	AT5G42740	AT5G49910	AT5G61780
GO:0048046	1	AT5G49910				
GO:0051082	4	AT5G20890	AT5G26360	AT5G48030	AT5G49910	
GO:0051085	1	AT5G48030				
GO:0051707	1	AT2G28790				

Cluster 43



Cluster 43

AT1G20510
AT1G32380
AT1G52060
AT1G52670
AT1G54220
AT1G63010
AT1G74960
AT1G76010
AT2G17265
AT2G31060
AT3G14390
AT3G21110
AT3G24200
AT3G48560
AT4G00620
AT4G11120
AT4G19710
AT4G20360
AT4G27860
AT4G36250
AT5G04990
AT5G13280
AT5G15530
AT5G42650
AT5G64050
AT5G64300

Cluster 43 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0003746	translation elongation factor activity	3	26	9.50E-07
GO:0004072	aspartate kinase activity	2	26	4.48E-06
GO:0009507	chloroplast	12	26	7.11E-06
GO:0009695	jasmonic acid biosynthetic process	2	26	2.24E-04
GO:0004413	homoserine kinase activity	1	26	0.001246703
GO:0004639	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	1	26	0.001246703
GO:0006081	cellular aldehyde metabolic process	1	26	0.001246703
GO:0009978	allene oxide synthase activity	1	26	0.001246703
GO:0019373	epoxygenase P450 pathway	1	26	0.001246703
GO:0031407	oxylipin metabolic process	1	26	0.001246703
GO:0006633	fatty acid biosynthetic process	2	26	0.001533946
GO:0004315	3-oxoacyl-[acyl-carrier-protein] synthase activity	1	26	0.002490418
GO:0004818	glutamate-tRNA ligase activity	1	26	0.002490418
GO:0009374	biotin binding	1	26	0.002490418
GO:0043039	tRNA aminoacylation	1	26	0.002490418
GO:0003935	GTP cyclohydrolase II activity	1	26	0.003731148
GO:0003984	acetolactate synthase activity	1	26	0.003731148
GO:0004312	fatty-acid synthase activity	1	26	0.003731148
GO:0004412	homoserine dehydrogenase activity	1	26	0.003731148
GO:0006090	pyruvate metabolic process	1	26	0.003731148
GO:0008686	3,4-dihydroxy-2-butanone-4-phosphate synthase activity	1	26	0.003731148

Cluster 43 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009067	aspartate family amino acid biosynthetic process	1	26	0.003731148
GO:0009088	threonine biosynthetic process	1	26	0.003731148
GO:0004737	pyruvate decarboxylase activity	1	26	0.0049689
GO:0006725	cellular aromatic compound metabolic process	1	26	0.0049689
GO:0004742	dihydrolipoyllysine-residue acetyltransferase activity	1	26	0.006203677
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	1	26	0.006203677
GO:0006424	glutamyl-tRNA aminoacylation	1	26	0.006203677
GO:0006636	unsaturated fatty acid biosynthetic process	1	26	0.006203677
GO:0008652	amino acid biosynthetic process	1	26	0.006203677
GO:0009082	branched chain family amino acid biosynthetic process	1	26	0.006203677
GO:0016836	hydro-lyase activity	1	26	0.006203677
GO:0004029	aldehyde dehydrogenase (NAD) activity	1	26	0.007435487
GO:0006164	purine nucleotide biosynthetic process	1	26	0.007435487
GO:0006744	ubiquinone biosynthetic process	1	26	0.007435487
GO:0009086	methionine biosynthetic process	1	26	0.007435487
GO:0009611	response to wounding	2	26	0.007508082
GO:0007005	mitochondrion organization	1	26	0.008664333
GO:0005739	mitochondrion	4	26	0.012048091
GO:0009231	riboflavin biosynthetic process	1	26	0.012333141
GO:0009698	phenylpropanoid metabolic process	1	26	0.013550185
GO:0016207	4-coumarate-CoA ligase activity	1	26	0.015975463
GO:0004028	3-chloroallyl aldehyde dehydrogenase activity	1	26	0.017183709
GO:0018119	peptidyl-cysteine S-nitrosylation	1	26	0.017183709
GO:0008152	metabolic process	3	26	0.026629337
GO:0006414	translational elongation	1	26	0.02674488
GO:0009295	nucleoid	1	26	0.030282622
GO:0048481	ovule development	1	26	0.032626772
GO:0000325	plant-type vacuole	1	26	0.033794558
GO:0009620	response to fungus	1	26	0.033794558
GO:0009535	chloroplast thylakoid membrane	2	26	0.034424943
GO:0009658	chloroplast organization	1	26	0.043034577
GO:0004497	monooxygenase activity	1	26	0.046453035
GO:0005774	vacuolar membrane	1	26	0.047586918
GO:0010287	plastoglobule	1	26	0.056557827
GO:0016020	membrane	4	26	0.05852385
GO:0009570	chloroplast stroma	2	26	0.062046752
GO:0009941	chloroplast envelope	2	26	0.066531413
GO:0005777	peroxisome	1	26	0.121235928
GO:0009753	response to jasmonic acid stimulus	1	26	0.123123047
GO:0009536	plastid	1	26	0.138770399
GO:0009579	thylakoid	1	26	0.172907922
GO:0005525	GTP binding	1	26	0.176920323
GO:0019825	oxygen binding	1	26	0.190154562
GO:0009733	response to auxin stimulus	1	26	0.212018804
GO:0005730	nucleolus	1	26	0.222931161
GO:0048046	apoplast	1	26	0.224920978
GO:0016021	integral to membrane	1	26	0.231427684
GO:0005783	endoplasmic reticulum	1	26	0.240216754
GO:0006952	defense response	1	26	0.274373653
GO:0003676	nucleic acid binding	1	26	0.278872615
GO:0005622	intracellular	1	26	0.303168609
GO:0005488	binding	1	26	0.323173877

Cluster 43

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0000325	1	AT1G63010					
GO:0003676	1	AT1G76010					
GO:0003746	3	AT2G31060	AT4G11120	AT4G20360			
GO:0003935	1	AT5G64300					
GO:0003984	1	AT3G48560					
GO:0004028	1	AT4G36250					
GO:0004029	1	AT4G36250					
GO:0004072	2	AT4G19710	AT5G13280				
GO:0004312	1	AT1G74960					
GO:0004315	1	AT1G74960					
GO:0004412	1	AT4G19710					
GO:0004413	1	AT2G17265					
GO:0004497	1	AT3G24200					
GO:0004639	1	AT3G21110					
GO:0004737	1	AT3G48560					
GO:0004742	1	AT1G54220					
GO:0004818	1	AT5G64050					
GO:0005488	1	AT1G52670					
GO:0005525	1	AT2G31060					
GO:0005622	1	AT2G31060					
GO:0005730	1	AT4G20360					
GO:0005739	4	AT1G54220	AT4G11120	AT5G42650	AT5G64050		
GO:0005774	1	AT1G63010					
GO:0005777	1	AT1G20510					
GO:0005783	1	AT4G36250					
GO:0006081	1	AT4G36250					
GO:0006086	1	AT1G54220					
GO:0006090	1	AT1G54220					
GO:0006164	1	AT3G21110					
GO:0006414	1	AT4G11120					
GO:0006424	1	AT5G64050					
GO:0006633	2	AT1G74960	AT5G15530				
GO:0006636	1	AT1G74960					
GO:0006725	1	AT3G24200					
GO:0006744	1	AT3G24200					
GO:0006952	1	AT5G42650					
GO:0007005	1	AT5G64050					
GO:0008152	3	AT1G54220	AT3G24200	AT4G36250			
GO:0008652	1	AT5G13280					
GO:0008686	1	AT5G64300					
GO:0009067	1	AT4G19710					
GO:0009082	1	AT3G48560					
GO:0009086	1	AT2G17265					
GO:0009088	1	AT2G17265					
GO:0009231	1	AT5G64300					
GO:0009295	1	AT4G20360					
GO:0009374	1	AT5G15530					
GO:0009507	12	AT1G52670	AT1G74960	AT2G17265	AT3G21110	AT3G48560	AT4G19710
		AT4G20360	AT5G13280	AT5G15530	AT5G42650	AT5G64050	AT5G64300
GO:0009535	2	AT4G20360	AT5G42650				
GO:0009536	1	AT1G74960					
GO:0009570	2	AT2G17265	AT4G20360				
GO:0009579	1	AT5G42650					
GO:0009611	2	AT1G20510	AT5G42650				
GO:0009620	1	AT5G42650					
GO:0009658	1	AT5G64050					
GO:0009695	2	AT1G20510	AT5G42650				
GO:0009698	1	AT1G20510					
GO:0009733	1	AT3G21110					
GO:0009753	1	AT5G42650					

Cluster 43 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)			
GO:0009941	2	AT4G20360	AT5G42650		
GO:0009978	1	AT5G42650			
GO:0010287	1	AT5G42650			
GO:0016020	4	AT4G20360	AT4G36250	AT5G42650	AT5G64300
GO:0016021	1	AT4G27860			
GO:0016207	1	AT1G20510			
GO:0016836	1	AT5G42650			
GO:0018119	1	AT4G20360			
GO:0019373	1	AT5G42650			
GO:0019825	1	AT5G42650			
GO:0031407	1	AT5G42650			
GO:0043039	1	AT5G64050			
GO:0048046	1	AT4G20360			
GO:0048481	1	AT5G64050			

Cluster 44

Cluster 44

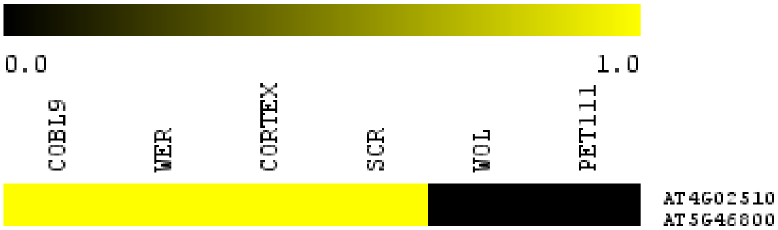
AT1G22520
AT1G27400
AT1G50430
AT3G24170
AT5G18280

Cluster 44 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009918	sterol delta7 reductase activity	1	5	2.40E-04
GO:0004362	glutathione-disulfide reductase activity	1	5	4.79E-04
GO:0004551	nucleotide diphosphatase activity	1	5	4.79E-04
GO:0006749	glutathione metabolic process	1	5	4.79E-04
GO:0030176	integral to endoplasmic reticulum membrane	1	5	0.001437125
GO:0016132	brassinosteroid biosynthetic process	1	5	0.00239337
GO:0016126	sterol biosynthetic process	1	5	0.005253299
GO:0009846	pollen germination	1	5	0.00596622
GO:0045454	cell redox homeostasis	1	5	0.010933639
GO:0009826	unidimensional cell growth	1	5	0.018658499
GO:0022625	cytosolic large ribosomal subunit	1	5	0.023522999
GO:0005777	peroxisome	1	5	0.026055215
GO:0016887	ATPase activity	1	5	0.026743933
GO:0005794	Golgi apparatus	1	5	0.029947276
GO:0005840	ribosome	1	5	0.042585818
GO:0005886	plasma membrane	2	5	0.049853434
GO:0003735	structural constituent of ribosome	1	5	0.064467462
GO:0006412	translation	1	5	0.067034781
GO:0005773	vacuole	1	5	0.09748675
GO:0005739	mitochondrion	1	5	0.158671062
GO:0009507	chloroplast	1	5	0.348502152

Cluster 44

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0003735	1	AT1G27400	
GO:0004362	1	AT3G24170	
GO:0004551	1	AT5G18280	
GO:0005739	1	AT1G22520	
GO:0005773	1	AT1G27400	
GO:0005777	1	AT3G24170	
GO:0005794	1	AT5G18280	
GO:0005840	1	AT1G27400	
GO:0005886	2	AT1G27400	AT1G50430
GO:0006412	1	AT1G27400	
GO:0006749	1	AT3G24170	
GO:0009507	1	AT1G27400	
GO:0009826	1	AT1G50430	
GO:0009846	1	AT5G18280	
GO:0009918	1	AT1G50430	
GO:0016126	1	AT1G50430	
GO:0016132	1	AT1G50430	
GO:0016887	1	AT5G18280	
GO:0022625	1	AT1G27400	
GO:0030176	1	AT1G50430	
GO:0045454	1	AT3G24170	

Cluster 45



Cluster 45
AT4G02510
AT5G46800

Cluster 45 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009536	plastid	2	2	3.86E-05
GO:0015822	ornithine transport	1	2	9.59E-05
GO:0045036	protein targeting to chloroplast	1	2	8.63E-04
GO:0005739	mitochondrion	2	2	0.001357963
GO:0009707	chloroplast outer membrane	1	2	0.002107681
GO:0006839	mitochondrial transport	1	2	0.004019892
GO:0005743	mitochondrial inner membrane	1	2	0.007166997
GO:0004888	transmembrane receptor activity	1	2	0.010114245
GO:0009507	chloroplast	2	2	0.012574049
GO:0006810	transport	1	2	0.030125688
GO:0009941	chloroplast envelope	1	2	0.034855244
GO:0005488	binding	1	2	0.041583373
GO:0016020	membrane	1	2	0.119837161

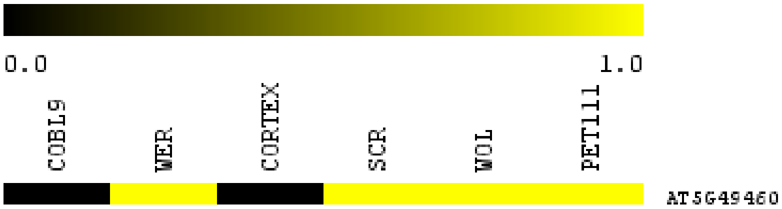
Cluster 45

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0004888	1	AT4G02510	
GO:0005488	1	AT5G46800	
GO:0005739	2	AT4G02510	AT5G46800

Cluster 45 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0005743	1	AT5G46800	
GO:0006810	1	AT5G46800	
GO:0006839	1	AT5G46800	
GO:0009507	2	AT4G02510	AT5G46800
GO:0009536	2	AT4G02510	AT5G46800
GO:0009707	1	AT4G02510	
GO:0009941	1	AT4G02510	
GO:0015822	1	AT5G46800	
GO:0016020	1	AT4G02510	
GO:0045036	1	AT4G02510	

Cluster 46

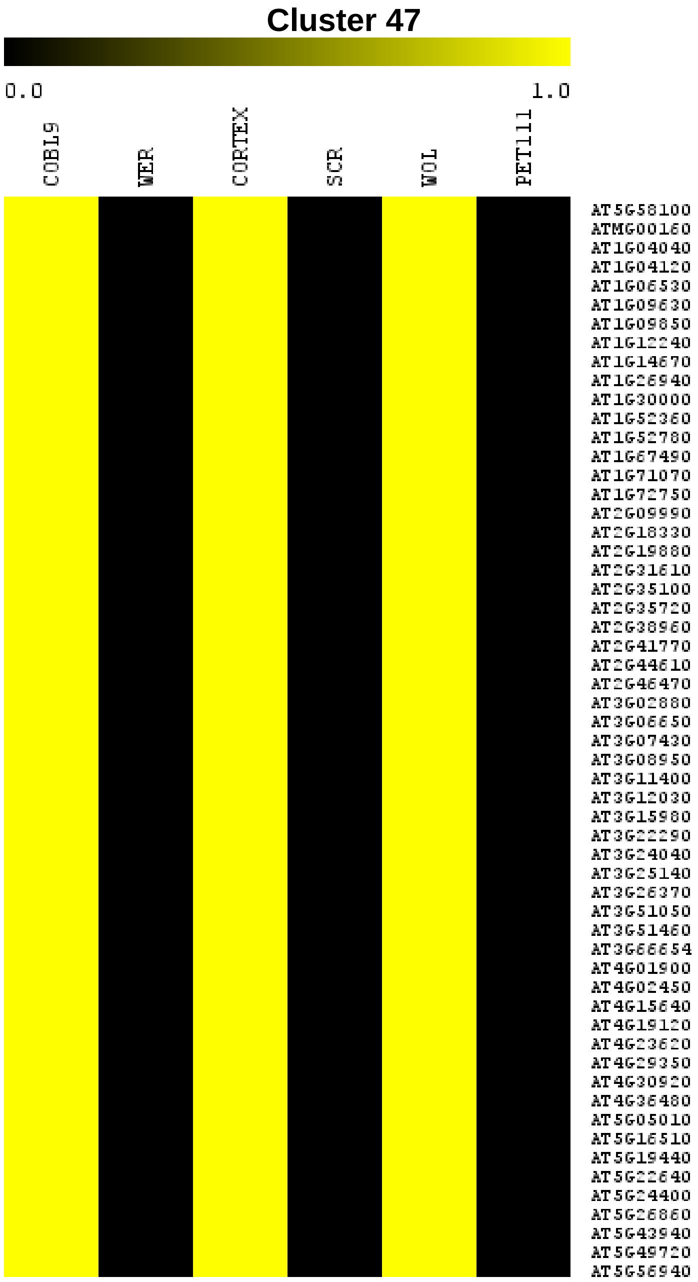


Cluster 46
AT5G49460

Cluster 46 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009346	citrate lyase complex	1	1	2.40E-04
GO:0003878	ATP citrate synthase activity	1	1	2.88E-04
GO:0006085	acetyl-CoA biosynthetic process	1	1	2.88E-04
GO:0005829	cytosol	1	1	0.008247423
GO:0005886	plasma membrane	1	1	0.08002877

Cluster 46

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0003878	1	AT5G49460
GO:0005829	1	AT5G49460
GO:0005886	1	AT5G49460
GO:0006085	1	AT5G49460
GO:0009346	1	AT5G49460



Cluster 47

AT1G04040
AT1G04120
AT1G06530
AT1G09630
AT1G09850
AT1G12240
AT1G14670
AT1G26940
AT1G30000
AT1G52360
AT1G52780
AT1G67490
AT1G71070
AT1G72750
AT2G09990
AT2G18330
AT2G19880
AT2G31610
AT2G35100
AT2G35720
AT2G38960
AT2G41770
AT2G44610
AT2G46470
AT3G02880
AT3G06650
AT3G07430
AT3G08950
AT3G11400
AT3G12030
AT3G15980
AT3G22290
AT3G24040
AT3G25140
AT3G26370
AT3G51050
AT3G51460
AT3G66654
AT4G01900
AT4G02450
AT4G15640
AT4G19120
AT4G23620
AT4G29350
AT4G30920
AT4G36480
AT5G05010
AT5G16510
AT5G19440
AT5G22640
AT5G24400
AT5G26860
AT5G43940

Cluster 47 (con.)

AT5G49720
AT5G56940
AT5G58100
ATMG00160

Cluster 47 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005794	Golgi apparatus	6	56	1.15E-06
GO:0045489	pectin biosynthetic process	2	56	2.12E-05
GO:0006461	protein complex assembly	3	56	3.09E-05
GO:0030126	COPI vesicle coat	2	56	1.05E-04
GO:0005886	plasma membrane	13	56	2.83E-04
GO:0005739	mitochondrion	8	56	7.85E-04
GO:0009504	cell plate	2	56	8.20E-04
GO:0008565	protein transporter activity	3	56	8.81E-04
GO:0016192	vesicle-mediated transport	3	56	0.001070306
GO:0007160	cell-matrix adhesion	1	56	0.002685207
GO:0008120	ceramide glucosyltransferase activity	1	56	0.002685207
GO:0008281	sulfonylurea receptor activity	1	56	0.002685207
GO:0008305	integrin complex	1	56	0.002685207
GO:0010307	acetylglutamate kinase regulator activity	1	56	0.002685207
GO:0031520	plasma membrane of cell tip	1	56	0.002685207
GO:0043812	phosphatidylinositol-4-phosphate phosphatase activity	1	56	0.002685207
GO:0046292	formaldehyde metabolic process	1	56	0.002685207
GO:0051903	S-(hydroxymethyl)glutathione dehydrogenase activity	1	56	0.002685207
GO:0009505	plant-type cell wall	4	56	0.003376065
GO:0006886	intracellular protein transport	3	56	0.003483808
GO:0009536	plastid	3	56	0.004744316
GO:0005198	structural molecule activity	2	56	0.005248165
GO:0004558	alpha-glucosidase activity	1	56	0.005356251
GO:0004758	serine C-palmitoyltransferase activity	1	56	0.005356251
GO:0005624	membrane fraction	1	56	0.005356251
GO:0008154	actin polymerization or depolymerization	1	56	0.005356251
GO:0032940	secretion by cell	1	56	0.005356251
GO:0016020	membrane	9	56	0.006051205
GO:0016051	carbohydrate biosynthetic process	2	56	0.006811602
GO:0016757	transferase activity, transferring glycosyl groups	4	56	0.00708799
GO:0005769	early endosome	1	56	0.008013186
GO:0008097	5S rRNA binding	1	56	0.008013186
GO:0008466	glycogenin glucosyltransferase activity	1	56	0.008013186
GO:0010289	homogalacturonan biosynthetic process	1	56	0.008013186
GO:0030148	sphingolipid biosynthetic process	1	56	0.008013186
GO:0042450	arginine biosynthetic process via ornithine	1	56	0.008013186
GO:0045039	protein import into mitochondrial inner membrane	1	56	0.008013186
GO:0006467	protein thiol-disulfide exchange	1	56	0.013284948
GO:0008810	cellulase activity	1	56	0.013284948
GO:0009346	citrate lyase complex	1	56	0.013284948
GO:0030007	cellular potassium ion homeostasis	1	56	0.013284948
GO:0048768	root hair cell tip growth	1	56	0.013284948
GO:0003878	ATP citrate synthase activity	1	56	0.015899884
GO:0006085	acetyl-CoA biosynthetic process	1	56	0.015899884
GO:0009913	epidermal cell differentiation	1	56	0.015899884
GO:0004559	alpha-mannosidase activity	1	56	0.01850093

Cluster 47 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004022	alcohol dehydrogenase activity	1	56	0.021088139
GO:0004439	phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity	1	56	0.021088139
GO:0005852	eukaryotic translation initiation factor 3 complex	1	56	0.023661566
GO:0009718	anthocyanin biosynthetic process	1	56	0.023661566
GO:0043622	cortical microtubule organization	1	56	0.023661566
GO:0010053	root epidermal cell differentiation	1	56	0.026221264
GO:0005515	protein binding	7	56	0.026453836
GO:0005783	endoplasmic reticulum	3	56	0.028748968
GO:0004564	beta-fructofuranosidase activity	1	56	0.028767286
GO:0010286	heat acclimation	1	56	0.028767286
GO:0015629	actin cytoskeleton	1	56	0.028767286
GO:0006487	protein amino acid N-linked glycosylation	1	56	0.031299687
GO:0016671	oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor	1	56	0.031299687
GO:0009793	embryonic development ending in seed dormancy	3	56	0.032379468
GO:0005777	peroxisome	2	56	0.032566705
GO:0010584	pollen exine formation	1	56	0.036323834
GO:0019575	sucrose catabolic process, using beta-fructofuranosidase	1	56	0.038815687
GO:0005768	endosome	1	56	0.04129413
GO:0008375	acetylglucosaminyltransferase activity	1	56	0.04129413
GO:0006807	nitrogen compound metabolic process	1	56	0.046210993
GO:0005744	mitochondrial inner membrane presequence translocase complex	1	56	0.051074842
GO:0007010	cytoskeleton organization	1	56	0.051074842
GO:0000910	cytokinesis	1	56	0.053487016
GO:0030244	cellulose biosynthetic process	1	56	0.053487016
GO:0016049	cell growth	1	56	0.058272121
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	2	56	0.059117221
GO:0047262	polygalacturonate 4-alpha-galacturonosyltransferase activity	1	56	0.060645154
GO:0048316	seed development	1	56	0.063005243
GO:0050660	FAD binding	1	56	0.067686789
GO:0005525	GTP binding	2	56	0.068720488
GO:0000325	plant-type vacuole	1	56	0.070008348
GO:0005840	ribosome	2	56	0.074224312
GO:0008236	serine-type peptidase activity	1	56	0.079167665
GO:0005773	vacuole	3	56	0.08510904
GO:0006457	protein folding	2	56	0.086630873
GO:0003993	acid phosphatase activity	1	56	0.088126299
GO:0009744	response to sucrose stimulus	1	56	0.090334971
GO:0042538	hyperosmotic salinity response	1	56	0.090334971
GO:0005774	vacuolar membrane	1	56	0.096887402
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	1	56	0.103330471
GO:0016021	integral to membrane	2	56	0.116052898
GO:0003779	actin binding	1	56	0.119987147
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	56	0.126040211
GO:0006413	translational initiation	1	56	0.128034854
GO:0016758	transferase activity, transferring hexosyl groups	1	56	0.133950291
GO:0003735	structural constituent of ribosome	2	56	0.13630355
GO:0046658	anchored to plasma membrane	1	56	0.137837294
GO:0009651	response to salt stress	2	56	0.139310688
GO:0006412	translation	2	56	0.143487444

Cluster 47 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005975	carbohydrate metabolic process	2	56	0.144673306
GO:0005618	cell wall	2	56	0.14762268
GO:0003743	translation initiation factor activity	1	56	0.156606329
GO:0006810	transport	2	56	0.156903631
GO:0009055	electron carrier activity	1	56	0.163809751
GO:0005743	mitochondrial inner membrane	1	56	0.16558399
GO:0009826	unidimensional cell growth	1	56	0.172575771
GO:0015031	protein transport	1	56	0.179401301
GO:0003824	catalytic activity	2	56	0.184609433
GO:0009941	chloroplast envelope	2	56	0.184609433
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	56	0.186063259
GO:0042254	ribosome biogenesis	1	56	0.195755272
GO:0005507	copper ion binding	1	56	0.21555396
GO:0009416	response to light stimulus	1	56	0.217010722
GO:0009611	response to wounding	1	56	0.217010722
GO:0031072	heat shock protein binding	1	56	0.217010722
GO:0016887	ATPase activity	1	56	0.226950752
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1	56	0.245520229
GO:0005524	ATP binding	2	56	0.267881489
GO:0004674	protein serine/threonine kinase activity	1	56	0.295316033
GO:0009535	chloroplast thylakoid membrane	1	56	0.345505753
GO:0003723	RNA binding	1	56	0.362420375
GO:0006508	proteolysis	1	56	0.369923141
GO:0009570	chloroplast stroma	1	56	0.371244355

Cluster 47

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000325	1	AT1G04120
GO:0000910	1	AT1G09630
GO:0003723	1	AT3G11400
GO:0003735	2	AT4G23620 AT5G56940
GO:0003743	1	AT3G11400
GO:0003755	1	AT1G26940
GO:0003779	1	AT4G29350
GO:0003824	2	AT2G35100 AT5G24400
GO:0003878	1	AT3G06650
GO:0003993	1	AT1G04040
GO:0004022	1	AT5G19440
GO:0004439	1	AT3G51460
GO:0004553	2	AT1G12240 AT5G49720
GO:0004558	1	AT1G67490
GO:0004559	1	AT1G30000
GO:0004564	1	AT1G12240
GO:0004674	1	AT3G02880
GO:0004758	1	AT4G36480
GO:0005198	2	AT1G52360 AT3G15980
GO:0005507	1	AT3G08950
GO:0005515	7	AT1G52360 AT2G38960 AT2G44610 AT3G15980 AT4G29350 AT4G36480 AT5G05010
GO:0005524	2	AT3G02880 AT5G26860
GO:0005525	2	AT1G09630 AT2G44610
GO:0005618	2	AT1G04040 AT3G02880
GO:0005624	1	AT2G44610

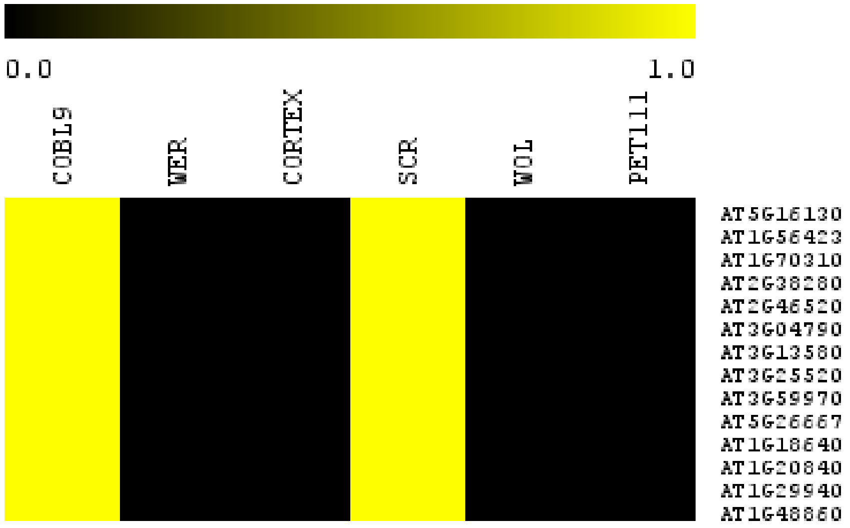
Cluster 47 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005739	8	AT1G06530	AT1G72750	AT2G35720	AT2G46470	AT3G08950	AT3G25140
		AT4G15640	AT5G26860				
GO:0005743	1	AT1G72750					
GO:0005744	1	AT1G72750					
GO:0005768	1	AT1G09630					
GO:0005769	1	AT5G49720					
GO:0005773	3	AT1G04040	AT1G09850	AT1G12240			
GO:0005774	1	AT1G04120					
GO:0005777	2	AT5G24400	AT5G43940				
GO:0005783	3	AT1G67490	AT2G38960	AT4G36480			
GO:0005794	6	AT1G14670	AT1G30000	AT3G25140	AT3G26370	AT5G16510	AT5G49720
GO:0005840	2	AT4G23620	AT5G56940				
GO:0005852	1	AT3G11400					
GO:0005886	13	AT1G04040	AT1G04120	AT1G06530	AT1G09630	AT2G44610	AT3G02880
		AT3G11400	AT3G51050	AT3G51460	AT4G02450	AT4G29350	AT5G19440
		AT5G49720					
GO:0005975	2	AT1G12240	AT5G24400				
GO:0006085	1	AT3G06650					
GO:0006412	2	AT4G23620	AT5G56940				
GO:0006413	1	AT3G11400					
GO:0006457	2	AT1G26940	AT2G35720				
GO:0006461	3	AT1G52360	AT3G15980	AT5G05010			
GO:0006467	1	AT2G38960					
GO:0006487	1	AT1G30000					
GO:0006508	1	AT1G09850					
GO:0006807	1	AT4G01900					
GO:0006810	2	AT1G14670	AT5G05010				
GO:0006886	3	AT1G52360	AT3G15980	AT5G05010			
GO:0007010	1	AT4G29350					
GO:0007160	1	AT3G51050					
GO:0007169	1	AT3G02880					
GO:0008097	1	AT4G23620					
GO:0008120	1	AT2G19880					
GO:0008154	1	AT4G29350					
GO:0008236	1	AT5G26860					
GO:0008281	1	AT1G04120					
GO:0008305	1	AT3G51050					
GO:0008375	1	AT1G71070					
GO:0008466	1	AT5G16510					
GO:0008565	3	AT1G52360	AT3G15980	AT5G05010			
GO:0008810	1	AT5G49720					
GO:0009055	1	AT2G38960					
GO:0009346	1	AT3G06650					
GO:0009416	1	AT4G01900					
GO:0009504	2	AT1G09630	AT5G49720				
GO:0009505	4	AT1G04040	AT1G12240	AT3G02880	AT5G16510		
GO:0009535	1	AT5G22640					
GO:0009536	3	AT1G06530	AT2G35720	AT3G08950			
GO:0009570	1	AT5G24400					
GO:0009611	1	AT5G43940					
GO:0009651	2	AT1G04120	AT5G16510				
GO:0009718	1	AT4G01900					
GO:0009744	1	AT4G01900					
GO:0009793	3	AT3G07430	AT5G22640	AT5G24400			
GO:0009826	1	AT5G49720					
GO:0009913	1	AT1G67490					
GO:0009941	2	AT3G07430	AT5G22640				
GO:0010053	1	AT1G67490					
GO:0010286	1	AT5G43940					
GO:0010289	1	AT3G25140					

Cluster 47 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0010307	1	AT4G01900					
GO:0010584	1	AT5G58100					
GO:0015031	1	AT1G72750					
GO:0015450	1	AT1G72750					
GO:0015629	1	AT4G29350					
GO:0016020	9	AT1G14670	AT1G71070	AT1G72750	AT2G35100	AT2G46470	AT3G02880
		AT3G06650	AT3G24040	AT5G05010			
GO:0016021	2	AT1G14670	AT3G51050				
GO:0016049	1	AT4G36480					
GO:0016051	2	AT1G71070	AT3G25140				
GO:0016192	3	AT1G52360	AT3G15980	AT5G05010			
GO:0016671	1	AT2G38960					
GO:0016757	4	AT1G71070	AT2G35100	AT3G24040	AT3G25140		
GO:0016758	1	AT3G25140					
GO:0016887	1	AT2G18330					
GO:0019575	1	AT1G12240					
GO:0030007	1	AT1G04120					
GO:0030126	2	AT1G52360	AT3G15980				
GO:0030148	1	AT4G36480					
GO:0030244	1	AT5G49720					
GO:0031072	1	AT2G35720					
GO:0031520	1	AT3G51460					
GO:0032940	1	AT2G44610					
GO:0042254	1	AT5G56940					
GO:0042450	1	AT4G01900					
GO:0042538	1	AT5G49720					
GO:0042626	1	AT1G04120					
GO:0043622	1	AT5G49720					
GO:0043812	1	AT3G51460					
GO:0045039	1	AT2G46470					
GO:0045489	2	AT2G35100	AT3G25140				
GO:0046292	1	AT5G43940					
GO:0046658	1	AT3G02880					
GO:0047262	1	AT3G25140					
GO:0048316	1	AT5G43940					
GO:0048768	1	AT3G51460					
GO:0050660	1	AT2G38960					
GO:0051903	1	AT5G43940					

Cluster 48



Cluster 48
AT1G18640
AT1G20840
AT1G29940
AT1G48860
AT1G56423
AT1G70310
AT2G38280
AT2G46520
AT3G04790
AT3G13580
AT3G25520
AT3G59970
AT5G16130
AT5G26667

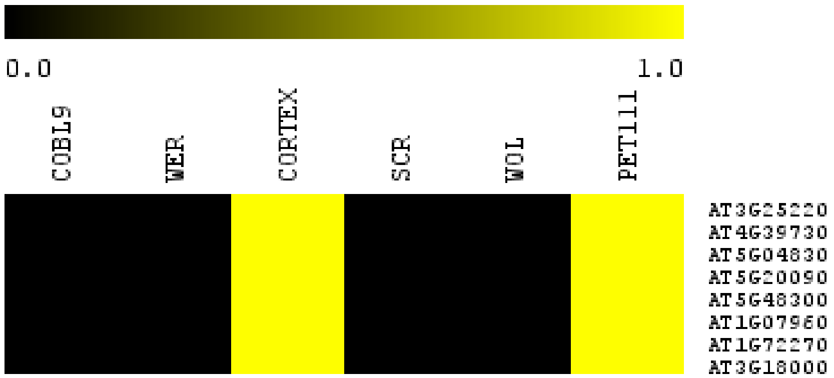
Cluster 48 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022626	cytosolic ribosome	3	14	1.68E-04
GO:0003876	AMP deaminase activity	1	14	6.71E-04
GO:0004647	phosphoserine phosphatase activity	1	14	6.71E-04
GO:0003735	structural constituent of ribosome	3	14	7.84E-04
GO:0006412	translation	3	14	8.82E-04
GO:0016020	membrane	5	14	0.001180548
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	1	14	0.001341767
GO:0022625	cytosolic large ribosomal subunit	2	14	0.001957586
GO:0004766	spermidine synthase activity	1	14	0.002011395
GO:0008097	5S rRNA binding	1	14	0.002011395
GO:0008295	spermidine biosynthetic process	1	14	0.002011395
GO:0004751	ribose-5-phosphate isomerase activity	1	14	0.002680189
GO:0006564	L-serine biosynthetic process	1	14	0.002680189
GO:0009955	adaxial/abaxial pattern formation	1	14	0.002680189
GO:0005337	nucleoside transmembrane transporter activity	1	14	0.004015271
GO:0019253	reductive pentose-phosphate cycle	1	14	0.006675442
GO:0009750	response to fructose stimulus	1	14	0.007338407
GO:0000059	protein import into nucleus, docking	1	14	0.008661848
GO:0005730	nucleolus	2	14	0.010295194
GO:0006913	nucleocytoplasmic transport	1	14	0.011955967
GO:0005643	nuclear pore	1	14	0.015229468
GO:0005792	microsom	1	14	0.015881702
GO:0005886	plasma membrane	4	14	0.01780227
GO:0015934	large ribosomal subunit	1	14	0.022359031
GO:0009705	plant-type vacuole membrane	1	14	0.024927148
GO:0005737	cytoplasm	2	14	0.02936112
GO:0003899	DNA-directed RNA polymerase activity	1	14	0.029390174
GO:0006350	transcription	1	14	0.031290801
GO:0005773	vacuole	2	14	0.031698763
GO:0009624	response to nematode	1	14	0.033813724
GO:0008565	protein transporter activity	1	14	0.045623401
GO:0009507	chloroplast	4	14	0.048173604
GO:0015144	carbohydrate transmembrane transporter activity	1	14	0.048683762
GO:0005351	sugar:hydrogen symporter activity	1	14	0.049902412
GO:0022627	cytosolic small ribosomal subunit	1	14	0.051117931
GO:0042254	ribosome biogenesis	1	14	0.058942862

Cluster 48 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005634	nucleus	3	14	0.078001142
GO:0042742	defense response to bacterium	1	14	0.082773182
GO:0009579	thylakoid	1	14	0.102662897
GO:0005840	ribosome	1	14	0.110143484
GO:0009535	chloroplast thylakoid membrane	1	14	0.142587111
GO:0009793	embryonic development ending in seed dormancy	1	14	0.1573007
GO:0009570	chloroplast stroma	1	14	0.190329855
GO:0009941	chloroplast envelope	1	14	0.196922836

Cluster 48

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**				
GO:0000059	1	AT2G46520				
GO:0003735	3	AT3G13580	AT3G25520	AT5G16130		
GO:0003876	1	AT2G38280				
GO:0003899	1	AT1G29940				
GO:0004647	1	AT1G18640				
GO:0004751	1	AT3G04790				
GO:0004766	1	AT1G70310				
GO:0005337	1	AT1G20840				
GO:0005351	1	AT1G20840				
GO:0005634	3	AT1G29940	AT2G46520	AT3G25520		
GO:0005643	1	AT2G46520				
GO:0005730	2	AT3G25520	AT5G16130			
GO:0005737	2	AT2G46520	AT3G25520			
GO:0005773	2	AT1G20840	AT3G25520			
GO:0005792	1	AT2G38280				
GO:0005840	1	AT3G25520				
GO:0005886	4	AT1G20840	AT1G70310	AT3G25520	AT5G16130	
GO:0006350	1	AT1G29940				
GO:0006412	3	AT3G13580	AT3G25520	AT5G16130		
GO:0006564	1	AT1G18640				
GO:0006913	1	AT3G25520				
GO:0008097	1	AT3G25520				
GO:0008295	1	AT1G70310				
GO:0008565	1	AT2G46520				
GO:0009168	1	AT2G38280				
GO:0009507	4	AT1G18640	AT3G04790	AT3G13580	AT3G25520	
GO:0009535	1	AT3G04790				
GO:0009570	1	AT3G04790				
GO:0009579	1	AT3G04790				
GO:0009624	1	AT1G20840				
GO:0009705	1	AT1G20840				
GO:0009750	1	AT1G20840				
GO:0009793	1	AT2G38280				
GO:0009941	1	AT3G04790				
GO:0009955	1	AT3G25520				
GO:0015144	1	AT1G20840				
GO:0015934	1	AT3G13580				
GO:0016020	5	AT1G20840	AT2G46520	AT3G13580	AT3G25520	AT5G16130
GO:0019253	1	AT3G04790				
GO:0022625	2	AT3G13580	AT3G25520			
GO:0022626	3	AT3G13580	AT3G25520	AT5G16130		
GO:0022627	1	AT5G16130				
GO:0042254	1	AT3G25520				
GO:0042742	1	AT3G04790				

Cluster 49



Cluster 49
AT1G07960
AT1G72270
AT3G18000
AT3G25220
AT4G39730
AT5G04830
AT5G20090
AT5G48300

Cluster 49 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0030931	heterotetrameric ADPG pyrophosphorylase complex	1	8	3.84E-04
GO:0008878	glucose-1-phosphate adenylyltransferase activity	1	8	0.002297746
GO:0019252	starch biosynthetic process	1	8	0.003824435
GO:0005528	FK506 binding	1	8	0.008379906
GO:0048573	photoperiodism, flowering	1	8	0.009513024
GO:0045454	cell redox homeostasis	1	8	0.017380792
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	8	0.020348685
GO:0005739	mitochondrion	2	8	0.03036572
GO:0009579	thylakoid	1	8	0.061601067
GO:0006457	protein folding	1	8	0.073074808
GO:0048046	apoplast	1	8	0.085251506
GO:0009535	chloroplast thylakoid membrane	1	8	0.087519342
GO:0005783	endoplasmic reticulum	1	8	0.092979863
GO:0005886	plasma membrane	2	8	0.1087124
GO:0009570	chloroplast stroma	1	8	0.120496729
GO:0005773	vacuole	1	8	0.146267346
GO:0012505	endomembrane system	2	8	0.169035632
GO:0009507	chloroplast	2	8	0.172530362
GO:0008150	biological_process	3	8	0.263338367
GO:0016020	membrane	1	8	0.322377166

Cluster 49

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**		
GO:0003755	1	AT3G25220		
GO:0005528	1	AT3G25220		
GO:0005739	2	AT1G72270	AT5G20090	
GO:0005773	1	AT4G39730		
GO:0005783	1	AT3G25220		
GO:0005886	2	AT4G39730	AT5G20090	
GO:0006457	1	AT3G25220		
GO:0008150	3	AT4G39730	AT5G04830	AT5G20090

Cluster 49 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0008878	1	AT5G48300	
GO:0009507	2	AT4G39730	AT5G48300
GO:0009535	1	AT4G39730	
GO:0009570	1	AT5G48300	
GO:0009579	1	AT4G39730	
GO:0012505	2	AT1G07960	AT3G25220
GO:0016020	1	AT5G20090	
GO:0019252	1	AT5G48300	
GO:0030931	1	AT5G48300	
GO:0045454	1	AT1G07960	
GO:0048046	1	AT5G48300	
GO:0048573	1	AT5G48300	

Cluster 50

Cluster 50
AT1G14360
AT1G55850
AT3G20130
AT3G21190
AT4G16170
AT5G38530
AT5G39410
AT5G53070

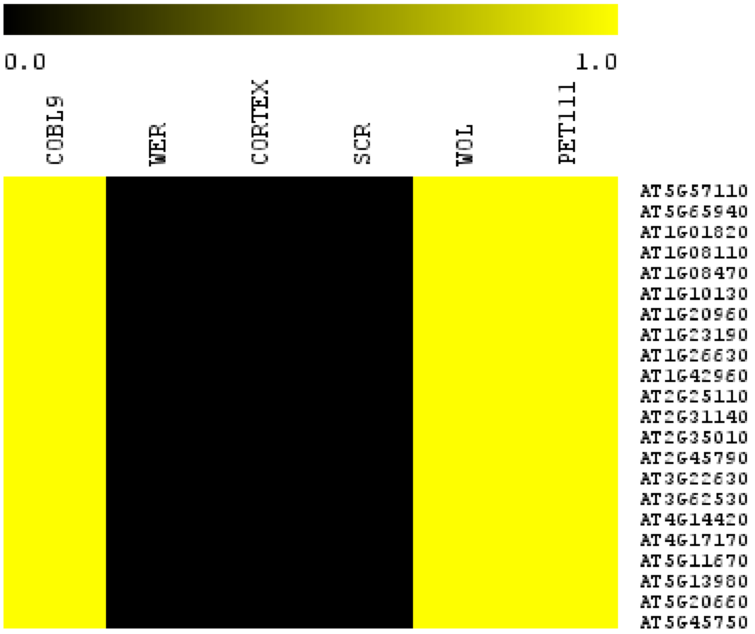
Cluster 50 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0015165	pyrimidine nucleotide sugar transmembrane transporter activity	1	8	7.67E-04
GO:0004834	tryptophan synthase activity	1	8	0.001150031
GO:0005783	endoplasmic reticulum	2	8	0.004173795
GO:0000271	polysaccharide biosynthetic process	1	8	0.00648627
GO:0000162	tryptophan biosynthetic process	1	8	0.007244491
GO:0009832	plant-type cell wall biogenesis	1	8	0.009135573
GO:0016759	cellulose synthase activity	1	8	0.013273535
GO:0042254	ribosome biogenesis	1	8	0.034587528
GO:0005794	Golgi apparatus	1	8	0.047045342
GO:0005840	ribosome	1	8	0.066358807
GO:0019825	oxygen binding	1	8	0.069056573
GO:0003735	structural constituent of ribosome	1	8	0.099004369
GO:0006412	translation	1	8	0.102766969
GO:0016757	transferase activity, transferring glycosyl groups	1	8	0.103079046
GO:0005886	plasma membrane	2	8	0.1087124
GO:0003824	catalytic activity	1	8	0.125256373

Cluster 50 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009941	chloroplast envelope	1	8	0.125256373
GO:0005488	binding	1	8	0.146267346
GO:0005773	vacuole	1	8	0.146267346
GO:0012505	endomembrane system	2	8	0.169035632
GO:0008152	metabolic process	1	8	0.177092172
GO:0005739	mitochondrion	1	8	0.22683916
GO:0016020	membrane	1	8	0.322377166

Cluster 50

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000162	1	AT5G38530	
GO:0000271	1	AT1G55850	
GO:0003735	1	AT5G53070	
GO:0003824	1	AT5G39410	
GO:0004834	1	AT5G38530	
GO:0005488	1	AT5G39410	
GO:0005739	1	AT5G39410	
GO:0005773	1	AT5G39410	
GO:0005783	2	AT1G55850	AT4G16170
GO:0005794	1	AT3G21190	
GO:0005840	1	AT5G53070	
GO:0005886	2	AT1G55850	AT5G39410
GO:0006412	1	AT5G53070	
GO:0008152	1	AT5G39410	
GO:0009832	1	AT1G55850	
GO:0009941	1	AT5G39410	
GO:0012505	2	AT1G14360	AT3G20130
GO:0015165	1	AT1G14360	
GO:0016020	1	AT5G39410	
GO:0016757	1	AT1G55850	
GO:0016759	1	AT1G55850	
GO:0019825	1	AT3G20130	
GO:0042254	1	AT5G53070	

Cluster 51



Cluster 51
AT1G01820
AT1G08110
AT1G08470
AT1G10130
AT1G20960
AT1G23190
AT1G26630
AT1G42960
AT2G25110
AT2G31140
AT2G35010
AT2G45790
AT3G22630
AT3G62530
AT4G14420
AT4G17170
AT5G11670
AT5G13980
AT5G20660
AT5G45750
AT5G57110
AT5G65940

Cluster 51 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005388	calcium-transporting ATPase activity	2	22	8.20E-05
GO:0005886	plasma membrane	8	22	1.66E-04
GO:0046686	response to cadmium ion	4	22	1.78E-04
GO:0005516	calmodulin binding	3	22	4.91E-04
GO:0005773	vacuole	4	22	0.001001851
GO:0008233	peptidase activity	2	22	0.001053969
GO:0004615	phosphomannomutase activity	1	22	0.001054903
GO:0015410	manganese-transporting ATPase activity	1	22	0.001054903
GO:0019307	mannose biosynthetic process	1	22	0.001054903
GO:0034050	host programmed cell death induced by symbiont	1	22	0.001054903
GO:0043621	protein self-association	1	22	0.001054903
GO:0055071	manganese ion homeostasis	1	22	0.001054903
GO:0016020	membrane	6	22	0.00177015
GO:0048046	apoplast	3	22	0.001887184
GO:0006574	valine catabolic process	1	22	0.002107681
GO:0005783	endoplasmic reticulum	3	22	0.00245684
GO:0004614	phosphoglucomutase activity	1	22	0.003158338
GO:0006013	mannose metabolic process	1	22	0.003158338
GO:0005975	carbohydrate metabolic process	3	22	0.003393081
GO:0003860	3-hydroxyisobutyryl-CoA hydrolase activity	1	22	0.004206876
GO:0004473	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	1	22	0.004206876
GO:0005779	integral to peroxisomal membrane	1	22	0.004206876
GO:0004470	malic enzyme activity	1	22	0.00629761
GO:0006828	manganese ion transport	1	22	0.00629761

Cluster 51 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0016652	oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	1	22	0.00629761
GO:0004462	lactoylglutathione lyase activity	1	22	0.007339811
GO:0004559	alpha-mannosidase activity	1	22	0.007339811
GO:0009051	pentose-phosphate shunt, oxidative branch	1	22	0.008379906
GO:0016559	peroxisome fission	1	22	0.009417898
GO:0006108	malate metabolic process	1	22	0.010453789
GO:0012501	programmed cell death	1	22	0.010453789
GO:0019853	L-ascorbic acid biosynthetic process	1	22	0.010453789
GO:0048235	pollen sperm cell differentiation	1	22	0.010453789
GO:0009821	alkaloid biosynthetic process	1	22	0.012519283
GO:0005525	GTP binding	2	22	0.013690093
GO:0006816	calcium ion transport	1	22	0.014576413
GO:0007031	peroxisome organization	1	22	0.014576413
GO:0016844	strictosidine synthase activity	1	22	0.014576413
GO:0005778	peroxisomal membrane	1	22	0.017646477
GO:0006888	ER to Golgi vesicle-mediated transport	1	22	0.018665675
GO:0005839	proteasome core complex	1	22	0.020697855
GO:0016049	cell growth	1	22	0.023730629
GO:0006635	fatty acid beta-oxidation	1	22	0.024737434
GO:0009706	chloroplast inner membrane	1	22	0.031727685
GO:0003924	GTPase activity	1	22	0.03469293
GO:0005618	cell wall	2	22	0.036334146
GO:0045454	cell redox homeostasis	1	22	0.046372394
GO:0009624	response to nematode	1	22	0.052104316
GO:0009617	response to bacterium	1	22	0.053999139
GO:0006413	translational initiation	1	22	0.054943598
GO:0007264	small GTPase mediated signal transduction	1	22	0.061499957
GO:0005737	cytoplasm	2	22	0.063278834
GO:0004601	peroxidase activity	1	22	0.065203599
GO:0008026	ATP-dependent helicase activity	1	22	0.067043809
GO:0048364	root development	1	22	0.067043809
GO:0003743	translation initiation factor activity	1	22	0.068876307
GO:0015031	protein transport	1	22	0.080601132
GO:0009611	response to wounding	1	22	0.101414062
GO:0005794	Golgi apparatus	1	22	0.118763854
GO:0009536	plastid	1	22	0.120375241
GO:0042742	defense response to bacterium	1	22	0.12357692
GO:0009507	chloroplast	4	22	0.136040364
GO:0006511	ubiquitin-dependent protein catabolic process	1	22	0.165536173
GO:0009733	response to auxin stimulus	1	22	0.187219799
GO:0005730	nucleolus	1	22	0.197468248
GO:0009505	plant-type cell wall	1	22	0.197468248
GO:0009535	chloroplast thylakoid membrane	1	22	0.203678483
GO:0009793	embryonic development ending in seed dormancy	1	22	0.222003993
GO:0009651	response to salt stress	1	22	0.227624368
GO:0006508	proteolysis	1	22	0.252714118
GO:0009941	chloroplast envelope	1	22	0.268234084
GO:0005634	nucleus	2	22	0.280653136
GO:0006355	regulation of transcription, DNA-dependent	1	22	0.361987516
GO:0005739	mitochondrion	1	22	0.368771516

Cluster 51

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0003743	1	AT1G26630					
GO:0003860	1	AT5G65940					
GO:0003924	1	AT4G17170					
GO:0004462	1	AT1G08110					
GO:0004470	1	AT5G11670					
GO:0004473	1	AT5G11670					
GO:0004559	1	AT5G13980					
GO:0004601	1	AT1G10130					
GO:0004614	1	AT1G23190					
GO:0004615	1	AT2G45790					
GO:0005388	2	AT1G10130	AT5G57110				
GO:0005516	3	AT1G08110	AT1G10130	AT5G57110			
GO:0005525	2	AT4G17170	AT5G45750				
GO:0005618	2	AT5G11670	AT5G13980				
GO:0005634	2	AT1G26630	AT5G45750				
GO:0005730	1	AT1G20960					
GO:0005737	2	AT1G23190	AT2G45790				
GO:0005739	1	AT1G42960					
GO:0005773	4	AT3G22630	AT4G17170	AT5G13980	AT5G45750		
GO:0005778	1	AT1G01820					
GO:0005779	1	AT1G01820					
GO:0005783	3	AT1G08470	AT2G25110	AT4G14420			
GO:0005794	1	AT1G10130					
GO:0005839	1	AT3G22630					
GO:0005886	8	AT1G08470	AT1G23190	AT3G22630	AT4G17170	AT5G11670	AT5G13980
		AT5G45750	AT5G57110				
GO:0005975	3	AT1G08110	AT1G23190	AT5G13980			
GO:0006013	1	AT5G13980					
GO:0006108	1	AT5G11670					
GO:0006355	1	AT5G45750					
GO:0006413	1	AT1G26630					
GO:0006508	1	AT5G20660					
GO:0006511	1	AT3G22630					
GO:0006574	1	AT5G65940					
GO:0006635	1	AT5G65940					
GO:0006816	1	AT1G10130					
GO:0006828	1	AT1G10130					
GO:0006888	1	AT4G17170					
GO:0007031	1	AT1G01820					
GO:0007264	1	AT5G45750					
GO:0008026	1	AT1G20960					
GO:0008233	2	AT3G22630	AT5G20660				
GO:0009051	1	AT5G11670					
GO:0009505	1	AT5G13980					
GO:0009507	4	AT1G08110	AT1G23190	AT1G42960	AT5G11670		
GO:0009535	1	AT1G42960					
GO:0009536	1	AT1G42960					
GO:0009611	1	AT1G26630					
GO:0009617	1	AT1G26630					
GO:0009624	1	AT5G57110					
GO:0009651	1	AT2G45790					
GO:0009706	1	AT1G42960					
GO:0009733	1	AT5G65940					
GO:0009793	1	AT1G20960					
GO:0009821	1	AT1G08470					
GO:0009941	1	AT1G42960					
GO:0012501	1	AT1G26630					
GO:0015031	1	AT5G45750					
GO:0015410	1	AT1G10130					

Cluster 51 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0016020	6	AT1G20960	AT1G42960	AT2G25110	AT4G17170	AT5G11670	AT5G57110
GO:0016049	1	AT4G17170					
GO:0016559	1	AT1G01820					
GO:0016652	1	AT5G11670					
GO:0016844	1	AT1G08470					
GO:0019307	1	AT2G45790					
GO:0019853	1	AT2G45790					
GO:0034050	1	AT1G26630					
GO:0042742	1	AT1G26630					
GO:0043621	1	AT5G57110					
GO:0045454	1	AT2G35010					
GO:0046686	4	AT1G08110	AT1G23190	AT1G26630	AT5G11670		
GO:0048046	3	AT3G22630	AT5G11670	AT5G13980			
GO:0048235	1	AT4G17170					
GO:0048364	1	AT1G10130					
GO:0055071	1	AT1G10130					

Cluster 52

Cluster 52

AT1G10760
AT1G20050
AT1G48850
AT1G53210
AT1G74030
AT2G04400
AT3G17810
AT3G62030

Cluster 52 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009507	chloroplast	6	8	4.37E-05
GO:0000247	C-8 sterol isomerase activity	1	8	3.84E-04
GO:0004107	chorismate synthase activity	1	8	3.84E-04
GO:0019595	non-phosphorylated glucose catabolic process	1	8	3.84E-04
GO:0050521	alpha-glucan, water dikinase activity	1	8	3.84E-04
GO:0000015	phosphopyruvate hydratase complex	1	8	7.67E-04
GO:0004425	indole-3-glycerol-phosphate synthase activity	1	8	7.67E-04
GO:0019496	serine-isocitrate lyase pathway	1	8	7.67E-04
GO:0004634	phosphopyruvate hydratase activity	1	8	0.001150031
GO:0010353	response to trehalose stimulus	1	8	0.001150031
GO:0006207	'de novo' pyrimidine base biosynthetic process	1	8	0.00153286

Cluster 52 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0010555	response to mannitol stimulus	1	8	0.00153286
GO:0019564	aerobic glycerol catabolic process	1	8	0.00153286
GO:0019642	anaerobic glycolysis	1	8	0.00153286
GO:0019683	glyceraldehyde-3-phosphate catabolic process	1	8	0.00153286
GO:0019656	glucose catabolic process to D-lactate and ethanol	1	8	0.001915431
GO:0009642	response to light intensity	1	8	0.002297746
GO:0019650	glucose catabolic process to butanediol	1	8	0.002297746
GO:0009610	response to symbiotic fungus	1	8	0.002679803
GO:0019658	glucose catabolic process to lactate and acetate	1	8	0.003061604
GO:0006094	gluconeogenesis	1	8	0.003443148
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	1	8	0.003824435
GO:0019344	cysteine biosynthetic process	1	8	0.003824435
GO:0009061	anaerobic respiration	1	8	0.004205466
GO:0019654	acetate fermentation	1	8	0.00458624
GO:0005983	starch catabolic process	1	8	0.004966759
GO:0009073	aromatic amino acid family biosynthetic process	1	8	0.004966759
GO:0009631	cold acclimation	1	8	0.006865508
GO:0000162	tryptophan biosynthetic process	1	8	0.007244491
GO:0009570	chloroplast stroma	2	8	0.007263904
GO:0009941	chloroplast envelope	2	8	0.007899243
GO:0016126	sterol biosynthetic process	1	8	0.008379906
GO:0000325	plant-type vacuole	1	8	0.010643849
GO:0005774	vacuolar membrane	1	8	0.015144268
GO:0006096	glycolysis	1	8	0.016263668
GO:0031977	thylakoid lumen	1	8	0.01700867
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	1	8	0.020348685
GO:0042742	defense response to bacterium	1	8	0.049150866
GO:0005509	calcium ion binding	1	8	0.058173989
GO:0022626	cytosolic ribosome	1	8	0.06057546
GO:0009579	thylakoid	1	8	0.061601067
GO:0006979	response to oxidative stress	1	8	0.069056573
GO:0006457	protein folding	1	8	0.073074808
GO:0009737	response to abscisic acid stimulus	1	8	0.073408126
GO:0007165	signal transduction	1	8	0.081664797
GO:0005730	nucleolus	1	8	0.084276101
GO:0048046	apoplast	1	8	0.085251506
GO:0009535	chloroplast thylakoid membrane	1	8	0.087519342
GO:0009793	embryonic development ending in seed dormancy	1	8	0.097426962
GO:0009651	response to salt stress	1	8	0.100576089
GO:0005886	plasma membrane	2	8	0.1087124
GO:0005773	vacuole	1	8	0.146267346
GO:0005739	mitochondrion	1	8	0.22683916
GO:0016020	membrane	1	8	0.322377166

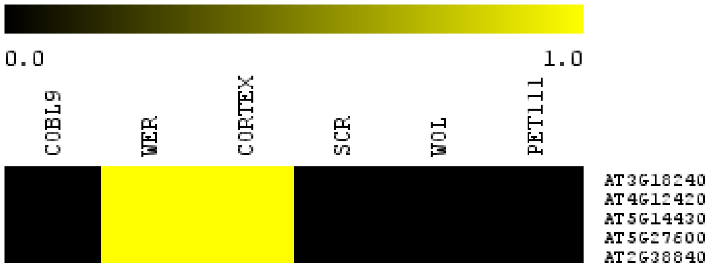
Cluster 52

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0000015	1	AT1G74030
GO:0000162	1	AT2G04400
GO:0000247	1	AT1G20050
GO:0000325	1	AT1G53210
GO:0003755	1	AT3G62030
GO:0004107	1	AT1G48850
GO:0004425	1	AT2G04400

Cluster 52 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0004634	1	AT1G74030					
GO:0005509	1	AT1G53210					
GO:0005730	1	AT1G48850					
GO:0005739	1	AT1G10760					
GO:0005773	1	AT1G53210					
GO:0005774	1	AT1G53210					
GO:0005886	2	AT1G20050	AT1G53210				
GO:0005983	1	AT1G10760					
GO:0006094	1	AT1G74030					
GO:0006096	1	AT1G74030					
GO:0006207	1	AT3G17810					
GO:0006457	1	AT3G62030					
GO:0006979	1	AT3G62030					
GO:0007165	1	AT3G62030					
GO:0009061	1	AT1G74030					
GO:0009073	1	AT1G48850					
GO:0009507	6	AT1G10760	AT1G48850	AT1G74030	AT2G04400	AT3G17810	AT3G62030
GO:0009535	1	AT3G62030					
GO:0009570	2	AT1G10760	AT3G62030				
GO:0009579	1	AT3G62030					
GO:0009610	1	AT1G10760					
GO:0009631	1	AT1G10760					
GO:0009642	1	AT3G62030					
GO:0009651	1	AT3G62030					
GO:0009737	1	AT3G62030					
GO:0009793	1	AT1G48850					
GO:0009941	2	AT1G10760	AT3G62030				
GO:0010353	1	AT1G10760					
GO:0010555	1	AT3G62030					
GO:0016020	1	AT1G53210					
GO:0016126	1	AT1G20050					
GO:0016627	1	AT3G17810					
GO:0019344	1	AT3G62030					
GO:0019496	1	AT1G74030					
GO:0019564	1	AT1G74030					
GO:0019595	1	AT1G74030					
GO:0019642	1	AT1G74030					
GO:0019650	1	AT1G74030					
GO:0019654	1	AT1G74030					
GO:0019656	1	AT1G74030					
GO:0019658	1	AT1G74030					
GO:0019683	1	AT1G74030					
GO:0022626	1	AT3G62030					
GO:0031977	1	AT3G62030					
GO:0042742	1	AT3G62030					
GO:0048046	1	AT3G62030					
GO:0050521	1	AT1G10760					

Cluster 53



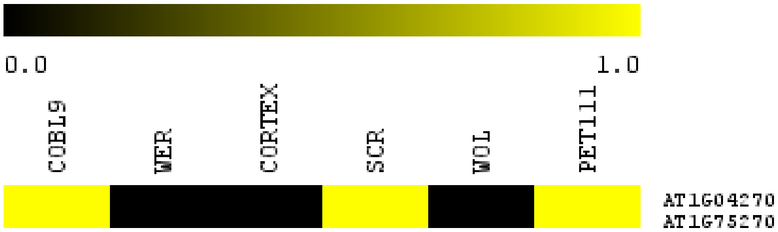
Cluster 53
AT2G38840
AT3G18240
AT4G12420
AT5G14430
AT5G27600

Cluster 53 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0001676	long-chain fatty acid metabolic process	1	5	9.58E-04
GO:0006955	immune response	1	5	9.58E-04
GO:0009505	plant-type cell wall	2	5	0.001253418
GO:0004467	long-chain-fatty-acid-CoA ligase activity	1	5	0.001676324
GO:0009932	cell tip growth	1	5	0.002154447
GO:0010193	response to ozone	1	5	0.004539554
GO:0003924	GTPase activity	1	5	0.008100044
GO:0046658	anchored to plasma membrane	1	5	0.014222925
GO:0005507	copper ion binding	1	5	0.024905556
GO:0005777	peroxisome	1	5	0.026055215
GO:0005794	Golgi apparatus	1	5	0.029947276
GO:0005525	GTP binding	1	5	0.040573406
GO:0031225	anchored to membrane	1	5	0.047253631
GO:0005886	plasma membrane	2	5	0.049853434
GO:0048046	apoplast	1	5	0.05516543
GO:0009651	response to salt stress	1	5	0.065538689
GO:0005618	cell wall	1	5	0.068526648
GO:0005515	protein binding	1	5	0.227022106
GO:0016020	membrane	1	5	0.245693865
GO:0012505	endomembrane system	1	5	0.345663617

Cluster 53

GO Identifier	#Loci	Associated Loci (Left to Right)	
GO:0001676	1	AT5G27600	
GO:0003924	1	AT2G38840	
GO:0004467	1	AT5G27600	
GO:0005507	1	AT4G12420	
GO:0005515	1	AT5G27600	
GO:0005525	1	AT2G38840	
GO:0005618	1	AT4G12420	
GO:0005777	1	AT5G27600	
GO:0005794	1	AT5G14430	
GO:0005886	2	AT4G12420	AT5G14430
GO:0006955	1	AT2G38840	
GO:0009505	2	AT4G12420	AT5G14430
GO:0009651	1	AT5G27600	
GO:0009932	1	AT4G12420	
GO:0010193	1	AT5G27600	
GO:0012505	1	AT2G38840	
GO:0016020	1	AT4G12420	
GO:0031225	1	AT4G12420	
GO:0046658	1	AT4G12420	
GO:0048046	1	AT4G12420	

Cluster 54

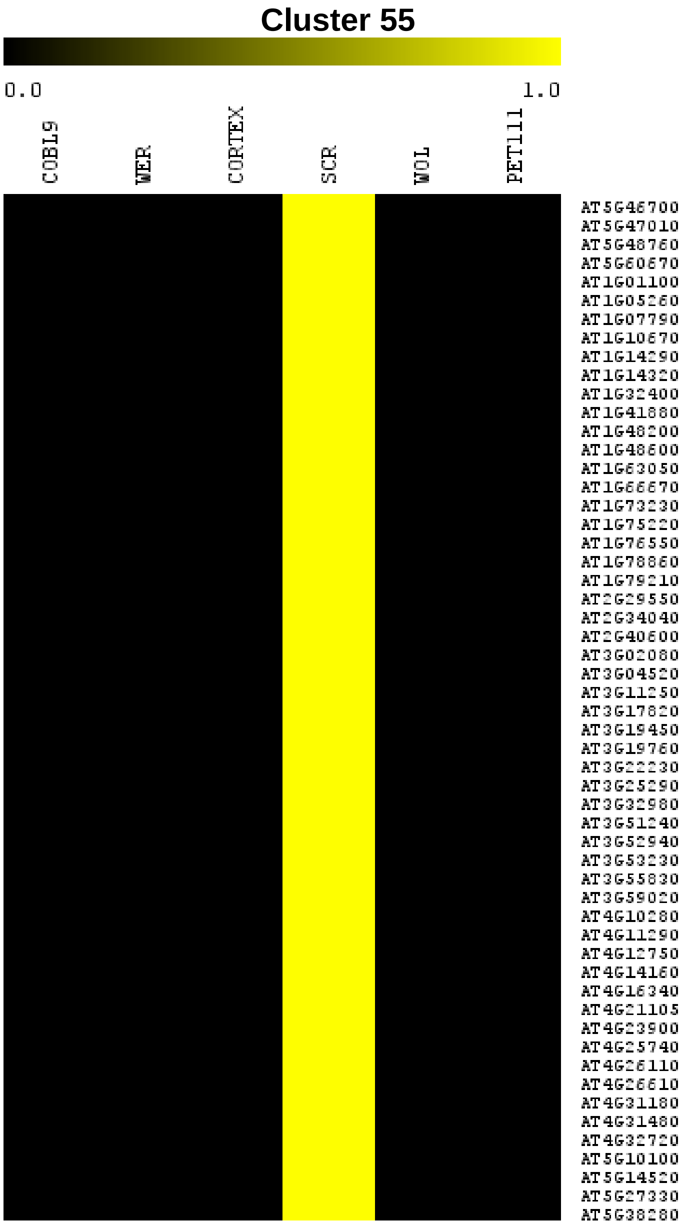


Cluster 54
AT1G04270
AT1G75270

Cluster 54 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045174	glutathione dehydrogenase (ascorbate) activity	1	2	2.88E-04
GO:0043295	glutathione binding	1	2	6.71E-04
GO:0005886	plasma membrane	2	2	0.006401074
GO:0022627	cytosolic small ribosomal subunit	1	2	0.007642958
GO:0022626	cytosolic ribosome	1	2	0.01588786
GO:0003735	structural constituent of ribosome	1	2	0.026866072
GO:0006412	translation	1	2	0.027984924

Cluster 54

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0003735	1	AT1G04270	
GO:0005886	2	AT1G04270	AT1G75270
GO:0006412	1	AT1G04270	
GO:0022626	1	AT1G04270	
GO:0022627	1	AT1G04270	
GO:0043295	1	AT1G75270	
GO:0045174	1	AT1G75270	



Cluster 55

AT1G01100
AT1G05260
AT1G07790
AT1G10670
AT1G14290
AT1G14320
AT1G32400
AT1G41880
AT1G48200
AT1G48600
AT1G63050
AT1G66670
AT1G73230
AT1G75220
AT1G76550
AT1G78860
AT1G79210
AT2G29550
AT2G34040
AT2G40600
AT3G02080
AT3G04520
AT3G11250
AT3G17820
AT3G19450
AT3G19760
AT3G22230
AT3G25290
AT3G32980
AT3G51240
AT3G52940
AT3G53230
AT3G55830
AT3G59020
AT4G10280
AT4G11290
AT4G12750
AT4G14160
AT4G16340
AT4G21105
AT4G23900
AT4G25740
AT4G26110
AT4G26610
AT4G31180
AT4G31480
AT4G32720
AT5G10100
AT5G14520
AT5G27330
AT5G38280
AT5G46700
AT5G47010
AT5G48760
AT5G60670

Cluster 55 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0022626	cytosolic ribosome	8	55	1.21E-08
GO:0003735	structural constituent of ribosome	8	55	6.97E-07
GO:0006412	translation	6	55	1.13E-04
GO:0005840	ribosome	5	55	1.14E-04
GO:0022625	cytosolic large ribosomal subunit	4	55	1.34E-04
GO:0005886	plasma membrane	12	55	8.26E-04
GO:0006414	translational elongation	2	55	0.001499183
GO:0042254	ribosome biogenesis	3	55	0.001798132
GO:0006422	aspartyl-tRNA aminoacylation	1	55	0.002637257
GO:0045486	naringenin 3-dioxygenase activity	1	55	0.002637257
GO:0050613	delta14-sterol reductase activity	1	55	0.002637257
GO:0051020	GTPase binding	1	55	0.002637257
GO:0015934	large ribosomal subunit	2	55	0.003531236
GO:0000170	sphingosine hydroxylase activity	1	55	0.005260857
GO:0004793	threonine aldolase activity	1	55	0.005260857
GO:0004815	aspartate-tRNA ligase activity	1	55	0.005260857
GO:0006183	GTP biosynthetic process	1	55	0.005260857
GO:0006228	UTP biosynthetic process	1	55	0.005260857
GO:0006241	CTP biosynthetic process	1	55	0.005260857
GO:0006567	threonine catabolic process	1	55	0.005260857
GO:0010317	pyrophosphate-dependent phosphofructokinase complex, alpha-subunit complex	1	55	0.005260857
GO:0016337	cell-cell adhesion	1	55	0.005260857
GO:0046520	sphingoid biosynthetic process	1	55	0.005260857
GO:0046686	response to cadmium ion	4	55	0.005364563
GO:0007568	aging	2	55	0.006059268
GO:0006334	nucleosome assembly	2	55	0.007402579
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1	55	0.00787085
GO:0006542	glutamine biosynthetic process	1	55	0.00787085
GO:0045995	regulation of embryonic development	1	55	0.00787085
GO:0043481	anthocyanin accumulation in tissues in response to UV light	1	55	0.010467289
GO:0045793	positive regulation of cell size	1	55	0.010467289
GO:0046786	viral replication complex formation and maintenance	1	55	0.010467289
GO:0047334	diphosphate-fructose-6-phosphate 1-phosphotransferase activity	1	55	0.010467289
GO:0004601	peroxidase activity	2	55	0.012443531
GO:0004550	nucleoside diphosphate kinase activity	1	55	0.013050226
GO:0009346	citrate lyase complex	1	55	0.013050226
GO:0016246	RNA interference	1	55	0.013050226
GO:0016020	membrane	8	55	0.015243643
GO:0003878	ATP citrate synthase activity	1	55	0.015619712
GO:0006085	acetyl-CoA biosynthetic process	1	55	0.015619712
GO:0006916	anti-apoptosis	1	55	0.015619712
GO:0009956	radial pattern formation	1	55	0.015619712
GO:0045551	cinnamyl-alcohol dehydrogenase activity	1	55	0.015619712
GO:0022627	cytosolic small ribosomal subunit	2	55	0.017687969
GO:0004356	glutamate-ammonia ligase activity	1	55	0.018175799
GO:0005085	guanyl-nucleotide exchange factor activity	1	55	0.018175799
GO:0009840	chloroplastic endopeptidase Clp complex	1	55	0.018175799
GO:0010015	root morphogenesis	1	55	0.018175799
GO:0004129	cytochrome-c oxidase activity	1	55	0.020718538
GO:0042128	nitrate assimilation	1	55	0.020718538

Cluster 55 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0045298	tubulin complex	1	55	0.020718538
GO:0005730	nucleolus	3	55	0.021344117
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	1	55	0.02324798
GO:0010025	wax biosynthetic process	1	55	0.025764175
GO:0019252	starch biosynthetic process	1	55	0.025764175
GO:0030127	COPII vesicle coat	1	55	0.025764175
GO:0035251	UDP-glucosyltransferase activity	1	55	0.025764175
GO:0005783	endoplasmic reticulum	3	55	0.027555944
GO:0003724	RNA helicase activity	1	55	0.028267175
GO:0009534	chloroplast thylakoid	1	55	0.03075703
GO:0000059	protein import into nucleus, docking	1	55	0.03323379
GO:0005654	nucleoplasm	1	55	0.03323379
GO:0009933	meristem structural organization	1	55	0.03323379
GO:0009651	response to salt stress	3	55	0.03366747
GO:0004805	trehalose-phosphatase activity	1	55	0.035697505
GO:0016117	carotenoid biosynthetic process	1	55	0.035697505
GO:0005618	cell wall	3	55	0.037467674
GO:0007017	microtubule-based process	1	55	0.038148227
GO:0009269	response to desiccation	1	55	0.038148227
GO:0005794	Golgi apparatus	2	55	0.040240628
GO:0009532	plastid stroma	1	55	0.040586003
GO:0003713	transcription coactivator activity	1	55	0.043010885
GO:0010087	phloem or xylem histogenesis	1	55	0.043010885
GO:0010305	leaf vascular tissue pattern formation	1	55	0.043010885
GO:0005992	trehalose biosynthetic process	1	55	0.045422921
GO:0005839	proteasome core complex	1	55	0.050208655
GO:0010182	sugar mediated signaling	1	55	0.052582451
GO:0016126	sterol biosynthetic process	1	55	0.054943598
GO:0005643	nuclear pore	1	55	0.057292145
GO:0005200	structural constituent of cytoskeleton	1	55	0.061951632
GO:0008283	cell proliferation	1	55	0.064262668
GO:0009813	flavonoid biosynthetic process	1	55	0.064262668
GO:0009911	positive regulation of flower development	1	55	0.064262668
GO:0015995	chlorophyll biosynthetic process	1	55	0.064262668
GO:0005829	cytosol	2	55	0.065042851
GO:0009620	response to fungus	1	55	0.068847569
GO:0009809	lignin biosynthetic process	1	55	0.073383224
GO:0009790	embryonic development	1	55	0.075632703
GO:0005737	cytoplasm	3	55	0.075707831
GO:0010224	response to UV-B	1	55	0.077870013
GO:0005773	vacuole	3	55	0.082290385
GO:0043565	sequence-specific DNA binding	1	55	0.086698502
GO:0009640	photomorphogenesis	1	55	0.08887567
GO:0009744	response to sucrose stimulus	1	55	0.08887567
GO:0042538	hyperosmotic salinity response	1	55	0.08887567
GO:0008643	carbohydrate transport	1	55	0.091040949
GO:0006096	glycolysis	1	55	0.101690621
GO:0006633	fatty acid biosynthetic process	1	55	0.110001027
GO:0008415	acyltransferase activity	1	55	0.133845873
GO:0005524	ATP binding	3	55	0.145251197
GO:0008026	ATP-dependent helicase activity	1	55	0.150694471
GO:0006810	transport	2	55	0.153641485

Cluster 55 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0008565	protein transporter activity	1	55	0.156119656
GO:0009055	electron carrier activity	1	55	0.161451208
GO:0048366	leaf development	1	55	0.163207776
GO:0006281	DNA repair	1	55	0.164954105
GO:0015144	carbohydrate transmembrane transporter activity	1	55	0.164954105
GO:0005351	sugar:hydrogen symporter activity	1	55	0.168416204
GO:0005507	copper ion binding	1	55	0.212778907
GO:0005488	binding	2	55	0.215047137
GO:0007275	multicellular organismal development	1	55	0.241350617
GO:0042742	defense response to bacterium	1	55	0.250044971
GO:0005525	GTP binding	1	55	0.293387961
GO:0009409	response to cold	1	55	0.304646383
GO:0006511	ubiquitin-dependent protein catabolic process	1	55	0.306280431
GO:0006979	response to oxidative stress	1	55	0.30788897
GO:0005215	transporter activity	1	55	0.330329203
GO:0009793	embryonic development ending in seed dormancy	1	55	0.356138391
GO:0003723	RNA binding	1	55	0.361051912
GO:0016757	transferase activity, transferring glycosyl groups	1	55	0.361592749
GO:0009570	chloroplast stroma	1	55	0.370909758
GO:0003824	catalytic activity	1	55	0.371648878
GO:0009941	chloroplast envelope	1	55	0.371648878

Cluster 55

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000059	1	AT3G59020					
GO:0000170	1	AT1G14290					
GO:0000184	1	AT5G47010					
GO:0003713	1	AT5G14520					
GO:0003723	1	AT4G32720					
GO:0003724	1	AT5G47010					
GO:0003735	8	AT1G01100	AT1G14320	AT3G02080	AT3G11250	AT3G22230	AT4G25740
		AT5G48760	AT5G60670				
GO:0003824	1	AT1G14290					
GO:0003878	1	AT1G10670					
GO:0004129	1	AT4G21105					
GO:0004356	1	AT3G17820					
GO:0004550	1	AT4G23900					
GO:0004601	2	AT1G05260	AT4G11290				
GO:0004675	1	AT5G38280					
GO:0004793	1	AT3G04520					
GO:0004805	1	AT5G10100					
GO:0004815	1	AT4G31180					
GO:0005085	1	AT4G16340					
GO:0005200	1	AT2G29550					
GO:0005215	1	AT4G14160					
GO:0005351	1	AT1G75220					
GO:0005488	2	AT2G34040	AT4G16340				
GO:0005507	1	AT3G17820					
GO:0005524	3	AT3G53230	AT4G23900	AT4G31180			
GO:0005525	1	AT4G16340					
GO:0005618	3	AT2G29550	AT3G02080	AT4G32720			
GO:0005643	1	AT3G59020					
GO:0005654	1	AT4G32720					
GO:0005730	3	AT1G14320	AT3G19760	AT3G53230			
GO:0005737	3	AT3G59020	AT4G26110	AT4G31180			

Cluster 55 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0005773	3	AT1G14320	AT1G32400	AT2G29550			
GO:0005783	3	AT1G05260	AT1G14290	AT5G27330			
GO:0005794	2	AT1G14290	AT3G55830				
GO:0005829	2	AT1G10670	AT3G17820				
GO:0005839	1	AT1G79210					
GO:0005840	5	AT1G01100	AT3G02080	AT3G11250	AT3G22230	AT5G60670	
GO:0005886	12	AT1G01100	AT1G14320	AT1G75220	AT2G29550	AT3G17820	AT3G25290
		AT3G53230	AT4G16340	AT4G21105	AT4G26110	AT5G46700	AT5G47010
GO:0005992	1	AT5G10100					
GO:0006085	1	AT1G10670					
GO:0006096	1	AT1G76550					
GO:0006183	1	AT4G23900					
GO:0006228	1	AT4G23900					
GO:0006241	1	AT4G23900					
GO:0006281	1	AT4G26110					
GO:0006334	2	AT1G07790	AT4G26110				
GO:0006412	6	AT1G14320	AT3G02080	AT3G11250	AT3G22230	AT4G25740	AT5G48760
GO:0006414	2	AT1G01100	AT3G11250				
GO:0006422	1	AT4G31180					
GO:0006511	1	AT1G79210					
GO:0006542	1	AT3G17820					
GO:0006567	1	AT3G04520					
GO:0006633	1	AT1G10670					
GO:0006810	2	AT1G75220	AT4G14160				
GO:0006916	1	AT2G34040					
GO:0006979	1	AT4G11290					
GO:0007017	1	AT2G29550					
GO:0007275	1	AT3G25290					
GO:0007568	2	AT1G10670	AT5G46700				
GO:0008026	1	AT3G19760					
GO:0008283	1	AT5G14520					
GO:0008415	1	AT1G63050					
GO:0008565	1	AT3G59020					
GO:0008643	1	AT1G75220					
GO:0009055	1	AT4G21105					
GO:0009269	1	AT1G05260					
GO:0009346	1	AT1G10670					
GO:0009409	1	AT1G05260					
GO:0009532	1	AT1G66670					
GO:0009534	1	AT1G66670					
GO:0009570	1	AT1G66670					
GO:0009620	1	AT5G38280					
GO:0009640	1	AT1G14290					
GO:0009651	3	AT1G73230	AT2G29550	AT3G11250			
GO:0009744	1	AT5G47010					
GO:0009790	1	AT4G32720					
GO:0009793	1	AT3G52940					
GO:0009809	1	AT3G19450					
GO:0009813	1	AT3G51240					
GO:0009840	1	AT1G66670					
GO:0009911	1	AT1G10670					
GO:0009933	1	AT5G46700					
GO:0009941	1	AT1G66670					
GO:0009956	1	AT5G46700					
GO:0010015	1	AT5G46700					
GO:0010025	1	AT1G10670					
GO:0010087	1	AT3G55830					
GO:0010182	1	AT5G47010					
GO:0010224	1	AT3G51240					
GO:0010305	1	AT5G46700					

Cluster 55 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)					
GO:0010317	1	AT1G76550					
GO:0015144	1	AT1G75220					
GO:0015934	2	AT1G14320	AT5G48760				
GO:0015995	1	AT1G10670					
GO:0016020	8	AT1G32400	AT1G63050	AT1G75220	AT3G11250	AT3G19760	AT3G25290
		AT3G52940	AT4G25740				
GO:0016117	1	AT1G10670					
GO:0016126	1	AT3G52940					
GO:0016246	1	AT5G47010					
GO:0016337	1	AT3G55830					
GO:0016757	1	AT3G55830					
GO:0019252	1	AT1G10670					
GO:0022625	4	AT1G14320	AT3G22230	AT5G48760	AT5G60670		
GO:0022626	8	AT1G01100	AT1G14320	AT3G02080	AT3G11250	AT3G17820	AT3G22230
		AT4G25740	AT5G48760				
GO:0022627	2	AT3G02080	AT4G25740				
GO:0030127	1	AT4G14160					
GO:0035251	1	AT3G55830					
GO:0042128	1	AT3G17820					
GO:0042254	3	AT3G22230	AT4G32720	AT5G60670			
GO:0042538	1	AT1G05260					
GO:0042742	1	AT1G79210					
GO:0043481	1	AT1G10670					
GO:0043565	1	AT4G12750					
GO:0045298	1	AT2G29550					
GO:0045486	1	AT3G51240					
GO:0045551	1	AT3G19450					
GO:0045793	1	AT1G10670					
GO:0045995	1	AT1G10670					
GO:0046520	1	AT1G14290					
GO:0046686	4	AT2G29550	AT3G17820	AT3G53230	AT4G31180		
GO:0046786	1	AT1G32400					
GO:0047334	1	AT1G76550					
GO:0048366	1	AT1G10670					
GO:0050613	1	AT3G52940					
GO:0051020	1	AT4G16340					

Cluster 56

Cluster 56

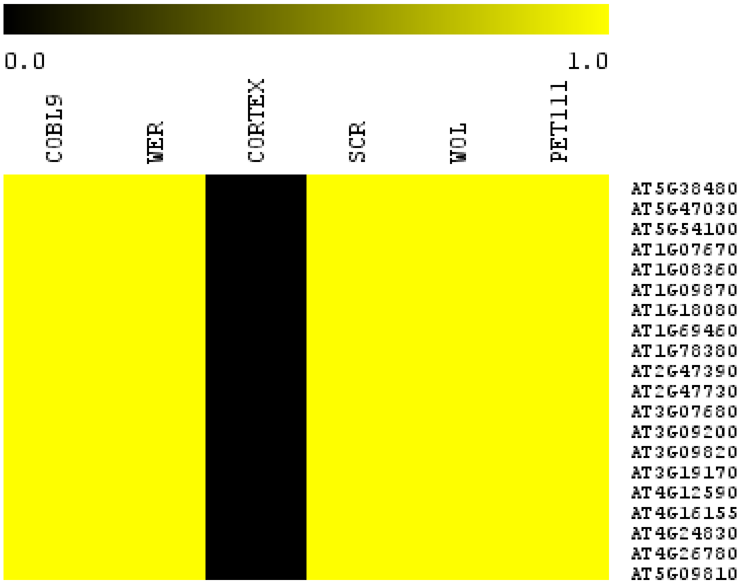
AT1G31230
AT3G04120
AT3G11940

Cluster 56 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004365	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	1	3	1.44E-04
GO:0004072	aspartate kinase activity	1	3	4.31E-04
GO:0004412	homoserine dehydrogenase activity	1	3	4.31E-04
GO:0009067	aspartate family amino acid biosynthetic process	1	3	4.31E-04
GO:0008943	glyceraldehyde-3-phosphate dehydrogenase activity	1	3	7.19E-04
GO:0006094	gluconeogenesis	1	3	0.00129366
GO:0005740	mitochondrial envelope	1	3	0.002011395
GO:0010154	fruit development	1	3	0.003015067
GO:0048316	seed development	1	3	0.003587987
GO:0042542	response to hydrogen peroxide	1	3	0.004589537
GO:0009744	response to sucrose stimulus	1	3	0.005304104
GO:0006096	glycolysis	1	3	0.006160676
GO:0006950	response to stress	1	3	0.012128977
GO:0009408	response to heat	1	3	0.013401599
GO:0005829	cytosol	1	3	0.024338155
GO:0006979	response to oxidative stress	1	3	0.027115656
GO:0009507	chloroplast	2	3	0.03349462
GO:0048046	apoplast	1	3	0.03387456
GO:0046686	response to cadmium ion	1	3	0.038935069
GO:0009651	response to salt stress	1	3	0.040432401
GO:0009570	chloroplast stroma	1	3	0.049213621
GO:0005739	mitochondrion	1	3	0.102623018
GO:0016020	membrane	1	3	0.168256477
GO:0005886	plasma membrane	1	3	0.203214985
GO:0005634	nucleus	1	3	0.207019295

Cluster 56

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0004072	1	AT1G31230	
GO:0004365	1	AT3G04120	
GO:0004412	1	AT1G31230	
GO:0005634	1	AT3G04120	
GO:0005739	1	AT3G04120	
GO:0005740	1	AT3G04120	
GO:0005829	1	AT3G04120	
GO:0005886	1	AT3G04120	
GO:0006094	1	AT3G04120	
GO:0006096	1	AT3G04120	
GO:0006950	1	AT3G04120	
GO:0006979	1	AT3G04120	
GO:0008943	1	AT3G04120	
GO:0009067	1	AT1G31230	
GO:0009408	1	AT3G04120	
GO:0009507	2	AT1G31230	AT3G04120
GO:0009570	1	AT1G31230	
GO:0009651	1	AT3G04120	
GO:0009744	1	AT3G04120	
GO:0010154	1	AT3G04120	
GO:0016020	1	AT3G04120	
GO:0042542	1	AT3G04120	
GO:0046686	1	AT3G04120	
GO:0048046	1	AT3G04120	
GO:0048316	1	AT3G04120	

Cluster 57



Cluster 57
AT1G07670
AT1G08360
AT1G09870
AT1G18080
AT1G69460
AT1G78380
AT2G47390
AT2G47730
AT3G07680
AT3G09200
AT3G09820
AT3G19170
AT4G12590
AT4G16155
AT4G24830
AT4G26780
AT5G09810
AT5G38480
AT5G47030
AT5G54100

Cluster 57 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0009570	chloroplast stroma	5	20	1.65E-05
GO:0009507	chloroplast	10	20	1.75E-05
GO:0043295	glutathione binding	2	20	1.83E-05
GO:0005886	plasma membrane	8	20	7.70E-05
GO:0046686	response to cadmium ion	4	20	1.21E-04
GO:0022626	cytosolic ribosome	3	20	5.03E-04
GO:0005739	mitochondrion	5	20	5.96E-04
GO:0009407	toxin catabolic process	2	20	6.93E-04
GO:0004364	glutathione transferase activity	2	20	7.97E-04

Cluster 57 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004055	argininosuccinate synthase activity	1	20	9.59E-04
GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	1	20	0.001916258
GO:0004001	adenosine kinase activity	1	20	0.001916258
GO:0006169	adenosine salvage	1	20	0.001916258
GO:0051605	protein maturation via proteolysis	1	20	0.001916258
GO:0009651	response to salt stress	3	20	0.002374136
GO:0000774	adenyl-nucleotide exchange factor activity	1	20	0.002871768
GO:0004148	dihydrolipoyl dehydrogenase activity	1	20	0.003825535
GO:0005753	mitochondrial proton-transporting ATP synthase complex	1	20	0.003825535
GO:0009941	chloroplast envelope	3	20	0.004669412
GO:0042631	cellular response to water deprivation	1	20	0.004777561
GO:0008320	protein transmembrane transporter activity	1	20	0.005727849
GO:0006526	arginine biosynthetic process	1	20	0.007623218
GO:0051087	chaperone binding	1	20	0.007623218
GO:0005856	cytoskeleton	1	20	0.008568304
GO:0045309	protein phosphorylated amino acid binding	1	20	0.011393194
GO:0005840	ribosome	2	20	0.012562263
GO:0009409	response to cold	2	20	0.013070281
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational mechanism	1	20	0.01420258
GO:0004252	serine-type endopeptidase activity	1	20	0.015135606
GO:0007010	cytoskeleton organization	1	20	0.018850598
GO:0005730	nucleolus	2	20	0.020075554
GO:0048046	apoplast	2	20	0.020532057
GO:0006414	translational elongation	1	20	0.020697855
GO:0005200	structural constituent of cytoskeleton	1	20	0.023455993
GO:0003735	structural constituent of ribosome	2	20	0.027477588
GO:0010319	stromule	1	20	0.028926594
GO:0006412	translation	2	20	0.029540929
GO:0008236	serine-type peptidase activity	1	20	0.029832465
GO:0005618	cell wall	2	20	0.030767824
GO:0003993	acid phosphatase activity	1	20	0.033439189
GO:0009845	seed germination	1	20	0.03433669
GO:0006508	proteolysis	2	20	0.036954543
GO:0042803	protein homodimerization activity	1	20	0.037910041
GO:0045454	cell redox homeostasis	1	20	0.04233942
GO:0005834	heterotrimeric G-protein complex	1	20	0.048471393
GO:0048364	root development	1	20	0.061342817
GO:0022625	cytosolic large ribosomal subunit	1	20	0.087606596
GO:0005507	copper ion binding	1	20	0.092354033
GO:0009416	response to light stimulus	1	20	0.09313993
GO:0009611	response to wounding	1	20	0.09313993
GO:0005524	ATP binding	2	20	0.098676235
GO:0006886	intracellular protein transport	1	20	0.100144808
GO:0042742	defense response to bacterium	1	20	0.113790818
GO:0009579	thylakoid	1	20	0.139667891
GO:0005829	cytosol	1	20	0.141051556
GO:0006979	response to oxidative stress	1	20	0.154583884
GO:0006457	protein folding	1	20	0.162441718
GO:0000166	nucleotide binding	1	20	0.171366344
GO:0009733	response to auxin stimulus	1	20	0.173868849
GO:0005783	endoplasmic reticulum	1	20	0.199476876

Cluster 57 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005515	protein binding	2	20	0.216591408
GO:0006952	defense response	1	20	0.231937555
GO:0016020	membrane	2	20	0.23679704
GO:0006499	N-terminal protein myristoylation	1	20	0.242121865
GO:0005634	nucleus	2	20	0.27382333
GO:0005737	cytoplasm	1	20	0.275433475
GO:0005773	vacuole	1	20	0.282731363

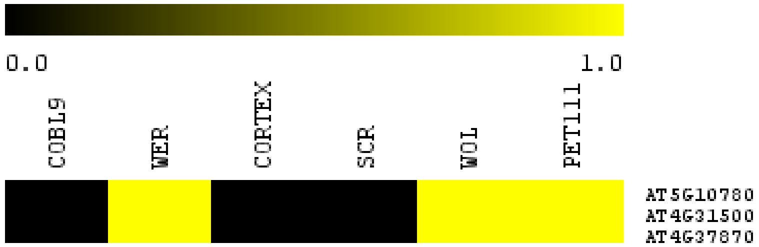
Cluster 57

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0000166	1	AT1G18080					
GO:0000275	1	AT5G47030					
GO:0000774	1	AT4G26780					
GO:0003735	2	AT1G08360	AT3G09200				
GO:0003993	1	AT1G09870					
GO:0004001	1	AT3G09820					
GO:0004055	1	AT4G24830					
GO:0004148	1	AT4G16155					
GO:0004252	1	AT2G47390					
GO:0004364	2	AT1G78380	AT2G47730				
GO:0005200	1	AT5G09810					
GO:0005507	1	AT3G09820					
GO:0005515	2	AT4G26780	AT5G38480				
GO:0005524	2	AT4G24830	AT5G38480				
GO:0005618	2	AT5G09810	AT5G38480				
GO:0005634	2	AT2G47730	AT3G09200				
GO:0005730	2	AT3G09200	AT5G09810				
GO:0005737	1	AT1G78380					
GO:0005739	5	AT3G19170	AT4G12590	AT5G09810	AT5G38480	AT5G47030	
GO:0005753	1	AT5G47030					
GO:0005773	1	AT5G38480					
GO:0005783	1	AT4G12590					
GO:0005829	1	AT3G09820					
GO:0005834	1	AT1G18080					
GO:0005840	2	AT1G08360	AT3G09200				
GO:0005856	1	AT5G09810					
GO:0005886	8	AT1G08360	AT1G09870	AT1G78380	AT2G47730	AT3G09200	AT3G09820
		AT5G09810	AT5G38480				
GO:0006169	1	AT3G09820					
GO:0006412	2	AT1G08360	AT3G09200				
GO:0006414	1	AT3G09200					
GO:0006457	1	AT4G26780					
GO:0006499	1	AT2G47730					
GO:0006508	2	AT2G47390	AT3G19170				
GO:0006526	1	AT4G24830					
GO:0006886	1	AT3G07680					
GO:0006952	1	AT2G47730					
GO:0006979	1	AT1G78380					
GO:0007010	1	AT5G09810					
GO:0008236	1	AT2G47390					
GO:0008320	1	AT3G07680					
GO:0009407	2	AT1G78380	AT2G47730				
GO:0009409	2	AT2G47730	AT3G09200				
GO:0009416	1	AT5G09810					
GO:0009507	10	AT1G18080	AT1G78380	AT2G47390	AT2G47730	AT3G09200	AT3G09820
		AT3G19170	AT4G16155	AT4G24830	AT5G38480		

Cluster 57 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)				
GO:0009570	5	AT1G78380	AT2G47390	AT2G47730	AT3G19170	AT4G24830
GO:0009579	1	AT2G47730				
GO:0009611	1	AT5G09810				
GO:0009651	3	AT2G47730	AT3G09200	AT5G47030		
GO:0009733	1	AT5G09810				
GO:0009845	1	AT5G09810				
GO:0009941	3	AT2G47730	AT3G19170	AT4G16155		
GO:0010319	1	AT2G47730				
GO:0016020	2	AT3G07680	AT3G09820			
GO:0022625	1	AT1G08360				
GO:0022626	3	AT1G08360	AT1G18080	AT3G09200		
GO:0042631	1	AT1G78380				
GO:0042742	1	AT2G47730				
GO:0042803	1	AT4G26780				
GO:0043295	2	AT1G78380	AT2G47730			
GO:0045309	1	AT5G38480				
GO:0045454	1	AT4G16155				
GO:0046686	4	AT1G18080	AT1G78380	AT3G09820	AT3G19170	
GO:0046933	1	AT5G47030				
GO:0048046	2	AT3G09820	AT3G19170			
GO:0048364	1	AT5G09810				
GO:0051087	1	AT4G26780				
GO:0051605	1	AT3G19170				

Cluster 58



Cluster 58
AT4G31500
AT4G37870
AT5G10780

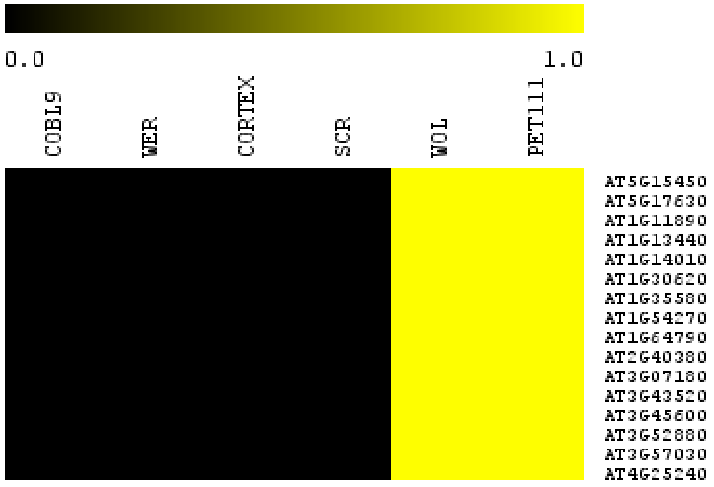
Cluster 58 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0004612	phosphoenolpyruvate carboxykinase (ATP) activity	1	3	1.44E-04
GO:0048830	adventitious root development	1	3	5.75E-04
GO:0009759	indole glucosinolate biosynthetic process	1	3	8.63E-04
GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	1	3	8.63E-04
GO:0009684	indoleacetic acid biosynthetic process	1	3	0.001006373
GO:0009641	shade avoidance	1	3	0.001150031
GO:0006094	gluconeogenesis	1	3	0.00129366
GO:0052544	callose deposition in cell wall during defense response	1	3	0.002298296
GO:0000162	tryptophan biosynthetic process	1	3	0.002728441
GO:0010114	response to red light	1	3	0.005732514
GO:0016020	membrane	2	3	0.011499264

Cluster 58 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0042742	defense response to bacterium	1	3	0.01903086
GO:0019825	oxygen binding	1	3	0.027115656
GO:0005730	nucleolus	1	3	0.033462623
GO:0005783	endoplasmic reticulum	1	3	0.037161276
GO:0046686	response to cadmium ion	1	3	0.038935069
GO:0005524	ATP binding	1	3	0.084606448
GO:0005739	mitochondrion	1	3	0.102623018
GO:0005886	plasma membrane	1	3	0.203214985
GO:0005575	cellular_component	1	3	0.422237836
GO:0003674	molecular_function	1	3	0.424399891
GO:0008150	biological_process	1	3	0.443314275

Cluster 58

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**	
GO:0000162	1	AT4G31500	
GO:0003674	1	AT5G10780	
GO:0004612	1	AT4G37870	
GO:0005524	1	AT4G37870	
GO:0005575	1	AT5G10780	
GO:0005730	1	AT4G37870	
GO:0005739	1	AT4G31500	
GO:0005783	1	AT4G31500	
GO:0005886	1	AT4G31500	
GO:0006094	1	AT4G37870	
GO:0008150	1	AT5G10780	
GO:0009641	1	AT4G31500	
GO:0009684	1	AT4G31500	
GO:0009759	1	AT4G31500	
GO:0010114	1	AT4G31500	
GO:0016020	2	AT4G31500	AT4G37870
GO:0016709	1	AT4G31500	
GO:0019825	1	AT4G31500	
GO:0042742	1	AT4G31500	
GO:0046686	1	AT4G37870	
GO:0048830	1	AT4G31500	
GO:0052544	1	AT4G31500	

Cluster 59



Cluster 59
AT1G11890
AT1G13440
AT1G14010
AT1G30620
AT1G35580
AT1G54270
AT1G64790
AT2G40380
AT3G07180
AT3G43520
AT3G45600
AT3G52880
AT3G57030
AT4G25240
AT5G15450
AT5G17630

Cluster 59 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005886	plasma membrane	9	16	8.45E-07
GO:0005782	peroxisomal matrix	1	16	7.67E-04
GO:0019567	arabinose biosynthetic process	1	16	7.67E-04
GO:0050373	UDP-arabinose 4-epimerase activity	1	16	7.67E-04
GO:0005783	endoplasmic reticulum	3	16	9.64E-04
GO:0046686	response to cadmium ion	3	16	0.001104278
GO:0015712	hexose phosphate transport	1	16	0.002298296
GO:0016656	monodehydroascorbate reductase (NADH) activity	1	16	0.003062191
GO:0005355	glucose transmembrane transporter activity	1	16	0.003824985
GO:0008943	glyceraldehyde-3-phosphate dehydrogenase activity	1	16	0.003824985
GO:0042744	hydrogen peroxide catabolic process	1	16	0.003824985
GO:0005794	Golgi apparatus	2	16	0.004120354
GO:0006094	gluconeogenesis	1	16	0.00686518
GO:0005829	cytosol	2	16	0.007236366
GO:0004564	beta-fructofuranosidase activity	1	16	0.008378704
GO:0009821	alkaloid biosynthetic process	1	16	0.009133827
GO:0016844	strictosidine synthase activity	1	16	0.010640799
GO:0018119	peptidyl-cysteine S-nitrosylation	1	16	0.010640799
GO:0009532	plastid stroma	1	16	0.012143413
GO:0006520	amino acid metabolic process	1	16	0.01289309
GO:0009225	nucleotide-sugar metabolic process	1	16	0.01364168
GO:0016020	membrane	4	16	0.013786955
GO:0009832	plant-type cell wall biogenesis	1	16	0.018110476
GO:0009507	chloroplast	5	16	0.020914181
GO:0009658	chloroplast organization	1	16	0.026931842
GO:0006096	glycolysis	1	16	0.032006674
GO:0015297	antiporter activity	1	16	0.032727411
GO:0007568	aging	1	16	0.03344709
GO:0046658	anchored to plasma membrane	1	16	0.044116207
GO:0008026	ATP-dependent helicase activity	1	16	0.049710525
GO:0003743	translation initiation factor activity	1	16	0.051098772
GO:0016192	vesicle-mediated transport	1	16	0.055238845
GO:0009408	response to heat	1	16	0.067439032
GO:0005507	copper ion binding	1	16	0.075391365

Cluster 59 GO identifier (con.)	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0005777	peroxisome	1	16	0.07866258
GO:0016887	ATPase activity	1	16	0.080613459
GO:0042742	defense response to bacterium	1	16	0.093394364
GO:0006979	response to oxidative stress	1	16	0.12830716
GO:0031225	anchored to membrane	1	16	0.135707028
GO:0005215	transporter activity	1	16	0.146250651
GO:0005730	nucleolus	1	16	0.15381657
GO:0009505	plant-type cell wall	1	16	0.15381657
GO:0048046	apoplast	1	16	0.155415703
GO:0005975	carbohydrate metabolic process	1	16	0.184352888
GO:0005618	cell wall	1	16	0.186763112
GO:0009570	chloroplast stroma	1	16	0.210213463
GO:0003824	catalytic activity	1	16	0.217155629
GO:0009941	chloroplast envelope	1	16	0.217155629
GO:0005634	nucleus	2	16	0.24332888
GO:0005488	binding	1	16	0.246438751
GO:0005524	ATP binding	1	16	0.303962515
GO:0005739	mitochondrion	1	16	0.335980303

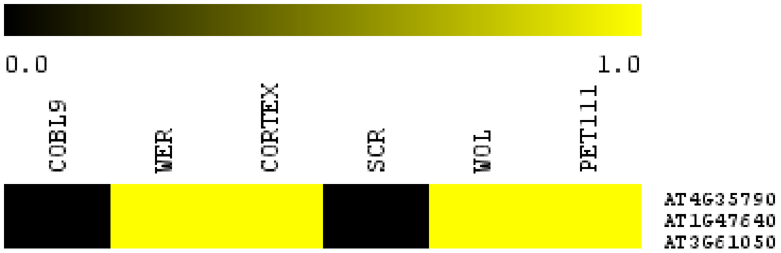
Cluster 59

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**					
GO:0003743	1	AT1G54270					
GO:0003824	1	AT1G30620					
GO:0004564	1	AT1G35580					
GO:0005215	1	AT1G11890					
GO:0005355	1	AT5G17630					
GO:0005488	1	AT1G64790					
GO:0005507	1	AT4G25240					
GO:0005524	1	AT5G15450					
GO:0005618	1	AT1G13440					
GO:0005634	2	AT1G13440	AT1G35580				
GO:0005730	1	AT1G13440					
GO:0005739	1	AT1G13440					
GO:0005777	1	AT3G52880					
GO:0005782	1	AT3G52880					
GO:0005783	3	AT1G11890	AT3G07180	AT3G57030			
GO:0005794	2	AT1G11890	AT1G30620				
GO:0005829	2	AT1G13440	AT1G35580				
GO:0005886	9	AT1G11890	AT1G13440	AT1G35580	AT1G54270	AT3G07180	AT3G45600
		AT3G52880	AT3G57030	AT4G25240			
GO:0005975	1	AT1G35580					
GO:0006094	1	AT1G13440					
GO:0006096	1	AT1G13440					
GO:0006520	1	AT1G35580					
GO:0006979	1	AT1G13440					
GO:0007568	1	AT3G45600					
GO:0008026	1	AT1G54270					
GO:0008943	1	AT1G13440					
GO:0009225	1	AT1G30620					
GO:0009408	1	AT5G15450					
GO:0009505	1	AT3G57030					
GO:0009507	5	AT1G13440	AT3G43520	AT3G52880	AT5G15450	AT5G17630	
GO:0009532	1	AT5G15450					
GO:0009570	1	AT5G15450					
GO:0009658	1	AT5G15450					

Cluster 59 (con.)

GO Identifier	#Loci	Associated Loci (Left to Right)			
GO:0009821	1	AT3G57030			
GO:0009832	1	AT1G30620			
GO:0009941	1	AT3G43520			
GO:0015297	1	AT5G17630			
GO:0015712	1	AT5G17630			
GO:0016020	4	AT1G11890	AT1G13440	AT1G35580	AT1G64790
GO:0016192	1	AT1G11890			
GO:0016656	1	AT3G52880			
GO:0016844	1	AT3G57030			
GO:0016887	1	AT5G15450			
GO:0018119	1	AT3G52880			
GO:0019567	1	AT1G30620			
GO:0031225	1	AT4G25240			
GO:0042742	1	AT1G13440			
GO:0042744	1	AT3G52880			
GO:0046658	1	AT4G25240			
GO:0046686	3	AT1G13440	AT1G54270	AT3G52880	
GO:0048046	1	AT3G52880			
GO:0050373	1	AT1G30620			

Cluster 60



Cluster 60
AT1G47640
AT3G61050
AT4G35790

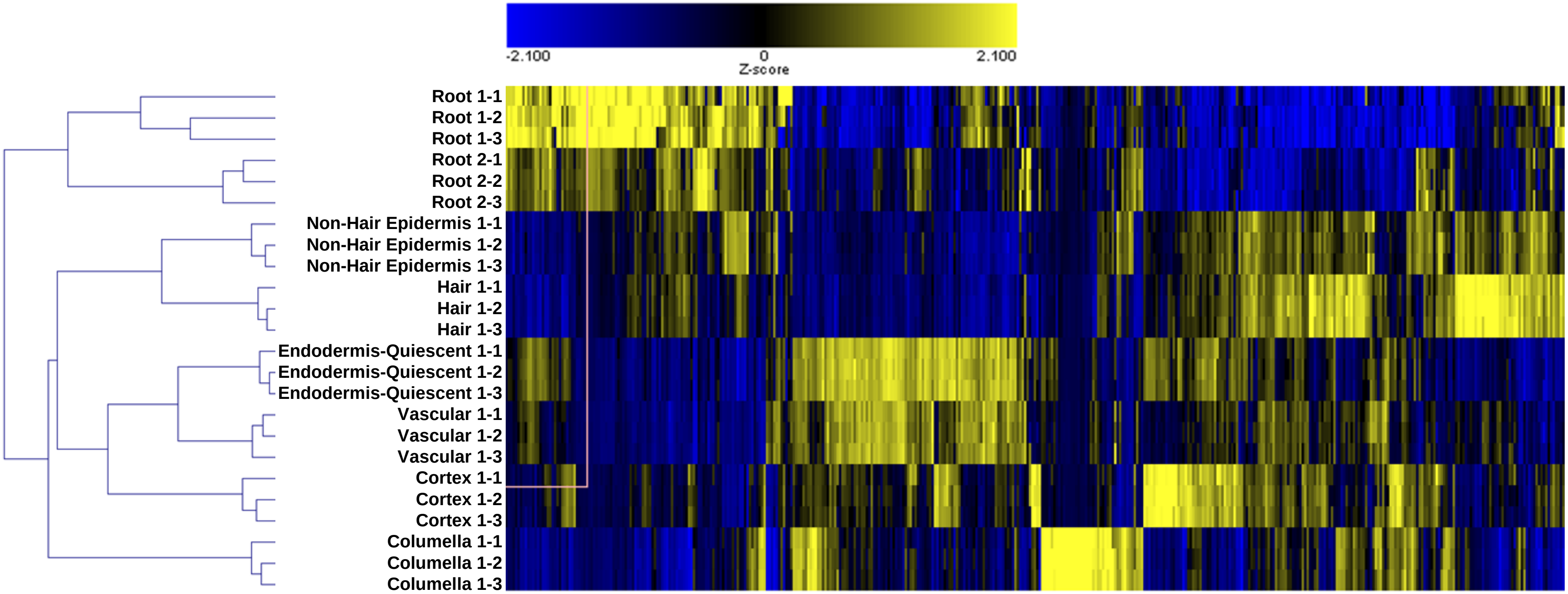
Cluster 60 GO identifier	Description	# Associated to the GO in Cluster	Total # in Cluster	p-value
GO:0046473	phosphatidic acid metabolic process	1	3	1.44E-04
GO:0015630	microtubule cytoskeleton	1	3	5.75E-04
GO:0012501	programmed cell death	1	3	0.001437263
GO:0004630	phospholipase D activity	1	3	0.001724384
GO:0009409	response to cold	1	3	0.026561027
GO:0005773	vacuole	1	3	0.061052959
GO:0005739	mitochondrion	1	3	0.102623018
GO:0016020	membrane	1	3	0.168256477
GO:0005886	plasma membrane	1	3	0.203214985
GO:0003674	molecular_function	1	3	0.424399891
GO:0008150	biological_process	1	3	0.443314275

Cluster 60

GO Identifier	#Loci	Associated Loci (Left to Right)
GO:0003674	1	AT1G47640
GO:0004630	1	AT4G35790
GO:0005739	1	AT1G47640
GO:0005773	1	AT4G35790

Cluster 60 (con.)

GO Identifier	**#Loci**	**Associated Loci (Left to Right)**
GO:0005886	1	AT4G35790
GO:0008150	1	AT1G47640
GO:0009409	1	AT4G35790
GO:0012501	1	AT4G35790
GO:0015630	1	AT4G35790
GO:0016020	1	AT4G35790
GO:0046473	1	AT4G35790



Supplementary Figure S6. Clustering of samples profiled by peak-integration proteomics.

A heat map of the unsupervised agglomerative cluster of samples profiled by peak-integration proteomics is shown. The y-axis shows technical and/or biological replicates of: whole sorted wild-type roots (Roots 1 and 2), non-hair epidermal cells, hair cells, endodermal/quiescent cells, cortex cells, and columella cells. The columns of the y-axis are Z-score protein expression values. Blue and yellow represent over 2-fold positive and negative enrichment, respectively. Note that technical replicates of the same sample cluster together, as do the biological replicates of whole wild-type roots. Striking differences between cell type profiles are visible; similarities between certain cell types are as well. For example, the epidermal hair and non-hair cells cluster together.

Supplementary Table S1. Raw data output from the Trans-Proteomic Pipeline of LTQ runs performed for the root cellular proteome. Tranche hash:
2vxeLdEgJYUtGS1qbaktSbd1JuYRLQAHeB3YfAeF+F/ZfEiZwzE2ctZqD76Ocvsy
uTHRXEWyWvO4KbhVIZYZHj36TEEAAAAAAAADxQ==

These raw data have been uploaded for public release and access at the Proteome Commons and are found at www.proteomecommons.org/tranche under the project “The Protein Expression Landscape of the *Arabidopsis* Root”. The data files for Supplementary Table S1, which include all raw data of the root cellular proteome, were too large for the file formats allowed in the Supplementary Information section. Thus, these data are found at Proteome Commons under the aforementioned project title and are accessible with the following Tranche hash:

2vxeLdEgJYUtGS1qbaktSbd1JuYRLQAHeB3YfAeF+F/ZfEiZwzE2ctZqD76Ocvsy
uTHRXEWyWvO4KbhVIZYZHj36TEEAAAAAAAADxQ==

All encryption at the tranche repository should be removed, but if a passphrase is requested, it is 'arabidopsis'.
A direct link to this table at the Proteome Commons is the following:
https://proteomecommons.org/dataset.jsp?i=76689

Supplementary Table S1 can also be found at the Duke Genome Express Repository at the following link:

https://discovery.genome.duke.edu/express/resources/2010/Final_Supplementary_Table_S1.xls

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01040	0	0	0	0	1	0
AT1G01090	1	1	1	1	1	1
AT1G01100	0	0	0	1	0	0
AT1G01180	0	0	0	0	0	1
AT1G01820	1	0	0	0	1	1
AT1G01910	1	0	0	0	0	0
AT1G01950	0	1	0	0	0	0
AT1G01960	0	0	1	0	0	0
AT1G02420	0	0	1	0	0	0
AT1G02500	0	0	1	1	1	0
AT1G02560	0	0	0	1	0	1
AT1G03230	0	1	0	0	0	0
AT1G03330	1	0	0	0	1	0
AT1G03860	1	1	1	1	1	1
AT1G03880	0	0	0	0	1	0
AT1G04040	1	0	1	0	1	0
AT1G04120	1	0	1	0	1	0
AT1G04170	1	0	0	0	1	0
AT1G04270	1	0	0	1	0	1
AT1G04410	1	1	1	1	1	1
AT1G04430	1	1	1	1	1	0
AT1G04690	0	0	0	0	1	0
AT1G04810	1	0	0	0	0	0
AT1G04850	0	0	0	0	1	0
AT1G04910	0	1	1	0	1	0
AT1G04980	1	0	1	0	1	1
AT1G05260	0	0	0	1	0	0
AT1G05500	1	0	0	0	0	1
AT1G05620	1	0	0	0	0	0
AT1G06000	0	0	0	0	1	0
AT1G06220	1	0	0	0	1	0
AT1G06290	1	1	1	1	1	1
AT1G06400	1	0	0	0	1	0
AT1G06430	0	0	1	0	0	0
AT1G06530	1	0	1	0	1	0
AT1G06800	0	0	1	0	0	0
AT1G06890	1	0	0	0	0	0
AT1G06900	1	0	0	0	1	0
AT1G06950	1	1	1	1	1	1
AT1G07410	0	1	0	0	0	0
AT1G07670	1	1	0	1	1	1
AT1G07750	0	0	0	0	1	0
AT1G07790	0	0	0	1	0	0
AT1G07810	1	1	1	0	1	0
AT1G07890	1	0	1	0	1	1
AT1G07960	0	0	1	0	0	1
AT1G08110	1	0	0	0	1	1
AT1G08200	0	0	0	1	1	0
AT1G08220	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G08360	1	1	0	1	1	1
AT1G08450	1	0	0	0	0	0
AT1G08470	1	0	0	0	1	1
AT1G08480	0	0	0	1	1	1
AT1G08640	0	0	0	0	1	0
AT1G08830	1	0	1	0	1	1
AT1G08840	0	0	0	0	1	0
AT1G09210	1	1	1	1	1	1
AT1G09270	1	0	0	0	1	0
AT1G09620	0	1	0	1	1	0
AT1G09630	1	0	1	0	1	0
AT1G09640	1	0	1	1	1	1
AT1G09760	1	0	0	0	1	0
AT1G09780	1	0	1	1	1	1
AT1G09830	1	0	0	0	1	0
AT1G09850	1	0	1	0	1	0
AT1G09870	1	1	0	1	1	1
AT1G10130	1	0	0	0	1	1
AT1G10270	1	0	0	0	1	0
AT1G10290	1	0	0	1	1	1
AT1G10510	0	1	0	0	0	0
AT1G10590	1	0	0	0	1	0
AT1G10670	0	0	0	1	0	0
AT1G10760	1	1	0	1	0	1
AT1G10840	0	0	0	1	1	0
AT1G10950	1	1	1	1	1	1
AT1G11580	0	0	1	1	1	0
AT1G11680	1	1	1	1	1	0
AT1G11840	1	0	1	1	1	1
AT1G11860	1	1	1	1	1	1
AT1G11890	0	0	0	0	1	1
AT1G11910	1	1	1	1	1	1
AT1G12000	0	0	1	1	1	0
AT1G12230	1	1	1	1	1	1
AT1G12240	1	0	1	0	1	0
AT1G12310	0	0	0	0	1	0
AT1G12640	1	0	1	0	0	0
AT1G12840	1	1	1	1	1	1
AT1G13000	1	0	0	0	0	1
AT1G13060	1	0	0	0	1	0
AT1G13280	1	1	1	1	1	1
AT1G13440	0	0	0	0	1	1
AT1G13560	0	0	0	0	1	0
AT1G14010	0	0	0	0	1	1
AT1G14060	1	0	0	0	0	0
AT1G14080	1	1	0	0	1	1
AT1G14210	1	0	0	0	0	0
AT1G14220	1	0	0	0	1	0
AT1G14290	0	0	0	1	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G14320	0	0	0	1	0	0
AT1G14360	1	1	1	0	0	0
AT1G14410	1	0	1	1	1	0
AT1G14610	1	0	0	0	1	0
AT1G14620	1	0	0	0	1	0
AT1G14670	1	0	1	0	1	0
AT1G14710	1	0	0	0	0	0
AT1G14810	1	1	1	1	1	1
AT1G14830	1	1	1	0	1	1
AT1G14850	1	0	0	0	1	0
AT1G14980	1	0	1	1	1	1
AT1G15120	1	0	1	0	0	0
AT1G15210	1	0	1	1	1	0
AT1G15480	1	1	0	0	1	0
AT1G15500	1	1	1	1	1	1
AT1G15690	1	1	1	1	1	1
AT1G15710	1	0	0	0	0	0
AT1G15750	0	0	0	0	1	0
AT1G15930	1	0	0	1	1	1
AT1G16300	1	0	0	0	0	0
AT1G16350	0	0	0	0	1	0
AT1G16560	0	0	1	0	0	0
AT1G16700	0	0	0	1	1	1
AT1G16870	1	0	0	0	1	0
AT1G16890	0	0	0	0	1	0
AT1G16920	1	0	0	0	1	0
AT1G17160	1	0	0	0	0	0
AT1G17180	1	0	0	0	0	1
AT1G17190	1	0	0	0	0	1
AT1G17290	1	1	1	1	1	1
AT1G17745	1	1	0	0	1	0
AT1G17890	1	0	0	0	0	0
AT1G18080	1	1	0	1	1	1
AT1G18260	1	1	1	0	1	0
AT1G18500	1	1	0	0	1	0
AT1G18540	1	0	1	1	1	0
AT1G18630	1	0	0	0	1	0
AT1G18640	1	0	0	1	0	0
AT1G18700	1	0	0	0	1	0
AT1G19130	1	0	0	0	0	0
AT1G19140	1	0	0	0	0	0
AT1G19360	1	1	1	1	1	1
AT1G19370	0	0	1	0	1	1
AT1G19440	0	0	0	0	1	0
AT1G19520	1	1	0	0	1	0
AT1G19580	1	0	1	1	0	1
AT1G19800	0	0	0	0	1	0
AT1G19900	0	0	0	0	1	0
AT1G19920	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G20050	1	1	0	1	0	1
AT1G20090	0	0	0	0	1	0
AT1G20200	1	0	0	0	1	0
AT1G20230	1	0	0	0	0	0
AT1G20300	0	1	0	0	0	0
AT1G20330	1	1	1	1	1	1
AT1G20430	1	0	1	0	1	1
AT1G20450	0	0	0	0	0	1
AT1G20510	1	1	0	0	0	0
AT1G20560	1	0	0	0	0	0
AT1G20575	1	0	1	1	1	1
AT1G20580	1	0	0	0	1	0
AT1G20620	0	0	1	0	0	0
AT1G20630	0	0	0	0	0	1
AT1G20840	1	0	0	1	0	0
AT1G20950	0	0	0	0	1	0
AT1G20960	1	0	0	0	1	1
AT1G21160	0	0	0	0	1	0
AT1G21370	1	0	0	0	0	0
AT1G21560	1	0	0	0	0	0
AT1G21650	1	0	1	0	0	0
AT1G21690	0	0	0	0	1	0
AT1G21720	0	1	0	1	0	0
AT1G21750	1	1	1	1	1	1
AT1G21900	1	0	1	0	0	1
AT1G22200	0	0	0	0	1	0
AT1G22300	1	1	1	1	1	1
AT1G22410	1	1	1	1	1	0
AT1G22450	1	1	1	0	1	0
AT1G22460	0	0	0	0	1	0
AT1G22520	1	0	1	1	0	0
AT1G22530	0	0	1	0	1	0
AT1G22840	1	0	1	0	1	1
AT1G23100	1	0	0	0	1	0
AT1G23170	1	0	0	0	0	0
AT1G23190	1	0	0	0	1	1
AT1G23310	0	0	0	0	0	1
AT1G23820	1	0	1	1	1	0
AT1G24090	0	0	0	0	0	1
AT1G24180	1	1	1	1	1	1
AT1G24280	0	1	0	0	0	0
AT1G24360	1	1	1	1	1	1
AT1G24510	1	0	0	1	1	0
AT1G25375	1	0	0	0	1	0
AT1G25380	1	0	0	0	0	0
AT1G25490	1	0	0	0	1	0
AT1G26160	1	0	0	0	0	0
AT1G26460	1	1	1	0	1	0
AT1G26630	1	0	0	0	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G26850	1	1	1	1	1	1
AT1G26940	1	0	1	0	1	0
AT1G27310	0	0	0	0	1	0
AT1G27390	1	0	0	0	1	0
AT1G27400	1	0	1	1	0	0
AT1G27450	1	0	0	0	0	1
AT1G27680	1	0	1	0	0	0
AT1G27770	1	1	1	0	0	1
AT1G27930	1	1	1	1	1	0
AT1G27970	0	0	0	0	1	0
AT1G27980	0	0	1	0	0	0
AT1G28130	0	0	0	0	0	1
AT1G28440	0	1	0	0	0	0
AT1G28510	0	0	0	0	0	1
AT1G29020	0	0	1	0	0	0
AT1G29150	1	0	0	1	1	0
AT1G29250	1	0	0	0	0	0
AT1G29330	0	1	0	0	0	0
AT1G29470	1	1	1	1	1	1
AT1G29790	1	1	1	0	1	1
AT1G29880	1	0	0	0	1	0
AT1G29900	1	1	1	1	1	1
AT1G29940	1	0	0	1	0	0
AT1G30000	1	0	1	0	1	0
AT1G30120	0	0	0	1	0	1
AT1G30230	0	0	0	1	1	0
AT1G30360	0	0	1	0	1	1
AT1G30400	1	1	0	0	1	1
AT1G30450	1	0	0	0	0	0
AT1G30510	1	1	1	1	1	1
AT1G30580	0	0	0	1	1	0
AT1G30620	0	0	0	0	1	1
AT1G30630	1	0	0	1	1	1
AT1G30690	0	0	0	0	1	0
AT1G30870	1	0	0	0	0	0
AT1G31180	1	1	1	0	1	1
AT1G31220	1	0	0	0	1	0
AT1G31230	0	1	0	1	0	1
AT1G31730	0	0	0	0	1	0
AT1G31812	0	0	0	0	0	1
AT1G31817	1	1	1	0	1	0
AT1G31850	1	1	1	0	1	0
AT1G31860	1	0	0	0	0	0
AT1G31950	0	1	0	0	0	0
AT1G32380	1	1	0	0	0	0
AT1G32400	0	0	0	1	0	0
AT1G32440	1	0	1	0	0	0
AT1G32900	0	0	0	0	0	1
AT1G33040	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G33230	0	0	0	0	0	1
AT1G33680	0	0	0	0	1	0
AT1G33750	1	1	0	0	0	1
AT1G33800	1	1	0	0	1	0
AT1G33810	0	0	0	0	1	0
AT1G34130	1	1	1	1	1	1
AT1G34430	1	1	1	1	1	1
AT1G35160	1	0	1	1	1	0
AT1G35580	0	0	0	0	1	1
AT1G35620	1	1	1	1	1	1
AT1G35720	1	1	1	1	1	1
AT1G36050	0	0	1	0	0	0
AT1G41880	0	0	0	1	0	0
AT1G42960	1	0	0	0	1	1
AT1G43170	1	0	1	1	1	1
AT1G43890	1	1	0	0	1	0
AT1G44170	1	0	1	0	1	1
AT1G44835	0	0	0	0	1	0
AT1G47128	0	0	1	0	0	0
AT1G47260	1	1	1	1	1	1
AT1G47290	1	1	1	0	1	0
AT1G47420	1	0	1	0	1	1
AT1G47600	0	0	0	0	0	1
AT1G47640	0	1	1	0	1	1
AT1G48030	1	1	1	1	1	1
AT1G48200	0	0	0	1	0	0
AT1G48230	1	0	0	0	0	0
AT1G48600	0	0	0	1	0	0
AT1G48610	1	0	0	0	0	0
AT1G48630	1	0	0	1	1	0
AT1G48850	1	1	0	1	0	1
AT1G48860	1	0	0	1	0	0
AT1G48900	1	0	0	0	0	0
AT1G48920	1	1	0	0	1	0
AT1G49140	1	0	0	0	0	0
AT1G49300	0	0	0	0	0	1
AT1G49410	0	0	0	0	1	0
AT1G49630	0	1	0	0	0	0
AT1G49670	1	0	0	0	0	1
AT1G49760	1	0	0	1	1	0
AT1G50030	0	0	0	0	1	0
AT1G50110	0	0	0	0	1	0
AT1G50140	1	0	0	0	0	0
AT1G50200	1	0	1	1	1	0
AT1G50380	0	1	1	0	1	0
AT1G50430	1	0	1	1	0	0
AT1G50500	1	0	0	0	0	0
AT1G50510	1	0	0	0	1	0
AT1G50700	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G50940	0	1	0	0	0	0
AT1G51160	0	0	0	0	1	0
AT1G51570	0	0	1	0	1	0
AT1G51630	1	1	1	0	1	0
AT1G51650	0	0	0	0	0	1
AT1G51710	0	0	0	0	1	0
AT1G51980	1	1	1	1	1	1
AT1G52060	1	1	0	0	0	0
AT1G52070	1	1	0	0	1	1
AT1G52280	0	0	0	0	0	1
AT1G52360	1	0	1	0	1	0
AT1G52600	1	0	1	1	1	1
AT1G52670	1	1	0	0	0	0
AT1G52740	0	0	0	0	1	0
AT1G52760	0	0	1	0	1	0
AT1G52780	1	0	1	0	1	0
AT1G53000	1	1	1	0	1	1
AT1G53210	1	1	0	1	0	1
AT1G53240	1	1	1	1	1	1
AT1G53310	1	0	0	1	1	0
AT1G53645	1	0	0	0	0	0
AT1G53750	0	0	0	1	1	0
AT1G53760	1	1	1	0	1	1
AT1G53840	1	1	1	0	1	0
AT1G54000	1	1	1	1	1	1
AT1G54010	1	1	1	0	1	1
AT1G54030	1	1	1	0	1	1
AT1G54100	1	0	0	0	1	0
AT1G54220	1	1	0	0	0	0
AT1G54270	0	0	0	0	1	1
AT1G54320	1	0	0	0	0	1
AT1G54550	0	0	1	0	0	0
AT1G54990	0	1	1	0	1	0
AT1G55160	1	0	0	0	0	1
AT1G55490	1	0	0	1	1	0
AT1G55850	1	1	1	0	0	0
AT1G55890	1	1	1	0	1	0
AT1G55900	1	1	1	0	1	1
AT1G56070	1	1	1	1	1	1
AT1G56110	1	1	0	1	1	0
AT1G56190	1	1	1	1	1	0
AT1G56330	1	1	1	0	0	1
AT1G56340	1	1	1	1	1	1
AT1G56423	1	0	0	1	0	0
AT1G56450	1	0	0	1	1	1
AT1G56550	1	0	0	0	0	0
AT1G57620	0	1	0	0	0	1
AT1G57720	1	1	1	1	1	1
AT1G58080	1	0	1	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G58270	1	1	1	0	1	1
AT1G59610	1	1	1	1	1	1
AT1G59780	0	0	1	0	0	0
AT1G59820	1	0	0	0	1	0
AT1G59900	1	0	0	0	0	1
AT1G60770	1	1	0	0	1	0
AT1G61730	0	0	0	0	1	0
AT1G61770	1	1	0	0	1	1
AT1G61790	1	1	1	1	1	1
AT1G61870	1	1	0	0	1	0
AT1G62020	1	0	1	1	1	1
AT1G62130	0	0	1	0	0	0
AT1G62330	0	1	1	0	1	0
AT1G62640	1	1	1	1	1	0
AT1G62660	1	1	1	1	1	1
AT1G62730	1	0	0	0	0	0
AT1G62810	1	0	0	0	0	0
AT1G63000	1	1	0	0	1	1
AT1G63010	1	1	0	0	0	0
AT1G63050	0	0	0	1	0	0
AT1G63110	1	0	0	0	0	0
AT1G63450	1	0	0	0	0	0
AT1G63660	0	0	0	0	1	0
AT1G63770	1	0	1	1	1	1
AT1G63940	1	1	1	1	1	1
AT1G64090	1	1	1	1	1	1
AT1G64190	1	1	1	1	1	1
AT1G64520	1	0	0	0	1	0
AT1G64650	1	0	1	1	1	1
AT1G64790	0	0	0	0	1	1
AT1G64850	0	0	0	0	0	1
AT1G64880	1	1	1	1	1	0
AT1G65020	0	0	0	0	1	0
AT1G65220	0	0	0	0	1	0
AT1G65260	0	0	0	0	0	1
AT1G65270	1	1	1	1	1	1
AT1G65540	1	0	0	0	0	0
AT1G65820	0	0	0	0	0	1
AT1G65930	1	0	1	1	1	1
AT1G66270	1	1	1	1	1	1
AT1G66280	1	1	1	1	1	1
AT1G66430	0	0	0	0	1	0
AT1G66580	1	0	0	0	0	0
AT1G66670	0	0	0	1	0	0
AT1G67120	0	0	0	0	1	0
AT1G67230	1	0	0	0	1	0
AT1G67330	1	1	1	0	1	0
AT1G67360	0	1	0	0	1	0
AT1G67430	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G67490	1	0	1	0	1	0
AT1G67500	0	0	1	0	0	0
AT1G67560	0	1	0	0	0	0
AT1G67730	1	1	1	1	1	1
AT1G67850	0	0	0	0	0	1
AT1G67930	1	0	0	0	0	0
AT1G69460	1	1	0	1	1	1
AT1G69526	0	0	0	0	0	1
AT1G69640	1	0	0	0	1	0
AT1G69740	0	0	1	0	1	0
AT1G69830	0	0	0	0	0	1
AT1G70190	0	1	0	0	0	0
AT1G70310	1	0	0	1	0	0
AT1G70330	1	0	1	0	0	0
AT1G70410	1	0	0	0	0	0
AT1G70570	0	0	1	0	0	0
AT1G70580	0	0	0	0	1	0
AT1G70600	1	0	1	1	1	1
AT1G70730	1	0	0	0	0	0
AT1G70770	1	1	1	1	1	1
AT1G70940	0	0	0	0	0	1
AT1G71070	1	0	1	0	1	0
AT1G71220	1	1	1	1	1	1
AT1G71260	0	1	0	0	0	0
AT1G71780	1	0	0	0	1	0
AT1G72150	0	0	0	0	1	0
AT1G72175	0	0	0	0	0	1
AT1G72270	0	0	1	0	0	1
AT1G72280	1	0	0	0	0	0
AT1G72370	1	0	1	1	1	1
AT1G72480	1	0	0	0	0	0
AT1G72540	0	0	0	0	1	0
AT1G72730	0	0	1	0	0	0
AT1G72750	1	0	1	0	1	0
AT1G72860	0	0	1	0	0	0
AT1G73160	1	0	0	0	0	0
AT1G73180	0	0	0	0	1	0
AT1G73230	0	0	0	1	0	0
AT1G73590	0	0	0	0	1	0
AT1G73940	0	0	1	0	0	0
AT1G74020	1	1	1	1	0	1
AT1G74030	1	1	0	1	0	1
AT1G74260	1	1	1	1	1	0
AT1G74380	1	1	1	0	1	0
AT1G74560	0	0	0	0	1	0
AT1G74910	1	0	0	0	0	0
AT1G74920	1	0	0	0	0	0
AT1G74960	1	1	0	0	0	0
AT1G75140	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G75220	0	0	0	1	0	0
AT1G75270	1	0	0	1	0	1
AT1G75280	0	0	0	0	1	0
AT1G75330	1	1	0	0	1	1
AT1G75640	0	0	0	0	1	0
AT1G75680	0	1	1	0	1	0
AT1G75780	1	0	1	0	0	0
AT1G75940	1	0	0	0	0	0
AT1G75990	0	0	0	0	1	0
AT1G76010	1	1	0	0	0	0
AT1G76030	0	0	0	0	0	1
AT1G76090	1	1	1	1	1	0
AT1G76140	1	0	0	0	1	0
AT1G76200	0	0	0	0	0	1
AT1G76400	1	1	1	1	1	1
AT1G76490	0	0	1	1	0	0
AT1G76550	0	0	0	1	0	0
AT1G76690	1	0	0	0	0	0
AT1G76860	0	0	0	0	1	0
AT1G77260	1	0	0	0	1	0
AT1G77330	1	0	0	0	0	1
AT1G77510	1	1	1	1	1	1
AT1G77590	1	0	1	1	1	0
AT1G77710	1	0	0	0	0	0
AT1G77940	1	0	1	0	1	1
AT1G78240	0	1	1	0	1	0
AT1G78300	1	1	1	1	1	0
AT1G78380	1	1	0	1	1	1
AT1G78570	0	0	1	0	1	0
AT1G78660	1	0	0	0	0	0
AT1G78850	1	0	0	0	1	0
AT1G78860	0	0	0	1	0	0
AT1G78900	1	1	1	1	1	1
AT1G78920	1	1	1	0	1	1
AT1G79010	1	1	1	0	1	1
AT1G79210	0	0	0	1	0	0
AT1G79230	1	1	1	0	1	1
AT1G79440	1	1	1	0	1	1
AT1G79500	0	0	0	0	1	0
AT1G79530	1	1	1	1	1	1
AT1G79550	1	1	1	1	1	1
AT1G79690	1	1	1	0	1	0
AT1G79750	1	1	1	1	1	1
AT1G79930	0	0	0	1	0	1
AT1G79940	1	1	1	0	1	1
AT1G79990	0	0	0	1	1	0
AT1G80070	1	0	0	0	1	0
AT1G80230	1	0	1	0	1	1
AT1G80270	1	1	1	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G80480	0	1	0	0	0	0
AT1G80500	0	0	0	0	1	0
AT1G80560	1	1	1	0	1	1
AT1G80600	1	1	1	1	1	1
AT1G80670	1	0	0	0	0	0
AT2G01140	1	1	1	1	1	1
AT2G01250	1	0	1	1	1	1
AT2G01410	1	1	1	0	1	1
AT2G01470	1	1	1	0	1	1
AT2G01690	0	0	0	0	1	0
AT2G01720	1	1	1	0	1	1
AT2G01970	1	0	1	1	1	1
AT2G02040	1	0	1	0	0	0
AT2G02050	1	0	1	0	1	1
AT2G02740	1	0	1	0	0	0
AT2G03120	0	0	0	0	0	1
AT2G03510	1	0	1	0	1	1
AT2G04030	1	1	1	1	1	0
AT2G04280	1	1	0	0	1	0
AT2G04350	0	0	0	0	0	1
AT2G04400	1	1	0	1	0	1
AT2G04780	0	0	1	0	0	0
AT2G05710	1	1	1	1	1	1
AT2G05840	1	0	0	0	1	0
AT2G05990	1	1	1	1	1	1
AT2G06050	1	1	1	0	1	1
AT2G07050	1	1	1	1	1	1
AT2G09990	1	0	1	0	1	0
AT2G13560	1	0	0	0	1	0
AT2G14170	1	1	1	1	1	1
AT2G14720	1	0	1	0	0	1
AT2G15270	0	0	0	0	1	0
AT2G15390	1	0	0	0	0	0
AT2G15620	1	0	1	0	1	1
AT2G16005	1	0	0	0	0	1
AT2G16460	1	0	1	1	1	0
AT2G16570	1	0	0	0	0	0
AT2G16600	1	0	0	1	1	1
AT2G16640	0	0	0	0	1	0
AT2G16760	0	0	0	0	1	0
AT2G17130	1	1	1	0	1	1
AT2G17265	1	1	0	0	0	0
AT2G17420	1	1	1	1	1	1
AT2G17500	1	0	0	0	0	0
AT2G17630	1	1	1	0	1	1
AT2G17720	1	1	1	0	1	0
AT2G17790	0	0	0	0	1	0
AT2G18020	1	1	1	1	1	1
AT2G18030	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G18230	0	0	0	0	0	1
AT2G18330	1	0	1	0	1	0
AT2G18520	1	0	0	0	1	0
AT2G18960	1	1	1	1	1	1
AT2G18980	1	0	0	0	0	0
AT2G19080	1	0	0	1	1	1
AT2G19160	1	0	0	0	0	0
AT2G19520	0	0	0	0	1	0
AT2G19730	1	0	0	0	1	0
AT2G19760	0	0	0	0	0	1
AT2G19860	1	0	0	0	0	0
AT2G19880	1	0	1	0	1	0
AT2G19940	1	1	1	0	1	1
AT2G20060	1	1	0	0	1	1
AT2G20360	1	1	1	1	1	1
AT2G20370	1	0	0	0	1	0
AT2G20420	1	1	1	1	1	1
AT2G20530	1	1	1	1	1	1
AT2G20580	1	0	1	1	1	0
AT2G20680	0	0	1	0	0	0
AT2G20810	0	0	1	0	1	0
AT2G20890	0	0	0	0	1	0
AT2G20940	1	1	1	0	1	0
AT2G20990	1	1	1	0	1	1
AT2G21160	1	1	1	1	1	0
AT2G21170	1	1	1	1	1	1
AT2G21250	1	0	0	0	0	0
AT2G21390	1	0	0	1	1	1
AT2G21410	1	1	0	0	0	1
AT2G21590	0	0	0	0	0	1
AT2G21600	0	0	1	0	1	1
AT2G21620	0	0	0	0	1	0
AT2G21660	1	1	1	1	1	1
AT2G21870	1	1	1	1	1	1
AT2G22125	1	0	0	0	0	0
AT2G22170	1	0	1	0	1	1
AT2G22230	0	0	1	1	0	1
AT2G22250	1	0	0	0	1	0
AT2G22420	0	0	0	0	0	1
AT2G22480	1	1	1	1	1	0
AT2G22500	1	0	0	0	0	0
AT2G22780	1	1	1	1	1	1
AT2G22795	1	1	1	0	1	1
AT2G22970	1	0	0	0	0	0
AT2G23070	0	0	0	0	1	0
AT2G23350	1	0	0	1	1	0
AT2G23370	0	1	0	0	0	0
AT2G24170	1	0	0	0	0	0
AT2G24180	1	1	1	0	0	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G24200	1	1	1	1	1	1
AT2G24420	1	0	0	0	1	0
AT2G25110	1	0	0	0	1	1
AT2G25160	0	0	1	0	0	0
AT2G25830	1	0	0	0	0	0
AT2G25980	1	1	0	0	1	1
AT2G26080	1	1	1	1	1	1
AT2G26140	1	1	1	0	1	0
AT2G26230	1	1	1	1	1	1
AT2G26240	0	1	0	0	0	0
AT2G26640	1	0	1	0	0	0
AT2G26730	0	0	0	0	1	0
AT2G27000	0	0	0	0	1	0
AT2G27020	1	0	1	1	1	1
AT2G27040	0	0	0	0	1	0
AT2G27190	1	0	0	0	0	0
AT2G27530	1	1	1	1	1	1
AT2G27720	0	1	0	0	1	0
AT2G27730	1	1	1	0	1	1
AT2G27860	1	0	0	0	0	1
AT2G28000	1	1	1	1	1	1
AT2G28190	1	0	1	1	1	1
AT2G28430	1	0	0	0	0	1
AT2G28490	0	0	0	0	1	0
AT2G28520	1	0	1	0	0	1
AT2G28760	0	0	0	0	0	1
AT2G28790	0	0	0	1	1	0
AT2G28900	0	0	0	0	0	1
AT2G29080	1	1	1	0	1	1
AT2G29550	0	0	0	1	0	0
AT2G29960	1	0	1	0	1	1
AT2G30050	1	0	0	1	1	0
AT2G30110	1	0	0	0	1	0
AT2G30200	1	1	1	1	1	1
AT2G30490	1	1	1	1	1	1
AT2G30860	1	0	0	1	1	1
AT2G30870	1	1	1	1	1	0
AT2G30920	1	0	0	0	0	0
AT2G30930	1	0	0	0	1	0
AT2G30950	0	0	0	0	0	1
AT2G30970	1	1	1	1	1	1
AT2G31060	1	1	0	0	0	0
AT2G31140	1	0	0	0	1	1
AT2G31320	0	0	0	0	1	0
AT2G31360	0	0	0	0	1	0
AT2G31390	1	1	1	1	1	1
AT2G31610	1	0	1	0	1	0
AT2G31670	1	0	1	1	1	0
AT2G31810	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G32060	0	0	0	0	1	0
AT2G32240	1	0	0	0	1	0
AT2G32520	0	0	0	0	0	1
AT2G32730	0	0	0	0	1	0
AT2G32920	1	1	1	1	1	1
AT2G33040	1	1	1	1	1	1
AT2G33150	1	1	1	1	1	1
AT2G33210	1	1	1	1	1	1
AT2G33220	1	0	1	1	1	1
AT2G33340	0	0	0	0	1	0
AT2G34040	0	0	0	1	0	0
AT2G34300	1	1	1	1	1	1
AT2G34480	1	0	1	1	1	1
AT2G34560	1	0	0	0	0	0
AT2G34585	1	0	0	0	0	0
AT2G34590	1	0	1	1	1	0
AT2G34630	1	1	0	0	1	0
AT2G34660	1	0	1	1	1	1
AT2G35010	1	0	0	0	1	1
AT2G35040	1	1	1	0	1	0
AT2G35100	1	0	1	0	1	0
AT2G35120	1	0	1	0	0	0
AT2G35490	0	0	0	0	0	1
AT2G35605	1	0	0	0	1	0
AT2G35610	1	1	0	0	1	0
AT2G35630	0	0	0	0	1	0
AT2G35720	1	0	1	0	1	0
AT2G35790	1	0	0	0	0	0
AT2G35810	1	0	0	0	0	0
AT2G36070	1	0	0	0	1	0
AT2G36130	1	0	0	0	1	0
AT2G36160	1	0	1	0	0	1
AT2G36290	0	0	1	1	0	0
AT2G36380	1	0	0	0	1	0
AT2G36460	0	0	0	0	0	1
AT2G36530	1	1	1	1	1	1
AT2G36580	0	0	0	0	1	0
AT2G36850	1	0	1	1	1	1
AT2G36880	0	1	1	0	1	0
AT2G36910	0	0	0	0	1	0
AT2G37020	0	0	0	0	1	0
AT2G37040	0	0	0	0	1	0
AT2G37050	0	0	0	0	1	0
AT2G37170	1	0	1	1	1	0
AT2G37230	1	1	1	0	1	0
AT2G37250	1	1	0	0	1	0
AT2G37500	1	0	0	0	1	0
AT2G37550	1	0	0	0	0	0
AT2G37670	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G37690	1	1	1	1	1	0
AT2G37860	1	0	1	0	1	1
AT2G38040	1	1	1	1	1	1
AT2G38230	0	0	0	0	0	1
AT2G38280	1	0	0	1	0	0
AT2G38360	1	0	0	0	1	0
AT2G38550	1	0	0	1	1	1
AT2G38650	1	0	0	0	0	0
AT2G38670	1	1	0	0	0	1
AT2G38750	1	1	1	0	1	1
AT2G38760	1	1	1	0	1	1
AT2G38840	0	1	1	0	0	0
AT2G38960	1	0	1	0	1	0
AT2G39040	0	0	0	0	1	0
AT2G39630	1	0	0	0	0	1
AT2G39750	0	0	0	0	0	1
AT2G39800	0	0	1	0	0	0
AT2G39960	1	1	1	1	1	1
AT2G39990	1	0	0	0	1	0
AT2G40290	0	0	0	0	1	0
AT2G40380	0	0	0	0	1	1
AT2G40510	1	0	0	0	1	0
AT2G40600	0	0	0	1	0	0
AT2G40660	0	0	0	0	1	0
AT2G40800	1	0	0	0	0	0
AT2G40840	1	0	0	0	0	1
AT2G40890	0	0	1	0	0	0
AT2G41150	0	0	1	0	0	0
AT2G41220	1	1	1	1	1	1
AT2G41475	1	0	0	0	1	0
AT2G41530	1	0	1	1	1	0
AT2G41600	1	0	0	0	0	0
AT2G41620	1	0	0	0	1	0
AT2G41740	1	0	0	0	1	0
AT2G41770	1	0	1	0	1	0
AT2G41790	0	0	0	0	1	0
AT2G41840	1	0	0	1	1	0
AT2G42210	1	1	1	0	1	1
AT2G42490	1	1	1	0	1	1
AT2G42590	1	0	0	0	1	0
AT2G42710	1	1	0	0	1	0
AT2G42770	0	0	0	0	1	0
AT2G42790	1	0	0	0	0	1
AT2G42810	0	0	0	0	1	0
AT2G42910	1	0	0	1	1	0
AT2G43070	1	0	0	0	0	0
AT2G43090	1	0	0	1	1	1
AT2G43350	0	1	0	0	0	0
AT2G43360	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G43400	0	0	0	0	1	0
AT2G43610	0	1	0	0	0	1
AT2G43630	0	0	0	0	1	0
AT2G43710	1	1	1	1	1	0
AT2G43750	1	1	1	1	1	1
AT2G43770	0	0	0	0	1	0
AT2G43950	1	0	1	0	1	1
AT2G44040	1	0	0	0	0	0
AT2G44050	1	1	1	0	1	1
AT2G44060	1	0	1	0	1	1
AT2G44100	0	0	0	0	1	0
AT2G44120	1	0	0	1	1	0
AT2G44350	1	1	1	1	1	1
AT2G44530	1	0	1	0	0	0
AT2G44610	1	0	1	0	1	0
AT2G44640	0	0	1	1	1	0
AT2G44790	1	0	1	1	1	1
AT2G45030	0	1	0	0	1	0
AT2G45060	1	0	1	1	1	1
AT2G45070	1	0	0	0	0	0
AT2G45140	1	0	0	0	1	0
AT2G45290	0	1	0	1	1	0
AT2G45300	1	1	0	1	1	0
AT2G45440	0	1	0	0	0	0
AT2G45740	0	0	0	0	0	1
AT2G45750	1	0	0	0	1	0
AT2G45790	1	0	0	0	1	1
AT2G45820	0	0	0	0	1	0
AT2G45960	1	1	1	1	1	1
AT2G45990	1	0	0	0	0	0
AT2G46170	0	0	0	1	0	1
AT2G46280	1	0	0	1	1	0
AT2G46470	1	0	1	0	1	0
AT2G46520	1	0	0	1	0	0
AT2G47000	1	1	0	0	1	1
AT2G47380	0	0	0	0	0	1
AT2G47390	1	1	0	1	1	1
AT2G47470	1	1	1	1	1	1
AT2G47510	1	1	1	1	1	1
AT2G47540	1	0	0	0	0	0
AT2G47610	1	0	0	1	1	0
AT2G47650	1	0	1	1	1	1
AT2G47730	1	1	0	1	1	1
AT2G47800	1	1	0	0	0	1
AT2G47840	1	0	1	0	1	1
AT2G48020	0	0	1	0	0	0
AT3G01120	1	1	1	1	1	1
AT3G01190	1	0	0	0	0	0
AT3G01280	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G01290	1	0	0	0	0	0
AT3G01380	1	0	0	0	1	0
AT3G01390	1	0	1	0	1	1
AT3G01720	1	0	0	0	1	0
AT3G01800	1	1	0	0	1	0
AT3G01910	1	1	1	0	1	0
AT3G02080	0	0	0	1	0	0
AT3G02090	1	1	1	1	1	1
AT3G02200	0	0	0	1	1	0
AT3G02230	1	1	1	1	1	1
AT3G02260	0	0	0	0	1	0
AT3G02350	1	1	1	0	1	0
AT3G02360	1	0	0	1	1	0
AT3G02420	1	0	1	0	0	0
AT3G02520	1	0	1	1	1	1
AT3G02530	1	0	0	1	1	0
AT3G02560	1	0	0	0	1	0
AT3G02630	1	1	0	1	1	0
AT3G02650	1	1	1	0	1	0
AT3G02660	1	0	0	0	0	0
AT3G02780	1	0	1	0	1	1
AT3G02880	1	0	1	0	1	0
AT3G02900	1	0	0	0	0	1
AT3G03050	1	0	0	0	0	0
AT3G03060	0	1	0	1	0	0
AT3G03100	1	0	1	1	1	1
AT3G03220	0	0	0	0	1	0
AT3G03250	1	1	1	1	1	1
AT3G03330	0	0	0	0	1	0
AT3G03600	1	0	0	1	1	1
AT3G03640	1	1	0	0	0	1
AT3G03810	0	0	0	0	0	1
AT3G03960	1	0	1	1	1	0
AT3G03990	0	0	0	0	1	0
AT3G04080	1	0	1	0	1	1
AT3G04120	0	1	0	1	0	1
AT3G04520	0	0	0	1	0	0
AT3G04570	1	0	0	0	0	0
AT3G04600	0	0	0	0	1	0
AT3G04790	1	0	0	1	0	0
AT3G04820	0	0	0	0	1	0
AT3G04830	1	1	1	1	1	1
AT3G04840	1	1	1	1	1	1
AT3G04920	1	0	1	1	1	0
AT3G04940	0	0	0	0	1	0
AT3G05060	1	0	0	1	1	0
AT3G05100	0	0	1	0	0	0
AT3G05230	1	1	1	1	1	1
AT3G05420	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G05560	1	0	1	0	0	1
AT3G05970	1	1	1	0	1	1
AT3G06040	1	0	0	0	0	0
AT3G06050	1	0	1	0	1	1
AT3G06300	1	1	1	0	1	1
AT3G06350	1	1	0	0	1	0
AT3G06530	1	0	0	0	1	0
AT3G06650	1	0	1	0	1	0
AT3G06810	1	1	0	0	0	1
AT3G06860	1	1	1	0	1	1
AT3G07060	1	1	1	0	1	0
AT3G07100	0	0	0	0	1	0
AT3G07110	1	0	0	1	1	0
AT3G07140	0	0	1	0	1	0
AT3G07160	0	0	0	0	1	0
AT3G07180	0	0	0	0	1	1
AT3G07290	0	0	1	0	0	0
AT3G07330	0	1	0	0	0	0
AT3G07390	0	0	0	0	1	0
AT3G07430	1	0	1	0	1	0
AT3G07470	1	0	0	0	0	0
AT3G07480	1	0	1	1	1	1
AT3G07610	0	0	0	0	1	0
AT3G07630	1	0	0	0	1	0
AT3G07680	1	1	0	1	1	1
AT3G07770	1	1	1	1	1	1
AT3G07950	1	0	0	0	0	0
AT3G08530	1	0	1	0	1	1
AT3G08550	1	0	0	0	0	0
AT3G08580	1	1	1	1	1	1
AT3G08590	1	0	1	1	1	0
AT3G08610	0	0	0	0	0	1
AT3G08630	1	1	1	0	1	1
AT3G08640	1	0	0	0	0	1
AT3G08950	1	0	1	0	1	0
AT3G09200	1	1	0	1	1	1
AT3G09260	1	1	1	1	1	1
AT3G09300	0	0	0	0	1	0
AT3G09410	0	0	1	0	0	0
AT3G09440	1	0	1	1	1	0
AT3G09500	1	0	0	0	1	0
AT3G09630	1	0	0	1	1	0
AT3G09690	1	0	0	0	0	0
AT3G09740	1	0	0	0	0	0
AT3G09810	1	1	0	0	1	1
AT3G09820	1	1	0	1	1	1
AT3G09840	1	1	0	1	1	0
AT3G10050	1	0	0	0	0	0
AT3G10260	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G10370	1	0	1	0	1	1
AT3G10380	0	0	0	0	1	0
AT3G10410	1	0	0	0	0	1
AT3G10690	1	1	1	0	1	0
AT3G10730	0	0	1	0	0	0
AT3G10920	1	1	1	1	1	1
AT3G11070	1	0	1	0	1	1
AT3G11130	1	1	1	1	1	1
AT3G11170	1	0	0	0	0	0
AT3G11250	0	0	0	1	0	0
AT3G11400	1	0	1	0	1	0
AT3G11630	1	1	1	0	1	1
AT3G11710	1	0	0	0	1	0
AT3G11730	1	0	0	0	0	0
AT3G11830	1	0	0	1	1	0
AT3G11940	0	1	0	1	0	1
AT3G11964	1	0	0	0	1	0
AT3G12030	1	0	1	0	1	0
AT3G12050	0	0	0	0	1	0
AT3G12120	1	1	1	1	1	0
AT3G12260	1	1	1	1	1	1
AT3G12290	1	0	0	0	0	0
AT3G12370	1	0	0	0	0	0
AT3G12670	0	0	0	0	1	0
AT3G12780	1	1	1	1	1	1
AT3G12800	1	0	1	0	0	0
AT3G13110	0	1	0	0	0	0
AT3G13160	1	1	1	1	1	1
AT3G13300	0	0	0	0	1	0
AT3G13460	1	0	0	0	0	0
AT3G13470	1	1	0	1	1	0
AT3G13530	0	1	0	0	0	0
AT3G13580	1	0	0	1	0	0
AT3G13772	1	0	1	1	1	1
AT3G13860	1	1	1	1	1	1
AT3G13870	1	1	1	0	1	1
AT3G13920	1	0	1	1	1	1
AT3G13930	1	1	1	1	1	1
AT3G14067	1	0	0	0	1	0
AT3G14220	1	1	0	0	0	1
AT3G14290	0	0	0	0	0	1
AT3G14390	1	1	0	0	0	0
AT3G14790	0	1	0	0	0	0
AT3G14840	0	0	1	0	0	0
AT3G14990	0	0	0	1	0	1
AT3G15000	1	0	1	0	1	1
AT3G15020	1	1	1	1	1	1
AT3G15090	1	1	1	1	1	1
AT3G15290	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G15640	1	0	1	0	1	1
AT3G15660	1	0	0	0	0	0
AT3G15730	1	0	1	1	1	1
AT3G15950	1	1	1	1	1	1
AT3G15980	1	0	1	0	1	0
AT3G16110	1	1	1	0	1	0
AT3G16200	1	0	0	0	0	0
AT3G16400	0	0	0	0	1	0
AT3G16410	1	1	0	0	1	1
AT3G16420	1	1	1	0	1	1
AT3G16430	1	1	0	0	0	1
AT3G16450	1	1	0	0	0	1
AT3G16460	1	1	1	0	1	1
AT3G16480	1	1	1	1	1	1
AT3G16640	1	0	1	1	1	1
AT3G16950	1	1	1	1	1	1
AT3G17210	0	0	0	0	1	0
AT3G17240	1	1	1	1	1	1
AT3G17390	1	1	1	0	1	1
AT3G17465	1	1	0	0	1	0
AT3G17810	1	1	0	1	0	1
AT3G17820	0	0	0	1	0	0
AT3G17910	1	0	0	0	0	0
AT3G17940	0	0	1	0	1	1
AT3G17970	1	1	0	1	0	0
AT3G18000	0	0	1	0	0	1
AT3G18060	0	0	0	0	1	0
AT3G18130	0	1	0	1	1	0
AT3G18190	1	0	0	1	1	0
AT3G18240	0	1	1	0	0	0
AT3G18410	1	0	1	0	0	0
AT3G18430	0	0	0	0	0	1
AT3G18580	1	0	0	0	1	0
AT3G18760	1	0	0	0	0	0
AT3G18820	1	0	0	0	1	0
AT3G18830	0	1	0	0	0	0
AT3G18860	1	0	0	0	1	0
AT3G19170	1	1	0	1	1	1
AT3G19390	1	0	0	0	1	0
AT3G19430	0	1	0	0	0	1
AT3G19450	0	0	0	1	0	0
AT3G19508	1	0	0	0	0	0
AT3G19760	0	0	0	1	0	0
AT3G19820	1	1	1	1	1	1
AT3G19870	0	0	0	0	0	1
AT3G20000	1	1	1	1	1	1
AT3G20050	1	0	0	1	1	0
AT3G20130	1	1	1	0	0	0
AT3G20320	0	0	1	1	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G20330	1	0	0	0	1	0
AT3G20370	1	1	1	0	1	1
AT3G20390	1	0	1	0	1	1
AT3G20410	0	0	0	0	1	0
AT3G20670	0	0	0	0	0	1
AT3G20790	0	0	0	0	1	0
AT3G20940	1	1	1	0	1	1
AT3G21110	1	1	0	0	0	0
AT3G21140	1	1	0	1	1	0
AT3G21160	0	1	0	0	0	0
AT3G21190	1	1	1	0	0	0
AT3G21400	1	0	0	0	0	0
AT3G21465	1	0	0	0	0	0
AT3G21540	1	0	0	0	0	0
AT3G22110	1	0	1	1	1	0
AT3G22200	1	1	1	1	1	1
AT3G22230	0	0	0	1	0	0
AT3G22290	1	0	1	0	1	0
AT3G22310	1	1	0	0	1	0
AT3G22320	1	0	0	0	1	0
AT3G22330	0	0	0	1	1	0
AT3G22370	1	0	1	0	0	0
AT3G22630	1	0	0	0	1	1
AT3G22845	1	1	0	0	0	1
AT3G22890	0	1	1	1	1	1
AT3G22960	1	1	1	1	1	1
AT3G23160	0	0	1	0	0	0
AT3G23180	1	1	0	0	0	1
AT3G23190	1	0	0	0	0	0
AT3G23300	1	1	1	0	1	1
AT3G23400	1	0	1	0	0	1
AT3G23510	1	0	0	0	0	0
AT3G23530	1	1	1	0	1	0
AT3G23600	1	0	0	0	0	0
AT3G23750	1	1	1	0	1	0
AT3G23820	1	1	1	0	1	0
AT3G23940	1	1	1	1	1	1
AT3G23990	1	1	1	1	1	1
AT3G24040	1	0	1	0	1	0
AT3G24160	1	0	0	0	1	0
AT3G24170	1	0	1	1	0	0
AT3G24200	1	1	0	0	0	0
AT3G24503	1	0	0	0	0	0
AT3G24830	1	1	0	1	1	0
AT3G25110	1	1	0	1	1	0
AT3G25140	1	0	1	0	1	0
AT3G25220	0	0	1	0	0	1
AT3G25230	0	0	1	1	1	0
AT3G25290	0	0	0	1	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G25520	1	0	0	1	0	0
AT3G25530	1	0	0	0	1	0
AT3G25585	0	0	1	0	0	0
AT3G25780	1	0	1	0	1	1
AT3G25800	0	0	0	0	1	0
AT3G25860	1	1	1	1	1	1
AT3G26370	1	0	1	0	1	0
AT3G26520	1	1	1	1	1	1
AT3G26720	1	1	1	1	1	0
AT3G26950	0	0	1	0	0	0
AT3G27020	1	0	0	0	0	0
AT3G27080	1	0	0	0	1	0
AT3G27230	1	0	0	0	0	0
AT3G27240	1	1	1	1	1	1
AT3G27280	1	1	1	1	0	1
AT3G27300	1	0	0	0	0	0
AT3G27325	1	0	1	0	0	0
AT3G27380	1	1	1	1	1	1
AT3G27430	1	0	0	0	0	0
AT3G27570	1	1	0	0	1	0
AT3G27740	1	1	1	1	1	0
AT3G27890	1	0	0	0	0	0
AT3G27930	1	0	0	0	1	0
AT3G28480	1	0	0	0	0	0
AT3G28710	1	0	1	1	1	0
AT3G28715	1	1	1	1	1	1
AT3G28720	1	1	1	0	1	0
AT3G28860	0	0	1	1	1	0
AT3G29250	1	0	0	0	0	0
AT3G29320	1	1	0	0	0	1
AT3G29360	1	0	0	0	0	0
AT3G32980	0	0	0	1	0	0
AT3G42050	1	1	1	1	1	1
AT3G43300	1	0	1	0	1	1
AT3G43520	0	0	0	0	1	1
AT3G44100	1	0	1	0	1	1
AT3G44110	0	0	0	0	1	0
AT3G44160	0	1	0	0	0	0
AT3G44190	0	0	1	0	0	0
AT3G44310	0	0	1	0	0	0
AT3G44320	0	0	1	1	0	0
AT3G44330	1	1	1	1	1	1
AT3G44830	0	0	0	0	0	1
AT3G45300	0	0	0	0	0	1
AT3G45600	0	0	0	0	1	1
AT3G46040	0	0	0	0	0	1
AT3G46210	0	0	0	0	1	0
AT3G46560	1	0	0	0	0	0
AT3G46740	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G46830	1	0	1	0	1	1
AT3G46940	0	0	0	0	1	0
AT3G46970	1	0	0	0	0	1
AT3G47370	0	0	0	0	1	0
AT3G47520	1	1	1	1	1	1
AT3G47670	0	1	0	0	0	0
AT3G47730	0	0	0	0	0	1
AT3G47930	1	1	1	0	1	1
AT3G47960	0	0	1	0	0	0
AT3G48000	1	1	1	1	1	1
AT3G48110	1	0	0	0	0	0
AT3G48140	1	0	1	0	0	0
AT3G48170	1	1	0	0	0	1
AT3G48340	1	1	1	0	1	1
AT3G48410	1	0	1	0	1	1
AT3G48560	1	1	0	0	0	0
AT3G48680	1	0	1	0	0	1
AT3G48730	1	0	1	0	0	0
AT3G48870	0	1	1	1	1	0
AT3G48890	1	0	0	0	0	0
AT3G48930	0	0	1	0	1	0
AT3G49010	1	0	0	0	1	0
AT3G49080	1	0	0	0	1	0
AT3G49190	0	1	0	0	0	0
AT3G49240	0	1	0	0	1	0
AT3G49560	1	1	0	0	1	0
AT3G49680	1	1	1	0	1	0
AT3G49720	1	1	1	1	1	1
AT3G49910	1	0	0	1	1	1
AT3G51050	1	0	1	0	1	0
AT3G51100	0	0	0	0	1	0
AT3G51160	1	0	0	0	0	1
AT3G51240	0	0	0	1	0	0
AT3G51260	1	1	1	1	1	1
AT3G51440	1	0	0	0	0	0
AT3G51460	1	0	1	0	1	0
AT3G51550	0	0	1	0	0	0
AT3G51670	0	0	0	0	1	0
AT3G51800	1	0	0	0	1	0
AT3G51830	1	0	0	0	0	0
AT3G51840	1	1	1	0	1	1
AT3G51980	1	0	0	0	0	0
AT3G52140	0	0	0	0	1	0
AT3G52180	0	0	0	0	0	1
AT3G52190	1	0	0	0	0	0
AT3G52200	1	1	1	0	1	1
AT3G52230	0	0	0	0	0	1
AT3G52300	1	1	1	1	1	1
AT3G52570	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G52580	0	0	0	0	1	0
AT3G52640	1	0	0	0	0	0
AT3G52730	1	0	0	0	1	0
AT3G52850	0	0	1	0	0	0
AT3G52880	0	0	0	0	1	1
AT3G52930	1	1	1	1	1	1
AT3G52940	0	0	0	1	0	0
AT3G52960	1	1	1	1	1	0
AT3G53180	1	0	0	0	0	0
AT3G53230	0	0	0	1	0	0
AT3G53420	0	0	1	1	0	1
AT3G53430	0	1	0	0	0	0
AT3G53460	0	1	0	0	0	0
AT3G53480	1	1	0	0	0	1
AT3G53520	1	1	1	1	1	1
AT3G53580	1	1	0	0	1	1
AT3G53740	1	0	0	0	1	0
AT3G53900	1	0	0	0	0	0
AT3G53990	1	0	0	0	0	0
AT3G54110	1	1	1	1	1	1
AT3G54470	0	0	0	0	1	0
AT3G54640	0	1	0	0	0	0
AT3G54660	1	0	1	0	0	0
AT3G54840	1	0	0	0	0	0
AT3G54960	1	1	1	1	1	1
AT3G54980	0	1	0	0	1	0
AT3G55010	1	0	0	1	1	1
AT3G55030	1	0	0	0	0	1
AT3G55360	1	1	1	1	1	0
AT3G55410	1	1	1	1	1	1
AT3G55440	1	1	1	1	1	1
AT3G55610	0	0	1	0	0	0
AT3G55760	0	1	0	0	0	0
AT3G55830	0	0	0	1	0	0
AT3G55920	1	0	0	0	0	0
AT3G56070	1	1	1	1	1	1
AT3G56090	1	1	1	1	1	0
AT3G56150	1	1	1	1	1	0
AT3G56170	0	0	0	0	0	1
AT3G56190	1	0	1	1	1	1
AT3G56310	1	0	1	0	0	1
AT3G56460	1	1	0	0	1	1
AT3G56490	0	0	0	0	1	0
AT3G56900	1	0	0	0	0	0
AT3G56950	1	0	0	0	0	0
AT3G57010	0	1	1	1	1	1
AT3G57020	1	0	1	0	1	1
AT3G57030	0	0	0	0	1	1
AT3G57050	1	0	1	0	1	1

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G57150	1	0	0	1	1	0
AT3G57220	0	0	0	0	1	0
AT3G57280	1	1	1	0	1	1
AT3G57290	1	0	0	0	1	0
AT3G57410	0	0	0	0	1	0
AT3G57420	0	0	1	0	0	0
AT3G57560	1	0	0	0	0	0
AT3G57610	1	1	1	1	1	1
AT3G57630	1	0	0	0	0	0
AT3G57650	1	0	0	1	1	1
AT3G57660	1	0	0	0	0	0
AT3G57680	0	1	0	0	0	0
AT3G58010	0	0	0	0	0	1
AT3G58140	1	0	0	0	0	0
AT3G58510	0	0	0	0	1	0
AT3G58610	1	1	1	1	1	1
AT3G58730	1	1	1	1	1	1
AT3G58750	1	1	0	0	1	1
AT3G58840	1	0	0	0	0	0
AT3G59020	0	0	0	1	0	0
AT3G59280	0	0	0	0	1	0
AT3G59360	0	1	0	0	0	0
AT3G59650	1	0	0	0	1	0
AT3G59760	1	1	1	1	1	1
AT3G59820	1	1	0	0	1	0
AT3G59890	0	0	0	0	1	0
AT3G59920	1	0	1	1	1	0
AT3G59970	1	0	0	1	0	0
AT3G59990	0	0	0	0	1	0
AT3G60100	0	0	1	0	0	0
AT3G60245	0	0	0	0	1	0
AT3G60340	0	0	0	0	0	1
AT3G60440	1	0	0	0	0	0
AT3G60600	1	0	0	0	1	0
AT3G60750	1	1	1	1	1	1
AT3G60770	0	0	0	0	1	0
AT3G60820	1	1	1	0	1	1
AT3G60850	1	0	0	0	0	0
AT3G60860	0	0	0	0	1	0
AT3G60900	0	1	0	0	0	1
AT3G61050	0	1	1	0	1	1
AT3G61070	1	1	1	1	1	1
AT3G61130	1	0	1	0	0	1
AT3G61430	1	0	1	1	0	1
AT3G61440	1	0	1	1	1	1
AT3G61520	1	0	0	0	0	0
AT3G61580	0	0	0	0	1	0
AT3G62030	1	1	0	1	0	1
AT3G62360	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G62530	1	0	0	0	1	1
AT3G62580	0	0	1	0	0	0
AT3G62600	1	1	1	0	1	1
AT3G62700	0	0	1	1	1	0
AT3G62830	1	1	1	1	1	1
AT3G62870	0	0	0	1	0	1
AT3G63130	0	0	0	0	1	0
AT3G63150	1	0	0	0	1	0
AT3G63190	1	0	0	0	0	0
AT3G63410	0	1	1	1	1	1
AT3G63460	1	0	1	1	1	1
AT3G66654	1	0	1	0	1	0
AT3G66658	1	0	1	1	1	0
AT4G00040	1	0	0	0	0	0
AT4G00090	1	0	0	0	1	0
AT4G00100	1	0	0	0	0	0
AT4G00290	1	0	0	0	0	0
AT4G00430	0	1	0	0	0	0
AT4G00490	1	1	0	0	0	1
AT4G00570	1	1	1	0	1	1
AT4G00620	1	1	0	0	0	0
AT4G00630	1	1	1	0	1	1
AT4G00710	1	0	0	0	0	0
AT4G00740	1	1	1	0	1	1
AT4G00750	0	0	0	0	0	1
AT4G00860	1	0	1	1	1	1
AT4G01100	1	1	1	1	1	1
AT4G01210	0	0	0	0	1	0
AT4G01320	1	1	1	1	1	0
AT4G01610	1	0	1	0	0	0
AT4G01660	1	0	0	0	0	0
AT4G01690	0	1	0	0	0	1
AT4G01750	0	0	0	0	0	1
AT4G01850	1	1	1	0	1	0
AT4G01900	1	0	1	0	1	0
AT4G02450	1	0	1	0	1	0
AT4G02500	1	1	1	0	1	0
AT4G02510	1	1	1	1	0	0
AT4G02580	1	1	1	1	1	1
AT4G02620	1	0	1	0	0	1
AT4G02930	1	1	1	1	1	1
AT4G03190	0	0	0	0	1	0
AT4G03550	0	0	1	0	1	0
AT4G03560	1	0	1	1	1	1
AT4G04190	0	0	1	0	0	0
AT4G04470	1	0	0	0	0	0
AT4G04860	1	0	0	0	0	0
AT4G04910	1	0	0	0	1	0
AT4G04940	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G05020	1	1	1	1	1	1
AT4G05160	1	1	1	0	1	1
AT4G05390	1	0	1	0	1	1
AT4G05400	1	0	0	0	1	0
AT4G05420	0	0	0	1	1	0
AT4G05530	1	0	0	0	0	1
AT4G08390	1	1	1	1	1	1
AT4G08520	0	0	0	0	1	0
AT4G08770	0	0	0	1	1	0
AT4G08790	0	0	0	0	1	0
AT4G08810	1	0	1	0	0	0
AT4G09000	1	1	1	1	1	1
AT4G09020	1	1	0	0	0	1
AT4G09320	1	1	1	1	1	1
AT4G09720	1	1	0	0	0	1
AT4G09990	1	0	0	0	0	0
AT4G10260	0	0	0	0	1	0
AT4G10280	0	0	0	1	0	0
AT4G10320	1	0	0	1	1	0
AT4G10450	1	0	0	1	1	0
AT4G10480	1	0	1	1	1	0
AT4G10750	1	1	1	0	1	1
AT4G11010	1	1	1	1	1	1
AT4G11120	1	1	0	0	0	0
AT4G11150	1	1	1	1	1	1
AT4G11290	0	0	0	1	0	0
AT4G11380	1	0	0	0	1	0
AT4G11420	0	0	0	1	1	0
AT4G11600	1	0	0	0	0	0
AT4G11610	1	0	0	0	1	0
AT4G11820	1	0	0	1	1	0
AT4G11850	0	0	0	0	1	0
AT4G12130	1	0	0	0	0	0
AT4G12420	0	1	1	0	0	0
AT4G12590	1	1	0	1	1	1
AT4G12600	1	0	0	1	1	0
AT4G12650	1	1	1	1	1	1
AT4G12750	0	0	0	1	0	0
AT4G13050	1	0	0	0	0	0
AT4G13200	1	0	0	0	0	0
AT4G13430	1	1	1	1	1	1
AT4G13720	1	0	0	0	1	0
AT4G13780	0	0	0	1	1	0
AT4G13850	1	0	0	0	1	0
AT4G13930	1	1	1	1	1	1
AT4G13940	1	1	1	1	1	1
AT4G14160	0	0	0	1	0	0
AT4G14360	0	0	1	0	1	0
AT4G14420	1	0	0	0	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G14430	0	0	0	0	0	1
AT4G14570	1	0	0	1	1	0
AT4G14680	0	0	0	0	1	0
AT4G14800	1	0	0	1	1	0
AT4G14880	1	1	1	0	1	1
AT4G15000	0	0	0	1	1	0
AT4G15640	1	0	1	0	1	0
AT4G16120	0	0	1	0	1	0
AT4G16143	0	0	0	1	1	0
AT4G16155	1	1	0	1	1	1
AT4G16170	1	1	1	0	0	0
AT4G16180	1	0	0	0	0	0
AT4G16210	1	0	0	0	0	0
AT4G16340	0	0	0	1	0	0
AT4G16450	1	0	1	1	1	1
AT4G16500	1	0	0	0	0	0
AT4G16660	1	1	1	1	1	1
AT4G16760	1	1	1	1	1	0
AT4G17040	1	0	0	0	0	0
AT4G17140	1	0	0	0	0	1
AT4G17170	1	0	0	0	1	1
AT4G17270	0	0	0	0	1	0
AT4G17420	1	0	0	0	0	0
AT4G17530	1	0	0	0	0	1
AT4G18030	1	1	1	1	1	1
AT4G18100	1	0	0	1	1	0
AT4G18230	1	0	0	0	0	0
AT4G18360	0	0	1	0	0	0
AT4G18440	1	0	0	0	1	0
AT4G18760	0	0	1	0	0	0
AT4G18800	0	1	0	0	0	1
AT4G18830	0	0	0	0	1	0
AT4G19006	0	0	0	0	1	0
AT4G19120	1	0	1	0	1	0
AT4G19460	0	0	0	0	0	1
AT4G19640	0	0	0	0	0	1
AT4G19710	1	1	0	0	0	0
AT4G20020	1	0	0	0	0	0
AT4G20360	1	1	0	0	0	0
AT4G20460	1	0	0	0	0	0
AT4G20830	1	0	0	0	1	0
AT4G20850	1	1	1	1	1	1
AT4G20890	0	1	0	0	0	0
AT4G20980	0	0	0	0	1	0
AT4G21105	0	0	0	1	0	0
AT4G21150	1	1	1	1	1	1
AT4G21180	1	0	0	0	0	0
AT4G21540	1	0	0	0	0	0
AT4G21570	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G21710	0	1	0	1	0	0
AT4G22214	1	0	0	0	0	0
AT4G22240	1	0	0	0	0	1
AT4G22310	0	0	0	0	0	1
AT4G22330	0	0	0	1	1	1
AT4G22930	1	1	1	1	1	0
AT4G23100	1	0	1	1	1	0
AT4G23430	0	1	0	0	0	0
AT4G23460	0	0	0	0	1	0
AT4G23540	0	0	0	0	1	0
AT4G23590	1	1	0	0	0	1
AT4G23620	1	0	1	0	1	0
AT4G23630	0	0	0	0	0	1
AT4G23640	1	0	0	0	0	0
AT4G23650	0	0	0	0	1	0
AT4G23690	0	0	0	0	1	0
AT4G23710	1	0	0	0	1	0
AT4G23850	0	0	0	0	0	1
AT4G23900	0	0	0	1	0	0
AT4G23920	0	0	0	0	0	1
AT4G24190	1	1	1	1	1	1
AT4G24280	1	1	1	1	1	0
AT4G24310	0	1	0	0	0	0
AT4G24330	1	1	1	1	1	1
AT4G24520	1	0	0	0	1	0
AT4G24550	0	0	0	0	1	0
AT4G24620	1	1	1	1	1	1
AT4G24820	1	0	1	1	1	0
AT4G24830	1	1	0	1	1	1
AT4G25240	0	0	0	0	1	1
AT4G25360	0	0	1	0	0	0
AT4G25450	0	0	0	0	0	1
AT4G25570	1	0	0	0	0	0
AT4G25630	1	0	0	1	1	0
AT4G25740	0	0	0	1	0	0
AT4G26010	1	0	0	0	0	0
AT4G26110	0	0	0	1	0	0
AT4G26210	0	0	0	0	1	0
AT4G26300	1	0	0	1	1	0
AT4G26410	1	1	1	1	1	1
AT4G26570	1	0	0	0	0	1
AT4G26610	0	0	0	1	0	0
AT4G26780	1	1	0	1	1	1
AT4G26900	1	1	1	1	1	0
AT4G26910	1	1	1	0	1	1
AT4G26970	1	1	0	0	1	1
AT4G27080	0	1	0	0	0	0
AT4G27090	1	0	0	1	1	1
AT4G27160	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G27170	0	0	0	0	1	0
AT4G27400	0	0	0	0	0	1
AT4G27500	1	0	0	0	1	0
AT4G27585	1	1	1	0	1	1
AT4G27640	1	0	0	0	0	0
AT4G27720	1	0	0	0	0	0
AT4G27760	1	1	1	0	1	1
AT4G27860	1	1	0	0	0	0
AT4G28050	1	0	0	0	0	0
AT4G28220	1	1	0	0	0	1
AT4G28390	0	0	0	0	0	1
AT4G28510	1	1	1	1	1	1
AT4G28520	0	0	1	0	1	0
AT4G29010	1	1	1	0	1	1
AT4G29120	0	0	0	0	1	0
AT4G29130	1	1	1	1	1	1
AT4G29350	1	0	1	0	1	0
AT4G29430	1	0	0	0	0	0
AT4G29480	1	0	1	0	1	1
AT4G29520	1	1	1	1	1	1
AT4G29680	1	1	1	0	0	1
AT4G29690	1	1	1	0	1	1
AT4G29840	1	1	1	1	1	1
AT4G29900	0	0	0	0	1	0
AT4G30010	1	0	1	1	1	1
AT4G30080	0	0	0	0	1	0
AT4G30160	1	0	0	0	1	0
AT4G30170	1	0	1	0	0	0
AT4G30190	1	1	1	0	1	1
AT4G30210	1	0	0	0	1	0
AT4G30440	0	0	1	0	1	0
AT4G30920	1	0	1	0	1	0
AT4G30930	1	1	0	1	1	0
AT4G30996	1	1	1	0	1	0
AT4G31180	0	0	0	1	0	0
AT4G31300	1	0	0	1	1	0
AT4G31340	1	1	1	1	1	1
AT4G31460	1	0	0	0	0	0
AT4G31480	0	0	0	1	0	0
AT4G31500	0	1	0	0	1	1
AT4G31700	0	0	0	0	1	0
AT4G31810	1	1	1	0	1	1
AT4G31880	1	0	0	0	1	0
AT4G31990	1	1	1	1	1	1
AT4G32120	0	1	0	0	0	0
AT4G32130	1	1	0	0	1	1
AT4G32400	1	0	1	0	1	1
AT4G32410	1	1	1	1	1	0
AT4G32470	1	1	1	0	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G32520	1	1	1	0	1	0
AT4G32720	0	0	0	1	0	0
AT4G32880	1	0	0	0	0	0
AT4G32920	0	0	0	0	0	1
AT4G33010	1	1	1	1	1	0
AT4G33090	1	1	1	1	1	1
AT4G33120	1	1	1	0	1	1
AT4G33250	1	0	0	0	1	0
AT4G33360	1	1	1	1	1	1
AT4G33530	1	0	0	0	1	0
AT4G33580	1	1	0	1	0	0
AT4G33650	0	0	0	0	1	0
AT4G33680	1	1	1	1	1	1
AT4G34140	1	0	0	0	0	0
AT4G34180	1	0	0	0	0	0
AT4G34200	1	1	1	1	1	1
AT4G34450	1	1	1	1	1	1
AT4G34640	1	1	1	0	1	1
AT4G34670	0	0	0	1	1	0
AT4G34700	1	1	1	1	1	1
AT4G34870	1	1	1	1	1	1
AT4G34960	0	1	0	1	0	0
AT4G35000	1	1	1	1	1	1
AT4G35090	1	1	1	1	1	1
AT4G35100	1	1	1	1	1	1
AT4G35260	1	1	1	1	1	1
AT4G35490	0	0	0	0	1	0
AT4G35580	0	0	0	0	1	0
AT4G35630	1	0	1	1	1	1
AT4G35790	0	1	1	0	1	1
AT4G35830	1	0	1	1	1	1
AT4G35850	1	1	1	0	1	1
AT4G35860	1	0	0	0	0	0
AT4G36080	0	0	1	0	1	0
AT4G36195	1	0	1	0	0	0
AT4G36250	1	1	0	0	0	0
AT4G36480	1	0	1	0	1	0
AT4G36680	1	1	0	0	1	0
AT4G37190	0	0	0	0	1	0
AT4G37640	1	0	1	0	1	1
AT4G37820	1	1	0	0	1	1
AT4G37830	1	0	1	0	1	1
AT4G37870	0	1	0	0	1	1
AT4G37910	1	1	1	1	1	1
AT4G38220	1	1	1	1	1	1
AT4G38350	1	0	1	0	1	1
AT4G38510	1	1	1	0	1	1
AT4G38630	0	0	0	0	1	0
AT4G38740	1	0	1	1	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G38790	0	0	0	0	0	1
AT4G38800	0	0	0	1	1	0
AT4G39080	1	1	1	1	1	1
AT4G39120	1	0	0	0	1	0
AT4G39200	0	0	0	0	1	0
AT4G39260	1	0	0	1	1	1
AT4G39460	0	1	0	0	0	0
AT4G39660	1	1	1	1	1	1
AT4G39690	1	1	1	0	1	0
AT4G39730	0	0	1	0	0	1
AT4G39740	1	0	0	0	1	0
AT4G39980	1	1	1	0	1	0
AT5G01220	1	0	0	0	0	0
AT5G01500	0	0	1	0	1	1
AT5G01600	0	0	1	1	0	0
AT5G01750	0	0	1	0	0	0
AT5G02050	1	0	0	0	0	0
AT5G02240	0	0	0	0	0	1
AT5G02260	0	1	0	0	0	0
AT5G02500	1	1	1	1	1	1
AT5G02530	0	0	0	0	1	0
AT5G02740	1	1	1	1	1	1
AT5G02870	1	0	0	0	1	0
AT5G02960	1	0	0	0	1	0
AT5G03080	1	0	0	0	0	1
AT5G03160	1	1	1	0	1	1
AT5G03290	1	1	1	0	1	1
AT5G03300	0	0	0	1	1	0
AT5G03630	1	1	1	1	1	1
AT5G03860	0	0	1	0	0	0
AT5G04430	1	0	0	0	1	0
AT5G04590	1	1	1	1	1	1
AT5G04610	0	0	0	0	0	1
AT5G04710	1	0	0	0	0	0
AT5G04740	1	0	1	0	0	0
AT5G04830	0	0	1	0	0	1
AT5G04960	1	0	0	0	0	0
AT5G04990	1	1	0	0	0	0
AT5G05000	1	0	1	1	1	0
AT5G05010	1	0	1	0	1	0
AT5G05170	1	1	1	1	1	0
AT5G05520	1	1	1	0	1	1
AT5G05670	1	0	0	0	1	0
AT5G05690	0	0	0	0	1	0
AT5G05780	1	0	0	0	1	0
AT5G05990	1	0	0	0	0	0
AT5G06060	0	0	0	0	1	0
AT5G07340	1	1	1	0	1	1
AT5G07350	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G07440	1	1	1	1	1	1
AT5G07980	0	0	1	0	0	0
AT5G07990	0	0	1	0	0	0
AT5G08060	1	0	1	1	1	1
AT5G08160	1	1	1	1	1	1
AT5G08180	1	0	0	0	1	0
AT5G08280	1	0	0	1	1	0
AT5G08300	1	1	1	1	1	1
AT5G08530	1	1	1	1	1	1
AT5G08540	1	1	0	0	1	1
AT5G08580	0	0	0	0	0	1
AT5G08610	0	0	0	0	1	0
AT5G08670	0	0	0	0	1	0
AT5G09420	0	0	0	0	1	0
AT5G09450	1	0	0	0	0	0
AT5G09510	0	0	0	0	1	0
AT5G09590	1	1	1	1	1	1
AT5G09650	1	1	1	0	1	1
AT5G09810	1	1	0	1	1	1
AT5G09840	1	0	0	0	1	0
AT5G09900	1	0	0	0	1	0
AT5G10100	0	0	0	1	0	0
AT5G10160	1	1	1	1	1	1
AT5G10450	1	0	0	1	1	0
AT5G10540	0	0	0	0	1	0
AT5G10560	0	0	0	0	0	1
AT5G10730	1	0	1	0	1	1
AT5G10780	0	1	0	0	1	1
AT5G10830	1	0	0	0	0	0
AT5G10840	1	1	1	1	1	1
AT5G10860	1	1	0	0	0	1
AT5G10920	1	1	0	0	1	0
AT5G11240	0	0	0	0	1	0
AT5G11520	1	1	1	0	1	1
AT5G11560	1	1	1	1	1	1
AT5G11670	1	0	0	0	1	1
AT5G11700	0	0	0	0	1	0
AT5G11730	0	0	1	0	0	0
AT5G11770	1	1	1	1	1	1
AT5G11880	1	1	1	1	1	1
AT5G12040	1	0	1	1	1	0
AT5G12200	1	0	0	0	0	0
AT5G12290	1	1	0	0	1	0
AT5G12470	1	1	1	1	1	1
AT5G12860	1	0	1	1	1	0
AT5G12950	0	1	0	0	0	0
AT5G13000	0	0	0	0	1	0
AT5G13110	0	0	0	1	1	0
AT5G13120	1	0	0	1	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G13280	1	1	0	0	0	0
AT5G13420	1	1	1	1	1	1
AT5G13450	1	1	1	1	1	1
AT5G13490	1	1	1	1	1	1
AT5G13520	0	0	0	0	1	0
AT5G13640	1	0	1	0	0	0
AT5G13710	1	1	1	1	1	1
AT5G13930	0	0	1	0	1	0
AT5G13980	1	0	0	0	1	1
AT5G14030	1	1	1	1	1	1
AT5G14040	1	1	1	1	1	1
AT5G14060	1	0	0	0	0	0
AT5G14105	0	0	0	0	1	0
AT5G14220	0	0	1	0	0	0
AT5G14430	0	1	1	0	0	0
AT5G14520	0	0	0	1	0	0
AT5G14580	1	0	0	0	0	0
AT5G14590	1	1	0	0	1	0
AT5G14950	1	1	1	0	1	0
AT5G15090	1	1	1	1	1	1
AT5G15200	1	0	0	1	1	1
AT5G15350	1	0	1	1	1	0
AT5G15450	0	0	0	0	1	1
AT5G15490	0	0	0	0	0	1
AT5G15520	0	0	0	0	0	1
AT5G15530	1	1	0	0	0	0
AT5G15550	1	0	0	0	1	0
AT5G15610	0	0	0	0	1	0
AT5G15640	1	0	1	1	1	0
AT5G15650	1	1	1	1	1	1
AT5G15910	1	0	1	0	1	1
AT5G15940	0	1	0	0	0	0
AT5G15980	1	1	1	0	1	0
AT5G16050	1	0	1	1	1	0
AT5G16130	1	0	0	1	0	0
AT5G16170	0	0	0	0	0	1
AT5G16230	0	1	0	0	0	0
AT5G16290	1	0	0	0	0	0
AT5G16370	0	1	0	0	0	0
AT5G16390	1	0	0	0	0	0
AT5G16440	1	0	0	0	1	0
AT5G16450	0	0	0	0	1	0
AT5G16510	1	0	1	0	1	0
AT5G16550	0	0	0	0	1	0
AT5G16590	1	0	1	1	1	0
AT5G16620	1	0	0	0	1	0
AT5G16660	1	0	0	0	0	0
AT5G16930	1	0	0	0	0	0
AT5G17190	0	1	0	0	0	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G17310	0	1	1	1	1	0
AT5G17530	1	1	0	0	1	0
AT5G17630	0	0	0	0	1	1
AT5G17710	0	1	0	0	1	0
AT5G17770	1	1	1	1	1	1
AT5G17820	1	1	0	1	1	0
AT5G17920	1	1	1	1	1	1
AT5G18170	1	1	1	1	1	1
AT5G18280	1	0	1	1	0	0
AT5G18380	0	0	0	1	1	1
AT5G18480	1	1	1	0	1	1
AT5G18520	0	0	1	0	1	1
AT5G18900	1	0	0	0	0	0
AT5G19130	0	0	0	0	1	0
AT5G19370	1	0	0	0	0	0
AT5G19440	1	0	1	0	1	0
AT5G19510	1	0	0	0	1	0
AT5G19520	0	0	1	1	0	1
AT5G19550	1	0	0	0	1	0
AT5G19690	1	1	1	1	1	1
AT5G19750	0	1	0	0	0	0
AT5G19760	1	1	1	1	1	1
AT5G19820	1	0	0	1	1	0
AT5G20000	0	0	0	1	1	0
AT5G20080	1	0	1	1	1	1
AT5G20090	0	0	1	0	0	1
AT5G20290	1	1	0	1	1	0
AT5G20350	1	0	0	0	0	0
AT5G20490	1	0	0	0	0	0
AT5G20500	1	0	1	0	1	1
AT5G20520	1	0	0	0	1	0
AT5G20660	1	0	0	0	1	1
AT5G20680	1	0	1	0	0	0
AT5G20720	1	1	1	1	1	1
AT5G20890	0	0	0	1	1	0
AT5G20950	0	0	1	0	0	0
AT5G20960	0	0	1	1	0	1
AT5G20980	1	0	0	0	0	0
AT5G22020	0	0	1	0	0	0
AT5G22060	0	0	1	0	0	0
AT5G22330	1	0	0	0	0	0
AT5G22350	1	0	0	0	0	0
AT5G22440	1	1	0	1	1	0
AT5G22640	1	0	1	0	1	0
AT5G22650	1	0	0	0	1	0
AT5G22740	1	0	0	0	0	0
AT5G22790	0	0	0	0	0	1
AT5G22880	1	0	1	0	1	1
AT5G23140	0	1	0	0	0	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G23250	1	0	0	0	1	0
AT5G23300	1	1	1	1	1	1
AT5G23540	1	0	0	0	1	0
AT5G23575	1	1	1	1	1	1
AT5G23630	1	1	1	0	1	1
AT5G23670	1	0	0	0	1	0
AT5G23740	1	0	0	0	0	0
AT5G23820	1	1	1	0	1	1
AT5G23830	1	1	1	0	1	1
AT5G24350	0	0	0	0	1	0
AT5G24400	1	0	1	0	1	0
AT5G24650	1	0	0	1	1	0
AT5G24690	0	0	0	0	1	0
AT5G24960	0	0	0	0	0	1
AT5G25100	1	1	1	0	1	1
AT5G25265	1	1	1	0	1	0
AT5G25940	1	0	0	0	0	0
AT5G26030	1	1	1	0	1	0
AT5G26260	1	1	1	1	1	1
AT5G26280	1	1	1	1	0	1
AT5G26360	0	0	0	1	1	0
AT5G26570	0	1	0	0	0	1
AT5G26667	1	0	0	1	0	0
AT5G26710	1	0	0	0	1	0
AT5G26780	1	1	1	1	1	0
AT5G26830	1	0	0	1	1	0
AT5G26860	1	0	1	0	1	0
AT5G27120	1	1	0	1	1	0
AT5G27330	0	0	0	1	0	0
AT5G27395	1	0	0	0	0	0
AT5G27430	1	0	0	0	0	0
AT5G27540	1	1	1	1	1	1
AT5G27600	0	1	1	0	0	0
AT5G27640	0	0	0	0	1	0
AT5G27670	0	0	0	0	0	1
AT5G27770	0	0	0	0	1	0
AT5G27850	1	0	1	1	1	1
AT5G28060	0	0	0	1	1	0
AT5G28220	1	0	0	0	0	0
AT5G28540	1	1	1	1	1	1
AT5G33320	1	1	1	1	1	1
AT5G34850	1	1	1	1	1	1
AT5G35080	0	0	1	0	1	0
AT5G35160	1	0	1	1	1	1
AT5G35360	1	1	1	1	1	1
AT5G35590	1	0	1	1	1	0
AT5G35630	1	1	1	1	1	1
AT5G35940	1	1	0	0	1	1
AT5G36210	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G36230	1	0	1	1	1	0
AT5G36880	1	1	0	0	1	0
AT5G37310	1	0	0	0	0	1
AT5G37510	1	1	1	1	1	1
AT5G37830	0	0	0	0	1	0
AT5G38280	0	0	0	1	0	0
AT5G38460	1	0	0	0	0	0
AT5G38480	1	1	0	1	1	1
AT5G38530	1	1	1	0	0	0
AT5G39320	1	0	0	0	1	0
AT5G39410	1	1	1	0	0	0
AT5G39730	0	0	0	0	0	1
AT5G39740	0	0	0	0	1	0
AT5G40480	1	1	1	1	1	1
AT5G40510	1	1	0	0	1	0
AT5G40580	1	0	0	0	0	0
AT5G40650	1	0	0	0	1	0
AT5G40660	0	1	0	0	0	0
AT5G40770	1	1	1	1	1	1
AT5G40810	1	1	1	1	1	1
AT5G40890	1	1	1	0	1	1
AT5G40930	1	0	0	0	1	0
AT5G41210	1	0	0	0	0	1
AT5G41520	1	0	0	1	1	0
AT5G41600	1	1	1	0	0	1
AT5G41670	1	1	1	1	1	1
AT5G41970	0	0	1	1	1	0
AT5G42020	1	1	1	1	1	1
AT5G42080	1	1	1	1	1	1
AT5G42090	1	0	1	0	1	1
AT5G42150	1	1	1	0	1	1
AT5G42390	0	1	0	0	0	0
AT5G42420	0	0	0	0	0	1
AT5G42570	1	0	1	1	1	1
AT5G42590	0	1	1	0	0	1
AT5G42650	1	1	0	0	0	0
AT5G42740	0	0	0	1	1	0
AT5G42790	1	0	0	1	1	1
AT5G42960	1	1	1	1	1	1
AT5G42980	1	1	1	0	1	1
AT5G43010	0	0	0	0	1	0
AT5G43060	1	1	1	1	1	1
AT5G43430	1	0	0	0	0	0
AT5G43600	0	0	1	0	0	0
AT5G43780	0	0	1	0	0	0
AT5G43830	1	0	0	0	0	0
AT5G43940	1	0	1	0	1	0
AT5G43970	1	0	1	0	0	1
AT5G44020	1	1	1	0	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G44120	0	1	0	0	1	0
AT5G44240	0	0	1	0	0	0
AT5G44320	0	1	0	0	1	0
AT5G44510	0	0	0	0	1	0
AT5G44710	1	0	0	0	0	0
AT5G44820	1	0	0	0	0	0
AT5G45390	0	1	0	0	0	0
AT5G45620	1	0	0	0	1	0
AT5G45750	1	0	0	0	1	1
AT5G46160	1	0	0	0	0	0
AT5G46180	0	0	0	0	0	1
AT5G46290	1	1	1	1	1	1
AT5G46430	0	0	0	0	1	0
AT5G46700	0	0	0	1	0	0
AT5G46800	1	1	1	1	0	0
AT5G47010	0	0	0	1	0	0
AT5G47030	1	1	0	1	1	1
AT5G47040	1	0	0	0	0	0
AT5G47320	1	0	0	0	1	0
AT5G47420	1	0	0	0	0	0
AT5G47690	0	0	0	0	1	0
AT5G47770	1	0	1	1	1	0
AT5G47780	1	0	0	0	0	0
AT5G47890	1	0	0	1	1	1
AT5G47990	1	1	1	0	1	1
AT5G48000	1	1	1	0	1	1
AT5G48010	1	1	1	0	1	0
AT5G48030	0	0	0	1	1	0
AT5G48180	1	0	0	0	0	0
AT5G48230	1	0	1	1	1	0
AT5G48300	0	0	1	0	0	1
AT5G48480	0	0	0	0	1	0
AT5G48580	1	1	1	0	1	0
AT5G48760	0	0	0	1	0	0
AT5G48810	1	1	1	0	1	1
AT5G48880	0	0	1	0	0	0
AT5G49030	0	1	0	0	0	0
AT5G49270	1	0	0	0	0	0
AT5G49460	0	1	0	1	1	1
AT5G49555	0	1	0	0	0	0
AT5G49680	1	0	0	0	0	0
AT5G49720	1	0	1	0	1	0
AT5G49810	1	0	0	0	1	0
AT5G49910	0	0	0	1	1	0
AT5G50370	1	0	1	1	1	1
AT5G50375	0	0	1	1	0	0
AT5G50850	1	1	1	1	1	1
AT5G50920	1	1	1	0	1	1
AT5G51200	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G51220	1	1	1	1	1	1
AT5G51570	1	0	1	0	0	0
AT5G51820	0	0	0	0	1	0
AT5G52210	1	0	0	0	0	0
AT5G52240	1	1	0	0	1	1
AT5G52520	0	1	0	0	0	0
AT5G52840	1	1	1	1	1	1
AT5G52920	1	1	1	1	1	0
AT5G53070	1	1	1	0	0	0
AT5G53090	1	0	0	0	1	0
AT5G53340	1	0	0	0	0	0
AT5G53400	0	0	0	0	1	0
AT5G53460	1	1	1	1	1	1
AT5G53480	1	0	1	1	1	0
AT5G53560	1	1	1	1	1	1
AT5G53850	1	0	0	0	1	0
AT5G54100	1	1	0	1	1	1
AT5G54370	1	1	0	0	0	1
AT5G54500	1	0	0	0	0	0
AT5G54750	1	0	0	0	1	0
AT5G54800	1	0	1	0	1	1
AT5G54810	0	1	0	0	0	0
AT5G54830	0	1	0	0	0	0
AT5G55070	1	1	1	1	1	1
AT5G55200	1	0	0	0	0	0
AT5G55610	1	1	1	0	1	1
AT5G55940	1	1	1	1	1	1
AT5G56010	0	0	0	0	1	0
AT5G56030	1	0	0	1	1	0
AT5G56350	1	0	0	0	0	0
AT5G56360	1	1	1	1	1	1
AT5G56500	1	1	1	1	1	1
AT5G56680	0	0	0	0	1	0
AT5G56730	1	0	0	0	0	0
AT5G56940	1	0	1	0	1	0
AT5G57020	0	0	0	0	1	0
AT5G57110	1	0	0	0	1	1
AT5G57290	0	0	0	0	1	0
AT5G57490	0	1	1	1	1	1
AT5G57500	0	1	0	0	0	1
AT5G57655	1	1	1	0	0	1
AT5G57870	1	0	0	1	1	0
AT5G58030	0	0	0	1	1	0
AT5G58070	0	0	0	0	0	1
AT5G58100	1	0	1	0	1	0
AT5G58270	1	0	0	0	0	0
AT5G58710	1	1	0	0	1	1
AT5G58784	1	0	0	0	0	0
AT5G59010	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G59290	0	1	0	0	0	1
AT5G59870	1	0	1	1	0	1
AT5G59880	1	0	1	0	0	1
AT5G59910	1	0	0	0	0	0
AT5G59980	0	0	1	0	0	0
AT5G60040	0	0	0	0	1	0
AT5G60120	0	0	1	0	0	0
AT5G60160	1	1	1	1	1	0
AT5G60640	1	1	1	1	1	1
AT5G60660	1	0	1	0	1	1
AT5G60670	0	0	0	1	0	0
AT5G60700	1	1	0	0	0	1
AT5G60730	1	0	0	0	0	0
AT5G60920	0	0	1	0	1	0
AT5G60960	1	0	0	0	1	0
AT5G60980	1	0	0	0	1	0
AT5G61020	0	0	0	0	1	0
AT5G61030	1	0	0	0	1	0
AT5G61140	0	0	0	0	1	0
AT5G61170	0	0	0	0	1	0
AT5G61240	1	1	1	0	1	1
AT5G61580	1	0	0	0	0	0
AT5G61780	0	0	0	1	1	0
AT5G61790	1	1	1	1	1	1
AT5G61840	0	0	1	0	0	0
AT5G62190	0	0	0	0	1	0
AT5G62200	0	0	0	0	0	1
AT5G62270	1	0	0	0	0	0
AT5G62390	1	0	0	1	1	1
AT5G62530	1	1	1	1	1	1
AT5G62670	0	0	0	0	1	0
AT5G62740	0	0	0	0	0	1
AT5G62890	0	1	0	0	1	0
AT5G63310	0	0	1	0	0	0
AT5G63400	1	1	1	1	1	1
AT5G63510	1	1	0	0	1	0
AT5G63570	1	1	0	1	1	0
AT5G63620	0	1	0	0	0	0
AT5G63840	1	1	1	1	1	1
AT5G63890	1	0	1	1	1	0
AT5G64030	1	1	1	0	1	1
AT5G64050	1	1	0	0	0	0
AT5G64100	1	0	1	0	0	0
AT5G64270	0	0	0	0	1	0
AT5G64290	1	0	1	1	1	0
AT5G64300	1	1	0	0	0	0
AT5G64350	0	0	0	0	0	1
AT5G64440	1	1	1	1	0	1
AT5G64670	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G64740	1	0	0	0	1	0
AT5G64860	1	0	0	0	0	1
AT5G65020	1	1	1	1	1	1
AT5G65110	1	1	0	0	0	1
AT5G65270	0	0	0	0	1	0
AT5G65430	1	0	0	1	1	0
AT5G65620	1	0	0	0	1	0
AT5G65700	0	0	0	0	1	0
AT5G65720	1	1	0	0	1	0
AT5G65750	1	1	0	0	0	1
AT5G65780	1	1	0	0	1	0
AT5G65810	1	1	1	0	1	1
AT5G65940	1	0	0	0	1	1
AT5G66060	1	0	0	0	0	0
AT5G66120	1	0	1	1	1	0
AT5G66140	1	0	0	1	1	1
AT5G66280	0	0	0	0	0	1
AT5G66510	1	1	1	1	1	1
AT5G66530	1	0	1	0	0	0
AT5G66680	1	1	1	1	1	1
AT5G66760	1	1	1	1	1	1
AT5G66860	1	1	1	1	1	1
AT5G67500	1	1	1	1	1	1
AT5G67590	1	0	1	1	1	1
ATCG00120	0	1	1	0	1	0
ATCG00480	1	1	1	1	1	0
ATCG00490	0	0	1	0	0	0
ATCG00500	1	1	1	1	1	0
ATCG01130	1	0	1	1	1	0
ATMG00070	1	1	1	1	1	1
ATMG00160	1	0	1	0	1	0
ATMG00510	1	1	1	1	1	1
ATMG00560	1	0	0	0	0	0
ATMG00580	1	0	0	0	1	0
ATMG00640	1	1	1	1	1	1
False Discovery Rate (FDR)	0.0320233					
REV_AT1G06230	0	1	0	0	0	0
REV_AT1G07630	1	0	0	0	0	0
REV_AT1G08590	1	0	0	0	0	0
REV_AT1G09020	0	1	0	1	0	0
REV_AT1G13490	0	0	0	1	0	0
REV_AT1G26640	0	0	1	0	0	0
REV_AT1G31730	1	0	0	0	0	0
REV_AT1G34930	1	0	0	0	0	0
REV_AT1G36180	0	0	0	0	1	0
REV_AT1G50380	0	0	0	0	1	0
REV_AT1G55040	1	0	0	0	0	0
REV_AT1G59790	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
REV_AT1G67110	1	0	0	0	0	0
REV_AT1G80760	0	1	0	0	0	0
REV_AT2G03450	1	0	0	0	0	0
REV_AT2G17880	1	0	0	0	0	0
REV_AT2G20330	0	0	1	0	0	0
REV_AT2G27120	1	0	0	0	0	0
REV_AT2G31830	0	0	0	0	1	0
REV_AT2G32750	0	0	1	0	0	0
REV_AT2G33050	1	1	1	0	1	0
REV_AT2G37670	0	0	0	0	0	1
REV_AT3G06490	1	0	0	0	0	0
REV_AT3G06860	0	0	0	0	1	0
REV_AT3G12950	0	0	0	0	1	0
REV_AT3G13180	0	0	1	0	0	0
REV_AT3G14670	1	0	0	0	1	0
REV_AT3G15120	1	0	1	0	1	0
REV_AT3G18110	1	0	0	0	0	0
REV_AT3G18310	1	0	0	0	1	0
REV_AT3G19040	0	0	0	0	1	0
REV_AT3G22790	0	0	0	0	1	0
REV_AT3G28840	1	0	1	0	1	0
REV_AT3G29300	0	0	0	1	0	0
REV_AT3G50870	0	0	1	0	0	0
REV_AT3G54760	0	0	1	0	0	0
REV_AT3G57350	0	0	0	0	0	1
REV_AT4G00440	0	0	0	0	1	0
REV_AT4G01200	0	1	0	0	0	0
REV_AT4G10120	0	0	1	0	0	0
REV_AT4G10710	0	0	1	0	1	0
REV_AT4G11660	0	0	0	0	1	0
REV_AT4G14370	0	0	0	0	1	0
REV_AT4G14850	1	0	0	0	0	0
REV_AT4G18820	1	0	0	0	0	0
REV_AT4G20650	1	0	0	0	0	0
REV_AT4G21860	0	0	1	0	0	0
REV_AT4G24900	1	0	0	0	0	0
REV_AT4G25820	0	0	1	0	0	0
REV_AT4G26640	1	0	0	0	0	0
REV_AT4G32430	0	0	1	0	0	0
REV_AT4G32850	0	0	0	0	1	0
REV_AT4G36490	0	0	1	0	0	0
REV_AT5G07210	0	0	0	0	1	0
REV_AT5G07390	1	0	0	0	0	0
REV_AT5G12300	0	0	0	0	1	0
REV_AT5G15700	0	0	1	0	0	0
REV_AT5G16420	0	0	1	0	0	0
REV_AT5G21120	1	0	0	0	0	0
REV_AT5G22220	0	1	0	0	0	0
REV_AT5G24740	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S2. The 1,995 proteins of the root cellular proteome

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
REV_AT5G44750	0	0	0	0	0	1
REV_AT5G44790	0	0	1	0	0	0
REV_AT5G45370	0	0	1	0	0	0
REV_AT5G48780	0	0	0	0	1	0
REV_AT5G61190	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S3. Root proteins found in a single cell population

Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01910	AT1G01950	AT1G01960	AT1G01100	AT1G01040	AT1G01180
AT1G04810	AT1G03230	AT1G02420	AT1G05260	AT1G03880	AT1G20450
AT1G05620	AT1G07410	AT1G06430	AT1G07790	AT1G04690	AT1G20630
AT1G06890	AT1G10510	AT1G06800	AT1G10670	AT1G04850	AT1G23310
AT1G08450	AT1G20300	AT1G16560	AT1G14290	AT1G06000	AT1G24090
AT1G14060	AT1G24280	AT1G20620	AT1G14320	AT1G07750	AT1G28130
AT1G14210	AT1G28440	AT1G27980	AT1G32400	AT1G08640	AT1G28510
AT1G14710	AT1G29330	AT1G29020	AT1G41880	AT1G08840	AT1G31812
AT1G15710	AT1G31950	AT1G36050	AT1G48200	AT1G12310	AT1G32900
AT1G16300	AT1G49630	AT1G47128	AT1G48600	AT1G13560	AT1G33230
AT1G17160	AT1G50940	AT1G50700	AT1G63050	AT1G15750	AT1G47600
AT1G17890	AT1G67560	AT1G54550	AT1G66670	AT1G16350	AT1G49300
AT1G19130	AT1G70190	AT1G59780	AT1G73230	AT1G16890	AT1G51650
AT1G19140	AT1G71260	AT1G62130	AT1G75220	AT1G19440	AT1G52280
AT1G20230	AT1G80480	AT1G67500	AT1G76550	AT1G19800	AT1G64850
AT1G20560	AT2G23370	AT1G70570	AT1G78860	AT1G19900	AT1G65260
AT1G21370	AT2G26240	AT1G72730	AT1G79210	AT1G19920	AT1G65820
AT1G21560	AT2G43350	AT1G72860	AT2G29550	AT1G20090	AT1G67850
AT1G23170	AT2G45440	AT1G73940	AT2G34040	AT1G20950	AT1G69526
AT1G25380	AT3G07330	AT1G75140	AT2G40600	AT1G21160	AT1G69830
AT1G26160	AT3G13110	AT2G04780	AT3G02080	AT1G21690	AT1G70940
AT1G29250	AT3G13530	AT2G20680	AT3G04520	AT1G22200	AT1G72175
AT1G30450	AT3G14790	AT2G25160	AT3G11250	AT1G22460	AT1G76030
AT1G30870	AT3G18830	AT2G39800	AT3G17820	AT1G27310	AT1G76200
AT1G31860	AT3G21160	AT2G40890	AT3G19450	AT1G27970	AT2G03120
AT1G48230	AT3G44160	AT2G41150	AT3G19760	AT1G30690	AT2G04350
AT1G48610	AT3G47670	AT2G48020	AT3G22230	AT1G31730	AT2G18230
AT1G48900	AT3G49190	AT3G05100	AT3G25290	AT1G33040	AT2G19760
AT1G49140	AT3G53430	AT3G07290	AT3G32980	AT1G33680	AT2G21590
AT1G50140	AT3G53460	AT3G09410	AT3G51240	AT1G33810	AT2G22420
AT1G50500	AT3G54640	AT3G10730	AT3G52940	AT1G44835	AT2G28760
AT1G53645	AT3G55760	AT3G14840	AT3G53230	AT1G49410	AT2G28900
AT1G56550	AT3G57680	AT3G23160	AT3G55830	AT1G50030	AT2G30950
AT1G62730	AT3G59360	AT3G25585	AT3G59020	AT1G50110	AT2G32520
AT1G62810	AT4G00430	AT3G26950	AT4G10280	AT1G51160	AT2G35490
AT1G63110	AT4G20890	AT3G44190	AT4G11290	AT1G51710	AT2G36460
AT1G63450	AT4G23430	AT3G44310	AT4G12750	AT1G52740	AT2G38230
AT1G65540	AT4G24310	AT3G47960	AT4G14160	AT1G61730	AT2G39750
AT1G66580	AT4G27080	AT3G51550	AT4G16340	AT1G63660	AT2G45740
AT1G67930	AT4G32120	AT3G52850	AT4G21105	AT1G65020	AT2G47380
AT1G70410	AT4G39460	AT3G55610	AT4G23900	AT1G65220	AT3G03810
AT1G70730	AT5G02260	AT3G57420	AT4G25740	AT1G66430	AT3G08610
AT1G72280	AT5G12950	AT3G60100	AT4G26110	AT1G67120	AT3G14290
AT1G72480	AT5G15940	AT3G62580	AT4G26610	AT1G67430	AT3G18430
AT1G73160	AT5G16230	AT4G04190	AT4G31180	AT1G70580	AT3G19870
AT1G74910	AT5G16370	AT4G18360	AT4G31480	AT1G72150	AT3G20670
AT1G74920	AT5G19750	AT4G18760	AT4G32720	AT1G72540	AT3G44830
AT1G75940	AT5G40660	AT4G25360	AT5G10100	AT1G73180	AT3G45300
AT1G76690	AT5G42390	AT5G01750	AT5G14520	AT1G73590	AT3G46040

Supplementary Tables pertaining to Figure 1
Supplementary Table S3. Root proteins found in a single cell population

Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G77710	AT5G45390	AT5G03860	AT5G27330	AT1G74560	AT3G47730
AT1G78660	AT5G49030	AT5G07980	AT5G38280	AT1G75280	AT3G52180
AT1G80670	AT5G49555	AT5G07990	AT5G46700	AT1G75640	AT3G52230
AT2G15390	AT5G52520	AT5G11730	AT5G47010	AT1G75990	AT3G56170
AT2G16570	AT5G54810	AT5G14220	AT5G48760	AT1G76860	AT3G58010
AT2G17500	AT5G54830	AT5G20950	AT5G60670	AT1G79500	AT3G60340
AT2G18030	AT5G63620	AT5G22020		AT1G80500	AT4G00750
AT2G18980		AT5G22060		AT2G01690	AT4G01750
AT2G19160		AT5G43600		AT2G15270	AT4G14430
AT2G19860		AT5G43780		AT2G16640	AT4G19460
AT2G21250		AT5G44240		AT2G16760	AT4G19640
AT2G22125		AT5G48880		AT2G17790	AT4G22310
AT2G22500		AT5G59980		AT2G19520	AT4G23630
AT2G22970		AT5G60120		AT2G20890	AT4G23850
AT2G24170		AT5G61840		AT2G21620	AT4G23920
AT2G25830		AT5G63310		AT2G23070	AT4G25450
AT2G27190		ATCG00490		AT2G26730	AT4G27400
AT2G30920				AT2G27000	AT4G28390
AT2G34560				AT2G27040	AT4G32920
AT2G34585				AT2G28490	AT4G38790
AT2G35790				AT2G31320	AT5G02240
AT2G35810				AT2G31360	AT5G04610
AT2G37550				AT2G32060	AT5G08580
AT2G37670				AT2G32730	AT5G10560
AT2G38650				AT2G33340	AT5G15490
AT2G40800				AT2G35630	AT5G15520
AT2G41600				AT2G36580	AT5G16170
AT2G43070				AT2G36910	AT5G22790
AT2G44040				AT2G37020	AT5G24960
AT2G45070				AT2G37040	AT5G27670
AT2G45990				AT2G37050	AT5G39730
AT2G47540				AT2G39040	AT5G42420
AT3G01190				AT2G40290	AT5G46180
AT3G01290				AT2G40660	AT5G58070
AT3G02660				AT2G41790	AT5G62200
AT3G03050				AT2G42770	AT5G62740
AT3G04570				AT2G42810	AT5G64350
AT3G05420				AT2G43400	AT5G66280
AT3G06040				AT2G43630	
AT3G07470				AT2G43770	
AT3G07950				AT2G44100	
AT3G08550				AT2G45820	
AT3G09690				AT3G02260	
AT3G09740				AT3G03220	
AT3G10050				AT3G03330	
AT3G10260				AT3G03990	
AT3G11170				AT3G04600	
AT3G11730				AT3G04820	
AT3G12290				AT3G04940	

Supplementary Tables pertaining to Figure 1
Supplementary Table S3. Root proteins found in a single cell population

Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G12370				AT3G07100	
AT3G13460				AT3G07160	
AT3G15290				AT3G07390	
AT3G15660				AT3G07610	
AT3G16200				AT3G09300	
AT3G17910				AT3G10380	
AT3G18760				AT3G12050	
AT3G19508				AT3G12670	
AT3G21400				AT3G13300	
AT3G21465				AT3G16400	
AT3G21540				AT3G17210	
AT3G23190				AT3G18060	
AT3G23510				AT3G20410	
AT3G23600				AT3G20790	
AT3G24503				AT3G25800	
AT3G27020				AT3G44110	
AT3G27230				AT3G46210	
AT3G27300				AT3G46940	
AT3G27430				AT3G47370	
AT3G27890				AT3G51100	
AT3G28480				AT3G51670	
AT3G29250				AT3G52140	
AT3G29360				AT3G52580	
AT3G46560				AT3G54470	
AT3G48110				AT3G56490	
AT3G48890				AT3G57220	
AT3G51440				AT3G57410	
AT3G51830				AT3G58510	
AT3G51980				AT3G59280	
AT3G52190				AT3G59890	
AT3G52570				AT3G59990	
AT3G52640				AT3G60245	
AT3G53180				AT3G60770	
AT3G53900				AT3G60860	
AT3G53990				AT3G61580	
AT3G54840				AT3G63130	
AT3G55920				AT4G01210	
AT3G56900				AT4G03190	
AT3G56950				AT4G04940	
AT3G57560				AT4G08520	
AT3G57630				AT4G08790	
AT3G57660				AT4G10260	
AT3G58140				AT4G11850	
AT3G58840				AT4G14680	
AT3G60440				AT4G17270	
AT3G60850				AT4G18830	
AT3G61520				AT4G19006	
AT3G63190				AT4G20980	
AT4G00040				AT4G23460	

Supplementary Tables pertaining to Figure 1
Supplementary Table S3. Root proteins found in a single cell population

Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G00100				AT4G23540	
AT4G00290				AT4G23650	
AT4G00710				AT4G23690	
AT4G01660				AT4G24550	
AT4G04470				AT4G26210	
AT4G04860				AT4G27160	
AT4G09990				AT4G27170	
AT4G11600				AT4G29120	
AT4G12130				AT4G29900	
AT4G13050				AT4G30080	
AT4G13200				AT4G31700	
AT4G16180				AT4G33650	
AT4G16210				AT4G35490	
AT4G16500				AT4G35580	
AT4G17040				AT4G37190	
AT4G17420				AT4G38630	
AT4G18230				AT4G39200	
AT4G20020				AT5G02530	
AT4G20460				AT5G05690	
AT4G21180				AT5G06060	
AT4G21540				AT5G08610	
AT4G21570				AT5G08670	
AT4G22214				AT5G09420	
AT4G23640				AT5G09510	
AT4G25570				AT5G10540	
AT4G26010				AT5G11240	
AT4G27640				AT5G11700	
AT4G27720				AT5G13000	
AT4G28050				AT5G13520	
AT4G29430				AT5G14105	
AT4G31460				AT5G15610	
AT4G32880				AT5G16450	
AT4G34140				AT5G16550	
AT4G34180				AT5G19130	
AT4G35860				AT5G24350	
AT5G01220				AT5G24690	
AT5G02050				AT5G27640	
AT5G04710				AT5G27770	
AT5G04960				AT5G37830	
AT5G05990				AT5G39740	
AT5G07350				AT5G43010	
AT5G09450				AT5G44510	
AT5G10830				AT5G46430	
AT5G12200				AT5G47690	
AT5G14060				AT5G48480	
AT5G14580				AT5G51820	
AT5G16290				AT5G53400	
AT5G16390				AT5G56010	
AT5G16660				AT5G56680	

Supplementary Tables pertaining to Figure 1
Supplementary Table S3. Root proteins found in a single cell population

Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis /Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G16930				AT5G57020	
AT5G18900				AT5G57290	
AT5G19370				AT5G59010	
AT5G20350				AT5G60040	
AT5G20490				AT5G61020	
AT5G20980				AT5G61140	
AT5G22330				AT5G61170	
AT5G22350				AT5G62190	
AT5G22740				AT5G62670	
AT5G23740				AT5G64270	
AT5G25940				AT5G65270	
AT5G27395				AT5G65700	
AT5G27430					
AT5G28220					
AT5G38460					
AT5G40580					
AT5G43430					
AT5G43830					
AT5G44710					
AT5G44820					
AT5G46160					
AT5G47040					
AT5G47420					
AT5G47780					
AT5G48180					
AT5G49270					
AT5G49680					
AT5G52210					
AT5G53340					
AT5G54500					
AT5G55200					
AT5G56350					
AT5G56730					
AT5G58270					
AT5G58784					
AT5G59910					
AT5G60730					
AT5G61580					
AT5G62270					
AT5G64670					
AT5G66060					
ATMG00560					

Supplementary Tables pertaining to Figure 1
Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G14220	ribonuclease T2 family protein, contains similarity to S-like ribonuclease PD1 GI:9957752 from (Prunus dulcis); contains ribonuclease T2 family histidine protein motif	1	0	0	0	1	0
AT1G15210	ABC transporter family protein, Similar to gb:Z70524 GI:1514643 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF:00005 ABC transporter family. ESTs gb:N97039 and gb:T43169 come from this gene	1	0	1	1	1	0
AT1G17180	ATGSTU25__glutathione S-transferase, putative, Second of three repeated putative glutathione transferases. 72% identical to glutathione transferase (Arabidopsis thaliana) (gi:4006934). Location of ests 191A10T7 (gb:R90188) and 171N13T7 (gb:R65532)	1	0	0	0	0	1
AT1G30870	cationic peroxidase, putative, similar to cationic peroxidase (gi:1232069); similar to EST gb:AI100412	1	0	0	0	0	0
AT1G47600	glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to thioglucosidase (GI:871992) (Arabidopsis thaliana)	0	0	0	0	0	1
AT1G56550	expressed protein	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G66270	beta-glucosidase (PSR3.2), nearly identical to GI:2286069 from (Arabidopsis thaliana) (Plant Mol. Biol. 34 (1), 57-68 (1997)); similar to thioglucoside glucohydrolase (GI:984052) (Arabidopsis thaliana)	1	1	1	1	1	1
AT1G67330	expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)	1	1	1	0	1	0
AT1G78860	curculin-like (mannose-binding) lectin family protein, low similarity to Ser/Thr protein kinase (Zea mays) GI:2598067; contains Pfam profile PF01453: Lectin (probable mannose binding) but not the protein kinase domain of the Z. mays protein	0	0	0	1	0	0
AT2G15390	FUT4_ATFUT4__xyloglucan fucosyltransferase, putative (FUT4), identical to SP:Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SP:Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}	1	0	0	0	0	0
AT2G16005	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain	1	0	0	0	0	1
AT2G18980	peroxidase, putative, identical to peroxidase ATP22a (Arabidopsis thaliana) gi:1620369:emb:CAA70034	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G38840	guanylate-binding family protein, similar to SP:Q01514 Interferon-induced guanylate-binding protein 1 (Guanine nucleotide-binding protein 1) (Interferon-gamma inducible protein MAG-1) {Mus musculus}; contains Pfam profile PF02263: Guanylate-binding protein, N-terminal domain	0	1	1	0	0	0
AT3G01190	peroxidase 27 (PER27) (P27) (PRXR7), identical to SP:Q43735 Peroxidase 27 precursor (EC 1.11.1.7) (Atperox P27) (PRXR7) (ATP12a) {Arabidopsis thaliana}	1	0	0	0	0	0
AT3G01720	expressed protein	1	0	0	0	1	0
AT3G08610	expressed protein	0	0	0	0	0	1
AT3G16410	jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, epithiospecifier (Arabidopsis thaliana) GI:16118845; contains Pfam profiles PF01419 jacalin-like lectin family, PF01344 Kelch motif	1	1	0	0	1	1
AT3G16430	jacalin lectin family protein, similar to myrosinase binding protein (Brassica napus) GI:1711296; contains Pfam profile PF01419 jacalin-like lectin domain	1	1	0	0	0	1
AT3G19390	cysteine proteinase, putative / thiol protease, putative, contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from (Arabidopsis thaliana)	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G21400	expressed protein	1	0	0	0	0	0
AT3G48340	similar to cysteine proteinase, putative [Arabidopsis thaliana] (TAIR:At3g48350.1); similar to cysteine proteinase [Glycine max] (GB:BAC77522.1); contains InterPro domain Papain cysteine protease (C1) (InterPro:IPR000668); contains InterPro domain Eukaryotic thiol (cysteine) protease (InterPro:IPR000169)	1	1	1	0	1	1
AT3G53480	ABC transporter family protein, PDR5-like ABC transporter, Spirodela polyrrhiza, EMBL:Z70524	1	1	0	0	0	1
AT4G08770	peroxidase, putative, identical to class III peroxidase ATP38 (Arabidopsis thaliana) gi:17530568:gb:AAL40851; similar to peroxidase C2 precursor (Armoracia rusticana) SWISS-PROT: P17179; identical to cDNA class III peroxidase ATP38 GI:17530567	0	0	0	1	1	0
AT4G23710	vacuolar ATP synthase subunit G 2 (VATG2) / V-ATPase G subunit 2 (VAG2) / vacuolar proton pump G subunit 2, identical to Swiss-Prot:O82629 vacuolar ATP synthase subunit G 2 (V-ATPase G subunit 2, Vacuolar proton pump G subunit 2) (Arabidopsis thaliana)	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G26010	peroxidase, putative, peroxidase ATP13a - Arabidopsis thaliana, PID:e264765; identical to cDNA class III peroxidase ATP35, GI:17530565	1	0	0	0	0	0
AT4G27860	integral membrane family protein, contains Pfam PF01988: Integral membrane protein	1	1	0	0	0	0
AT4G29690	type I phosphodiesterase/nucleotide pyrophosphatase family protein, similar to SP:P22413 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) (Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) {Homo sapiens}; contains Pfam profile PF01663: Type I phosphodiesterase / nucleotide pyrophosphatase	1	1	1	0	1	1
AT4G30170	peroxidase, putative, identical to peroxidase ATP8a (Arabidopsis thaliana) gi:1546706:emb:CAA67361	1	0	1	0	0	0
AT5G02260	ATEXPA9_ATEXP9_ATHEXP ALPHA 1.10_EXP9__expansin, putative (EXP9), similar to expansin precursor GI:4138914 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069	0	1	0	0	0	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G04960	pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase	1	0	0	0	0	0
AT5G17820	peroxidase 57 (PER57) (P57) (PRXR10), identical to SP:Q43729 Peroxidase 57 precursor (EC 1.11.1.7) (Atperox P57) (PRXR10) (ATP13a) {Arabidopsis thaliana}	1	1	0	1	1	0
AT5G23830	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain	1	1	1	0	1	1
AT5G26260	meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain	1	1	1	1	1	1
AT5G35940	jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	1	1	0	0	1	1
AT5G40510	expressed protein	1	1	0	0	1	0
AT5G42590	CYP71A16__cytochrome P450 71A16, putative (CYP71A16), Identical to Cytochrome P450 71A16 (SP:Q9FH66) (Arabidopsis thaliana)	0	1	1	0	0	1
AT5G47990	CYP705A5__cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max);	1	1	1	0	1	1

Supplementary Tables pertaining to Figure 1

Supplementary Table S4. Proteins from the root cellular proteome also identified as root organ-specific biomarkers by Baerenfaller et al. 2008

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G48000	CYP708A2__cytochrome P450 family protein, similar to steroid 22-alpha-hydroxylase; DWF4; CYP90B1 (GI:2935342) (Arabidopsis thaliana)	1	1	1	0	1	1
AT5G48010	ATPEN1_04C11__Encodes an oxidosqualene cyclase involved in the biosynthesis of thalianol, a tricyclic triterpenoid of unknown function.	1	1	1	0	1	0
AT5G60660	PIP2;4_PIP2F__major intrinsic family protein / MIP family protein, similar to mipC protein GI:1657948 from (Mesembryanthemum crystallinum)	1	0	1	0	1	1
AT5G64100	peroxidase, putative, identical to peroxidase ATP3a (Arabidopsis thaliana) gi:1546698:emb:CAA67340	1	0	1	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S5. Known regulators of cellular development detected in a single root cell population

Locus	Protein Name	Root Cells Identified	Literature reference supporting a root developmental role
At3g03050	CELLUASE SYNTHASE-LIKE D3 (CSLD3)	Root Hairs (COBL9)	CSLD3. Wang X, Cnops G, Vanderhaeghen R, De Block S, Van Montagu M, Van Lijsebettens M (2001) AtCSLD3, a cellulose synthase-like gene important for root hair growth in Arabidopsis. Plant Physiol 126:575-586
	KOJAK (KJK)		KJK. Favery B, Ryan E, Foreman J, Linstead P, Boudonck K, Steer M, Shaw P, Dolan L (2001) KOJAK encodes a cellulose synthase-like protein required for root hair cell morphogenesis in Arabidopsis. Genes Dev 15:79-89
At3g08550	ABA-INSENSITIVE8 (ABI8)	Root Hairs (COBL9)	ABI8. Brocard-Gifford I, Lynch TJ, Garcia ME, Malhotra B, Finkelstein RR (2004) The Arabidopsis thaliana ABSCISIC ACID-INSENSITIVE8 encodes a novel protein mediating abscisic acid and sugar responses essential for growth. Plant Cell16:406-421
	ELONGATION DEFECTIVE 1 (ELD1)		ELD1. Cheng JC, Lertpiriyapong K, Wang S, Sung ZR (2000) The role of the Arabidopsis ELD1 gene in cell development and photomorphogenesis in darkness. Plant Physiol 123:509-520
	KOBITO1 (KOB1)		KOB1. Pagant S, Bichet A, Sugimoto K, Lerouxel O, Desprez T, McCann M, Lerouge P, Vernhettes S, Höfte H (2002) KOBITO1 encodes a novel plasma membrane protein necessary for normal synthesis of cellulose during cell expansion in Arabidopsis. Plant Cell 14:2001-2013
At4g23640	TINY ROOT HAIR 1 (TRH1)	Root Hairs (COBL9)	TRH1. Rigas S, Debrosses G, Haralampidis K, Vicente-Agullo F, Feldmann KA, Grabov A, Dolan L, Hatzopoulos P (2001) TRH1 encodes a potassium transporter required for tip growth in Arabidopsis root hairs. Plant Cell 13:139-151
At5g20350	TIP GROWTH DEFECTIVE 1 (TIP1)	Root Hairs (COBL9)	TIP1. Schiefelbein J, Galway M, Masucci J, Ford S (1993) Pollen tube and root-hair tip growth is disrupted in a mutant of Arabidopsis thaliana. Plant Physiol 103:979-985
			TIP1. Hemsley PA, Kemp AC, Grierson CS (2005) The TIP GROWTH DEFECTIVE1 S-acyl transferase regulates plant cell growth in Arabidopsis. Plant Cell 17:2554-2563
At5g49270	COBRA-LIKE 9 (COBL9)	Root Hairs (COBL9)	COBL9. Roudier F, Schindelman G, DeSalle R, Benfey PN (2002) The COBRA family of putative GPI-anchored proteins in Arabidopsis. A new fellowship in expansion. Plant Physiol 130:538-548
	DEFORMED ROOT HAIRS 9 (DER9)		DER9. Ringli C, Baumberger N, Keller B (2005) The Arabidopsis root hair mutants der2-der9 are affected at different stages of root hair development. Plant Cell Physiol 46:1046-1053
	MUTANT ROOT HAIRS 4 (MRH4)		MRH4. Jones MA, Raymond MJ, Smirnoff N (2006) Analysis of the root-hair morphogenesis transcriptome reveals the molecular identity of six genes with roles in root-hair development in Arabidopsis. Plant J 45:83-100

Supplementary Tables pertaining to Figure 1
Supplementary Table S5. Known regulators of cellular development detected in a single root cell population

Locus	Protein Name	Root Cells Identified	Literature reference supporting a root developmental role
	SHAVEN 2 (SHV2)		SHV2. Parker JS, Cavell AC, Dolan L, Roberts K, Grierson CS (2000) Genetic interactions during root hair morphogenesis in Arabidopsis. Plant Cell 12:1961-1974
At5g49680	KINKY POLLEN (KIP)	Root Hairs (COBL9)	KIP. Procissi A, Guyon A, Pierson ES, Giritch A, Knuiman B, Grandjean O, Tonelli C, Derksen J, Pelletier G, Bonhomme S (2003) KINKY POLLEN encodes a SABRE-like protein required for tip growth in Arabidopsis and conserved among eukaryotes. Plant J 36:894-904
At1g01950	ARMADILLO REPEAT KINESIN2 (ARK2)	Non-Hair Epidermis (WER)	ARK2. Sakai T, Honing H, Nishioka M, Uehara Y, Takahashi M, Fujisawa N, Saji K, Seki M, Shinozaki K, Jones MA, Smirnoff N, Okada K, Wasteneys GO (2008) Armadillo repeat-containing kinesins and a NIMA-related kinase are required for epidermal-cell morphogenesis in Arabidopsis. Plant J 53:157-171.
At3g54640	TRYPTOPHAN-REQUIRING 3 (TRP3)	Non-Hair Epidermis (WER)	TRP3. Rutherford R, Gallois P, Masson PH (1998) Mutations in Arabidopsis thaliana genes involved in the tryptophan biosynthesis pathway affect root waving on tilted agar surfaces. Plant J 16:145-154
At2g40890	CYTOCHROME P450, FAMILY 98, SUBFAMILY1, POLYPEPTIDE 3 (CYP98A3)	Cortex (CORTEX)	CYP98A3. Abdulrazzak N, Pollet B, Ehlting J, Larsen K, Asnaghi C, Ronseau S, Proux C, Erhardt M, Seltzer V, Renou JP, Ullmann P, Pauly M, Lapierre C, Werck-Reichhart D (2006) A coumaroyl-ester-3-hydroxylase insertion mutant reveals the existence of nonredundant meta-hydroxylation pathways and essential roles for phenolic precursors in cell expansion and plant growth. Plant Physiol 140:30-48
At3g52940	FACKEL (FK)	Endodermis/Quiescent (SCR)	FK. Schrick K, Mayer U, Horrichs A, Kuhnt C, Bellini C, Dangl J, Schmidt J, Jürgens G (2000) FACKEL is a sterol C-14 reductase required for organized cell division and expansion in Arabidopsis embryogenesis. Genes Dev 14:1471-1484
	EXTRA-LONG-LIFESPAN 1 (ELL1)		ELL1. Jang JC, Fujioka S, Tasaka M, Seto H, Takatsuto S, Ishii A, Aida M, Yoshida S, Sheen J (2000) A critical role of sterols in embryonic patterning and meristem programming revealed by the fackel mutants of Arabidopsis thaliana. Genes Dev 14:1485-1497
	HYDRA2 (HYD2)		HYD2. Souter M, Topping J, Pullen M, Friml J, Palme K, Hackett R, Grierson D, Lindsey K (2002) hydra Mutants of Arabidopsis are defective in sterol profiles and auxin and ethylene signaling. Plant Cell 14:1017-1031
At3g55830	ECTOPICALLY PARTING CELLS (EPC1)	Endodermis/Quiescent (SCR)	EPC1. Singh SK, Eland C, Harholt J, Scheller HV, Marchant A (2005) Cell adhesion in Arabidopsis thaliana is mediated by ECTOPICALLY PARTING CELLS 1--a glycosyltransferase (GT64) related to the animal exostosins. Plant J 43:384-397

Supplementary Tables pertaining to Figure 1
Supplementary Table S5. Known regulators of cellular development detected in a single root cell population

Locus	Protein Name	Root Cells Identified	Literature reference supporting a root developmental role
At1g01040	SHORT INTEGUMENTS (SIN1)	Vasculature (WOL)	SIN1. Robinson-Beers K, Pruitt RE, Gasser CS (1992) Ovule Development in Wild-Type Arabidopsis and Two Female-Sterile Mutants. Plant Cell 4:1237-1249
	SUSPENSOR1 (SUS1)		SUS1. Schwartz BW, Yeung EC, Meinke DW (1994) Disruption of morphogenesis and transformation of the suspensor in abnormal suspensor mutants of Arabidopsis. Development 120:3235-3245
	CARPEL FACTORY (CAF)		CAF1. Jacobsen SE, Running MP, Meyerowitz EM (1999) Disruption of an RNA helicase/RNAse III gene in Arabidopsis causes unregulated cell division in floral meristems. Development 126:5231-5243
	DICER-LIKE1 (DCL1)		DCL1. SIN1. SUS1. CAF1. Golden TA, Schauer SE, Lang JD, Pien S, Mushegian AR, Grossniklaus U, Meinke DW, Ray A (2002) SHORT INTEGUMENTS1/SUSPENSOR1/CARPEL FACTORY, a Dicer homolog, is a maternal effect gene required for embryo development in Arabidopsis. Plant Physiol 130:808-822
At1g15750	TOPLESS		TPL. Long JA, Woody S, Poethig S, Meyerowitz EM, Barton MK (2002) Transformation of shoots into roots in Arabidopsis embryos mutant at the TOPLESS locus. Development 129:2797-2806
			TPL. Smith ZR, Long JA (2010) Control of Arabidopsis apical-basal embryo polarity by antagonistic transcription factors. Nature 464:423-426
At1g50030	TARGET OF RAPAMYCIN (TOR)	Vasculature (WOL)	TOR. Menand B, Desnos T, Nussaume L, Berger F, Bouchez D, Meyer C, Robaglia C (2002) Expression and disruption of the Arabidopsis TOR (target of rapamycin) gene. PNAS 99:6422-6427
			TOR. Deprost D, Yao L, Sormani R, Moreau M, Leterreux G, Nicolaï M, Bedu M, Robaglia C, Meyer C (2007) The Arabidopsis TOR kinase links plant growth, yield, stress resistance and mRNA translation. EMBO Rep 8:864-870
At1g73590	PIN-FORMED (PIN1)	Vasculature (WOL)	PIN1. Okada K, Ueda J, Komaki MK, Bell CJ, Shimura Y (1991) Requirement of the Auxin Polar Transport System in Early Stages of Arabidopsis Floral Bud Formation. Plant Cell 3:677-684
			PIN1. Gälweiler L, Guan C, Müller A, Wisman E, Mendgen K, Yephremov A, Palme K (1998) Regulation of polar auxin transport by AtPIN1 in Arabidopsis vascular tissue. Science 282:2226-2230
At2g35630	MICROTUBULE ORGANIZATION 1 (MOR1)	Vasculature (WOL)	MOR1. Whittington AT, Vugrek O, Wei KJ, Hasenbein NG, Sugimoto K, Rashbrooke MC, Wasteneys GO (2001) MOR1 is essential for organizing cortical microtubules in plants. Nature 411:610-613
At2g36910	Arabidopsis thaliana P-GLYCOPROTEIN PROTEIN1 (AtPGP1)	Vasculature (WOL)	AtPGP1. Sidler M, Hassa P, Hasan S, Ringli C, Dudler R (1998) Involvement of an ABC transporter in a developmental pathway regulating hypocotyl cell elongation in the light. Plant Cell 10:1623-1636

Supplementary Tables pertaining to Figure 1
Supplementary Table S5. Known regulators of cellular development detected in a single root cell population

Locus	Protein Name	Root Cells Identified	Literature reference supporting a root developmental role
			PGP1. Blakeslee JJ, Bandyopadhyay A, Lee OR, Mravec J, Titapiwatanakun B, Sauer M, Makam SN, Cheng Y, Bouchard R, Adamec J, Geisler M, Nagashima A, Sakai T, Martinoia E, Friml J, Peer WA, Murphy AS (2007) Interactions among PIN-FORMED and P-glycoprotein auxin transporters in Arabidopsis. Plant Cell 19:131-147
At3g02260	TRANSPORT INHIBITOR RESISTANT3 (TIR3)	Vasculature (WOL)	TIR3. Ruegger M, Dewey E, Hobbie L, Brown D, Bernasconi P, Turner J, Muday G, Estelle M (1997) Reduced naphthylphthalamic acid binding in the tir3 mutant of Arabidopsis is associated with a reduction in polar auxin transport and diverse morphological defects. Plant Cell 9:745-757
	BIG		BIG. Gil P, Dewey E, Friml J, Zhao Y, Snowden KC, Putterill J, Palme K, Estelle M, Chory J (2001) BIG: a calossin-like protein required for polar auxin transport in Arabidopsis. Genes Dev 15:1985-1997
At3g13300	VARICOSE (VCS)	Vasculature (WOL)	VCS1. Deyholos MK, Cavaness GF, Hall B, King E, Punwani J, Van Norman J, Sieburth LE (2003) VARICOSE, a WD-domain protein, is required for leaf blade development. Development 130:6577-6588
			VCS1. Xu J, Yang JY, Niu QW, Chua NH (2006) Arabidopsis DCP2, DCP1, and VARICOSE form a decapping complex required for postembryonic development. Plant Cell 18:3386-3398
			VCS1. Goeres DC, Van Norman JM, Zhang W, Fauver NA, Spencer ML, Sieburth LE (2007) Components of the Arabidopsis mRNA decapping complex are required for early seedling development. Plant Cell 19:1549-1564
At4g03190	AUXIN SIGNALING F BOX 1 (AFB1)	Vasculature (WOL)	AFB1. Dharmasiri N, Dharmasiri S, Weijers D, Lechner E, Yamada M, Hobbie L, Ehrismann JS, Jürgens G, Estelle M (2005) Plant development is regulated by a family of auxin receptor F box proteins. Dev Cell 9:109-119
At1g70940	PIN-FORMED 3 (PIN3)	Columella (PET111)	PIN3. Friml J, Wiśniewska J, Benková E, Mendgen K, Palme K (2002) Lateral relocation of auxin efflux regulator PIN3 mediates tropism in Arabidopsis. Nature 415:806-809

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G03230	extracellular dermal glycoprotein, putative / EDGP, putative, similar to extracellular dermal glycoprotein EDGP precursor (Daucus carota) GI:285741	0	1	0	0	0	0
AT1G04910	expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as `growth regulator protein` based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	0	1	1	0	1	0
AT1G06220	elongation factor Tu family protein, similar to Cryptosporidium parvum elongation factor-2 GB:U21667 GI:706974 from (Cryptosporidium parvum)	1	0	0	0	1	0
AT1G07670	calcium-transporting ATPase 4, endoplasmic reticulum-type (ECA4), identical to SP:Q9XES1 Calcium-transporting ATPase 4, endoplasmic reticulum-type (EC 3.6.3.8) {Arabidopsis thaliana); contains InterPro Accession IPR006069: Cation transporting ATPase	1	1	0	1	1	1
AT1G07810	ECA1_ACA3_ATECA1__calcium-transporting ATPase 1, endoplasmic reticulum-type (ECA1), identical to SP:P92939 Calcium-transporting ATPase 1, endoplasmic reticulum-type (EC 3.6.3.8) {Arabidopsis thaliana); contains InterPro Accession	1	1	1	0	1	0

Supplementary Tables pertaining to Figure 1

Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	IPR006069: Cation transporting ATPase						
AT1G08200	AXS2__expressed protein	0	0	0	1	1	0
AT1G11680	EMB1738_CYP51G1_CYP51_CYP51A2__obtusifoliol 14-demethylase (CYP51), identical to obtusifoliol 14-demethylase (GI:14624983) (Arabidopsis thaliana)	1	1	1	1	1	0
AT1G13440	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, very strong similarity to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	0	0	0	0	1	1
AT1G14010	emp24/gp25L/p24 family protein, similar to SP:P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family	0	0	0	0	1	1
AT1G16300	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to glyceraldehyde-3-phosphate dehydrogenase (Pinus sylvestris) GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain						
AT1G16700	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative, very strong similarity to SP:Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}; contains Pfam profile PF00037: iron-sulfur cluster-binding protein	0	0	0	1	1	1
AT1G16890	ubiquitin-conjugating enzyme, putative, nearly identical to ubiquitin-conjugating enzyme E2 (Catharanthus roseus) GI:5381319; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	0	0	0	0	1	0
AT1G17745	PGDH__D-3-phosphoglycerate dehydrogenase / 3-PGDH, identical to SP:O04130	1	1	0	0	1	0
AT1G23170	expressed protein, Location of ESTs gb:AA395014, gb:T23026, gb:N65311 and gb:N37226; expression supported by MPSS	1	0	0	0	0	0
AT1G30230	elongation factor 1-beta / EF-1-beta, identical to SP:P48006 Elongation factor 1-beta (EF-1-beta) {Arabidopsis thaliana}	0	0	0	1	1	0
AT1G30450	CCC1_ATCCC1__cation-chloride cotransporter, putative, similar to cation-chloride co-transporter GB:AAC49874 GI:2582381 from (Nicotiana tabacum), Cation-Chloride Cotransporter (CCC) Family Member, PMID:11500563	1	0	0	0	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G31180	3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to SP:P29102 3-isopropylmalate dehydrogenase, chloroplast precursor {Brassica napus}; EST gb:F14478 comes from this gene	1	1	1	0	1	1
AT1G32380	ribose-phosphate pyrophosphokinase 2 / phosphoribosyl diphosphate synthetase 2 (PRS2), identical to SP:Q42583 from (Arabidopsis thaliana); strong similarity to phosphoribosyl diphosphate synthetase 1 (ribose-phosphate pyrophosphokinase 1 (PRS I) (Arabidopsis thaliana) GI:633140, SP:Q42581	1	1	0	0	0	0
AT1G35160	GRF4_GF14 PHI__14-3-3 protein GF14 phi (GRF4), identical to GF14 protein phi chain GI:1493805, SP:P46077 from (Arabidopsis thaliana)	1	0	1	1	1	0
AT1G47600	glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to thioglucosidase (GI:871992) (Arabidopsis thaliana)	0	0	0	0	0	1
AT1G47640	expressed protein, similar to seven transmembrane domain protein GI:3550427 from (Homo sapiens)	0	1	1	0	1	1
AT1G48860	3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP synthase, putative, strong similarity to 5-enolpyruvylshikimate-3-phosphate	1	0	0	1	0	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(EPSP) synthase SP:P05466 from (Arabidopsis thaliana)						
AT1G48900	signal recognition particle 54 kDa protein 3 / SRP54 (SRP-54C), identical to SP:P49967 Signal recognition particle 54 kDa protein 3 (SRP54) {Arabidopsis thaliana}	1	0	0	0	0	0
AT1G51630	expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;	1	1	1	0	1	0
AT1G52780	expressed protein	1	0	1	0	1	0
AT1G54000	myrosinase-associated protein, putative, similar to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216391, GI:1216389 from (Brassica napus); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase; contains 1 predicted transmembrane domain	1	1	1	1	1	1
AT1G54010	myrosinase-associated protein, putative, similar to myrosinase-associated protein GI:1769969 from (Brassica napus); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif	1	1	1	0	1	1
AT1G54270	EIF4A1_RH4_TIF4A1_EIF4A-2__eukaryotic translation initiation factor 4A-2 / eIF-4A-2, similar to eukaryotic translation initiation factor 4A GI:19696 from (Nicotiana plumbaginifolia)	0	0	0	0	1	1
AT1G56190	phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC	1	1	1	1	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase						
AT1G56423		1	0	0	1	0	0
AT1G56550	expressed protein	1	0	0	0	0	0
AT1G57720	elongation factor 1B-gamma, putative / eEF-1B gamma, putative, similar to elongation factor 1B gamma GI:3868758 from (Oryza sativa)	1	1	1	1	1	1
AT1G65540	calcium-binding EF hand family protein, similar to leucine zipper-EF-hand containing transmembrane protein 1 (Homo sapiens) GI:4235226; contains Pfam profile PF00036: EF hand	1	0	0	0	0	0
AT1G66270	beta-glucosidase (PSR3.2), nearly identical to GI:2286069 from (Arabidopsis thaliana) (Plant Mol. Biol. 34 (1), 57-68 (1997)); similar to thioglucoside glucohydrolase (GI:984052) (Arabidopsis thaliana)	1	1	1	1	1	1
AT1G66280	glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase 1 (GI:12043529) (Arabidopsis thaliana)	1	1	1	1	1	1
AT1G66580	60S ribosomal protein L10 (RPL10C), contains Pfam profile: PF00826: Ribosomal L10	1	0	0	0	0	0
AT1G69460	emp24/gp25L/p24 family protein, similar to SP:Q28735 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Oryctolagus cuniculus}; contains Pfam	1	1	0	1	1	1

Supplementary Tables pertaining to Figure 1
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	profile: PF01105: emp24/gp25L/p24 family						
AT1G70330	ENT1,AT__equilibrative nucleoside transporter family protein, contains similarity to SWISS-PROT:Q14542 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, ei-type, 36 kDa nucleolar protein HNP36, Hydrophobic nucleolar protein, 36 kDa, Delayed-early response protein 12) (Homo sapiens)	1	0	1	0	0	0
AT1G70600	60S ribosomal protein L27A (RPL27aC), identical to 60S ribosomal protein L27A GB:P49637 (Arabidopsis thaliana)	1	0	1	1	1	1
AT1G76690	OPR2__12-oxophytodienoate reductase (OPR2), identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 (Arabidopsis thaliana)	1	0	0	0	0	0
AT1G78570	RHM1__NAD-dependent epimerase/dehydratase family protein, similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	0	0	1	0	1	0
AT1G78850	curculin-like (mannose-binding) lectin family protein, low similarity to ser/thr protein kinase from Zea mays	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(GI:2598067); contains Pfam lectin (probable mannose binding) domain PF01453 but not the protein kinase domain of the Z. mays protein						
AT1G79930	HSP91__heat shock protein, putative, contains Pfam profile: PF00012 Heat shock hsp70 proteins; similar to heat-shock proteins GB:CAA94389, GB:AAD55461 (Arabidopsis thaliana)	0	0	0	1	0	1
AT2G01410	expressed protein	1	1	1	0	1	1
AT2G09990	40S ribosomal protein S16 (RPS16A), Same as GB:Q42340	1	0	1	0	1	0
AT2G14720	VSR-2__vacuolar sorting receptor, putative, identical to GB:U79960 GI:1737220; contains a calcium-binding EGF-like domain signature	1	0	1	0	0	1
AT2G19160	expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266	1	0	0	0	0	0
AT2G21250	mannose 6-phosphate reductase (NADPH-dependent), putative, 6-phosphate reductase (Apium graveolens)(GI:1835701), NADP-dependent D-sorbitol-6-phosphate dehydrogenase (Malus domestica)(SP:P28475)	1	0	0	0	0	0
AT2G22795	expressed protein	1	1	1	0	1	1
AT2G22970	SCPL11__serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase I precursor (SP:P37890) (Oryza sativa)	1	0	0	0	0	0
AT2G23370	expressed protein	0	1	0	0	0	0
AT2G26640	beta-ketoacyl-CoA synthase, putative, similar to beta-ketoacyl-CoA synthase (Simmondsia chinensis)(GI:1045614)	1	0	1	0	0	0

Supplementary Tables pertaining to Figure 1
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G30870	ATGSTF10_ATGSTF4_ERD13__glutathione S-transferase, putative, supported by cDNA GI:443698 GB:D17673	1	1	1	1	1	0
AT2G30950	VAR2_FTSH2__FtsH protease (VAR2), identical to zinc dependent protease VAR2 GI:7650138 from (Arabidopsis thaliana)	0	0	0	0	0	1
AT2G31140	expressed protein	1	0	0	0	1	1
AT2G37170	PIP2B_PIP2;2__plasma membrane intrinsic protein 2B (PIP2B) / aquaporin PIP2.2 (PIP2.2), identical to SP:P43287 Plasma membrane intrinsic protein 2B {Arabidopsis thaliana}	1	0	1	1	1	0
AT2G37230	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat	1	1	1	0	1	0
AT2G38230	ATPDX1.1__Encodes a protein predicted to function in tandem with PDX2 to form glutamine amidotransferase complex with involved in vitamin B6 biosynthesis.	0	0	0	0	0	1
AT2G38840	guanylate-binding family protein, similar to SP:Q01514 Interferon-induced guanylate-binding protein 1 (Guanine nucleotide-binding protein 1) (Interferon-gamma inducible protein MAG-1) {Mus musculus}; contains Pfam profile PF02263: Guanylate-binding protein, N-terminal domain	0	1	1	0	0	0
AT2G39800	P5CS1_ATP5CS__delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1), identical to SP:P54887:P5C1_ARATH	0	0	1	0	0	0
AT2G40380	prenylated rab acceptor (PRA1) family protein, contains Pfam profile PF03208:	0	0	0	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	Prenylated rab acceptor (PRA1)						
AT2G40510	40S ribosomal protein S26 (RPS26A)	1	0	0	0	1	0
AT2G41150	expressed protein, an isoform contains a GA donor splice site supported by FL-cDNA alignment which truncates the ORF.	0	0	1	0	0	0
AT2G41475		1	0	0	0	1	0
AT2G41770	expressed protein, contains Pfam domain PF03385: Protein of unknown function, DUF288	1	0	1	0	1	0
AT2G45030	mitochondrial elongation factor, putative, similar to SP:P25039 Elongation factor G 1, mitochondrial precursor (mEF-G-1) {Saccharomyces cerevisiae}; contains Pfam profiles PF00009: Elongation factor Tu GTP binding domain, PF03764: Elongation factor G domain IV, PF00679: Elongation factor G C-terminus	0	1	0	0	1	0
AT2G45300	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase, nearly identical to SP:P05466	1	1	0	1	1	0
AT2G46280	TRIP-1_TIF3I1__eukaryotic translation initiation factor 3 subunit 2 / TGF-beta receptor interacting protein 1 / eIF-3 beta / eIF3i / TRIP-1 (TIF3I1), identical to eukaryotic translation initiation factor 3 subunit 2 (SP:Q38884) {Arabidopsis thaliana}; contains Pfam PF00400: WD domain, G-beta repeat (5 copies)	1	0	0	1	1	0
AT2G47380	cytochrome c oxidase subunit Vc family protein / COX5C family protein, contains Pfam profile: PF05799	0	0	0	0	0	1

Supplementary Tables pertaining to Figure 1
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	cytochrome c oxidase subunit Vc (COX5C)						
AT2G47510	FUM1__fumarate hydratase, putative / fumarase, putative, similar to SP:P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase	1	1	1	1	1	1
AT3G04120	GAPC__glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, identical to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}	0	1	0	1	0	1
AT3G06810	acyl-CoA dehydrogenase-related, low similarity to acyl-CoA dehydrogenase (Acinetobacter sp. NCIMB9871) GI:14587418; contains Pfam profiles PF01636: Phosphotransferase enzyme family, PF00441: Acyl-CoA dehydrogenase C-terminal domain, PF02770: Acyl-CoA dehydrogenase middle domain	1	1	0	0	0	1
AT3G07290	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535: PPR repeat	0	0	1	0	0	0
AT3G08530	clathrin heavy chain, putative, similar to Swiss-Prot:Q00610 clathrin heavy chain 1 (CLH-17) (Homo sapiens)	1	0	1	0	1	1
AT3G09410	pectinacetylesterase family protein, similar to pectinacetylesterase precursor GB:CAA67728 (Vigna radiata); contains Pfam profile: PF03283 pectinacetylesterase	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 1
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G09630	60S ribosomal protein L4/L1 (RPL4A), strong similarity to 60S ribosomal protein L1 GB:P49691	1	0	0	1	1	0
AT3G11070	outer membrane OMP85 family protein, contains Pfam profile PF01103: outer membrane protein, OMP85 family	1	0	1	0	1	1
AT3G11130	clathrin heavy chain, putative, similar to Swiss-Prot:Q00610 clathrin heavy chain 1 (CLH-17) (Homo sapiens)	1	1	1	1	1	1
AT3G11170	FAD7_FADD__omega-3 fatty acid desaturase, chloroplast (FAD7) (FADD), identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabidopsis thaliana (Mouse-ear cress)); identical to Pfam profile PF00487: Fatty acid desaturase; identical to cDNA plastid fatty acid desaturase GI:809491	1	0	0	0	0	0
AT3G11940	ATRPS5A_AML1__40S ribosomal protein S5 (RPS5B), similar to 40S ribosomal protein S5 GB:AAC98068 GI:4056502 from (Arabidopsis thaliana)	0	1	0	1	0	1
AT3G12800	short-chain dehydrogenase/reductase (SDR) family protein, contains Pfam profile PF00106:oxidoreductase, short chain dehydrogenase/reductase family	1	0	1	0	0	0
AT3G13300	VCS__transducin family protein / WD-40 repeat family protein, contains 2 WD-40 repeats (PF00400); autoantigen locus HUMAUTANT (GI:533202) (Homo sapiens) and autoantigen locus HSU17474 (GI:596134) (Homo sapiens)	0	0	0	0	1	0
AT3G13530	MAPKKK7__MAP3K epsilon protein kinase, identical to MAP3K epsilon	0	1	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	protein kinase (Arabidopsis thaliana) gi:3549652:emb:CAA12272						
AT3G13920	EIF4A1_RH4_TIF4A1_EIF4A-2__eukaryotic translation initiation factor 4A-1 / eIF-4A-1, eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile PF00270: DEAD/DEAH box helicase; contains Pfam profile PF00271: Helicase conserved C-terminal domain	1	0	1	1	1	1
AT3G14390	diaminopimelate decarboxylase, putative / DAP carboxylase, putative, similar to diaminopimelate decarboxylase (Arabidopsis thaliana) GI:6562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain	1	1	0	0	0	0
AT3G16400	ATMLP-470__jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, epithiospecifier (Arabidopsis thaliana) GI:16118845; contains Pfam profiles PF01419 jacalin-like lectin family, PF01344 Kelch motif	0	0	0	0	1	0
AT3G16410	jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, epithiospecifier (Arabidopsis thaliana) GI:16118845; contains Pfam profiles PF01419 jacalin-like lectin family, PF01344 Kelch motif	1	1	0	0	1	1
AT3G16420	PBP1__jacalin lectin family protein, similar to myrosinase binding protein	1	1	1	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(Brassica napus) GI:1711296; contains Pfam profile: PF01419 jacalin-like lectin domain						
AT3G16430	jacalin lectin family protein, similar to myrosinase binding protein (Brassica napus) GI:1711296; contains Pfam profile PF01419 jacalin-like lectin domain	1	1	0	0	0	1
AT3G17390	MTO3_SAMS3__S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Catharanthus roseus) SWISS-PROT:Q96552	1	1	1	0	1	1
AT3G17970	chloroplast outer membrane translocon subunit, putative, similar to Toc64 (Pisum sativum) GI:7453538; contains Pfam profile PF00515 TPR Domain	1	1	0	1	0	0
AT3G18000	NMT1__phosphoethanolamine N-methyltransferase 1 / PEAMT 1 (NMT1), identical to Phosphoethanolamine N-methyltransferase 1 (EC 2.1.1.103) (PEAMT 1) (AtNMT1) (SP:Q9FR44){Arabidopsis thaliana}; strong similarity to phosphoethanolamine N-methyltransferase from (Spinacia oleracea) GI:7407189, (Triticum aestivum) GI:17887465; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family	0	0	1	0	0	1
AT3G18240	expressed protein	0	1	1	0	0	0
AT3G18410	NADH-ubiquinone oxidoreductase-related, similar to NADH-ubiquinone	1	0	1	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	oxidoreductase 12 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-12KD) (CI-12KD). (Swiss-Prot:Q03015) (Neurospora crassa)						
AT3G18580	single-strand-binding family protein, contains Pfam domain PF00436: Single-strand binding protein family	1	0	0	0	1	0
AT3G19508		1	0	0	0	0	0
AT3G22290	expressed protein	1	0	1	0	1	0
AT3G22330	DEAD box RNA helicase, putative, similar to RNA helicases GI:3775995, GI:3775987 from (Arabidopsis thaliana); contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain	0	0	0	1	1	0
AT3G23180	lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum)	1	1	0	0	0	1
AT3G23510	cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative, similar to cyclopropane synthase (Sterculia foetida) GI:21069167; contains Pfam profile PF02353: Cyclopropane-fatty-acyl-phospholipid synthase	1	0	0	0	0	0
AT3G28710	H+-transporting two-sector ATPase, putative, similar to SP:P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14) (Vacuolar proton pump d subunit) (V-ATPase 41 KDa accessory protein) {Dictyostelium discoideum}; contains Pfam profile PF01992: ATP synthase (C/AC39) subunit	1	0	1	1	1	0
AT3G28715	H+-transporting two-sector ATPase,	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	putative, similar to SP:P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14) (Vacuolar proton pump d subunit) (V-ATPase 41 KDa accessory protein) {Dictyostelium discoideum}; contains Pfam profile PF01992: ATP synthase (C/AC39) subunit						
AT3G32980	peroxidase 32 (PER32) (P32) (PRXR3), identical to SP:Q9LHB9 Peroxidase 32 precursor (EC 1.11.1.7) (Atperox P32) (PRXR3) (ATP16a) {Arabidopsis thaliana}	0	0	0	1	0	0
AT3G44160	chloroplast outer membrane protein-related, low similarity to chloroplastic outer envelope membrane protein (OEP75) (Pisum sativum) GI:633607	0	1	0	0	0	0
AT3G44310	ATNIT1_NIT1__The protein undergoes thiolation following treatment with the oxidant tert-butylhydroperoxide.	0	0	1	0	0	0
AT3G47960	proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family	0	0	1	0	0	0
AT3G48340	similar to cysteine proteinase, putative [Arabidopsis thaliana] (TAIR:At3g48350.1); similar to cysteine proteinase [Glycine max] (GB:BAC77522.1); contains InterPro domain Papain cysteine protease (C1) (InterPro:IPR000668); contains InterPro domain Eukaryotic thiol (cysteine) protease (InterPro:IPR000169)	1	1	1	0	1	1
AT3G48680	bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats);	1	0	1	0	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	ferripyochelin binding protein - Methanobacterium thermoautotrophicum, EMBL:AE000918.1						
AT3G48870	ATHSP93-III_HSP93-III_ATCLPC__Similar to ATP-dependent Clp protease ATP-binding subunit (ClpC), identical to AtClpC GI:5360574 from (Arabidopsis thaliana); contains Pfam profiles PF02861: Clp amino terminal domain and PF02151: UvrB/uvrC motif. May function redundantly with TIC complex in chloroplast protein import.	0	1	1	1	1	0
AT3G49080	ribosomal protein S9 family protein, contains Pfam profile PF00380: ribosomal protein S9	1	0	0	0	1	0
AT3G51980	expressed protein	1	0	0	0	0	0
AT3G52640	nicastrin-related, contains weak similarity to Nicastrin precursor (Swiss-Prot:Q92542) (Homo sapiens)	1	0	0	0	0	0
AT3G54470	uridine 5`-monophosphate synthase / UMP synthase (PYRE-F) (UMPS), identical to SP:Q42586 Uridine 5`-monophosphate synthase (UMP synthase) (Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRtase); Orotidine 5`-phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)) {Arabidopsis thaliana}	0	0	0	0	1	0
AT3G55610	delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2), identical to SP:P54888	0	0	1	0	0	0
AT3G59890	dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae}; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus						
AT3G59970	MTHFR1__methylenetetrahydrofolate reductase 1 (MTHFR1), identical to methylenetetrahydrofolate reductase MTHFR1 (Arabidopsis thaliana) GI:5911425	1	0	0	1	0	0
AT3G61520	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat	1	0	0	0	0	0
AT3G62530	PBS lyase HEAT-like repeat-containing protein, contains Pfam profile: PF03130 PBS lyase HEAT-like repeat	1	0	0	0	1	1
AT3G62830	AUD1_UXS2_ATUXS2__NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains non-consensus CA donor splice site at exon 1 and TA acceptor splice site at exon 2	1	1	1	1	1	1
AT3G66654	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type	1	0	1	0	1	0
AT4G00290	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, weak	1	0	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	similarity to SP:P77338 Potassium efflux system kefA {Escherichia coli}; contains Pfam profile PF00924: Mechanosensitive ion channel						
AT4G00620	tetrahydrofolate dehydrogenase/cyclohydrolase, putative, similar to SP:P07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)) {Saccharomyces cerevisiae}; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain	1	1	0	0	0	0
AT4G01660	ABC1At_ATATH10__ABC1 family protein, contains Pfam domain, PF03109: ABC1 family	1	0	0	0	0	0
AT4G01750	expressed protein, T15B16.8	0	0	0	0	0	1
AT4G03190	GRH1_ATGER1_ATGRH1__F-box family protein (FBL18), almost identical to GRR1-like protein 1 GI:12658970 from (Arabidopsis thaliana); similar to leucine-rich repeats containing F-box protein FBL3 (GI:5919219) (Homo sapiens); similar to F-box protein FBL2 (GI:6063090) (Homo sapiens)	0	0	0	0	1	0
AT4G08520	clathrin adaptor complex small chain	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain						
AT4G08810	SUB1__expressed protein	1	0	1	0	0	0
AT4G11850	phospholipase D gamma 1 / PLD gamma 1 (PLDGAMMA1), identical to phospholipase D gamma 1 SP:Q9T053 from (Arabidopsis thaliana)	0	0	0	0	1	0
AT4G13930	SHM4__glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	1	1	1	1	1	1
AT4G17140	pleckstrin homology (PH) domain-containing protein, contains Pfam profile PF00169: PH domain	1	0	0	0	0	1
AT4G17530	RAB1C__Ras-related GTP-binding protein, putative, very strong similarity to RAB1C (Lotus corniculatus var. japonicus) GI:1370166; contains Pfam profile PF00071: Ras family	1	0	0	0	0	1
AT4G18760	leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611	0	0	1	0	0	0
AT4G18830	ATOFP5_OFP5__ovate family protein, 52% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G19006	26S proteasome regulatory subunit, putative (RPN9), similar to 26S proteasome subunit p40.5 (Homo sapiens) gi:3618343:dbj:BAA33214	0	0	0	0	1	0
AT4G21180	DNAJ heat shock N-terminal domain-containing protein / sec63 domain-containing protein, similar to SP:Q9UGP8 Translocation protein SEC63 homolog {Homo sapiens}; contains Pfam profiles PF00226 DnaJ domain, PF02889 Sec63 domain	1	0	0	0	0	0
AT4G21540	Encodes a putative sphingosine kinase (SphK) containing the five conserved domains (C1-C5) previously identified in SphKs.	1	0	0	0	0	0
AT4G21570	expressed protein, contains Pfam profile PF03619: Domain of unknown function	1	0	0	0	0	0
AT4G22214	Encodes a defensin-like (DEFL) family protein.	1	0	0	0	0	0
AT4G22240	plastid-lipid associated protein PAP, putative, similar to plastid-lipid associated proteins PAP2 (Brassica rapa) GI:14248550 GI:14248556; contains Pfam profile PF04755: PAP_fibrillin	1	0	0	0	0	1
AT4G23430	short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily; contains Pfam PF00106: oxidoreductase, short chain dehydrogenase/reductase family	0	1	0	0	0	0
AT4G24310	expressed protein, contains Pfam profile PF05078: Protein of unknown	0	1	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	function (DUF679)						
AT4G25450	ATNAP8__ABC transporter family protein, similar to multidrug resistance protein 2 SP:P21440 from (Mus musculus)	0	0	0	0	0	1
AT4G27585	band 7 family protein, similar to stomatin-like protein (Zea mays) GI:7716464; contains Pfam profile PF01145: SPFH domain / Band 7 family	1	1	1	0	1	1
AT4G28510	ATPHB1__prohibitin, putative, similar to SP:P24142 Prohibitin (B-cell receptor associated protein 32) (BAP 32) {Rattus norvegicus}; contains Pfam profile PF01145: SPFH domain / Band 7 family	1	1	1	1	1	1
AT4G29120	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein, similar to SP:P23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) {Escherichia coli}; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase	0	0	0	0	1	0
AT4G30920	cytosol aminopeptidase family protein, contains Pfam profiles: PF00883 cytosol aminopeptidase family catalytic domain, PF02789: cytosol aminopeptidase family N-terminal domain	1	0	1	0	1	0
AT4G31480	coatomer beta subunit, putative / beta-coat protein, putative / beta-COP, putative, similar to Coatomer beta subunit (Beta-coat protein) (Beta-COP) from {Rattus norvegicus} SP:P23514, {Mus musculus} SP:Q9JIF7, {Homo sapiens} SP:P53618; contains Pfam	0	0	0	1	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	profile: PF01602 Adaptin N terminal region						
AT4G33120	coclaurine N-methyltransferase, putative, similar to coclaurine N-methyltransferase (Coptis japonica) GI:16754879	1	1	1	0	1	1
AT4G33580	carbonic anhydrase family protein / carbonate dehydratase family protein, similar to SP:P46512 Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase 1) {Flaveria linearis}; contains Pfam profile PF00484: Carbonic anhydrase	1	1	0	1	0	0
AT4G35100	PIP3_PIP2;7_PIP3A_SIMIP__plasma membrane intrinsic protein (SIMIP), nearly identical to plasma membrane intrinsic protein (Arabidopsis thaliana) GI:2306917	1	1	1	1	1	1
AT4G35630	PSAT__phosphoserine aminotransferase, chloroplast (PSAT), identical to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q96255)(Arabidopsis thaliana); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V	1	0	1	1	1	1
AT4G35860	ATGB2__Ras-related GTP-binding protein, putative, similar to Rab2-like GTP-binding protein GI:1765896 from (Arabidopsis thaliana)	1	0	0	0	0	0
AT4G36080	FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profiles PF00454: Phosphatidylinositol 3- and 4-	0	0	1	0	1	0

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	kinase, PF02259: FAT domain, PF02260: FATC domain						
AT4G36195	serine carboxypeptidase S28 family protein, contains Pfam PF05577: Serine carboxypeptidase S28	1	0	1	0	0	0
AT4G38790	ER lumen protein retaining receptor family protein, similar to SP:P35402 ER lumen protein retaining receptor (HDEL receptor) {Arabidopsis thaliana}; contains Pfam profile PF00810: ER lumen protein retaining receptor	0	0	0	0	0	1
AT4G39200	40S ribosomal protein S25 (RPS25E), ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089	0	0	0	0	1	0
AT5G02960	40S ribosomal protein S23 (RPS23B), ribosomal protein S23, Fragaria x ananassa, PIR:S56673	1	0	0	0	1	0
AT5G04990	sad1/unc-84 protein-related, contains weak similarity to Sad1/unc-84 protein-like 1 (Swiss-Prot:O94901) (Homo sapiens)	1	1	0	0	0	0
AT5G07980	dentin sialophosphoprotein-related, contains weak similarity to Swiss-Prot:Q9NZW4 dentin sialophosphoprotein precursor (Homo sapiens)	0	0	1	0	0	0
AT5G08610	DEAD box RNA helicase (RH26), strong similarity to RNA helicase RH26 (Arabidopsis thaliana) GI:3776025; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain; identical to cDNA DEAD box RNA helicase, RH26 GI:3776024	0	0	0	0	1	0
AT5G08670	ATP synthase beta chain 1,	0	0	0	0	1	0

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	mitochondrial, identical to SP:P83483 ATP synthase beta chain 1, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; strong similarity to SP:P17614 ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14) {Nicotiana plumbaginifolia}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain; supporting cDNA gi:26452102:dbj:AK118538.1:						
AT5G10840	endomembrane protein 70, putative, TM4 family;	1	1	1	1	1	1
AT5G11880	diaminopimelate decarboxylase, putative / DAP carboxylase, putative, similar to diaminopimelate decarboxylase (Arabidopsis thaliana) GI:6562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain	1	1	1	1	1	1
AT5G12950	expressed protein, putative secreted protein SCF41.30c, Streptomyces coelicolor, EMBL:SCF41_30	0	1	0	0	0	0
AT5G14060	CARAB-AK-LYS__aspartate kinase, lysine-sensitive, nearly identical to gi:2257743	1	0	0	0	0	0
AT5G15200	40S ribosomal protein S9 (RPS9B), 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528	1	0	0	1	1	1
AT5G15650	RGP2__reversibly glycosylated	1	1	1	1	1	1

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	polypeptide-2 (RGP2), identical to reversibly glycosylated polypeptide-2 (Arabidopsis thaliana) GI:2317731						
AT5G16170	expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266	0	0	0	0	0	1
AT5G16370	AMP-binding protein, putative, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to cDNA adenosine monophosphate binding protein 5 AMPBP5 (AMPBP5) GI:20799718	0	1	0	0	0	0
AT5G17630	glucose-6-phosphate/phosphate translocator, putative, similar to glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) gi:2997593:gb:AAC08526	0	0	0	0	1	1
AT5G17920	ATMETS_ATMS1_ATCIMS__The protein underdoes thiolation following treatment with the oxidant tert-butylhydroperoxide.	1	1	1	1	1	1
AT5G18380	40S ribosomal protein S16 (RPS16C)	0	0	0	1	1	1
AT5G18480	glycogenin glucosyltransferase (glycogenin)-related, low similarity to glycogenin-1 from Mus musculus (SP:Q9R062), Rattus norvegicus (SP:O08730), Homo sapiens (SP:P46976); contains Pfam profile PF01501: Glycosyl transferase family 8	1	1	1	0	1	1
AT5G20000	RPT6A__26S proteasome AAA-ATPase subunit, putative, almost identical to 26S proteasome AAA-ATPase subunit RPT6a GI:6652888 from (Arabidopsis thaliana); almost	0	0	0	1	1	0

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	identical to a member of conserved Sug1 CAD family AtSUG1 GI:13537115 from (Arabidopsis thaliana)						
AT5G20490	XIK_ATXIK__myosin, putative, similar to myosin (GI:433663) (Arabidopsis thaliana); myosin-like protein my5, common sunflower, PIR:T14279	1	0	0	0	0	0
AT5G22020	strictosidine synthase family protein, similar to SP:P15324 Strictosidine synthase precursor (EC 4.3.3.2) {Rauvolfia mannii}; contains Pfam profile PF03088: Strictosidine synthase	0	0	1	0	0	0
AT5G22350	expressed protein	1	0	0	0	0	0
AT5G23575	transmembrane protein, putative, similar to cleft lip and palate transmembrane protein 1 (Homo sapiens) GI:4039014; contains Pfam profile PF05602: Cleft lip and palate transmembrane protein 1 (CLPTM1)	1	1	1	1	1	1
AT5G24690	expressed protein	0	0	0	0	1	0
AT5G24960	CYP71A14__cytochrome P450 71A14, putative (CYP71A14), identical to Cytochrome P450 71A14 (SP:P58045) (Arabidopsis thaliana); cytochrome P450 - Nepeta racemosa, EMBL:Y09423	0	0	0	0	0	1
AT5G25265	expressed protein	1	1	1	0	1	0
AT5G26260	meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain	1	1	1	1	1	1
AT5G26280	meprin and TRAF homology domain-containing protein / MATH domain-	1	1	1	1	0	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	containing protein, low similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain						
AT5G26667	uridylate kinase / uridine monophosphate kinase / UMP kinase (PYR6), identical to uridylate kinase / UMP/CMP kinase SP:O04905 from (Arabidopsis thaliana)	1	0	0	1	0	0
AT5G27120	SAR DNA-binding protein, putative, strong similarity to SAR DNA-binding protein-1 (Pisum sativum) GI:3132696; contains Pfam profile PF01798: Putative snoRNA binding domain; has similarity to MAR binding NOP58 protein	1	1	0	1	1	0
AT5G27395		1	0	0	0	0	0
AT5G27640	TIF3B1_ATEIF3B-1_ATTIF3B1_EIF3B_EIF3B-1__eukaryotic translation initiation factor 3 subunit 9 / eIF-3 eta / eIF3b (TIF3B1), nearly identical to SP:Q9C5Z1 Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) {Arabidopsis thaliana}	0	0	0	0	1	0
AT5G28540	luminal binding protein 1 (BiP-1) (BP1), SWISS-PROT:Q9LKR3 PMID:8888624	1	1	1	1	1	1
AT5G33320	CUE1_ARAPPT_PPT__triose phosphate/phosphate translocator, putative, similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator (Cauliflower) {Brassica oleracea}	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G35590	PAA1__20S proteasome alpha subunit A1 (PAA1) (PRC1), identical to proteasome subunit alpha type 6-1 SP:O81146 GI:12643647 from (Arabidopsis thaliana); identical to cDNA proteasome subunit prc1 GI:2511587	1	0	1	1	1	0
AT5G39740	60S ribosomal protein L5 (RPL5B), ribosomal protein L5, rice	0	0	0	0	1	0
AT5G41210	ATGSTT1_GST10__glutathione S-transferase (GST10), identical to glutathione transferase AtGST 10 (Arabidopsis thaliana) GI:4049401	1	0	0	0	0	1
AT5G42020	BIP__luminal binding protein 2 (BiP-2) (BP2), similar to SWISS-PROT: Q39043; GI:1303695; luminal binding protein (BiP) (Arabidopsis thaliana)	1	1	1	1	1	1
AT5G44820	expressed protein, similar to unknown protein (pir::T04881)	1	0	0	0	0	0
AT5G46430	60S ribosomal protein L32 (RPL32B)	0	0	0	0	1	0
AT5G53480	importin beta-2, putative, similar to importin-beta2 (Oryza sativa (japonica cultivar-group)) GI:3983665; contains Pfam profile PF03810: Importin-beta N-terminal domain	1	0	1	1	1	0
AT5G54810	TSB1_TRP2_TRPB__tryptophan synthase, beta subunit 1 (TSB1), identical to SP:P14671	0	1	0	0	0	0
AT5G56010	HSP81-3__heat shock protein, putative, strong similarity to SP:P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 1
Supplementary Table S6. Proteins of the root cellular proteome that lack RNA expression data

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	protein						
AT5G56030	HSP81-2__heat shock protein 81-2 (HSP81-2), nearly identical to SP:P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thaliana}	1	0	0	1	1	0
AT5G56680	EMB2755__asparaginyl-tRNA synthetase 1, cytoplasmic / asparagine-tRNA ligase 1 (SYNC1), identical to SP:Q9SW96	0	0	0	0	1	0
AT5G57020	NMT1_ATNMT1__myristoyl-CoA:protein N-myristoyltransferase 1 (NMT1), identical to N-myristoyltransferase 1 (NMT1) (Arabidopsis thaliana) GI:7339834	0	0	0	0	1	0
AT5G60700	glycosyltransferase family protein 2, contains Pfam profile PF00535: glycosyl transferase, group 2 family protein	1	1	0	0	0	1
AT5G62270	expressed protein	1	0	0	0	0	0
AT5G66860	expressed protein	1	1	1	1	1	1
ATCG01130	YCF1.2__hypothetical protein	1	0	1	1	1	0
ATMG00560	RPL2__encodes a mitochondrial ribosomal protein L2, a constituent of the large subunit of the ribosomal complex	1	0	0	0	0	0

Supplementary Tables pertaining to Figures 1 and 2

Supplementary Table S7. GO analysis of root proteins found in a single cell type

The p-values of statistical enrichment for the GO identifiers in each of the cell types; p-values ≤0.005 are in bold and considered to be enriched GO terms

GO Identifier	GO Term Description	Root Hairs (COBL9) Cluster 33 p-value	Columella (PET111) Cluster 7 p-value	Vasculature (WOL) Cluster 6 p-value	Non-Hair Epidermis (WER) Cluster 34 p-value	Endodermis (SCR) Cluster 55 p-value	Cortex (COR) Cluster 25 p-value
GO:0000095	S-adenosylmethionine transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0000910	cytokinesis	1	1	**0.001088727**	1	1	1
GO:0003735	structural constituent of ribosome	**0.001161272**	0.216797404	**8.9622E-07**	0.13630355	**6.9726E-07**	1
GO:0004474	malate synthase activity	1	1	1	1	1	**0.003116759**
GO:0004587	ornithine-oxo-acid transaminase activity	1	**0.004171661**	1	1	1	1
GO:0004781	sulfate adenylyltransferase (ATP) activity	1	1	**0.00058232**	1	1	0.012352598
GO:0004812	aminoacyl-tRNA ligase activity	0.20345508	1	0.184170328	**0.001696729**	1	1
GO:0005046	KDEL sequence binding	1	1	1	**0.002685207**	1	1
GO:0005365	myo-inositol transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0005635	nuclear envelope	1	1	**2.01368E-05**	1	1	0.050441304
GO:0005730	nucleolus	0.150610182	0.059931641	**1.09458E-07**	1	0.021344117	1
GO:0005737	cytoplasm	0.142586898	0.158911764	**0.002479565**	1	0.07570783	1
GO:0005739	mitochondrion	**1.64491E-05**	**1.39672E-05**	1	**6.36441E-07**	1	0.059012425
GO:0005759	mitochondrial matrix	**0.003948399**	0.107751418	1	1	1	1

Supplementary Tables pertaining to Figures 1 and 2

Supplementary Table S7. GO analysis of root proteins found in a single cell type

The p-values of statistical enrichment for the GO identifiers in each of the cell types; p-values ≤0.005 are in bold and considered to be enriched GO terms

GO Identifier	GO Term Description	Root Hairs (COBL9) Cluster 33 p-value	Columella (PET111) Cluster 7 p-value	Vasculature (WOL) Cluster 6 p-value	Non-Hair Epidermis (WER) Cluster 34 p-value	Endodermis (SCR) Cluster 55 p-value	Cortex (COR) Cluster 25 p-value
GO:0005773	vacuole	0.007903408	**1.99823E-06**	0.078678573	1	0.082290385	0.110630464
GO:0005777	peroxisome	0.094722455	**0.001102895**	0.204234749	1	1	**0.004643314**
GO:0005783	endoplasmic reticulum	**0.000709048**	**0.004204992**	0.012061162	0.352785108	0.027555944	0.007994995
GO:0005794	Golgi apparatus	**0.000551139**	0.315427882	1	**0.004550286**	0.040240628	0.053040507
GO:0005840	ribosome	0.013698279	0.359131328	**8.30651E-05**	0.304080007	**0.000114399**	1
GO:0005886	plasma membrane	0.015383636	**0.000317324**	**1.30189E-10**	1	**0.000825516**	0.008471668
GO:0006014	D-ribose metabolic process	0.102575599	1	**0.004114794**	1	1	1
GO:0006177	GMP biosynthetic process	1	1	**0.000294065**	1	1	1
GO:0006412	translation	**0.000449235**	0.224118866	**7.47586E-06**	0.362676123	**0.000113364**	1
GO:0006414	translational elongation	1	1	0.177930872	1	**0.001499183**	1
GO:0006418	tRNA aminoacylation for protein translation	0.216164466	1	0.023633949	**0.002001514**	1	1
GO:0006422	aspartyl-tRNA aminoacylation	1	1	1	1	**0.002637257**	1
GO:0006606	protein import into nucleus	1	1	**5.21273E-05**	1	1	1
GO:0006621	protein retention in ER lumen	1	1	1	**0.002685207**	1	1
GO:0006744	ubiquinone biosynthetic process	**0.001843583**	1	1	1	1	1
GO:0006913	nucleocytoplasmic transport	1	1	**0.000688081**	0.046210993	1	1
GO:0008026	ATP-dependent	1	1	**0.000528917**	1	0.150694471	0.172438039

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	helicase activity						
GO:0008470	isovaleryl-CoA dehydrogenase activity	1	**0.004171661**	1	1	1	1
GO:0008540	proteasome regulatory particle, base subcomplex	0.083950502	1	**5.21273E-05**	1	1	1
GO:0009225	nucleotide-sugar metabolic process	0.168558262	**0.002465571**	1	0.046210993	1	1
GO:0009411	response to UV	1	1	1	1	1	**2.25502E-05**
GO:0009507	chloroplast	0.032838734	0.027947013	0.028861089	**4.44343E-06**	1	0.051240009
GO:0009535	chloroplast thylakoid membrane	0.225518358	**0.003221857**	0.215178789	0.345505753	1	0.360144099
GO:0009570	chloroplast stroma	0.106148019	0.123164952	0.192383583	**3.89768E-05**	0.370909759	0.204151046
GO:0009606	tropism	1	**0.004171661**	1	1	1	1
GO:0009658	chloroplast organization	1	1	0.253161042	**0.004084833**	1	1
GO:0009733	response to auxin stimulus	1	0.369762843	**0.005240254**	1	1	1
GO:0009813	flavonoid biosynthetic process	1	1	1	1	0.064262668	**0.002890829**
GO:0009926	auxin polar transport	0.274599331	0.129940908	**0.005038795**	1	1	1
GO:0009932	cell tip growth	**0.00011377**	1	1	1	1	1
GO:0009940	amino-terminal vacuolar sorting propeptide binding	1	1	1	1	1	**0.003116759**

Supplementary Tables pertaining to Figures 1 and 2

Supplementary Table S7. GO analysis of root proteins found in a single cell type

The p-values of statistical enrichment for the GO identifiers in each of the cell types; p-values ≤0.005 are in bold and considered to be enriched GO terms

GO Identifier	GO Term Description	Root Hairs (COBL9) Cluster 33 p-value	Columella (PET111) Cluster 7 p-value	Vasculature (WOL) Cluster 6 p-value	Non-Hair Epidermis (WER) Cluster 34 p-value	Endodermis (SCR) Cluster 55 p-value	Cortex (COR) Cluster 25 p-value
GO:0009941	chloroplast envelope	0.165965595	**0.00013303**	**0.002869342**	0.014243383	0.371648878	0.022377523
GO:0010109	regulation of photosynthesis	1	1	1	**0.002685207**	1	1
GO:0010170	glucose-1-phosphate adenylyltransferase complex	1	**0.004171661**	1	1	1	1
GO:0010483	pollen tube reception	1	1	1	1	1	**0.003116759**
GO:0012506	vesicle membrane	1	**0.004171661**	1	1	1	1
GO:0015148	D-xylose transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0015575	mannitol transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0015576	sorbitol transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0015591	D-ribose transmembrane transporter activity	1	1	1	**0.002685207**	1	1
GO:0015629	actin cytoskeleton	1	**0.000912038**	1	1	1	1
GO:0015805	S-adenosylmethionine transport	1	1	1	**0.002685207**	1	1
GO:0015934	large ribosomal subunit	0.265324623	1	1	0.083671869	**0.003531236**	1
GO:0016020	membrane	0.089648457	0.005807738	0.060769552	0.08175283	0.015243643	**0.001832108**

Supplementary Tables pertaining to Figures 1 and 2

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GO:0016035	zeta DNA polymerase complex	1	1	1	1	1	**0.003116759**
GO:0016036	cellular response to phosphate starvation	**0.002600203**	0.094439263	1	1	1	0.072374962
GO:0016328	lateral plasma membrane	1	**0.004171661**	1	1	1	1
GO:0016337	cell-cell adhesion	1	1	1	1	0.005260857	1
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1	1	1	**0.002685207**	1	1
GO:0016711	flavonoid 3'-monooxygenase activity	1	1	1	1	1	**0.003116759**
GO:0016757	transferase activity, transferring glycosyl groups	**0.004904106**	0.224705427	0.226765563	0.362927861	0.361592749	1
GO:0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	**0.000160705**	1	1	1	1	1
GO:0022625	cytosolic large ribosomal subunit	1	1	**0.002789866**	0.206616656	**0.000134093**	1
GO:0022626	cytosolic ribosome	0.27270635	0.027503954	**6.15069E-06**	1	**1.21267E-08**	0.311850841
GO:0022627	cytosolic small ribosomal subunit	0.049858161	0.039508169	**1.23734E-06**	1	0.017687969	1
GO:0030149	sphingolipid	1	1	1	1	1	**0.003116759**

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	catabolic process						
GO:0030276	clathrin binding	1	1	**0.00332469**	1	1	1
GO:0031210	phosphatidylcholine binding	1	**0.004171661**	1	1	1	1
GO:0042254	ribosome biogenesis	1	1	0.052058885	0.195755272	**0.001798132**	1
GO:0043680	filiform apparatus	1	1	1	1	1	**0.003116759**
GO:0045486	naringenin 3-dioxygenase activity	1	1	1	1	**0.002637257**	1
GO:0045735	nutrient reservoir activity	1	1	**0.000154281**	1	1	1
GO:0046409	p-coumarate 3-hydroxylase activity	1	1	1	1	1	**0.003116759**
GO:0048481	ovule development	1	1	1	**0.002329645**	1	1
GO:0048589	developmental growth	1	1	**0.000960945**	1	1	1
GO:0050613	delta14-sterol reductase activity	1	1	1	1	**0.002637257**	1
GO:0050660	FAD binding	0.228197404	1	1	**0.002329645**	1	1
GO:0051020	GTPase binding	1	1	1	1	**0.002637257**	1
GO:0003824	catalytic	1	0.371648878	0.087760987	0.035335458	0.371693061	**0.003622847**
GO:0015031	protein transport	1	1	0.150515996	0.053894255	0.019526495	**0.004662127**

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01090	CA1_PDH-E1 ALPHA__pyruvate dehydrogenase E1 component alpha subunit, chloroplast, identical to pyruvate dehydrogenase E1 alpha subunit GB:AAB86803 GI:2454182 from (Arabidopsis thaliana); identical to cDNA pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein GI:2454181	1	1	1	1	1	1
AT1G02500	SAM1_SAM-1__S-adenosylmethionine synthetase 1 (SAM1), identical to S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1, AdoMet synthetase 1) (Arabidopsis thaliana) SWISS-PROT:P23686	0	0	1	1	1	0
AT1G04410	malate dehydrogenase, cytosolic, putative, strong similarity to malate dehydrogenase from Mesembryanthemum crystallinum (SP:O24047), Medicago sativa (SP:O48905), Prunus persica (GI:15982948); contains InterPro entry IPR001236: Lactate/malate dehydrogenase	1	1	1	1	1	1
AT1G05620	inosine-uridine preferring nucleoside hydrolase family protein, similar to Chain A, Crystal Structure Of Nucleoside Hydrolase From Leishmania MajorGI:8569431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase	1	0	0	0	0	0
AT1G06000	UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from (Solanum berthaultii)	0	0	0	0	1	0
AT1G06290	ACX3_ATACX3__acyl-CoA oxidase (ACX3), identical to acyl-CoA oxidase ACX3 (Arabidopsis thaliana) GI:8163758, GI:8515709	1	1	1	1	1	1
AT1G06800	lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G07890	APX1_CS1__L-ascorbate peroxidase 1, cytosolic (APX1), identical to SP:Q05431 L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP) {Arabidopsis thaliana}, L-ascorbate peroxidase (Arabidopsis thaliana) gi:16173:emb:CAA42168; strong similarity to cytosolic ascorbate peroxidase (Spinacia oleracea) gi:1384110:dbj:BAA12890	1	0	1	0	1	1
AT1G08110	lactoylglutathione lyase, putative / glyoxalase I, putative, similar to lactoylglutathione lyase SP:O04885 from (Brassica juncea)	1	0	0	0	1	1
AT1G08200	AXS2__expressed protein	0	0	0	1	1	0
AT1G08480	expressed protein	0	0	0	1	1	1
AT1G08830	CSD1__superoxide dismutase (Cu-Zn) (SODCC) / copper/zinc superoxide dismutase (CSD1), identical to SWISS-PROT: P24704	1	0	1	0	1	1
AT1G09620	similar to leucyl-tRNA synthetase, putative / leucine--tRNA ligase, putative [Arabidopsis thaliana] (TAIR:At4g04350.1); similar to leucyl tRNA synthetase [Homo sapiens] (GB:BAA95667.1); similar to SYLC_HUMAN Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) (GB:Q9P2J5); similar to KIAA1352 protein [Homo sapiens] (GB:BAA92590.1); similar to MGC82093 protein [Xenopus laevis] (GB:AAH79713.1); similar to PREDICTED: similar to Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) [Canis familiaris] (GB:XP_535229.1); contains InterPro domain Aminoacyl-tRNA synthetase, class I (InterPro:IPR001412); contains InterPro domain Leucyl-tRNA synthetase archae/euk cytosolic, class Ia (InterPro:IPR004493); contains InterPro domain Aminoacyl-tRNA synthetase, class Ia (InterPro:IPR002300)	0	1	0	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G09780	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative, strong similarity to SP:Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}; contains Pfam profile PF01676: Metalloenzyme superfamily	1	0	1	1	1	1
AT1G09830	phosphoribosylamine--glycine ligase (PUR2), Identical to phosphoribosylamine--glycine ligase, chloroplast (precursor) SP:P52420 from (Arabidopsis thaliana)	1	0	0	0	1	0
AT1G10670	ACLA-1__expressed protein	0	0	0	1	0	0
AT1G11580	pectin methylesterase, putative, similar to pectin methylesterase GI:1617583 from (Lycopersicon esculentum)	0	0	1	1	1	0
AT1G11840	ATGLX1__lactoylglutathione lyase, putative / glyoxalase I, putative, highly similar to putative lactoylglutathione lyase SP:Q39366 from (Brassica oleracea)	1	0	1	1	1	1
AT1G11860	aminomethyltransferase, putative, similar to aminomethyltransferase, mitochondrial precursor SP:O49849 from (Flaveria anomala)	1	1	1	1	1	1
AT1G12000	pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative, strong similarity to SP:Q41141 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.90) (PFP) ((PPI-PFK) {Ricinus communis}; contains Pfam profile PF00365: Phosphofructokinase	0	0	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G12240	ATBETAFRUCT4__beta-fructosidase (BFRUCT4) / beta-fructofuranosidase / invertase, vacuolar, identical to beta-fructosidase GI:1871503 from (Arabidopsis thaliana); contains Pfam profile PF00251:Glycosyl hydrolases family 32; identical to cDNA beta-fructosidase (vacuolar form) GI:1321683; similar to SP:Q43857	1	0	1	0	1	0
AT1G12640	membrane bound O-acyl transferase (MBOAT) family protein, low similarity to porcupine from (Xenopus laevis) GI:6714514, GI:6714520, GI:6714518, GI:6714516; contains Pfam profile PF03062: MBOAT family	1	0	1	0	0	0
AT1G13280	AOC4__allene oxide cyclase family protein, similar to ERD12 (GI:15320414), allene oxide cyclase GI:8977961 from (Lycopersicon esculentum); contains Pfam profile PF06351: Allene oxide cyclase	1	1	1	1	1	1
AT1G13440	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, very strong similarity to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	0	0	0	0	1	1
AT1G13560	AAPT1__aminoalcoholphosphotransferase (AAPT1), identical to aminoalcoholphosphotransferase GI:3661593 from (Arabidopsis thaliana)	0	0	0	0	1	0
AT1G14290	acid phosphatase, putative, similar to acid phosphatase (Lupinus albus) GI:5360721; contains Pfam profile PF01598 sterol desaturase	0	0	0	1	0	0

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Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G14610	TWN2_VALRS__valyl-tRNA synthetase / valine--tRNA ligase (VALRS), nearly identical to SP:P93736 Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) {Arabidopsis thaliana}	1	0	0	0	1	0
AT1G14810	semialdehyde dehydrogenase family protein, similar to SP:O31219 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH) {Legionella pneumophila}; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain	1	1	1	1	1	1
AT1G15690	AVP1_ATAVP3_AVP-3__pyrophosphate-energized vacuolar membrane proton pump / pyrophosphate-energized inorganic pyrophosphatase (AVP-3), identical to pyrophosphate-energized vacuolar membrane proton pump (pyrophosphate-energized inorganic pyrophosphatase) SP:P31414 from (Arabidopsis thaliana)	1	1	1	1	1	1
AT1G15710	prephenate dehydrogenase family protein, contains Pfam profile: PF02153 prephenate dehydrogenase	1	0	0	0	0	0
AT1G16300	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to glyceraldehyde-3-phosphate dehydrogenase (Pinus sylvestris) GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	1	0	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G16350	inosine-5`-monophosphate dehydrogenase, putative, strong similarity to SP:P47996 gb:L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsis thaliana; member of the PF:00478 IMP dehydrogenase family	0	0	0	0	1	0
AT1G16700	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative, very strong similarity to SP:Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}; contains Pfam profile PF00037: iron-sulfur cluster-binding protein	0	0	0	1	1	1
AT1G17290	ALAAT1__alanine aminotransferase, putative, similar to alanine aminotransferase from Panicum miliaceum (SP:P34106), GB:AAC62456 GI:3694807 from (Zea mays), GI:4730884 from Oryza sativa	1	1	1	1	1	1
AT1G17745	PGDH__D-3-phosphoglycerate dehydrogenase / 3-PGDH, identical to SP:O04130	1	1	0	0	1	0
AT1G17890	GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase, putative, similar to GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1)GI:6016479 from (Arabidopsis thaliana)	1	0	0	0	0	0
AT1G18500	2-isopropylmalate synthase, putative, strong similarity to 2-isopropylmalate synthase (IMS1) (Arabidopsis thaliana) GI:12330687; contains Pfam profile PF00682: HMGL-like	1	1	0	0	1	0
AT1G18640	PSP__3-phosphoserine phosphatase (PSP), nearly identical to 3-phosphoserine phosphatase GI:3759177 from (Arabidopsis thaliana)	1	0	0	1	0	0
AT1G19440	very-long-chain fatty acid condensing enzyme, putative, similar to GB:AAD37122 from (Arabidopsis thaliana)	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G19580	bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)	1	0	1	1	0	1
AT1G19920	APS2_ASA1_AMT1_TRP5_WEI2__sulfate adenylyltransferase 2 / ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2), identical to ATP sulfurylase (APS2) (Arabidopsis thaliana) GI:1575324	0	0	0	0	1	0
AT1G20510	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to SP:P14912 and SP:P14913 from Petroselinum crispum; contains Pfam AMP-binding enzyme domain PF00501	1	1	0	0	0	0
AT1G20575	dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichol-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative, similar to DPM1 from Homo sapiens (SP:O60762); member of glycosyltransferase family 2	1	0	1	1	1	1
AT1G20620	CAT3_SEN2_ATSEN2__catalase 3 (SEN2), almost identical to catalase 3 SP:Q42547, GI:3123188 from (Arabidopsis thaliana); identical to catalase 3 (SEN2) mRNA, partial cds GI:3158369	0	0	1	0	0	0
AT1G20630	CAT1__catalase 1, identical to catalase 1 GI:2511725 from (Arabidopsis thaliana)	0	0	0	0	0	1
AT1G20950	pyrophosphate--fructose-6-phosphate 1-phosphotransferase-related / pyrophosphate-dependent 6-phosphofructose-1-kinase-related, similar to pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit SP:Q41140 from (Ricinus communis)	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G22410	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative, similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate GI:170224 from (Nicotiana tabacum), SP:P21357 from Solanum tuberosum; contains Pfam Class-II DAHP synthetase family domain PF01474	1	1	1	1	1	0
AT1G22450	COX6B_ATCOX6B2__cytochrome c oxidase subunit 6b, putative (COX6b), nearly identical to subunit 6b of cytochrome c oxidase (Arabidopsis thaliana) GI:6518353	1	1	1	0	1	0
AT1G23190	phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative, strong similarity to SP:P93805 Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase	1	0	0	0	1	1
AT1G23310	GGT1_AOAT1__glutamate:glyoxylate aminotransferase 1 (GGT1), identical to glutamate:glyoxylate aminotransferase 1 (Arabidopsis thaliana) GI:24461827; similar to alanine aminotransferase GI:4730884 from (Oryza sativa); contains Pfam profile PF00155: aminotransferase, classes I and II	0	0	0	0	0	1
AT1G23820	SPDS1__spermidine synthase 1 (SPDSYN1) / putrescine aminopropyltransferase 1, identical to SP:Q9ZUB3 Spermidine synthase 1 (EC 2.5.1.16) (Putrescine aminopropyltransferase 1) (SPDSY 1) {Arabidopsis thaliana}	1	0	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G24180	IAR4__pyruvate dehydrogenase E1 component alpha subunit, mitochondrial, putative, similar to SP:P52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) {Arabidopsis thaliana}; contains Pfam profile PF00676: Dehydrogenase E1 component	1	1	1	1	1	1
AT1G24280	G6PD3__Encodes a plastidic glucose-6-phosphate dehydrogenase that is sensitive to reduction by DTT and whose mRNA is most highly expressed in root.	0	1	0	0	0	0
AT1G24360	3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase, identical to 3-oxoacyl-(acyl-carrier protein) reductase SP:P33207 from (Arabidopsis thaliana)	1	1	1	1	1	1
AT1G27450	APT1_APRT_APT_ATAPT1_ATAPT1__adenine phosphoribosyltransferase 1 (APT1), nearly identical to SP:P31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}	1	0	0	0	0	1
AT1G27680	APL2__glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase, identical to SP:P55230	1	0	1	0	0	0
AT1G28130	GH3.17__encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro. Lines carrying insertions in this gene are hypersensitive to auxin.	0	0	0	0	0	1
AT1G29880	glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP:O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}	1	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G29900	CARB__carbamoyl-phosphate synthase family protein, similar to carbamoylphosphate synthetase GI:6552726 from (Medicago sativa); contains Pfam profiles PF02786: Carbamoyl-phosphate synthase L chain ATP binding domain, PF00289: Carbamoyl-phosphate synthase L chain N-terminal domain, PF02787: Carbamoyl-phosphate synthetase large chain oligomerisation domain	1	1	1	1	1	1
AT1G30120	PDH-E1 BETA__pyruvate dehydrogenase E1 component beta subunit, chloroplast, identical to pyruvate dehydrogenase E1 beta subunit (Arabidopsis thaliana) GI:2454184; identical to cDNA pyruvate dehydrogenase E1 beta subunit mRNA, nuclear gene encoding plastid protein GI:2454183	0	0	0	1	0	1
AT1G30620	MUR4_UXE1__UDP-D-xylose 4-epimerase, putative (MUR4), similar to SP:P55180 UDP-glucose 4-epimerase (EC 5.1.3.2) from Bacillus subtilis, GI:3021357 UDP-galactose 4-epimerase from Cyamopsis tetragonoloba; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains TIGRfam profile TIGR01179: UDP-glucose 4-epimerase	0	0	0	0	1	1
AT1G31180	3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to SP:P29102 3-isopropylmalate dehydrogenase, chloroplast precursor {Brassica napus}; EST gb:F14478 comes from this gene	1	1	1	0	1	1
AT1G31220	phosphoribosylglycinamide formyltransferase, similar to phosphoribosylglycinamide formyltransferase, chloroplast precursor (Arabidopsis thaliana) SWISS-PROT:P52422	1	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G31230	AK-HSDH I__bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH, nearly identical to gb:X71364 (PIR:S46497) aspartate kinase / homoserine dehydrogenase from Arabidopsis thaliana; contains ACT domain	0	1	0	1	0	1
AT1G31860	AT-IE__histidine biosynthesis bifunctional protein (HISIE), identical to histidine biosynthesis bifunctional protein hisIE, chloroplast (precursor) SP: O82768 from (Arabidopsis thaliana); identical to cDNA phosphoribosyl-ATP pyrophosphohydrolase GI:3461883	1	0	0	0	0	0
AT1G32380	ribose-phosphate pyrophosphokinase 2 / phosphoribosyl diphosphate synthetase 2 (PRS2), identical to SP:Q42583 from (Arabidopsis thaliana); strong similarity to phosphoribosyl diphosphate synthetase 1 (ribose-phosphate pyrophosphokinase 1 (PRS I) (Arabidopsis thaliana) GI:633140, SP:Q42581	1	1	0	0	0	0
AT1G32440	pyruvate kinase, putative, similar to pyruvate kinase isozyme G, chloroplast precursor (Nicotiana tabacum) SWISS-PROT:Q40546	1	0	1	0	0	0
AT1G34430	EMB3003__dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide S-acetyltransferase (LTA2) (Arabidopsis thaliana) GI:5881963; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain	1	1	1	1	1	1
AT1G35580	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase	0	0	0	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G44170	ALDH3H1_ALDH4__aldehyde dehydrogenase, putative (ALDH), similar to aldehyde dehydrogenase ALDH (Craterostigma plantagineum) gi:17065918:emb:CAC84900	1	0	1	0	1	1
AT1G47260	APFI__bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)	1	1	1	1	1	1
AT1G47420	expressed protein, identical to hypothetical protein GB:AAD46040 GI:5668814 from (Arabidopsis thaliana)	1	0	1	0	1	1
AT1G48600	phosphoethanolamine N-methyltransferase 2, putative (NMT2), very similar to :PEM2_ARATH Putative phosphoethanolamine N-methyltransferase 2 (EC 2.1.1.103) (SP:Q944H0){Arabidopsis thaliana}; very similar to Halotolerance protein Hal3b (SP:P94063)(Arabidopsis thaliana); to similar to GB:AAF61950 from (Spinacia oleracea)	0	0	0	1	0	0
AT1G48850	EMB1144__chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase, putative, similar to chorismate synthase from Lycopersicon esculentum (SP:Q42884), Corydalis sempervirens (SP:P27793); contains Pfam chorismate synthase domain PF01264	1	1	0	1	0	1
AT1G48860	3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP synthase, putative, strong similarity to 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase SP:P05466 from (Arabidopsis thaliana)	1	0	0	1	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G49140	NADH-ubiquinone oxidoreductase-related, similar to NADH-ubiquinone oxidoreductase 12 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-12KD) (CI-12KD). (Swiss-Prot:Q03015) (Neurospora crassa)	1	0	0	0	0	0
AT1G50200	ALATS_ACD__aminoacyl-tRNA synthetase family protein, contains Pfam profiles: PF01411 tRNA synthetases class II (A), PF02272 DHHA1 domain	1	0	1	1	1	0
AT1G53000	cytidylyltransferase family, contains Pfam profile: PF02348 cytidylyltransferase	1	1	1	0	1	1
AT1G53240	malate dehydrogenase (NAD), mitochondrial, identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 SP:Q9ZP06 from (Arabidopsis thaliana); contains InterPro entry IPR001236: Lactate/malate dehydrogenase	1	1	1	1	1	1
AT1G53840	ATPME1__pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase	1	1	1	0	1	0
AT1G54100	ALDH7B4__aldehyde dehydrogenase, putative / antiquitin, putative, strong similarity to SP:Q41247 Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1) (Brassica turgor-responsive/drought-induced gene 26 protein) (Btg-26) {Brassica napus}; similar to turgor-responsive protein 26G (aldehyde dehydrogenase family 7 member A1) (Pisum sativum) SWISS-PROT:P25795	1	0	0	0	1	0
AT1G54220	dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide S-acetyltransferase GI:5669871 (Zea mays); contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain	1	1	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G55850	ATCSLE1_CSLE1__cellulose synthase family protein, similar to cellulose synthase catalytic subunit (gi:13925881) from Nicotiana alata, cellulose synthase-5 (gi:9622882) from Zea mays	1	1	1	0	0	0
AT1G56190	phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase	1	1	1	1	1	0
AT1G58080	ATATP-PRT1_ATATP-PRT2__ATP phosphoribosyl transferase 1 (ATP-PRT1), identical to ATP phosphoribosyl transferase GI:6683617 from (Arabidopsis thaliana)	1	0	1	0	0	0
AT1G59900	AT-E1 ALPHA__pyruvate dehydrogenase E1 component alpha subunit, mitochondrial (PDHE1-A), identical to SP:P52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) {Arabidopsis thaliana}	1	0	0	0	0	1
AT1G62640	KAS III__3-oxoacyl-(acyl-carrier-protein) synthase III, chloroplast / beta-ketoacyl-ACP synthase III / 3-ketoacyl-acyl carrier protein synthase III (KAS III), identical to SP:P49243 3-oxoacyl-(acyl-carrier-protein) synthase III, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase III) (KAS III) {Arabidopsis thaliana}	1	1	1	1	1	0
AT1G63000	NRS/ER__expressed protein	1	1	0	0	1	1
AT1G63050	membrane bound O-acyl transferase (MBOAT) family protein, low similarity to porcupine from (Xenopus laevis) GI:6714514, GI:6714520, GI:6714518, GI:6714516; contains Pfam profile PF03062: MBOAT family	0	0	0	1	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G63660	GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative, similar to SP:P38625 GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase) {Saccharomyces cerevisiae}; contains Pfam profile PF00117: glutamine amidotransferase class-I	0	0	0	0	1	0
AT1G64190	6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate	1	1	1	1	1	1
AT1G66430	pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase	0	0	0	0	1	0
AT1G67560	lipoxygenase family protein, similar to 13-lipoxygenase GB:CAA65269 (Solanum tuberosum), gi:1654140 (Lycopersicon esculentum)	0	1	0	0	0	0
AT1G67730	b-keto acyl reductase, putative (GLOSSY8), similar to b-keto acyl reductase GI:2586127 from (Hordeum vulgare)	1	1	1	1	1	1
AT1G69640	acid phosphatase, putative, similar to GI:5360721 from (Lupinus albus)	1	0	0	0	1	0
AT1G69740	porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative, similar to delta-aminolevulinic acid dehydratase (Alad) GI:493019 (SP:P43210) from Glycine max, SP:P24493 from Spinacia oleracea, SP:P30124 from Pisum sativum	0	0	1	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G69830	AMY3_ATAMY3__Encodes a plastid-localized α-amylase. Expression is reduced in the SEX4 mutant. Loss of function mutations show normal diurnal pattern of starch accumulation/degradation. Expression follows circadian rhythms.	0	0	0	0	0	1
AT1G70310	SPDS2__spermidine synthase 2 (SPDSYN2) / putrescine aminopropyltransferase 2, identical to SP:O48661 Spermidine synthase 2 (EC 2.5.1.16) (Putrescine aminopropyltransferase 2) (SPDSY 2) {Arabidopsis thaliana}	1	0	0	1	0	0
AT1G70410	carbonic anhydrase, putative / carbonate dehydratase, putative, similar to SP:P42737 Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase 2) {Arabidopsis thaliana}; contains Pfam profile PF00484: Carbonic anhydrase	1	0	0	0	0	0
AT1G70580	AOAT2_GGT2__glutamate:glyoxylate aminotransferase 2 (GGT2), identical to glutamate:glyoxylate aminotransferase 2 (Arabidopsis thaliana) GI:24461829; similar to alanine aminotransferase from Panicum miliaceum (SP:P34106), GI:4730884 from Oryza sativa; contains Pfam profile PF00155: aminotransferase, classes I and II	0	0	0	0	1	0
AT1G70730	phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative, strong similarity to SP:P93804 Phosphoglucomutase, cytoplasmic 1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase	1	0	0	0	0	0
AT1G74030	enolase, putative, similar to Swiss-Prot:P15007 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) (Drosophila melanogaster)	1	1	0	1	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G74260	AIR synthase-related family protein, contains Pfam profiles: PF00586 AIR synthase related protein, N-terminal domain, PF02769 AIR synthase related protein, C-terminal domain	1	1	1	1	1	0
AT1G74920	ALDH10A8__betaine-aldehyde dehydrogenase, putative, identical to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) (Arabidopsis thaliana) SWISS-PROT:Q9S795; strong similarity to betaine aldehyde dehydrogenase (Amaranthus hypochondriacus) GI:2388710	1	0	0	0	0	0
AT1G74960	FAB1_KAS2__3-ketoacyl-ACP synthase, putative, similar to 3-ketoacyl-ACP synthase (Cuphea pulcherrima) gi:3800747:gb:AAC68860; identical to cDNA beta-ketoacyl-ACP synthetase 2 nuclear gene for plastid product GI:14582700	1	1	0	0	0	0
AT1G75270	dehydroascorbate reductase, putative, similar to GI:6939839 from (Oryza sativa)	1	0	0	1	0	1
AT1G75330	OTC__ornithine carbamoyltransferase, chloroplast / ornithine transcarbamylase / OTCase (OTC), identical to SP:O50039 Ornithine carbamoyltransferase, chloroplast precursor (EC 2.1.3.3) (OTCase) (Ornithine transcarbamylase) {Arabidopsis thaliana}	1	1	0	0	1	1
AT1G75680	glycosyl hydrolase family 9 protein, similar to endo-beta-1,4-glucanase GB:AAC12685 GI:3025470 from (Pinus radiata)	0	1	1	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G76490	HMG1_HMGR1__similar to 3-hydroxy-3-methylglutaryl-CoA reductase 2 / HMG-CoA reductase 2 (HMGR2) [Arabidopsis thaliana] (TAIR:At2g17370.1); similar to 3-hydroxy-3-methylglutaryl coenzyme A reductase [Hevea brasiliensis] (GB:AAU08214.1); similar to HMG-CoA reductase [Cucumis melo] (GB:BAA36291.1); similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase [Hevea brasiliensis] (GB:AAQ63055.1); similar to hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus] (GB:CAA48610.1); similar to 3-hydroxy-3-methylglutaryl coenzyme A reductase; HMG-CoA reductase; EuHMGR [Eucommia ulmoides] (GB:AAV54051.1); contains InterPro domain 3-hydroxy-3-methylglutaryl Coenzyme A reductase (InterPro:IPR004554); contains InterPro domain Hydroxymethylglutaryl-coenzyme A reductase (InterPro:IPR002202)	0	0	1	1	0	0
AT1G76550	pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative, strong similarity to SP:Q41140 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (PPI-PFK) {Ricinus communis}; contains Pfam profile PF00365: Phosphofructokinase	0	0	0	1	0	0
AT1G77590	LACS9__long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9), similar to LACS 3 (SP:O95573) from Homo Sapiens, LACS 3 (SP:Q63151) from Rattus norvegicus; contains Pfam HMM hit: AMP-binding enzymes PF00501	1	0	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G78570	RHM1__NAD-dependent epimerase/dehydratase family protein, similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	0	0	1	0	1	0
AT1G78660	ATGGH1__gamma-glutamyl hydrolase, putative / gamma-Glu-X carboxypeptidase, putative / conjugase, putative, similar to SP:O65355 Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) {Arabidopsis thaliana}	1	0	0	0	0	0
AT1G78920	AVP2__vacuolar-type H+-translocating inorganic pyrophosphatase (AVPL1), identical to vacuolar-type H+-translocating inorganic pyrophosphatase GI:6901676 from (Arabidopsis thaliana)	1	1	1	0	1	1
AT1G79010	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY), identical to SP:Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}	1	1	1	0	1	1
AT1G79230	ST1_ATMST1_ATRDH1_MST1__mercaptopyruvate sulfurtransferase (MST1) (RDH1), identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:5834508 from (Arabidopsis thaliana)	1	1	1	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G79440	ALDH5F1_SSADH_SSADH1__succinate-semialdehyde dehydrogenase (SSADH1), similar to succinate-semialdehyde dehydrogenase (NADP+) (SSDH) (Escherichia coli) SWISS-PROT:P25526; identical to succinic semialdehyde dehydrogenase mRNA, nuclear gene encoding mitochondrial protein GI:6684441; contains TIGRfam profile TIGR01780:succinic semialdehyde dehydrogenase; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein	1	1	1	0	1	1
AT1G79500	KDSA__2-dehydro-3-deoxyphosphooctonate aldolase / phospho-2-dehydro-3-deoxyoctonate aldolase / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase (KDSA), identical to Swiss-Prot:Q9AV97 2-dehydro-3-deoxyphosphooctonate aldolase (EC 4.1.2.16) (Phospho-2- dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) (Arabidopsis thaliana)	0	0	0	0	1	0
AT1G79530	GAPC__glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to glyceraldehyde-3-phosphate dehydrogenase (Pinus sylvestris) GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G79550	PGK__phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase	1	1	1	1	1	1
AT1G79690	ATNUDT3__MutT/nudix family protein, contains Pfam NUDIX domain (PF00293); very low similarity to Chain A and Chain B of Escherichia coli isopentenyl diphosphate:dimethylallyl diphosphate isomerase (gi:15826361) (gi:15826360)	1	1	1	0	1	0
AT1G80230	cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb	1	0	1	0	1	1
AT1G80560	3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 SP:P29102 from (Brassica napus)	1	1	1	0	1	1
AT1G80600	acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative, similar to SP:O04866 Acetylornithine aminotransferase, mitochondrial precursor (EC 2.6.1.11) (ACOAT) (Acetylornithine transaminase) (AOTA) {Alnus glutinosa}; contains Pfam profile PF00202: aminotransferase, class III	1	1	1	1	1	1
AT2G01140	fructose-bisphosphate aldolase, putative, similar to plastidic aldolase NPALDP1 from Nicotiana paniculata (GI:4827251); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G02050	NADH-ubiquinone oxidoreductase B18 subunit, putative, contains Pfam PF05676: NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7); similar to NADH-ubiquinone oxidoreductase B18 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B18) (CI-B18) (Cell adhesion protein SQM1) (Swiss-Prot:P17568) (Homo sapiens); similar to NADH:ubiquinoe oxidoreductase NDUFB7 subunit (GI:9651635) (Homo sapiens)	1	0	1	0	1	1
AT2G04350	long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8), similar to LACS 4 (SP:O35547) from Rattus norvegicus, LACS 4 (SP:O60488) from Homo sapiens; contains Pfam HMM hit: AMP-binding enzymes PF00501	0	0	0	0	0	1
AT2G04400	indole-3-glycerol phosphate synthase (IGPS), nearly identical to SP:P49572	1	1	0	1	0	1
AT2G05710	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative, nearly identical to SP:P49608 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Cucurbita maxima}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain	1	1	1	1	1	1
AT2G05990	ENR1_ENR-A_MOD1_ENR1__enoyl-(acyl-carrier protein) reductase (NADH), chloroplast, putative / NADH-dependent enoyl-ACP reductase, putative, strong similarity to enoyl-(acyl-carrier protein) reductase (NADH) SP:P80030 from (Brassica napus)	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G06050	OPR3_OPDA-REDUCTASE__12-oxophytodienoate reductase (OPR3) / delayed dehiscence1 (DDE1), nearly identical to DELAYED DEHISCENCE1 (GI:7688991) and to OPR3 (GI:10242314); contains Pfam profile PF00724:oxidoreductase, FAD/FMN-binding; identical to cDNA OPDA-reductase homolog GI:5059114	1	1	1	0	1	1
AT2G07050	CAS1__cycloartenol synthase (CAS1) / 2,3-epoxysqualene--cycloartenol cyclase / (S)-2,3-epoxysqualene mutase, identical to cycloartenol synthase (SP:P38605 : GI:452446) (PMID:7505443)	1	1	1	1	1	1
AT2G14170	ALDH6B2__methylmalonate-semialdehyde dehydrogenase, putative, similar to methylmalonate-semialdehyde dehydrogenase (acylating), mitochondrial precursor (MMSDH) (Rattus norvegicus) SWISS-PROT:Q02253	1	1	1	1	1	1
AT2G15620	NIR1_ATHNIR_NIR__ferredoxin--nitrite reductase, putative, strong similarity to ferredoxin--nitrite reductase (Nicotiana tabacum) GI:19893; contains Pfam profiles PF03460: Nitrite/Sulfite reductase ferredoxin-like half domain, PF01077: Nitrite and sulphite reductase 4Fe-4S domain	1	0	1	0	1	1
AT2G16570	ATASE_ATASE1__amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase, identical to amidophosphoribosyltransferase (Arabidopsis thaliana) GI:469193; identical to cDNA amidophosphoribosyltransferase GI:469192	1	0	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G17130	IDH2__isocitrate dehydrogenase subunit 2 / NAD+ isocitrate dehydrogenase subunit 2, nearly identical to NAD+ dependent isocitrate dehydrogenase subunit 2 (Arabidopsis thaliana) GI:1766048	1	1	1	0	1	1
AT2G17265	HSK__homoserine kinase (HSK), identical to homoserine kinase (Arabidopsis thaliana) gi:4927412:gb:AAD33097	1	1	0	0	0	0
AT2G17420	NTRA_ATNTRA_NTR2__similar to thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [Arabidopsis thaliana] (TAIR:At4g35460.1); similar to NADPH-thioredoxin reductase [Triticum aestivum] (GB:CAD19162.1); contains InterPro domain Thioredoxin reductase (InterPro:IPR005982); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class I (InterPro:IPR001100); contains InterPro domain FAD-dependent pyridine nucleotide-disulphide oxidoreductase (InterPro:IPR001327); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II, active site (InterPro:IPR008255); contains InterPro domain Adrenodoxin reductase (InterPro:IPR000759); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II (InterPro:IPR000103)	1	1	1	1	1	1
AT2G17630	phosphoserine aminotransferase, putative, similar to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q96255) (Arabidopsis thaliana); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V	1	1	1	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G18230	inorganic pyrophosphatase (soluble) (PPA) / pyrophosphate phospho-hydrolase / PPase, nearly identical to SP:P21216 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase) {Arabidopsis thaliana}	0	0	0	0	0	1
AT2G19860	ATHXK2__hexokinase 2 (HXK2), identical to hexokinase 2 (Arabidopsis thaliana) Swiss-Prot:P93834	1	0	0	0	0	0
AT2G19940	semialdehyde dehydrogenase family protein, similar to N-acetyl-glutamyl-phosphate reductase (Campylobacter jejuni) GI:6650362; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain	1	1	1	0	1	1
AT2G20360	expressed protein	1	1	1	1	1	1
AT2G20370	MUR3__exostosin family protein, contains Pfam profile: PF03016	1	0	0	0	1	0
AT2G20420	succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative, identical to SP:O82662 Succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS-beta) {Arabidopsis thaliana}; similar to SP:O97580 Succinyl-CoA ligase (ADP-forming) beta-chain, mitochondrial precursor (EC 6.2.1.5) {Sus scrofa}; contains Pfam profiles PF00549: CoA-ligase, PF02222: ATP-grasp domain	1	1	1	1	1	1
AT2G20810	glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8	0	0	1	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G21170	TIM__triosephosphate isomerase, chloroplast, putative, similar to Triosephosphate isomerase, chloroplast precursor: SP:P48496 from Spinacia oleracea, SP:P46225 from Secale cereale	1	1	1	1	1	1
AT2G21590	APL4__glucose-1-phosphate adenylyltransferase large subunit, putative / ADP-glucose pyrophosphorylase, putative, strong similarity to SP:P55231	0	0	0	0	0	1
AT2G22230	beta-hydroxyacyl-ACP dehydratase, putative, similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase	0	0	1	1	0	1
AT2G22480	phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase	1	1	1	1	1	0
AT2G22780	PMDH1__malate dehydrogenase, glyoxysomal, putative, strong similarity to glyoxysomal malate dehydrogenase (EC 1.1.1.37) SP:P19446 {Citrullus lanatus}, SP:P46488 {Cucumis sativus}, (Medicago sativa) GI:2827078, SP:Q42972 {Oryza sativa}, SP:Q9ZP05 {Arabidopsis thaliana}, SP:P37228 {Glycine max}; contains InterPro entry IPR001236: Lactate/malate dehydrogenase	1	1	1	1	1	1
AT2G26080	glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative, strong similarity to SP:P26969 Glycine dehydrogenase (decarboxylating), mitochondrial precursor (EC 1.4.4.2) {Pisum sativum}; contains Pfam profile PF02347: Glycine cleavage system P-protein	1	1	1	1	1	1
AT2G26230	uricase / urate oxidase / nodulin 35, putative, identical to uricase SP:O04420 from (Arabidopsis thaliana)	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G26640	beta-ketoacyl-CoA synthase, putative, similar to beta-ketoacyl-CoA synthase (Simmondsia chinensis)(GI:1045614)	1	0	1	0	0	0
AT2G27730	expressed protein, contains 1 transmembrane domain; similar to Unknown mitochondrial protein At2g27730 (Swiss-Prot:Q9ZUX4) (Arabidopsis thaliana) similar to F1F0-ATPase inhibitor protein (GI:5821432) (Oryza sativa)	1	1	1	0	1	1
AT2G27860	AXS1__expressed protein	1	0	0	0	0	1
AT2G28190	CSD2_CZSOD2__superoxide dismutase (Cu-Zn), chloroplast (SODCP) / copper/zinc superoxide dismutase (CSD2), identical to GP:3273753:AF061519	1	0	1	1	1	1
AT2G28760	NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	0	0	0	0	0	1
AT2G30200	expressed protein	1	1	1	1	1	1
AT2G30490	ATC4H_C4H_CYP73A5__trans-cinnamate 4-monooxygenase / cinnamic acid 4-hydroxylase (C4H) (CA4H) / cytochrome P450 73 (CYP73) (CYP73A5), identical to SP:P92994: Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73). {Arabidopsis thaliana}; molecular marker C4H (GB:U71080)	1	1	1	1	1	1
AT2G30860	ATGSTF9_ATGSTF7_GLUTTR__glutathione S-transferase, putative, identical to GB:Y12295	1	0	0	1	1	1
AT2G30870	ATGSTF10_ATGSTF4_ERD13__glutathione S-transferase, putative, supported by cDNA GI:443698 GB:D17673	1	1	1	1	1	0

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AT2G30920	EMB3002_ATCOQ3_COQ3__hexaprenyldihydroxybenzoate methyltransferase, identical to hexaprenyldihydroxybenzoate methyltransferase SP:O49354 from (Arabidopsis thaliana)	1	0	0	0	0	0
AT2G30970	ASP1__aspartate aminotransferase, mitochondrial / transaminase A (ASP1), identical to SP:P46643 Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}	1	1	1	1	1	1
AT2G31360	ADS2__delta 9 desaturase (ADS2), identical to delta 9 acyl-lipid desaturase (ADS2) GI:2970036 from (Arabidopsis thaliana)	0	0	0	0	1	0
AT2G31390	STH__pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase	1	1	1	1	1	1
AT2G33150	PED1__acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative, similar to 3-ketoacyl-CoA thiolase (E.C. 2.3.1.16) from (Arabidopsis thaliana) GI:2981616, (Cucumis sativus) GI:393707, (Cucurbita cv. Kurokawa Amakuri) GI:1694621; contains InterPro accession IPR002155: Thiolase	1	1	1	1	1	1
AT2G33220	expressed protein	1	0	1	1	1	1
AT2G34630	geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative, identical to GI:11322965 A. thaliana geranyl diphosphate synthase	1	1	0	0	1	0

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AT2G35040	AICARFT/IMPCHase bienzyme family protein, similar to SP:P12048 Bifunctional purine biosynthesis protein purH (Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)) {Bacillus subtilis}; contains Pfam profiles PF01808: AICARFT/IMPCHase bienzyme, PF02142: MGS-like domain	1	1	1	0	1	0
AT2G35120	glycine cleavage system H protein, mitochondrial, putative, similar to SP:Q39732 Glycine cleavage system H protein, mitochondrial precursor {Flaveria anomala}; contains Pfam profile PF01597: Glycine cleavage H-protein	1	0	1	0	0	0
AT2G36460	fructose-bisphosphate aldolase, putative, similar to PIR:S65073 fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic (Oryza sativa); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I	0	0	0	0	0	1
AT2G36530	LOS2__enolase, identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D-glycerate hydro-lyase) (Arabidopsis thaliana)	1	1	1	1	1	1
AT2G36580	pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Glycine max) SWISS-PROT:Q42806	0	0	0	0	1	0
AT2G36880	S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltransferase 3, AdoMet synthetase 3) (Lycopersicon esculentum) SWISS-PROT:P43282	0	1	1	0	1	0
AT2G37040	PAL1__phenylalanine ammonia-lyase 1 (PAL1), nearly identical to SP:P35510	0	0	0	0	1	0

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AT2G37250	ADK_ATPADK1__adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase	1	1	0	0	1	0
AT2G37690	phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative, similar to SP:P55195 Phosphoribosylaminoimidazole carboxylase, chloroplast precursor (EC 4.1.1.21) (AIR carboxylase) (AIRC) {Vigna aconitifolia}; contains Pfam profiles PF02222: ATP-grasp domain, PF00731: AIR carboxylase	1	1	1	1	1	0
AT2G38040	CAC3__acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family, contains Pfam profile: PF03255: Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit	1	1	1	1	1	1
AT2G38280	FAC1__AMP deaminase, putative / myoadenylate deaminase, putative, similar to SP:P15274 AMP deaminase (EC 3.5.4.6) (Myoadenylate deaminase) {Saccharomyces cerevisiae}; contains Pfam profile PF00962: Adenosine/AMP deaminase	1	0	0	1	0	0
AT2G38650	glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8	1	0	0	0	0	0
AT2G38670	ethanolamine-phosphate cytidylyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:phosphoethanolamine cytidylyltransferase, putative, similar to SP:Q99447 Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) {Homo sapiens}; contains Pfam profile PF01467: Cytidylyltransferase	1	1	0	0	0	1
AT2G39800	P5CS1_ATP5CS__delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1), identical to SP:P54887:P5C1_ARATH	0	0	1	0	0	0

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AT2G40840	DPE2__glycoside hydrolase family 77 protein, contains Pfam profiles PF02446: 4-alpha-glucanotransferase, PF00686: Starch binding domain; contains a non-consensus AT-AC intron between at intron 5	1	0	0	0	0	1
AT2G40890	CYP98A3_REF8__cytochrome P450 98A3, putative (CYP98A3), identical to Cytochrome P450 98A3 (SP:O22203) (Arabidopsis thaliana); similar to gi:17978651 from Pinus taeda	0	0	1	0	0	0
AT2G41220	GLU2__glutamate synthase, chloroplast (GLU2) / ferredoxin-dependent glutamate synthase (Fd-GOGAT 2), identical to SP:Q9T0P4 Ferredoxin-dependent glutamate synthase 2, chloroplast precursor (EC 1.4.7.1) (Fd-GOGAT 2) {Arabidopsis thaliana}	1	1	1	1	1	1
AT2G41530	esterase, putative, similar to SP:P10768 Esterase D (EC 3.1.1.1) {Homo sapiens}; contains Pfam profile: PF00756 putative esterase	1	0	1	1	1	0
AT2G42790	CSY3__citrate synthase, glyoxysomal, putative, strong similarity to SP:P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase	1	0	0	0	0	1
AT2G42910	ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4), identical to phosphoribosyl diphosphate synthase (prs4) (Arabidopsis thaliana) GI:4902472	1	0	0	1	1	0
AT2G43350	ATGPX3__glutathione peroxidase, putative	0	1	0	0	0	0
AT2G43360	BIO2_BIOB__biotin synthase (BioB) (BIO2), identical to SP:P54967 Pfam profile PF04055: radical SAM domain protein	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G43710	SSI2_FAB2__acyl-(acyl-carrier-protein) desaturase / stearoyl-ACP desaturase (SSI2), identical to gi:15149310; contains Pfam profile PF03405: Fatty acid desaturase; identical to cDNA stearoyl ACP desaturase (SSI2), SSI2-FAB2 allele, GI:15149309	1	1	1	1	1	0
AT2G43750	OASB_ACS1_ATCS-B_CPACS1__cysteine synthase, chloroplast / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase / cpACS1 (OASB), identical to SP:P47999 Cysteine synthase, chloroplast precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (cpACS1) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.7-4) GI:6983575	1	1	1	1	1	1
AT2G44040	dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae} ; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus	1	0	0	0	0	0
AT2G44050	COS1__6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase, identical to 6,7-dimethyl-8-ribityllumazine synthase, chloroplast (precursor) SP:O80575 from (Arabidopsis thaliana)	1	1	1	0	1	1
AT2G44350	ATCS_CSY4__citrate synthase, mitochondrial, putative, strong similarity to SP:P20115 Citrate synthase, mitochondrial precursor {Arabidopsis thaliana}; contains Pfam profile PF00285: Citrate synthase	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G44530	ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative, very strong similarity to phosphoribosyl pyrophosphate synthase (Spinacia oleracea) GI:4902849; contains Pfam profile PF00156: Phosphoribosyl transferase domain	1	0	1	0	0	0
AT2G45290	transketolase, putative, strong similarity to transketolase 1 (Capsicum annuum) GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain	0	1	0	1	1	0
AT2G45300	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase, nearly identical to SP:P05466	1	1	0	1	1	0
AT2G45440	DHDPS2__dihydrodipicolinate synthase 2 (DHDPS2), identical to dihydrodipicolinate synthase 2 (DHDPS2) (Arabidopsis thaliana) GI:11066382	0	1	0	0	0	0
AT2G45790	eukaryotic phosphomannomutase family protein, contains Pfam profile: PF03332 eukaryotic phosphomannomutase	1	0	0	0	1	1
AT2G47380	cytochrome c oxidase subunit Vc family protein / COX5C family protein, contains Pfam profile: PF05799 cytochrome c oxidase subunit Vc (COX5C)	0	0	0	0	0	1
AT2G47510	FUM1__fumarate hydratase, putative / fumarase, putative, similar to SP:P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G47650	UXS4__NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains non-consensus AT donor splice site at exon 1 and non-consensus AC acceptor splice site at exon 2	1	0	1	1	1	1
AT3G01910	SOX__sulfite oxidase, putative, similar to sulfite oxidase GB:3212610 SP:P07850 (Gallus gallus), Moco containing protein (Oryza sativa (japonica cultivar-group)) GI:22759584; contains Pfam profiles: PF00174: Oxidoreductase molybdopterin binding domain and PF03404: Mo-co oxidoreductase dimerisation domain	1	1	1	0	1	0
AT3G02350	glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8	1	1	1	0	1	0
AT3G02360	6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate ;similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 (Glycine max)	1	0	0	1	1	0
AT3G02630	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from Sesamum indicum GI:575942, Cucumis sativus SP:P32061, Ricinus communis SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase	1	1	0	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G02780	IPP2_IDI2_IPIAT1__isopentenyl-diphosphate delta-isomerase II / isopentenyl diphosphate:dimethylallyl diphosphate isomerase II (IPP2), identical to isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP2) GB:U49259 (Arabidopsis thaliana)	1	0	1	0	1	1
AT3G03050	ATCSLD3_KOJAK_CSLD3_ATCSLD3_KJK__cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143 from (Arabidopsis thaliana), cellulose synthase-7 (gi:9622886) from Zea mays; contains Pfam profile PF03552: Cellulose synthase	1	0	0	0	0	0
AT3G03100	NADH:ubiquinone oxidoreductase family protein, contains Pfam PF05071: NADH:ubiquinone oxidoreductase 17.2 kD subunit; similar to ethylene-regulated ER6 protein (GI:5669654) (Lycopersicon esculentum); identical to Probable NADH-ubiquinone oxidoreductase subunit B17.2 (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B17.2) (CI-B17.2) (Swiss-Prot:Q9M9M9) (Arabidopsis thaliana)	1	0	1	1	1	1
AT3G03250	UGP__Is thought to encodes a cytosolic UDP-glucose pyrophosphorylase with strong similarity to UTP--glucose-1-phosphate uridylyltransferase (SwissProt P19595, EC 2.7.7.9, UDP-glucose pyrophosphorylase Solanum tuberosum).	1	1	1	1	1	1
AT3G04120	GAPC__glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, identical to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}	0	1	0	1	0	1
AT3G04520	threonine aldolase family protein, similar to L-allo-threonine aldolase SP:O07051 from (Aeromonas jandaei)	0	0	0	1	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G04600	tRNA synthetase class I (W and Y) family protein, contains Pfam profile: PF00579 tRNA synthetases class I (W and Y)	0	0	0	0	1	0
AT3G04790	ribose 5-phosphate isomerase-related, similar to ribose-5-phosphate isomerase GI:18654317 from (Spinacia oleracea)	1	0	0	1	0	0
AT3G04940	ATCYSD1__cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	0	0	0	0	1	0
AT3G05970	LACS6__long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase (LACS6), strong similarity to AMP-binding protein (MF39P) gi:1617274 from Brassica napus, similar to putative long-chain-fatty-acid--CoA ligase (brain isozyme) GB:P33124 (Rattus norvegicus); contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA AtLACS6 for long-chain acyl-CoA synthetase GI:22531705	1	1	1	0	1	1
AT3G06350	EMB3004__dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative, similar to dehydroquinate dehydratase/shikimate dehydrogenase (Nicotiana tabacum)(GI:535771), dehydroquinate dehydratase/shikimate:NADP oxidoreductase (Lycopersicon esculentum)(GI:3169883)	1	1	0	0	1	0
AT3G06650	ACLB-1__ATP-citrate synthase, putative / ATP-citrate (pro-S-)-lyase, putative / citrate cleavage enzyme, putative, strong similarity to ATP:citrate lyase (Capsicum annuum) GI:13160653; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain	1	0	1	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G06810	acyl-CoA dehydrogenase-related, low similarity to acyl-CoA dehydrogenase (Acinetobacter sp. NCIMB9871) GI:14587418; contains Pfam profiles PF01636: Phosphotransferase enzyme family, PF00441: Acyl-CoA dehydrogenase C-terminal domain, PF02770: Acyl-CoA dehydrogenase middle domain	1	1	0	0	0	1
AT3G06860	MFP2_ATMPF2__fatty acid multifunctional protein (MFP2), identical to fatty acid multifunctional protein (AtMFP2) GB:AF123254 (gi:4337027) (Arabidopsis thaliana) (fatty acid beta-oxidation); contains Pfam profiles PF02737 (3-hydroxyacyl-CoA dehydrogenase, NAD binding domain), PF00378 (enoyl-CoA hydratase/isomerase family protein), PF00725 (3-hydroxyacyl-CoA dehydrogenase)	1	1	1	0	1	1
AT3G07630	prephenate dehydratase family protein, similar to P-protein: chorismate mutase, prephenate dehydratase GB:P43900 (Haemophilus influenzae)	1	0	0	0	1	0
AT3G08590	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative, strong similarity to SP:Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}; contains Pfam profile PF01676: Metalloenzyme superfamily	1	0	1	1	1	0
AT3G08610	expressed protein	0	0	0	0	0	1
AT3G09810	AT3G09805__isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase (NAD+) GB:CAA65502 GI:3021506 (Nicotiana tabacum)	1	1	0	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G09820	ADK1__adenosine kinase 1 (ADK1) / adenosine 5`-phosphotransferase 1, identical to adenosine kinase 1 /adenosine 5`-phosphotransferase 1 SP:Q9SF85 from (Arabidopsis thaliana)	1	1	0	1	1	1
AT3G10050	OMR1__threonine ammonia-lyase / threonine dehydratase / threonine deaminase (OMR1), identical to SP:Q9ZSS6 Threonine dehydratase biosynthetic, chloroplast precursor (EC 4.3.1.19, formerly EC 4.2.1.16) (Threonine deaminase) (TD) {Arabidopsis thaliana}	1	0	0	0	0	0
AT3G10370	mitochondrial FAD-dependent glycerol-3-phosphate dehydrogenase. possibly involved in storage lipid catabolism and glycerol assimilation, and in glycerol-3-phosphate shuttle which transports reducing power from cytosol to mitochondrion.	1	0	1	0	1	1
AT3G10920	MSD1__superoxide dismutase (Mn), mitochondrial (SODA) / manganese superoxide dismutase (MSD1), identical to manganese superoxide dismutase (Arabidopsis thaliana) gi:3273751:gb:AAC24832	1	1	1	1	1	1
AT3G11170	FAD7_FADD__omega-3 fatty acid desaturase, chloroplast (FAD7) (FADD), identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabidopsis thaliana (Mouse-ear cress)); identical to Pfam profile PF00487: Fatty acid desaturase; identical to cDNA plastid fatty acid desaturase GI:809491	1	0	0	0	0	0
AT3G11710	lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative, similar to SP:Q43776 Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) {Lycopersicon esculentum}; contains Pfam profile PF00152: tRNA synthetases class II (D, K and N)	1	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G12120	FAD2__omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) / delta-12 desaturase, identical to omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) SP:P46313 (Arabidopsis thaliana (Mouse-ear cress)) (Plant Cell 6:147-158(1994))	1	1	1	1	1	0
AT3G12260	complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)	1	1	1	1	1	1
AT3G12290	tetrahydrofolate dehydrogenase/cyclohydrolase, putative, similar to SP:P07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)) {Saccharomyces cerevisiae}; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain	1	0	0	0	0	0
AT3G12670	EMB2742__CTP synthase, putative / UTP--ammonia ligase, putative, similar to SP:P17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I	0	0	0	0	1	0
AT3G12780	PGK1__phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase	1	1	1	1	1	1
AT3G13110	AtSerat2;2_SAT-1_SAT-A__serine O-acetyltransferase (SAT-1), identical to serine acetyltransferase (Sat-1) GI:1184048 (Arabidopsis thaliana)	0	1	0	0	0	0

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AT3G13930	dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide S-acetyltransferase (Zea mays) GI:5669871; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain	1	1	1	1	1	1
AT3G14390	diaminopimelate decarboxylase, putative / DAP carboxylase, putative, similar to diaminopimelate decarboxylase (Arabidopsis thaliana) GI:6562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain	1	1	0	0	0	0
AT3G14790	RHM3__NAD-dependent epimerase/dehydratase family protein, similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, Saccharopolyspora spinosa GI:15077647, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	0	1	0	0	0	0
AT3G15020	malate dehydrogenase (NAD), mitochondrial, putative, similar to mitochondrial NAD-dependent malate dehydrogenase GB:CAA10320 SP:Q9ZP06 (Arabidopsis thaliana); contains InterPro entry IPR001236: Lactate/malate dehydrogenase	1	1	1	1	1	1

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AT3G15290	3-hydroxybutyryl-CoA dehydrogenase, putative, similar to S(+)-beta-hydroxybutyryl CoA dehydrogenase (3-hydroxybutyryl-CoA dehydrogenase) (Paracoccus denitrificans) GI:12003356; contains Pfam profiles PF02737: 3-hydroxyacyl-CoA dehydrogenase NAD binding, PF00725: 3-hydroxyacyl-CoA dehydrogenase C-terminal	1	0	0	0	0	0
AT3G15640	cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb	1	0	1	0	1	1
AT3G15730	PLDALPHA1_PLD__phospholipase D alpha 1 / PLD alpha 1 (PLDALPHA1) (PLD1) / choline phosphatase 1, identical to SP:Q38882 Phospholipase D alpha 1 (EC 3.1.4.4) (AtPLDalpha1) (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1) (PLDalpha) (Arabidopsis thaliana)	1	0	1	1	1	1
AT3G16400	ATMLP-470__jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, epithiospecifier (Arabidopsis thaliana) GI:16118845; contains Pfam profiles PF01419 jacalin-like lectin family, PF01344 Kelch motif	0	0	0	0	1	0
AT3G16410	jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, epithiospecifier (Arabidopsis thaliana) GI:16118845; contains Pfam profiles PF01419 jacalin-like lectin family, PF01344 Kelch motif	1	1	0	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G17240	LPD2__dihydrolipoamide dehydrogenase 2, mitochondrial / lipoamide dehydrogenase 2 (MTLPD2), nearly identical to GB:AAF34796 (gi:6984216) from (Arabidopsis thaliana); alternative splice form exists	1	1	1	1	1	1
AT3G17390	MTO3_SAMS3__S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Catharanthus roseus) SWISS-PROT:Q96552	1	1	1	0	1	1
AT3G17810	dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein, low similarity to SP:Q12882 Dihydropyrimidine dehydrogenase (NADP+) precursor (EC 1.3.1.2) (DPD) (DHPDHase) (Dihydrouracil dehydrogenase) (Dihydrothymine dehydrogenase) {Homo sapiens}; contains Pfam profile PF01180: Dihydroorotate dehydrogenase	1	1	0	1	0	1
AT3G17820	ATGSKB6__glutamine synthetase (GS1), identical to glutamine synthetase, cytosolic isozyme (glutamate-- ammonia ligase, GS1) (Arabidopsis thaliana) SWISS-PROT:Q9LVI8	0	0	0	1	0	0
AT3G18000	NMT1__phosphoethanolamine N-methyltransferase 1 / PEAMT 1 (NMT1), identical to Phosphoethanolamine N-methyltransferase 1 (EC 2.1.1.103) (PEAMT 1) (AtNMT1) (SP:Q9FR44){Arabidopsis thaliana}; strong similarity to phosphoethanolamine N-methyltransferase from (Spinacia oleracea) GI:7407189, (Triticum aestivum) GI:17887465; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family	0	0	1	0	0	1

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AT3G19450	ATCAD4_CAD4_CAD-C__cinnamyl-alcohol dehydrogenase (CAD), identical to SP:P48523 Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Arabidopsis thaliana)	0	0	0	1	0	0
AT3G20330	aspartate carabmoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB), identical to SP:P49077 Aspartate carbamoyltransferase, chloroplast precursor (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase) {Arabidopsis thaliana}	1	0	0	0	1	0
AT3G21110	PUR7_PURC__phosphoribosylamidoimidazole-succinocarboxamide synthase / SAICAR synthetase (PUR7), identical to phosphoribosylamidoimidazole-succinocarboxamide synthase, chloroplast (precursor) SP:P38025 from (Arabidopsis thaliana)	1	1	0	0	0	0
AT3G22200	POP2_GABA-T__4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine--oxoglutarate aminotransferase, identical to gamma-aminobutyrate transaminase subunit precursor (Arabidopsis thaliana) (EC 2.6.1.19) GI:14030435; contains Pfam profile PF00202: aminotransferase, class III; identical to cDNA gamma-aminobutyrate transaminase subunit precursor, nuclear gene for mitochondrial product GI:14030434	1	1	1	1	1	1
AT3G22370	AOX1A__alternative oxidase 1a, mitochondrial (AOX1A), identical to GB:Q39219 (SP:Q39219) from (Arabidopsis thaliana)	1	0	1	0	0	0
AT3G22890	APS1__sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509	0	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G22960	pyruvate kinase, putative, similar to pyruvate kinase isozyme A, chloroplast precursor (Ricinus communis) SWISS-PROT:Q43117	1	1	1	1	1	1
AT3G23820	GAE6__NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile: PF01370 NAD dependent epimerase/dehydratase family	1	1	1	0	1	0
AT3G24170	glutathione reductase, putative, identical to GB:P48641 from (Arabidopsis thaliana)	1	0	1	1	0	0
AT3G24503	ALDH2C4_ALDH1A_REF1__aldehyde dehydrogenase (ALDH1a), identical to aldehyde dehydrogenase ALDH1a (Arabidopsis thaliana) gi:20530143:gb:AAM27004	1	0	0	0	0	0
AT3G25110	acyl-(acyl carrier protein) thioesterase / acyl-ACP thioesterase / oleoyl-(acyl-carrier protein) hydrolase / S-acyl fatty acid synthase thioesterase, identical to acyl-(acyl carrier protein) thioesterase (Arabidopsis thaliana) GI:804946	1	1	0	1	1	0
AT3G25140	QUA1__glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8	1	0	1	0	1	0
AT3G25585	AAPT2__aminoalcoholphosphotransferase, putative, strong similarity to aminoalcoholphosphotransferase (Arabidopsis thaliana) GI:3661593; contains Pfam profile PF01066: CDP-alcohol phosphatidyltransferase	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G25780	AOC2__allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative, similar to allene oxide cyclase GI:8977961 from (Lycopersicon esculentum); similar to early-responsive to dehydration (ERD12) protein (GI:15320414); contains Pfam profile PF06351: Allene oxide cyclase	1	0	1	0	1	1
AT3G25860	LTA2_PLE2__dihydrolipoamide S-acetyltransferase (LTA2), identical to dihydrolipoamide S-acetyltransferase (LTA2) (Arabidopsis thaliana) GI:5881963	1	1	1	1	1	1
AT3G27300	G6PD5__glucose-6-phosphate 1-dehydrogenase / G6PD (ACG9), identical to glucose-6-phosphate 1-dehydrogenase (acg9) (Arabidopsis thaliana) GI:5732195	1	0	0	0	0	0
AT3G27380	SDH2-1__succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-1), nearly identical to mitochondrial succinate dehydrogenase iron-sulphur subunit (sdh2-1) (gi:12049598) from Arabidopsis thaliana	1	1	1	1	1	1
AT3G27740	CARA__carbamoyl-phosphate synthase (glutamine-hydrolyzing) (CARA) / glutamine-dependent carbamoyl-phosphate synthase small subunit, identical to carbamoyl phosphate synthetase small subunit GI:2462781 (Arabidopsis thaliana)	1	1	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G29360	UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	1	0	0	0	0	0
AT3G44310	ATNIT1_NIT1__The protein undergoes thiolation following treatment with the oxidant tert-butylhydroperoxide.	0	0	1	0	0	0
AT3G44320	NIT3__nitrilase 3 (NIT3), identical to SP:P46010 Nitrilase 3 (EC 3.5.5.1) {Arabidopsis thaliana}	0	0	1	1	0	0
AT3G44830	lecithin:cholesterol acyltransferase family protein / LACT family protein, similar to lecithin:cholesterol acyltransferase (Rattus norvegicus) GI:2306762; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)	0	0	0	0	0	1
AT3G45300	IVD_ATIVD__isovaleryl-CoA-dehydrogenase (IVD), identical to isovaleryl-CoA-dehydrogenase precursor (Arabidopsis thaliana) GI:5596622	0	0	0	0	0	1
AT3G46940	deoxyuridine 5`-triphosphate nucleotidohydrolase family, contains Pfam profile: PF00692 deoxyuridine 5`-triphosphate nucleotidohydrolase	0	0	0	0	1	0
AT3G46970	ATPHS2_PHS2__Encodes a cytosolic alpha-glucan phosphorylase.	1	0	0	0	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G47520	MDH__malate dehydrogenase (NAD), chloroplast (MDH), identical to chloroplast NAD-malate dehydrogenase (Arabidopsis thaliana) GI:3256066; contains InterPro entry IPR001236: Lactate/malate dehydrogenase; contains Pfam profiles PF00056: lactate/malate dehydrogenase, NAD binding domain and PF02866: lactate/malate dehydrogenase, alpha/beta C-terminal domain	1	1	1	1	1	1
AT3G47930	ATGLDH__L-galactono-1,4-lactone dehydrogenase, putative, strong similarity to L-galactono-1,4-lactone dehydrogenase, Brassica oleracea, Z97060 (gi:2760543), and gi:3986289 from Ipomea batatas	1	1	1	0	1	1
AT3G48000	ALDH2B4_ALDH2__aldehyde dehydrogenase (ALDH2), identical to aldehyde dehydrogenase (Arabidopsis thaliana) GI:8574427; similar to mitochondrial aldehyde dehydrogenase (Arabidopsis thaliana) gi:19850249:gb:AAL99612; identical to cDNA aldehyde dehydrogenase AtALDH2a GI:20530140	1	1	1	1	1	1
AT3G48170	ALDH10A9__betaine-aldehyde dehydrogenase, putative, similar to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) (Arabidopsis thaliana) SWISS-PROT:Q9S795	1	1	0	0	0	1
AT3G48560	CSR1_AHAS_ALS_IMR1_TZP5__acetolactate synthase, chloroplast / acetohydroxy-acid synthase (ALS), nearly identical to SP:P17597 Acetolactate synthase, chloroplast precursor (EC 2.2.1.6, formerly EC 4.1.3.18) (Acetohydroxy-acid synthase) (ALS) {Arabidopsis thaliana}	1	1	0	0	0	0

Supplementary Tables pertaining to Figure 2

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G48680	bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats); ferripyochelin binding protein - Methanobacterium thermoautotrophicum, EMBL:AE000918.1	1	0	1	0	0	1
AT3G48730	glutamate-1-semialdehyde 2,1-aminomutase 2 (GSA 2) / glutamate-1-semialdehyde aminotransferase 2 (GSA-AT 2), identical to GSA2 (SP:Q42522)	1	0	1	0	0	0
AT3G49680	branched-chain amino acid aminotransferase 3 / branched-chain amino acid transaminase 3 (BCAT3), identical to SP:Q9M401 Branched-chain amino acid aminotransferase 3, chloroplast precursor (EC 2.6.1.42) (Atbcat-3){Arabidopsis thaliana}	1	1	1	0	1	0
AT3G51160	MUR1_GMD2_MUR_1__GDP-D-mannose-4,6-dehydratase (MUR1), almost identical to GDP-D-mannose-4,6-dehydratase (MUR1) GI:1764100 from (Arabidopsis thaliana)	1	0	0	0	0	1
AT3G51240	F3H_TT6__naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H), identical to GI:3790548	0	0	0	1	0	0
AT3G51840	ACX4_ATG6_ATSCX__short-chain acyl-CoA oxidase, identical to Short-chain acyl CoA oxidase (Arabidopsis thaliana) GI:5478795; contains InterPro entry IPR006089: Acyl-CoA dehydrogenase	1	1	1	0	1	1
AT3G52880	ATMDAR1__monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407	0	0	0	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G52930	fructose-bisphosphate aldolase, putative, similar to SP:O65735:ALF_CICAR Fructose-bisphosphate aldolase, cytoplasmic isozyme {Cicer arietinum}, cytosolic aldolase (Fragaria x ananassa) GI:10645188; contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I	1	1	1	1	1	1
AT3G53520	UXS1_ATUXS1__NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	1	1	1	1	1	1
AT3G53580	diaminopimelate epimerase family protein, contains Pfam profile PF01678: Diaminopimelate epimerase	1	1	0	0	1	1
AT3G53900	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:P50926 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Lactococcus lactis}; contains Pfam profile PF00156: Phosphoribosyl transferase domain	1	0	0	0	0	0
AT3G54470	uridine 5`-monophosphate synthase / UMP synthase (PYRE-F) (UMPS), identical to SP:Q42586 Uridine 5`-monophosphate synthase (UMP synthase) (Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRtase); Orotidine 5`- phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)) {Arabidopsis thaliana}	0	0	0	0	1	0
AT3G54640	TSA1_TRP3__tryptophan synthase, alpha subunit (TSA1), identical to gi:619753	0	1	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G54660	GR_EMB2360__gluthatione reductase, chloroplast, nearly identical to SP:P42770 Glutathione reductase, chloroplast precursor (EC 1.8.1.7) (GR) (GRASE) {Arabidopsis thaliana}; identical to cDNA glutathione reductase GI:451197	1	0	1	0	0	0
AT3G55010	phosphoribosylformylglycinamidine cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5), identical to phosphoribosylformylglycinamidine cyclo-ligase, chloroplast precursor SP:Q05728 from (Arabidopsis thaliana); contains Pfam profiles: PF02769 AIR synthase related protein, C-terminal domain, PF00586 AIR synthase related protein, N-terminal domain	1	0	0	1	1	1
AT3G55030	phosphatidylglycerolphosphate synthase, putative, similar to phosphatidylglycerolphosphate synthase GI:13365519 from (Arabidopsis thaliana); contains non-consensus CG acceptor splice site at exon 4	1	0	0	0	0	1
AT3G55360	CER10_ECR__Enoyl-CoA reductase (ECA) is involved in all very long chain fatty acids (VLCFA) elongation reactions that are required for cuticular wax, storage lipid and sphingolipid metabolism. The protein is located in the ER, but in contrast to its yeast homolog TSC13 is not particularly enriched in the nuclear envelope-vacuole junction. Mutants in this gene show abnormal organ morphology and stem glossiness. Cells in all tissues are only about 1/3 of the size of wild type cells. The morphological changes are most likely to result from the reduction in the VLCFA content of sphingolipids. Mutants also show abnormalities in the endocytic membrane organization and transport.	1	1	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G55440	ATCTIMC__triosephosphate isomerase, cytosolic, putative, strong similarity to triosephosphate isomerase, cytosolic from Petunia hybrida (SP:P48495), from Coptis japonica (SP:P21820)	1	1	1	1	1	1
AT3G55610	delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2), identical to SP:P54888	0	0	1	0	0	0
AT3G56310	alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative, similar to alpha-galactosidase SP:Q42656 from (Coffea arabica)	1	0	1	0	0	1
AT3G57050	CBL__cystathionine beta-lyase, chloroplast / beta-cystathionase / cysteine lyase (CBL), identical to SP:P53780 Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL) (Beta-cystathionase) (Cysteine lyase) {Arabidopsis thaliana}	1	0	1	0	1	1
AT3G57560	aspartate/glutamate/uridylate kinase family protein, similar to acetylglutamate kinase from Porphyra purpurea (SP:P31595), Campylobacter jejuni (GI:6650364) contains Pfam profile PF00696: Amino acid kinase family	1	0	0	0	0	0
AT3G57610	adenylosuccinate synthetase (ADSS), identical to adenylosuccinate synthetase, chloroplast precursor (EC 6.3.4.4) (IMP-- aspartate ligase) (AdSS) (AMPSase) (Swiss-Prot:Q96529) (Arabidopsis thaliana)	1	1	1	1	1	1
AT3G57650	LPAT2__acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative, similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GI:4583544 from (Brassica napus)	1	0	0	1	1	1
AT3G58140	phenylalanyl-tRNA synthetase class IIc family protein, similar to phenylalanine-tRNA synthetase (Homo sapiens) GI:3983103; contains Pfam profile PF01409: tRNA synthetases class II core domain (F)	1	0	0	0	0	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G58750	CSY2__citrate synthase, glyoxysomal, putative, strong similarity to SP:P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase	1	1	0	0	1	1
AT3G59760	OASC_ATCS-C__cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to SP:Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}	1	1	1	1	1	1
AT3G59890	dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae}; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus	0	0	0	0	1	0
AT3G59970	MTHFR1__methylenetetrahydrofolate reductase 1 (MTHFR1), identical to methylenetetrahydrofolate reductase MTHFR1 (Arabidopsis thaliana) GI:5911425	1	0	0	1	0	0
AT3G60100	CSY5__citrate synthase, mitochondrial, putative, strong similarity to SP:Q43175 Citrate synthase, mitochondrial precursor {Solanum tuberosum}; contains Pfam profile PF00285: Citrate synthase	0	0	1	0	0	0
AT3G60750	transketolase, putative, strong similarity to transketolase 1 (Capsicum annuum) GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain	1	1	1	1	1	1
AT3G61130	glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8	1	0	1	0	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G61440	ARATH;BSAS3;1_ATCYSC1__encodes a cysteine synthase isomer. The isomer is however less effective in cysteine biosynthesis. It is involved in beta-cyanoalanine biosynthesis, a intermediate of cyanide detoxification pathway.	1	0	1	1	1	1
AT3G61580	delta-8 sphingolipid desaturase (SLD1), identical to delta-8 sphingolipid desaturase GI:3819710 from (Arabidopsis thaliana); contains Pfam profile PF00487: Fatty acid desaturase; contains Pfam profile PF00173: Heme/Steroid binding domain	0	0	0	0	1	0
AT3G62830	AUD1_UXS2_ATUXS2__NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains non-consensus CA donor splice site at exon 1 and TA acceptor splice site at exon 2	1	1	1	1	1	1
AT3G63410	APG1_VTE3__chloroplast inner envelope membrane protein, putative (APG1), similar to SP:P23525 37 kDa inner envelope membrane protein, chloroplast precursor (E37) {Spinacia oleracea}; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family	0	1	1	1	1	1
AT4G00490	beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative, similar to beta-amylase from SP:O64407 (Vigna unguiculata); contains Pfam profile PF01373: Glycosyl hydrolase family 14	1	1	0	0	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G00620	tetrahydrofolate dehydrogenase/cyclohydrolase, putative, similar to SP:P07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)) {Saccharomyces cerevisiae}; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain	1	1	0	0	0	0
AT4G01690	PPOX__protoporphyrinogen oxidase (PPOX), identical to SP:P55826	0	1	0	0	0	1
AT4G01850	S-adenosylmethionine synthetase 2 (SAM2), identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Arabidopsis thaliana) SWISS-PROT:P17562	1	1	1	0	1	0
AT4G02580	NADH-ubiquinone oxidoreductase 24 kDa subunit, putative, similar to NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Polypeptide II) (Swiss-Prot:P04394) (Bos taurus)	1	1	1	1	1	1
AT4G08790	nitrilase, putative, similar to nitrilase 1 (Mus musculus) GI:3228668; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family	0	0	0	0	1	0
AT4G09320	NDPK1__nucleoside diphosphate kinase 1 (NDK1), identical to identical to Nucleoside diphosphate kinase I (NDK I) (NDP kinase I) (NDPK I) (SP:P39207) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain;	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G10260	pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase	0	0	0	0	1	0
AT4G10320	isoleucyl-tRNA synthetase, putative / isoleucine--tRNA ligase, putative, similar to SP:P41252 Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS) (IRS) {Homo sapiens}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)	1	0	0	1	1	0
AT4G11010	NDPK3__nucleoside diphosphate kinase 3, mitochondrial (NDK3), identical to Nucleoside diphosphate kinase III, mitochondrial precursor (NDK III) (NDP kinase III) (NDPK III) (SP:O49203) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain;	1	1	1	1	1	1
AT4G11600	ATGPX6_LSC803_PHGPX__glutathione peroxidase, putative	1	0	0	0	0	0
AT4G11820	BAP1_MVA1__hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase, identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) (Arabidopsis thaliana)	1	0	0	1	1	0
AT4G11850	phospholipase D gamma 1 / PLD gamma 1 (PLDGAMMA1), identical to phospholipase D gamma 1 SP:Q9T053 from (Arabidopsis thaliana)	0	0	0	0	1	0
AT4G13430	aconitase family protein / aconitate hydratase family protein, contains Pfam profile PF00330: Aconitase family (aconitate hydratase	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G13780	methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, similar to methionyl-tRNA synthetase (Oryza sativa) GI:4091008; contains Pfam profiles PF00133: tRNA synthetases class I (I, L, M and V), PF01588: Putative tRNA binding domain	0	0	0	1	1	0
AT4G13930	SHM4__glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	1	1	1	1	1	1
AT4G13940	EMB1395_HOG1_SAHH_SAHH1__adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH), identical to SP:O23255 Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) {Arabidopsis thaliana}; strong similarity to SP:P50248 Adenosylhomocysteinase (EC 3.3.1.1) {Nicotiana sylvestris}	1	1	1	1	1	1
AT4G14430	enoyl-CoA hydratase/isomerase family protein, low siimilarity to 2-cyclohexenylcarbonyl CoA isomerase (Streptomyces collinus) GI:8133118, enoyl-CoA isomerase (Escherichia coli) GI:2764829; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein	0	0	0	0	0	1
AT4G14680	APS3__sulfate adenylyltransferase 3 / ATP-sulfurylase 3 (APS3), identical to ATP sulfurylase (APS3) (Arabidopsis thaliana) GI:1575327	0	0	0	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G14880	OASA1_CYTACS1__cysteine synthase / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase (OAS1), nearly identical to SP:P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.5-8) GI:6983573	1	1	1	0	1	1
AT4G16210	enoyl-CoA hydratase/isomerase family protein, similar to 3-hydroxybutyryl-CoA dehydratase (Crotonase) from Clostridium acetobutylicum (SP:P52046), FadB1x (enoyl-CoA hydratase) from Pseudomonas putida (GI:13310130); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein	1	0	0	0	0	0
AT4G16450	expressed protein	1	0	1	1	1	1
AT4G16760	ACX1_ATACX1__acyl-CoA oxidase (ACX1), identical to acyl-CoA oxidase (Arabidopsis thaliana) GI:3044214	1	1	1	1	1	0
AT4G18360	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) (Spinacia oleracea) SWISS-PROT:P05414	0	0	1	0	0	0
AT4G18440	adenylosuccinate lyase, putative / adenylosuccinase, putative, similar to SP:P25739 Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) {Escherichia coli}; contains Pfam profile PF00206: Lyase	1	0	0	0	1	0
AT4G19710	AK-HSDH_AK-HSDH II__bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative, similar to gb:X71364 (PIR:S46497) aspartate kinase / homoserine dehydrogenase from Arabidopsis thaliana	1	1	0	0	0	0

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Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G20460	NAD-dependent epimerase/dehydratase family protein, similar to UDP-galactose 4-epimerase from Cyamopsis tetragonoloba GI:3021357 (EMBL:AJ005082), Bacillus subtilis SP:P55180; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	1	0	0	0	0	0
AT4G21540	Encodes a putative sphingosine kinase (SphK) containing the five conserved domains (C1-C5) previously identified in SphKs.	1	0	0	0	0	0
AT4G22930	PYR4__dihydroorotase, mitochondrial / DHOase (PYR4), identical to SP:O04904 Dihydroorotase, mitochondrial precursor (EC 3.5.2.3) (DHOase) {Arabidopsis thaliana}	1	1	1	1	1	0
AT4G23100	GSH1_RML1_CAD2_GSH1__glutamate-cysteine ligase / gamma-glutamylcysteine synthetase (GSH1), identical to glutamate-cysteine ligase SP:P46309 from (Arabidopsis thaliana); contains Pfam profile: PF04107 glutamate-cysteine ligase family 2(GCS2). Two mRNA species are detected for this locus which differ in the length of their 5` UTRs. The ratio of the two species appears to be developmentally regulated. Both encode a protein that is localized to the chloroplast.	1	0	1	1	1	0
AT4G23590	aminotransferase class I and II family protein, similar to nicotianamine aminotransferase from Hordeum vulgare (GI:6498122, GI:6469087); contains Pfam profile PF00155 aminotransferase, classes I and II	1	1	0	0	0	1
AT4G23850	long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase, nearly identical to acyl-CoA synthetase (MF7P) from Brassica napus (gi:1617270)	0	0	0	0	0	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G23900	nucleoside diphosphate kinase 4 (NDK4), contains Pfam PF00334 : Nucleoside diphosphate kinase domain; identical to nucleoside diphosphate kinase 4 (GI:11990430) (Arabidopsis thaliana)	0	0	0	1	0	0
AT4G23920	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP:Q42605, Cyamopsis tetragonoloba GI:3021357 (AJ005082)	0	0	0	0	0	1
AT4G24620	PGI1_PGI__glucose-6-phosphate isomerase, putative, similar to glucose-6-phosphate isomerase (Spinacia oleracea) GI:3413511; contains Pfam profile PF00342: glucose-6-phosphate isomerase	1	1	1	1	1	1
AT4G25570	ACYB-2__cytochrome B561 family protein, contains Pfam domain, PF03188: Cytochrome b561	1	0	0	0	0	0
AT4G26300	EMB1027__arginyl-tRNA synthetase, putative / arginine--tRNA ligase, putative, similar to SP:P37880 Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) {Cricetulus longicaudatus}; contains Pfam profiles PF00750: arginyl-tRNA synthetase, PF03485: arginyl-tRNA synthetase N-terminal domain	1	0	0	1	1	0
AT4G26900	AT-HF_HISHF__imidazole glycerol phosphate synthase hisHF, chloroplast / IGP synthase / ImGPP synthase / IGPS, identical to SP:Q9SZ30 Imidazole glycerol phosphate synthase hisHF, chloroplast precursor (IGP synthase) {Arabidopsis thaliana}	1	1	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G26910	2-oxoacid dehydrogenase family protein, similar to SP:P36957 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) {Homo sapiens}; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme	1	1	1	0	1	1
AT4G26970	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative, strong similarity to SP:P49608 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Cucurbita maxima}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain	1	1	0	0	1	1
AT4G29010	AIM1__abnormal inflorescence meristem 1 / fatty acid multifunctional protein (AIM1), identical to gi:4337025; contains Pfam profiles PF02737 (3-hydroxyacyl-CoA dehydrogenase, NAD binding domain), PF00378 (enoyl-CoA hydratase/isomerase family protein), PF00725 (3-hydroxyacyl-CoA dehydrogenase)	1	1	1	0	1	1
AT4G29130	ATHXK1_GIN2_HXK1__hexokinase 1 (HXK1), identical to hexokinase 1 (Arabidopsis thaliana) Swiss-Prot:Q42525	1	1	1	1	1	1
AT4G29840	MTO2_TS__threonine synthase, chloroplast, identical to SP:Q9S7B5 Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS) {Arabidopsis thaliana}	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G30440	GAE1__NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	0	0	1	0	1	0
AT4G31180	aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative, similar to Aspartyl-tRNA synthetase (Aspartate--tRNA ligase) (AspRS) (Homo sapiens) GI:20178330	0	0	0	1	0	0
AT4G31500	CYP83B1_ATR4_RED1_RNT1_SUR2__cytochrome P450 83B1 (CYP83B1), Identical to Cytochrome P450 (SP:O65782)(Arabidopsis thaliana)	0	1	0	0	1	1
AT4G31810	enoyl-CoA hydratase/isomerase family protein, similar to CHY1 (gi:8572760); contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein	1	1	1	0	1	1
AT4G31990	ASP5_AAT3_ATAAT1__aspartate aminotransferase, chloroplast / transaminase A (ASP5) (AAT1), nearly identical to SP:P46248 Aspartate aminotransferase, chloroplast precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}	1	1	1	1	1	1
AT4G32410	CESA1_RSW1_CESA9_CESA09__cellulose synthase, catalytic subunit, putative, similar to cellulose synthase-1 (gi:9622874) and -2 (gi:9622876) from Zea mays	1	1	1	1	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G32520	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	1	1	1	0	1	0
AT4G33010	glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative, strong similarity to SP:P49361 Glycine dehydrogenase (decarboxylating) A, mitochondrial precursor (EC 1.4.4.2) {Flaveria pringlei}; contains Pfam profile PF02347: Glycine cleavage system P-protein	1	1	1	1	1	0
AT4G33580	carbonic anhydrase family protein / carbonate dehydratase family protein, similar to SP:P46512 Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase 1) {Flaveria linearis}; contains Pfam profile PF00484: Carbonic anhydrase	1	1	0	1	0	0
AT4G33680	AGD2__aminotransferase class I and II family protein, low similarity to Aromatic Aminotransferase from Pyrococcus horikoshii GP:14278621; contains Pfam profile PF00155 aminotransferase, classes I and II	1	1	1	1	1	1
AT4G34640	SQS1_ERG9__farnesyl-diphosphate farnesyltransferase 1 / squalene synthase 1 (SQS1), identical to SP:P53799 Farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase) {Arabidopsis thaliana}; non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana	1	1	1	0	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G35000	APX3__L-ascorbate peroxidase 3 (APX3), identical to ascorbate peroxidase 3 (Arabidopsis thaliana) GI:2444019, L-ascorbate peroxidase (Arabidopsis thaliana) gi:1523791:emb:CAA66926; similar to ascorbate peroxidase (Gossypium hirsutum) gi:1019946:gb:AAB52954	1	1	1	1	1	1
AT4G35090	CAT2__catalase 2, identical to catalase 2 SP:P25819, GI:17865693 from (Arabidopsis thaliana)	1	1	1	1	1	1
AT4G35260	IDH1__isocitrate dehydrogenase subunit 1 / NAD+ isocitrate dehydrogenase subunit 1, nearly identical to NAD+ dependent isocitrate dehydrogenase subunit 1 (Arabidopsis thaliana) GI:1766046	1	1	1	1	1	1
AT4G35630	PSAT__phosphoserine aminotransferase, chloroplast (PSAT), identical to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q96255)(Arabidopsis thaliana); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V	1	0	1	1	1	1
AT4G35790	ATPLDDELTA_PLDDELTA__phospholipase D delta / PLD delta (PLDDELTA), identical to phospholipase D delta SP: Q9C5Y0 from (Arabidopsis thaliana); supporting cDNA gi:11761141:dbj:AB031047.1:	0	1	1	0	1	1
AT4G35830	aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO), identical to SP:Q42560 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Arabidopsis thaliana}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain	1	0	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G36250	ALDH3F1__aldehyde dehydrogenase family protein, contais aldehyde dehydrogenase (NADP) family protein domain, Pfam:PF00171	1	1	0	0	0	0
AT4G36480	ATLCB1__aminotransferase class I and II family protein, similar to Serine palmitoyltransferase 1 (EC 2.3.1.50) from Homo sapiens (SP:O15269), Mus musculus (SP:O35704), Cricetulus griseus (SP:O54695)	1	0	1	0	1	0
AT4G37830	cytochrome c oxidase-related, contains weak similarity to cytochrome c oxidase polypeptide VIa-liver, mitochondrial precursor (EC 1.9.3.1) (Swiss-Prot:P10818) (Rattus norvegicus)	1	0	1	0	1	1
AT4G37870	phosphoenolpyruvate carboxykinase (ATP), putative / PEP carboxykinase, putative / PEPCK, putative, similar to phosphoenolpyruvate carboxykinase (Lycopersicon esculentum) GI:16950587, SP:Q9SLZ0 Phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK) {Zea mays}; contains Pfam profile PF01293: phosphoenolpyruvate carboxykinase	0	1	0	0	1	1
AT4G38800	phosphorylase family protein, contains weak similarity to Swiss-Prot:O51931 nucleosidase (Includes: 5`-methylthioadenosine nucleosidase (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase (Buchnera aphidicola)	0	0	0	1	1	0
AT4G39120	inositol monophosphatase family protein, low similarity to Mono-phosphatase (Streptomyces anulatus) GI:1045231; contains Pfam profile PF00459: Inositol monophosphatase family	1	0	0	0	1	0
AT4G39980	DHS1__2-dehydro-3-deoxyphosphoheptonate aldolase 1 / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 / DAHP synthetase 1 (DHS1), nearly identical to SP:P29965	1	1	1	0	1	0

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G01220	SQD2__UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2), identical to GI:20302857	1	0	0	0	0	0
AT5G03290	isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase (NAD+) (Nicotiana tabacum) GI:3021506	1	1	1	0	1	1
AT5G03300	ADK2__adenosine kinase 2 (ADK2), contains Pfam profile: PF00294 pfkB family carbohydrate kinase; identical to cDNA adenosine kinase 2 (ADK2) GI:12017763	0	0	0	1	1	0
AT5G03630	monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182	1	1	1	1	1	1
AT5G03860	malate synthase, putative, strong similarity to glyoxysomal malate synthase from Brassica napus (SP:P13244)	0	0	1	0	0	0
AT5G04590	SIR__sulfite reductase / ferredoxin (SIR), identical to sulfite reductase (Arabidopsis thaliana) GI:804953, GI:2584721	1	1	1	1	1	1
AT5G04960	pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase	1	0	0	0	0	0
AT5G05170	CESA3_ATCESA3_ATH-B_CEV1_IXR1__cellulose synthase, catalytic subunit (Ath-B), nearly identical to gi:2827143, cellulose synthase, catalytic subunit (Ath-B)	1	1	1	1	1	0
AT5G05690	CPD_CBB3_CYP90_CYP90A_CYP90A1_DWF3__cytochrome P450 90A1 (CYP90A1) (CYP90) (CPD), identical to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana)	0	0	0	0	1	0
AT5G07440	GDH2__glutamate dehydrogenase 2 (GDH2), identical to glutamate dehydrogenase 2 (GDH 2) (Arabidopsis thaliana) SWISS-PROT:Q38946	1	1	1	1	1	1

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G07990	TT7_CYP75B1_D501_F3`H__flavonoid 3`-monooxygenase / flavonoid 3`-hydroxylase (F3`H) / cytochrome P450 75B1 (CYP75B1) / transparent testa 7 protein (TT7), identical to SP:Q9SD85 Flavonoid 3`-monooxygenase (EC 1.14.13.21) (Flavonoid 3`-hydroxylase) (AtF3`H) (Cytochrome P450 75B1) (TRANSPARENT TESTA 7 protein) {Arabidopsis thaliana}; similar to gi:10334806, gi:10334808	0	0	1	0	0	0
AT5G08280	hydroxymethylbilane synthase / porphobilinogen deaminase, chloroplast / pre-uroporphyrinogen synthase, identical to SP:Q43316	1	0	0	1	1	0
AT5G08300	succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative, identical to SP:P53586 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, alpha chain) (SCS-alpha) {Arabidopsis thaliana}; strong similarity to SP:P13086 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor {Rattus norvegicus}; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain	1	1	1	1	1	1
AT5G08530	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial, putative, similar to NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) from {Homo sapiens} SP:P49821, {Bos taurus} SP:P25708, {Aspergillus niger} SP:Q92406; contains Pfam profile PF01512: Respiratory-chain NADH dehydrogenase 51 Kd subunit	1	1	1	1	1	1

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AT5G09420	chloroplast outer membrane translocon subunit, putative, similar to component of chloroplast outer membrane translocon Toc64 (Pisum sativum) GI:7453538; contains Pfam profiles PF01425: Amidase, PF00515: TPR Domain	0	0	0	0	1	0
AT5G09650	inorganic pyrophosphatase family protein, similar to SP:Q15181 Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate {Homo sapiens}; contains Pfam profile PF00719: inorganic pyrophosphatase	1	1	1	0	1	1
AT5G10100	trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase	0	0	0	1	0	0
AT5G10920	argininosuccinate lyase, putative / arginosuccinase, putative, similar to argininosuccinate lyase (Nostoc punctiforme) GI:7672743; contains Pfam profile PF00206: Lyase	1	1	0	0	1	0
AT5G11520	ASP3_YLS4_YSL4__aspartate aminotransferase, chloroplast / transaminase A (ASP3) (YLS4), identical to SP:P46644 Aspartate aminotransferase, chloroplast precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}; identical to cDNA YLS4 mRNA for aspartate aminotransferase (ASP3), partial cds GI:13122285	1	1	1	0	1	1
AT5G11770	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial, identical to NADH-ubiquinone oxidoreductase 20 kDa subunit mitochondrial (precursor) SP:Q42577 from (Arabidopsis thaliana); contains Pfam profile: PF01058 NADH ubiquinone oxidoreductase, 20 Kd subunit	1	1	1	1	1	1

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AT5G11880	diaminopimelate decarboxylase, putative / DAP carboxylase, putative, similar to diaminopimelate decarboxylase (Arabidopsis thaliana) GI:6562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain	1	1	1	1	1	1
AT5G12200	dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2), identical to dihydropyrimidine amidohydrolase (PYD2) (Arabidopsis thaliana) GI:28194047; similar to SP:Q9EQF5 Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP) {Mus musculus}; contains Pfam profile PF01979: Amidohydrolase family	1	0	0	0	0	0
AT5G13110	G6PD2__Encodes a plastidic glucose-6-phosphate dehydrogenase that is sensitive to reduction by DTT and whose mRNA is most highly expressed in root.	0	0	0	1	1	0
AT5G13280	AK-LYS1_AK__aspartate kinase, identical to aspartate kinase (Arabidopsis thaliana) GI:4376158	1	1	0	0	0	0
AT5G13640	ATPDAT__lecithin:cholesterol acyltransferase family protein / LACT family protein, similar to SP:P40345 Phospholipid:diacylglycerol acyltransferase (EC 2.3.1.158) (PDAT) {Saccharomyces cerevisiae}; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)	1	0	1	0	0	0
AT5G13930	CHS_ATCHS_TT4__chalcone synthase / naringenin-chalcone synthase, identical to SP:P13114	0	0	1	0	1	0
AT5G14060	CARAB-AK-LYS__aspartate kinase, lysine-sensitive, nearly identical to gi:2257743	1	0	0	0	0	0

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AT5G14220	protoporphyrinogen oxidase, putative, similar to protoporphyrinogen IX oxidase, mitochondrial (PPO II) from Nicotiana tabacum (SP:O24164), Glycine max, AB025102, Spinacia oleracea (GI:14349153); contains Pfam amine oxidase, flavin-containing domain (PF015930)	0	0	1	0	0	0
AT5G14950	glycosyl hydrolase family 38 protein, similar to alpha-mannosidase II SP:P27046 from (Mus musculus)	1	1	1	0	1	0
AT5G15490	UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	0	0	0	0	0	1
AT5G16230	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from Spinacia oleracea SP:P28645, Ricinus communis SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase	0	1	0	0	0	0
AT5G16390	CAC1_BCCP_BCCP1_CAC1A__biotin carboxyl carrier protein 1 (BCCP1), identical to biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor (Arabidopsis thaliana) gi:9759121:dbj:BAB09606	1	0	0	0	0	0

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AT5G16440	IPP1_IDI1__similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At1g79690.1); similar to isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Adonis palaestina] (GB:AAF29973.1); similar to isopentenyl pyrophosphate isomerase [Pueraria montana var. lobata] (GB:AAQ84167.1); contains InterPro domain Isopentenyl-diphosphate delta-isomerase (InterPro:IPR002667); contains InterPro domain NUDIX hydrolase (InterPro:IPR000086)	1	0	0	0	1	0
AT5G17310	UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative, strong similarity to SP:P19595 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) {Solanum tuberosum}; contains Pfam profile PF01704: UTP--glucose-1-phosphate uridylyltransferase	0	1	1	1	1	0
AT5G17530	phosphoglucosamine mutase family protein, low similarity to phosphoglucomutase/phosphomannomutase (Sphingomonas paucimobilis) GI:6103619; contains InterPro accession IPR006352: Phosphoglucosamine mutase	1	1	0	0	1	0
AT5G17920	ATMETS_ATMS1_ATCIMS__The protein underdoes thiolation following treatment with the oxidant tert-butylhydroperoxide.	1	1	1	1	1	1
AT5G18170	GDH1__glutamate dehydrogenase 1 (GDH1), identical to glutamate dehydrogenase 1 (GDH 1) (Arabidopsis thaliana) SWISS-PROT:Q43314	1	1	1	1	1	1
AT5G19440	similar to Eucalyptus gunnii alcohol dehydrogenase of unknown physiological function (GI:1143445), apple tree, PIR:T16995; NOT a cinnamyl-alcohol dehydrogenase	1	0	1	0	1	0

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Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G19550	ASP2_AAT2__aspartate aminotransferase, cytoplasmic isozyme 1 / transaminase A (ASP2), identical to SP:P46645 Aspartate aminotransferase, cytoplasmic isozyme 1 (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}	1	0	0	0	1	0
AT5G20960	AAO1_AO1_ATAO_ATAO1__aldehyde oxidase 1 (AAO1), identical to aldehyde oxidase AAO1 from Arabidopsis thaliana (gi:3172023) isoform contains a GA-donor splice site at intron 10	0	0	1	1	0	1
AT5G20980	ATMS3__5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative, strong similarity to SP:O50008 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) {Arabidopsis thaliana}; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent	1	0	0	0	0	0
AT5G23250	succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative, similar to SP:P36967 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, alpha chain) (SCS-alpha) {Dictyostelium discoideum}; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G23300	PYRD__dihydroorotate dehydrogenase, mitochondrial / dihydroorotate oxidase / DHOdehase (PYRD), nearly identical to SP:P32746 Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHOdehase) {Arabidopsis thaliana}; identical to cDNA pyrD mRNA for dihydroorotate dehydrogenase GI:16448	1	1	1	1	1	1
AT5G23670	LCB2_ATLCB2__serine C-palmitoyltransferase (LCB2), identical to serine palmitoyltransferase (Arabidopsis thaliana) GI:9309380; similar to serine palmitoyltransferase from Solanum tuberosum (GI:4995890), Homo sapiens (SP:O15270), Mus musculus (SP:P97363); contains Pfam profile PF00155: aminotransferase, classes I and II	1	0	0	0	1	0
AT5G26030	ferrochelatase I, identical to Swiss-Prot:P42043 ferrochelatase I, chloroplast/mitochondrial precursor (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme synthetase) (Arabidopsis thaliana)	1	1	1	0	1	0
AT5G26667	uridylate kinase / uridine monophosphate kinase / UMP kinase (PYR6), identical to uridylate kinase / UMP/CMP kinase SP:O04905 from (Arabidopsis thaliana)	1	0	0	1	0	0
AT5G26710	glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative, identical to gi:3435196	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G26780	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, strong similarity to SP:P50433 Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) {Solanum tuberosum}; contains Pfam profile PF00464: serine hydroxymethyltransferase	1	1	1	1	1	0
AT5G26830	threonyl-tRNA synthetase / threonine--tRNA ligase (THRRS), identical to SP:O04630 Threonyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS) {Arabidopsis thaliana}	1	0	0	1	1	0
AT5G27600	LACS7__AMP-binding protein, putative, similar to AMP-binding protein (MF39P) gi:1617274 from Brassica napus, long-chain-fatty-acid--CoA ligase - Brassica napus, EMBL:Z72152; contains Pfam AMP-binding enzyme domain PF00501	0	1	1	0	0	0
AT5G35360	CAC2__acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2), identical to acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2) (Arabidopsis thaliana) GI:1905876	1	1	1	1	1	1
AT5G35630	GS2_ATGSL1_GLN2__glutamine synthetase (GS2), identical to glutamine synthetase, chloroplast precursor (glutamate-- ammonia ligase, GS2) (Arabidopsis thaliana) SWISS-PROT:Q43127	1	1	1	1	1	1
AT5G36880	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative, similar to SP:P27550 (Escherichia coli) and gi:8439651 (Homo sapiens); contains Pfam AMP-binding enzyme domain PF00501	1	1	0	0	1	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G37510	EMB1467__NADH-ubiquinone dehydrogenase, mitochondrial, putative, similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial from Solanum tuberosum (SP:Q43644)	1	1	1	1	1	1
AT5G37830	hydantoinase/oxoprolinase family protein, contains Pfam profiles: PF02538 hydantoinase B/oxoprolinase, PF01968 hydantoinase/oxoprolinase, PF05378 hydantoinase/oxoprolinase N-terminal region	0	0	0	0	1	0
AT5G39320	UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	1	0	0	0	1	0
AT5G40650	SDH2-2__succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-2), nearly identical to mitochondrial succinate dehydrogenase iron-sulphur subunit (sdh2-2) (gi:12049600) from Arabidopsis thaliana	1	0	0	0	1	0
AT5G41670	6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G42650	AOS_CYP74A__allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A), identical to Allene oxide synthase, chloroplast precursor (Hydroperoxide dehydrase) (Cytochrome P450 74A) (SP:Q96242) {Arabidopsis thaliana}	1	1	0	0	0	0
AT5G42740	glucose-6-phosphate isomerase, cytosolic (PGIC), identical to SP:P34795 Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) {Arabidopsis thaliana}; contains Pfam profile PF00342: glucose-6-phosphate isomerase	0	0	0	1	1	0
AT5G43780	APS4__sulfate adenylyltransferase 4 / ATP-sulfurylase 4 (APS4), identical to ATP sulfurylase precursor (APS4) (Arabidopsis thaliana) GI:4633131	0	0	1	0	0	0
AT5G43940	alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase / GSH-FDH (ADHIII), identical to gi:1143388	1	0	1	0	1	0
AT5G46180	delta-OAT__ornithine aminotransferase, putative / ornithine--oxo-acid aminotransferase, putative, similar to SP:Q92413 Ornithine aminotransferase (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase) (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile PF00202: aminotransferase, class III	0	0	0	0	0	1
AT5G46290	KAS I__3-oxoacyl-(acyl-carrier-protein) synthase I, identical to Swiss-Prot:P52410 3-oxoacyl-(acyl-carrier-protein) synthase I, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase I) (KAS I) (Arabidopsis thaliana)	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G47770	FPS1__farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1) / FPP synthetase 1 / farnesyl diphosphate synthase 1, identical to SP:Q09152 Farnesyl pyrophosphate synthetase 1, mitochondrial precursor (FPP synthetase 1) (FPS 1) (Farnesyl diphosphate synthetase 1) (Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)) {Arabidopsis thaliana}	1	0	1	1	1	0
AT5G47780	glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8; strong similarity to unknown protein (emb:CAB71043.1)	1	0	0	0	0	0
AT5G47990	CYP705A5__cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max);	1	1	1	0	1	1
AT5G48000	CYP708A2__cytochrome P450 family protein, similar to steroid 22-alpha-hydroxylase; DWF4; CYP90B1 (GI:2935342) (Arabidopsis thaliana)	1	1	1	0	1	1
AT5G48010	ATPEN1_04C11__Encodes an oxidosqualene cyclase involved in the biosynthesis of thalianol, a tricyclic triterpenoid of unknown function.	1	1	1	0	1	0
AT5G48180	kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aberrant protein 1 (Cell polarity protein tea1) (SP:P87061) (Schizosaccharomyces pombe)	1	0	0	0	0	0
AT5G48230	EMB1276__acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative, strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) (Raphanus sativus) GI:1542941; contains InterPro accession IPR002155: Thiolase	1	0	1	1	1	0

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G48300	ADG1_APS1__glucose-1-phosphate adenylyltransferase small subunit 1 (APS1) / ADP-glucose pyrophosphorylase (ADG1), identical to SP:P55228	0	0	1	0	0	1
AT5G48880	PKT1_PKT2_KAT5__acetyl-CoA C-acyltransferase 1 / 3-ketoacyl-CoA thiolase 1 (PKT1), identical to 3-keto-acyl-CoA-thiolase 1 (Arabidopsis thaliana) GI:3169568	0	0	1	0	0	0
AT5G49030	tRNA synthetase class I (I, L, M and V) family protein, similar to SP:P41972 Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS) {Staphylococcus aureus}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)	0	1	0	0	0	0
AT5G49460	ACLB-2__ATP-citrate synthase, putative / ATP-citrate (pro-S-)-lyase, putative / citrate cleavage enzyme, putative, strong similarity to ATP:citrate lyase (Capsicum annuum) GI:13160653; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain	0	1	0	1	1	1
AT5G49720	KOR1_DEC_KOR_OR16PEP_RSW2__endo-1,4-beta-glucanase KORRIGAN (KOR) / cellulase (OR16pep), identical to endo-1,4-beta-D-glucanase KORRIGAN (Arabidopsis thaliana) GI:3978258; similar to endo-1,4-beta-D-glucanase; cellulase GI:5689613 from (Brassica napus); identical to cDNA cellulase (OR16pep) GI:1022806	1	0	1	0	1	0
AT5G49810	MMT__methionine S-methyltransferase, identical to methionine S-methyltransferase (Arabidopsis thaliana) GI:5733429	1	0	0	0	1	0
AT5G50370	adenylate kinase, putative, similar to adenylate kinase (ATP-AMP transphosphorylase) (Arabidopsis thaliana) SWISS-PROT:O82514	1	0	1	1	1	1

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G50850	pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2), identical to SP:Q38799 Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) {Arabidopsis thaliana}	1	1	1	1	1	1
AT5G51820	PGM_ATPGMP_PGM1_STF1__phosphoglucomutase, chloroplast (PGM) (PGMP) / glucose phosphomutase, identical to SP:Q9SCY0 Phosphoglucomutase, chloroplast precursor (EC 5.4.2.2) (Glucose phosphomutase) (PGM) {Arabidopsis thaliana}	0	0	0	0	1	0
AT5G52840	NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13Kd-B) (CI-13Kd-B) (Complex I subunit B13) (Swiss-Prot:Q63362) (Rattus norvegicus)	1	1	1	1	1	1
AT5G52920	pyruvate kinase, putative, similar to pyruvate kinase isozyme G, chloroplast precursor (Nicotiana tabacum) SWISS-PROT:Q40546	1	1	1	1	1	0
AT5G53460	GLT1__glutamate synthase (NADH), chloroplast, putative, similar to SP:Q03460 Glutamate synthase (NADH), chloroplast precursor (EC 1.4.1.14) (NADH- GOGAT) {Medicago sativa}	1	1	1	1	1	1
AT5G54810	TSB1_TRP2_TRPB__tryptophan synthase, beta subunit 1 (TSB1), identical to SP:P14671	0	1	0	0	0	0
AT5G55070	2-oxoacid dehydrogenase family protein, similar to SP:Q01205 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) {Rattus norvegicus}; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G56350	pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Nicotiana tabacum) SWISS-PROT:Q42954	1	0	0	0	0	0
AT5G56680	EMB2755__asparaginyl-tRNA synthetase 1, cytoplasmic / asparagine-tRNA ligase 1 (SYNC1), identical to SP:Q9SW96	0	0	0	0	1	0
AT5G57655	xylose isomerase family protein, contains similarity to Xylose isomerase (EC 5.3.1.5) (Swiss-Prot:P22842) (Thermoanaerobacter ethanolicus)	1	1	1	0	0	1
AT5G59290	UXS3_ATUXS3__UDP-glucuronic acid decarboxylase (UXS3), identical to UDP-glucuronic acid decarboxylase (Arabidopsis thaliana) GI:14595666; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; identical to cDNA UDP-glucuronic acid decarboxylase (UXS3) GI:14595665	0	1	0	0	0	1
AT5G61580	phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase	1	0	0	0	0	0
AT5G63310	NDPK2_NDPK1A_NDPK IA_NDPK IA IA__nucleotide diphosphate kinase II, chloroplast (NDPK2), identical to SP:O64903 Nucleoside diphosphate kinase II, chloroplast precursor (NDK II) (NDP kinase II) (NDPK II) (NDPK Ia) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain; contains Pfam profile PF00334: Nucleoside diphosphate kinase	0	0	1	0	0	0
AT5G63400	ADK1__adenylate kinase, identical to adenylate kinase (ATP-AMP transphosphorylase) (Arabidopsis thaliana) SWISS-PROT:O82514	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G63510	bacterial transferase hexapeptide repeat-containing protein, contains similarity to acetyltransferase; contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)	1	1	0	0	1	0
AT5G63570	GSA1__glutamate-1-semialdehyde 2,1-aminomutase 1 (GSA 1) / glutamate-1-semialdehyde aminotransferase 1 (GSA-AT 1), identical to GSA 1 (SP:P42799)	1	1	0	1	1	0
AT5G63890	ATHDH__histidinol dehydrogenase, putative / HDH, putative, strong similarity to SP:P24226 Histidinol dehydrogenase, chloroplast precursor (EC 1.1.1.23) (HDH) {Brassica oleracea var.capitata}; contains Pfam profile PF00815: histidinol dehydrogenase	1	0	1	1	1	0
AT5G64050	ATERS_ERS__glutamate-tRNA ligase family protein / glutamyl-tRNA synthetase family protein, similar to SP:P22250 from Bacillus subtilis, SP:P22249 from Bacillus stearothermophilus; contains Pfam tRNA synthetases class I (E and Q), catalytic domain PF00749	1	1	0	0	0	0
AT5G64300	ATGCH__similar to riboflavin biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At2g22450.1); similar to GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase [Lycopersicon esculentum] (GB:CAA05308.1); similar to putative riboflavin biosynthesis protein ribA [Oryza sativa (japonica cultivar-group)] (GB:XP_483002.1); contains InterPro domain GTP cyclohydrolase II (InterPro:IPR000926); contains InterPro domain 3,4-Dihydroxy-2-butanone 4-phosphate synthase (InterPro:IPR000422)	1	1	0	0	0	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G64740	CESA6_E112_IXR2_PRC1__cellulose synthase, catalytic subunit, putative, similar to gi:2827141 cellulose synthase catalytic subunit (Ath-A), Arabidopsis thaliana	1	0	0	0	1	0
AT5G64860	DPE1__4-alpha-glucanotransferase, putative / disproportionating enzyme, putative, similar to 4-alpha-glucanotransferase SP:Q06801 from (Solanum tuberosum)	1	0	0	0	0	1
AT5G65110	ACX2_ATACX2__acyl-CoA oxidase (ACX2), identical to acyl-CoA oxidase (Arabidopsis thaliana) GI:3044212	1	1	0	0	0	1
AT5G65720	cysteine desulfurase, mitochondrial (NIFS), identical to Cysteine desulfurase, mitochondrial precursor (SP:O49543) {Arabidopsis thaliana}; identical to cDNA GI:12656131; contains Pfam profile PF00266: aminotransferase, class V	1	1	0	0	1	0
AT5G65780	branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5), nearly identical to SP:Q9FYA6 Branched-chain amino acid aminotransferase 5, chloroplast precursor (EC 2.6.1.42) (Atbcat-5) {Arabidopsis thaliana}; contains Pfam profile: PF01063 aminotransferase class IV	1	1	0	0	1	0
AT5G65940	CHY1__3-hydroxyisobutyryl-coenzyme A hydrolase / CoA-thioester hydrolase (CHY1), identical to gi:8572760; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein	1	0	0	0	1	1
AT5G66120	3-dehydroquinate synthase, putative, similar to aroB (Neisseria gonorrhoeae)(GI:2661441); contains 3-dehydroquinate synthase domain PF01761	1	0	1	1	1	0
AT5G66280	GMD1__GDP-D-mannose 4,6-dehydratase, putative, strong similarity to GDP-D-mannose-4,6-dehydratase (Arabidopsis thaliana) GI:1764100	0	0	0	0	0	1

Supplementary Tables pertaining to Figure 2
Supplementary Table S8. Proteins of the root cellular proteome that are in the AraCyc Plant Metabolic Network

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G66510	bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)	1	1	1	1	1	1
AT5G66760	SDH1-1__succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial / flavoprotein subunit of complex II, identical to SP:O82663 Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) {Arabidopsis thaliana}	1	1	1	1	1	1
AT5G67590	FRO1__NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 21 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-21KD) (CI-21KD). (Swiss-Prot:P25711) (Neurospora crassa); contains Pfam PF04800: ETC complex I subunit conserved region	1	0	1	1	1	1
ATCG00490	RBCL__large subunit of RUBISCO.	0	0	1	0	0	0
ATCG00500	ACCD_ACCD__carboxytransferase beta subunit	1	1	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01040	0	0	0	0	1	0
AT1G01090	1	1	1	1	1	1
AT1G04170	1	0	0	0	1	0
AT1G04410	1	1	1	1	1	1
AT1G04690	0	0	0	0	1	0
AT1G04850	0	0	0	0	1	0
AT1G05260	0	0	0	1	0	0
AT1G06220	1	0	0	0	1	0
AT1G06950	1	1	1	1	1	1
AT1G07890	1	0	1	0	1	1
AT1G10270	1	0	0	0	1	0
AT1G10290	1	0	0	1	1	1
AT1G10840	0	0	0	1	1	0
AT1G11910	1	1	1	1	1	1
AT1G12840	1	1	1	1	1	1
AT1G13440	0	0	0	0	1	1
AT1G14320	0	0	0	1	0	0
AT1G15750	0	0	0	0	1	0
AT1G16890	0	0	0	0	1	0
AT1G19920	0	0	0	0	1	0
AT1G20090	0	0	0	0	1	0
AT1G20200	1	0	0	0	1	0
AT1G20450	0	0	0	0	0	1
AT1G20620	0	0	1	0	0	0
AT1G20630	0	0	0	0	0	1
AT1G20950	0	0	0	0	1	0
AT1G20960	1	0	0	0	1	1
AT1G21560	1	0	0	0	0	0
AT1G21750	1	1	1	1	1	1
AT1G22300	1	1	1	1	1	1
AT1G22450	1	1	1	0	1	0
AT1G22840	1	0	1	0	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G23190	1	0	0	0	1	1
AT1G23820	1	0	1	1	1	0
AT1G25490	1	0	0	0	1	0
AT1G27310	0	0	0	0	1	0
AT1G27390	1	0	0	0	1	0
AT1G27450	1	0	0	0	0	1
AT1G27970	0	0	0	0	1	0
AT1G29150	1	0	0	1	1	0
AT1G30400	1	1	0	0	1	1
AT1G31180	1	1	1	0	1	1
AT1G31817	1	1	1	0	1	0
AT1G32400	0	0	0	1	0	0
AT1G35160	1	0	1	1	1	0
AT1G35580	0	0	0	0	1	1
AT1G47128	0	0	1	0	0	0
AT1G47260	1	1	1	1	1	1
AT1G48030	1	1	1	1	1	1
AT1G50030	0	0	0	0	1	0
AT1G50940	0	1	0	0	0	0
AT1G51650	0	0	0	0	0	1
AT1G51710	0	0	0	0	1	0
AT1G51980	1	1	1	1	1	1
AT1G52070	1	1	0	0	1	1
AT1G52740	0	0	0	0	1	0
AT1G54010	1	1	1	0	1	1
AT1G54030	1	1	1	0	1	1
AT1G55490	1	0	0	1	1	0
AT1G56340	1	1	1	1	1	1
AT1G59820	1	0	0	0	1	0
AT1G62020	1	0	1	1	1	1
AT1G64520	1	0	0	0	1	0
AT1G65930	1	0	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G70310	1	0	0	1	0	0
AT1G72150	0	0	0	0	1	0
AT1G73590	0	0	0	0	1	0
AT1G75990	0	0	0	0	1	0
AT1G76030	0	0	0	0	0	1
AT1G78300	1	1	1	1	1	0
AT1G78570	0	0	1	0	1	0
AT1G78900	1	1	1	1	1	1
AT1G79530	1	1	1	1	1	1
AT1G79690	1	1	1	0	1	0
AT1G80670	1	0	0	0	0	0
AT2G01250	1	0	1	1	1	1
AT2G01470	1	1	1	0	1	1
AT2G02050	1	0	1	0	1	1
AT2G04030	1	1	1	1	1	0
AT2G04400	1	1	0	1	0	1
AT2G06050	1	1	1	0	1	1
AT2G13560	1	0	0	0	1	0
AT2G15620	1	0	1	0	1	1
AT2G16640	0	0	0	0	1	0
AT2G17790	0	0	0	0	1	0
AT2G18960	1	1	1	1	1	1
AT2G19080	1	0	0	1	1	1
AT2G19520	0	0	0	0	1	0
AT2G19940	1	1	1	0	1	1
AT2G20370	1	0	0	0	1	0
AT2G20580	1	0	1	1	1	0
AT2G20890	0	0	0	0	1	0
AT2G21170	1	1	1	1	1	1
AT2G21390	1	0	0	1	1	1
AT2G21620	0	0	0	0	1	0
AT2G21660	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G22780	1	1	1	1	1	1
AT2G26640	1	0	1	0	0	0
AT2G26730	0	0	0	0	1	0
AT2G27040	0	0	0	0	1	0
AT2G28000	1	1	1	1	1	1
AT2G28900	0	0	0	0	0	1
AT2G29960	1	0	1	0	1	1
AT2G30490	1	1	1	1	1	1
AT2G30870	1	1	1	1	1	0
AT2G30950	0	0	0	0	0	1
AT2G34480	1	0	1	1	1	1
AT2G34660	1	0	1	1	1	1
AT2G35720	1	0	1	0	1	0
AT2G36910	0	0	0	0	1	0
AT2G38230	0	0	0	0	0	1
AT2G38280	1	0	0	1	0	0
AT2G39630	1	0	0	0	0	1
AT2G42590	1	0	0	0	1	0
AT2G42810	0	0	0	0	1	0
AT2G43350	0	1	0	0	0	0
AT2G43750	1	1	1	1	1	1
AT2G44610	1	0	1	0	1	0
AT2G45140	1	0	0	0	1	0
AT2G45820	0	0	0	0	1	0
AT2G45960	1	1	1	1	1	1
AT2G46280	1	0	0	1	1	0
AT2G47730	1	1	0	1	1	1
AT3G01280	1	1	1	1	1	1
AT3G01290	1	0	0	0	0	0
AT3G02090	1	1	1	1	1	1
AT3G02230	1	1	1	1	1	1
AT3G02520	1	0	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G02880	1	0	1	0	1	0
AT3G03600	1	0	0	1	1	1
AT3G04940	0	0	0	0	1	0
AT3G05420	1	0	0	0	0	0
AT3G08530	1	0	1	0	1	1
AT3G09260	1	1	1	1	1	1
AT3G09440	1	0	1	1	1	0
AT3G09840	1	1	0	1	1	0
AT3G10380	0	0	0	0	1	0
AT3G10730	0	0	1	0	0	0
AT3G11070	1	0	1	0	1	1
AT3G11130	1	1	1	1	1	1
AT3G11730	1	0	0	0	0	0
AT3G13110	0	1	0	0	0	0
AT3G13300	0	0	0	0	1	0
AT3G13460	1	0	0	0	0	0
AT3G13580	1	0	0	1	0	0
AT3G13920	1	0	1	1	1	1
AT3G14220	1	1	0	0	0	1
AT3G15000	1	0	1	0	1	1
AT3G15730	1	0	1	1	1	1
AT3G15980	1	0	1	0	1	0
AT3G16420	1	1	1	0	1	1
AT3G16480	1	1	1	1	1	1
AT3G16640	1	0	1	1	1	1
AT3G17240	1	1	1	1	1	1
AT3G17970	1	1	0	1	0	0
AT3G19390	1	0	0	0	1	0
AT3G20000	1	1	1	1	1	1
AT3G20050	1	0	0	1	1	0
AT3G21160	0	1	0	0	0	0
AT3G22320	1	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G23820	1	1	1	0	1	0
AT3G24830	1	1	0	1	1	0
AT3G25230	0	0	1	1	1	0
AT3G27080	1	0	0	0	1	0
AT3G28860	0	0	1	1	1	0
AT3G32980	0	0	0	1	0	0
AT3G44110	0	0	0	0	1	0
AT3G48680	1	0	1	0	0	1
AT3G49080	1	0	0	0	1	0
AT3G49240	0	1	0	0	1	0
AT3G51160	1	0	0	0	0	1
AT3G51240	0	0	0	1	0	0
AT3G51260	1	1	1	1	1	1
AT3G52180	0	0	0	0	0	1
AT3G52300	1	1	1	0	1	1
AT3G52850	0	0	1	0	0	0
AT3G52930	1	1	1	1	1	1
AT3G52960	1	1	1	1	1	0
AT3G53420	0	0	1	1	0	1
AT3G53430	0	1	0	0	0	0
AT3G54660	1	0	1	0	0	0
AT3G54840	1	0	0	0	0	0
AT3G56070	1	1	1	1	1	1
AT3G56150	1	1	1	1	1	0
AT3G56460	1	1	0	0	1	1
AT3G57290	1	0	0	0	1	0
AT3G57560	1	0	0	0	0	0
AT3G59760	1	1	1	1	1	1
AT3G59920	1	0	1	1	1	0
AT3G60600	1	0	0	0	1	0
AT3G60750	1	1	1	1	1	1
AT3G62030	1	1	0	1	0	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G62830	1	1	1	1	1	1
AT3G63130	0	0	0	0	1	0
AT4G00570	1	1	1	0	1	1
AT4G01900	1	0	1	0	1	0
AT4G02510	1	1	1	1	0	0
AT4G03190	0	0	0	0	1	0
AT4G03560	1	0	1	1	1	1
AT4G05420	0	0	0	1	1	0
AT4G09000	1	1	1	1	1	1
AT4G09320	1	1	1	1	1	1
AT4G11420	0	0	0	1	1	0
AT4G11850	0	0	0	0	1	0
AT4G14880	1	1	1	0	1	1
AT4G16143	0	0	0	1	1	0
AT4G16760	1	1	1	1	1	0
AT4G17170	1	0	0	0	1	1
AT4G18830	0	0	0	0	1	0
AT4G19640	0	0	0	0	0	1
AT4G20850	1	1	1	1	1	1
AT4G20890	0	1	0	0	0	0
AT4G21105	0	0	0	1	0	0
AT4G23430	0	1	0	0	0	0
AT4G23630	0	0	0	0	0	1
AT4G23650	0	0	0	0	1	0
AT4G25630	1	0	0	1	1	0
AT4G26570	1	0	0	0	0	1
AT4G26610	0	0	0	1	0	0
AT4G27090	1	0	0	1	1	1
AT4G27160	0	0	0	0	1	0
AT4G27500	1	0	0	0	1	0
AT4G29130	1	1	1	1	1	1
AT4G29350	1	0	1	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G30190	1	1	1	0	1	1
AT4G31480	0	0	0	1	0	0
AT4G31500	0	1	0	0	1	1
AT4G32410	1	1	1	1	1	0
AT4G32470	1	1	1	0	1	1
AT4G32880	1	0	0	0	0	0
AT4G33650	0	0	0	0	1	0
AT4G34450	1	1	1	1	1	1
AT4G34670	0	0	0	1	1	0
AT4G35000	1	1	1	1	1	1
AT4G35090	1	1	1	1	1	1
AT4G36250	1	1	0	0	0	0
AT4G37870	0	1	0	0	1	1
AT4G38510	1	1	1	0	1	1
AT4G38800	0	0	0	1	1	0
AT4G39260	1	0	0	1	1	1
AT5G02500	1	1	1	1	1	1
AT5G04830	0	0	1	0	0	1
AT5G04990	1	1	0	0	0	0
AT5G05000	1	0	1	1	1	0
AT5G05170	1	1	1	1	1	0
AT5G06060	0	0	0	0	1	0
AT5G09420	0	0	0	0	1	0
AT5G10450	1	0	0	1	1	0
AT5G11670	1	0	0	0	1	1
AT5G13120	1	0	0	1	1	0
AT5G13930	0	0	1	0	1	0
AT5G15650	1	1	1	1	1	1
AT5G16050	1	0	1	1	1	0
AT5G16620	1	0	0	0	1	0
AT5G17190	0	1	0	0	0	1
AT5G18520	0	0	1	0	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G20290	1	1	0	1	1	0
AT5G22880	1	0	1	0	1	1
AT5G23540	1	0	0	0	1	0
AT5G26830	1	0	0	1	1	0
AT5G27600	0	1	1	0	0	0
AT5G27640	0	0	0	0	1	0
AT5G27850	1	0	1	1	1	1
AT5G35630	1	1	1	1	1	1
AT5G38480	1	1	0	1	1	1
AT5G38530	1	1	1	0	0	0
AT5G40810	1	1	1	1	1	1
AT5G40930	1	0	0	0	1	0
AT5G41600	1	1	1	0	0	1
AT5G41670	1	1	1	1	1	1
AT5G42020	1	1	1	1	1	1
AT5G42080	1	1	1	1	1	1
AT5G42650	1	1	0	0	0	0
AT5G42980	1	1	1	0	1	1
AT5G43060	1	1	1	1	1	1
AT5G43430	1	0	0	0	0	0
AT5G45390	0	1	0	0	0	0
AT5G46430	0	0	0	0	1	0
AT5G48810	1	1	1	0	1	1
AT5G50920	1	1	1	0	1	1
AT5G53560	1	1	1	1	1	1
AT5G56030	1	0	0	1	1	0
AT5G59880	1	0	1	0	0	1
AT5G62190	0	0	0	0	1	0
AT5G62740	0	0	0	0	0	1
AT5G63310	0	0	1	0	0	0
AT5G63510	1	1	0	0	1	0
AT5G63570	1	1	0	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G64350	0	0	0	0	0	1
AT5G64740	1	0	0	0	1	0
AT5G65430	1	0	0	1	1	0
AT5G65720	1	1	0	0	1	0
AT5G66530	1	0	1	0	0	0
At1g01040	0	0	0	0	1	0
At1g01090	1	1	1	1	1	1
At1g01820	1	0	0	0	1	1
At1g03860	1	1	1	1	1	1
At1g04410	1	1	1	1	1	1
At1g04690	0	0	0	0	1	0
At1g04810	1	0	0	0	0	0
At1g04850	0	0	0	0	1	0
At1g06220	1	0	0	0	1	0
At1g06950	1	1	1	1	1	1
At1g07890	1	0	1	0	1	1
At1g08830	1	0	1	0	1	1
At1g09270	1	0	0	0	1	0
At1g09760	1	0	0	0	1	0
At1g10270	1	0	0	0	1	0
At1g10290	1	0	0	1	1	1
At1g10840	0	0	0	1	1	0
At1g11860	1	1	1	1	1	1
At1g11910	1	1	1	1	1	1
At1g13440	0	0	0	0	1	1
At1g14320	0	0	0	1	0	0
At1g14620	1	0	0	0	1	0
At1g14810	1	1	1	1	1	1
At1g14850	1	0	0	0	1	0
At1g15750	0	0	0	0	1	0
At1g16890	0	0	0	0	1	0
At1g18540	1	0	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At1g19520	1	1	0	0	1	0
At1g20090	0	0	0	0	1	0
At1g20200	1	0	0	0	1	0
At1g20450	0	0	0	0	0	1
At1g20620	0	0	1	0	0	0
At1g20630	0	0	0	0	0	1
At1g20960	1	0	0	0	1	1
At1g21750	1	1	1	1	1	1
At1g22300	1	1	1	1	1	1
At1g22450	1	1	1	0	1	0
At1g23190	1	0	0	0	1	1
At1g23310	0	0	0	0	0	1
At1g23820	1	0	1	1	1	0
At1g24510	1	0	0	1	1	0
At1g25490	1	0	0	0	1	0
At1g26630	1	0	0	0	1	1
At1g27310	0	0	0	0	1	0
At1g27970	0	0	0	0	1	0
At1g29150	1	0	0	1	1	0
At1g30400	1	1	0	0	1	1
At1g32380	1	1	0	0	0	0
At1g32400	0	0	0	1	0	0
At1g35160	1	0	1	1	1	0
At1g35580	0	0	0	0	1	1
At1g35720	1	1	1	1	1	1
At1g43170	1	0	1	1	1	1
At1g47128	0	0	1	0	0	0
At1g47260	1	1	1	1	1	1
At1g48600	0	0	0	1	0	0
At1g48920	1	1	0	0	1	0
At1g49760	1	0	0	1	1	0
At1g50030	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At1g51650	0	0	0	0	0	1
At1g51710	0	0	0	0	1	0
At1g51980	1	1	1	1	1	1
At1g52070	1	1	0	0	1	1
At1g52360	1	0	1	0	1	0
At1g52740	0	0	0	0	1	0
At1g53310	1	0	0	1	1	0
At1g53750	0	0	0	1	1	0
At1g54030	1	1	1	0	1	1
At1g54270	0	0	0	0	1	1
At1g55490	1	0	0	1	1	0
At1g55890	1	1	1	0	1	0
At1g56070	1	1	1	1	1	1
At1g56110	1	1	0	1	1	0
At1g56340	1	1	1	1	1	1
At1g57720	1	1	1	1	1	1
At1g59610	1	1	1	1	1	1
At1g61870	1	1	0	0	1	0
At1g64090	1	1	1	1	1	1
At1g64520	1	0	0	0	1	0
At1g65020	0	0	0	0	1	0
At1g65260	0	0	0	0	0	1
At1g70310	1	0	0	1	0	0
At1g72150	0	0	0	0	1	0
At1g72730	0	0	1	0	0	0
At1g74030	1	1	0	1	0	1
At1g75990	0	0	0	0	1	0
At1g76010	1	1	0	0	0	0
At1g76030	0	0	0	0	0	1
At1g78300	1	1	1	1	1	0
At1g78380	1	1	0	1	1	1
At1g78900	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At1g79530	1	1	1	1	1	1
At1g79690	1	1	1	0	1	0
At1g79930	0	0	0	1	0	1
At1g80070	1	0	0	0	1	0
At1g80480	0	1	0	0	0	0
At1g80670	1	0	0	0	0	0
At2g01250	1	0	1	1	1	1
At2g01470	1	1	1	0	1	1
At2g04030	1	1	1	1	1	0
At2g05710	1	1	1	1	1	1
At2g13560	1	0	0	0	1	0
At2g16570	1	0	0	0	0	0
At2g16600	1	0	0	1	1	1
At2g16640	0	0	0	0	1	0
At2g18960	1	1	1	1	1	1
At2g19520	0	0	0	0	1	0
At2g20370	1	0	0	0	1	0
At2g20530	1	1	1	1	1	1
At2g20580	1	0	1	1	1	0
At2g20890	0	0	0	0	1	0
At2g21390	1	0	0	1	1	1
At2g21660	1	1	1	1	1	1
At2g22780	1	1	1	1	1	1
At2g23350	1	0	0	1	1	0
At2g26640	1	0	1	0	0	0
At2g27040	0	0	0	0	1	0
At2g28000	1	1	1	1	1	1
At2g28900	0	0	0	0	0	1
At2g29080	1	1	1	0	1	1
At2g29960	1	0	1	0	1	1
At2g30050	1	0	0	1	1	0
At2g30490	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At2g30950	0	0	0	0	0	1
At2g32730	0	0	0	0	1	0
At2g33210	1	1	1	1	1	1
At2g33340	0	0	0	0	1	0
At2g34660	1	0	1	1	1	1
At2g35040	1	1	1	0	1	0
At2g36130	1	0	0	0	1	0
At2g36910	0	0	0	0	1	0
At2g37690	1	1	1	1	1	0
At2g38280	1	0	0	1	0	0
At2g38750	1	1	1	0	1	1
At2g39630	1	0	0	0	0	1
At2g39800	0	0	1	0	0	0
At2g41620	1	0	0	0	1	0
At2g42590	1	0	0	0	1	0
At2g43350	0	1	0	0	0	0
At2g43710	1	1	1	1	1	0
At2g43750	1	1	1	1	1	1
At2g44350	1	1	1	1	1	1
At2g44530	1	0	1	0	0	0
At2g45740	0	0	0	0	0	1
At2g45820	0	0	0	0	1	0
At2g45960	1	1	1	1	1	1
At2g46280	1	0	0	1	1	0
At2g47470	1	1	1	1	1	1
At3g01280	1	1	1	1	1	1
At3g01290	1	0	0	0	0	0
At3g02090	1	1	1	1	1	1
At3g02230	1	1	1	1	1	1
At3g02520	1	0	1	1	1	1
At3g02530	1	0	0	1	1	0
At3g03600	1	0	0	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At3g03960	1	0	1	1	1	0
At3g04940	0	0	0	0	1	0
At3g05060	1	0	0	1	1	0
At3g05420	1	0	0	0	0	0
At3g07160	0	0	0	0	1	0
At3g08530	1	0	1	0	1	1
At3g08580	1	1	1	1	1	1
At3g09260	1	1	1	1	1	1
At3g09440	1	0	1	1	1	0
At3g09840	1	1	0	1	1	0
At3g10690	1	1	1	0	1	0
At3g10730	0	0	1	0	0	0
At3g11070	1	0	1	0	1	1
At3g11130	1	1	1	1	1	1
At3g11630	1	1	1	0	1	1
At3g11730	1	0	0	0	0	0
At3g11830	1	0	0	1	1	0
At3g12780	1	1	1	1	1	1
At3g13110	0	1	0	0	0	0
At3g13300	0	0	0	0	1	0
At3g13460	1	0	0	0	0	0
At3g13470	1	1	0	1	1	0
At3g13580	1	0	0	1	0	0
At3g13920	1	0	1	1	1	1
At3g14790	0	1	0	0	0	0
At3g14990	0	0	0	1	0	1
At3g15730	1	0	1	1	1	1
At3g15980	1	0	1	0	1	0
At3g16200	1	0	0	0	0	0
At3g16420	1	1	1	0	1	1
At3g16480	1	1	1	1	1	1
At3g17210	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At3g17970	1	1	0	1	0	0
At3g18000	0	0	1	0	0	1
At3g18190	1	0	0	1	1	0
At3g19390	1	0	0	0	1	0
At3g19760	0	0	0	1	0	0
At3g20050	1	0	0	1	1	0
At3g20390	1	0	1	0	1	1
At3g21140	1	1	0	1	1	0
At3g21160	0	1	0	0	0	0
At3g22310	1	1	0	0	1	0
At3g22320	1	0	0	0	1	0
At3g23820	1	1	1	0	1	0
At3g23990	1	1	1	1	1	1
At3g25230	0	0	1	1	1	0
At3g28860	0	0	1	1	1	0
At3g29360	1	0	0	0	0	0
At3g44110	0	0	0	0	1	0
At3g47930	1	1	1	0	1	1
At3g48680	1	0	1	0	0	1
At3g49240	0	1	0	0	1	0
At3g51160	1	0	0	0	0	1
At3g51260	1	1	1	1	1	1
At3g51550	0	0	1	0	0	0
At3g52180	0	0	0	0	0	1
At3g52850	0	0	1	0	0	0
At3g53230	0	0	0	1	0	0
At3g53430	0	1	0	0	0	0
At3g55010	1	0	0	1	1	1
At3g55440	1	1	1	1	1	1
At3g55610	0	0	1	0	0	0
At3g55760	0	1	0	0	0	0
At3g56150	1	1	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At3g56900	1	0	0	0	0	0
At3g57290	1	0	0	0	1	0
At3g57560	1	0	0	0	0	0
At3g59760	1	1	1	1	1	1
At3g60600	1	0	0	0	1	0
At3g60750	1	1	1	1	1	1
At3g61070	1	1	1	1	1	1
At3g62030	1	1	0	1	0	1
At3g62830	1	1	1	1	1	1
At3g63130	0	0	0	0	1	0
At3g63410	0	1	1	1	1	1
At4g00570	1	1	1	0	1	1
At4g01900	1	0	1	0	1	0
At4g02500	1	1	1	0	1	0
At4g02510	1	1	1	1	0	0
At4g03190	0	0	0	0	1	0
At4g05420	0	0	0	1	1	0
At4g09000	1	1	1	1	1	1
At4g09320	1	1	1	1	1	1
At4g11420	0	0	0	1	1	0
At4g13850	1	0	0	0	1	0
At4g14880	1	1	1	0	1	1
At4g16143	0	0	0	1	1	0
At4g16760	1	1	1	1	1	0
At4g18830	0	0	0	0	1	0
At4g19006	0	0	0	0	1	0
At4g19640	0	0	0	0	0	1
At4g20360	1	1	0	0	0	0
At4g20850	1	1	1	1	1	1
At4g20890	0	1	0	0	0	0
At4g23430	0	1	0	0	0	0
At4g23630	0	0	0	0	0	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At4g24190	1	1	1	1	1	1
At4g24280	1	1	1	1	1	0
At4g24820	1	0	1	1	1	0
At4g26570	1	0	0	0	0	1
At4g26610	0	0	0	1	0	0
At4g27160	0	0	0	0	1	0
At4g27500	1	0	0	0	1	0
At4g28510	1	1	1	1	1	1
At4g29130	1	1	1	1	1	1
At4g29350	1	0	1	0	1	0
At4g30190	1	1	1	0	1	1
At4g31480	0	0	0	1	0	0
At4g31500	0	1	0	0	1	1
At4g32410	1	1	1	1	1	0
At4g32470	1	1	1	0	1	1
At4g33650	0	0	0	0	1	0
At4g34450	1	1	1	1	1	1
At4g34670	0	0	0	1	1	0
At4g34870	1	1	1	1	1	1
At4g35000	1	1	1	1	1	1
At4g35090	1	1	1	1	1	1
At4g35830	1	0	1	1	1	1
At4g38740	1	0	1	1	1	1
At4g38800	0	0	0	1	1	0
At4g39260	1	0	0	1	1	1
At4g39690	1	1	1	0	1	0
At5g02500	1	1	1	1	1	1
At5g02530	0	0	0	0	1	0
At5g02870	1	0	0	0	1	0
At5g04830	0	0	1	0	0	1
At5g04990	1	1	0	0	0	0
At5g05000	1	0	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At5g05170	1	1	1	1	1	0
At5g05780	1	0	0	0	1	0
At5g08670	0	0	0	0	1	0
At5g09900	1	0	0	0	1	0
At5g10450	1	0	0	1	1	0
At5g13110	0	0	0	1	1	0
At5g13120	1	0	0	1	1	0
At5g13420	1	1	1	1	1	1
At5g13490	1	1	1	1	1	1
At5g15650	1	1	1	1	1	1
At5g15980	1	1	1	0	1	0
At5g16050	1	0	1	1	1	0
At5g16620	1	0	0	0	1	0
At5g17770	1	1	1	1	1	1
At5g19440	1	0	1	0	1	0
At5g20290	1	1	0	1	1	0
At5g20890	0	0	0	1	1	0
At5g22330	1	0	0	0	0	0
At5g22650	1	0	0	0	1	0
At5g22880	1	0	1	0	1	1
At5g23540	1	0	0	0	1	0
At5g24690	0	0	0	0	1	0
At5g26360	0	0	0	1	1	0
At5g26710	1	0	0	0	1	0
At5g26830	1	0	0	1	1	0
At5g26860	1	0	1	0	1	0
At5g27120	1	1	0	1	1	0
At5g27600	0	1	1	0	0	0
At5g27640	0	0	0	0	1	0
At5g27850	1	0	1	1	1	1
At5g28540	1	1	1	1	1	1
At5g35630	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At5g38480	1	1	0	1	1	1
At5g40480	1	1	1	1	1	1
At5g40770	1	1	1	1	1	1
At5g40810	1	1	1	1	1	1
At5g41600	1	1	1	0	0	1
At5g41670	1	1	1	1	1	1
At5g42020	1	1	1	1	1	1
At5g42080	1	1	1	1	1	1
At5g42650	1	1	0	0	0	0
At5g42740	0	0	0	1	1	0
At5g43060	1	1	1	1	1	1
At5g44120	0	1	0	0	1	0
At5g45390	0	1	0	0	0	0
At5g45620	1	0	0	0	1	0
At5g46430	0	0	0	0	1	0
At5g49910	0	0	0	1	1	0
At5g50920	1	1	1	0	1	1
At5g51200	1	0	0	0	1	0
At5g53480	1	0	1	1	1	0
At5g53560	1	1	1	1	1	1
At5g56030	1	0	0	1	1	0
At5g56500	1	1	1	1	1	1
At5g59880	1	0	1	0	0	1
At5g60960	1	0	0	0	1	0
At5g62270	1	0	0	0	0	0
At5g62390	1	0	0	1	1	1
At5g62740	0	0	0	0	0	1
At5g63310	0	0	1	0	0	0
At5g63510	1	1	0	0	1	0
At5g64350	0	0	0	0	0	1
At5g64740	1	0	0	0	1	0
At5g65430	1	0	0	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
At5g65700	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Interactors (No Neciprocal or Self-Interactions)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/ Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/ Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT5G42980	AT1G04410	1	1	1	0	1	1	1	1	1	1	1	1
AT2G16640	AT1G06950	0	0	0	0	1	0	1	1	1	1	1	1
AT4G02510	AT1G06950	1	1	1	1	0	0	1	1	1	1	1	1
AT5G42980	AT1G07890	1	1	1	0	1	1	1	0	1	0	1	1
AT3G14990	AT1G08830	0	0	0	1	0	1	1	0	1	0	1	1
AT3G56150	AT1G10840	1	1	1	1	1	0	0	0	0	1	1	0
AT4G11420	AT1G10840	0	0	0	1	1	0	0	0	0	1	1	0
AT2G41620	AT1G13440	1	0	0	0	1	0	0	0	0	0	1	1
AT2G41620	AT1G14850	1	0	0	0	1	0	1	0	0	0	1	0
AT2G20580	AT1G20200	1	0	1	1	1	0	1	0	0	0	1	0
AT2G41620	AT1G20620	1	0	0	0	1	0	0	0	1	0	0	0
AT4G09320	AT1G20620	1	1	1	1	1	1	0	0	1	0	0	0
AT4G09320	AT1G20630	1	1	1	1	1	1	0	0	0	0	0	1
AT1G06220	AT1G20960	1	0	0	0	1	0	1	0	0	0	1	1
AT5G42980	AT1G21750	1	1	1	0	1	1	1	1	1	1	1	1
AT1G73590	AT1G25490	0	0	0	0	1	0	1	0	0	0	1	0
AT2G20580	AT1G29150	1	0	1	1	1	0	1	0	0	1	1	0
AT4G30190	AT1G35160	1	1	1	0	1	1	1	0	1	1	1	0
AT1G21750	AT1G47128	1	1	1	1	1	1	0	0	1	0	0	0
AT2G41620	AT1G48920	1	0	0	0	1	0	1	1	0	0	1	0
AT2G20580	AT1G51650	1	0	1	1	1	0	0	0	0	0	0	1
AT2G20580	AT1G53750	1	0	1	1	1	0	0	0	0	1	1	0
AT4G23630	AT1G64090	0	0	0	0	0	1	1	1	1	1	1	1
AT2G20580	AT1G64520	1	0	1	1	1	0	1	0	0	0	1	0
AT5G42980	AT1G65930	1	1	1	0	1	1	1	0	1	1	1	1
AT1G23820	AT1G70310	1	0	1	1	1	0	1	0	0	1	0	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Interactors (No Neciprocal or Self-Interactions)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT2G36910	AT1G73590	0	0	0	0	1	0	0	0	0	0	1	0
AT2G38280	AT2G01470	1	0	0	1	0	0	1	1	1	0	1	1
AT5G42980	AT2G15620	1	1	1	0	1	1	1	0	1	0	1	1
AT5G05000	AT2G16640	1	0	1	1	1	0	0	0	0	0	1	0
AT5G42980	AT2G21170	1	1	1	0	1	1	1	1	1	1	1	1
AT4G01900	AT2G21390	1	0	1	0	1	0	1	0	0	1	1	1
AT2G20580	AT2G32730	1	0	1	1	1	0	0	0	0	0	1	0
AT1G35720	AT2G38750	1	1	1	1	1	1	1	1	1	0	1	1
AT5G42980	AT2G47730	1	1	1	0	1	1	1	1	0	1	1	1
AT2G38280	AT3G09840	1	0	0	1	0	0	1	1	0	1	1	0
AT5G04990	AT3G10730	1	1	0	0	0	0	0	0	1	0	0	0
AT2G41620	AT3G12780	1	0	0	0	1	0	1	1	1	1	1	1
AT3G53420	AT3G15730	0	0	1	1	0	1	1	0	1	1	1	1
AT4G01900	AT3G15980	1	0	1	0	1	0	1	0	1	0	1	0
AT3G09260	AT3G16420	1	1	1	1	1	1	1	1	1	0	1	1
AT1G21750	AT3G19390	1	1	1	1	1	1	1	0	0	0	1	0
AT1G27390	AT3G20000	1	0	0	0	1	0	1	1	1	1	1	1
AT2G19080	AT3G20000	1	0	0	1	1	1	1	1	1	1	1	1
AT5G09420	AT3G20000	0	0	0	0	1	0	1	1	1	1	1	1
AT3G20000	AT3G27080	1	1	1	1	1	1	1	0	0	0	1	0
AT1G73590	AT3G28860	0	0	0	0	1	0	0	0	1	1	1	0
AT1G47260	AT3G48680	1	1	1	1	1	1	1	0	1	0	0	1
AT1G20090	AT3G51550	0	0	0	0	1	0	0	0	1	0	0	0
AT5G42980	AT3G52960	1	1	1	0	1	1	1	1	1	1	1	0
AT1G27390	AT3G54660	1	0	0	0	1	0	1	0	1	0	0	0
AT2G19080	AT3G54660	1	0	0	1	1	1	1	0	1	0	0	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Interactors (No Neciprocal or Self-Interactions)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/ Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/ Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT3G27080	AT3G54660	1	0	0	0	1	0	1	0	1	0	0	0
AT5G09420	AT3G54660	0	0	0	0	1	0	1	0	1	0	0	0
AT5G40930	AT3G54660	1	0	0	0	1	0	1	0	1	0	0	0
AT3G57290	AT3G56150	1	0	0	0	1	0	1	1	1	1	1	0
AT5G27640	AT3G56150	0	0	0	0	1	0	1	1	1	1	1	0
AT1G10840	AT3G57290	0	0	0	1	1	0	1	0	0	0	1	0
AT5G27640	AT3G57290	0	0	0	0	1	0	1	0	0	0	1	0
AT3G13110	AT3G59760	0	1	0	0	0	0	1	1	1	1	1	1
AT5G42980	AT3G60750	1	1	1	0	1	1	1	1	1	1	1	1
AT2G41620	AT3G62030	1	0	0	0	1	0	1	1	0	1	0	1
AT5G42980	AT3G62030	1	1	1	0	1	1	1	1	0	1	0	1
AT1G62020	AT4G01900	1	0	1	1	1	1	1	0	1	0	1	0
AT3G57560	AT4G01900	1	0	0	0	0	0	1	0	1	0	1	0
AT2G46280	AT4G05420	1	0	0	1	1	0	0	0	0	1	1	0
AT3G53420	AT4G11850	0	0	1	1	0	1	0	0	0	0	1	0
AT3G13110	AT4G14880	0	1	0	0	0	0	1	1	1	0	1	1
AT2G20580	AT4G19006	1	0	1	1	1	0	0	0	0	0	1	0
AT2G41620	AT4G20360	1	0	0	0	1	0	1	1	0	0	0	0
AT1G06950	AT4G23430	1	1	1	1	1	1	0	1	0	0	0	0
AT2G41620	AT4G24190	1	0	0	0	1	0	1	1	1	1	1	1
AT2G20580	AT4G24820	1	0	1	1	1	0	1	0	1	1	1	0
AT2G18960	AT4G27500	1	1	1	1	1	1	1	0	0	0	1	0
AT1G76030	AT4G29130	0	0	0	0	0	1	1	1	1	1	1	1
AT3G01280	AT4G29130	1	1	1	1	1	1	1	1	1	1	1	1
AT1G78300	AT4G30190	1	1	1	1	1	0	1	1	1	0	1	1
AT4G01900	AT4G31480	1	0	1	0	1	0	0	0	0	1	0	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Interactors (No Neciprocal or Self-Interactions)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/ Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/ Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT4G01900	AT4G34450	1	0	1	0	1	0	1	1	1	1	1	1
AT4G09320	AT4G35090	1	1	1	1	1	1	1	1	1	1	1	1
AT4G26570	AT4G38800	1	0	0	0	0	1	0	0	0	1	1	0
AT2G21660	AT4G39260	1	1	1	1	1	1	1	0	0	1	1	1
AT2G41620	AT5G02500	1	0	0	0	1	0	1	1	1	1	1	1
AT4G02510	AT5G05000	1	1	1	1	0	0	1	0	1	1	1	0
AT4G32410	AT5G05170	1	1	1	1	1	0	1	1	1	1	1	0
AT2G20580	AT5G05780	1	0	1	1	1	0	1	0	0	0	1	0
AT2G20580	AT5G09900	1	0	1	1	1	0	1	0	0	0	1	0
AT3G09840	AT5G10450	1	1	0	1	1	0	1	0	0	1	1	0
AT4G35000	AT5G10450	1	1	1	1	1	1	1	0	0	1	1	0
AT3G02230	AT5G15650	1	1	1	1	1	1	1	1	1	1	1	1
AT2G42590	AT5G16050	1	0	0	0	1	0	1	0	1	1	1	0
AT1G06950	AT5G16620	1	1	1	1	1	1	1	0	0	0	1	0
AT4G23430	AT5G16620	0	1	0	0	0	0	1	0	0	0	1	0
AT2G20580	AT5G23540	1	0	1	1	1	0	1	0	0	0	1	0
AT1G10840	AT5G27640	0	0	0	1	1	0	0	0	0	0	1	0
AT5G26710	AT5G35630	1	0	0	0	1	0	1	1	1	1	1	1
AT5G42980	AT5G35630	1	1	1	0	1	1	1	1	1	1	1	1
AT2G41620	AT5G40480	1	0	0	0	1	0	1	1	1	1	1	1
AT3G20000	AT5G40930	1	1	1	1	1	1	1	0	0	0	1	0
AT4G23630	AT5G41600	0	0	0	0	0	1	1	1	1	0	0	1
AT5G62390	AT5G42020	1	0	0	1	1	1	1	1	1	1	1	1
AT1G59610	AT5G42080	1	1	1	1	1	1	1	1	1	1	1	1
AT1G48030	AT5G42980	1	1	1	1	1	1	1	1	1	0	1	1
AT1G21750	AT5G43060	1	1	1	1	1	1	1	1	1	1	1	1

Supplementary Tables pertaining to Figure 2
Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases
Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Interactors (No Neciprocal or Self-Interactions)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/ Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/ Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT1G50940	AT5G43430	0	1	0	0	0	0	1	0	0	0	0	0
AT2G20580	AT5G45620	1	0	1	1	1	0	1	0	0	0	1	0
AT5G16620	AT5G50920	1	0	0	0	1	0	1	1	1	0	1	1
AT2G41620	AT5G51200	1	0	0	0	1	0	1	0	0	0	1	0
AT3G05420	AT5G59880	1	0	0	0	0	0	1	0	1	0	0	1
AT1G47260	AT5G63510	1	1	1	1	1	1	1	1	0	0	1	0
AT4G32410	AT5G64740	1	1	1	1	1	0	1	0	0	0	1	0
AT5G05170	AT5G64740	1	1	1	1	1	0	1	0	0	0	1	0
AT5G42980	AT5G66530	1	1	1	0	1	1	1	0	1	0	0	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Self Interactors

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01040	0	0	0	0	1	0
AT1G10290	1	0	0	1	1	1
AT1G27450	1	0	0	0	0	1
AT1G29150	1	0	0	1	1	0
AT1G32400	0	0	0	1	0	0
AT1G35720	1	1	1	1	1	1
AT1G47260	1	1	1	1	1	1
AT2G13560	1	0	0	0	1	0
AT2G18960	1	1	1	1	1	1
AT2G21660	1	1	1	1	1	1
AT2G36910	0	0	0	0	1	0
AT2G38280	1	0	0	1	0	0
AT2G38750	1	1	1	0	1	1
AT2G39630	1	0	0	0	0	1
AT3G09260	1	1	1	1	1	1
AT3G09840	1	1	0	1	1	0
AT3G10730	0	0	1	0	0	0
AT3G13110	0	1	0	0	0	0
AT3G13300	0	0	0	0	1	0
AT3G52850	0	0	1	0	0	0
AT3G59760	1	1	1	1	1	1
AT3G62830	1	1	1	1	1	1
AT4G00570	1	1	1	0	1	1
AT4G01900	1	0	1	0	1	0
AT4G16760	1	1	1	1	1	0
AT4G20850	1	1	1	1	1	1
AT4G23630	0	0	0	0	0	1
AT4G29130	1	1	1	1	1	1
AT4G33650	0	0	0	0	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Self Interactors

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G39260	1	0	0	1	1	1
AT5G04990	1	1	0	0	0	0
AT5G42080	1	1	1	1	1	1
AT5G63310	0	0	1	0	0	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases
Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Reciprocal Interactors (only one pair was considered for the full list in columns I-V of this file)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT4G23430	AT1G06950	0	1	0	0	0	0	1	1	1	1	1	1
AT5G27640	AT1G10840	0	0	0	0	1	0	0	0	0	1	1	0
AT3G19390	AT1G21750	1	0	0	0	1	0	1	1	1	1	1	1
AT5G43060	AT1G21750	1	1	1	1	1	1	1	1	1	1	1	1
AT1G70310	AT1G23820	1	0	0	1	0	0	1	0	1	1	1	0
AT3G20000	AT1G27390	1	1	1	1	1	1	1	0	0	0	1	0
AT2G38750	AT1G35720	1	1	1	0	1	1	1	1	1	1	1	1
AT5G63510	AT1G47260	1	1	0	0	1	0	1	1	1	1	1	1
AT5G43430	AT1G50940	1	0	0	0	0	0	0	1	0	0	0	0
AT5G42080	AT1G59610	1	1	1	1	1	1	1	1	1	1	1	1
AT3G28860	AT1G73590	0	0	1	1	1	0	0	0	0	0	1	0
AT4G29130	AT1G76030	1	1	1	1	1	1	0	0	0	0	0	1
AT4G27500	AT2G18960	1	0	0	0	1	0	1	1	1	1	1	1
AT3G20000	AT2G19080	1	1	1	1	1	1	1	0	0	1	1	1
AT4G39260	AT2G21660	1	0	0	1	1	1	1	1	1	1	1	1
AT4G05420	AT2G46280	0	0	0	1	1	0	1	0	0	1	1	0
AT4G29130	AT3G01280	1	1	1	1	1	1	1	1	1	1	1	1
AT5G10450	AT3G09840	1	0	0	1	1	0	1	1	0	1	1	0
AT3G59760	AT3G13110	1	1	1	1	1	1	0	1	0	0	0	0
AT4G14880	AT3G13110	1	1	1	0	1	1	0	1	0	0	0	0
AT3G27080	AT3G20000	1	0	0	0	1	0	1	1	1	1	1	1
AT5G40930	AT3G20000	1	0	0	0	1	0	1	1	1	1	1	1
AT4G01900	AT3G57560	1	0	1	0	1	0	1	0	0	0	0	0
AT5G05000	AT4G02510	1	0	1	1	1	0	1	1	1	1	0	0
AT5G41600	AT4G23630	1	1	1	0	0	1	0	0	0	0	0	1
AT5G05170	AT4G32410	1	1	1	1	1	0	1	1	1	1	1	0

Supplementary Tables pertaining to Figure 2

Supplementary Table S9. Proteins of the root cellular proteome that are also found in The Arabidopsis Information Resource (TAIR) and BioGRID databases

Proteins of the Root Cellular Proteome found in TAIR and BioGRID databases

TAIR and BioGRID Reciprocal Interactors (only one pair was considered for the full list in columns I-V of this file)

Interactor A Locus	Interactor B Locus	A Root Hairs (COBL9)	A Non-Hair Epidermis (WER)	A Cortex (CORTEX)	A Endodermis/ Quiescent (SCR)	A Vasculature (WOL)	A Columella (PET111)	B Root Hairs (COBL9)	B Non-Hair Epidermis (WER)	B Cortex (CORTEX)	B Endodermis/ Quiescent (SCR)	B Vasculature (WOL)	B Columella (PET111)
AT5G64740	AT4G32410	1	0	0	0	1	0	1	1	1	1	1	0
AT5G10450	AT4G35000	1	0	0	1	1	0	1	1	1	1	1	1
AT5G64740	AT5G05170	1	0	0	0	1	0	1	1	1	1	1	0

Supplementary Tables pertaining to Figure 2
Supplementary Table S10. Pearson Correlation Coefficients (PCCs) of RNA and protein profiles of genomic features

Pearson Correlation Coefficient Between Root Cellular Proteome by GeLC-MS/MS Proteomics and Thresholded Microarrays of Dinneny et al. 2008

	Root Hairs (COBL9)	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Total Number of Proteins in the Root Cellular Proteome in this category**
Short CDS							
CDS≤800 bps	0.18	0.28	0.36	0.26	0.22	0.36	97
CDS≤900 bps	0.19	0.15	0.36	0.24	0.26	0.29	130
CDS≤1000 bps	0.18	0.18	0.35	0.24	0.24	0.31	177
CDS≤1100 bps	0.18	0.16	0.28	0.27	0.27	0.33	244
Long CDS							
CDS≥2500 bps	0.34	0.28	0.34	0.39	0.37	0.4	669
CDS≥3000 bps	0.37	0.26	0.38	0.36	0.38	0.4	579
CDS≥3500 bps	0.35	0.27	0.36	0.36	0.34	0.39	423
CDS≥4000 bps	0.37	0.3	0.37	0.36	0.3	0.41	248
CDS≥4500 bps	0.37	0.37	0.39	0.36	0.34	0.42	200
CDS≥5000 bps	0.42	0.42	0.41	0.41	0.36	0.39	172
CDS≥5500 bps	0.39	0.33	0.36	0.46	0.34	0.43	108
Short 3'UTRs							
3'UTR≤150 bps	0.31	0.25	0.38	0.38	0.24	0.42	185
3'UTR≤175 bps	0.3	0.21	0.37	0.29	0.26	0.38	337
3'UTR≤200 bps	0.3	0.2	0.33	0.34	0.26	0.37	559
Long 3'UTRs							
3'UTR≥300 bps	0.33	0.35	0.36	0.4	0.38	0.42	464
3'UTR≥350 bps	0.33	0.44	0.37	0.45	0.36	0.43	252
3'UTR≥400 bps	0.49	0.54	0.44	0.48	0.46	0.46	145

Supplementary Table S11. Peptide-level annotated quantitative output from label-free proteomics using peak integration. Tranche hash: CeUzpnLVCqXrNWTg1/6JY4R2t15IfV1pKCkaX2yMVqYtEck6tedT5cKhlT00y+NjM75q3a5KREfWBTMQJgD30zh4WQAAAAAAAAD+g==

These raw data have been uploaded for public release and access at the Proteome Commons and are found at www.proteomecommons.org/tranche under the project "The Protein Expression Landscape of the *Arabidopsis* Root". The data files for Supplementary Table S11, which contain peptide-level data output from label-free proteomics using peak integration of the six cell types (root hairs, non-hair epidermis, cortex, endodermis/quiescent center, vasculature, columella) and whole roots that were isolated by FACS, are found at Proteome Commons under the aforementioned project title and are accessible with the following Tranche hash:

2vxeLdEgJYUtGS1qbaktSbd1JuYRLQAHeB3YfAeF+F/ZfEiZwzE2ctZqD76OcvsyuTHRXEWyWvO4KbhVIZYZHj36TEEAAAAAAAADxQ==

All encryption at the tranche repository should be removed, but if a passphrase is requested, it is 'arabidopsis'.

Supplementary Table S11 can also be found at the Duke Genome Express Repository at the following:

https://discovery.genome.duke.edu/express/resources/2010/Final_Supplementary_Table_S11.xls

Supplementary MS/MS Spectra of Supplementary Table S11:

Data-dependent acquisition (DDA) MS/MS spectra that were used to generate the peptide-level quantitative output mentioned above have been uploaded in a Scaffold 3 (.sf3) file to www.proteomecommons.org/tranche under the project "The Protein Expression Landscape of the *Arabidopsis* Root", at the following hash:
X23FuCTH8OflWJlsmY6qRkJNQ1xRB/O054rp+yohmAuHn6nwn3zm5VmheEFVCYwlUKp4fn2DYtRfEjgpa33/dfRXveEAAAAAAAAExQ==

Data-independent acquisition (MSE) spectra were too large for Tranche upload and have thus been added to a Duke-based public, non-editable repository called Express. This data is available as a Scaffold 3 (.sf3) file at the following link: https://discovery.genome.duke.edu/express/resources/2010/Petricka_MSESpectra_LabelFreeSupplemental_Condensed.sf3

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G01090.1	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)	4.3035	4.3975	4.462	4.3879	4.262	4.2045
AT1G02780.1	| Symbols: EMB2386 | EMB2386 (EMBRYO DEFECTIVE 2386); structural constituent of ribosome | chr1:608120-609391 REVERSE	4.7852	4.6865	4.7801	5.0038	4.9457	4.9515
AT1G04040.1	| Symbols: | acid phosphatase class B family protein | chr1:1042563-1043818 REVERSE	4.5854	4.1787	3.4836	3.4918	4.2366	3.5197
AT1G04270.1	RPS15 (RIBOSOMAL PROTEIN S15); structural constituent of ribosome	4.3578	4.4281	4.3348	4.568	4.4208	4.4056
AT1G04410.1	malate dehydrogenase, cytosolic, putative	4.9808	4.9913	5.2186	5.3315	5.2178	5.4524
AT1G04430.1	dehydration-responsive protein-related	4.2382	4.3564	4.3535	4.3056	4.0263	3.9485
AT1G04480.1	60S ribosomal protein L23 (RPL23A)	4.5462	4.4302	4.4987	4.8039	4.5807	4.4876
AT1G07660.1	histone H4	5.4627	5.6604	5.5348	5.4869	5.463	5.5973
AT1G07810.1	| Symbols: ATECA1, ACA3, ECA1 | ECA1 (CALCIUM-TRANSPORTING ATPASE 1, ENDOPLASMIC RETICULUM-TYPE); calcium-transporting ATPase | chr1:2416678-2420569 FORWARD	4.6557	4.5589	4.5623	4.3804	4.4823	4.2271
AT1G07890.3	Symbols: APX1, CS1 | APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase | chr1:2438005-2439349 FORWARD	4.2865	4.2887	4.4674	4.6124	4.4281	4.6162
AT1G07920.1	elongation factor 1-alpha / EF-1-alpha	5.7317	5.8537	5.9881	5.983	5.9425	5.8325
AT1G08830.1	Symbols: CSD1 | CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); superoxide dismutase | chr1:2827700-2829053 FORWARD; Duplicate proteins:	3.8208	3.8168	3.9022	3.9451	3.9459	4.3706

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	AT1G08830.2						
AT1G08880.1	| Symbols: | histone H2A, putative | chr1:2847147-2847679 REVERSE	4.7062	4.8711	4.4733	4.6059	4.5889	4.7366
AT1G09080.1	luminal binding protein 3 (BiP-3) (BP3)	3.8075	3.893	4.0949	4.0637	4.3407	4.4234
AT1G09210.1	calreticulin 2 (CRT2)	5.5183	5.3491	5.2665	5.2307	5.3066	5.3141
AT1G10760.1	Symbols: SEX1, SOP1, SOP, GWD1, GWD | SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase | chr1:3581210-3590043 REVERSE	4.0786	4.36	4.2025	4.0885	3.9743	5.2205
AT1G11580.1	pectin methylesterase, putative	2.7402	3.0167	4.5972	4.5721	3.9457	3.4316
AT1G11910.1	aspartyl protease family protein	5.0338	5.2292	4.9196	5.0226	5.0018	5.4009
AT1G12230.1	Symbols: | transaldolase, putative | chr1:4148050-4150708 FORWARD	4.1275	4.2259	4.4737	4.3449	4.2253	4.1231
AT1G12840.1	DET3 (DE-ETIOLATED 3)	4.8177	4.7421	4.7159	4.6478	4.6457	4.6319
AT1G13280.1	| Symbols: AOC4 | AOC4 (ALLENE OXIDE CYCLASE 4) | chr1:4547621-4548549 FORWARD	3.8655	4.0783	4.042	3.8541	3.7912	4.7924
AT1G13440.1	GAPC-2; glyceraldehyde-3-phosphate dehydrogenase	5.7341	5.7026	5.9401	6.0085	5.8597	6.076
AT1G14670.1	endomembrane protein 70, putative	4.8889	4.8576	4.8497	4.6575	4.6676	4.6831
AT1G14980.1	CPN10 (CHAPERONIN 10)	5.1199	4.973	4.876	4.8478	4.9295	4.7909
AT1G15690.1	AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase	5.4904	5.5383	5.6253	5.4745	5.4197	5.3664
AT1G15930.2	40S ribosomal protein S12 (RPS12A)	4.9478	4.8987	5.0684	5.2023	5.0841	4.9229
AT1G16030.1	HSP70B (heat shock protein 70B); ATP binding	4.4988	4.482	4.6051	4.4895	4.4756	4.3266
AT1G16300.1	GAPCP-2; glyceraldehyde-3-phosphate dehydrogenase	4.4686	4.2944	4.0976	4.1043	4.2884	4.2691
AT1G16920.1	Symbols: RAB11, ATRABA1B | ATRABA1B (ARABIDOPSIS RAB GTPASE HOMOLOG A1B); GTP binding | chr1:5787489-5789147 REVERSE	4.8311	4.7451	4.7661	4.6551	4.6637	4.6822

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G18080.1	ATARCA (Arabidopsis thaliana Homolog of the Tobacco ArcA); nucleotide binding	5.273	5.2574	5.4381	5.6562	5.5971	5.3821
AT1G18540.1	60S ribosomal protein L6 (RPL6A)	4.8398	4.7961	4.8875	5.0494	5.0199	4.8908
AT1G20260.1	Symbols: | hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism | chr1:7016971-7020290 FORWARD	5.6748	5.5842	5.6299	5.4609	5.4978	5.5632
AT1G20440.1	Symbols: COR47, RD17 | COR47 (COLD-REGULATED 47) | chr1:7084722-7085664 REVERSE	4.2005	4.367	4.3168	4.4418	4.6026	5.8538
AT1G20450.1	| Symbols: LTI45, ERD10, LTI29 | ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10) | chr1:7088225-7089097 REVERSE	3.8053	4.2575	4.06	4.1044	4.0586	5.5525
AT1G20840.1	TMT1 (TONOPLAST MONOSACCHARIDE TRANSPORTER1); carbohydrate transporter/ nucleoside transporter/ sugar porter	4.3762	4.2011	4.7365	4.3945	4.1351	4.1164
AT1G21750.1	ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	4.8076	4.5485	4.6275	4.4241	4.3814	4.4547
AT1G21750.2	ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	6.1452	5.8932	5.9708	5.8034	5.8671	5.8633
AT1G22300.1	GRF10 (GENERAL REGULATORY FACTOR 10); protein phosphorylated amino acid binding	4.0811	4.1499	4.3115	4.4045	4.3411	4.5578
AT1G22410.1	| Symbols: | 2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase,	4.2109	4.2561	4.5771	4.3643	4.3295	3.9828

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	putative / DAHP synthetase, putative | chr1:7912109-7914731 FORWARD						
AT1G22780.1	| Symbols: RPS18A, PFL1, PFL | PFL (POINTED FIRST LEAVES); structural constituent of ribosome | chr1:8067979-8069152 FORWARD	3.7662	3.8216	3.61	3.9144	3.1877	3.8395
AT1G23190.1	| Symbols: | phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative | chr1:8219935-8224175 FORWARD	4.177	4.2886	4.3981	4.2977	4.4128	4.8801
AT1G24180.1	IAR4 (IAA-conjugate-resistant 4); pyruvate dehydrogenase (acetyl-transferring)	4.9549	4.8369	4.7678	4.6518	4.7952	4.7708
AT1G24360.1	3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase	4.9346	4.9776	5.1476	5.1216	4.9667	4.8718
AT1G26630.1	| Symbols: FBR12 | FBR12 (FUMONISIN B1-RESISTANT12); translation initiation factor | chr1:9205955-9207085 FORWARD	4.5074	4.6234	4.7433	4.8167	4.8245	4.779
AT1G26850.1	dehydration-responsive family protein	4.654	4.4763	4.7452	4.6327	4.6664	4.2054
AT1G27400.1	Symbols: | 60S ribosomal protein L17 (RPL17B) | chr1:25262209-25263627 FORWARD	4.6769	4.7217	4.9164	4.956	4.897	4.7943
AT1G30120.1	PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyruvate dehydrogenase (acetyl-transferring)	5.0366	5.0207	5.2325	5.1892	5.0169	4.7865
AT1G30580.1	GTP binding	4.4272	4.5201	4.7378	4.8076	4.7916	4.6639
AT1G31812.1	| Symbols: ACBP | ACBP (ACYL-COA-BINDING PROTEIN); acyl-CoA binding | chr1:11411113-11412080 REVERSE	4.5534	4.6605	4.7536	4.9337	4.8305	5.1815
AT1G32900.1	Symbols: | starch synthase, putative |	2.6594	2.8141	3.0109	2.099	2.5071	4.7327

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	chr1:11920582-11923506 REVERSE						
AT1G33120.1	60S ribosomal protein L9 (RPL90B)	5.58	5.5641	5.5941	5.7217	5.6838	5.5383
AT1G34430.1	EMB3003 (EMBRYO DEFECTIVE 3003); dihydrolipoyllysine-residue acetyltransferase	4.4488	4.4485	4.6788	4.6342	4.4348	4.4431
AT1G35720.1	ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding	5.1761	4.9839	4.829	4.8852	5.0041	5.1259
AT1G42960.1	| Symbols: | expressed protein localized to the inner membrane of the chloroplast. | chr1:16128303-16129520 FORWARD	4.588	4.7268	4.6918	4.6679	4.4964	4.6045
AT1G43170.1	ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	4.9834	4.9605	5.1265	5.2511	5.2427	4.9975
AT1G47260.1	APFI; carbonate dehydratase	5.4354	5.446	5.3547	5.3266	5.281	5.2841
AT1G47420.1	Identical to Unknown protein At1g47420, mitochondrial precursor [Arabidopsis Thaliana] (GB:Q9SX77); similar to APFI, carbonate dehydratase [Arabidopsis thaliana] (TAIR:AT1G47260.1); similar to unknown [Hordeum vulgare subsp. vulgare] (GB:AAL77110.1)	4.4087	4.4561	4.4324	4.1966	4.2093	4.4842
AT1G48830.1	| Symbols: | 40S ribosomal protein S7 (RPS7A) | chr1:18063522-18064603 REVERSE	4.2862	4.3724	4.4587	4.5592	4.5616	4.5192
AT1G48920.1	| Symbols: ATNUC-L1, PARL1 | nucleolin, putative | chr1:18101854-18105090 FORWARD	4.7892	4.8517	4.6408	4.9105	4.9319	4.5352
AT1G50430.1	DWF5 (DWARF 5); sterol delta7 reductase	4.5633	4.5316	4.5933	4.5155	4.3795	4.1361
AT1G51980.1	mitochondrial processing peptidase alpha subunit, putative	5.5132	5.509	5.4267	5.3551	5.3279	5.3627

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G52070.1	| Symbols: | jacalin lectin family protein | chr1:19368809-19370569 REVERSE	4.8357	5.2877	3.9004	4.0216	3.9628	4.991
AT1G52360.1	Symbols: | coatomer protein complex, subunit beta 2 (beta prime), putative | chr1:19499282-19505397 FORWARD	4.1953	4.1769	4.3176	4.2435	4.2994	4.249
AT1G52670.1	Symbols: | biotin/lipoyl attachment domain-containing protein | chr1:19615119-19617420 REVERSE	3.9387	3.9012	4.0656	4.0162	3.8274	3.5629
AT1G53240.1	malate dehydrogenase (NAD), mitochondrial	5.5681	5.5015	5.3211	5.3758	5.4696	5.5697
AT1G53310.1	ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); phosphoenolpyruvate carboxylase	3.7746	3.871	3.9123	4.1441	3.7979	4.3982
AT1G54000.1	myrosinase-associated protein, putative	5.8383	6.0064	5.255	5.054	5.4244	5.8615
AT1G54010.1	myrosinase-associated protein, putative	5.0316	5.6632	4.4402	4.5121	4.5837	4.8613
AT1G54580.1	| Symbols: ACP2 | ACP2 (ACYL CARRIER PROTEIN 2) | chr1:20393239-20394437 FORWARD	5.2755	5.2605	5.457	5.4045	5.3149	5.1876
AT1G55060.1	UBQ12 (UBIQUITIN 12)	5.146	5.2463	5.3233	5.4076	5.3788	5.4059
AT1G55490.1	CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding	5.1988	5.2003	5.2831	5.1802	5.173	5.0126
AT1G56070.1	LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding	5.7203	5.7486	5.8758	5.9831	5.9424	5.7818
AT1G56110.1	NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOLAR PROTEIN NOP56)	4.6603	4.7391	4.446	4.6407	4.7161	4.2451
AT1G56330.1	SAR1 (SECRETION-ASSOCIATED RAS); GTP binding	5.2853	5.1892	5.2897	5.2421	5.2243	5.2953

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G56340.2	CRT1 (CALRETICULIN 1); calcium ion binding	5.8892	5.7529	5.6947	5.6603	5.7033	5.7562
AT1G56410.1	ERD2/HSP70T-1 (EARLY-RESPONSIVE TO DEHYDRATION 2); ATP binding	4.8329	4.7919	4.7467	4.8083	4.7899	4.7104
AT1G57660.1	Symbols: | 60S ribosomal protein L21 (RPL21E) | chr1:21355567-21356364 FORWARD; Duplicate proteins: AT1G57860.1	4.6306	4.6292	4.7346	4.8694	4.8381	4.6452
AT1G57720.1	elongation factor 1B-gamma, putative / eEF-1B gamma, putative	4.8988	4.8729	5.0267	5.1038	5.0457	4.8692
AT1G58270.1	ZW9	5.174	4.743	4.3926	4.3824	4.6678	4.5733
AT1G61790.1	OST3/OST6 family protein	5.08	5.0412	4.9727	4.9127	4.893	4.822
AT1G62640.1	Symbols: KAS III | KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr1:23192502-23194737 FORWARD; Duplicate proteins: AT1G6	4.0512	4.1518	4.3773	4.2593	4.0923	4.2567
AT1G62660.1	| Symbols: | beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar | chr1:23203614-23207180 FORWARD	4.4684	4.2257	4.8381	4.3733	4.3117	4.2557
AT1G63940.1	monodehydroascorbate reductase, putative	5.3439	5.3014	5.3177	5.1887	5.2929	5.4642
AT1G64190.1	| Symbols: | 6-phosphogluconate dehydrogenase family protein | chr1:23829212-23830675 REVERSE	4.7168	4.6751	4.8689	4.703	4.682	4.7478
AT1G65930.1	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	5.0055	4.9722	5.3552	5.417	5.2747	5.2338
AT1G66270.2	beta-glucosidase (PSR3.2)	6.1169	5.9323	5.1801	5.1359	5.6453	5.4408

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G66280.1	glycosyl hydrolase family 1 protein	5.6261	5.7475	4.7866	4.7981	5.2722	5.6851
AT1G66580.1	60S ribosomal protein L10 (RPL10C)	5.2067	5.2206	5.3132	5.4638	5.4692	5.2873
AT1G67140.1	Symbols: SWEETIE | SWEETIE (SWEETIE); binding | chr1:25101016-25117372 REVERSE	4.1636	4.2337	4.1876	4.3219	4.4361	4.4564
AT1G70600.1	| Symbols: | 60S ribosomal protein L27A (RPL27aC) | chr1:26624831-26625271 REVERSE	4.5333	4.5272	4.5075	4.8645	4.7356	4.5807
AT1G70770.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23170.1); similar to Os01g0128400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041912.1); similar to hypothetical protein [Platanus x acerifolia] (GB:CAL07978.1); contains domain FAMI	5.6064	5.5481	5.5259	5.3838	5.4812	5.2712
AT1G72370.1	P40 (40S ribosomal protein SA); structural constituent of ribosome	4.9684	5.0681	5.0829	5.3146	5.2746	5.0359
AT1G74030.1	enolase, putative	4.9835	4.9961	5.1768	5.096	5.0235	4.9595
AT1G74050.1	60S ribosomal protein L6 (RPL6C)	5.1572	5.1037	5.2176	5.4179	5.4227	5.1736
AT1G76090.1	SMT3 (S-adenosyl-methionine-sterol-C-methyltransferase 3); S-adenosylmethionine-dependent methyltransferase	4.781	4.4459	5.1331	4.7999	4.4259	3.9332
AT1G77510.1	ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase	5.7392	5.5499	5.5126	5.3626	5.4307	5.6935
AT1G78300.1	GRF2 (GENERAL REGULATORY FACTOR 2); protein phosphorylated amino acid binding	4.1006	4.0907	4.3406	4.3361	4.3253	4.2465
AT1G78380.1	| Symbols: GST8, ATGSTU19 | ATGSTU19 (GLUTATHIONE TRANSFERASE 8); glutathione transferase | chr1:29491552-	4.1064	4.429	4.1469	4.2344	4.1681	5.1389

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	29492712 REVERSE						
AT1G78570.1	Symbols: RHM1, ROL1, ATRHM1 | RHM1 (RHAMNOSE BIOSYNTHESIS 1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic | chr1:29550110-29552207 FORWARD	4.3609	4.3431	4.4649	4.0542	4.3067	4.0217
AT1G78900.1	VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism	5.8624	5.7834	5.8111	5.6755	5.738	5.6665
AT1G79440.1	| Symbols: SSADH1, SSADH, ALDH5F1 | ALDH5F1 (SUCCINIC SEMIALDEHYDE DEHYDROGENASE); 3-chloroallyl aldehyde dehydrogenase/ succinate-semialdehyde dehydrogenase | chr1:29887418-29892168 REVERSE	4.3236	4.4096	4.4837	4.2941	4.2009	4.5889
AT1G79530.1	GAPCP-1; glyceraldehyde-3-phosphate dehydrogenase	5.1886	5.1927	5.2567	5.1289	5.1121	5.1624
AT1G79550.1	PGK (PHOSPHOGLYCERATE KINASE)	4.8457	4.8922	5.2159	5.2934	5.1916	5.1945
AT1G79930.1	Symbols: HSP91 | HSP91; ATP binding | chr1:30063924-30067067 REVERSE	3.7006	3.887	3.881	4.0282	4.0509	3.9498
AT2G01140.1	fructose-bisphosphate aldolase, putative	5.3412	5.3473	5.4567	5.3614	5.3324	5.3299
AT2G01250.1	60S ribosomal protein L7 (RPL7B)	5.0661	5.0365	5.1296	5.3206	5.2864	5.074
AT2G01720.1	ribophorin I family protein	5.335	5.3252	5.2619	5.2093	5.2754	5.2896
AT2G03120.1	signal peptide peptidase family protein	4.8033	4.7449	4.6511	4.5204	4.6408	4.7148
AT2G04030.1	CR88 (EMBRYO DEFECTIVE 1956); ATP binding	5.0074	5.0149	4.906	4.832	4.9329	4.8494
AT2G04390.1	Symbols: | 40S ribosomal protein S17 (RPS17A) | chr2:1527911-1528336 FORWARD	5.032	5.0923	5.056	5.1602	5.1261	4.9948
AT2G05710.1	| Symbols: | aconitate hydratase,	5.0683	4.9923	4.9377	4.8899	4.9529	5.073

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	cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141588-2146347 FORWARD						
AT2G05990.1	| Symbols: ENR1, MOD1 | MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase | chr2:2322873-2324864 FORWARD	4.7194	4.7455	4.9988	4.8283	4.6922	4.5987
AT2G07050.1	CAS1 (CYCLOARTENOL SYNTHASE 1)	4.0729	4.1524	4.3671	4.24	4.1678	4.0075
AT2G07698.1	ATP synthase alpha chain, mitochondrial, putative	4.5565	4.4797	3.9055	3.9364	4.2092	4.1492
AT2G07707.1	Identical to Hypothetical protein ymf19 (ORFB) (YMF19) [Arabidopsis Thaliana] (GB:P93303;GB:Q4PL89); similar to Hypothetical protein ymf19 (ORF158) (GB:Q03152); contains InterPro domain ATPase, F0 complex, subunit 8, mitochondrial, plant; (InterPro:	4.6499	4.6902	4.6341	4.5405	4.5812	4.5868
AT2G14720.1	VSR-2 (Vacuolar sorting receptor 2); calcium ion binding / peptidase	4.4456	4.5842	4.5067	4.5217	4.3922	4.4662
AT2G16360.1	Symbols: | 40S ribosomal protein S25 (RPS25A) | chr2:7076713-7077366 REVERSE	4.8567	4.9148	5.0151	5.1212	5.0741	4.8965
AT2G16600.1	ROC3 (rotamase CyP 3); peptidyl-prolyl cis-trans isomerase	4.613	4.7662	4.7644	4.8798	4.8591	5.1447
AT2G17720.1	| Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr2:7704595-7706256 FORWARD	5.0021	4.6061	4.6291	4.5376	4.6379	4.2928
AT2G18020.1	EMB2296 (EMBRYO DEFECTIVE 2296); structural constituent of ribosome	5.2426	5.2352	5.2954	5.422	5.4429	5.1936
AT2G18230.1	Symbols: AtPPa2 | AtPPa2	3.2731	3.4755	3.3495	3.6272	3.6346	4.5709

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	(Arabidopsis thaliana pyrophosphorylase 2); inorganic diphosphatase/ pyrophosphatase | chr2:7932139-7933560 REVERSE						
AT2G19750.1	| Symbols: | 40S ribosomal protein S30 (RPS30A) | chr2:8522119-8522888 FORWARD	4.5115	4.4117	4.6312	4.8641	4.8824	4.5344
AT2G20360.1	catalytic/ coenzyme binding	4.8233	4.8873	4.8168	4.7202	4.778	4.7487
AT2G20420.1	succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative	5.493	5.3984	5.3078	5.221	5.3648	5.3691
AT2G20530.1	Symbols: ATPHB6 | ATPHB6 (PROHIBITIN 6) | chr2:8842300-8843787 FORWARD; Duplicate proteins: AT2G20530.2	4.454	4.4949	4.2554	4.3848	4.3275	4.2249
AT2G21160.1	translocon-associated protein alpha (TRAP alpha) family protein	5.3968	5.3386	5.2922	5.2152	5.1911	5.0368
AT2G21170.1	| Symbols: TIM | TIM (TRIOSEPHOSPHATE ISOMERASE) | chr2:9078128-9080187 REVERSE	4.4375	4.5333	4.5899	4.4263	4.3445	4.8003
AT2G21390.1	coatomer protein complex, subunit alpha, putative	4.1564	4.2242	4.4437	4.3092	4.3379	4.4411
AT2G21410.1	(VACUOLAR PROTON ATPASE A2); ATPase	4.8539	4.8363	4.9183	4.67	4.6913	4.7379
AT2G21660.1	ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	5.3764	5.3356	5.513	5.6543	5.6108	5.4813
AT2G21870.1	| Symbols: | Identical to Probable ATP synthase 24 kDa subunit, mitochondrial precursor (EC 3.6.3.14) [Arabidopsis Thaliana] (GB:Q9SJ12;GB:Q8LBN3); similar to	5.1717	5.1749	5.1299	4.9462	4.9356	5.0004

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	hypothetical protein MtrDRAFT_AC155898g5v1 [Medicago truncatula] (GB:ABE87707.1) | chr2:9327536						
AT2G22170.1	lipid-associated family protein	5.0687	5.1616	5.2935	4.9886	5.0082	5.4028
AT2G25980.1	| Symbols: | jacalin lectin family protein | chr2:11084796-11086720 REVERSE	4.7767	5.025	4.2015	4.2023	4.3901	4.5048
AT2G27030.3	Symbols: CAM4, ACAM-4 | CAM4 (calmodulin 4); calcium ion binding / signal transducer | chr1:24774431-24775785 REVERSE; Duplicate proteins: AT5G37780.1	4.6833	4.6666	4.6584	4.8375	4.7662	5.1234
AT2G27710.1	60S acidic ribosomal protein P2 (RPP2B)	4.8508	4.8521	5.0271	5.2105	5.115	4.9996
AT2G27730.1	| Symbols: | Identical to Uncharacterized mitochondrial protein At2g27730 [Arabidopsis Thaliana] (GB:Q9ZUX4;GB:Q8LBD1); similar to hypothetical protein [Vitis vinifera] (GB:CAN62125.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48731.1);	5.0473	4.9905	4.9249	4.809	4.7963	4.6357
AT2G27860.1	AXS1 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 1)	4.0347	3.9441	4.1922	4.3391	4.2712	4.321
AT2G28000.1	CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded protein binding	5.2885	5.2846	5.3103	5.2584	5.2647	5.1384
AT2G29550.1	Symbols: TUB7 | TUB7; structural constituent of cytoskeleton | chr2:12644258-12645932 REVERSE	3.9376	4.1862	4.2623	4.481	4.3263	4.1965
AT2G30200.1	Symbols: | binding / catalytic/ transferase | chr2:12883340-	4.3596	4.3729	4.4217	4.4006	4.3784	4.2338

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	12885482 REVERSE						
AT2G30490.1	| Symbols: ATC4H, C4H, CYP73A5 | ATC4H (CINNAMATE-4-HYDROXYLASE) | chr2:13000938-13002760 REVERSE	3.8467	3.9516	4.6679	4.1431	4.1294	3.9353
AT2G30860.1	ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase	4.4767	4.8856	5.0045	5.2214	4.8722	5.5216
AT2G30970.1	| Symbols: ASP1 | ASP1 (ASPARTATE AMINOTRANSFERASE 1) | chr2:13186089-13188763 FORWARD	4.4746	4.4891	4.4235	4.2028	4.3273	4.2792
AT2G31390.1	pfkB-type carbohydrate kinase family protein	4.5078	4.6801	4.8838	4.9388	4.7695	5.0982
AT2G31610.1	40S ribosomal protein S3 (RPS3A)	5.1926	5.2646	5.3064	5.4885	5.4381	5.2642
AT2G32060.1	| Symbols: | 40S ribosomal protein S12 (RPS12C) | chr2:13646305-13647181 REVERSE	4.1252	4.139	4.306	4.604	4.5095	4.3075
AT2G33040.1	ATP synthase gamma chain, mitochondrial (ATPC)	5.3631	5.386	5.3075	5.2667	5.1975	5.2353
AT2G33150.1	PED1 (PEROXISOME DEFECTIVE 1); acetyl-CoA C-acyltransferase	5.1306	5.1322	5.0595	4.8156	4.9201	5.3018
AT2G33210.1	chaperonin, putative	5.3523	5.2495	5.2044	5.1726	5.1828	5.0186
AT2G33220.1	Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: photorespiration; LOCATED IN: mitochondrion, mitochondrial membrane, plastid, respiratory chain complex I; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS I	4.6539	4.686	4.6229	4.534	4.541	4.5811
AT2G33730.1	Symbols: | DEAD box RNA helicase, putative | chr2:14265679-14267880	4.0651	4.0163	4.0274	3.9308	4.0571	3.8455

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	REVERSE						
AT2G34250.1	Symbols: | protein transport protein sec61, putative | chr2:14462635-14464572 FORWARD; Duplicate proteins: AT2G34250.2	5.1957	5.1431	5.0984	4.9878	5.0094	4.9107
AT2G34480.1	60S ribosomal protein L18A (RPL18aB)	4.5096	4.4775	4.6301	4.7982	4.678	4.5161
AT2G35605.1	Symbols: | SWIB complex BAF60b domain-containing protein | chr2:14946161-14947027 FORWARD	4.7187	4.6519	4.4563	4.5714	4.6485	4.5013
AT2G36160.1	40S ribosomal protein S14 (RPS14A)	4.5601	4.5064	4.6799	4.7777	4.8026	4.5889
AT2G36460.1	| Symbols: | fructose-bisphosphate aldolase, putative | chr2:15304008-15305466 REVERSE	5.4599	5.4291	5.6665	5.7777	5.6612	5.5897
AT2G36530.1	LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase	5.2833	5.2727	5.549	5.7399	5.6265	5.5763
AT2G36620.1	| Symbols: RPL24B, RPL24, STV1 | STV1 (SHORT VALVE1); structural constituent of ribosome | chr3:19671727-19672890 REVERSE	4.9965	4.9872	5.063	5.2849	5.265	5.0579
AT2G36880.1	MAT3 (METHIONINE ADENOSYLTRANSFERASE 3); methionine adenosyltransferase	4.4394	4.714	4.8883	4.9006	4.6952	4.5134
AT2G37270.1	ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	5.0103	5.093	4.9782	5.2392	5.2076	4.9828
AT2G38040.1	| Symbols: CAC3 | CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit); acetyl-CoA carboxylase | chr2:15924690-15927827 FORWARD	4.3097	4.383	4.5288	4.433	4.2342	4.1345
AT2G38750.1	| Symbols: ANNAT4 | ANNAT4 (ANNEXIN 4, ANNEXIN ARABIDOPSIS 4); calcium ion binding	5.1136	5.1967	4.3326	3.9249	4.6725	4.0714

Supplementary Tables pertaining to Figure 2

Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics

Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	/ calcium-dependent phospholipid binding | chr2:16203660-16205509 REVERSE						
AT2G39460.1	Symbols: ATRPL23A, RPL23A, RPL23AA | RPL23AA (RIBOSOMAL PROTEIN L23AA); RNA binding / nucleotide binding / structural constituent of ribosome | chr2:16475049-16475904 FORWARD; Duplicate proteins: AT2G39460.2	5.002	4.9818	5.0707	5.2152	5.2035	5.0003
AT2G39800.1	Symbols: P5CS1, ATP5CS | P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1); delta1-pyrroline-5-carboxylate synthetase | chr2:16598516-16602939 REVERSE	3.2499	3.2953	4.2227	3.8961	3.4994	3.2284
AT2G40510.1	| Symbols: | 40S ribosomal protein S26 (RPS26A) | chr2:16925584-16926701 FORWARD	4.9703	4.9714	5.1174	5.2796	5.2553	5.1347
AT2G41840.1	Symbols: XW6 | XW6; structural constituent of ribosome | chr1:21689115-21690085 FORWARD	4.8556	4.907	4.927	5.1642	5.1242	4.8918
AT2G42100.1	| Symbols: | actin, putative | chr2:17567289-17569023 FORWARD	4.1304	3.9842	4.0795	3.9631	4.0827	4.0595
AT2G42210.2	Symbols: ATOEP16-3, OEP16-3 | mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | chr2:17590600-17591591 FORWARD	4.8924	4.9143	4.8142	4.7672	4.7939	4.7207
AT2G43090.1	| Symbols: | aconitase C-terminal domain-containing protein | chr2:17926034-17926789 FORWARD	4.6848	4.7237	4.6896	4.5592	4.6201	4.7079
AT2G43535.1	| Symbols: | trypsin inhibitor, putative | chr2:18078207-18078637 FORWARD	4.1544	4.8705	3.9495	3.57	3.4676	4.8485

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G43610.1	Symbols: | glycoside hydrolase family 19 protein | chr2:18088058-18089184 REVERSE	3.004	3.649	2.6684	3.1517	2.8679	3.6161
AT2G44790.1	UCC2 (UCLACYANIN 2); copper ion binding	4.4538	4.28	4.6034	4.7585	4.527	4.2034
AT2G45740.1	Symbols: PEX11C | PEX11C (PEROXIN 11C) | chr1:296213-297723 REVERSE	4.4388	4.5927	4.6147	4.3525	4.232	4.8222
AT2G47470.1	Symbols: ATPDIL2-1, UNE5, MEE30, PDI11, ATPDI11 | UNE5 (UNFERTILIZED EMBRYO SAC 5); protein disulfide isomerase | chr2:19481503-19483683 FORWARD	5.4676	5.3934	5.3784	5.365	5.3089	5.5573
AT2G47510.1	FUM1 (FUMARASE 1); fumarate hydratase	4.0259	3.9991	3.9059	3.8645	3.8369	3.7587
AT3G01280.1	porin, putative	5.747	5.8046	5.7006	5.7013	5.6453	5.5641
AT3G01390.1	VMA10 (VACUOLAR MEMBRANE ATPASE 10)	4.7619	4.7414	4.7112	4.5846	4.566	4.8521
AT3G02090.1	MPPBETA; metalloendopeptidase	5.8455	5.852	5.7469	5.6936	5.7102	5.6846
AT3G02230.1	RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)	4.9919	4.8057	4.902	4.9072	4.9681	5.055
AT3G02530.1	chaperonin, putative	3.7203	3.6968	3.9781	4.1774	4.1933	4.0086
AT3G02630.1	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative	4.3966	4.4878	4.5704	4.4928	4.3467	4.4607
AT3G02780.1	| Symbols: IPP2, IPIAT1, IDI2 | IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE ISOMERASE 2, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase | chr3:602585-604655 REVERSE	4.0008	3.9799	4.1638	4.1604	4.1365	4.3256

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G03780.1	AtMS2 (Arabidopsis thaliana methionine synthase 2); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	5.452	5.4967	5.7159	5.7985	5.7333	5.8861
AT3G03960.1	chaperonin, putative	4.3701	4.4418	4.4568	4.6892	4.6379	4.5256
AT3G04120.1	GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	4.6678	4.5824	4.7637	4.9271	4.7032	4.7936
AT3G04840.1	40S ribosomal protein S3A (RPS3aA)	4.923	4.9337	4.918	5.2009	5.1918	4.9543
AT3G05020.1	ACP1 (ACYL CARRIER PROTEIN 1)	5.2945	5.305	5.4908	5.4405	5.2695	5.0172
AT3G05560.1	60S ribosomal protein L22-2 (RPL22B)	5.0878	5.0859	5.1322	5.1463	5.0521	4.9845
AT3G05590.1	RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	5.1825	5.1476	5.2053	5.4258	5.4333	5.1747
AT3G06300.1	| Symbols: AT-P4H-2 | AT-P4H-2 (A. THALIANA P4H ISOFORM 2); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors / procolla	4.7894	4.4161	4.2912	4.2111	4.4467	3.9979
AT3G06860.1	MFP2 (MULTIFUNCTIONAL PROTEIN); enoyl-CoA hydratase	4.0015	3.9532	3.846	3.6598	3.8333	4.2926
AT3G07770.1	| Symbols: | ATP binding | chr3:2479617-2483976 FORWARD	4.567	4.476	4.2387	4.3247	4.2677	4.0243
AT3G08580.1	AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	5.9422	5.9418	5.8863	5.8363	5.7693	5.7975
AT3G09200.1	60S acidic ribosomal protein P0 (RPP0B)	5.3473	5.3242	5.4664	5.6316	5.6232	5.4354
AT3G09260.1	PYK10 (phosphate starvation-response 3.1); hydrolase, hydrolyzing O-glycosyl compounds	6.1616	6.2885	5.4886	5.3711	5.8827	6.0015

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT3G09440.1	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	4.6749	4.6095	4.6888	4.6688	4.7628	4.7725
AT3G09630.1	| Symbols: | 60S ribosomal protein L4/L1 (RPL4A) | chr3:2953818-2955449 FORWARD	5.007	5	4.9952	5.2103	5.1781	5.0169
AT3G09680.1	| Symbols: | 40S ribosomal protein S23 (RPS23B) | chr5:693278-694394 REVERSE	4.7311	4.7191	4.8585	5.0996	5.0144	4.7837
AT3G09820.1	ADK1 (ADENOSINE KINASE 1)	4.4109	4.4406	4.5619	4.7175	4.6819	4.5432
AT3G09840.1	CDC48 (CELL DIVISION CYCLE 48); ATPase	4.6297	4.6245	4.7774	4.9173	4.9194	4.9818
AT3G10090.1	40S ribosomal protein S28 (RPS28A)	4.5493	4.6105	4.8105	4.9296	4.884	4.757
AT3G10370.1	Symbols: SDP6 | SDP6 (SUGAR-DEPENDENT 6); glycerol-3-phosphate dehydrogenase | chr3:3216502-3219027 FORWARD	3.7075	3.6736	3.4259	3.2406	3.5349	3.6771
AT3G11130.1	clathrin heavy chain, putative	4.3704	4.2747	4.4342	4.396	4.3538	4.4011
AT3G11250.1	60S acidic ribosomal protein P0 (RPP0C)	4.0284	4.0735	4.2471	4.2876	4.2108	3.9583
AT3G11830.1	chaperonin, putative	4.0768	4.1694	4.3164	4.5326	4.4695	4.2993
AT3G12580.1	HSP70 (heat shock protein 70); ATP binding	4.4765	4.4086	4.538	4.5068	4.5777	4.4892
AT3G12780.1	PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase	4.2843	4.3436	4.6534	4.4609	4.3546	4.5626
AT3G13860.1	chaperonin, putative	4.6321	4.541	4.4083	4.3689	4.4366	4.4217
AT3G13870.1	RHD3 (ROOT HAIR DEFECTIVE 3)	4.6401	4.5249	4.426	4.3423	4.3335	4.4839
AT3G13920.1	EIF4A1 (eukaryotic translation initiation factor 4A-1); ATP-dependent helicase	5.3863	5.4692	5.5585	5.5498	5.5456	5.4142
AT3G13930.1	| Symbols: | dihydrolipoamide S-acetyltransferase, putative | chr3:4596247-4600150 FORWARD	5.1271	5.0705	5.0596	4.9264	4.9908	5.0276
AT3G14990.1	Symbols: | 4-methyl-5(b-	3.5112	3.8125	4.0581	4.2327	4.1698	4.9944

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative | chr3:5047510-5049621 FORWARD						
AT3G15000.1	Identical to Unknown mitochondrial protein At3g15000 [Arabidopsis Thaliana] (GB:Q9LKA5); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53260.1); similar to Os09g0509000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063625.1); simi	4.9187	4.9095	4.7901	4.8011	4.9231	4.6631
AT3G15020.1	malate dehydrogenase (NAD), mitochondrial, putative	5.5452	5.4912	5.4518	5.3591	5.4737	5.509
AT3G15730.1	| Symbols: PLD, PLDALPHA1 | PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D | chr3:5330842-5333481 FORWARD	3.7714	3.6665	3.8443	3.8962	3.7938	4.2931
AT3G15950.1	| Symbols: | (TSA1-LIKE); unknown protein | chr3:5397789-5402616 REVERSE	6.0657	5.9345	5.1331	5.0702	5.5965	5.5535
AT3G16410.1	| Symbols: | jacalin lectin family protein | chr3:5572151-5574365 FORWARD	5.1239	5.318	4.533	4.4454	4.7804	4.9839
AT3G16420.1	PBP1 (PYK10-BINDING PROTEIN 1)	5.4951	5.5968	5.005	4.9619	5.1392	5.7362
AT3G16460.1	jacalin lectin family protein	6.1121	6.1421	5.2974	5.2755	5.625	5.8886
AT3G16480.1	MPPALPHA (mitochondrial processing peptidase alpha subunit); metalloendopeptidase	4.754	4.774	4.7212	4.6037	4.5373	4.5259
AT3G17240.1	LPD2 (LIPOAMIDE DEHYDROGENASE 2); FAD binding / dihydrolipoyl dehydrogenase/ disulfide oxidoreductase/ oxidoreductase	4.8004	4.6925	4.7045	4.6127	4.6907	4.7509
AT3G17390.1	MTO3 (S-adenosylmethionine synthase 3); methionine	5.3861	5.5389	5.6434	5.6138	5.5871	5.461

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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	adenosyltransferase						
AT3G17810.1	| Symbols: | dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein | chr3:6094285-6096295 FORWARD	4.3236	4.3639	4.3315	4.1861	4.1545	4.5406
AT3G18000.1	| Symbols: XIPOTL1, PEAMT, NMT1 | NMT1 (N-METHYLTRANSFERASE 1); phosphoethanolamine N-methyltransferase | chr3:6154584-6157337 FORWARD	3.9431	4.0984	4.6957	4.4883	4.2225	4.4926
AT3G18130.1	guanine nucleotide-binding family protein / activated protein kinase C receptor (RACK1)	4.2937	4.349	4.4611	4.6508	4.5746	4.2999
AT3G18190.1	chaperonin, putative	4.4387	4.5279	4.6778	4.8599	4.8636	4.6418
AT3G18780.2	| Symbols: DER1, LSR2, ENL2, ACT2 | ACT2 (ACTIN 2); structural constituent of cytoskeleton | chr3:6475541-6476838 FORWARD	5.6561	5.3042	5.5148	5.5106	5.6992	5.3024
AT3G19820.1	DWF1 (DIMINUTO 1); catalytic	5.7369	5.7698	5.9862	5.8156	5.6221	5.4318
AT3G20000.1	TOM40 (translocase of the outer mitochondrial membrane 40); voltage-gated ion-selective channel	4.9937	5.0125	4.9129	4.9045	4.8835	4.8013
AT3G20050.1	| Symbols: ATTCP-1 | ATTCP-1 (Arabidopsis thaliana T-complex protein 1 alpha subunit); ATP binding / protein binding / unfolded protein binding | chr3:6998550-7002272 REVERSE	3.9372	4.0782	4.1769	4.4782	4.5947	4.3751
AT3G20370.1	| Symbols: | meprin and TRAF homology domain-containing protein / MATH domain-containing protein | chr3:7105487-7107085 FORWARD	5.1122	4.8314	4.0459	3.8266	4.5114	4.7024
AT3G22200.1	Symbols: POP2, GABA-T, HER1 | POP2 (POLLEN-PISTIL	4.4365	4.3276	4.1881	4.0101	4.1732	4.6819

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase | chr3:7835286-7838863 FORWARD						
AT3G22790.1	Symbols: | kinase interacting family protein | chr3:8052446-8057888 REVERSE	4.1676	4.0954	4.3498	4.4651	4.4457	4.1944
AT3G22960.1	| Symbols: | pyruvate kinase, putative | chr3:8139376-8141778 FORWARD	4.5401	4.5646	4.7703	4.6696	4.5142	4.4899
AT3G23990.1	HSP60 (Heat shock protein 60); ATP binding / protein binding / unfolded protein binding	5.8109	5.7646	5.6665	5.6175	5.6417	5.6391
AT3G25860.1	LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE); dihydrolipoyllysine-residue acetyltransferase	5.1489	5.1783	5.3634	5.2945	5.1158	5.0308
AT3G27240.1	| Symbols: | cytochrome c1, putative | chr3:10057381-10059607 REVERSE	4.5913	4.6229	4.5959	4.4873	4.5814	4.5106
AT3G42050.1	| Symbols: | vacuolar ATP synthase subunit H family protein | chr3:14239832-14243214 REVERSE	4.8446	4.7727	4.814	4.6928	4.7037	4.7862
AT3G43980.1	Symbols: | 40S ribosomal protein S29 (RPS29A) | chr3:15778555-15779235 REVERSE; Duplicate proteins: AT3G44010.1,AT4G33865.1	3.8741	3.8449	3.8862	3.9157	3.9238	3.8418
AT3G44110.1	| Symbols: ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3) | chr3:15880102-15882046 REVERSE	4.6584	4.5435	4.7726	4.7446	4.6781	4.459
AT3G44330.1	similar to PREDICTED: similar to nicalin [Tribolium castaneum] (GB:XP_971811.1); similar to Os08g0102100 [Oryza sativa (japonica cultivar-group)]	4.8023	4.7689	4.8324	4.6998	4.6984	4.5755

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(GB:NP_001060766.1); contains InterPro domain Nicastrin; (InterPro:IPR008710)						
AT3G45030.1	40S ribosomal protein S20 (RPS20A)	5.1647	5.1658	5.3132	5.4458	5.446	5.2964
AT3G46040.1	RPS15AD (ribosomal protein S15A D); structural constituent of ribosome	4.4014	4.4435	4.4543	4.5927	4.4724	4.4211
AT3G46430.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G59613.1); similar to mitochondrial ATP synthase 6 KD subunit [Oryza sativa (japonica cultivar-group)] (GB:BAB21526.1)	4.3145	4.301	4.1325	4.2632	3.999	3.8452
AT3G47520.1	MDH (malate dehydrogenase); malate dehydrogenase	5.4958	5.4767	5.595	5.474	5.476	5.435
AT3G48000.1	| Symbols: ALDH2, ALDH2B4 | ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD) | chr3:17728067-17730828 REVERSE	4.5333	4.9012	5.1262	4.5337	4.2413	5.1701
AT3G48340.1	| Symbols: | cysteine-type peptidase | chr3:17908919-17910059 FORWARD	5.3197	5.0337	4.0398	4.1866	4.7924	4.5722
AT3G48870.1	ATCLPC (CASEINOLYTIC PROTEASE C); ATP binding / ATPase	4.6316	4.7102	4.8497	4.7602	4.7193	4.7503
AT3G48930.1	EMB1080 (EMBRYO DEFECTIVE 1080); structural constituent of ribosome	4.8503	4.8714	5.0293	5.2007	5.1526	4.943
AT3G49010.1	Symbols: ATBBC1, BBC1, RSU2 | ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome | chr3:18166971-18168047 REVERSE	4.8492	4.8595	4.9253	5.0743	5.1014	4.8402
AT3G49720.1	similar to unknown protein [Arabidopsis thaliana]	5.0195	5.0182	4.9533	4.7816	4.8745	4.811

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(TAIR:AT5G65810.1); similar to Os01g0144000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042001.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78370.1); contains dom						
AT3G49910.1	| Symbols: | 60S ribosomal protein L26 (RPL26A) | chr3:18515296-18515736 FORWARD	4.1579	4.172	4.3339	4.4869	4.3645	4.3128
AT3G51800.1	Symbols: ATG2 | ATG2; aminopeptidase/ metalloexopeptidase | chr3:19211261-19213568 REVERSE	3.7834	3.8019	3.8363	4.2056	4.2568	3.9705
AT3G52200.1	| Symbols: LTA3 | LTA3 (Dihydrolipoamide S-acetyltransferase 3); dihydrolipoyllysine-residue acetyltransferase | chr3:19371295-19377069 FORWARD	4.6468	4.5472	4.4784	4.3806	4.4196	4.5413
AT3G52300.1	ATP synthase D chain-related	5.4492	5.4733	5.4224	5.3321	5.3282	5.3363
AT3G52580.1	40S ribosomal protein S14 (RPS14C)	5.1432	5.0862	5.2597	5.3923	5.3786	5.1303
AT3G52730.1	| Symbols: | ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein | chr3:19554124-19555145 REVERSE	4.6371	4.6306	4.5251	4.4378	4.4527	4.2571
AT3G52930.1	fructose-bisphosphate aldolase, putative	5.5683	5.5524	5.8128	5.8669	5.7527	5.6383
AT3G52960.1	peroxiredoxin type 2, putative	4.9005	4.8725	5.0996	4.9412	4.8105	4.8031
AT3G52990.1	Symbols: | pyruvate kinase, putative | chr3:19649046-19652237 FORWARD	4.0785	4.0358	4.1614	4.2643	4.1787	4.1578
AT3G53430.1	| Symbols: | 60S ribosomal protein L12 (RPL12B) | chr3:19820873-19821373 REVERSE	5.4739	5.4452	5.5971	5.6892	5.7109	5.4987
AT3G54560.1	Symbols: HTA9 | HTA9 (HISTONE H2A PROTEIN 9); DNA binding |	4.4008	4.6521	4.6544	4.5218	4.3663	4.5634

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	chr1:19645409-19646221 FORWARD						
AT3G54960.1	ATPDIL1-3 (PDI-LIKE 1-3); thiol-disulfide exchange intermediate	5.5307	5.122	4.9639	4.7323	5.0842	4.9861
AT3G55360.1	ATTSC13/CER10/ECR/TSC13 (ENOYL-COA REDUCTASE); 3-oxo-5-alpha-steroid 4-dehydrogenase/ fatty acid elongase/ trans-2-enoyl-CoA reductase (NADPH)	4.3896	4.4377	4.4518	4.3359	4.2545	4.0549
AT3G55410.1	| Symbols: | 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative | chr3:20552874-20556705 FORWARD	4.9533	4.8934	4.7269	4.6654	4.7844	4.7053
AT3G55440.1	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase	4.7648	4.7728	4.9382	5.1329	5.0795	5.185
AT3G56130.1	| Symbols: | biotin/lipoyl attachment domain-containing protein | chr3:20837831-20839986 FORWARD	4.1667	4.1596	4.2587	4.2384	4.0718	3.8964
AT3G57010.1	strictosidine synthase family protein	4.2169	4.4836	4.6949	4.9575	4.8002	4.5937
AT3G57610.1	adenylosuccinate synthetase (ADSS)	4.4158	4.4343	4.5338	4.5027	4.3997	4.4199
AT3G58610.1	| Symbols: | ketol-acid reductoisomerase | chr3:21682538-21685616 FORWARD	5.236	5.2361	5.2607	5.1631	5.2035	5.103
AT3G60750.1	transketolase, putative	5.4188	5.3885	5.6072	5.406	5.3649	5.4938
AT3G60770.1	40S ribosomal protein S13 (RPS13A)	4.8602	4.8762	4.9476	5.1277	5.0925	4.8806
AT3G61440.1	ATCYSC1 (BETA-SUBSTITUTED ALA SYNTHASE 3;1); L-3-cyanoalanine synthase/ cysteine synthase	4.3458	4.402	4.6445	4.4443	4.2977	4.5729
AT3G62360.1	similar to LOC495699 protein [Xenopus laevis] (GB:AAH86296.1); contains InterPro domain	5.3191	5.2744	5.2936	5.1941	5.1984	5.0488

Supplementary Tables pertaining to Figure 2
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Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	Carboxypeptidase regulatory region; (InterPro:IPR008969); contains InterPro domain Cna B-type; (InterPro:IPR008454); contains InterPro domain Borrelia outer surf						
AT3G62830.1	Symbols: UXS2, ATUXS2, AUD1 | AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase | chr3:23232539-23235353 FORWARD; Duplicate proteins: AT3G62830.2	4.5912	4.4251	4.3553	4.2445	4.3343	4.5807
AT4G00490.1	Symbols: BAM2, BMY9 | BAM2 (BETA-AMYLASE 2); beta-amylase | chr4:222422-224862 FORWARD	4.0842	4.0415	4.0324	3.93	3.8331	4.6723
AT4G00860.1	ATOZI1 (Arabidopsis thaliana ozone-induced protein 1)	4.6568	4.6419	4.6332	4.5827	4.3948	4.5688
AT4G01100.1	mitochondrial substrate carrier family protein	4.9291	4.807	4.7611	4.7383	4.8193	4.4809
AT4G01850.1	MAT2/SAM-2 (S-adenosylmethionine synthetase 2); methionine adenosyltransferase	4.8284	4.6919	4.658	4.8043	4.793	4.6068
AT4G02450.1	Symbols: | glycine-rich protein | chr4:1073987-1075765 REVERSE	4.6206	4.6874	4.8319	5.0508	4.9584	4.8488
AT4G02930.1	elongation factor Tu, putative / EF-Tu, putative	5.1353	5.0099	4.9639	4.848	4.9155	4.8432
AT4G05020.1	NDB2 (NAD(P)H DEHYDROGENASE B2); disulfide oxidoreductase	4.3335	4.2066	4.2164	3.8954	4.1697	4.2196
AT4G09000.2	Symbols: GRF1, GF14 CHI | 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1) | chr4:5775387-5777157 FORWARD	4.3582	4.408	4.5783	4.7434	4.739	4.8332
AT4G09020.1	Symbols: ATISA3, ISA3 | ISA3 (ISOAMYLASE 3); alpha-amylase/ isoamylase | chr4:5784099-5788839	3.9904	4.1767	3.9523	3.9121	3.8667	4.9168

Supplementary Tables pertaining to Figure 2

Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics

Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	FORWARD						
AT4G09320.1	NDPK1 (nucleoside diphosphate kinase 1); ATP binding / nucleoside diphosphate kinase	4.8838	4.9275	5.0623	5.2222	5.221	5.107
AT4G11010.1	| Symbols: NDPK3 | NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3); ATP binding / nucleoside diphosphate kinase | chr4:6732776-6734294 REVERSE	4.6302	4.557	4.5037	4.5118	4.299	4.4473
AT4G11150.1	TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1)	5.1781	5.0848	5.1882	4.9489	5.0096	5.008
AT4G11820.2	| Symbols: HMGS, EMB2778, MVA1 | MVA1 (HYDROXYMETHYLGLUTARYL-COA SYNTHASE) | chr4:7109118-7111895 REVERSE	3.8329	3.9139	4.3463	4.417	4.1772	3.8392
AT4G12650.1	endomembrane protein 70, putative	4.8412	4.888	4.7873	4.7037	4.7249	4.7977
AT4G13850.1	| Symbols: GR-RBP2, GRP2, ATGRP2 | ATGRP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding | chr4:8021310-8022061 FORWARD	5.3827	5.2356	5.16	5.1835	5.2129	5.0167
AT4G13930.1	SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4); glycine hydroxymethyltransferase	4.4792	4.4473	4.8639	4.8404	4.8052	4.7143
AT4G13940.1	HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase	5.6033	5.6233	5.8223	5.9336	5.8692	5.786
AT4G14800.1	| Symbols: PBD2 | PBD2 (20S PROTEASOME BETA SUBUNIT 2); peptidase | chr4:8500393-8502053 FORWARD	4.1125	4.1244	4.3132	4.413	4.3879	4.4414
AT4G14960.2	TUA6 (tubulin alpha-6 chiain)	5.4113	5.5047	5.7634	5.7426	5.6512	5.5096

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AT4G16155.1	Symbols: LPD1, ptlpd1 | LPD1 (LIPOAMIDE DEHYDROGENASE 1); dihydrolipoyl dehydrogenase | chr3:5786508-5790383 REVERSE	4.6793	4.6907	4.962	4.8394	4.6393	4.4602
AT4G16450.1	Symbols: | unknown protein | chr4:9280132-9280541 FORWARD	4.591	4.6259	4.606	4.5507	4.5936	4.5184
AT4G16660.1	heat shock protein 70, putative / HSP70, putative	4.7744	4.5723	4.5095	4.4285	4.5179	4.7335
AT4G17530.1	RAB1C; GTP binding	4.9535	4.7389	4.8327	4.7352	4.6628	4.5612
AT4G18030.1	dehydration-responsive family protein	4.6261	4.7645	4.8121	4.6818	4.6219	4.3457
AT4G18100.1	60S ribosomal protein L32 (RPL32A)	4.7145	4.6337	4.7505	4.9791	4.9609	4.6693
AT4G21150.1	ribophorin II (RPN2) family protein	5.6213	5.6093	5.5482	5.4655	5.4869	5.3946
AT4G23620.1	| Symbols: | 50S ribosomal protein-related | chr4:12315026-12316669 REVERSE	4.161	4.0235	3.9649	3.8695	3.9571	3.8414
AT4G23710.1	| Symbols: VHA-G2, VAG2, VATG2 | VAG2/VATG2/VHA-G2 (VACUOLAR ATP SYNTHASE SUBUNIT G2) | chr4:12350587-12351364 FORWARD	4.5821	4.3589	4.4049	4.2986	4.4225	3.9934
AT4G24190.1	SHD (SHEPHERD); ATP binding	5.8716	5.8089	5.7345	5.6844	5.6873	5.8602
AT4G24280.1	CPHSC70-1 (chloroplast heat shock protein 70-1); ATP binding / unfolded protein binding	4.6619	4.6147	4.7204	4.619	4.6016	4.5162
AT4G24830.1	arginosuccinate synthase family	5.1177	5.0998	5.0778	5.0247	5.1305	4.9972
AT4G25630.1	FIB2 (FIBRILLARIN 2)	5.3594	5.4537	5.2508	5.4363	5.4918	5.1198
AT4G27090.1	60S ribosomal protein L14 (RPL14B)	5.154	5.2241	5.2172	5.3362	5.3229	5.2434
AT4G27500.1	| Symbols: PPI1 | PPI1 (PROTON PUMP INTERACTOR 1) | chr4:13743620-13745906 FORWARD	4.6939	4.4071	4.4474	4.2278	4.3261	4.1767
AT4G29130.1	ATHXK1 (GLUCOSE INSENSITIVE 2); ATP binding / hexokinase	4.6875	4.7244	4.5839	4.4743	4.5097	4.6265
AT4G29690.1	type I phosphodiesterase/nucleotide pyrophosphatase family protein	4.7962	5.2679	4.6773	4.6816	4.5758	5.2433

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AT4G29840.1	| Symbols: TS, MTO2 | MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase | chr4:14599440-14601020 REVERSE	4.5329	4.5463	4.6277	4.4613	4.5531	4.4398
AT4G30190.1	| Symbols: PMA2, AHA2 | AHA2 (Arabidopsis H(+)-ATPase 2); ATPase | chr4:14770826-14775926 REVERSE	5.067	5.2049	4.984	4.8031	4.8878	4.9867
AT4G31340.1	| Symbols: | myosin heavy chain-related | chr4:15205668-15208901 FORWARD	4.9857	4.8282	4.9502	4.7312	4.7706	4.5413
AT4G31700.1	RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	4.4477	4.4531	4.5262	4.7556	4.7276	4.5424
AT4G32470.1	ubiquinol-cytochrome C reductase complex 14 kDa protein, putative	5.0818	5.084	4.9913	4.9382	4.9608	4.9511
AT4G33680.1	| Symbols: AGD2 | AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase | chr4:16171850-16174633 REVERSE	4.5316	4.5051	4.5135	4.4507	4.5509	4.5427
AT4G34200.1	EDA9 (embryo sac development arrest 9); NAD binding / amino acid binding / cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor / phosphoglycerate dehydrogenase	5.675	5.6575	5.8032	5.639	5.652	5.6439
AT4G34450.1	coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	4.6361	4.6799	4.883	4.8056	4.7926	4.8423
AT4G34670.1	40S ribosomal protein S3A (RPS3aB)	3.5027	3.4451	3.4687	3.7811	3.7258	3.585
AT4G34870.1	ROC5 (ROTAMASE CYP 5); peptidyl-prolyl cis-trans isomerase	4.8598	4.9691	5.0564	5.1146	4.9769	5.3747
AT4G35090.1	CAT2 (CATALASE 2); catalase	5.0527	5.0496	5.0797	4.7672	4.8482	5.2645
AT4G35100.1	PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water	4.476	4.3355	4.8199	4.7087	4.5672	4.0719

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	channel						
AT4G35630.1	PSAT (phosphoserine aminotransferase); phosphoserine transaminase	4.941	5.0277	5.2299	5.0287	5.0216	5.0884
AT4G36130.1	| Symbols: | 60S ribosomal protein L8 (RPL8C) | chr4:17097616-17098659 FORWARD	4.3618	4.3572	4.3281	4.462	4.5366	4.2255
AT4G37910.1	MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding	5.599	5.4984	5.3624	5.331	5.4615	5.2293
AT4G38510.1	(VACUOLAR ATP SYNTHASE SUBUNIT B2); hydrogen ion transporting ATP synthase, rotational mechanism	4.9208	4.8143	4.8748	4.685	4.7787	4.6379
AT4G38740.1	| Symbols: ROC1 | ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans isomerase | chr4:18083614-18084132 REVERSE	5.2921	5.3395	5.5419	5.5646	5.5587	5.598
AT4G39260.1	| Symbols: GR-RBP8, ATGRP8, CCR1 | ATGRP8/GR-RBP8 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 1, GLYCINE-RICH PROTEIN 8); RNA binding | chr4:18274160-18274952 REVERSE	4.6902	4.6175	4.7743	4.987	4.9994	4.784
AT4G39980.1	DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1); 3-deoxy-7-phosphoheptulonate synthase	4.6671	4.6774	4.8616	4.6525	4.6177	4.4674
AT4G40030.2	histone H3.2	4.8262	4.8983	4.7856	4.8076	4.8875	4.8775
AT5G02490.1	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	4.3178	4.2504	4.3207	4.3311	4.4141	4.053
AT5G02500.1	HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding	6.0607	5.9649	6.048	6.088	6.0833	6.0653
AT5G02870.1	60S ribosomal protein L4/L1 (RPL4D)	4.5237	4.5426	4.5943	4.8027	4.8265	4.6761

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G03160.1	Symbols: ATP58IPK | ATP58IPK (ARABIDOPSIS HOMOLOG OF MAMALLIAN P58IPK); binding / heat shock protein binding | chr5:750286-752671 FORWARD	4.2493	4.0983	3.8785	3.9901	3.9701	4.06
AT5G05170.1	Symbols: CESA3, IXR1, ATCESA3, ATH-B, CEV1 | CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups | chr5:1530401-1535090 REVERSE	4.181	4.1135	4.4428	4.1384	4.1788	3.8188
AT5G07090.1	Symbols: | 40S ribosomal protein S4 (RPS4A) | chr2:7546598-7548138 FORWARD	5.3608	5.3734	5.4951	5.6635	5.6079	5.415
AT5G07350.2	Symbols: | tudor domain-containing protein / nuclease family protein | chr5:2319790-2324892 REVERSE	4.262	4.326	4.4335	4.366	4.336	4.3017
AT5G07440.1	GDH2 (GLUTAMATE DEHYDROGENASE 2); oxidoreductase	5.3248	5.3553	5.0598	4.7531	5.0378	5.255
AT5G08300.1	| Symbols: | succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative | chr5:2667580-2669673 FORWARD	4.7184	4.5519	4.4052	4.3227	4.4671	4.4793
AT5G08530.1	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial, putative	4.9701	5.0115	4.9132	4.8288	4.8201	4.8779
AT5G08670.1	ATP synthase beta chain 1, mitochondrial	6.2722	6.2788	6.2426	6.1358	6.1548	6.1494
AT5G09590.1	mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP binding / unfolded protein binding	5.1222	5.026	4.9514	4.9099	4.9953	4.9118

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G09810.1	| Symbols: ACT2/7, ACT7 | ACT7 (actin 7) | chr5:3052810-3054221 FORWARD	4.9713	4.8854	5.0453	5.1143	5.1249	4.926
AT5G10360.1	EMB3010 (EMBRYO DEFECTIVE 3010); structural constituent of ribosome	5.2222	5.1734	5.2704	5.5203	5.526	5.2471
AT5G11520.1	| Symbols: YLS4, ASP3 | ASP3 (ASPARTATE AMINOTRANSFERASE 3) | chr5:3685258-3687722 REVERSE	4.5216	4.4099	4.5433	4.3754	4.547	4.5842
AT5G11560.1	catalytic	5.2009	5.1692	5.1053	5.0443	5.0062	4.9488
AT5G11770.1	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial	4.6907	4.733	4.4593	4.5806	4.6323	4.5679
AT5G12250.1	Symbols: TUB6 | TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton | chr5:3961317-3962971 REVERSE	4.5474	4.5608	4.8763	4.562	4.4657	4.3343
AT5G13420.1	transaldolase, putative	4.7427	4.7394	4.9989	4.8942	4.7622	4.6776
AT5G13440.1	| Symbols: | ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative | chr5:4308434-4310025 REVERSE	5.2059	5.1951	5.0985	5.0298	5.0462	4.9731
AT5G13450.1	ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative	5.4446	5.4135	5.297	5.2833	5.2887	5.1892
AT5G13630.1	Symbols: GUN5, CCH, CHLH, CCH1 | GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase | chr5:4387567-4392082 REVERSE	3.942	3.974	3.8538	3.9168	3.8295	3.6198
AT5G13710.1	SMT1 (STEROL METHYLTRANSFERASE 1)	4.7216	4.6641	5.1517	5.0927	4.7632	4.5055
AT5G14030.1	translocon-associated protein beta	5.2844	5.2454	5.2145	5.0886	5.1049	4.9258

Supplementary Tables pertaining to Figure 2

Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics

Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	(TRAPB) family protein						
AT5G14040.1	mitochondrial phosphate transporter	5.3556	5.315	5.2356	5.1566	5.2202	5.1975
AT5G14670.1	Symbols: ATARFA1F | ATARFA1F (ARABIDOPSIS THALIANA ADP-RIBOSYLATION FACTOR A1F); GTP binding / copper ion binding / phospholipase activator/ protein binding | chr1:3513189-3514230 REVERSE	4.9674	5.0741	5.0686	5.082	4.9268	5.1084
AT5G15090.1	porin, putative / voltage-dependent anion-selective channel protein, putative	5.8086	5.8374	5.7249	5.673	5.6689	5.5175
AT5G15200.1	40S ribosomal protein S9 (RPS9B)	5.011	5.0296	5.1263	5.3166	5.3144	5.0957
AT5G15490.1	| Symbols: | UDP-glucose 6-dehydrogenase, putative | chr5:5027875-5029317 REVERSE	4.6517	4.6082	4.7426	4.752	4.8633	5.0968
AT5G15520.1	40S ribosomal protein S19 (RPS19B)	5.0788	5.1244	5.1271	5.3795	5.1985	5.0804
AT5G15650.1	RGP2 (Reversibly glycosylated polypeptide-3); DNA binding / alpha-1,4-glucan-protein synthase (UDP-forming)	5.4914	5.4101	5.3763	5.4464	5.4531	5.8287
AT5G16130.1	| Symbols: | 40S ribosomal protein S7 (RPS7C) | chr5:5268987-5269915 FORWARD	4.6018	4.6827	4.7459	4.8483	4.7581	4.6171
AT5G16390.1	| Symbols: CAC1A, BCCP, BCCP1, CAC1-A, BCCP-1, CAC1 | BCCP/BCCP-1/BCCP1/CAC1-A/CAC1A (BIOTIN CARBOXYL CARRIER, BIOTIN CARBOXYL CARRIER PROTEIN 1); biotin binding | chr5:5361557-5363023 REVERSE	4.7288	4.7242	4.8433	4.795	4.6995	4.6157
AT5G17770.1	ATCBR (NADH:CYTOCHROME B5 REDUCTASE 1)	4.9422	4.9774	5.0638	5.1211	4.9845	4.8421
AT5G17920.1	ATCIMS (COBALAMIN-	5.6811	5.6952	5.9072	6.0074	5.9189	6.0626

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase						
AT5G18380.1	40S ribosomal protein S16 (RPS16C)	4.4741	4.5457	4.6995	4.8725	4.8075	4.6319
AT5G19510.1	| Symbols: | elongation factor 1B alpha-subunit 2 (eEF1Balpha2) | chr5:6581856-6583139 REVERSE	4.8497	4.7981	5.001	5.0809	5.0379	4.8625
AT5G19760.1	dicarboxylate/tricarboxylate carrier (DTC)	5.5621	5.5536	5.5725	5.4297	5.4172	5.5644
AT5G20010.1	| Symbols: RAN1, ATRAN1, RAN-1 | RAN-1 (RAS RELATED NUCLEAR PROTEIN); GTP binding | chr5:6760366-6761749 FORWARD	4.6819	4.7692	4.9299	5.1254	5.0692	5.0592
AT5G20160.2	Symbols: | ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr4:7453296-7454208 FORWARD	4.6522	4.6853	4.1015	4.6761	4.7475	4.2223
AT5G20290.1	40S ribosomal protein S8 (RPS8A)	5.4335	5.4168	5.5477	5.7212	5.6863	5.4879
AT5G20720.1	CPN20 (CHAPERONIN 20); calmodulin binding	5.2557	5.2684	5.3165	5.2688	5.2301	5.254
AT5G20890.1	chaperonin, putative	4.152	4.1506	4.3069	4.4619	4.4457	4.2758
AT5G20980.1	ATMS3 (METHIONINE SYNTHASE 3); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase	5.1308	5.1246	5.405	5.504	5.338	5.5135
AT5G22880.1	histone H2B, putative	5.3018	5.4661	5.3473	5.3372	5.3714	5.3721
AT5G23300.1	PYRD (PYRIMIDINE D); dihydroorotate dehydrogenase	4.4402	4.4646	4.3728	4.3924	4.4167	4.2794
AT5G23820.1	| Symbols: | MD-2-related lipid recognition domain-containing protein / ML domain-containing protein |	4.9953	5.4862	4.6988	4.6035	4.6454	5.7432

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	chr5:8031389-8032812 FORWARD						
AT5G23860.1	| Symbols: TUB8 | TUB8 (tubulin beta-8) | chr5:8042965-8044531 FORWARD	3.205	3.2583	3.574	3.6054	3.6703	3.5784
AT5G25100.1	endomembrane protein 70, putative	5.3517	5.3354	5.3355	5.1753	5.1567	5.1417
AT5G26260.1	meprin and TRAF homology domain-containing protein / MATH domain-containing protein	5.7521	5.6522	4.842	4.7997	5.3183	5.3447
AT5G26280.1	Symbols: | meprin and TRAF homology domain-containing protein / MATH domain-containing protein | chr5:9208724-9210403 FORWARD	4.3434	4.0864	3.5868	3.7906	3.8446	3.8584
AT5G26360.1	chaperonin, putative	4.1691	4.2912	4.431	4.4674	4.4568	4.4006
AT5G27670.1	| Symbols: | histone H2A, putative | chr5:9792810-9793368 REVERSE	4.3318	4.5947	4.305	4.3696	4.3824	4.7496
AT5G28060.1	40S ribosomal protein S24 (RPS24B)	4.8221	4.8558	4.9314	5.1344	5.0793	4.8795
AT5G28540.1	luminal binding protein 1 (BiP-1) (BP1)	5.3369	5.1344	5.1363	5.0197	5.117	5.1899
AT5G35360.1	CAC2 (acetyl co-enzyme A carboxylase biotin carboxylase subunit)	5.368	5.3857	5.5498	5.4695	5.3266	5.2268
AT5G35630.1	| Symbols: GLN2, ATGSL1, GS2 | GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase | chr5:13848450-13850469 FORWARD	5.0746	4.9099	4.6781	4.455	4.8256	4.8091
AT5G35940.1	| Symbols: | jacalin lectin family protein | chr5:14108055-14110038 FORWARD	4.558	5.0478	4.0844	4.1224	4.255	4.5952
AT5G37510.2	| Symbols: EMB1467 | EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase | chr5:14914720-14917677 FORWARD	5.4447	5.4567	5.3778	5.3006	5.2893	5.284
AT5G38480.1	GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding	4.6577	4.7412	4.906	5.0553	4.9957	5.2305

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT5G38530.1	| Symbols: | tryptophan synthase-related | chr5:15441327-15443524 FORWARD	4.2323	4.3374	4.2582	3.9762	4.1382	4.3268
AT5G39320.1	| Symbols: | UDP-glucose 6-dehydrogenase, putative | chr5:15760482-15761924 FORWARD	3.8965	3.585	3.7541	3.9777	4.0409	3.7308
AT5G39740.1	| Symbols: | 60S ribosomal protein L5 (RPL5B) | chr5:15920593-15922413 FORWARD	5.0808	5.1046	5.1815	5.3055	5.3289	5.098
AT5G40770.1	ATPHB3 (PROHIBITIN 3)	4.2862	4.3845	4.2067	4.1715	3.8804	4.2406
AT5G41790.1	Symbols: CIP1 | CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding | chr5:16727530-16732391 FORWARD	4.5985	4.5665	4.6304	4.5905	4.5972	4.5765
AT5G42020.1	BIP (LUMINAL BINDING PROTEIN); ATP binding	6.2818	6.1113	6.0026	5.9738	6.021	6.1321
AT5G42020.2	BIP (LUMINAL BINDING PROTEIN); ATP binding	4.4413	4.3303	4.3882	4.5366	4.5033	4.3306
AT5G42080.1	ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding	4.4594	4.3819	4.3763	4.3086	4.3306	4.3056
AT5G42960.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G45170.1); similar to pore protein of 24 kD (OEP24) [Pisum sativum] (GB:CAA04468.1)	3.995	4.0853	4.0793	4.0153	3.9008	3.675
AT5G42980.1	ATTRX3 (thioredoxin H-type 3); thiol-disulfide exchange intermediate	4.8301	4.9631	5.049	5.1798	5.1175	5.3696
AT5G43060.1	| Symbols: | cysteine proteinase, putative / thiol protease, putative | chr5:17287012-17289345 REVERSE	4.6008	4.6899	4.7141	4.533	4.4568	4.8492
AT5G44020.1	acid phosphatase class B family protein	4.9493	4.4697	4.3956	4.4859	4.6599	4.0657
AT5G44340.1	| Symbols: TUB4 | TUB4 (tubulin beta-4 chain) | chr5:17876669-17878221	4.0513	4.0871	4.3739	4.3591	4.2321	4.0997

Supplementary Tables pertaining to Figure 2
Supplementary Table S12. Root cell type proteins quantified by peak-integration proteomics
Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	REVERSE						
AT5G47030.1	ATP synthase delta' chain, mitochondrial	5.1663	5.077	5.0317	4.9713	4.974	4.8571
AT5G47770.1	| Symbols: FPS1 | FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); dimethylallyltranstransferase/ geranyltranstransferase | chr5:19362523-19364641 FORWARD	4.0541	4.1116	4.4567	4.398	4.1997	4.2351
AT5G47990.1	Symbols: CYP705A5, THAD, THAD1 | CYP705A5; oxygen binding / thalian-diol desaturase | chr5:19434827-19436444 FORWARD	4.2952	4.4063	4.1436	3.3959	3.9095	3.9733
AT5G48810.1	Symbols: ATB5-B, B5 #3, ATCB5-D, CB5-D | CB5-D (CYTOCHROME B5 ISOFORM D); heme binding | chr5:19789249-19790180 REVERSE	4.8755	4.7291	4.8051	4.5832	4.4551	4.4536
AT5G49460.1	| Symbols: ACLB-2 | ACLB-2 (ATP-citrate lyase B-2) | chr5:20072274-20075421 FORWARD	4.2261	4.3264	4.7652	4.7885	4.5931	4.5574
AT5G50850.1	pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2)	5.0322	4.9514	4.9107	4.8065	4.9438	4.9994
AT5G52470.1	FIB1 (FIBRILLARIN 1)	4.2214	4.3374	4.1268	4.385	4.4422	4.0602
AT5G52840.1	NADH-ubiquinone oxidoreductase-related	5.1293	5.1088	5.0276	4.9665	5.0107	4.9853
AT5G52920.1	pyruvate kinase, putative	4.3667	4.4066	4.5002	4.5903	4.4677	4.1385
AT5G53460.1	| Symbols: GLT1 | GLT1 (NADH-dependent glutamate synthase 1 gene) | chr5:21717744-21726855 FORWARD	4.2191	4.2435	3.7467	3.9608	4.2063	4.3079
AT5G53560.1	ATB5-A (Cytochrome b5 A)	5.2221	5.2178	5.2209	4.9937	4.9387	4.9595
AT5G54100.1	Symbols: | band 7 family protein | chr5:21954035-21956500 REVERSE	4.2729	4.2819	4.1678	3.9686	4.0027	4.2652
AT5G56030.1	HSP81-2 (EARLY-RESPONSIVE TO	5.509	5.5747	5.7839	5.8255	5.7665	5.6537

Supplementary Tables pertaining to Figure 2
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Label-free proteomic log intensity values obtained by peak integration for proteins with ≥2 unique peptides

Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	DEHYDRATION 8); ATP binding						
AT5G59880.1	ADF3 (ACTIN DEPOLYMERIZING FACTOR 3); actin binding	3.9962	4.1696	4.2802	4.4018	4.4743	4.6313
AT5G60390.2	calmodulin binding / translation elongation factor	3.6537	3.7451	3.6626	3.5894	3.6608	3.5719
AT5G60960.1	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:24545649-24547214 REVERSE	4.1816	4.012	3.9663	3.9794	3.9122	3.6564
AT5G61790.1	calnexin 1 (CNX1)	5.9547	5.9095	5.7849	5.7158	5.7421	5.8655
AT5G62190.1	Symbols: PRH75 | PRH75; ATP-dependent helicase/ DEAD/H-box RNA helicase binding | chr5:24980542-24983879 REVERSE	4.0812	4.3023	3.9705	4.2075	4.254	3.8659
AT5G62530.1	| Symbols: ATP5CDH, P5CDH, ALDH12A1 | ALDH12A1 (Aldehyde dehydrogenase 12A1); 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase | chr5:25116994-25120385 REVERSE	4.2998	4.3836	4.2905	4.1599	4.1962	4.384
AT5G62690.1	TUB2 (Tubulin beta-2); structural molecule	5.2831	5.3855	5.4457	5.5021	5.3887	5.2884
AT5G63400.1	ADK1 (ADENYLATE KINASE 1); adenylate kinase	5.2564	5.2215	5.2192	5.1147	5.0827	5.2033
AT5G63510.1	GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase	4.8769	4.9133	4.8363	4.6967	4.778	4.7823
AT5G63840.1	| Symbols: RSW3 | RSW3 (RADIAL SWELLING 3); hydrolase, hydrolyzing O-glycosyl compounds | chr5:25562282-25566148 FORWARD	4.5712	4.4677	4.5058	4.4155	4.4832	4.4025
AT5G65020.1	ANNAT2 (ANNEXIN ARABIDOPSIS 2); calcium ion binding / calcium-dependent phospholipid binding	4.691	4.8918	4.7896	4.713	4.6607	5.4369
AT5G65350.1	Symbols: | histone H3 |	4.9524	5.0812	4.9234	5.0152	5.0532	4.9992

Supplementary Tables pertaining to Figure 2
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Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
	chr5:26119406-26119825 REVERSE						
AT5G66510.2	| Symbols: GAMMA CA3 | GAMMA CA3 (GAMMA CARBONIC ANHYDRASE 3) | chr5:26567242-26568722 REVERSE	4.9281	4.9616	4.9024	4.7886	4.7895	4.7803
AT5G66680.1	DGL1 (defective glycosylation 1); dolichyl-diphosphooligosaccharide-protein glycotransferase	5.6146	5.6109	5.5374	5.4463	5.4494	5.3617
AT5G66760.1	SDH1-1 (Succinate dehydrogenase 1-1)	5.3232	5.3297	5.289	5.167	5.1983	5.2393
AT5G67500.1	porin, putative	5.2982	5.3013	5.2772	5.2238	5.2102	5.243
ATMG00070.1	NADH dehydrogenase subunit 9	4.6526	4.6382	4.5944	4.5527	4.426	4.4415
ATMG00510.1	NADH dehydrogenase subunit 7	4.2684	4.2954	4.3309	4.1962	4.1861	4.2528
ATMG01190.1	ATPase subunit 1	6.168	6.1773	6.174	6.0389	6.0924	6.0597
P00330	ADH1_YEAST Alcohol dehydrogenase I (EC 1.1.1.1).	5.833	5.83	5.9568	5.8184	5.8736	5.8987

Supplementary Tables pertaining to Figure 2
Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT1G01090	1	1	1	1	1	1	4.3035	4.3975	4.462	4.3879	4.262	4.2045
AT1G04040	1	0	1	0	1	0	4.5854	4.1787	3.4836	3.4918	4.2366	3.5197
AT1G04270	1	0	0	1	0	1	4.3578	4.4281	4.3348	4.568	4.4208	4.4056
AT1G04410	1	1	1	1	1	1	4.9808	4.9913	5.2186	5.3315	5.2178	5.4524
AT1G04430	1	1	1	1	1	0	4.2382	4.3564	4.3535	4.3056	4.0263	3.9485
AT1G07810	1	1	1	0	1	0	4.6557	4.5589	4.5623	4.3804	4.4823	4.2271
AT1G07890	1	0	1	0	1	1	4.2865	4.2887	4.4674	4.6124	4.4281	4.6162
AT1G08830	1	0	1	0	1	1	3.8208	3.8168	3.9022	3.9451	3.9459	4.3706
AT1G09210	1	1	1	1	1	1	5.5183	5.3491	5.2665	5.2307	5.3066	5.3141
AT1G10760	1	1	0	1	0	1	4.0786	4.36	4.2025	4.0885	3.9743	5.2205
AT1G11580	0	0	1	1	1	0	2.7402	3.0167	4.5972	4.5721	3.9457	3.4316
AT1G11910	1	1	1	1	1	1	5.0338	5.2292	4.9196	5.0226	5.0018	5.4009
AT1G12230	1	1	1	1	1	1	4.1275	4.2259	4.4737	4.3449	4.2253	4.1231
AT1G12840	1	1	1	1	1	1	4.8177	4.7421	4.7159	4.6478	4.6457	4.6319
AT1G13280	1	1	1	1	1	1	3.8655	4.0783	4.042	3.8541	3.7912	4.7924
AT1G13440	0	0	0	0	1	1	5.7341	5.7026	5.9401	6.0085	5.8597	6.076
AT1G14670	1	0	1	0	1	0	4.8889	4.8576	4.8497	4.6575	4.6676	4.6831
AT1G14980	1	0	1	1	1	1	5.1199	4.973	4.876	4.8478	4.9295	4.7909
AT1G15690	1	1	1	1	1	1	5.4904	5.5383	5.6253	5.4745	5.4197	5.3664
AT1G15930	1	0	0	1	1	1	4.9478	4.8987	5.0684	5.2023	5.0841	4.9229
AT1G16300	1	0	0	0	0	0	4.4686	4.2944	4.0976	4.1043	4.2884	4.2691
AT1G16920	1	0	0	0	1	0	4.8311	4.7451	4.7661	4.6551	4.6637	4.6822
AT1G18080	1	1	0	1	1	1	5.273	5.2574	5.4381	5.6562	5.5971	5.3821
AT1G18540	1	0	1	1	1	0	4.8398	4.7961	4.8875	5.0494	5.0199	4.8908
AT1G20450	0	0	0	0	0	1	3.8053	4.2575	4.06	4.1044	4.0586	5.5525
AT1G20840	1	0	0	1	0	0	4.3762	4.2011	4.7365	4.3945	4.1351	4.1164
AT1G21750	1	1	1	1	1	1	6.1452	5.8932	5.9708	5.8034	5.8671	5.8633

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G21750	1	1	1	1	1	1	4.8076	4.5485	4.6275	4.4241	4.3814	4.4547
AT1G22300	1	1	1	1	1	1	4.0811	4.1499	4.3115	4.4045	4.3411	4.5578
AT1G22410	1	1	1	1	1	0	4.2109	4.2561	4.5771	4.3643	4.3295	3.9828
AT1G23190	1	0	0	0	1	1	4.177	4.2886	4.3981	4.2977	4.4128	4.8801
AT1G24180	1	1	1	1	1	1	4.9549	4.8369	4.7678	4.6518	4.7952	4.7708
AT1G24360	1	1	1	1	1	1	4.9346	4.9776	5.1476	5.1216	4.9667	4.8718
AT1G26630	1	0	0	0	1	1	4.5074	4.6234	4.7433	4.8167	4.8245	4.779
AT1G26850	1	1	1	1	1	1	4.654	4.4763	4.7452	4.6327	4.6664	4.2054
AT1G27400	1	0	1	1	0	0	4.6769	4.7217	4.9164	4.956	4.897	4.7943
AT1G30120	0	0	0	1	0	1	5.0366	5.0207	5.2325	5.1892	5.0169	4.7865
AT1G30580	0	0	0	1	1	0	4.4272	4.5201	4.7378	4.8076	4.7916	4.6639
AT1G31812	0	0	0	0	0	1	4.5534	4.6605	4.7536	4.9337	4.8305	5.1815
AT1G32900	0	0	0	0	0	1	2.6594	2.8141	3.0109	2.099	2.5071	4.7327
AT1G34430	1	1	1	1	1	1	4.4488	4.4485	4.6788	4.6342	4.4348	4.4431
AT1G35720	1	1	1	1	1	1	5.1761	4.9839	4.829	4.8852	5.0041	5.1259
AT1G42960	1	0	0	0	1	1	4.588	4.7268	4.6918	4.6679	4.4964	4.6045
AT1G43170	1	0	1	1	1	1	4.9834	4.9605	5.1265	5.2511	5.2427	4.9975
AT1G47260	1	1	1	1	1	1	5.4354	5.446	5.3547	5.3266	5.281	5.2841
AT1G47420	1	0	1	0	1	1	4.4087	4.4561	4.4324	4.1966	4.2093	4.4842
AT1G48920	1	1	0	0	1	0	4.7892	4.8517	4.6408	4.9105	4.9319	4.5352
AT1G50430	1	0	1	1	0	0	4.5633	4.5316	4.5933	4.5155	4.3795	4.1361
AT1G51980	1	1	1	1	1	1	5.5132	5.509	5.4267	5.3551	5.3279	5.3627
AT1G52070	1	1	0	0	1	1	4.8357	5.2877	3.9004	4.0216	3.9628	4.991
AT1G52360	1	0	1	0	1	0	4.1953	4.1769	4.3176	4.2435	4.2994	4.249
AT1G52670	1	1	0	0	0	0	3.9387	3.9012	4.0656	4.0162	3.8274	3.5629
AT1G53240	1	1	1	1	1	1	5.5681	5.5015	5.3211	5.3758	5.4696	5.5697
AT1G53310	1	0	0	1	1	0	3.7746	3.871	3.9123	4.1441	3.7979	4.3982

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT1G54000	1	1	1	1	1	1	5.8383	6.0064	5.255	5.054	5.4244	5.8615
AT1G54010	1	1	1	0	1	1	5.0316	5.6632	4.4402	4.5121	4.5837	4.8613
AT1G55490	1	0	0	1	1	0	5.1988	5.2003	5.2831	5.1802	5.173	5.0126
AT1G56070	1	1	1	1	1	1	5.7203	5.7486	5.8758	5.9831	5.9424	5.7818
AT1G56110	1	1	0	1	1	0	4.6603	4.7391	4.446	4.6407	4.7161	4.2451
AT1G56330	1	1	1	0	0	1	5.2853	5.1892	5.2897	5.2421	5.2243	5.2953
AT1G56340	1	1	1	1	1	1	5.8892	5.7529	5.6947	5.6603	5.7033	5.7562
AT1G57720	1	1	1	1	1	1	4.8988	4.8729	5.0267	5.1038	5.0457	4.8692
AT1G58270	1	1	1	0	1	1	5.174	4.743	4.3926	4.3824	4.6678	4.5733
AT1G61790	1	1	1	1	1	1	5.08	5.0412	4.9727	4.9127	4.893	4.822
AT1G62640	1	1	1	1	1	0	4.0512	4.1518	4.3773	4.2593	4.0923	4.2567
AT1G62660	1	1	1	1	1	1	4.4684	4.2257	4.8381	4.3733	4.3117	4.2557
AT1G63940	1	1	1	1	1	1	5.3439	5.3014	5.3177	5.1887	5.2929	5.4642
AT1G64190	1	1	1	1	1	1	4.7168	4.6751	4.8689	4.703	4.682	4.7478
AT1G65930	1	0	1	1	1	1	5.0055	4.9722	5.3552	5.417	5.2747	5.2338
AT1G66270	1	1	1	1	1	1	6.1169	5.9323	5.1801	5.1359	5.6453	5.4408
AT1G66280	1	1	1	1	1	1	5.6261	5.7475	4.7866	4.7981	5.2722	5.6851
AT1G66580	1	0	0	0	0	0	5.2067	5.2206	5.3132	5.4638	5.4692	5.2873
AT1G70600	1	0	1	1	1	1	4.5333	4.5272	4.5075	4.8645	4.7356	4.5807
AT1G70770	1	1	1	1	1	1	5.6064	5.5481	5.5259	5.3838	5.4812	5.2712
AT1G72370	1	0	1	1	1	1	4.9684	5.0681	5.0829	5.3146	5.2746	5.0359
AT1G74030	1	1	0	1	0	1	4.9835	4.9961	5.1768	5.096	5.0235	4.9595
AT1G76090	1	1	1	1	1	0	4.781	4.4459	5.1331	4.7999	4.4259	3.9332
AT1G77510	1	1	1	1	1	1	5.7392	5.5499	5.5126	5.3626	5.4307	5.6935
AT1G78300	1	1	1	1	1	0	4.1006	4.0907	4.3406	4.3361	4.3253	4.2465
AT1G78380	1	1	0	1	1	1	4.1064	4.429	4.1469	4.2344	4.1681	5.1389
AT1G78570	0	0	1	0	1	0	4.3609	4.3431	4.4649	4.0542	4.3067	4.0217

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT1G78900	1	1	1	1	1	1	5.8624	5.7834	5.8111	5.6755	5.738	5.6665
AT1G79440	1	1	1	0	1	1	4.3236	4.4096	4.4837	4.2941	4.2009	4.5889
AT1G79530	1	1	1	1	1	1	5.1886	5.1927	5.2567	5.1289	5.1121	5.1624
AT1G79550	1	1	1	1	1	1	4.8457	4.8922	5.2159	5.2934	5.1916	5.1945
AT1G79930	0	0	0	1	0	1	3.7006	3.887	3.881	4.0282	4.0509	3.9498
AT2G01140	1	1	1	1	1	1	5.3412	5.3473	5.4567	5.3614	5.3324	5.3299
AT2G01250	1	0	1	1	1	1	5.0661	5.0365	5.1296	5.3206	5.2864	5.074
AT2G01720	1	1	1	0	1	1	5.335	5.3252	5.2619	5.2093	5.2754	5.2896
AT2G03120	0	0	0	0	0	1	4.8033	4.7449	4.6511	4.5204	4.6408	4.7148
AT2G04030	1	1	1	1	1	0	5.0074	5.0149	4.906	4.832	4.9329	4.8494
AT2G05710	1	1	1	1	1	1	5.0683	4.9923	4.9377	4.8899	4.9529	5.073
AT2G05990	1	1	1	1	1	1	4.7194	4.7455	4.9988	4.8283	4.6922	4.5987
AT2G07050	1	1	1	1	1	1	4.0729	4.1524	4.3671	4.24	4.1678	4.0075
AT2G14720	1	0	1	0	0	1	4.4456	4.5842	4.5067	4.5217	4.3922	4.4662
AT2G16600	1	0	0	1	1	1	4.613	4.7662	4.7644	4.8798	4.8591	5.1447
AT2G17720	1	1	1	0	1	0	5.0021	4.6061	4.6291	4.5376	4.6379	4.2928
AT2G18020	1	1	1	1	1	1	5.2426	5.2352	5.2954	5.422	5.4429	5.1936
AT2G18230	0	0	0	0	0	1	3.2731	3.4755	3.3495	3.6272	3.6346	4.5709
AT2G20360	1	1	1	1	1	1	4.8233	4.8873	4.8168	4.7202	4.778	4.7487
AT2G20420	1	1	1	1	1	1	5.493	5.3984	5.3078	5.221	5.3648	5.3691
AT2G20530	1	1	1	1	1	1	4.454	4.4949	4.2554	4.3848	4.3275	4.2249
AT2G21160	1	1	1	1	1	0	5.3968	5.3386	5.2922	5.2152	5.1911	5.0368
AT2G21170	1	1	1	1	1	1	4.4375	4.5333	4.5899	4.4263	4.3445	4.8003
AT2G21390	1	0	0	1	1	1	4.1564	4.2242	4.4437	4.3092	4.3379	4.4411
AT2G21410	1	1	0	0	0	1	4.8539	4.8363	4.9183	4.67	4.6913	4.7379
AT2G21660	1	1	1	1	1	1	5.3764	5.3356	5.513	5.6543	5.6108	5.4813
AT2G21870	1	1	1	1	1	1	5.1717	5.1749	5.1299	4.9462	4.9356	5.0004

Supplementary Tables pertaining to Figure 2
Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT2G22170	1	0	1	0	1	1	5.0687	5.1616	5.2935	4.9886	5.0082	5.4028
AT2G25980	1	1	0	0	1	1	4.7767	5.025	4.2015	4.2023	4.3901	4.5048
AT2G27730	1	1	1	0	1	1	5.0473	4.9905	4.9249	4.809	4.7963	4.6357
AT2G27860	1	0	0	0	0	1	4.0347	3.9441	4.1922	4.3391	4.2712	4.321
AT2G28000	1	1	1	1	1	1	5.2885	5.2846	5.3103	5.2584	5.2647	5.1384
AT2G29550	0	0	0	1	0	0	3.9376	4.1862	4.2623	4.481	4.3263	4.1965
AT2G30200	1	1	1	1	1	1	4.3596	4.3729	4.4217	4.4006	4.3784	4.2338
AT2G30490	1	1	1	1	1	1	3.8467	3.9516	4.6679	4.1431	4.1294	3.9353
AT2G30860	1	0	0	1	1	1	4.4767	4.8856	5.0045	5.2214	4.8722	5.5216
AT2G30970	1	1	1	1	1	1	4.4746	4.4891	4.4235	4.2028	4.3273	4.2792
AT2G31390	1	1	1	1	1	1	4.5078	4.6801	4.8838	4.9388	4.7695	5.0982
AT2G31610	1	0	1	0	1	0	5.1926	5.2646	5.3064	5.4885	5.4381	5.2642
AT2G32060	0	0	0	0	1	0	4.1252	4.139	4.306	4.604	4.5095	4.3075
AT2G33040	1	1	1	1	1	1	5.3631	5.386	5.3075	5.2667	5.1975	5.2353
AT2G33150	1	1	1	1	1	1	5.1306	5.1322	5.0595	4.8156	4.9201	5.3018
AT2G33210	1	1	1	1	1	1	5.3523	5.2495	5.2044	5.1726	5.1828	5.0186
AT2G33220	1	0	1	1	1	1	4.6539	4.686	4.6229	4.534	4.541	4.5811
AT2G34480	1	0	1	1	1	1	4.5096	4.4775	4.6301	4.7982	4.678	4.5161
AT2G35605	1	0	0	0	1	0	4.7187	4.6519	4.4563	4.5714	4.6485	4.5013
AT2G36160	1	0	1	0	0	1	4.5601	4.5064	4.6799	4.7777	4.8026	4.5889
AT2G36460	0	0	0	0	0	1	5.4599	5.4291	5.6665	5.7777	5.6612	5.5897
AT2G36530	1	1	1	1	1	1	5.2833	5.2727	5.549	5.7399	5.6265	5.5763
AT2G36880	0	1	1	0	1	0	4.4394	4.714	4.8883	4.9006	4.6952	4.5134
AT2G38040	1	1	1	1	1	1	4.3097	4.383	4.5288	4.433	4.2342	4.1345
AT2G38750	1	1	1	0	1	1	5.1136	5.1967	4.3326	3.9249	4.6725	4.0714
AT2G39800	0	0	1	0	0	0	3.2499	3.2953	4.2227	3.8961	3.4994	3.2284
AT2G40510	1	0	0	0	1	0	4.9703	4.9714	5.1174	5.2796	5.2553	5.1347

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT2G41840	1	0	0	1	1	0	4.8556	4.907	4.927	5.1642	5.1242	4.8918
AT2G42210	1	1	1	0	1	1	4.8924	4.9143	4.8142	4.7672	4.7939	4.7207
AT2G43090	1	0	0	1	1	1	4.6848	4.7237	4.6896	4.5592	4.6201	4.7079
AT2G43610	0	1	0	0	0	1	3.004	3.649	2.6684	3.1517	2.8679	3.6161
AT2G44790	1	0	1	1	1	1	4.4538	4.28	4.6034	4.7585	4.527	4.2034
AT2G45740	0	0	0	0	0	1	4.4388	4.5927	4.6147	4.3525	4.232	4.8222
AT2G47470	1	1	1	1	1	1	5.4676	5.3934	5.3784	5.365	5.3089	5.5573
AT2G47510	1	1	1	1	1	1	4.0259	3.9991	3.9059	3.8645	3.8369	3.7587
AT3G01280	1	1	1	1	1	1	5.747	5.8046	5.7006	5.7013	5.6453	5.5641
AT3G01390	1	0	1	0	1	1	4.7619	4.7414	4.7112	4.5846	4.566	4.8521
AT3G02090	1	1	1	1	1	1	5.8455	5.852	5.7469	5.6936	5.7102	5.6846
AT3G02230	1	1	1	1	1	1	4.9919	4.8057	4.902	4.9072	4.9681	5.055
AT3G02530	1	0	0	1	1	0	3.7203	3.6968	3.9781	4.1774	4.1933	4.0086
AT3G02630	1	1	0	1	1	0	4.3966	4.4878	4.5704	4.4928	4.3467	4.4607
AT3G02780	1	0	1	0	1	1	4.0008	3.9799	4.1638	4.1604	4.1365	4.3256
AT3G03960	1	0	1	1	1	0	4.3701	4.4418	4.4568	4.6892	4.6379	4.5256
AT3G04120	0	1	0	1	0	1	4.6678	4.5824	4.7637	4.9271	4.7032	4.7936
AT3G04840	1	1	1	1	1	1	4.923	4.9337	4.918	5.2009	5.1918	4.9543
AT3G05560	1	0	1	0	0	1	5.0878	5.0859	5.1322	5.1463	5.0521	4.9845
AT3G06300	1	1	1	0	1	1	4.7894	4.4161	4.2912	4.2111	4.4467	3.9979
AT3G06860	1	1	1	0	1	1	4.0015	3.9532	3.846	3.6598	3.8333	4.2926
AT3G07770	1	1	1	1	1	1	4.567	4.476	4.2387	4.3247	4.2677	4.0243
AT3G08580	1	1	1	1	1	1	5.9422	5.9418	5.8863	5.8363	5.7693	5.7975
AT3G09200	1	1	0	1	1	1	5.3473	5.3242	5.4664	5.6316	5.6232	5.4354
AT3G09260	1	1	1	1	1	1	6.1616	6.2885	5.4886	5.3711	5.8827	6.0015
AT3G09440	1	0	1	1	1	0	4.6749	4.6095	4.6888	4.6688	4.7628	4.7725
AT3G09630	1	0	0	1	1	0	5.007	5	4.9952	5.2103	5.1781	5.0169

Supplementary Tables pertaining to Figure 2
Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT3G09820	1	1	0	1	1	1	4.4109	4.4406	4.5619	4.7175	4.6819	4.5432
AT3G09840	1	1	0	1	1	0	4.6297	4.6245	4.7774	4.9173	4.9194	4.9818
AT3G10370	1	0	1	0	1	1	3.7075	3.6736	3.4259	3.2406	3.5349	3.6771
AT3G11130	1	1	1	1	1	1	4.3704	4.2747	4.4342	4.396	4.3538	4.4011
AT3G11250	0	0	0	1	0	0	4.0284	4.0735	4.2471	4.2876	4.2108	3.9583
AT3G11830	1	0	0	1	1	0	4.0768	4.1694	4.3164	4.5326	4.4695	4.2993
AT3G12780	1	1	1	1	1	1	4.2843	4.3436	4.6534	4.4609	4.3546	4.5626
AT3G13860	1	1	1	1	1	1	4.6321	4.541	4.4083	4.3689	4.4366	4.4217
AT3G13870	1	1	1	0	1	1	4.6401	4.5249	4.426	4.3423	4.3335	4.4839
AT3G13920	1	0	1	1	1	1	5.3863	5.4692	5.5585	5.5498	5.5456	5.4142
AT3G13930	1	1	1	1	1	1	5.1271	5.0705	5.0596	4.9264	4.9908	5.0276
AT3G14990	0	0	0	1	0	1	3.5112	3.8125	4.0581	4.2327	4.1698	4.9944
AT3G15000	1	0	1	0	1	1	4.9187	4.9095	4.7901	4.8011	4.9231	4.6631
AT3G15020	1	1	1	1	1	1	5.5452	5.4912	5.4518	5.3591	5.4737	5.509
AT3G15730	1	0	1	1	1	1	3.7714	3.6665	3.8443	3.8962	3.7938	4.2931
AT3G15950	1	1	1	1	1	1	6.0657	5.9345	5.1331	5.0702	5.5965	5.5535
AT3G16410	1	1	0	0	1	1	5.1239	5.318	4.533	4.4454	4.7804	4.9839
AT3G16420	1	1	1	0	1	1	5.4951	5.5968	5.005	4.9619	5.1392	5.7362
AT3G16460	1	1	1	0	1	1	6.1121	6.1421	5.2974	5.2755	5.625	5.8886
AT3G16480	1	1	1	1	1	1	4.754	4.774	4.7212	4.6037	4.5373	4.5259
AT3G17240	1	1	1	1	1	1	4.8004	4.6925	4.7045	4.6127	4.6907	4.7509
AT3G17390	1	1	1	0	1	1	5.3861	5.5389	5.6434	5.6138	5.5871	5.461
AT3G17810	1	1	0	1	0	1	4.3236	4.3639	4.3315	4.1861	4.1545	4.5406
AT3G18000	0	0	1	0	0	1	3.9431	4.0984	4.6957	4.4883	4.2225	4.4926
AT3G18130	0	1	0	1	1	0	4.2937	4.349	4.4611	4.6508	4.5746	4.2999
AT3G18190	1	0	0	1	1	0	4.4387	4.5279	4.6778	4.8599	4.8636	4.6418
AT3G19820	1	1	1	1	1	1	5.7369	5.7698	5.9862	5.8156	5.6221	5.4318

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT3G20000	1	1	1	1	1	1	4.9937	5.0125	4.9129	4.9045	4.8835	4.8013
AT3G20050	1	0	0	1	1	0	3.9372	4.0782	4.1769	4.4782	4.5947	4.3751
AT3G20370	1	1	1	0	1	1	5.1122	4.8314	4.0459	3.8266	4.5114	4.7024
AT3G22200	1	1	1	1	1	1	4.4365	4.3276	4.1881	4.0101	4.1732	4.6819
AT3G22960	1	1	1	1	1	1	4.5401	4.5646	4.7703	4.6696	4.5142	4.4899
AT3G23990	1	1	1	1	1	1	5.8109	5.7646	5.6665	5.6175	5.6417	5.6391
AT3G25860	1	1	1	1	1	1	5.1489	5.1783	5.3634	5.2945	5.1158	5.0308
AT3G27240	1	1	1	1	1	1	4.5913	4.6229	4.5959	4.4873	4.5814	4.5106
AT3G42050	1	1	1	1	1	1	4.8446	4.7727	4.814	4.6928	4.7037	4.7862
AT3G44110	0	0	0	0	1	0	4.6584	4.5435	4.7726	4.7446	4.6781	4.459
AT3G44330	1	1	1	1	1	1	4.8023	4.7689	4.8324	4.6998	4.6984	4.5755
AT3G46040	0	0	0	0	0	1	4.4014	4.4435	4.4543	4.5927	4.4724	4.4211
AT3G47520	1	1	1	1	1	1	5.4958	5.4767	5.595	5.474	5.476	5.435
AT3G48000	1	1	1	1	1	1	4.5333	4.9012	5.1262	4.5337	4.2413	5.1701
AT3G48340	1	1	1	0	1	1	5.3197	5.0337	4.0398	4.1866	4.7924	4.5722
AT3G48870	0	1	1	1	1	0	4.6316	4.7102	4.8497	4.7602	4.7193	4.7503
AT3G48930	0	0	1	0	1	0	4.8503	4.8714	5.0293	5.2007	5.1526	4.943
AT3G49010	1	0	0	0	1	0	4.8492	4.8595	4.9253	5.0743	5.1014	4.8402
AT3G49720	1	1	1	1	1	1	5.0195	5.0182	4.9533	4.7816	4.8745	4.811
AT3G49910	1	0	0	1	1	1	4.1579	4.172	4.3339	4.4869	4.3645	4.3128
AT3G51800	1	0	0	0	1	0	3.7834	3.8019	3.8363	4.2056	4.2568	3.9705
AT3G52200	1	1	1	0	1	1	4.6468	4.5472	4.4784	4.3806	4.4196	4.5413
AT3G52300	1	1	1	1	1	1	5.4492	5.4733	5.4224	5.3321	5.3282	5.3363
AT3G52580	0	0	0	0	1	0	5.1432	5.0862	5.2597	5.3923	5.3786	5.1303
AT3G52730	1	0	0	0	1	0	4.6371	4.6306	4.5251	4.4378	4.4527	4.2571
AT3G52930	1	1	1	1	1	1	5.5683	5.5524	5.8128	5.8669	5.7527	5.6383
AT3G52960	1	1	1	1	1	0	4.9005	4.8725	5.0996	4.9412	4.8105	4.8031

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT3G53430	0	1	0	0	0	0	5.4739	5.4452	5.5971	5.6892	5.7109	5.4987
AT3G54960	1	1	1	1	1	1	5.5307	5.122	4.9639	4.7323	5.0842	4.9861
AT3G55360	1	1	1	1	1	0	4.3896	4.4377	4.4518	4.3359	4.2545	4.0549
AT3G55410	1	1	1	1	1	1	4.9533	4.8934	4.7269	4.6654	4.7844	4.7053
AT3G55440	1	1	1	1	1	1	4.7648	4.7728	4.9382	5.1329	5.0795	5.185
AT3G57010	0	1	1	1	1	1	4.2169	4.4836	4.6949	4.9575	4.8002	4.5937
AT3G57610	1	1	1	1	1	1	4.4158	4.4343	4.5338	4.5027	4.3997	4.4199
AT3G58610	1	1	1	1	1	1	5.236	5.2361	5.2607	5.1631	5.2035	5.103
AT3G60750	1	1	1	1	1	1	5.4188	5.3885	5.6072	5.406	5.3649	5.4938
AT3G60770	0	0	0	0	1	0	4.8602	4.8762	4.9476	5.1277	5.0925	4.8806
AT3G61440	1	0	1	1	1	1	4.3458	4.402	4.6445	4.4443	4.2977	4.5729
AT3G62360	1	1	1	1	1	1	5.3191	5.2744	5.2936	5.1941	5.1984	5.0488
AT3G62830	1	1	1	1	1	1	4.5912	4.4251	4.3553	4.2445	4.3343	4.5807
AT4G00490	1	1	0	0	0	1	4.0842	4.0415	4.0324	3.93	3.8331	4.6723
AT4G00860	1	0	1	1	1	1	4.6568	4.6419	4.6332	4.5827	4.3948	4.5688
AT4G01100	1	1	1	1	1	1	4.9291	4.807	4.7611	4.7383	4.8193	4.4809
AT4G01850	1	1	1	0	1	0	4.8284	4.6919	4.658	4.8043	4.793	4.6068
AT4G02450	1	0	1	0	1	0	4.6206	4.6874	4.8319	5.0508	4.9584	4.8488
AT4G02930	1	1	1	1	1	1	5.1353	5.0099	4.9639	4.848	4.9155	4.8432
AT4G05020	1	1	1	1	1	1	4.3335	4.2066	4.2164	3.8954	4.1697	4.2196
AT4G09000	1	1	1	1	1	1	4.3582	4.408	4.5783	4.7434	4.739	4.8332
AT4G09020	1	1	0	0	0	1	3.9904	4.1767	3.9523	3.9121	3.8667	4.9168
AT4G09320	1	1	1	1	1	1	4.8838	4.9275	5.0623	5.2222	5.221	5.107
AT4G11010	1	1	1	1	1	1	4.6302	4.557	4.5037	4.5118	4.299	4.4473
AT4G11150	1	1	1	1	1	1	5.1781	5.0848	5.1882	4.9489	5.0096	5.008
AT4G11820	1	0	0	1	1	0	3.8329	3.9139	4.3463	4.417	4.1772	3.8392
AT4G12650	1	1	1	1	1	1	4.8412	4.888	4.7873	4.7037	4.7249	4.7977

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
AT4G13850	1	0	0	0	1	0	5.3827	5.2356	5.16	5.1835	5.2129	5.0167
AT4G13930	1	1	1	1	1	1	4.4792	4.4473	4.8639	4.8404	4.8052	4.7143
AT4G13940	1	1	1	1	1	1	5.6033	5.6233	5.8223	5.9336	5.8692	5.786
AT4G14800	1	0	0	1	1	0	4.1125	4.1244	4.3132	4.413	4.3879	4.4414
AT4G16155	1	1	0	1	1	1	4.6793	4.6907	4.962	4.8394	4.6393	4.4602
AT4G16450	1	0	1	1	1	1	4.591	4.6259	4.606	4.5507	4.5936	4.5184
AT4G16660	1	1	1	1	1	1	4.7744	4.5723	4.5095	4.4285	4.5179	4.7335
AT4G17530	1	0	0	0	0	1	4.9535	4.7389	4.8327	4.7352	4.6628	4.5612
AT4G18030	1	1	1	1	1	1	4.6261	4.7645	4.8121	4.6818	4.6219	4.3457
AT4G18100	1	0	0	1	1	0	4.7145	4.6337	4.7505	4.9791	4.9609	4.6693
AT4G21150	1	1	1	1	1	1	5.6213	5.6093	5.5482	5.4655	5.4869	5.3946
AT4G23620	1	0	1	0	1	0	4.161	4.0235	3.9649	3.8695	3.9571	3.8414
AT4G23710	1	0	0	0	1	0	4.5821	4.3589	4.4049	4.2986	4.4225	3.9934
AT4G24190	1	1	1	1	1	1	5.8716	5.8089	5.7345	5.6844	5.6873	5.8602
AT4G24280	1	1	1	1	1	0	4.6619	4.6147	4.7204	4.619	4.6016	4.5162
AT4G24830	1	1	0	1	1	1	5.1177	5.0998	5.0778	5.0247	5.1305	4.9972
AT4G25630	1	0	0	1	1	0	5.3594	5.4537	5.2508	5.4363	5.4918	5.1198
AT4G27090	1	0	0	1	1	1	5.154	5.2241	5.2172	5.3362	5.3229	5.2434
AT4G27500	1	0	0	0	1	0	4.6939	4.4071	4.4474	4.2278	4.3261	4.1767
AT4G29130	1	1	1	1	1	1	4.6875	4.7244	4.5839	4.4743	4.5097	4.6265
AT4G29690	1	1	1	0	1	1	4.7962	5.2679	4.6773	4.6816	4.5758	5.2433
AT4G29840	1	1	1	1	1	1	4.5329	4.5463	4.6277	4.4613	4.5531	4.4398
AT4G30190	1	1	1	0	1	1	5.067	5.2049	4.984	4.8031	4.8878	4.9867
AT4G31340	1	1	1	1	1	1	4.9857	4.8282	4.9502	4.7312	4.7706	4.5413
AT4G31700	0	0	0	0	1	0	4.4477	4.4531	4.5262	4.7556	4.7276	4.5424
AT4G32470	1	1	1	0	1	1	5.0818	5.084	4.9913	4.9382	4.9608	4.9511
AT4G33680	1	1	1	1	1	1	4.5316	4.5051	4.5135	4.4507	4.5509	4.5427

Supplementary Tables pertaining to Figure 2
Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT4G34200	1	1	1	1	1	1	5.675	5.6575	5.8032	5.639	5.652	5.6439
AT4G34450	1	1	1	1	1	1	4.6361	4.6799	4.883	4.8056	4.7926	4.8423
AT4G34670	0	0	0	1	1	0	3.5027	3.4451	3.4687	3.7811	3.7258	3.585
AT4G34870	1	1	1	1	1	1	4.8598	4.9691	5.0564	5.1146	4.9769	5.3747
AT4G35090	1	1	1	1	1	1	5.0527	5.0496	5.0797	4.7672	4.8482	5.2645
AT4G35100	1	1	1	1	1	1	4.476	4.3355	4.8199	4.7087	4.5672	4.0719
AT4G35630	1	0	1	1	1	1	4.941	5.0277	5.2299	5.0287	5.0216	5.0884
AT4G37910	1	1	1	1	1	1	5.599	5.4984	5.3624	5.331	5.4615	5.2293
AT4G38510	1	1	1	0	1	1	4.9208	4.8143	4.8748	4.685	4.7787	4.6379
AT4G38740	1	0	1	1	1	1	5.2921	5.3395	5.5419	5.5646	5.5587	5.598
AT4G39260	1	0	0	1	1	1	4.6902	4.6175	4.7743	4.987	4.9994	4.784
AT4G39980	1	1	1	0	1	0	4.6671	4.6774	4.8616	4.6525	4.6177	4.4674
AT5G02500	1	1	1	1	1	1	6.0607	5.9649	6.048	6.088	6.0833	6.0653
AT5G02870	1	0	0	0	1	0	4.5237	4.5426	4.5943	4.8027	4.8265	4.6761
AT5G03160	1	1	1	0	1	1	4.2493	4.0983	3.8785	3.9901	3.9701	4.06
AT5G05170	1	1	1	1	1	0	4.181	4.1135	4.4428	4.1384	4.1788	3.8188
AT5G07350	1	0	0	0	0	0	4.262	4.326	4.4335	4.366	4.336	4.3017
AT5G07440	1	1	1	1	1	1	5.3248	5.3553	5.0598	4.7531	5.0378	5.255
AT5G08300	1	1	1	1	1	1	4.7184	4.5519	4.4052	4.3227	4.4671	4.4793
AT5G08530	1	1	1	1	1	1	4.9701	5.0115	4.9132	4.8288	4.8201	4.8779
AT5G08670	0	0	0	0	1	0	6.2722	6.2788	6.2426	6.1358	6.1548	6.1494
AT5G09590	1	1	1	1	1	1	5.1222	5.026	4.9514	4.9099	4.9953	4.9118
AT5G09810	1	1	0	1	1	1	4.9713	4.8854	5.0453	5.1143	5.1249	4.926
AT5G11520	1	1	1	0	1	1	4.5216	4.4099	4.5433	4.3754	4.547	4.5842
AT5G11560	1	1	1	1	1	1	5.2009	5.1692	5.1053	5.0443	5.0062	4.9488
AT5G11770	1	1	1	1	1	1	4.6907	4.733	4.4593	4.5806	4.6323	4.5679
AT5G13420	1	1	1	1	1	1	4.7427	4.7394	4.9989	4.8942	4.7622	4.6776

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT5G13450	1	1	1	1	1	1	5.4446	5.4135	5.297	5.2833	5.2887	5.1892
AT5G13710	1	1	1	1	1	1	4.7216	4.6641	5.1517	5.0927	4.7632	4.5055
AT5G14030	1	1	1	1	1	1	5.2844	5.2454	5.2145	5.0886	5.1049	4.9258
AT5G14040	1	1	1	1	1	1	5.3556	5.315	5.2356	5.1566	5.2202	5.1975
AT5G15090	1	1	1	1	1	1	5.8086	5.8374	5.7249	5.673	5.6689	5.5175
AT5G15200	1	0	0	1	1	1	5.011	5.0296	5.1263	5.3166	5.3144	5.0957
AT5G15490	0	0	0	0	0	1	4.6517	4.6082	4.7426	4.752	4.8633	5.0968
AT5G15520	0	0	0	0	0	1	5.0788	5.1244	5.1271	5.3795	5.1985	5.0804
AT5G15650	1	1	1	1	1	1	5.4914	5.4101	5.3763	5.4464	5.4531	5.8287
AT5G16130	1	0	0	1	0	0	4.6018	4.6827	4.7459	4.8483	4.7581	4.6171
AT5G16390	1	0	0	0	0	0	4.7288	4.7242	4.8433	4.795	4.6995	4.6157
AT5G17770	1	1	1	1	1	1	4.9422	4.9774	5.0638	5.1211	4.9845	4.8421
AT5G17920	1	1	1	1	1	1	5.6811	5.6952	5.9072	6.0074	5.9189	6.0626
AT5G18380	0	0	0	1	1	1	4.4741	4.5457	4.6995	4.8725	4.8075	4.6319
AT5G19510	1	0	0	0	1	0	4.8497	4.7981	5.001	5.0809	5.0379	4.8625
AT5G19760	1	1	1	1	1	1	5.5621	5.5536	5.5725	5.4297	5.4172	5.5644
AT5G20290	1	1	0	1	1	0	5.4335	5.4168	5.5477	5.7212	5.6863	5.4879
AT5G20720	1	1	1	1	1	1	5.2557	5.2684	5.3165	5.2688	5.2301	5.254
AT5G20890	0	0	0	1	1	0	4.152	4.1506	4.3069	4.4619	4.4457	4.2758
AT5G20980	1	0	0	0	0	0	5.1308	5.1246	5.405	5.504	5.338	5.5135
AT5G22880	1	0	1	0	1	1	5.3018	5.4661	5.3473	5.3372	5.3714	5.3721
AT5G23300	1	1	1	1	1	1	4.4402	4.4646	4.3728	4.3924	4.4167	4.2794
AT5G23820	1	1	1	0	1	1	4.9953	5.4862	4.6988	4.6035	4.6454	5.7432
AT5G25100	1	1	1	0	1	1	5.3517	5.3354	5.3355	5.1753	5.1567	5.1417
AT5G26260	1	1	1	1	1	1	5.7521	5.6522	4.842	4.7997	5.3183	5.3447
AT5G26280	1	1	1	1	0	1	4.3434	4.0864	3.5868	3.7906	3.8446	3.8584
AT5G26360	0	0	0	1	1	0	4.1691	4.2912	4.431	4.4674	4.4568	4.4006

Supplementary Tables pertaining to Figure 2
Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						Peak-integration log intensity values					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT5G27670	0	0	0	0	0	1	4.3318	4.5947	4.305	4.3696	4.3824	4.7496
AT5G28060	0	0	0	1	1	0	4.8221	4.8558	4.9314	5.1344	5.0793	4.8795
AT5G28540	1	1	1	1	1	1	5.3369	5.1344	5.1363	5.0197	5.117	5.1899
AT5G35360	1	1	1	1	1	1	5.368	5.3857	5.5498	5.4695	5.3266	5.2268
AT5G35630	1	1	1	1	1	1	5.0746	4.9099	4.6781	4.455	4.8256	4.8091
AT5G35940	1	1	0	0	1	1	4.558	5.0478	4.0844	4.1224	4.255	4.5952
AT5G37510	1	1	1	1	1	1	5.4447	5.4567	5.3778	5.3006	5.2893	5.284
AT5G38480	1	1	0	1	1	1	4.6577	4.7412	4.906	5.0553	4.9957	5.2305
AT5G38530	1	1	1	0	0	0	4.2323	4.3374	4.2582	3.9762	4.1382	4.3268
AT5G39320	1	0	0	0	1	0	3.8965	3.585	3.7541	3.9777	4.0409	3.7308
AT5G39740	0	0	0	0	1	0	5.0808	5.1046	5.1815	5.3055	5.3289	5.098
AT5G40770	1	1	1	1	1	1	4.2862	4.3845	4.2067	4.1715	3.8804	4.2406
AT5G42020	1	1	1	1	1	1	6.2818	6.1113	6.0026	5.9738	6.021	6.1321
AT5G42020	1	1	1	1	1	1	4.4413	4.3303	4.3882	4.5366	4.5033	4.3306
AT5G42080	1	1	1	1	1	1	4.4594	4.3819	4.3763	4.3086	4.3306	4.3056
AT5G42960	1	1	1	1	1	1	3.995	4.0853	4.0793	4.0153	3.9008	3.675
AT5G42980	1	1	1	0	1	1	4.8301	4.9631	5.049	5.1798	5.1175	5.3696
AT5G43060	1	1	1	1	1	1	4.6008	4.6899	4.7141	4.533	4.4568	4.8492
AT5G44020	1	1	1	0	1	1	4.9493	4.4697	4.3956	4.4859	4.6599	4.0657
AT5G47030	1	1	0	1	1	1	5.1663	5.077	5.0317	4.9713	4.974	4.8571
AT5G47770	1	0	1	1	1	0	4.0541	4.1116	4.4567	4.398	4.1997	4.2351
AT5G47990	1	1	1	0	1	1	4.2952	4.4063	4.1436	3.3959	3.9095	3.9733
AT5G48810	1	1	1	0	1	1	4.8755	4.7291	4.8051	4.5832	4.4551	4.4536
AT5G49460	0	1	0	1	1	1	4.2261	4.3264	4.7652	4.7885	4.5931	4.5574
AT5G50850	1	1	1	1	1	1	5.0322	4.9514	4.9107	4.8065	4.9438	4.9994
AT5G52840	1	1	1	1	1	1	5.1293	5.1088	5.0276	4.9665	5.0107	4.9853
AT5G52920	1	1	1	1	1	0	4.3667	4.4066	4.5002	4.5903	4.4677	4.1385

Supplementary Tables pertaining to Figure 2

Supplementary Table S13. Proteins found in both GeLC-MS/MS and peak-integration proteomic approaches coupled with FACS

	GeLC-MS/MS binary values						**Peak-integration log intensity values**					
Locus	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
AT5G53460	1	1	1	1	1	1	4.2191	4.2435	3.7467	3.9608	4.2063	4.3079
AT5G53560	1	1	1	1	1	1	5.2221	5.2178	5.2209	4.9937	4.9387	4.9595
AT5G54100	1	1	0	1	1	1	4.2729	4.2819	4.1678	3.9686	4.0027	4.2652
AT5G56030	1	0	0	1	1	0	5.509	5.5747	5.7839	5.8255	5.7665	5.6537
AT5G59880	1	0	1	0	0	1	3.9962	4.1696	4.2802	4.4018	4.4743	4.6313
AT5G60960	1	0	0	0	1	0	4.1816	4.012	3.9663	3.9794	3.9122	3.6564
AT5G61790	1	1	1	1	1	1	5.9547	5.9095	5.7849	5.7158	5.7421	5.8655
AT5G62190	0	0	0	0	1	0	4.0812	4.3023	3.9705	4.2075	4.254	3.8659
AT5G62530	1	1	1	1	1	1	4.2998	4.3836	4.2905	4.1599	4.1962	4.384
AT5G63400	1	1	1	1	1	1	5.2564	5.2215	5.2192	5.1147	5.0827	5.2033
AT5G63510	1	1	0	0	1	0	4.8769	4.9133	4.8363	4.6967	4.778	4.7823
AT5G63840	1	1	1	1	1	1	4.5712	4.4677	4.5058	4.4155	4.4832	4.4025
AT5G65020	1	1	1	1	1	1	4.691	4.8918	4.7896	4.713	4.6607	5.4369
AT5G66510	1	1	1	1	1	1	4.9281	4.9616	4.9024	4.7886	4.7895	4.7803
AT5G66680	1	1	1	1	1	1	5.6146	5.6109	5.5374	5.4463	5.4494	5.3617
AT5G66760	1	1	1	1	1	1	5.3232	5.3297	5.289	5.167	5.1983	5.2393
AT5G67500	1	1	1	1	1	1	5.2982	5.3013	5.2772	5.2238	5.2102	5.243
ATMG00070	1	1	1	1	1	1	4.6526	4.6382	4.5944	4.5527	4.426	4.4415
ATMG00510	1	1	1	1	1	1	4.2684	4.2954	4.3309	4.1962	4.1861	4.2528

Supplementary Tables pertaining to Figure 3

Supplementary Table S14. Root hair proteins of this study that were also found in the root hair transcriptome studies of Jones et al. (48), Won et al. (49), or Deal et al. (50)

Loci in the list of 606 genes comprising the 'root-hair morphogenesis transcriptome' of Jones *et al.* 2006	**Loci in the list of 904 genes of Won et al. 2009 with an Root Hair Element (RHE) in their proximal promoter**	**Loci in the list of 638 genes of Won et al. 2009 down-regulated 2-fold in 3 root hair arrays**	**Loci in the list of 946 genes of Deal et al. 2009 enriched in hair versus non-hair cells (>1.3, p<0.02))**
AND in the list of Proteins identified only in root hairs (238 proteins) by FACS coupled with GeLC-MS/MS in this study			
AT2G40800	AT1G14710	AT1G30870	AT1G30870
AT3G09740	AT1G19140	AT1G63450	AT2G19160
AT3G11730	AT1G63450	AT2G37670	AT2G37670
AT3G23190	AT1G75940	AT2G47540	AT3G53990
AT4G11600	AT2G18030	AT3G01290	AT4G16500
AT4G26010	AT2G34560	AT3G23190	AT4G26010
AT4G35860	AT3G01190	AT4G09990	AT5G04960
AT5G01220	AT3G27300	AT4G26010	AT5G49270
AT5G04960	AT4G27640	AT5G04960	AT5G59910
	AT4G34180	AT5G49270	
	AT5G46160	AT5G49680	
	AT5G56730		
AND in the list of Proteins identified in this study of whole roots sorted by FACS of wild-type and/or hairy mutant roots but not in hairless mutant roots (202 proteins)			
AT2G19760	AT1G20580	AT1G58270	AT1G04270
AT4G04910	AT1G58270	AT2G38750	AT1G18540
	AT1G76010	AT3G16450	AT1G63660
	AT3G02530	AT5G47990	AT2G09990
	AT3G44110		AT2G21580
	AT5G35940		AT2G27530
			AT2G32060
			AT3G11510
			AT3G53020
			AT4G21960
			AT4G27090
			AT4G39200
			AT5G27770
			AT5G35530
			AT5G47700
			AT5G67630

Supplementary Tables pertaining to Figure 3

Supplementary Table S15. Novel candidate regulators of root hair development and function

Proteins identified only in root hairs in the Root Cellular Proteome that have available homozygous insertion lines from the Arabidopsis Biological Resource Center (ABRC)

Locus	Insertion Line Name
At1g01910	SALK_012980C
At1g06890	SALK_073566C
At1g14210	SALK_035618C
At1g15710	SALK_131009C
At1g15710	SALK_081796C
At1g17160	SALK_137479C
At1g17160	SALK_005371C
At1g17890	SALK_020145C
At1g21560	SALK_044476C
At1g23170	SALK_046821C
At1g26160	SALK_123482C
At1g26160	SALK_005997C
At1g29250	SALK_069210C
At1g30450	SALK_048175C
At1g31860	SALK_027157C
At1g48230	SALK_063985C
At1g48900	SALK_112379C
At1g63450	SALK_028024C
At1g66580	SALK_126907C
At1g72280	SALK_050000C
At1g72480	SALK_143646C
At1g74910	SALK_065562C
At1g75940	SALK_133498C
At1g76690	SALK_042219C
At1g76690	SALK_021194C
At2g19860	SALK_150524C
At2g19860	SALK_080584C
At2g21250	SALK_021705C
At2g38650	SALK_046348C
At2g38650	SALK_015189C
At2g45990	SALK_141449C
At2g45990	SALK_142699C
At3g01290	SALK_124393C
At3g01290	SALK_033877C
At3g02660	SALK_045570C
At3g02660	SALK_016722C
At3g03050	SALK_070920C
At3g05420	SALK_019656C
At3g07470	SALK_015333C
At3g11170	SALK_147096C
At3g11730	SALK_033433C
At3g13460	SALK_002225C
At3g23510	SALK_069357C
At3g23510	SALK_018286C
At3g27020	SALK_119560C
At3g27020	SALK_093392C
At3g29250	SALK_148412C
At3g29250	SALK_082262C
At3g48110	SALK_102661C

Supplementary Tables pertaining to Figure 3

Supplementary Table S15. Novel candidate regulators of root hair development and function

Proteins identified only in root hairs in the Root Cellular Proteome that have available homozygous insertion lines from the Arabidopsis Biological Resource Center (ABRC)

At3g48890	SALK_056475C
At3g48890	SALK_042103C
At3g51440	SALK_046142C
At3g51980	SALK_012739C
At3g52190	SALK_147561C
At3g52190	SALK_037068C
At3g52570	SALK_141979C
At3g53180	SALK_016332C
At3g54840	SALK_004698C
At3g55920	SALK_034811C
At3g60850	SALK_013745C
At4g00710	SALK_022072C
At4g04860	SALK_067527C
At4g13050	SALK_111046C
At4g13050	SALK_062204C
At4g21540	SALK_000250C
At4g21540	SALK_022916C
At4g25570	SALK_058385C
At4g29430	SALK_118515C
At4g32880	SALK_023733C
At5g04710	SALK_035555C
At5g10830	SALK_133463C
At5g10830	SALK_099512C
At5g12200	SALK_064708C
At5g12200	SALK_038919C
At5g14060	SALK_003685C
At5g16930	SALK_083164C
At5g20490	SALK_067972C
At5g22740	SALK_149092C
At5g23740	SALK_069193C
At5g38460	SALK_130472C
At5g38460	SALK_077252C
At5g43830	SALK_016986C
At5g47040	SALK_043857C
At5g49270	SALK_099933C
At5g49270	SALK_020771C

Supplementary Table S16. Raw data output from the Trans-Proteomic Pipeline of LTQ runs performed using wild-type, *caprice triptychon*, and *werewolf myb23* mutant sorted root samples. Tranche hash: FbsvAjRbRcuHV0c2hF7GQ8AQq/MZUm6GaUu3ZGOQehHW6zspVtGvrvQ28rzttWItW5sua/OynnxUDA68YBcPZcD4FtEAAAAAAAAEIQ==

These raw data have been uploaded for public release and access at the Proteome Commons and are found at www.proteomecommons.org/tranche under the project "The Protein Expression Landscape of the *Arabidopsis* Root". The data files for Supplementary Table S16, which includes all raw data of the proteome from whole roots of wild-type, *caprice triptychon*, or *werewolf myb23* mutants, were too large for the file formats allowed in the Supplementary Information section. Thus, these data are found at Proteome Commons under the aforementioned project title and are accessible with the following Tranche hash:

FbsvAjRbRcuHV0c2hF7GQ8AQq/MZUm6GaUu3ZGOQehHW6zspVtGvrvQ28rzttWItW5sua/OynnxUDA68YBcPZcD4FtEAAAAAAAAEIQ==

All encryption at the tranche repository should be removed, but if a passphrase is requested, it is 'arabidopsis'.

Supplementary Table S16 can also be found at the Duke Genome Express Repository at the following:

https://discovery.genome.duke.edu/express/resources/2010/Final_Supplementary_Table_S16.xls

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G01090	1	1	1
AT1G01100	1	0	1
AT1G01910	1	0	0
AT1G02080	1	0	0
AT1G02500	1	1	1
AT1G02690	0	0	1
AT1G02780	1	1	1
AT1G02840	1	0	1
AT1G03860	1	1	1
AT1G04080	1	0	0
AT1G04170	1	0	1
AT1G04190	1	0	0
AT1G04270	1	0	1
AT1G04410	1	1	1
AT1G04430	0	1	0
AT1G04690	1	1	1
AT1G05520	1	0	0
AT1G06220	1	0	1
AT1G06290	1	1	1
AT1G06530	1	0	0
AT1G06950	1	1	1
AT1G07140	1	0	1
AT1G07670	1	1	0
AT1G07830	1	0	0
AT1G07890	1	1	1
AT1G08200	0	1	0
AT1G08360	1	0	1
AT1G08480	1	1	1
AT1G08830	1	1	1
AT1G09210	1	1	1
AT1G09620	1	0	1
AT1G09640	1	1	1
AT1G09760	1	0	1
AT1G09770	1	0	0
AT1G09780	1	1	1
AT1G09830	0	0	1
AT1G10270	1	0	0
AT1G10290	1	0	1
AT1G10490	0	0	1
AT1G10760	0	1	0
AT1G10840	1	0	1
AT1G10950	0	1	1
AT1G11580	0	1	0
AT1G11650	1	0	0
AT1G11680	1	1	0
AT1G11840	0	0	1
AT1G11860	1	1	0
AT1G11910	1	1	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G12000	1	1	1
AT1G12230	1	0	0
AT1G12240	0	1	0
AT1G12270	1	0	0
AT1G12410	1	1	0
AT1G12840	1	1	1
AT1G13280	1	1	0
AT1G14210	0	1	0
AT1G14320	0	0	1
AT1G14410	0	1	0
AT1G14610	1	0	1
AT1G14620	1	1	1
AT1G14670	1	0	0
AT1G14710	0	0	1
AT1G14810	0	1	1
AT1G14830	1	1	1
AT1G14850	1	0	0
AT1G14980	1	0	0
AT1G15210	0	1	0
AT1G15390	1	0	0
AT1G15500	1	1	1
AT1G15690	1	1	1
AT1G15930	1	1	1
AT1G16300	0	1	0
AT1G16350	1	0	1
AT1G16870	0	0	1
AT1G17290	1	0	1
AT1G17470	1	0	0
AT1G17880	1	0	1
AT1G18080	1	1	1
AT1G18210	1	0	0
AT1G18500	1	0	1
AT1G18540	1	0	1
AT1G18850	1	0	1
AT1G19360	1	0	1
AT1G19580	0	0	1
AT1G19880	1	0	0
AT1G20010	1	0	0
AT1G20200	1	0	1
AT1G20220	0	0	1
AT1G20330	1	1	1
AT1G20440	0	1	0
AT1G20450	0	1	0
AT1G20580	1	0	1
AT1G20630	0	1	0
AT1G20950	1	1	1
AT1G20960	1	0	1
AT1G21160	0	1	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G21730	1	0	0
AT1G21750	1	1	1
AT1G22300	1	1	1
AT1G22410	1	1	1
AT1G22440	0	0	1
AT1G22450	1	1	1
AT1G23190	1	1	0
AT1G23290	1	0	0
AT1G23820	1	1	1
AT1G24180	1	1	1
AT1G24360	1	1	1
AT1G24510	1	1	1
AT1G25350	1	0	0
AT1G25490	1	1	1
AT1G26460	1	1	1
AT1G26630	1	1	1
AT1G26850	1	1	1
AT1G26940	1	1	1
AT1G27090	1	0	0
AT1G27130	1	0	0
AT1G27390	1	0	0
AT1G27400	0	0	1
AT1G27450	1	0	1
AT1G27930	0	0	1
AT1G27970	0	0	1
AT1G28290	1	1	0
AT1G29150	1	0	1
AT1G29880	1	0	1
AT1G29900	1	1	1
AT1G29940	0	0	1
AT1G30230	1	0	1
AT1G30400	0	0	1
AT1G30580	1	1	1
AT1G30630	1	1	1
AT1G31180	1	1	0
AT1G31230	1	0	0
AT1G31850	1	0	1
AT1G31970	1	0	0
AT1G32230	1	0	0
AT1G32380	1	0	0
AT1G33750	0	1	0
AT1G34130	1	1	1
AT1G34430	1	1	1
AT1G35160	1	1	1
AT1G35620	1	1	0
AT1G35720	1	1	1
AT1G43170	1	1	1
AT1G43890	0	1	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G44170	0	1	0
AT1G44835	1	0	0
AT1G45332	0	0	1
AT1G47260	1	1	1
AT1G47290	1	0	0
AT1G47420	1	1	1
AT1G47600	0	1	0
AT1G48030	1	1	1
AT1G48410	1	0	0
AT1G48630	1	1	1
AT1G48830	1	0	1
AT1G48850	0	1	0
AT1G48860	1	0	0
AT1G48900	1	0	0
AT1G48920	1	1	1
AT1G49600	1	0	1
AT1G49760	1	0	1
AT1G50060	0	1	0
AT1G50200	1	1	0
AT1G50380	1	0	0
AT1G50430	1	0	0
AT1G50920	1	0	1
AT1G51710	0	0	1
AT1G51980	1	1	1
AT1G52060	1	0	0
AT1G52070	0	1	1
AT1G52360	0	1	0
AT1G52600	1	0	0
AT1G52670	0	0	1
AT1G52980	1	0	0
AT1G53240	1	1	1
AT1G53260	0	0	1
AT1G53310	1	1	1
AT1G53390	1	0	0
AT1G53645	1	0	0
AT1G53750	1	0	1
AT1G53850	1	0	0
AT1G54000	1	1	1
AT1G54010	1	1	1
AT1G54030	1	0	1
AT1G54080	1	0	0
AT1G54270	1	0	0
AT1G55160	1	0	0
AT1G55440	1	0	0
AT1G55490	1	1	1
AT1G55890	1	1	1
AT1G56070	1	1	1
AT1G56110	1	1	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G56330	1	0	0
AT1G56340	1	1	1
AT1G56410	1	0	0
AT1G56450	1	1	1
AT1G57720	1	1	1
AT1G58080	0	1	0
AT1G58270	1	0	1
AT1G59610	1	1	0
AT1G59900	0	1	0
AT1G59990	1	0	0
AT1G60770	0	1	1
AT1G61580	0	0	1
AT1G61790	0	1	1
AT1G61870	1	1	0
AT1G62020	0	0	1
AT1G62330	0	1	0
AT1G62640	1	1	0
AT1G62660	1	0	0
AT1G62740	1	0	0
AT1G63000	1	0	1
AT1G63660	1	0	1
AT1G63770	1	1	1
AT1G63780	0	1	1
AT1G63940	1	1	1
AT1G64190	1	1	1
AT1G64520	1	1	1
AT1G64650	0	1	0
AT1G64790	1	1	1
AT1G64880	1	0	1
AT1G65270	1	1	1
AT1G65930	1	1	1
AT1G65980	0	0	1
AT1G66270	1	1	1
AT1G66280	1	1	1
AT1G66430	0	1	0
AT1G67430	1	0	0
AT1G67490	1	0	0
AT1G67730	1	1	1
AT1G69830	0	1	0
AT1G70310	1	0	1
AT1G70730	0	0	1
AT1G70770	1	1	1
AT1G71220	1	1	1
AT1G71260	1	1	0
AT1G72370	1	1	1
AT1G72440	1	0	0
AT1G72550	1	0	0
AT1G72730	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT1G72750	1	1	1
AT1G73230	1	0	1
AT1G73970	0	1	0
AT1G74020	0	1	0
AT1G74030	1	1	1
AT1G74230	1	0	1
AT1G74260	1	1	0
AT1G74380	0	0	1
AT1G74560	1	1	1
AT1G74920	0	1	0
AT1G75200	0	0	1
AT1G75330	1	1	0
AT1G76010	1	0	1
AT1G76090	1	1	1
AT1G76400	0	1	0
AT1G77510	1	1	1
AT1G77590	0	1	1
AT1G77940	1	1	1
AT1G78300	1	1	0
AT1G78380	1	1	1
AT1G78570	1	0	0
AT1G78660	1	0	0
AT1G78900	1	1	1
AT1G78920	1	0	1
AT1G79010	1	0	1
AT1G79230	0	1	0
AT1G79280	0	0	1
AT1G79440	1	1	1
AT1G79530	1	1	1
AT1G79550	1	1	1
AT1G79750	1	1	1
AT1G79920	1	0	1
AT1G79930	1	1	1
AT1G79940	1	1	1
AT1G79990	0	0	1
AT1G80070	1	0	1
AT1G80270	1	1	1
AT1G80410	1	0	1
AT1G80560	1	1	1
AT1G80600	1	1	1
AT2G01140	1	1	1
AT2G01250	1	1	1
AT2G01470	1	1	1
AT2G01720	1	1	1
AT2G02050	0	1	0
AT2G02560	0	0	1
AT2G02740	0	1	0
AT2G03120	1	1	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT2G03510	1	0	1
AT2G03820	1	0	0
AT2G04030	1	1	1
AT2G04280	1	0	0
AT2G04400	1	1	0
AT2G05710	1	1	1
AT2G05840	0	1	0
AT2G05990	1	1	1
AT2G06990	1	0	0
AT2G07050	1	1	1
AT2G09990	1	0	1
AT2G14170	1	1	1
AT2G16570	1	0	1
AT2G16600	1	1	1
AT2G16950	1	0	0
AT2G17130	1	1	0
AT2G17265	1	1	0
AT2G17420	1	1	1
AT2G17630	1	1	1
AT2G18020	1	1	1
AT2G18110	1	0	0
AT2G18330	0	1	1
AT2G18900	1	0	1
AT2G18960	0	1	0
AT2G19080	0	1	0
AT2G19480	0	0	1
AT2G19730	1	1	1
AT2G19760	1	0	1
AT2G19940	1	1	1
AT2G20060	1	1	1
AT2G20360	1	1	1
AT2G20420	1	1	1
AT2G20450	1	0	0
AT2G20530	1	0	0
AT2G20580	1	1	1
AT2G20990	1	1	0
AT2G21160	1	0	1
AT2G21170	1	1	1
AT2G21390	1	1	1
AT2G21580	1	0	1
AT2G21660	1	1	1
AT2G21870	1	1	1
AT2G22230	1	1	0
AT2G22250	0	1	0
AT2G22780	1	1	0
AT2G22795	0	1	0
AT2G23350	1	0	1
AT2G24200	1	1	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT2G25110	0	0	1
AT2G25280	1	0	0
AT2G25970	1	0	1
AT2G25980	1	0	1
AT2G26080	1	1	1
AT2G26140	1	1	0
AT2G27020	1	1	1
AT2G27530	1	0	1
AT2G27710	1	0	1
AT2G27720	1	1	1
AT2G27730	1	1	1
AT2G27840	1	0	0
AT2G27860	1	0	0
AT2G28000	1	1	1
AT2G28430	1	1	1
AT2G29080	1	0	0
AT2G29550	1	1	1
AT2G30050	1	0	1
AT2G30110	1	1	1
AT2G30200	1	1	1
AT2G30490	0	1	0
AT2G30860	1	1	1
AT2G30870	1	1	1
AT2G30970	1	1	1
AT2G31390	1	1	1
AT2G31660	1	0	0
AT2G31810	1	1	1
AT2G32060	1	0	1
AT2G32730	1	1	0
AT2G32920	1	1	1
AT2G33040	1	1	1
AT2G33150	1	1	1
AT2G33210	1	1	1
AT2G33220	1	1	1
AT2G33340	1	0	1
AT2G33410	1	0	1
AT2G33845	0	0	1
AT2G34357	1	0	0
AT2G34480	1	1	1
AT2G34590	1	1	0
AT2G34630	0	1	0
AT2G35040	1	1	1
AT2G35720	0	0	1
AT2G36070	0	1	0
AT2G36250	1	0	0
AT2G36390	0	1	0
AT2G36460	1	0	1
AT2G36530	1	1	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	**wild type**	***caprice triptychon***	***werewolf myb23***
AT2G36850	0	1	0
AT2G36880	1	0	0
AT2G37170	0	1	0
AT2G37220	1	0	0
AT2G37230	1	1	0
AT2G37250	1	0	0
AT2G37690	1	1	1
AT2G37990	1	0	0
AT2G38040	1	1	1
AT2G38750	1	0	1
AT2G38770	1	0	0
AT2G39800	1	0	0
AT2G39960	0	1	1
AT2G39990	1	1	1
AT2G40010	1	1	0
AT2G40290	1	1	0
AT2G40360	1	0	0
AT2G40510	1	0	1
AT2G40660	0	0	1
AT2G41220	1	1	0
AT2G41530	1	0	1
AT2G41840	1	1	1
AT2G42210	1	1	1
AT2G42710	1	0	1
AT2G42910	1	0	1
AT2G43090	1	1	1
AT2G43710	1	1	1
AT2G43750	1	1	1
AT2G43950	0	0	1
AT2G44060	1	0	0
AT2G44100	0	0	1
AT2G44120	1	1	1
AT2G44350	1	1	1
AT2G44610	0	1	1
AT2G44640	1	0	0
AT2G44790	0	1	0
AT2G44860	0	0	1
AT2G45030	1	0	0
AT2G45060	0	0	1
AT2G45290	1	0	0
AT2G45300	0	1	0
AT2G45440	1	1	0
AT2G45790	1	1	0
AT2G45990	0	1	0
AT2G46140	1	0	0
AT2G46280	1	1	1
AT2G46520	1	1	1
AT2G47000	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT2G47250	1	0	1
AT2G47470	1	1	1
AT2G47510	1	1	1
AT2G47610	1	0	1
AT2G47650	1	1	1
AT2G47730	1	1	1
AT2G47800	0	1	0
AT2G47990	1	0	0
AT3G01120	1	1	1
AT3G01280	1	1	1
AT3G01540	1	0	0
AT3G01910	0	0	1
AT3G02080	1	0	1
AT3G02090	1	1	1
AT3G02200	1	1	1
AT3G02230	1	1	1
AT3G02320	0	0	1
AT3G02360	1	1	0
AT3G02520	1	1	1
AT3G02530	1	0	1
AT3G02560	0	0	1
AT3G02650	1	1	1
AT3G02760	1	0	1
AT3G02780	1	1	0
AT3G03100	1	1	0
AT3G03250	1	1	1
AT3G03600	0	1	0
AT3G03640	0	1	0
AT3G03780	1	0	0
AT3G03920	1	0	1
AT3G03960	1	1	1
AT3G04080	0	1	0
AT3G04120	1	1	1
AT3G04600	1	0	1
AT3G04830	0	1	0
AT3G04840	1	1	1
AT3G04920	1	1	1
AT3G05060	1	0	1
AT3G05230	0	1	0
AT3G05420	1	0	0
AT3G05560	1	1	1
AT3G05970	1	0	0
AT3G06050	1	1	1
AT3G06350	0	1	0
AT3G06530	1	0	1
AT3G06720	0	0	1
AT3G06860	0	1	1
AT3G07050	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT3G07100	1	0	0
AT3G07110	1	1	1
AT3G07160	1	0	0
AT3G07480	1	1	1
AT3G07770	1	1	1
AT3G08530	0	0	1
AT3G08580	1	1	1
AT3G08590	1	1	0
AT3G08943	1	1	0
AT3G09200	1	1	1
AT3G09260	1	1	1
AT3G09440	1	1	1
AT3G09630	1	1	1
AT3G09820	1	1	1
AT3G09840	1	1	0
AT3G09940	0	0	1
AT3G10050	1	0	1
AT3G10690	1	1	0
AT3G10920	1	1	0
AT3G11070	1	1	1
AT3G11130	1	1	0
AT3G11400	0	0	1
AT3G11510	1	0	1
AT3G11630	1	1	1
AT3G11710	1	0	0
AT3G11830	1	1	1
AT3G11910	1	0	1
AT3G11940	0	0	1
AT3G11964	1	0	1
AT3G12260	1	1	1
AT3G12390	1	0	1
AT3G12670	1	0	1
AT3G12780	0	1	1
AT3G13160	1	1	1
AT3G13235	1	0	0
AT3G13300	0	1	0
AT3G13460	1	0	1
AT3G13580	1	1	1
AT3G13772	1	1	1
AT3G13860	1	1	1
AT3G13870	1	1	1
AT3G13920	1	0	1
AT3G13930	1	1	1
AT3G14067	0	1	0
AT3G14220	0	1	0
AT3G14290	0	0	1
AT3G14390	1	1	1
AT3G14550	0	1	0

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT3G14600	1	0	0
AT3G14990	1	0	0
AT3G15000	1	0	1
AT3G15020	0	1	0
AT3G15090	1	1	1
AT3G15290	0	0	1
AT3G15730	1	1	1
AT3G15950	1	1	1
AT3G16110	1	1	1
AT3G16410	1	1	1
AT3G16420	1	1	1
AT3G16430	1	0	0
AT3G16450	1	0	1
AT3G16460	1	1	1
AT3G16480	0	1	1
AT3G16640	1	1	1
AT3G16780	1	0	0
AT3G16950	1	1	1
AT3G17240	1	1	1
AT3G17390	1	1	1
AT3G17810	1	1	1
AT3G17820	1	0	1
AT3G17940	1	0	0
AT3G18000	1	0	1
AT3G18130	1	1	1
AT3G18190	1	1	1
AT3G18580	1	1	1
AT3G18600	1	0	1
AT3G19170	1	1	0
AT3G19760	1	1	0
AT3G19820	1	1	1
AT3G20000	1	1	1
AT3G20050	1	1	1
AT3G20330	0	0	1
AT3G20370	1	1	1
AT3G20390	1	1	1
AT3G20940	0	0	1
AT3G21110	1	1	0
AT3G21140	0	1	0
AT3G21540	1	0	0
AT3G22110	1	1	1
AT3G22200	0	0	1
AT3G22310	1	0	1
AT3G22330	1	0	1
AT3G22630	1	0	0
AT3G22660	1	0	1
AT3G22890	1	0	0
AT3G22960	1	1	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT3G23620	1	0	1
AT3G23830	1	0	1
AT3G23940	0	0	1
AT3G23990	1	1	1
AT3G24170	0	0	1
AT3G24830	1	1	1
AT3G25110	0	1	0
AT3G25140	0	1	0
AT3G25230	1	0	0
AT3G25520	1	0	1
AT3G25530	1	0	0
AT3G25780	1	1	0
AT3G25860	1	1	1
AT3G26340	0	0	1
AT3G26520	0	1	1
AT3G26720	1	1	0
AT3G27240	1	1	1
AT3G27280	1	1	0
AT3G27380	0	1	0
AT3G27430	1	0	0
AT3G27570	1	0	0
AT3G27740	1	1	0
AT3G28710	1	0	1
AT3G28715	0	1	0
AT3G28720	0	1	0
AT3G29320	0	1	0
AT3G29360	1	0	0
AT3G42050	1	1	1
AT3G44110	1	0	1
AT3G44320	1	0	0
AT3G44330	1	1	1
AT3G44340	1	0	1
AT3G44750	1	0	1
AT3G45450	1	0	0
AT3G46740	1	1	1
AT3G46940	1	0	0
AT3G47370	1	1	1
AT3G47520	1	1	1
AT3G47930	0	0	1
AT3G48000	1	1	1
AT3G48140	0	1	1
AT3G48170	1	1	0
AT3G48340	0	1	1
AT3G48410	1	1	1
AT3G48560	1	1	1
AT3G48680	1	1	1
AT3G48870	1	0	1
AT3G48890	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT3G48930	1	0	0
AT3G49010	1	1	1
AT3G49080	1	0	1
AT3G49100	0	0	1
AT3G49240	1	1	1
AT3G49430	0	0	1
AT3G49560	1	1	0
AT3G49680	1	1	1
AT3G49720	1	1	1
AT3G49910	1	1	1
AT3G51260	1	1	1
AT3G51800	1	1	1
AT3G52140	1	0	1
AT3G52200	0	1	0
AT3G52300	1	1	1
AT3G52930	1	1	1
AT3G52960	1	1	1
AT3G53020	1	0	1
AT3G53180	1	0	0
AT3G53520	1	1	0
AT3G53580	1	1	0
AT3G53740	0	1	0
AT3G53870	1	0	1
AT3G53990	1	0	0
AT3G54110	1	1	1
AT3G54470	1	0	1
AT3G54640	0	1	0
AT3G54960	1	1	1
AT3G55010	1	0	0
AT3G55360	0	1	1
AT3G55410	1	1	1
AT3G55440	1	1	1
AT3G55620	1	0	1
AT3G55920	1	0	0
AT3G56070	1	0	1
AT3G56150	1	1	1
AT3G56190	1	0	1
AT3G56490	0	0	1
AT3G57000	1	0	0
AT3G57010	1	1	1
AT3G57150	1	1	1
AT3G57290	1	1	1
AT3G57610	1	1	1
AT3G57650	0	1	0
AT3G57660	1	0	0
AT3G57940	1	0	0
AT3G58510	1	0	1
AT3G58610	1	1	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT3G58730	0	0	1
AT3G58750	0	1	0
AT3G59020	1	0	1
AT3G59650	1	0	1
AT3G59760	1	1	1
AT3G59920	1	0	1
AT3G59970	1	1	0
AT3G60750	1	1	1
AT3G60820	1	0	1
AT3G61070	1	1	0
AT3G61440	0	1	1
AT3G62030	0	1	1
AT3G62120	1	0	1
AT3G62360	1	1	1
AT3G62530	1	1	1
AT3G62830	0	0	1
AT3G62870	1	1	0
AT3G63130	1	0	0
AT3G63460	1	1	1
AT4G00100	1	1	1
AT4G00490	0	1	0
AT4G00570	1	1	1
AT4G00620	1	1	1
AT4G00860	1	1	1
AT4G01100	1	1	1
AT4G01320	0	1	1
AT4G01850	1	1	1
AT4G01900	1	0	0
AT4G02150	1	0	0
AT4G02230	0	0	1
AT4G02450	1	0	0
AT4G02510	0	1	0
AT4G02580	1	1	1
AT4G02620	1	0	0
AT4G02930	1	1	1
AT4G04910	1	0	1
AT4G04940	1	0	0
AT4G05020	0	1	0
AT4G05390	0	1	0
AT4G05410	1	0	0
AT4G05530	0	1	0
AT4G07410	1	0	0
AT4G08390	1	0	0
AT4G09000	1	1	1
AT4G09020	0	1	0
AT4G09320	1	1	1
AT4G10320	1	0	1
AT4G10450	1	0	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT4G10480	1	1	1
AT4G11010	0	1	0
AT4G11120	1	1	1
AT4G11150	1	1	1
AT4G11260	1	0	0
AT4G11420	1	1	1
AT4G11820	1	0	0
AT4G12130	1	0	0
AT4G12590	1	0	0
AT4G12600	1	0	1
AT4G12650	1	1	1
AT4G13430	1	1	1
AT4G13780	1	0	1
AT4G13850	1	0	0
AT4G13930	1	1	1
AT4G13940	1	1	1
AT4G14030	1	0	1
AT4G14160	1	0	0
AT4G14570	1	0	0
AT4G14800	0	1	1
AT4G14880	1	0	0
AT4G15000	1	0	1
AT4G16143	1	0	1
AT4G16155	1	1	1
AT4G16450	0	0	1
AT4G16660	1	1	1
AT4G16760	1	1	1
AT4G17040	0	1	0
AT4G17520	1	0	1
AT4G17770	1	0	0
AT4G18030	1	1	1
AT4G18100	1	1	1
AT4G18440	0	1	0
AT4G19030	0	1	0
AT4G19120	0	1	0
AT4G20020	1	0	1
AT4G20360	1	1	1
AT4G20850	1	1	1
AT4G20890	1	0	0
AT4G20980	1	0	0
AT4G21150	1	1	1
AT4G21960	1	0	1
AT4G22670	1	0	1
AT4G23460	1	0	0
AT4G23540	1	0	0
AT4G23590	0	0	1
AT4G23620	0	0	1
AT4G23650	1	0	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT4G23850	1	0	0
AT4G24190	1	1	1
AT4G24280	1	1	1
AT4G24330	1	1	0
AT4G24620	1	1	1
AT4G24800	1	0	0
AT4G24820	1	0	0
AT4G24830	1	1	1
AT4G25550	1	0	1
AT4G25630	1	1	1
AT4G25740	1	1	1
AT4G26110	1	1	1
AT4G26300	1	0	1
AT4G26410	1	0	0
AT4G26780	1	1	1
AT4G26900	1	1	1
AT4G26910	0	1	0
AT4G26970	1	1	0
AT4G27080	0	1	0
AT4G27090	1	0	1
AT4G27500	1	0	0
AT4G27585	1	0	1
AT4G27760	0	1	0
AT4G28360	0	0	1
AT4G28440	1	0	0
AT4G28470	1	1	0
AT4G28510	1	1	1
AT4G29010	0	1	0
AT4G29130	1	1	1
AT4G29350	1	1	1
AT4G29410	1	1	1
AT4G29510	0	0	1
AT4G29690	1	1	1
AT4G29840	1	1	1
AT4G30010	0	1	0
AT4G30190	1	0	1
AT4G30920	1	0	1
AT4G30930	1	0	0
AT4G30990	1	0	1
AT4G31120	1	0	1
AT4G31180	1	0	1
AT4G31300	1	1	1
AT4G31340	1	1	1
AT4G31480	0	1	0
AT4G31490	1	0	0
AT4G31500	0	1	0
AT4G31700	1	0	1
AT4G31810	1	1	1

Supplementary Tables pertaining to Figure 3
Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT4G31990	1	1	1
AT4G32470	1	1	0
AT4G32520	1	1	1
AT4G32720	1	0	1
AT4G33090	1	1	1
AT4G33120	0	1	1
AT4G33250	1	1	0
AT4G33360	1	1	1
AT4G33580	1	1	1
AT4G33650	1	0	0
AT4G33680	1	1	1
AT4G34110	1	1	1
AT4G34200	1	1	1
AT4G34450	1	1	1
AT4G34670	1	0	1
AT4G34700	1	1	1
AT4G34870	1	1	1
AT4G35000	1	1	1
AT4G35090	1	1	1
AT4G35100	1	1	1
AT4G35260	1	1	1
AT4G35490	1	0	0
AT4G35630	1	1	1
AT4G35830	1	0	1
AT4G35850	1	1	1
AT4G35860	1	0	0
AT4G36680	1	0	0
AT4G37400	0	0	1
AT4G37640	1	0	0
AT4G37830	1	0	1
AT4G37910	1	1	1
AT4G38220	1	1	1
AT4G38350	1	0	1
AT4G38510	1	1	1
AT4G38630	1	0	0
AT4G38680	1	0	1
AT4G38740	1	1	1
AT4G39080	1	1	1
AT4G39200	1	0	1
AT4G39260	1	0	1
AT4G39520	1	0	1
AT4G39660	1	1	1
AT4G39680	1	0	0
AT4G39690	0	0	1
AT4G39880	0	0	1
AT4G39980	1	1	1
AT5G02050	1	0	0
AT5G02490	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G02500	1	1	1
AT5G02740	1	0	1
AT5G02870	1	1	1
AT5G03160	0	0	1
AT5G03290	1	1	1
AT5G03300	1	0	1
AT5G03630	1	1	1
AT5G04430	1	1	1
AT5G04590	1	1	1
AT5G04600	1	0	1
AT5G04990	0	1	0
AT5G05000	1	0	1
AT5G05010	1	1	1
AT5G05170	0	1	0
AT5G05470	1	0	0
AT5G05780	1	1	1
AT5G06060	1	0	0
AT5G06110	1	0	0
AT5G06460	1	0	0
AT5G07340	0	1	1
AT5G07350	1	1	1
AT5G07440	1	1	1
AT5G08060	1	1	1
AT5G08180	0	0	1
AT5G08300	1	1	1
AT5G08530	1	1	1
AT5G09590	1	1	1
AT5G09650	1	1	1
AT5G09810	1	1	1
AT5G09900	1	0	1
AT5G10160	0	1	0
AT5G10360	1	0	0
AT5G10450	1	0	1
AT5G10540	1	0	0
AT5G10730	1	0	1
AT5G10840	0	0	1
AT5G10860	0	1	1
AT5G11520	0	1	0
AT5G11560	1	1	1
AT5G11670	1	0	0
AT5G11770	1	1	1
AT5G11880	1	1	1
AT5G12470	1	1	1
AT5G13110	1	1	0
AT5G13120	1	0	0
AT5G13280	1	0	0
AT5G13420	1	1	1
AT5G13450	1	1	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G13490	1	1	1
AT5G13520	1	0	0
AT5G13710	1	1	1
AT5G13780	1	0	0
AT5G13850	1	0	0
AT5G14030	1	1	1
AT5G14040	1	1	1
AT5G14240	1	0	0
AT5G14520	1	0	1
AT5G14590	1	1	0
AT5G14800	1	0	1
AT5G15090	1	1	1
AT5G15200	1	1	1
AT5G15450	0	1	0
AT5G15490	0	1	0
AT5G15550	1	0	1
AT5G15610	1	0	0
AT5G15650	1	1	1
AT5G15910	1	0	0
AT5G16050	1	1	0
AT5G16130	1	1	1
AT5G17020	1	0	0
AT5G17270	0	0	1
AT5G17770	0	1	1
AT5G17920	1	1	1
AT5G18170	1	1	1
AT5G18280	0	0	1
AT5G18380	0	1	0
AT5G19350	1	0	0
AT5G19440	1	0	1
AT5G19510	1	0	1
AT5G19520	1	0	0
AT5G19550	1	0	1
AT5G19690	1	0	1
AT5G19760	1	1	1
AT5G19820	1	0	0
AT5G20080	0	0	1
AT5G20090	0	0	1
AT5G20290	1	1	1
AT5G20660	0	1	0
AT5G20720	1	1	1
AT5G20890	1	1	1
AT5G20920	1	0	0
AT5G20960	1	0	0
AT5G22100	1	0	0
AT5G22330	1	0	0
AT5G22440	1	0	1
AT5G22650	1	0	1

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G22740	1	0	1
AT5G22880	1	1	1
AT5G23140	0	1	0
AT5G23300	0	1	1
AT5G23540	1	0	1
AT5G23575	1	1	0
AT5G23630	1	1	0
AT5G23740	0	1	0
AT5G23820	1	0	0
AT5G23830	1	0	0
AT5G23900	1	1	1
AT5G24650	1	1	1
AT5G25100	1	1	1
AT5G25780	1	0	0
AT5G26260	1	1	1
AT5G26280	1	0	0
AT5G26360	1	1	1
AT5G26710	1	0	1
AT5G26780	1	1	1
AT5G26830	1	1	1
AT5G26860	0	1	0
AT5G27120	1	0	1
AT5G27330	1	0	0
AT5G27470	1	0	1
AT5G27540	1	1	1
AT5G27640	1	0	1
AT5G27770	1	0	1
AT5G27850	1	1	1
AT5G28060	1	0	1
AT5G28540	0	1	1
AT5G28840	1	0	0
AT5G34850	0	1	0
AT5G35160	1	1	1
AT5G35360	1	1	1
AT5G35530	1	0	1
AT5G35590	1	0	1
AT5G35630	1	1	1
AT5G35940	1	0	1
AT5G36210	1	0	0
AT5G36230	1	1	1
AT5G37475	0	0	1
AT5G37510	1	1	1
AT5G37830	0	0	1
AT5G38470	1	0	0
AT5G38480	1	1	1
AT5G38530	0	0	1
AT5G39320	1	0	1
AT5G39740	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G39840	1	0	0
AT5G40480	1	1	1
AT5G40770	1	1	1
AT5G40810	0	1	1
AT5G40890	0	1	0
AT5G41520	1	1	1
AT5G41670	1	1	1
AT5G41970	1	0	1
AT5G42020	1	1	0
AT5G42080	1	1	1
AT5G42090	0	0	1
AT5G42150	1	0	0
AT5G42740	1	0	0
AT5G42790	1	0	1
AT5G42960	1	0	1
AT5G42980	1	1	1
AT5G43060	1	1	0
AT5G43780	0	1	0
AT5G43830	1	0	1
AT5G43940	1	0	1
AT5G43960	1	0	0
AT5G43970	0	1	1
AT5G45620	1	0	0
AT5G45750	1	1	0
AT5G46160	1	0	0
AT5G46290	1	1	1
AT5G46430	1	0	1
AT5G47030	0	0	1
AT5G47210	1	0	0
AT5G47320	1	0	0
AT5G47690	1	0	0
AT5G47700	1	0	1
AT5G47770	1	0	1
AT5G47890	1	1	1
AT5G47990	1	0	1
AT5G48030	1	0	0
AT5G48110	0	1	0
AT5G48180	1	0	0
AT5G48230	0	0	1
AT5G48580	1	1	1
AT5G48760	1	0	0
AT5G48810	1	0	1
AT5G49460	0	1	0
AT5G49810	1	0	0
AT5G49910	1	0	1
AT5G50375	0	1	1
AT5G50850	1	1	1
AT5G50920	0	1	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G52240	1	0	1
AT5G52470	0	0	1
AT5G52650	1	0	0
AT5G52840	1	1	1
AT5G52920	1	1	1
AT5G53070	1	0	0
AT5G53400	1	0	1
AT5G53460	1	1	1
AT5G53480	1	0	0
AT5G53560	1	0	1
AT5G54100	0	1	0
AT5G54580	1	0	1
AT5G54810	1	0	1
AT5G55070	1	1	1
AT5G55610	0	0	1
AT5G55920	0	0	1
AT5G55940	1	1	1
AT5G56010	0	0	1
AT5G56030	1	0	0
AT5G56360	1	1	0
AT5G56500	1	1	1
AT5G56680	1	0	1
AT5G56950	1	0	0
AT5G57020	1	0	0
AT5G57090	1	0	0
AT5G57110	0	1	0
AT5G57490	1	1	1
AT5G57870	1	0	1
AT5G58290	0	0	1
AT5G59840	1	0	0
AT5G59870	1	1	1
AT5G59880	1	1	1
AT5G60640	1	1	1
AT5G60700	0	1	0
AT5G60730	1	1	0
AT5G60790	0	0	1
AT5G60960	0	1	1
AT5G60980	1	0	1
AT5G61020	1	0	0
AT5G61170	0	0	1
AT5G61240	1	0	0
AT5G61780	1	0	1
AT5G61790	1	1	1
AT5G61840	0	0	1
AT5G62190	1	0	1
AT5G62390	1	0	1
AT5G62530	1	1	1
AT5G63190	0	1	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S17. Root hair proteins identified in wild type, *caprice triptychon* (hairless), and *werewolf myb23* (excessively hairy) mutant sorted roots by GeLC-MS/MS proteomics

Locus	wild type	*caprice triptychon*	*werewolf myb23*
AT5G63400	1	1	1
AT5G63510	0	1	0
AT5G63570	0	1	0
AT5G63840	1	1	1
AT5G63890	1	0	0
AT5G63950	1	0	0
AT5G64290	0	1	0
AT5G64670	1	0	1
AT5G64860	0	1	0
AT5G65020	1	1	1
AT5G65430	1	0	0
AT5G65620	1	1	0
AT5G65720	1	0	1
AT5G65750	0	1	0
AT5G66140	1	0	1
AT5G66280	0	1	0
AT5G66510	1	1	1
AT5G66540	1	0	0
AT5G66680	1	1	1
AT5G66760	1	1	1
AT5G66860	1	1	1
AT5G67500	1	1	1
AT5G67590	0	0	1
AT5G67630	1	0	1
ATCG00120	0	1	0
ATCG00480	0	0	1
ATCG00490	0	1	1
ATCG00500	1	1	1
ATMG00070	1	1	1
ATMG00090	1	0	1
ATMG00510	1	1	1
ATMG00640	1	1	1
False Discovery Rate (FDR)	0.011314186		
REV_AT1G63770	0	0	1
REV_AT1G65580	1	0	0
REV_AT1G70150	1	0	0
REV_AT1G74180	0	1	0
REV_AT2G36200	1	0	0
REV_AT2G45880	0	0	1
REV_AT3G14670	0	0	1
REV_AT3G49140	1	0	0
REV_AT4G07400	0	1	0
REV_AT4G13750	0	1	0
REV_AT4G32340	1	0	0
REV_AT5G48060	1	0	0
REV_AT5G48690	1	0	0

Supplementary Tables pertaining to Figure 3

Supplementary Table S18. Root hair proteins identified from genetics and FACS coupled with GeLC-MS/MS proteomics

Locus	Annotation
At1g14710	hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965
At1g70730	phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative, strong similarity to SP:P93804 Phosphoglucomutase, cytoplasmic 1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase
At2g16570	ATASE_ATASE1__amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase, identical to amidophosphoribosyltransferase (Arabidopsis thaliana) GI:469193; identical to cDNA amidophosphoribosyltransferase GI:469192
At3g10050	OMR1__threonine ammonia-lyase / threonine dehydratase / threonine deaminase (OMR1), identical to SP:Q9ZSS6 Threonine dehydratase biosynthetic, chloroplast precursor (EC 4.3.1.19, formerly EC 4.2.1.16) (Threonine deaminase) (TD) {Arabidopsis thaliana}
At3g13460	ECT2__Physically interacts with CIPK1.
At3g15290	3-hydroxybutyryl-CoA dehydrogenase, putative, similar to S(+)-beta-hydroxybutyryl CoA dehydrogenase (3-hydroxybutyryl-CoA dehydrogenase) (Paracoccus denitrificans) GI:12003356; contains Pfam profiles PF02737: 3-hydroxyacyl-CoA dehydrogenase NAD binding, PF00725: 3-hydroxyacyl-CoA dehydrogenase C-terminal
At4g20020	expressed protein
At5g22740	ATCSLA02_ATCSLA2_CSLA02__glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535
At5g43830	expressed protein, similar to auxin down-regulated protein ARG10 (Vigna radiata) GI:2970051, wali7 (aluminum-induced protein) (Triticum aestivum) GI:451193
At5g64670	ribosomal protein L15 family protein

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, $p < 0.05$)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
261581_at	AT1G01140	4.523198137	0.921060878	2.102934559	1.512124821	0.716350311	0.518938259
261057_at	AT1G01230	7.642145638	3.582403552	4.261009088	3.725502701	2.826259271	2.841741814
257484_at	AT1G01650	8.075087324	2.681742444	4.345283761	2.811676839	2.153745672	3.651670162
261562_at	AT1G01750	21.71934544	4.717357029	0.867972646	0.849712383	2.150325942	1.061526633
259443_at	AT1G02360	8.763601172	1.698078489	1.073647106	1.262533552	1.486714399	2.601658573
264835_at	AT1G03550	10.60646127	2.684188637	0.837420852	0.897577396	0.875632315	1.180160538
264330_at	AT1G04120	6.674759867	3.625071286	2.053235701	3.04895585	2.255802517	2.005990956
264324_at	AT1G04160	2.422892188	1.048737159	0.636322216	0.672641112	0.853698993	1.195368632
264574_at	AT1G05300	3.234333737	0.98167281	1.436248971	0.636333502	0.705685089	0.971694654
264572_at	AT1G05320	11.88069952	3.041907459	1.072649657	0.936245459	1.249523272	1.156886022
261252_at	AT1G05810	4.185002909	2.005477797	0.688363793	1.129779365	1.256274897	1.112392949
261414_at	AT1G07795	8.073638792	1.919204115	0.928627631	0.956823761	1.251472485	1.202810045
260648_at	AT1G08050	2.93120968	0.554602099	0.646869879	1.175563287	0.926563255	0.764325433
264645_at	AT1G08940	8.261826034	1.106971055	4.272156922	1.293000259	0.865759436	0.89347825
264643_at	AT1G08990	2.346536772	1.221654828	0.767997927	0.588499317	0.807274145	0.509149109
264253_at	AT1G09170	1.587458817	0.620717837	0.478816296	0.544223228	0.748781096	0.556935349
264522_at	AT1G10050	2.873343793	1.602482757	1.257099245	1.39299609	1.0919781	1.248930075
262786_at	AT1G10740	3.923625101	2.2264639	1.701298617	2.301967713	1.428330265	1.485758024
261846_at	AT1G11540	4.640862618	2.568890923	1.043460925	1.196267876	1.045892358	1.049400751
262814_at	AT1G11660	5.554977986	2.395749477	2.34392394	2.360729112	2.329429642	1.85773597
260992_at	AT1G12150	0.941788607	0.431818132	0.344843416	0.40546212	0.493790417	0.360411918
245566_at	AT1G12220	1.925765715	0.829683653	0.627251382	0.514499813	0.645780779	0.515622132
259525_at	AT1G12560	16.86527144	3.184538495	0.831941685	1.001270966	2.035134687	0.943289668
261199_at	AT1G12950	10.93995168	1.479249876	1.594859219	0.895934683	1.172788459	0.716806343
262793_at	AT1G13110	2.205292518	0.686407079	1.274903207	0.5933237	0.558500331	0.460566375
262660_at	AT1G14000	8.755942666	4.233761383	3.887846112	2.43177428	2.637859158	2.96001826
261475_at	AT1G14550	3.611141777	0.604873759	0.783887176	1.755510123	0.642520171	0.87821374
262587_at	AT1G15490	2.332331853	1.156833478	1.216073051	0.64760379	0.955672527	1.114452805
261766_at	AT1G15580	2.493125724	0.628198959	0.655352553	0.580138071	0.673190072	0.641825104
259486_at	AT1G15710	3.349547712	1.955732468	1.446796127	1.159425507	1.409721486	1.417230051
256075_at	AT1G18150	10.54486785	4.200111386	2.250938795	2.189797838	1.818813427	1.428776336

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
261677_at	AT1G18470	6.04997177	1.870925708	2.573182806	2.791439743	2.275061255	3.137060838
255774_at	AT1G18620	4.88980055	1.560440521	2.01910027	2.494938414	0.949071405	0.867160047
261429_at	AT1G18860	2.805640772	0.524613741	0.489994363	0.437861069	0.467106288	0.494965672
259462_at	AT1G18940	1.766510716	0.689764089	0.91383229	0.720577087	0.824918378	0.678663729
259481_at	AT1G18970	1.645335019	0.53695648	0.658246702	0.757687926	0.663609789	0.698792351
256010_at	AT1G19220	2.047240808	1.158871114	0.9081759	0.681580057	0.973525863	0.8022014
256011_at	AT1G19230	2.582668751	0.839188531	0.774521957	0.868189078	0.657519844	0.919320373
262801_at	AT1G21010	3.841892423	1.168172069	1.454733293	1.114448945	0.808336394	1.401784281
260899_at	AT1G21370	11.02950709	4.090569886	5.777314045	3.107166852	2.879492743	4.645647995
260856_at	AT1G21910	7.654191804	3.049880556	3.31301967	2.037812816	2.072948751	1.375162941
261927_at	AT1G22500	5.109480502	1.56045996	1.410037709	0.718912162	0.904955193	0.626920643
261937_at	AT1G22570	4.614647029	1.378315098	1.068587067	0.739548464	0.886990278	0.981368065
264211_at	AT1G22770	3.906281925	1.985321398	2.125952566	1.916513316	0.985872048	2.273347766
265175_at	AT1G23480	6.803569032	2.939685895	1.089197084	0.999594476	1.012455871	0.739792813
265132_at	AT1G23830	2.325846614	1.21483678	1.365566179	0.802828036	0.882767429	0.886853192
264861_at	AT1G24320	2.950823879	1.082382235	0.640967774	0.592156957	0.550320301	0.620160171
265013_at	AT1G24460	3.820953943	1.821606247	2.179848915	1.752218523	1.522843838	1.894173338
245650_at	AT1G24735	2.789080931	0.791475131	0.622125797	0.723837759	0.786560198	0.71152196
245821_at	AT1G26270	9.590203761	4.694388683	3.644439194	3.217100426	2.556258571	2.397041114
264988_at	AT1G27140	15.2594547	5.639903234	1.084267893	0.842621195	1.212446884	1.167994856
264447_at	AT1G27300	6.674754571	2.816972296	1.881367638	1.636341763	1.263527379	1.078500455
261647_at	AT1G27740	10.66682868	1.832108125	0.638323516	0.718053555	1.00185892	0.695227118
262743_at	AT1G29020	2.356663634	0.834397174	1.366947012	0.784103924	0.808802294	0.782188697
260882_at	AT1G29280	19.11609029	7.088161905	3.043711409	2.571514808	1.542429143	2.492010752
259789_at	AT1G29395	3.036579313	0.613684782	0.575543269	0.532091057	0.623003408	0.623002995
263228_at	AT1G30700	7.05326377	1.09485241	3.008535351	2.498410563	1.151056504	0.834466489
257418_at	AT1G30850	4.789274591	1.169383798	0.699818679	0.798143068	1.097478534	0.903930574
265102_at	AT1G30870	29.26649439	6.119595789	1.215674212	2.232677527	4.666007882	1.479413597
265161_at	AT1G30900	17.33903534	3.622714968	2.047849734	7.415677758	3.708726614	7.041172268
265155_at	AT1G30990	5.301927134	0.788957877	0.521143528	0.615334659	0.732453801	0.798050271
261216_at	AT1G33030	1.244769645	0.586498105	0.531680735	0.575158231	0.566355688	0.654534991

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
245767_at	AT1G33610	2.103880806	0.903803183	0.592650388	0.537211332	0.557169005	0.54428094
261999_at	AT1G33800	22.69838501	11.09446676	4.679716794	3.135452477	4.101656774	5.603385021
262038_at	AT1G35580	22.44323199	7.121703443	12.08765646	8.333368005	6.242052612	8.817129578
262026_at	AT1G35670	10.8551322	3.22291406	3.224914026	2.380316789	2.79167771	2.690099604
259454_at	AT1G44050	1.30119117	0.499818474	0.515953722	0.446076884	0.529245304	0.486012663
259453_at	AT1G44090	1.26293059	0.491191479	0.641581837	0.609338109	0.737755376	0.616656795
245798_at	AT1G45545	0.910526386	0.395436825	0.372380292	0.435279377	0.529899423	0.470884732
256141_at	AT1G48640	7.286527966	0.806594335	0.653526405	0.704950116	0.862998415	0.78764206
260758_at	AT1G48930	17.62360653	2.776921079	0.681641555	0.829626745	2.375412941	0.843420016
260752_at	AT1G49030	1.659206629	0.830082827	0.607135096	0.663795235	0.656204203	0.707508335
261690_at	AT1G50090	0.965908628	0.55327869	0.478801972	0.536576575	0.552324104	0.518712636
256205_at	AT1G50890	4.085457378	1.627919417	1.151463338	0.878781164	1.110024537	1.019025606
260517_at	AT1G51420	12.37705999	3.225214041	2.263287878	0.840446738	1.060974661	0.784612108
256170_at	AT1G51790	2.557004544	0.825833731	0.825367517	0.829259278	0.914645361	0.885202764
256169_at	AT1G51800	6.607327357	1.208160933	0.923368294	0.72966113	0.834377542	0.617522053
246375_at	AT1G51830	1.550133568	0.408331986	0.57744788	0.468159036	0.652246245	0.452628165
246366_at	AT1G51850	6.183257407	1.693643109	0.505632386	0.512157824	0.797068858	0.456623913
246373_at	AT1G51860	1.423957003	0.528848493	0.482846017	0.533799747	0.787927548	0.505872605
259836_at	AT1G52240	1.576777004	0.772351865	0.412058996	0.489450089	0.5349382	0.453289411
259637_at	AT1G52260	2.648487687	1.366185985	0.982567269	1.066372346	1.273339472	1.080341454
262138_at	AT1G52660	3.17186746	0.956903108	0.599555596	0.631722057	0.917749244	0.705602851
260646_at	AT1G53340	2.46062103	1.313384582	0.864313514	0.573113386	0.742737809	0.589544154
260614_at	AT1G53390	4.520149773	1.775192054	1.946557529	1.443231026	1.461621999	2.180647423
259963_at	AT1G53660	3.362714638	1.552555983	0.80594744	0.66161158	1.023906787	1.838508876
262254_at	AT1G53920	13.53464773	4.245135836	1.212248943	0.885928902	1.488923182	4.990646832
263003_at	AT1G54450	2.560347961	0.89357589	0.801229473	0.476515793	0.539459354	1.042798705
264192_at	AT1G54710	7.407644825	2.150285301	3.537647117	3.024592796	2.68898116	3.436769133
256349_at	AT1G54890	12.47812227	5.501607765	1.064277711	0.544474789	0.779046435	1.97788935
256352_at	AT1G54970	13.21852584	3.150213255	0.823250819	1.18968947	3.606409142	1.209866865
265124_at	AT1G55430	3.270084548	1.68362343	0.619067984	0.577715261	0.701789646	0.54722808
246400_at	AT1G57540	5.732682682	3.070169199	2.899961152	2.773282794	3.299269967	2.342611497

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
246404_at	AT1G57600	4.544504168	2.344123541	2.6362936	1.612855245	2.086679456	1.949346744
264929_at	AT1G60730	1.82165691	0.977710827	0.82566743	0.683141593	0.581618879	0.479585575
259724_at	AT1G60940	5.595907697	1.665902391	2.93821295	1.524144662	1.43151765	1.68838871
264757_at	AT1G61360	7.213609515	1.2128099	2.94247746	2.105354484	1.249997255	1.854088028
264283_at	AT1G61850	3.311710626	1.561103064	1.798530776	1.483573589	1.280606274	1.602585287
262641_at	AT1G62730	2.504203579	1.400996357	1.035569994	0.883670474	1.146095388	0.994338229
261099_at	AT1G62980	7.05326769	2.237412482	0.613998738	0.857909596	2.277379134	0.916859575
261107_at	AT1G63010	16.8613648	6.561839477	5.258248146	3.400931881	1.787287793	4.22549327
261550_at	AT1G63450	9.996851076	2.072149195	0.61475174	0.677585192	1.108367087	0.904885377
260320_at	AT1G63930	3.81911717	1.044131361	0.616450215	0.683619563	0.958375505	0.750529074
262877_at	AT1G64850	18.55240737	6.353278621	5.886428766	3.815938379	4.610129429	7.413434428
263109_at	AT1G65180	2.669900459	1.226925701	0.729012441	1.311893882	1.056926948	0.796703341
264683_at	AT1G65580	5.795168362	2.34038748	2.898432763	3.271035526	2.658239148	3.201060641
264685_at	AT1G65610	17.6260883	3.561258413	1.192173795	0.938866627	1.360219124	0.951694308
256360_at	AT1G66440	2.313820086	0.703281499	0.658217511	0.557667603	0.604479727	0.622376564
256362_at	AT1G66450	2.504072166	0.80104515	1.034856028	0.574416954	0.633799689	1.151099022
256358_at	AT1G66470	4.562613894	2.647737962	0.60388737	0.492552741	0.658728019	0.674309003
256380_at	AT1G66680	11.29846768	5.566999939	6.520246536	6.225837957	6.097120997	5.01309657
264229_at	AT1G67480	12.12271411	4.460237201	6.910883726	3.348165715	2.961034463	1.861327483
260190_at	AT1G67560	6.196143793	1.65371253	1.220551797	0.881773114	1.220801241	2.244829358
260002_at	AT1G67940	4.106531217	1.912107567	2.06461574	0.893895607	0.945444604	1.787837526
260003_at	AT1G68100	7.002823001	3.235091719	3.973316996	1.772954454	1.741943414	2.748678385
260432_at	AT1G68150	5.313228321	3.062617971	0.750964175	0.526867187	0.67910526	1.305091784
260042_at	AT1G68820	1.966829957	0.959215662	0.973555889	0.813539171	0.847448046	0.993376165
260344_at	AT1G69240	8.144929464	1.282624473	0.649279793	0.678106262	0.921664674	0.806011024
256299_at	AT1G69530	6.731855978	1.630071435	1.560333862	0.590190374	0.709612594	1.852810116
260403_at	AT1G69810	8.398319536	3.608032477	2.347738028	1.134340299	1.03272547	2.37191108
260366_at	AT1G70460	5.950723824	1.294135878	0.612226563	0.710559363	1.061261742	0.729645828
259947_at	AT1G71530	2.898502948	0.979726631	0.444790402	0.523881314	0.573358054	0.612087776
260174_at	AT1G71940	7.956934491	3.236764331	3.928830357	2.237957648	3.168395962	3.300353791
256334_at	AT1G72120	3.410757818	1.665479721	0.629359501	0.574142692	0.717416425	0.694217313

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
259846_at	AT1G72140	3.730028421	1.480287789	0.83072068	0.706374864	0.843723987	0.879233784
259853_at	AT1G72300	3.195406039	0.911855014	1.196371677	1.076389351	1.071520368	0.914361527
262364_at	AT1G72860	1.924570651	0.800816008	0.647741886	0.613561303	0.73654076	0.779518108
262365_at	AT1G72870	1.678117113	0.858512926	0.630378376	0.622873324	0.685891517	0.757937009
260093_at	AT1G73270	0.838254462	0.462922014	0.319435717	0.324444083	0.377132934	0.351622239
260381_at	AT1G73860	1.331470918	0.568133016	0.450936876	0.473699504	0.58656667	0.541203258
260335_at	AT1G74000	2.521040845	0.688475428	0.532618335	0.596650561	0.635481297	0.925915673
260254_at	AT1G74210	21.56085509	9.169931507	6.582511232	2.680723575	2.667213305	5.846931282
260225_at	AT1G74590	2.041144254	0.516857788	0.968829393	0.54556533	0.535825009	0.498976566
262223_at	AT1G74680	2.293048929	1.129717534	1.295863548	1.035770569	1.12501792	0.980565263
262216_at	AT1G74780	3.62915591	1.529300046	1.755722895	1.422089054	1.494379877	1.408627463
256509_at	AT1G75300	1.529629353	0.508567214	0.614819273	0.604118616	0.725981103	0.839615581
261771_at	AT1G76150	6.902516412	2.602831855	3.226871881	2.15247567	1.940674976	3.482747586
264960_at	AT1G76930	1.396381903	0.446103137	0.666455625	0.49971681	0.563508863	0.59557335
264479_at	AT1G77280	1.969149634	0.766564706	0.511213096	0.509917102	0.576067135	0.84656934
262188_at	AT1G77810	3.618290336	1.289205695	1.411087005	1.00947306	1.127364743	1.135495087
262133_at	AT1G78000	12.22809968	5.226817473	2.928819617	1.331831612	1.501867072	2.03287529
264144_at	AT1G79320	2.194425296	0.573086409	0.436362742	0.513115337	0.550412249	0.468927963
262942_at	AT1G79450	4.667520293	1.557731657	1.157174831	0.570532566	0.661606924	0.944723718
262945_at	AT1G79510	1.202811726	0.595541095	0.675905566	0.622894774	0.656845632	0.6192931
260161_at	AT1G79860	1.40819037	0.584621749	0.400135763	0.459303576	0.627456923	0.484045517
261894_at	AT1G80900	2.444690463	1.100557211	0.872693006	0.997140285	0.883551062	1.212839709
266342_at	AT2G01540	14.2256413	5.149693103	2.023035869	1.556043494	1.348464951	1.104792546
265868_at	AT2G01650	5.82235378	2.176844735	2.617708827	2.195175539	1.94954902	1.932329878
263594_at	AT2G01880	15.12509605	2.927664568	2.00827509	1.234424452	1.377285614	1.012306391
267216_at	AT2G02620	2.189389487	1.249470446	0.935731992	0.603118346	0.68705339	0.601714703
267215_at	AT2G02630	2.481371946	1.37552337	0.902271321	0.545481732	0.74699202	0.692923207
266743_at	AT2G02990	9.280031503	0.518327113	0.74079414	0.611527663	0.637199359	0.679095426
266721_at	AT2G03220	6.083056753	2.244310025	2.667541062	1.588627512	1.957395531	2.044845448
265718_at	AT2G03340	1.44725725	0.823730576	0.6009252	0.570505048	0.62726556	0.761062998
263616_at	AT2G04680	4.443991236	1.628749227	0.888522717	0.810110439	1.072065033	0.562272314

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
263565_at	AT2G15390	3.793711249	1.854523242	1.722786581	0.750288885	0.842964194	0.682665858
266522_at	AT2G16920	2.432145758	1.389631147	1.426763991	1.255549986	1.317773144	1.157834823
263583_at	AT2G17130	13.86631575	6.186794581	4.521354426	2.494431407	2.258890425	3.210084172
263070_at	AT2G17600	1.108954504	0.570314528	0.580527386	0.513163959	0.596625776	0.510894386
264592_at	AT2G17720	34.43488967	15.58390513	14.98286387	10.11208254	6.226802379	2.793568408
265329_at	AT2G18450	7.02003931	0.843409966	0.55200881	0.498218987	0.555632182	0.502526482
267439_at	AT2G19060	2.288053565	0.958446554	0.551840433	0.723507143	1.034236486	0.620912318
267280_at	AT2G19450	4.861079389	1.613031106	2.431515826	2.071591502	2.10803091	2.769176186
266693_at	AT2G19800	7.474315734	1.13283674	2.606657371	0.926778532	1.347862772	1.238485636
263754_at	AT2G21510	2.412271507	0.633548539	0.665580093	0.751994353	0.638113556	0.703961414
263749_at	AT2G21520	6.934102236	3.969235582	3.166299325	3.480837115	2.262941535	3.045773625
257432_at	AT2G21850	5.222349848	1.96354074	1.903548134	1.050393621	0.996165154	1.671806065
264053_at	AT2G22560	5.431429184	2.738807661	0.826239792	0.718632822	1.377542431	1.614975411
265289_at	AT2G22690	2.733673076	1.461533875	1.467923117	1.473284797	1.206183624	1.497629039
266826_at	AT2G22910	2.37904372	0.842299191	0.906617894	1.008370767	0.939037655	0.775256912
267261_at	AT2G23120	34.09627979	9.555101728	19.01731947	19.68290804	7.670417961	15.75079033
266561_at	AT2G23960	2.854662239	1.04239827	0.488240257	0.501267672	0.628559689	0.769766895
265691_at	AT2G24330	2.795210932	1.618822231	0.878082008	1.355207557	1.065593984	1.590939571
265666_at	AT2G27440	1.345441333	0.596760372	0.549789716	0.534007241	0.674302273	0.783358031
265636_at	AT2G27480	1.63271099	0.72920686	0.818170651	0.742601617	0.643259393	0.736401277
266247_at	AT2G27660	5.628221793	1.126020347	0.823551208	1.209767396	1.03348562	0.670896686
265275_at	AT2G28440	2.919964136	1.065947927	0.632544844	0.624769936	0.849658649	0.765466115
263436_at	AT2G28690	1.519367355	0.592598413	0.621720747	0.611733624	0.704856307	0.817364317
266784_at	AT2G28960	0.974205354	0.487260785	0.407668307	0.448180863	0.507808289	0.469863343
266670_at	AT2G29740	4.194084073	1.409788093	0.985223231	0.73629612	0.887402071	0.651177208
263484_at	AT2G29900	5.300162112	1.888952485	2.894842444	2.243066111	2.671217903	2.481152581
266336_at	AT2G32270	15.67809199	4.084997594	4.795697327	1.018960873	2.128945301	1.03030814
267045_at	AT2G34180	2.365868314	0.524977865	0.537303248	0.58885634	0.835678662	1.272465694
267427_at	AT2G34830	4.518704016	2.085866136	0.650143189	0.619472338	0.790268141	1.982459202
267428_at	AT2G34840	3.957730687	1.903317682	1.830928048	0.914430678	1.227943998	1.280304267
267409_at	AT2G34910	19.7184044	4.782341293	1.036783389	0.956244637	1.455196576	0.858390446

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
267412_at	AT2G34940	6.462008533	1.398229189	1.386146829	0.914879426	1.012712872	0.895345279
267418_at	AT2G35000	2.43688384	1.1273694	1.247392859	1.359822178	0.86442515	1.187316636
265796_at	AT2G35730	2.761134808	0.586375572	0.519412786	0.521519992	0.561647321	0.494571633
265802_at	AT2G35733	1.026784531	0.598236744	0.555689059	0.53539793	0.565186059	0.525774062
263948_at	AT2G35980	2.368344581	0.530315424	0.895651177	1.208120528	0.734887797	0.775919471
265208_at	AT2G36690	1.560056813	0.680421972	0.826093373	0.691316549	0.613941431	0.679577315
265471_at	AT2G37130	32.59042463	5.85364894	11.54957461	3.177536931	5.494709318	1.383787376
265958_at	AT2G37250	13.01248052	7.43121888	6.368496466	2.785299267	4.484771209	3.581681079
265955_at	AT2G37280	2.198947852	0.531594894	0.597872656	0.623288302	0.802192481	1.048598964
266004_at	AT2G37330	4.869389806	1.269096842	0.767122297	0.760372545	0.966835941	0.960079732
266011_at	AT2G37440	3.763772883	1.317115998	0.58564371	1.371782644	1.113285523	0.788548001
267158_at	AT2G37640	2.763816463	0.627513441	1.300261277	0.610032703	0.877975039	0.543717453
267160_at	AT2G37670	1.9831187	0.821726928	0.658934544	0.527714229	0.621620215	0.839815341
266094_at	AT2G37975	7.21507849	3.782819829	4.082052587	2.4951518	2.689963241	3.057746081
266405_at	AT2G38580	6.130104577	1.962339497	2.872548462	2.227593829	3.096593471	2.676348378
266168_at	AT2G38870	10.66924619	1.184693368	6.26494295	2.322079577	1.827112911	0.817816958
266196_at	AT2G39110	10.47976363	4.183033908	2.943948858	1.726992934	1.405095567	0.966346348
267013_at	AT2G39180	3.991526601	1.89583924	1.629492764	0.975159666	0.915367461	0.734699519
266963_at	AT2G39450	7.586105892	3.115797264	2.72839944	1.900642268	2.486283994	2.327195198
267622_at	AT2G39690	1.375822268	0.695772754	0.429102049	0.427847991	0.5873987	0.470776901
267355_at	AT2G39900	14.3826818	6.691799235	8.269039856	7.923497604	7.000197983	3.929949025
257382_at	AT2G40750	4.814185166	0.757716761	0.447681598	0.539166189	0.543450687	0.521764795
267077_at	AT2G40970	7.436810935	2.079815292	2.331105391	3.502901827	1.932631292	1.4217016
266368_at	AT2G41380	4.845586546	1.339178499	2.708098321	0.779208407	0.805949648	0.585158944
267582_at	AT2G41970	10.45101406	2.33106297	0.695785892	0.900905321	1.527694494	0.803994113
265852_at	AT2G42350	2.482037148	0.627948256	1.30547765	0.747890109	0.813411086	0.872293572
265243_at	AT2G43040	9.05497626	4.20892544	1.618731373	1.344097286	1.568288443	2.985956481
260540_at	AT2G43500	3.720934349	0.89213403	0.822485494	0.853706422	0.693468458	1.588709343
260551_at	AT2G43510	3.323534991	0.451095379	0.501863971	0.578379384	0.624522729	0.573895616
260568_at	AT2G43570	1.776753036	0.763655455	0.527296334	0.568598101	0.664195656	0.83105157
260556_at	AT2G43620	1.348391006	0.692484414	0.585705201	0.560479407	0.582695969	0.608680301

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
260567_at	AT2G43820	7.993573688	1.518886714	4.29402438	0.973286986	0.792926294	0.548222108
267191_at	AT2G44110	4.886959551	2.045126043	0.711582736	0.767355311	1.364172554	0.754656366
267366_at	AT2G44310	8.88448189	4.917438842	4.315086181	2.356683665	2.982841163	4.55667595
267384_at	AT2G44370	4.61155777	0.735015593	0.703256955	0.678875377	0.623770923	0.549449363
267385_at	AT2G44380	6.154266474	1.034326008	1.891201642	0.865399462	0.939433246	0.510082778
267392_at	AT2G44490	18.78474515	9.977773407	10.52106741	3.173361401	2.636835067	7.595212991
245148_at	AT2G45220	15.27066991	1.008036751	5.779309599	2.449249454	3.654054402	0.923882421
266920_at	AT2G45750	34.48351969	9.707075559	2.848463255	3.229964824	2.85907781	1.548906951
266913_at	AT2G45890	3.963477884	1.49312075	0.519398804	0.661542469	1.078900335	1.206659634
266553_at	AT2G46170	18.34063912	9.471696347	6.218897677	3.729242716	6.090601568	4.772606606
265460_at	AT2G46600	14.79606816	2.500822241	5.221098529	7.290810853	1.964474439	1.966962193
266711_at	AT2G46740	9.673056354	4.065676422	0.826213891	0.678476769	1.094313156	0.607251299
266712_at	AT2G46750	3.357734515	0.579755351	1.467259398	0.765694383	0.708229449	0.654711752
266765_at	AT2G46860	1.764491938	0.98508973	0.500666439	0.496498437	0.665226874	0.985998401
245152_at	AT2G47490	5.73375932	3.282882292	3.286436318	2.677706299	2.266900616	2.715020643
245172_at	AT2G47540	32.96739091	9.699127898	1.158309845	1.433289202	2.356085561	1.083314431
245151_at	AT2G47550	13.4250587	1.817021414	0.798986382	1.029337716	1.338660701	1.076701353
266505_at	AT2G47830	2.269920304	1.213583096	0.887048059	0.962193522	0.840880473	0.956092733
259271_at	AT3G01170	3.09645428	1.096382249	1.567438534	1.403232966	0.914204832	1.497082315
259191_at	AT3G01720	23.5379808	11.16311693	8.762230777	4.359676837	3.904103464	2.355777322
259195_at	AT3G01730	1.576817676	0.780036777	0.640815862	0.626855878	0.804894899	0.720405492
258976_at	AT3G01980	3.311436514	1.538863661	1.433625506	0.910342472	0.903743818	0.813140559
259120_at	AT3G02240	1.408113918	0.574340403	0.595103776	0.411870606	0.488698735	0.341007012
258617_at	AT3G03000	2.715802821	1.273376007	1.059572838	0.774993497	0.653373457	0.499754288
257529_at	AT3G03290	1.274369906	0.680265301	0.409163368	0.441423559	0.494582885	0.477953435
259352_at	AT3G05170	4.228062627	1.436779896	0.867664563	1.795071477	1.020169101	0.833375126
256396_at	AT3G06150	4.334162781	2.201362555	2.072172379	1.151630921	1.612197273	0.850790579
258911_at	AT3G06470	2.661014641	1.290726771	1.239798531	0.805609499	1.065344434	0.958464612
258832_at	AT3G07070	2.496995284	1.083196499	0.566554065	0.684024455	1.160331606	0.729202437
259256_at	AT3G07680	23.09076948	12.08404253	10.66737108	9.928758973	8.000331407	9.199218484
258637_at	AT3G07880	12.28722963	6.112187776	4.425681085	3.953455899	4.491110632	1.827509242

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
258648_at	AT3G07900	4.55235999	1.439356768	1.650212064	1.178614277	1.113371106	0.86328258
258693_at	AT3G08650	9.572019128	2.965711889	5.272298586	5.441697918	2.745707394	5.284087652
259216_at	AT3G09000	3.647224114	1.41264746	1.998966414	1.51511486	1.236097911	0.868429163
259033_at	AT3G09410	1.865924178	0.814408668	0.889511032	0.644881041	0.843009594	0.939645282
258706_at	AT3G09570	10.64242042	6.254772806	6.257107233	3.948157407	4.305162822	4.380872292
258700_at	AT3G09710	2.182753539	1.103458531	0.69640706	0.800702212	0.700326791	0.704240473
259137_at	AT3G10300	5.458083495	2.607706054	2.400973334	2.183791695	0.935049504	2.253509665
256250_at	AT3G11320	10.3583129	5.187835081	4.535038833	2.594106448	2.734792865	2.724080876
259232_at	AT3G11420	6.682563509	3.206348783	2.703167926	2.052156658	1.673533786	1.369102384
256778_at	AT3G13782	2.887384596	0.955470118	0.562528909	0.572054558	0.714142912	0.663827907
257609_at	AT3G13845	5.393557236	3.052023218	1.6942331	2.015393563	2.193011204	1.596505776
257277_at	AT3G14470	1.803993587	0.797866949	0.717805184	0.671157317	0.815892396	0.985326089
257217_at	AT3G14940	21.66482989	9.01674642	9.144446976	6.960980314	3.899949849	6.033681646
258388_at	AT3G15370	1.475868836	0.550970582	0.567817689	0.574245917	0.615143841	0.537473006
258401_at	AT3G15430	9.261255458	2.771125784	3.598055108	4.272750578	2.032442181	3.91168769
258399_at	AT3G15540	11.19910566	1.229719752	3.006444641	6.410496408	6.142001793	3.122199711
258224_at	AT3G15670	1.535799786	0.57246704	0.464215566	0.599155026	0.653140573	0.723072422
258276_at	AT3G15710	13.90240521	7.794729385	6.269796224	3.586776238	3.348048056	4.043597723
257887_at	AT3G17090	9.71412898	4.393695835	5.310521795	5.101056695	3.662302476	3.911063432
258189_at	AT3G17860	7.746246902	3.180362896	3.756039455	2.093407631	1.973207775	1.544373978
256799_at	AT3G18560	3.796115822	1.40800906	1.06748436	1.379331537	0.977782692	0.68976915
258005_at	AT3G19390	45.67980509	9.910036249	6.948052809	13.2628979	4.715079205	9.159141317
256567_at	AT3G19553	2.601628716	1.215159083	1.407701617	0.975322446	0.869876862	0.8827077
257991_at	AT3G19870	3.530502434	1.836891927	2.036387749	1.570358474	1.922319843	1.77578498
257095_at	AT3G20560	4.917538145	2.276891307	2.44607573	1.282244915	2.665728448	1.923010036
257973_at	AT3G20720	3.088828962	1.374896929	1.507739837	0.963275609	1.277173331	1.272756431
258035_at	AT3G21180	2.215404596	1.243599256	0.539101773	0.523795495	0.648844626	0.590682653
258173_at	AT3G21630	7.739120222	2.884535144	3.192048557	3.210376571	1.849461489	2.366671797
257949_at	AT3G21750	9.235258521	1.771031203	3.835444303	0.960044846	1.037093051	1.787826152
256935_at	AT3G22570	13.4012329	4.645923027	5.326161402	2.125651533	2.333377183	1.121699811
256829_at	AT3G22850	16.03999436	9.334540764	8.3176028	5.66847548	4.568495553	7.417546757

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
257924_at	AT3G23190	21.72218486	3.259058347	1.083496123	1.042912533	1.611341643	1.042869254
256900_at	AT3G24670	30.18156536	11.41166641	2.094507336	1.749738179	2.223382099	3.020972823
257104_at	AT3G25040	17.95179212	10.01019616	10.08243041	6.853821736	9.467707714	8.265611891
256883_at	AT3G26440	8.965695213	1.969032802	2.346368697	1.1751063	1.633034012	4.234792677
257144_at	AT3G27300	6.868998452	3.307803561	0.913901483	1.479300066	1.013707473	1.064181043
257739_at	AT3G27470	2.651521834	1.462637892	1.355414344	1.002599024	1.155034138	1.381147794
256847_at	AT3G27950	1.998175467	0.550151778	0.514926217	0.508795266	0.637481742	0.616697319
256735_at	AT3G29400	4.627570772	1.789604943	2.435428438	1.928651001	1.439250438	1.913458664
257285_at	AT3G29760	3.16762181	1.784761831	1.562461731	1.386379715	1.678241868	1.384823324
252692_at	AT3G43960	22.01521924	6.295677247	8.970492299	5.563284388	2.701750552	1.386677567
252510_at	AT3G46270	2.053416143	0.63522824	0.494982955	0.520964814	0.638433709	0.548979688
252529_at	AT3G46490	1.690607441	0.812806691	0.658570064	0.636599993	0.855506934	0.782715676
252494_at	AT3G46760	2.486445167	0.738753177	0.515436219	0.551952955	0.634019646	0.585028391
252448_at	AT3G47050	1.626564847	0.45645716	0.487790571	0.511937972	0.596530284	0.603057869
252415_at	AT3G47340	12.8771662	0.81905542	3.130852155	0.747995212	0.692121925	0.574987389
252383_at	AT3G47780	8.420880724	1.769524499	2.263143903	4.223285326	1.124125251	4.714211006
252303_at	AT3G49210	3.224002961	1.203311801	0.913361846	0.822875794	1.068035068	0.905221029
252238_at	AT3G49960	13.36251865	2.159284123	0.662687688	0.724338558	2.066518106	0.92980716
252194_at	AT3G50110	3.28175064	1.382726828	1.229962231	1.098779424	1.251344001	1.397473518
252243_at	AT3G50120	1.562246138	0.629592879	0.571001216	0.621793698	0.459350521	0.390073599
252244_at	AT3G50130	3.813882069	1.532344585	0.590535841	0.445962301	0.571419077	0.494836983
252218_at	AT3G50150	2.299149845	0.735467202	0.467967326	0.443074528	0.514705914	0.485620247
252184_at	AT3G50660	11.99408291	1.23125781	2.843733991	3.799528977	3.637862423	1.682901631
252098_at	AT3G51330	6.057998228	1.467795829	0.884668256	0.840253723	1.055335117	0.597809215
252103_at	AT3G51410	1.785999105	0.662241529	0.570533619	0.574461231	0.620933238	0.693967185
252037_at	AT3G51920	8.090151219	4.232698875	4.591015635	2.540978683	1.255234053	3.184677313
252042_at	AT3G51990	4.170829868	1.756698517	1.398947401	1.391456281	1.516504175	1.571276111
256682_at	AT3G52200	7.984891274	4.694835772	4.589842607	3.728121875	3.571322734	2.791408709
252046_at	AT3G52460	2.468624595	0.635392874	1.150910001	0.663535968	0.774807683	0.697114648
252002_at	AT3G52760	7.234846185	4.017213351	3.649580156	2.073689146	3.052234455	2.428564216
251970_at	AT3G53150	3.853976945	0.536046506	0.496296192	0.732434625	0.831544272	0.51179788

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
251973_at	AT3G53180	17.44707864	5.487026304	7.01058528	3.266296095	2.062995207	1.994137427
251964_at	AT3G53370	7.249020824	3.559157369	1.585260973	1.022706242	1.700443404	0.991775345
251922_at	AT3G54030	5.4829491	1.573673759	2.910459911	1.716553206	1.78744965	0.958804975
251918_at	AT3G54040	12.23507987	1.264748702	1.111264316	1.111210751	2.319559576	3.022688389
251902_at	AT3G54110	21.67162545	9.392183682	11.51431959	10.69408357	7.858446609	10.364703
251895_at	AT3G54420	5.264517031	0.881242167	0.651269795	0.632337589	0.604387016	0.781069654
251843_x_at	AT3G54590	14.28121929	6.944181503	1.511871871	1.30597595	2.094237622	1.461822267
251863_at	AT3G54870	1.809856989	0.655022484	0.519157448	0.546746883	0.900837546	0.556844673
251832_at	AT3G55150	5.200318271	2.464386055	0.787217867	0.583522102	0.924520637	0.655952259
251790_at	AT3G55470	2.331564401	1.23276411	1.121076324	0.788542287	0.614306968	0.929755726
251771_at	AT3G56000	4.60435877	2.321763368	0.763838489	0.649724063	0.942680229	0.677521521
251705_at	AT3G56400	4.355807572	0.653190732	0.640968356	0.947536888	0.915155092	0.80062936
246345_at	AT3G56760	7.177714261	1.971052858	3.158118144	2.361378722	1.842903622	2.117564877
251659_at	AT3G57090	8.191940908	3.560204502	3.842638508	4.508181456	3.411592869	3.108332666
251649_at	AT3G57330	11.8997992	4.491688951	3.477420562	1.331531406	1.248567922	1.745366774
251650_at	AT3G57360	3.755770958	1.49323331	0.746357638	0.968656695	1.439617648	0.689491785
251528_at	AT3G58600	5.771162411	2.957379016	3.267839347	2.485494203	2.351135617	2.819874536
251505_at	AT3G59050	6.475346946	1.487755463	2.360329649	2.575092181	1.377693395	3.170966565
251513_at	AT3G59220	12.82876121	2.576407172	1.847323118	0.791094367	0.895498279	1.131321244
251479_at	AT3G59700	2.671066575	0.574902743	0.713276091	0.451491928	0.510797327	0.458375648
251433_at	AT3G59830	1.056715023	0.54127093	0.437490534	0.445956503	0.480602859	0.50354099
251434_at	AT3G59850	4.869690977	2.67965971	0.656204855	0.54422517	0.711844356	0.794193335
251405_at	AT3G60330	2.637636264	0.758543671	0.513371367	0.591458916	0.959132737	0.597970303
251422_at	AT3G60540	4.166495789	2.065302766	0.933391384	1.257622068	1.067117314	1.587962903
251376_at	AT3G60630	7.66651144	3.246928103	4.232773771	2.193634683	3.214980964	2.30997282
251390_at	AT3G60860	13.06796449	4.877040563	7.283858116	4.735121957	4.159039705	5.137279057
251334_at	AT3G61390	1.437711756	0.486335551	0.70715691	0.579756123	0.625787096	0.623981509
255757_at	AT4G00460	4.551345154	1.797268843	0.631074526	0.505015933	0.665237609	0.542453188
255632_at	AT4G00680	4.514473217	1.806785472	0.517800295	0.668917123	1.579394832	0.653071769
255595_at	AT4G01700	22.27602292	3.237095138	1.418262424	1.523122123	1.292804128	1.840081927

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
255516_at	AT4G02270	7.93013998	2.952439528	0.95713522	1.206665242	3.144892266	2.642431315
255500_at	AT4G02390	2.375428581	0.895506432	0.739038475	0.890438518	1.370385728	0.965305555
255498_at	AT4G02620	25.27088902	13.44049723	14.5931983	10.99220851	9.544771523	8.922731599
255432_at	AT4G03330	2.885972481	1.035702974	0.552881496	0.638230113	0.95542203	0.650887907
255408_at	AT4G03490	2.896487105	1.010370239	0.786628801	0.678478225	0.770287024	0.822828463
255380_at	AT4G03560	21.29456221	8.60747289	11.95055545	4.031828951	4.611917988	4.99347139
255295_at	AT4G04760	2.55402657	0.831271196	0.881175573	0.735086909	0.817056777	0.954564434
255276_at	AT4G04930	1.645479217	0.501509092	0.476316073	0.511286785	0.503198946	0.627458433
255175_at	AT4G07960	4.226820284	1.329342315	0.613447613	0.661056646	0.889082185	0.699073669
255074_at	AT4G09100	4.250979095	0.631246147	0.49038155	0.553464728	0.647994396	0.520752271
255039_at	AT4G09570	9.822102974	2.072879749	4.145314581	3.591084946	1.68834362	2.337475009
255005_at	AT4G09990	23.18906269	6.882259296	1.22080574	1.440892545	3.997105863	4.500734934
255810_at	AT4G10140	8.367286378	3.214671312	4.690765911	2.739874667	2.858116039	4.644421253
254858_at	AT4G12070	2.825566939	1.231977115	1.268696065	1.385422284	1.27577464	0.954918875
254809_at	AT4G12410	4.233495039	0.5377109	0.709635627	1.11490582	1.118685962	1.065638209
254774_at	AT4G13440	4.77432324	2.636728469	0.830172256	0.663512271	0.851719191	0.688014804
245611_at	AT4G14390	3.383242585	0.886523883	0.696796673	0.92446555	0.755076148	0.732251531
245397_at	AT4G14560	8.141363682	2.965316658	1.252330255	1.531203362	1.982792274	4.180074523
245577_at	AT4G14780	1.23401673	0.688162313	0.721337422	0.688923704	0.685666265	0.658718152
245556_at	AT4G15400	1.680822341	0.621981974	0.963489921	0.587153547	0.631633746	0.5971374
245561_at	AT4G15500	2.445326928	1.372272837	1.042517787	0.919296959	0.918564657	0.795988551
245484_at	AT4G16210	7.255701671	3.227990117	3.411651512	1.934220883	1.75728261	1.863429591
245300_at	AT4G16350	1.871718581	0.881394576	0.534552657	0.541562196	0.657485796	0.57949774
245495_at	AT4G16400	2.00645634	0.72529074	1.010162586	0.936737632	1.088995138	1.103601682
245466_at	AT4G16600	2.849257546	0.621130092	0.633588218	0.645226602	0.806109825	0.724790435
245454_at	AT4G16920	1.739653613	0.479325369	0.547592747	0.434154763	0.455619004	0.490978206
245416_at	AT4G17350	4.53915381	1.682513565	1.100975826	1.857346662	1.672725476	1.522701338
245428_at	AT4G17570	2.155656955	1.041506388	1.030390777	0.900705962	1.226402433	1.153493402
254632_at	AT4G18630	1.73256645	0.663714914	0.430612245	0.446538193	0.531047758	0.510046334
254468_at	AT4G20460	13.0876895	4.470302291	3.746529008	3.537187832	1.671318347	1.008696536
254461_at	AT4G21230	2.508780192	0.975294344	1.108573274	0.674165261	0.884915714	0.767902815

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254347_at	AT4G22070	1.645989971	0.539691338	0.658612245	0.56859302	0.712304171	0.726394875
254318_at	AT4G22530	6.07985444	2.4811917	3.094165243	3.348562916	1.492829938	1.496082312
254267_at	AT4G22930	14.79169915	8.406197905	8.197732258	3.283791756	3.374895094	4.512784422
254261_at	AT4G23460	4.913570803	2.74656845	2.612006222	1.75471082	1.969443989	1.97147206
254215_at	AT4G23700	2.28855963	0.828926545	0.841309741	0.942579143	1.268657033	0.702580663
254205_at	AT4G24170	2.541415139	0.555319973	0.833824515	1.100229024	0.714342051	1.269944883
254167_at	AT4G24400	8.556951213	3.055077006	3.569932645	3.752792901	2.966528648	2.765008762
254085_at	AT4G24960	6.720333131	1.895884995	0.839744177	3.62693022	1.397698323	1.422131184
254091_at	AT4G25070	1.28823259	0.749282576	0.615659574	0.753322476	0.709125727	0.682521207
254093_at	AT4G25110	1.030427978	0.514093154	0.492396776	0.555914992	0.561845995	0.544909793
254097_at	AT4G25160	1.349778461	0.483458859	0.403225388	0.434632069	0.554325756	0.470818414
254040_at	AT4G25900	16.18073209	8.984956168	6.450858288	2.031652749	2.274305352	8.014971964
253998_at	AT4G26010	9.313683744	3.343634451	1.56439787	3.970742651	4.182537327	1.419425618
253989_at	AT4G26130	1.532684082	0.749840922	0.842386667	0.524493931	0.634376777	0.546125006
253963_at	AT4G26470	5.681725317	3.329103525	1.368537399	0.734244797	0.872016445	1.298110245
253931_at	AT4G26770	2.255410817	0.989911718	0.616450985	0.57473573	0.725410582	0.66927416
253950_at	AT4G26910	19.56289608	8.356714919	8.813141665	6.332822785	7.146649018	3.741329144
253954_at	AT4G26970	42.54898087	14.07009907	15.42773914	16.85525481	11.69411447	12.42542248
253899_at	AT4G27080	13.23630762	6.181312376	7.379709905	2.823811382	4.812224782	4.572839209
253910_at	AT4G27290	1.678443934	0.537109617	0.421651348	0.441669363	0.501822209	0.457714061
253866_at	AT4G27480	11.29045092	1.776975459	0.818744016	0.748103518	0.791237637	0.730851901
253868_at	AT4G27500	27.14706822	15.02365666	14.69241117	12.78624946	11.45519661	12.32247708
253793_at	AT4G28710	1.557815336	0.787492813	0.757428792	0.765030946	0.745952569	0.820964334
253743_at	AT4G28940	2.487584086	1.103004153	1.322137326	1.43162879	1.374468693	1.437255668
253705_at	AT4G29130	13.34716868	7.375211193	7.344171417	4.40209725	4.619935532	4.692424468
253619_at	AT4G30460	6.562656737	1.395371588	0.589257585	1.53032949	1.388205054	1.450272113
253622_at	AT4G30560	3.878105876	0.774425928	0.573499224	0.684043707	0.857306875	0.653154757
253627_at	AT4G30650	13.11129069	3.91211174	2.601327584	0.873741815	0.780974773	1.171705782
253401_at	AT4G32870	12.48706754	6.942178701	2.215154991	1.217460184	1.653533539	5.705287118
253407_at	AT4G32920	5.227763736	1.524990432	1.068684666	1.133264362	1.601093372	1.493190717
253408_at	AT4G32950	1.448583465	0.543809554	0.595107804	0.646084176	0.664739292	0.62853965

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
253334_at	AT4G33360	21.32800628	9.933270834	11.68753923	5.905846874	4.240005569	5.763250759
253309_at	AT4G33790	5.964971698	1.204887676	1.355141928	2.336731327	2.913939343	0.99393283
253211_at	AT4G34880	2.31077032	1.295630821	1.265611902	0.570946343	0.579843878	0.982016391
253193_at	AT4G35380	10.35755024	3.236258386	1.391939891	0.64126968	0.875293232	2.010794689
253147_at	AT4G35600	4.071440127	1.590257447	2.073189572	1.667791525	0.807479621	1.500991542
253161_at	AT4G35770	3.083024028	0.50759114	0.838970901	0.550977147	0.569690256	0.667361195
246239_at	AT4G36790	4.625789416	1.935309911	2.530307981	1.797133457	1.684245884	1.518588459
246250_at	AT4G36880	5.929685465	1.002287296	0.764896191	0.873111978	1.030960717	0.666406206
253100_at	AT4G37400	13.39416986	7.272346192	5.253612997	2.539776419	1.442233104	5.248813869
253063_at	AT4G37640	19.43243304	6.665421328	3.365535725	5.698896686	4.586725538	3.953022243
252964_at	AT4G38830	2.285198531	0.714144934	0.546185627	0.559639623	0.681374705	0.58046079
252931_at	AT4G38930	3.157412648	1.652847383	1.670206946	1.479408965	1.266783636	1.432269097
252936_at	AT4G39160	2.503743609	1.068510792	0.642753536	0.827859388	1.055940314	0.836815288
252940_at	AT4G39270	6.331801728	2.519490231	3.282470343	1.181871825	0.927012503	1.420282712
252834_at	AT4G40070	1.716236736	0.637932456	0.747426445	0.835525157	0.785054641	0.750415934
252833_at	AT4G40090	5.946773827	1.903089487	0.910895675	0.928715095	2.681102717	1.03291297
251135_at	AT5G01280	1.652413824	0.520290628	0.527845421	0.506393977	0.624713756	0.691418312
251053_at	AT5G01490	5.051894591	1.285985992	1.129202786	1.075101806	1.266406441	1.097014078
251054_at	AT5G01540	1.366871513	0.585790207	0.662358979	0.621665847	0.636968583	0.670641107
251023_at	AT5G02170	6.808518095	3.184217636	1.357796297	0.759632861	0.751344082	1.200685802
251044_at	AT5G02350	5.450977327	1.388910759	0.631936428	0.461455287	0.678321972	0.508380464
250929_at	AT5G03290	27.17209065	13.43308419	11.81860855	8.816235827	7.932391613	7.486235313
250922_at	AT5G03345	21.12970757	11.73869274	11.75184544	7.737895163	10.83611117	7.706720345
245705_at	AT5G04390	1.072123311	0.581134775	0.408289465	0.469732807	0.58013847	0.578433161
246952_at	AT5G04820	11.27574403	2.556153122	3.864293182	2.810327131	1.608399392	1.633199516
250771_at	AT5G05400	2.144596017	0.820286164	0.72013605	0.57354901	0.842211581	0.61543483
250778_at	AT5G05500	18.85910645	5.954150811	0.768500121	0.944910559	2.540750649	0.962593316
250754_at	AT5G05700	2.930038687	1.57204554	1.710872333	1.444790335	1.292816075	1.281075345
250723_at	AT5G06300	6.946365553	3.645085265	3.959455036	2.002126984	1.621896717	0.82240771
250670_at	AT5G06860	26.34733329	12.35455018	9.836196755	1.685113374	1.906097071	1.247939629
250653_at	AT5G06930	4.431232697	1.479017195	2.593706452	0.809350006	1.147998061	1.351417875

Supplementary Tables pertaining to Figure 3

Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
250673_at	AT5G07070	2.263454931	0.742123453	1.126455291	1.086599995	0.909461579	0.85908011
250632_at	AT5G07450	1.912752043	0.792239478	0.504086746	0.531580266	0.80986173	0.73576784
250407_at	AT5G10870	3.895942194	1.769543883	1.700219047	1.078333817	1.035255161	1.508379992
250395_at	AT5G10950	3.162264587	1.024282788	0.791167605	0.910257584	1.22058232	0.85532637
245904_at	AT5G11110	7.862524737	4.388461334	1.093931691	1.594767907	1.640753731	2.354147606
250327_at	AT5G12050	7.89358783	2.273571274	0.560239094	0.605830357	1.96969656	1.279980661
250323_at	AT5G12880	12.97385661	4.966051493	4.426201708	4.401764428	1.364730666	0.914082186
245979_at	AT5G13150	8.020604473	2.307000234	0.687349661	0.580167209	0.919587243	0.651737521
245986_at	AT5G13160	4.430257039	1.877931226	2.524771524	1.654366766	1.480558756	2.275319112
245853_at	AT5G13500	14.48042558	7.26215885	3.291276294	1.980211556	2.734438558	3.01665721
250210_at	AT5G13890	7.259488738	3.757412645	2.548292428	3.651160245	2.14435563	2.300141961
250231_at	AT5G13910	11.62877355	3.223185066	1.85161745	5.667857017	1.69338548	1.173556185
250204_at	AT5G13990	9.238265808	2.496163882	0.69093935	0.602629336	0.807274149	0.600549086
246540_at	AT5G15600	6.23684959	3.28361613	2.349131431	2.172232714	2.709787817	1.564050433
246482_at	AT5G15930	3.58985372	1.748024774	1.890566846	1.634595568	1.714965485	1.793479257
246488_at	AT5G16010	14.0750525	0.754137158	7.461563353	2.35283969	1.236339692	1.311095935
246507_at	AT5G16120	3.800776556	1.256839222	1.083858547	1.723256467	1.78063805	1.498767514
250130_at	AT5G16510	18.52886554	10.09656887	7.95354277	3.273278789	5.151681956	6.788080041
246459_at	AT5G16900	1.904548067	0.697386035	0.554491254	0.59226395	0.607284425	0.899612136
246460_at	AT5G16910	23.382693	7.009779079	7.615352929	5.84508864	3.441169433	3.716799621
246416_at	AT5G16920	1.037547387	0.464711309	0.41741015	0.445735467	0.488588155	0.542261037
249974_at	AT5G18780	3.337029788	0.89152684	1.420332893	1.259949712	1.049370088	1.227016684
245951_at	AT5G19550	11.59317697	6.695547447	5.114149663	3.442232389	4.170106969	2.680575738
246146_at	AT5G20050	6.717661974	2.770809568	3.698749025	2.105363561	1.464989542	2.97508085
246188_at	AT5G21050	3.594813223	1.219691943	1.146126488	0.774063803	0.87569031	1.118343849
249893_at	AT5G22555	1.009703564	0.405048786	0.488257766	0.520546414	0.575717488	0.518088886
249890_at	AT5G22570	10.1890693	0.538659503	0.538455843	1.168906563	0.668593669	4.940096655
249882_at	AT5G22890	1.610588763	0.81490316	0.679344969	0.472384343	0.561013994	0.620345806
249868_at	AT5G23030	1.598937677	0.749405078	0.46212012	0.545782927	0.843736394	0.515619614
249767_at	AT5G24090	6.283856341	3.141567928	1.529744433	1.054970449	1.155865351	0.764879446
249773_at	AT5G24140	3.706714277	1.215331614	1.011313995	0.703198155	1.093390007	0.632500368

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
249790_at	AT5G24290	9.120365083	3.092209555	3.610753085	1.266587047	1.133778072	2.314905772
249786_at	AT5G24310	8.632741039	1.527333345	0.659005005	0.993251394	1.342619599	1.304892815
246968_at	AT5G24870	3.935739821	0.903581394	0.792938409	0.680522181	0.712088395	0.732894026
246969_at	AT5G24880	2.886529896	0.704898108	0.431531589	0.548929275	0.640865769	0.422184143
246943_at	AT5G25440	2.119862026	0.673493892	0.711646627	0.752871473	0.693300736	0.701023475
246912_at	AT5G25820	3.548015457	1.242779914	0.931364889	0.671960375	0.729119761	1.068741499
246915_at	AT5G25880	2.796678753	0.765025506	0.821434851	0.909367272	0.901338599	0.86556672
246868_at	AT5G26010	2.6937536	1.183549451	1.168703277	0.679253469	0.989640346	0.586832824
246807_at	AT5G27100	4.303514897	1.230282029	0.775420987	0.724209767	0.858561375	0.735242624
255859_at	AT5G34930	6.922651718	2.568153986	2.036280196	1.276673794	1.719267217	1.609474289
249720_at	AT5G35700	7.705567526	4.020874453	2.633567051	1.88298418	2.888773354	2.6093874
249603_at	AT5G37210	1.35307409	0.76253381	0.638417686	0.597299285	0.665176696	0.710147125
249526_at	AT5G38560	5.713536697	2.161530408	3.226351405	1.644416655	1.75420081	3.098610476
249523_at	AT5G38630	13.95059879	7.524777556	8.177452864	6.369102069	5.203969568	5.770176552
249527_at	AT5G38710	3.850061008	0.471455046	1.895404434	0.687780251	0.544912691	1.041768607
249406_at	AT5G40210	3.663210861	0.950043059	0.742629017	0.715272685	0.788129267	0.968603561
249358_at	AT5G40510	18.47005746	9.378377311	1.725967209	0.99736733	1.859225214	1.627568323
249364_at	AT5G40590	2.850210214	0.511725495	0.498593931	0.469731746	0.51587175	0.42702145
249348_at	AT5G40860	3.232423344	0.715369175	0.61535581	0.667256624	0.810913963	0.668323757
249295_at	AT5G41280	1.633297159	0.75945754	0.652997676	0.614101879	0.664877401	0.861047308
249283_at	AT5G41800	3.927418606	1.811673959	1.358871753	0.83103696	0.993046279	1.473831806
249284_at	AT5G41810	5.631745836	2.669748881	2.35952257	1.57887439	0.760668698	2.384026749
249166_at	AT5G42840	2.323053235	0.987453817	0.934161636	0.672025613	0.827234897	0.775031979
249169_at	AT5G42880	1.604841468	0.621996779	0.715544879	0.80971795	0.919262534	0.4705876
249185_at	AT5G43030	6.201385656	3.246684562	2.496118299	0.81621984	1.0503369	1.241870729
249140_at	AT5G43190	6.1537175	1.721613587	2.29587057	1.177006423	1.179535466	1.612429587
249151_at	AT5G43360	1.287406188	0.562344859	0.617377338	0.579983879	0.668643132	0.646638923
249097_at	AT5G43520	2.56843944	0.644986897	0.689696773	0.697470206	0.658594924	0.602520463
254521_at	AT5G44820	6.841962989	1.916413575	0.980855352	0.478916603	0.663954812	0.536020969
249029_at	AT5G44870	1.17502233	0.553311476	0.645901657	0.635927174	0.636500685	0.580042945
248971_at	AT5G45000	1.23958975	0.592966073	0.455300293	0.482626096	0.568087504	0.571831775

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
248968_at	AT5G45280	33.5922454	19.23376925	6.314854752	4.083588372	4.464316433	17.88034752
248944_at	AT5G45500	11.86166468	3.328144463	2.961919151	1.863988242	1.920359874	2.004143219
248916_at	AT5G45840	1.837767374	0.726275612	0.431827058	0.496014332	0.630540925	0.463831419
248927_at	AT5G45900	6.211619934	2.337394506	2.184005953	1.62638641	1.633816077	2.048902093
248889_at	AT5G46230	7.467477658	3.912692635	1.395961061	0.767203293	0.942588055	2.068579134
248896_at	AT5G46350	1.128452617	0.482739215	0.58567703	0.486189975	0.528170841	0.584291324
248848_at	AT5G46520	1.033002664	0.395552738	0.413837827	0.386452463	0.411544114	0.448873474
248717_at	AT5G48175	4.913977208	0.686465637	0.757125453	0.688546001	0.721990406	0.585233875
248703_at	AT5G48430	5.896273359	0.896106438	0.98744582	0.733935946	0.804668704	0.838532479
248652_at	AT5G49270	26.35831667	7.037165721	1.699631882	1.95741069	2.557357167	1.480283545
248562_at	AT5G49680	4.531574955	2.098588537	0.756013934	0.716298602	0.841458557	1.624108895
248577_at	AT5G49870	2.719736063	0.401791216	0.419586078	0.447657422	0.530524983	0.483053734
248486_at	AT5G51060	17.51153053	6.497931076	5.55476262	2.053632541	1.762235332	1.071269601
248464_at	AT5G51160	3.456941032	0.893563556	1.029638813	0.71743154	0.722989583	0.952923748
248441_at	AT5G51270	1.272967327	0.667506578	0.472598987	0.57735282	0.634746297	0.635870274
248410_at	AT5G51570	8.888934691	4.916403957	4.167028708	3.016956009	2.523620558	2.914209189
248422_at	AT5G51640	4.783617579	2.253976148	2.272141537	1.722115461	1.699485995	2.655548205
248337_at	AT5G52310	12.18303981	0.576527049	4.02102642	2.562234748	1.216544632	1.508786369
248311_at	AT5G52570	1.680955959	0.602392927	0.619736348	0.914502915	0.643538886	0.689642871
248212_at	AT5G54020	4.746385224	1.562997089	1.958563523	1.277321672	1.081410042	0.783317653
248183_at	AT5G54040	3.033789309	0.734949448	0.48677376	0.477670953	0.79060684	0.544503946
248184_at	AT5G54050	1.112848787	0.459147903	0.389924327	0.407694745	0.477222448	0.446100011
248191_at	AT5G54130	1.813955798	0.628922623	0.488073183	0.595609772	0.898718546	0.930268345
248192_at	AT5G54140	3.1868222	1.603125196	1.431474302	0.842761514	0.969669421	1.567585434
248164_at	AT5G54490	12.39953106	1.32071199	2.376984482	4.930748485	1.810383194	5.614316232
248162_at	AT5G54500	18.76963794	5.053339414	10.44207374	10.17027372	6.89654573	7.866507718
248087_at	AT5G55060	3.631000152	1.487545128	2.122045849	1.890489216	1.723335092	1.929815669
248082_at	AT5G55400	4.750535434	1.663175031	1.255649222	1.301659005	1.441741409	2.273008241
247983_at	AT5G56630	16.60026136	5.88132296	8.534162826	8.390648068	4.285109015	8.835033888
247869_at	AT5G57520	0.976820276	0.463855764	0.443104989	0.432310542	0.513792399	0.491953023
247895_at	AT5G58010	7.142999889	1.383331552	0.929829614	0.922431727	1.054487133	0.930618224

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Root Hairs (COBL9) from micorarray expression data analysis (1.7 fold, p <0.05)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
247820_at	AT5G58380	4.748631993	1.785180744	2.0777236	1.869206572	1.73304431	1.915591822
247768_at	AT5G58900	5.91148402	1.41125626	2.067765467	0.974293895	1.251903455	1.802991181
247725_at	AT5G59410	6.245226008	3.617884516	3.60644131	1.606107496	2.485447723	2.985135717
247678_at	AT5G59520	11.98264861	2.874671419	5.316820101	1.804079937	2.753096263	1.454934803
247674_at	AT5G59930	2.205625354	1.033425642	0.521544477	0.59228612	0.643725762	0.529560953
247675_at	AT5G59940	3.920623982	2.047296785	1.162938059	0.934746556	1.147196088	0.990378654
247622_at	AT5G60350	3.019347218	0.609420586	0.642414119	0.864291079	0.705168514	0.628157472
247594_at	AT5G60800	4.350117688	0.995529961	1.380132833	1.937329078	1.66475587	0.712341133
247521_at	AT5G61450	2.845114927	1.579736553	1.611188276	1.303402349	1.129179101	1.425089188
247531_at	AT5G61550	1.760261759	0.80819396	0.466153649	0.533350653	0.688351666	0.558280903
247532_at	AT5G61560	1.333664737	0.559508418	0.768706832	0.768876676	0.689579083	0.736075107
247474_at	AT5G62280	3.816003134	2.022069143	1.898485336	1.177326794	0.872562979	0.619282952
247475_at	AT5G62310	3.354916932	0.798318015	0.465144378	0.482906666	0.658883752	0.610167719
247411_at	AT5G63000	3.923808585	2.232604964	2.100055543	2.185187063	2.185020507	2.177353461
247318_at	AT5G63990	8.056810738	1.743034829	1.191651487	1.180447332	1.390101313	3.377261724
247275_at	AT5G64370	9.643742068	3.556620935	5.625628182	4.701536899	2.989257796	5.045368797
247225_at	AT5G65090	2.782655767	0.760394107	0.718277235	0.671095776	0.782610152	0.741485736
247229_at	AT5G65160	3.284284861	0.739300295	0.540944779	0.690026951	0.776709466	0.57400348
247151_at	AT5G65640	4.414793574	1.321774676	2.516234307	1.1610262	0.772664916	1.614712318
247109_at	AT5G65870	5.18913642	0.421336417	0.628542086	0.58535125	0.524293824	0.466314588
247115_at	AT5G65930	5.679125034	3.008547687	2.219404515	1.413049335	1.920488581	1.311892756
247112_at	AT5G65950	8.672328323	5.000146318	4.819309497	3.316408899	4.733163287	3.422875872
246989_at	AT5G67350	1.754818049	0.951519155	0.825098133	0.832069046	0.755641785	0.84346408
246991_at	AT5G67400	12.33505964	2.81227114	1.068518193	1.380762721	4.361096306	1.42033322
246993_at	AT5G67450	5.828015185	2.12702889	0.6547113	0.600195636	0.745514404	0.873286023

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
261569_at	AT1G01060	0.869534222	3.212378395	1.453862761	1.09530978	1.043739413	0.930046603
261578_at	AT1G01100	12.1369886	27.4563013	8.690735867	12.10748341	14.22817033	8.202890902
264152_at	AT1G02140	3.998272372	11.93709957	3.710871341	3.779496844	5.319729586	3.741450502
262112_at	AT1G02870	0.633686437	5.520193874	1.000884879	2.072572165	3.075284568	1.207172745
263113_at	AT1G03150	1.433549734	3.137240529	1.328557044	1.225363873	1.432278686	1.163720068
264826_at	AT1G03410	0.541642936	1.717528487	0.571321052	0.54186126	0.577647389	0.639735171
265037_at	AT1G03860	5.206445903	10.00052889	3.216649019	2.456085737	3.954982159	1.950936747
264327_at	AT1G04170	6.111092812	10.43115512	4.380809268	3.17410119	5.855052582	3.229517072
264566_at	AT1G05270	0.823967491	1.656783641	0.780185996	0.732904791	0.75579673	0.694972411
256065_at	AT1G07070	1.563573954	7.165953509	1.647768926	2.31468929	3.899742758	1.386060056
256043_at	AT1G07210	1.269274098	3.07658018	0.924164884	0.856386554	1.656323583	0.900189105
261418_at	AT1G07830	1.041655527	5.498144349	1.220352599	2.078650831	2.674806207	1.174203251
261784_at	AT1G08220	1.418841045	3.016651901	1.206719528	1.134306655	1.612608424	1.322802953
245227_s_at	AT1G08410	0.467543786	0.926252261	0.417307596	0.439666819	0.450775827	0.487506944
264783_at	AT1G08650	0.771214033	2.974349936	0.972483892	0.844319124	0.814527125	0.882227524
264254_at	AT1G09150	1.721911862	4.58461791	2.066168809	2.156098936	2.546892281	2.045336406
264665_at	AT1G09660	0.624121705	2.495491837	1.162877976	0.772755599	0.879285315	0.719814342
263255_at	AT1G10490	0.761763598	2.187635709	0.842204515	0.931964647	1.216228324	0.988510856
260472_at	AT1G10990	0.838217329	1.835238007	0.787281438	0.676901846	0.650781032	0.662432809
256070_at	AT1G13730	0.98109847	5.670713023	1.963690871	1.803076162	3.165174286	1.051533111
260781_at	AT1G14620	1.990052594	6.231789828	1.69538039	2.318176848	3.453921447	1.685723552
262840_at	AT1G14900	1.269951327	3.586714558	1.840646297	1.569272965	2.08796207	1.660212393
260714_at	AT1G14980	6.63655	25.0791456	3.980066029	5.17876119	9.09498757	3.650734569
262569_at	AT1G15180	0.446526998	0.900464937	0.346086932	0.340927859	0.397957238	0.359270349
262602_at	AT1G15270	1.201068818	3.672137585	0.720084297	0.957835786	0.893079429	1.211741202
259505_at	AT1G15810	1.67910133	3.46440623	1.774134049	1.255262317	2.011389953	1.219364246
255902_at	AT1G17880	4.510510352	18.31850434	3.444439979	5.23718503	7.084749394	3.903525512
255780_at	AT1G18580	1.008299426	2.039630354	0.968949301	0.775149981	0.920460273	0.941506805
255777_at	AT1G18630	1.674520308	2.912957859	0.6198959	0.740201633	0.883490302	0.691061778
261406_at	AT1G18800	0.701183322	3.189408729	0.732924307	0.854692282	1.040932158	0.673287279

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, $p <0.5$)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
260670_at	AT1G19520	0.693407662	2.637371051	0.724148356	0.726867401	0.898358799	0.703700002
259515_at	AT1G20430	2.417386127	5.973433663	1.327362895	1.395058559	1.97840881	1.394032757
256092_at	AT1G20696	1.631080149	12.38439274	2.434317935	1.757518016	1.858950104	1.547129177
259551_at	AT1G21190	0.52863986	2.187766568	0.539712398	0.699970955	0.902831395	0.608439064
264206_at	AT1G22730	1.516371172	2.694737345	1.233087378	0.723758047	0.976820816	0.81569557
264203_at	AT1G22780	10.26173649	25.58309192	7.761523219	10.02038996	14.91077856	5.683218533
264895_at	AT1G23100	0.787947323	3.842935647	0.628110871	0.86304151	1.360110961	0.662829606
255732_at	AT1G25450	1.236703459	3.752342577	0.649770897	1.194509634	0.916700507	0.620104243
261011_at	AT1G26340	1.044495029	2.877316046	0.756087778	0.916832368	1.277822949	0.941313959
261019_at	AT1G26470	1.175845381	5.165890109	0.878449466	1.282537098	2.041018668	1.824332055
263691_at	AT1G26880	10.08767706	25.71985208	7.625985401	8.369450771	13.47701301	6.849155015
264977_at	AT1G27090	1.357379301	6.806886723	1.387581883	1.438072453	1.883634332	1.075177658
264446_at	AT1G27310	5.375107425	11.57705229	2.726202673	2.267528613	2.668973271	1.587577007
262292_at	AT1G27595	0.673741396	1.271068798	0.69957139	0.661960986	0.734374419	0.714384388
262297_at	AT1G27600	1.457157785	2.923472608	1.326575231	0.774561935	0.989062447	0.904028096
262295_at	AT1G27650	0.877006171	2.481393823	0.736742794	1.187014638	1.29457157	0.746434135
245688_at	AT1G28290	15.63342215	44.05054263	10.27705368	3.423185797	6.68429851	10.20229632
261439_at	AT1G28395	1.21643624	6.063155702	1.323092444	1.795988884	2.711039094	1.928582756
256192_at	AT1G30110	1.628377387	2.878465042	1.239757344	0.655895409	0.661447965	1.221554476
263224_at	AT1G30580	5.436485321	12.2599983	4.540303885	2.702324623	5.664619554	2.874810202
265103_at	AT1G31070	0.479956386	1.518338204	0.496043921	0.48438334	0.522100515	0.559567285
246575_at	AT1G31660	0.801364223	3.883785705	1.141971371	1.202830987	2.117744562	1.365711929
246634_at	AT1G31730	2.128659376	4.212878797	2.242571112	1.601538837	2.065025397	1.587347276
246266_at	AT1G31817	1.559251893	3.344900315	1.65464494	1.265750371	1.860016833	1.121803426
255751_at	AT1G31950	1.351196296	6.825177784	3.500261546	0.822523685	0.989691043	0.963566385
245758_at	AT1G32240	0.430838369	1.028306364	0.438300264	0.514349082	0.548802845	0.536769908
256466_at	AT1G32580	0.83114427	2.619170117	0.811306846	0.930982525	1.526474364	1.076071865
256423_at	AT1G33540	0.52746954	1.258322779	0.444143329	0.401912153	0.457172173	0.431877683
261988_at	AT1G33680	0.520596726	1.458180305	0.517114184	0.627943147	0.622915687	0.554587826
261993_at	AT1G33860	1.497562945	3.686858117	1.15159249	0.829067357	0.944605895	0.594579449
260507_at	AT1G47200	3.018119651	7.118111076	1.723378611	1.576660476	2.622201015	1.481343067

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
260506_at	AT1G47210	0.759124972	2.457490137	1.20480483	0.846839327	1.165693372	1.009872574
260725_at	AT1G48170	0.991604173	2.134319452	0.871865658	0.780690294	1.096543659	0.806063499
260768_at	AT1G49245	0.380818355	0.891122725	0.348129588	0.441053308	0.479189254	0.454777316
262415_at	AT1G49400	0.938037642	3.066327713	1.077707208	0.866169337	1.45264012	0.849735515
262402_at	AT1G49410	4.823765594	14.39366019	2.928679352	2.854520704	6.16746751	2.572089042
261603_at	AT1G49600	4.588139295	12.9943809	3.374886114	2.527895203	4.625820038	2.110361379
264239_at	AT1G54770	1.055947271	3.079389788	1.163680706	1.093479847	1.556054298	1.112162001
259653_at	AT1G55240	0.929572602	1.756400341	0.535713729	0.603268737	0.699115694	0.807854996
260596_at	AT1G55900	0.90488254	4.935977766	1.145500533	1.35422269	2.690067747	1.595426323
246378_at	AT1G57620	2.997821999	5.560881707	2.260881496	1.078528064	1.968873809	2.158426998
264913_at	AT1G60770	0.984310168	3.715587296	0.910987189	1.023872535	1.992262838	0.952588635
260323_at	AT1G63780	0.80491273	5.296134651	1.178407027	1.850582464	3.01791542	1.355086713
262336_at	AT1G64220	0.311953798	1.189923878	0.344208978	0.400568974	0.545731983	0.382465553
261975_at	AT1G64640	1.452077082	5.145516421	2.249326205	0.966012857	1.669330542	0.856200006
262875_at	AT1G64970	0.652357949	1.681703022	0.853980494	0.69837339	0.814295781	0.88463323
262925_at	AT1G65730	1.503352073	4.634132366	1.270049517	0.940713188	1.156193506	1.760544602
256368_at	AT1G66800	1.573642053	4.668256467	1.407603859	0.984817904	1.657658167	1.053319414
260200_at	AT1G67620	1.372272113	2.361260471	0.968897441	0.99066425	1.343734127	1.280826474
259996_at	AT1G67910	0.852720031	1.772583154	0.772044062	0.792779194	0.812882946	0.679021363
262230_at	AT1G68560	1.083610094	8.356626912	3.500062773	1.260908582	1.885136357	1.873630201
260338_at	AT1G69250	1.742739736	5.215727027	1.192626143	1.296187568	2.356789487	1.495159678
260368_at	AT1G69700	0.729677751	3.209655289	1.287547931	1.062087944	1.388411898	0.867996415
264702_at	AT1G70190	0.739737901	3.303000341	0.75827552	0.621033329	0.870659702	0.655652956
264337_at	AT1G70350	1.205752947	2.732540976	0.964650283	1.033980277	1.40812828	0.886135105
259749_at	AT1G71100	0.591722868	1.413506702	0.654288966	0.713425136	0.830346373	0.77264333
261508_at	AT1G71730	1.516025576	3.091933003	1.184815302	1.720971461	1.733418759	1.422485936
260095_at	AT1G73230	5.583203372	21.35993688	4.714048903	6.873709059	9.65027657	4.364372384
260258_at	AT1G74270	9.630609574	18.62151207	5.61384792	6.099909952	9.415603089	5.246464837
260230_at	AT1G74500	1.348646693	12.23683021	5.478792971	1.415534103	1.04609112	6.777976588
260235_at	AT1G74560	0.641099563	6.146843421	1.14100053	1.297860102	1.957214967	1.359953073
262685_at	AT1G76010	4.684224686	15.80757832	6.409728257	4.160077881	7.702553259	2.497189132

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
264948_at	AT1G77050	0.652136356	1.430745896	0.566893178	0.59979177	0.741346538	0.733485947
259678_at	AT1G77750	3.166462972	6.040524297	1.881168352	1.448546941	3.034777559	1.374095499
264101_at	AT1G79000	0.765663942	1.867593156	0.84235501	0.733157808	0.692521515	0.731019424
264118_at	AT1G79140	0.413288073	2.73978851	0.602174649	1.046910815	1.41422071	0.76203705
261352_at	AT1G79650	0.979042791	3.161229004	1.191026609	1.026187591	1.688789914	0.934781042
260166_at	AT1G79840	0.70056256	2.119976831	0.550112074	0.528000581	0.650687481	0.520016333
260282_at	AT1G80410	0.631081503	3.49940718	0.716960185	0.713773001	1.174105467	0.729439988
263406_at	AT2G04160	4.502941461	11.66120089	1.495552623	0.630092475	0.956066727	1.986460198
263810_at	AT2G04520	2.837539564	9.483228243	3.221621951	3.295255064	3.374487731	1.961764685
265776_at	AT2G07340	0.715773163	2.107042992	0.654958077	0.817358371	0.897534367	0.638682464
265779_at	AT2G07360	0.622366133	1.649341405	0.598353283	0.561229455	0.710076885	0.616919967
263636_at	AT2G11910	2.031521639	9.047618589	2.882039965	3.595667233	4.855834066	1.825591033
265831_at	AT2G14460	0.461297954	2.723606667	0.540518577	0.876026165	1.562436381	0.662413209
265895_at	AT2G15000	4.210258345	7.670965494	2.239305598	2.281300531	4.189882516	1.177336874
263610_at	AT2G16230	0.757488936	2.185896299	1.230945773	0.702221095	0.882388664	1.051665061
265352_at	AT2G16600	10.11693485	21.33543107	8.008912482	7.929172857	8.289549104	7.065591065
265930_at	AT2G18510	0.882144407	2.424614718	0.985233495	0.744484962	1.067489907	0.846776327
266074_at	AT2G18740	0.523170038	2.630395093	0.50262186	0.681155438	0.93807139	0.651493606
266705_at	AT2G19750	0.973374948	13.41266731	1.003799264	2.438025405	5.225777764	1.986302102
263371_at	AT2G20490	0.632891799	10.80508987	0.976622527	1.96307665	3.752994038	1.239093583
265443_at	AT2G20750	1.674704589	10.32175782	2.298517432	0.839148255	2.44519096	0.936609896
263432_at	AT2G22230	1.445485906	6.921100008	3.798675318	1.769875395	2.174416125	1.243451995
264043_at	AT2G22490	1.1263902	2.806520536	1.147612798	1.355655328	1.131397657	0.932322096
267287_at	AT2G23630	1.00664006	8.522893654	0.796189621	0.798699016	0.700611917	4.677324322
266656_at	AT2G25900	0.988001557	2.56488293	1.481270733	1.162800033	1.378294913	1.111857494
266262_at	AT2G27590	1.415866557	3.450645123	2.002313505	1.926814448	1.365193461	1.888683301
266256_at	AT2G27710	16.21636799	33.03353723	11.72873769	12.97699183	16.63572116	8.319943829
266264_at	AT2G27775	1.102823774	3.321821006	0.875545737	0.884344509	1.484169097	0.833921789
266253_at	AT2G27840	1.090814508	6.538319971	1.280570211	1.508084611	3.059966806	1.327778873
265254_at	AT2G28380	0.744628362	2.255601456	1.066445508	1.093757322	1.221188964	1.320359691
255865_at	AT2G30330	0.930685272	1.614648296	0.638256109	0.652210987	0.731688434	0.748818065

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
267516_at	AT2G30520	0.57700281	2.79609946	1.17886754	0.716681077	0.825816218	0.673668458
266471_at	AT2G31060	2.020675511	5.095542997	1.328566212	1.09721047	2.316510297	1.30078599
263251_at	AT2G31410	0.720500253	5.533402166	0.739042586	1.275839674	2.03395488	0.894968649
265730_at	AT2G32220	0.878063743	2.896652394	0.74074513	0.919514365	1.700407507	1.359888272
267062_at	AT2G32600	1.234159576	2.38281844	1.089518725	1.116224288	1.309506115	1.073070302
245164_at	AT2G33210	5.316966265	13.67060198	4.687820663	4.383625097	7.180914758	2.505737009
267457_at	AT2G33790	3.530782803	27.35794748	4.669588782	0.82106322	2.786333785	3.356531609
256723_at	AT2G34160	1.090626524	2.438895962	0.875312968	1.05528421	1.251572261	0.781962288
263939_at	AT2G36070	0.874768519	2.577040263	0.958383678	1.036648591	1.464444557	1.012456231
263289_at	AT2G36170	8.562294214	21.71698756	3.578062031	4.909181642	10.31568628	4.611468573
267174_at	AT2G37600	0.561113027	3.394188788	0.548222055	0.881431644	1.186326894	0.796957188
263263_at	AT2G38840	0.705714098	1.368767534	0.601847847	0.58447835	0.660971878	0.639187497
267019_at	AT2G39130	1.325423543	4.579357337	1.666726309	0.649124647	0.799265383	0.77133812
266981_at	AT2G39460	9.512284456	28.42499154	6.505540512	7.543636634	12.17234666	6.049975917
266372_at	AT2G41310	0.555398498	1.511046714	0.713046184	0.453980869	0.508069867	0.562078193
265883_at	AT2G42310	4.022029155	11.22925454	2.832831621	2.089014258	2.401600203	2.685739631
263975_at	AT2G42710	0.864024326	3.757462803	1.21140051	1.296065954	2.092646578	1.078281856
266451_at	AT2G43090	6.779678999	11.72052244	4.445928605	3.342258076	4.813370509	4.422794246
266447_at	AT2G43290	1.514282154	5.552332167	0.701320841	1.917826772	0.922472015	2.606433454
260558_at	AT2G43600	1.115921062	7.674446753	0.907823625	0.675213766	0.781943082	2.66440515
260557_at	AT2G43610	11.11780095	41.29720731	4.841927371	1.231431709	2.122209394	18.29364814
260585_at	AT2G43650	0.369470362	1.453752588	0.407751076	0.633076636	0.797714391	0.501372355
267188_at	AT2G44050	3.769766683	6.517577305	3.425432465	2.02931228	3.047073198	1.624191742
267211_at	AT2G44065	2.813131714	5.275795931	1.625409451	1.839012112	2.06567437	1.508962295
267213_at	AT2G44120	4.035776236	28.04889734	5.725164226	7.065256953	15.013255	4.001556647
266822_at	AT2G44860	0.681970335	7.57509471	1.251693621	2.482500847	3.530147764	1.167876434
266125_at	AT2G45050	0.63000691	4.430192774	0.992261749	0.658199096	0.842747149	0.89490052
266136_at	AT2G45060	1.655343824	3.276223229	1.180134979	0.770672224	0.913829681	0.766583916
266124_at	AT2G45080	0.733970737	2.36886722	0.801492778	0.7684579	0.871272966	1.284061458
267507_at	AT2G45710	1.931070721	6.399602438	1.242807859	1.607718809	2.684803286	1.488776815
266596_at	AT2G46150	0.644238082	2.955762447	0.729813818	0.58157372	0.521256103	0.61546721

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
245124_at	AT2G47580	2.378354813	4.578216033	2.061863721	2.090587093	2.450796413	1.853533062
259319_at	AT3G01090	2.290495422	4.214617638	1.797084779	1.162418783	1.462235631	1.446042078
258958_at	AT3G01390	2.887974262	6.336199139	1.743234863	1.506270161	1.398802417	1.827301558
258995_at	AT3G01790	2.276638836	9.431055289	2.390776088	3.018509248	4.600265956	2.518130194
258859_at	AT3G02120	0.396471238	1.954665305	0.585712826	0.919387583	0.94135666	0.796527532
259123_at	AT3G02200	2.344501713	7.219112633	1.989853169	2.311868052	3.576108117	1.838324775
258576_at	AT3G04230	1.087416842	6.720140684	1.015488334	1.689667038	3.647575692	0.972582539
258820_at	AT3G04600	1.454595479	3.451920701	1.462681207	1.243465968	1.69048373	1.734202719
259090_at	AT3G04920	3.301130984	17.98301336	2.19394498	3.805956618	5.609135895	2.232333869
259095_at	AT3G05020	1.937516231	8.981131903	3.286572573	2.391568559	1.931099486	1.275900813
258747_at	AT3G05810	1.112767286	2.725437853	0.784696085	0.925940783	1.317561949	0.757105175
258466_at	AT3G06040	1.619586227	6.932565607	1.072704744	0.990870205	1.883828962	1.096888129
258521_at	AT3G06680	1.410182683	8.772981306	1.499132413	2.634513695	3.486777203	1.838171713
258532_at	AT3G06700	8.820631106	19.03748844	4.64528159	5.738279119	10.00820173	4.477271386
258545_at	AT3G07050	0.550061825	5.204706166	0.758591964	1.093557061	1.670440435	0.877402975
258821_at	AT3G07230	4.743372374	13.21437419	3.475488365	3.676275422	4.749854294	5.352110396
259245_at	AT3G07660	0.864316409	3.366574002	0.902166929	0.8255089	1.266553185	0.958481153
259248_at	AT3G07770	0.829189131	6.658304666	1.819526091	2.588503266	3.8890598	2.275803971
258644_at	AT3G07810	2.775654285	5.473596694	2.831517273	1.530569526	2.005398977	1.558005551
258638_at	AT3G07950	3.012194099	8.465972643	3.126331267	1.233849961	1.933120855	1.549313076
258657_at	AT3G09890	1.179553938	3.137874665	1.086939406	0.993000304	1.347563157	0.914666787
259239_at	AT3G11510	12.75155479	33.91867988	8.095765244	8.496001174	17.9431143	8.421078171
259237_at	AT3G11630	1.925729979	8.685192505	5.00895486	3.198003706	4.98948658	2.835116242
257658_at	AT3G13230	0.733194667	7.289035414	1.376395393	2.088145318	3.624010127	1.850116962
256982_at	AT3G13460	2.139812098	7.114527803	2.116267303	2.770437037	2.997625791	1.33916955
256784_at	AT3G13674	0.805164551	2.233421797	0.829779782	0.73090117	1.206711657	0.676286318
257002_at	AT3G14100	1.729051533	4.037481985	2.187242259	1.579305211	2.114193698	2.048581238
257079_at	AT3G15230	0.396721849	1.630648	0.459399333	0.563872165	0.60499603	0.443469128
258397_at	AT3G15357	0.451911277	5.295032909	0.491756079	0.677144728	0.948346859	0.5379979
258338_at	AT3G16150	1.417985085	5.528199334	1.058288715	1.168280491	1.055478053	1.528900242
257755_at	AT3G18760	3.362518502	6.654465626	1.79127541	2.260991363	3.318731888	1.751075972

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
257085_at	AT3G20630	0.477140824	1.971435271	0.477535586	0.481969769	0.531384566	0.482252179
256812_at	AT3G21350	0.74480546	1.798882194	0.762089886	0.637747218	0.782330382	0.759137676
256794_at	AT3G22230	4.094477208	16.18533225	2.562412032	4.895706483	7.456541442	3.991464337
258454_at	AT3G22300	1.95827138	5.135707079	1.76013157	1.59402893	2.27719512	1.418610095
258296_at	AT3G23390	12.56991859	25.55687135	6.373718587	9.312226324	14.62974738	7.735117182
256890_at	AT3G23830	0.526817023	14.75335124	2.733484083	6.59708383	8.106110502	1.763560286
256916_at	AT3G24050	1.203306082	2.926392339	1.206216798	1.381664828	1.420340105	1.583508738
257239_at	AT3G24100	1.144194253	2.910446996	1.224981025	1.474192249	1.092012678	1.431015785
257906_at	AT3G25520	14.30362529	29.42750176	10.8065429	11.4076271	16.88491253	7.282712187
257709_at	AT3G27325	0.671418054	1.382220265	0.675417727	0.539685631	0.695065187	0.717094799
257141_at	AT3G28900	3.185160833	15.57682237	2.170838739	3.990566219	6.972557779	1.824749616
258001_at	AT3G28950	1.139784632	2.246022613	0.965644057	0.927683112	1.027180329	0.877241586
252711_at	AT3G43720	0.759199144	2.876758685	0.602928727	1.410705833	0.724279384	0.650610827
252643_at	AT3G44590	4.847875096	19.8328446	5.102133016	6.779093237	11.15729517	3.179618298
252492_at	AT3G46740	1.671560835	5.075509465	2.2650525	1.810540588	2.380126328	1.37448977
252288_at	AT3G49080	0.759313224	2.467911882	0.679713891	0.758510511	1.00905846	0.730522381
252295_at	AT3G49100	2.126358015	3.858771988	1.191154461	0.970162514	1.480259625	0.844053327
252256_at	AT3G49430	1.444480468	4.805054193	1.39620948	1.987549444	2.42826607	1.508380766
252235_at	AT3G49910	19.64267203	42.34712122	14.01935931	20.23429713	23.55293814	11.83006271
252115_at	AT3G51600	0.622797345	2.35819337	0.625530024	0.687167687	0.638414654	0.615080555
252034_at	AT3G52040	0.697776654	4.813211498	0.854618737	1.364892383	1.796523274	1.293407671
252041_at	AT3G52090	3.681095226	6.553450292	2.770752237	3.162936347	3.039695637	3.372269346
252031_at	AT3G52140	0.942331495	4.830782945	1.165037147	1.379547887	2.650625645	1.245040361
252055_at	AT3G52580	5.612070153	20.03792306	3.863651558	5.7115349	9.640775375	4.536623501
251997_at	AT3G53020	16.23005714	33.65030367	10.29032509	12.23582635	16.95047502	8.638567535
251938_at	AT3G53430	16.18203296	35.61462681	12.30807521	15.00948713	20.18923067	9.19847477
251952_at	AT3G53650	1.139443567	1.983064765	0.759561414	0.926182838	0.665421493	0.509295482
251953_at	AT3G53670	0.767768965	1.46810307	0.606019516	0.492059032	0.539778949	0.626103407
251921_at	AT3G53890	10.46911791	26.65868865	5.78264332	8.569796881	15.05753721	8.133475179
251861_at	AT3G54810	2.346988421	6.417661439	2.259748866	1.355172658	1.728242714	2.339197861
251783_at	AT3G55280	4.591013453	21.87276269	4.752733585	4.995934731	9.256401903	3.754804711

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
251740_at	AT3G56070	0.845100053	8.79233008	1.571068531	3.13241837	4.534213987	1.407097745
251486_at	AT3G59540	10.14497603	20.32539678	6.439629258	7.667811348	11.52812082	6.455075751
251483_at	AT3G59650	1.19210172	3.583565055	1.13540318	1.456699228	2.069245832	0.961773298
251412_at	AT3G60220	0.608837881	1.483498511	0.459074147	0.487774671	0.621801567	0.696964049
251410_at	AT3G60280	0.574252202	1.081741435	0.474943543	0.572191971	0.620715207	0.522287382
251357_at	AT3G61110	6.893072849	30.305314	4.096265458	5.515248475	11.45360486	4.852245701
251362_at	AT3G61240	1.639335632	4.473105741	2.616455511	2.290932112	2.469158554	2.009995451
251319_at	AT3G61610	0.591453371	1.532899522	0.804831484	0.584418818	0.782835157	0.695868758
251231_at	AT3G62760	0.688822168	1.393050978	0.698666891	0.696092585	0.756908558	0.751267758
251179_at	AT3G63460	3.176059733	8.307726754	2.176063909	1.52272438	1.921616034	1.781547018
255636_at	AT4G00730	1.034013282	3.942873958	0.785477405	0.67965068	0.745453299	1.031988252
255657_at	AT4G00810	10.38513601	17.96679251	7.556119785	7.060625951	10.27296069	5.831791817
255642_at	AT4G00820	0.777038432	3.365283713	1.054517135	0.797173552	1.362351597	1.557414707
255570_at	AT4G01100	4.094904677	11.76954988	4.692947173	2.091653357	3.625384338	1.969701828
255308_at	AT4G04910	3.548719857	8.252674716	4.791198672	2.361902805	3.980998021	2.461112389
254980_at	AT4G10450	1.425506906	13.8669588	3.431271464	4.256681011	5.690286104	2.280173593
254962_at	AT4G11050	0.695965153	2.901837795	0.614693202	0.525925373	0.623737573	0.60003089
254815_at	AT4G12420	2.175556691	7.375833475	3.842734918	2.74959743	3.244452504	2.321782934
254831_at	AT4G12600	1.037084129	19.15366655	2.747852731	6.971366739	10.79598406	3.048195522
254798_at	AT4G13050	1.916690587	3.330823009	1.855894372	1.324600656	1.409509203	1.377722194
254686_at	AT4G13720	2.650830199	5.66470939	2.270550299	1.874578414	2.802064111	1.48164627
254684_at	AT4G13850	4.973025975	25.18495981	5.171149037	7.305625264	10.11298508	3.584165164
245311_at	AT4G14320	9.029624089	27.32551851	5.352420306	6.526166937	11.92564121	5.085220585
245594_at	AT4G14570	0.824117985	2.16740786	0.936484241	0.747855674	0.741287741	0.729027141
245557_at	AT4G15410	1.588324743	4.349757786	1.545057026	1.123090274	1.765705439	1.757364453
245358_at	AT4G15900	1.316882362	3.29459167	1.40281183	1.544767319	1.727333469	1.548603231
245216_at	AT4G16143	1.061755311	3.784462	1.286889847	1.060711203	1.189030226	1.007813195
254357_at	AT4G22220	2.868958037	6.630571399	2.310657659	1.738508166	1.991786034	2.154639105
254355_at	AT4G22380	0.418382977	3.111473687	0.806126783	1.015278548	1.646629061	1.0433727
254219_at	AT4G23760	0.629242231	1.129234413	0.555423407	0.612568427	0.639069255	0.597607954
254169_at	AT4G24290	0.74393013	1.675845274	0.901259463	0.725226759	0.737618528	0.870037958

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254162_at	AT4G24440	1.043299194	2.589323932	0.968755338	1.031726939	1.174683374	1.361871206
254089_at	AT4G24800	1.467552078	3.896933611	1.307014663	1.342768333	1.969694593	1.333053461
254056_at	AT4G25250	3.147248847	13.64586101	1.51694166	0.668783588	1.284814207	1.08302161
253917_at	AT4G27380	0.783729983	2.658024675	0.744668584	0.936104342	1.492036774	0.774021045
253881_at	AT4G27640	0.671180334	2.281560318	0.639567094	0.667850558	0.799559821	0.781503741
253726_at	AT4G29430	1.259873413	2.543525619	1.064395573	1.027392234	1.288269062	0.731413843
253607_at	AT4G30330	0.548454058	2.105613415	0.658403084	0.846612722	1.019284879	0.558367204
253605_at	AT4G30990	0.495386547	1.117928758	0.4615487	0.472466822	0.545275782	0.506883401
253577_at	AT4G31080	0.996974677	2.159382741	0.865519843	0.698548786	0.836179034	0.865196019
253545_at	AT4G31310	0.7670089	2.042380758	0.705674454	0.757450842	0.674585571	0.699061624
253538_at	AT4G31460	2.036673931	4.404547547	1.60511509	1.910707493	2.468375996	1.297985488
253536_at	AT4G31580	2.723096744	9.000884007	2.896443025	3.265241869	5.162138898	2.291154335
253482_at	AT4G31985	6.35037229	16.84821636	2.975392767	4.592225669	8.538712531	4.787553241
253464_at	AT4G32030	0.993403809	3.103213926	0.886398508	0.946545191	0.786791965	0.967283319
253448_at	AT4G32640	1.57898071	3.22832321	1.756986652	0.983680575	1.579156341	1.332319579
253381_at	AT4G33350	0.972280518	2.09673716	1.115670438	0.922847806	1.22769231	1.214458479
253233_at	AT4G34290	0.557076159	1.614810955	0.548198418	0.660718214	0.718166582	0.65300705
253248_at	AT4G34670	13.44235939	36.21967069	15.33334971	15.90458348	20.83618986	8.173166271
253221_at	AT4G34870	14.82394979	31.44476654	10.49553369	6.645023423	9.665002057	8.510764972
253138_at	AT4G35490	2.949690775	8.891613617	2.190598458	2.334115693	4.897771996	2.086721667
253159_at	AT4G35570	1.296990783	3.718223194	1.383300993	1.280912566	2.121807062	1.284998445
246210_at	AT4G36420	0.629098947	3.320065353	0.564863783	0.591901624	0.824501447	0.676341518
246284_at	AT4G36780	1.222766524	2.508440726	1.130442151	1.046091853	0.837066003	0.937858255
253058_at	AT4G37660	1.102085338	3.544072182	0.847058157	0.959478041	1.519023449	0.960701433
253070_at	AT4G37850	0.408930104	1.1852198	0.649168425	0.657124551	0.572996266	0.561219308
252997_at	AT4G38400	0.771512984	2.101340102	0.725537823	0.850798103	1.184599008	0.937563666
252947_at	AT4G38600	1.299209946	3.841994958	1.383583191	1.330206884	1.657925119	1.526812732
252973_s_at	AT4G38740	7.379354491	31.91848091	11.91045765	11.38864217	12.75076957	12.21426524
252934_at	AT4G39120	0.849076337	2.316149138	1.258290225	0.892602796	1.26907796	0.953037147
252942_at	AT4G39300	1.194553316	5.978279457	1.135786075	1.190123242	2.196185988	1.403262147

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
252850_at	AT4G39880	2.496925955	6.521775524	2.429495493	2.202540048	3.747180802	1.423674063
252824_at	AT4G40030	11.58495188	19.86157625	8.18308209	11.05256517	10.48216732	8.814719046
245862_at	AT5G01010	2.2094385	4.288057024	2.077967958	1.474000615	1.666979998	1.916343554
250992_at	AT5G02260	3.221214528	13.77040078	2.588498013	0.627560987	0.801968371	5.401973136
250969_at	AT5G02740	2.552701657	5.114527767	1.78760385	1.324110947	2.592210732	1.708249917
250970_at	AT5G02770	0.851348527	2.745190361	1.017826189	0.917443226	1.179644873	0.95699493
250845_at	AT5G04600	1.275516966	7.366062261	1.894828074	3.159556454	4.157398076	2.602714626
250779_at	AT5G05470	1.118618514	2.552498227	1.036978011	0.881232558	1.42841096	0.899196402
250703_at	AT5G06360	1.802215131	10.77040892	2.100216796	3.625265891	5.684141722	2.64272086
250564_at	AT5G08060	3.857954581	6.674247705	2.985196705	2.100433591	2.068982565	1.829252855
250546_at	AT5G08180	0.914492567	8.415773105	2.18629562	3.355945452	4.856436587	1.886502421
245886_at	AT5G09510	1.536598252	6.735207362	1.544852177	2.279042113	3.546438227	1.612526571
250433_at	AT5G10400	1.107025982	7.469249967	3.655243482	3.233586609	4.035547899	1.783246023
250353_at	AT5G11630	2.437003947	6.051348034	1.255651264	1.219905522	2.044527083	1.510025818
250355_at	AT5G11700	1.385483616	2.65769508	1.481352759	1.185044341	0.973325718	1.115068465
250275_at	AT5G13030	0.788198633	1.657091921	0.706650692	0.680549253	0.816650384	0.740905052
250226_at	AT5G13780	2.617867535	9.299247885	2.113273169	2.710747256	3.025119407	1.363265949
250214_at	AT5G13870	0.506889834	5.424404941	0.646213331	0.642395179	0.596689066	0.960804524
246585_at	AT5G14750	0.512374866	3.660555047	0.839625513	0.429166189	0.676748993	0.719681613
246537_at	AT5G15940	1.076284251	2.056433692	0.631369091	0.624907332	0.700810651	0.84019682
246490_at	AT5G15950	3.510050553	8.37839712	0.803438322	0.781113121	0.897334683	1.213999299
250132_at	AT5G16560	0.49452662	2.002404914	0.495222797	0.46858472	0.540139854	0.507619984
249954_at	AT5G18920	0.54650419	1.421820125	0.518540024	0.567813613	0.735002629	0.560337332
245937_at	AT5G19750	1.593756009	4.494213166	2.38800243	1.481674134	2.026796007	1.103139917
246070_at	AT5G20160	1.152505618	15.71606531	2.261729092	4.60678689	8.890734092	3.869231678
246031_at	AT5G21160	0.771666628	3.562659776	1.138809852	1.505677456	1.854319319	1.525229715
249945_at	AT5G22440	8.120110497	23.11389821	6.891497693	8.044059159	10.88622808	4.143356196
249829_at	AT5G23290	1.780237715	4.48926509	1.374248245	1.488307235	2.387987234	1.320388927
249836_at	AT5G23420	0.333261442	1.369944034	0.471439361	0.497310638	0.602662926	0.420663318
249814_at	AT5G23840	3.454403462	8.163245914	2.652576851	1.085273623	1.170642861	1.853218862
246958_at	AT5G24690	0.653712982	3.006700749	1.02157083	1.058844418	1.191787453	0.962694823

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
246784_at	AT5G27430	2.561912153	5.219238719	1.547718657	1.302461099	1.594582823	1.540795925
246747_at	AT5G27700	12.31852922	30.97228418	8.705187758	10.46743773	17.50338273	9.345293905
246746_at	AT5G27820	0.839792538	4.067331467	0.65297461	0.600315491	1.196918683	0.758372709
246730_at	AT5G28060	4.461479022	15.49034037	4.137157938	4.686668744	6.720057962	1.907313277
249722_at	AT5G35430	0.557861477	1.153393368	0.475130924	0.467493655	0.507814437	0.532634102
249675_at	AT5G35940	1.942720275	12.87874047	2.134405553	0.74199573	1.055029343	7.444838626
249583_at	AT5G37770	1.197528045	5.386930756	1.156919907	1.763801601	1.115692571	1.685993433
249493_at	AT5G39080	0.687106697	1.8978199	0.886173591	0.672675054	0.861847475	0.938341191
249443_at	AT5G39600	1.711093127	3.221977188	1.132601308	1.09911368	1.511311409	1.026112993
249466_at	AT5G39740	5.534430537	22.49835156	5.474515787	5.381457678	10.63139776	4.327911653
249427_at	AT5G39850	0.788449235	3.385568373	0.842779646	1.031719971	1.749821161	1.272305575
249336_at	AT5G41070	0.569119495	2.126597467	0.60067741	0.545394491	0.627962379	0.726363008
249254_at	AT5G42110	0.708705991	2.073919936	0.835188687	0.603843445	0.926066479	1.104889758
249206_at	AT5G42630	1.665967713	3.605324996	0.592090418	0.964729531	0.568618146	0.833724725
249182_at	AT5G42960	1.376020625	3.37235712	1.184816021	1.172822275	1.194165436	0.896592344
249186_at	AT5G43040	1.651030124	3.707768883	0.960844959	0.758499753	0.90614446	0.916962137
249067_at	AT5G43960	1.983415632	6.290795742	2.058616049	1.658193476	3.213974812	1.869314485
249014_at	AT5G44710	1.837747444	4.145132172	1.581910782	1.61996938	2.380152441	0.983289771
248958_at	AT5G45590	2.145747033	4.852325705	1.051217846	1.079134467	1.915431444	0.921081044
248919_at	AT5G45920	1.786656605	4.591067181	1.749267772	1.579010143	1.530837498	2.043030886
248826_at	AT5G47080	0.667835892	2.180818335	1.063539	1.105658462	1.179271772	1.009327078
248800_at	AT5G47320	2.894287394	5.671622658	2.239135596	2.149779648	3.32085193	1.881645533
248768_at	AT5G47700	10.03481447	24.60509139	9.760998201	11.48581731	13.75445562	8.814655377
248664_at	AT5G48580	6.983791816	14.23136006	5.10436362	2.409777295	3.99244152	2.92477759
248655_at	AT5G48760	1.887800552	13.358938	2.404765445	2.914336948	6.273362229	2.305467956
248473_at	AT5G50810	1.701037601	7.797699868	1.566185782	2.389245173	4.458991748	2.014232686
248434_at	AT5G51440	0.802617306	2.810585841	0.973707537	0.78416857	0.519695875	1.191709205
248407_at	AT5G51500	1.355524436	3.741051379	1.072380795	0.590223884	0.903666377	1.467782445
248295_at	AT5G53070	0.693775415	2.634890091	0.623862171	0.710588399	1.403038003	0.726852915
248268_at	AT5G53480	0.82596205	3.2650191	0.817580856	0.780005626	0.85591601	0.742689353
248131_at	AT5G54830	0.977162769	2.262576459	0.880080333	0.631129624	0.853943056	0.882128914

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Non-Hair Epidermis (WER) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
248103_at	AT5G55160	4.755361508	9.513522598	4.117833756	5.378237005	5.500378968	2.423821555
247991_at	AT5G56320	0.506196195	5.547149126	0.579223398	0.528327951	0.825295755	0.817884048
247935_at	AT5G56940	3.773566038	8.247251609	2.481985383	2.771606684	4.677002095	2.03020412
247781_at	AT5G58784	1.092092941	4.868818304	0.73614075	0.745991649	0.831563817	1.045108585
247699_at	AT5G59840	0.64888866	1.870813184	0.716628061	0.750513895	0.795055865	0.675265199
247632_at	AT5G60460	3.372715837	6.739840442	2.082936461	1.747818415	1.132562325	1.330479236
247551_at	AT5G60980	1.988603786	4.395137915	2.206241039	1.195320313	1.932280188	1.163732746
247555_at	AT5G61020	1.686612178	11.15529628	1.582749208	1.676124235	3.658583133	1.531655478
247520_at	AT5G61310	0.727533647	3.127513202	0.791232236	1.253258935	1.820339819	1.216426248
247517_at	AT5G61780	5.218148849	12.02930422	4.364735734	2.425394063	4.526105561	2.811055877
247476_at	AT5G62330	3.60006554	6.391191923	1.144906038	0.507283838	1.125299206	1.07363012
247477_at	AT5G62340	1.77450901	27.88125623	9.905056975	1.00503119	1.75903063	16.23457129
247454_at	AT5G62440	0.867142756	6.01008702	1.565863352	2.415718957	3.446233564	1.683432165
247323_at	AT5G64170	1.227454417	2.556508798	0.984847859	0.818694722	0.880647967	1.012261274
247192_at	AT5G65360	2.089840139	11.37979247	6.038166779	5.606273491	6.683136522	4.307970822
247068_at	AT5G66800	0.958907934	2.048546336	1.017477984	0.672729226	0.929681008	0.815671204
247010_at	AT5G67510	5.088411906	17.47178311	3.243901633	4.616234994	10.02329526	3.177937738
247014_at	AT5G67630	0.435414279	2.032375487	0.587697808	0.774504118	1.107686712	0.794366206

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
259442_at	AT1G02310	1.666543819	0.530829893	5.689009822	2.950563907	0.939103175	0.849639119
259417_at	AT1G02340	0.707069942	0.580720016	1.221629263	0.685832052	0.612316673	0.508466669
262118_at	AT1G02850	0.726687529	0.647613082	5.245291954	0.920860783	0.715723094	0.755775476
264355_at	AT1G03210	2.459418379	3.418233759	7.192265583	4.035634716	2.109431643	2.62565038
263677_at	AT1G04520	0.765418806	0.953537452	3.006306124	1.331567265	1.524231258	0.84815375
265214_at	AT1G05000	0.720858258	0.546187614	1.459467302	0.723135204	0.736422842	0.621708476
263183_at	AT1G05570	1.667724559	1.036260341	7.809780195	1.614703609	1.273501765	1.144488958
263231_at	AT1G05680	1.713826365	4.016573036	11.17729873	0.661576554	0.628186116	0.485247825
260955_at	AT1G06000	6.213115785	7.114996706	19.97626083	11.25269296	4.023116842	2.525586671
262626_at	AT1G06430	0.808416069	0.618892735	1.514055517	0.68734792	0.659110202	0.648147836
262637_at	AT1G06640	1.194027685	0.84134806	13.9137244	6.002252911	1.976148128	1.3420765
262638_at	AT1G06650	0.583235718	0.495487221	1.38124129	0.509848278	0.515566915	0.538593436
262632_at	AT1G06680	0.809035208	0.626921684	2.443727291	1.266956554	1.189743425	1.20249599
261434_at	AT1G07650	0.64552967	0.563113163	2.858688428	1.113542952	0.749150365	0.734728386
261417_at	AT1G07700	0.478383537	0.67534863	1.557252372	0.644213237	0.543094234	0.651164908
261746_at	AT1G08380	0.506704	0.48031413	1.157740016	0.57344751	0.658908423	0.565744653
264804_at	AT1G08590	2.99139199	2.97538764	5.154214639	2.021050019	1.424298945	1.001909973
264672_at	AT1G09750	0.511754423	0.57488353	12.31979941	0.570477277	0.724601856	0.576746398
261834_at	AT1G10640	0.465216136	0.425342479	1.071984247	0.472183939	0.524271245	0.511359563
262825_at	AT1G11790	2.151755872	1.841331103	5.195513193	2.299833198	2.013889148	1.601573223
264371_at	AT1G12090	2.496977304	1.260559151	32.07568055	14.47077848	3.871899124	1.679623248
260969_at	AT1G12240	7.934822922	5.647472287	17.69177912	6.217141479	3.356619719	3.630603985
261203_at	AT1G12845	0.705724079	0.569876867	5.176111815	0.895093034	0.743949546	0.752314163
262826_at	AT1G13080	1.044374545	0.508140649	2.474066533	0.718139041	0.76981926	1.161509948
262609_at	AT1G13930	0.814564911	0.540162641	12.48159796	3.870124881	3.82229184	2.352721886
262653_at	AT1G14130	0.666450649	0.698038602	2.657631048	1.404316236	0.839220095	1.099342944
261480_at	AT1G14280	0.590330231	0.849015226	3.859740637	1.771289619	1.57444164	0.947251039
261471_at	AT1G14460	0.627488204	0.910242429	2.605886592	1.096859974	1.048449185	0.924721154
262585_at	AT1G15460	0.721397688	0.620781167	1.435766183	0.648214276	0.816418587	0.826147741
261768_at	AT1G15550	0.719760447	0.584581513	4.792605028	0.810570837	0.869788507	0.735958827
255764_at	AT1G16720	2.449211379	1.309071789	4.55069313	1.936917661	1.41510652	1.836065542

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
262483_at	AT1G17220	0.816526306	1.085473289	2.940254976	1.550141543	1.523866745	1.575228407
261060_at	AT1G17340	1.910561115	1.369419781	3.974872605	1.74709114	0.746111804	1.36097193
261428_at	AT1G18870	0.471885503	0.427668085	1.956220176	0.49625229	0.556598478	0.488686614
256012_at	AT1G19250	0.462230539	0.442595312	1.738892621	0.632019947	0.5731053	0.463329665
260676_at	AT1G19450	2.14074893	0.923910417	21.77574744	11.30890348	3.324777818	3.074373898
261230_at	AT1G20010	7.041923162	6.835280587	15.67449104	5.808057963	4.144446767	1.428613209
261226_at	AT1G20190	0.903862523	1.384541883	15.77908051	2.712744613	2.443004283	1.025507704
261455_at	AT1G21070	0.908707125	1.18125824	3.546965104	1.113865598	1.538028153	1.176531698
264209_at	AT1G22740	0.627281943	0.620744144	6.105624133	2.412591587	1.331705666	1.277480404
261273_at	AT1G26650	1.439427717	1.91915835	4.111678646	1.326760026	2.070464509	1.853067382
264449_at	AT1G27460	0.906191188	0.779507285	2.569148757	1.258428329	1.386332071	0.946088179
256191_at	AT1G30130	6.112997719	3.831278751	11.12081165	5.049045309	2.880173727	2.59741999
256309_at	AT1G30380	0.607046964	0.61771923	6.921888716	2.740002574	1.522079812	0.865819348
262557_at	AT1G31330	0.744619301	0.597247184	4.488529232	1.741843665	1.010218051	0.972093025
261618_at	AT1G33110	0.778546887	0.80124504	2.642928636	1.005115784	0.902417765	0.730425622
255982_at	AT1G34000	2.396184644	2.357504577	5.363427676	2.873471793	2.288344052	2.176767495
245740_at	AT1G44100	1.393154613	1.363467624	6.319206385	1.256235429	1.149195451	2.431690318
245737_at	AT1G44160	0.719132031	0.492374953	1.855297804	1.03448719	0.625460693	0.710851987
245213_at	AT1G44575	1.018038944	0.690203076	4.649693017	0.932203816	1.039547564	1.024322587
262444_at	AT1G47480	1.2953242	0.673083721	2.90776657	1.007603589	0.988520331	0.734774775
261635_at	AT1G50020	1.800569448	1.261656962	3.877691195	2.056066889	1.245780189	1.336731634
262473_at	AT1G50250	3.021516593	1.287255147	9.190832679	3.955978967	1.784869501	2.132915334
246371_at	AT1G51940	0.522783753	0.769328048	3.266233385	1.387886527	1.66998717	1.293057204
260639_at	AT1G53180	5.828157206	6.522371964	11.08835454	4.365665501	1.370182845	5.688176081
259965_at	AT1G53670	1.876165239	1.011004033	3.190915909	1.736460353	1.129019746	1.58011632
262954_at	AT1G54500	0.900016428	0.645403203	2.38335857	1.221676067	1.038601626	0.945652743
256150_at	AT1G55120	0.672412035	0.410205256	1.857967007	0.708161355	0.685468354	0.527215835
257510_at	AT1G55360	0.587744222	0.643641406	4.069159495	0.848757228	1.392099576	1.296361756
260592_at	AT1G55850	3.960353716	5.002634434	14.6165431	7.252925698	2.523226344	4.706200467
256022_at	AT1G58360	0.586145905	0.569505695	9.350237899	1.470728736	0.813194444	0.835437787
262913_at	AT1G59960	2.527106815	2.511951316	5.2828482	2.01865393	1.31140247	2.765455208

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
265033_at	AT1G61520	0.668682132	0.510188465	3.001758977	1.319838799	1.057684183	0.89405778
264424_at	AT1G61740	2.871885558	1.232128568	7.563847348	4.434210962	1.400769806	1.00232562
265111_at	AT1G62510	0.679038642	0.511528612	7.272327173	1.119434239	0.782185153	0.645027174
262643_at	AT1G62770	0.610927386	0.755983441	2.480454624	0.724194472	0.724724839	0.731324523
260317_at	AT1G63800	2.200569535	1.111485789	7.034408164	2.715529407	1.788653989	1.458103577
261953_at	AT1G64440	1.789212843	2.345367194	4.579389428	2.01555208	1.966916497	1.160777136
262882_at	AT1G64900	0.469065061	0.511191739	1.065770837	0.535747525	0.586460351	0.606241835
262863_at	AT1G64910	0.456925583	0.432774098	1.910629493	0.414171213	0.444278024	0.423895367
262864_at	AT1G64920	1.050093308	1.511764134	4.101613715	0.424051045	0.528860199	0.47320514
261907_at	AT1G65060	1.079089793	0.980992972	10.55821375	2.392330911	1.000663768	1.215685857
256324_at	AT1G66760	0.818777062	0.887468774	3.40102371	1.290445846	0.876679859	1.130243554
245195_at	AT1G67740	0.542803059	0.526500332	1.33537977	0.626006236	0.63761252	0.586911048
260008_at	AT1G68070	2.097921109	1.963310117	3.812191049	2.068866751	1.850918047	1.624942963
264315_at	AT1G70370	0.719465765	0.868472109	16.07980032	2.792352726	3.302570082	1.676872256
260309_at	AT1G70580	1.276725718	1.082606441	3.5901263	1.723152793	1.520959852	1.178159221
262304_at	AT1G70890	0.473157658	0.404568224	4.158191715	0.859072984	0.756836969	0.449838105
262313_at	AT1G70900	0.673685944	1.026171669	2.88047371	1.124837746	0.948824126	1.056611273
262315_at	AT1G70990	1.013029798	1.004969563	2.116058293	0.956847355	1.077353491	0.851330439
260429_at	AT1G72450	1.185472337	0.483874967	8.411877249	2.213908164	0.886228237	1.019826899
262381_at	AT1G72900	0.53172096	0.504619178	1.578097476	0.876618535	0.511815214	0.484729551
245736_at	AT1G73330	0.928953956	0.60696005	16.21417175	6.228414756	6.295588918	3.508829619
260077_at	AT1G73620	0.578056179	0.762781125	10.76591821	3.272469783	1.705982627	0.621947225
260072_at	AT1G73650	1.569466707	1.105903765	3.587521455	1.47133973	1.199369136	1.51095198
262177_at	AT1G74710	0.471261969	0.502274704	1.833021561	0.609418498	0.615177993	0.557252594
262218_at	AT1G74760	1.119540275	0.946576961	2.314242891	0.854822055	0.88471865	1.239850585
262980_at	AT1G75680	7.804360409	7.6169332	15.88649287	5.823804933	8.570800417	5.531746563
262978_at	AT1G75780	7.740788391	10.08364444	19.73189212	6.244605607	2.507833138	1.278029363
261769_at	AT1G76100	0.466924768	0.485777276	1.083587137	0.493294349	0.53535051	0.517512879
261728_at	AT1G76160	2.743451495	2.179905466	14.95422978	6.391866397	2.724213664	1.372755868
259975_at	AT1G76470	0.648221646	0.593140022	8.13387049	1.221992727	0.840816973	0.613885704
259983_at	AT1G76490	6.680472589	7.549820807	19.09175615	10.2407231	6.746842071	4.250249309

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
259882_at	AT1G76670	8.096127859	7.288934134	16.50375176	6.016953967	6.317799338	8.754952155
262134_at	AT1G77990	0.481899558	0.45532978	1.799688031	0.550093667	0.632497195	0.570698131
262164_at	AT1G78070	0.691003669	0.727614092	2.404356873	1.158183726	0.646148958	0.633392126
264300_at	AT1G78670	2.082823523	0.716425996	4.152183056	1.293227862	0.997154436	0.740309889
264100_at	AT1G78970	0.730911375	0.474257096	2.034720482	0.827083459	0.947303122	0.887935316
264092_at	AT1G79040	0.830200611	1.186600858	12.07274712	2.970285914	1.889674461	1.352886644
262935_at	AT1G79410	3.473092639	1.673957451	6.892611788	1.861397385	1.008974935	0.780439964
261346_at	AT1G79720	1.105570655	0.861333649	2.771589148	1.259170249	1.038599404	1.06007559
262049_at	AT1G80180	0.7724821	0.475168163	2.885330011	1.053194082	1.021432227	0.688140121
260300_at	AT1G80340	0.683544808	0.611299244	2.022199866	0.865060696	0.7495896	0.738315584
266330_at	AT2G01530	1.918263366	0.566872852	15.43525415	4.064724098	2.661042239	1.197382216
263595_at	AT2G01890	0.929784596	0.559300239	2.247505667	0.506473648	0.626834124	0.687721597
266110_at	AT2G02080	0.838067627	0.595929665	2.094278316	0.970011004	0.777610814	0.749448547
267481_at	AT2G02780	0.673337872	2.106383744	7.26821402	4.193933379	1.094472513	1.089137566
266745_at	AT2G02950	0.770163444	0.425353089	4.095444373	1.406255869	0.766788562	0.628500108
265710_at	AT2G03370	0.682528091	0.481749142	1.844701131	0.645176019	0.669562358	0.575659028
265569_at	AT2G05620	0.526197672	0.538071237	1.378818586	0.672023793	0.604844415	0.650121363
265530_at	AT2G06050	8.272937469	3.850908494	15.65201299	9.021257968	4.156863594	7.739400607
263772_at	AT2G06255	0.399529504	0.432035979	1.239074462	0.558089348	0.505942948	0.443630381
266215_at	AT2G06850	2.365433047	10.00974777	23.18250995	8.163199043	6.769992996	3.113085516
266500_at	AT2G06925	0.862071166	0.690851722	6.350120714	3.233406764	0.926330639	0.823286982
263350_at	AT2G13360	0.639204811	0.592107891	1.74149361	0.642609915	0.691550105	0.618226891
266614_at	AT2G14910	2.225593386	1.761784543	3.966886878	2.250288236	1.590934049	1.598744031
265472_at	AT2G15580	0.785077957	0.560965242	3.044295255	1.227020738	0.864809955	0.79264853
265479_at	AT2G15760	1.031341372	0.681126775	3.056536424	1.080817623	1.353270039	1.072815873
263098_at	AT2G16005	0.839337453	1.040841355	5.056780371	2.16408294	1.597010662	2.070545946
265924_at	AT2G18620	0.520903612	0.51439307	1.252034136	0.681078492	0.686812919	0.543942239
265433_at	AT2G20950	1.032038813	0.529677252	1.883475315	0.897434616	0.731836355	0.632150372
264006_at	AT2G22430	2.52132327	1.490104525	4.536019389	2.534097075	1.177182653	1.658666174
245076_at	AT2G23170	4.496469294	0.472033162	9.736142539	2.406421001	0.980641695	0.801511628
266578_at	AT2G23910	0.793430233	0.826105154	12.83449825	3.164066443	1.01392997	2.054345373

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
266001_at	AT2G24150	0.97664904	0.897806351	6.836054602	1.270150777	2.524170307	1.283373854
245031_at	AT2G26360	2.14590516	1.488860323	3.714358985	1.450563922	1.050148564	0.98315421
267612_at	AT2G26690	0.852875676	1.033796655	5.903481271	1.718656626	1.778462965	1.059507548
266313_at	AT2G26980	1.027944059	1.464464314	3.132184596	1.709729827	1.388285718	1.077600192
266140_at	AT2G28120	0.884339426	0.654474788	1.540963456	0.876903951	0.842719616	0.790665689
255818_at	AT2G33570	0.744372666	1.552171555	3.880870256	0.947314679	1.791806899	0.945202229
256725_at	AT2G34070	1.664237155	1.226818411	14.76553321	7.158787197	3.978252462	2.621708221
266996_at	AT2G34490	0.500435067	0.447809159	1.217694231	0.559435825	0.613190749	0.535313351
266901_at	AT2G34600	0.471494966	0.375278849	3.505331979	1.51331838	0.538820648	0.62748442
263942_at	AT2G35860	3.31284929	1.934348179	5.761907937	2.827311588	2.025901234	2.889919387
267181_at	AT2G37760	0.646814918	0.531036325	3.530417293	0.963656035	1.438039336	0.633776752
267093_at	AT2G38170	1.293846605	1.11443505	13.6068131	4.971184342	2.160858705	1.344494128
267089_at	AT2G38300	0.369040691	0.327407959	1.262877132	0.365408458	0.392835432	0.369906739
266172_at	AT2G39010	1.99527666	1.122943498	5.129140462	1.954439069	1.183143013	0.806728091
245061_at	AT2G39730	0.672276075	0.565514647	2.816854702	0.761899476	0.883288609	0.810713695
263830_at	AT2G40260	0.556736564	0.429605716	1.858175469	0.535974261	0.549715418	0.554888164
245117_at	AT2G41560	1.466836027	1.834143112	3.761936247	1.207384839	1.975722235	1.504971398
263977_at	AT2G42660	0.662897197	0.505851291	1.155047419	0.566580971	0.604631729	0.604105397
266873_at	AT2G44740	1.434050841	2.55178725	5.46645242	1.596451648	1.383973404	0.854728634
266123_at	AT2G45180	0.797279094	0.704493754	21.27096895	2.025039431	1.766366433	0.935304834
266583_at	AT2G46220	0.895787672	0.793616842	2.17514471	1.007747787	0.918542875	0.847066968
263787_at	AT2G46420	0.577090477	0.941620387	3.140122334	0.952686734	0.770855778	1.676226387
266735_at	AT2G46930	4.223396238	2.165452756	9.729366785	3.51978869	3.544426167	1.128210232
265768_at	AT2G48020	4.754682848	2.089936802	16.80413015	5.094057004	1.839738676	1.449043374
258602_at	AT3G02750	2.000672575	1.971398973	4.626489824	1.961698483	1.405496563	1.674447323
259351_at	AT3G05150	0.60163669	1.079613327	14.79183062	2.631281752	1.088810129	0.696105247
258913_at	AT3G06450	0.784602539	0.727610396	4.326227321	2.379677529	2.514740764	1.074119879
258515_at	AT3G06650	5.095798186	8.181361846	14.7017376	5.976907176	5.340054305	3.334191029
258528_at	AT3G06770	1.969014026	2.211526229	6.831088113	2.370973788	1.576855479	1.295757211
259228_at	AT3G07720	2.318836363	1.685740749	7.394423053	3.759318894	1.798639601	1.202688702
258676_at	AT3G08600	1.309685641	1.521148769	2.969187187	1.576360629	1.621705172	1.100401763

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
258704_at	AT3G09780	0.79064283	0.8166269	2.112063812	0.868915671	0.821731138	0.639359865
258920_at	AT3G10520	0.820477938	0.885779122	2.501134763	0.657561043	0.634876121	0.630453237
256415_at	AT3G11210	0.631719174	0.586757044	3.221835839	0.863335104	0.72263032	0.696794559
256252_at	AT3G11340	6.346121203	1.413856343	14.86219836	5.023665154	1.259838278	1.795422773
257697_at	AT3G12700	1.809109107	0.620402776	9.738818367	1.817562516	0.916124509	0.797635871
256962_at	AT3G13560	0.779263865	1.631524423	2.980246803	1.460184789	1.747735833	1.260879704
258094_at	AT3G14690	1.231267042	0.475561942	4.429317681	1.019558694	0.829171059	2.184435845
256600_at	AT3G14850	2.775037668	0.852996362	8.847785677	2.356366521	1.710281553	0.831765942
258393_at	AT3G15480	4.646061545	4.50439677	8.223462616	4.31376773	3.896139199	4.754284573
257651_at	AT3G16850	1.483875777	2.027173057	4.102105022	1.758705709	1.322863658	0.855233875
257892_at	AT3G17020	6.636383267	1.522093943	17.0498969	8.747110435	3.143649554	3.532719359
257805_at	AT3G18830	1.34324893	1.64336696	13.68811705	4.180333951	2.117462641	1.783143864
257143_at	AT3G20110	0.554950802	0.377664545	1.587862196	0.395864837	0.399220881	0.384872046
257112_at	AT3G20120	0.458365052	0.509032668	2.197305951	0.894688891	0.884710103	0.686185285
256697_at	AT3G20660	1.236200352	1.22305572	3.293117131	1.610863292	1.436169842	1.019394487
258038_at	AT3G21260	0.742024421	0.700138595	1.769876237	0.836459917	0.6374461	0.6188785
258167_at	AT3G21560	0.799468771	1.425102088	5.979060129	2.165510388	1.183865714	0.654081823
258181_at	AT3G21670	0.757204406	0.554409667	3.831240073	0.694108277	0.712599711	0.58003657
258295_at	AT3G23400	3.287482322	1.223618776	7.78659148	3.367357044	1.458731479	3.693709343
257253_at	AT3G24190	1.725258118	0.928757829	3.681330772	1.960133571	1.058982078	1.21016207
257628_at	AT3G26290	0.543362796	0.442975603	1.838623129	0.697440756	0.742885424	0.680981497
256870_at	AT3G26300	0.379357182	0.356935443	3.782104545	0.841432109	0.523757293	0.46056891
256880_at	AT3G26450	0.392843018	0.382632358	2.077085708	0.747525737	0.562215431	0.422144853
256877_at	AT3G26470	2.861452828	0.668348136	5.331058249	1.077687643	0.743819263	0.664638591
257834_at	AT3G26720	1.571369967	1.918733848	7.727951091	3.290928571	2.891001076	1.972100925
256751_at	AT3G27170	1.142634616	0.527507688	3.779370527	0.896799963	0.759605741	0.640860966
258244_at	AT3G27770	9.797369075	6.615175982	16.7550204	6.161142218	4.561004953	3.966366457
256848_at	AT3G27960	3.546451207	2.052544053	6.218384835	3.14697836	2.781509309	3.324526555
257297_at	AT3G28040	1.019160117	0.693676459	3.798845387	1.617896247	0.857157763	0.797149713
257272_at	AT3G28130	0.462924687	0.467919043	2.260640262	0.77063815	0.668039081	0.472883207
257071_at	AT3G28180	5.748690649	5.361596889	10.93208972	6.324315146	3.950876187	3.363031816

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
256736_at	AT3G29410	0.57291624	0.494245008	1.753767216	0.713848107	0.609959724	0.605061767
252677_at	AT3G44320	4.638662606	5.447829639	15.55993847	7.328571386	2.415082908	5.478648862
252652_at	AT3G44720	0.880422471	0.568604013	2.047778879	1.1648736	1.063704182	0.883950996
252607_at	AT3G44990	0.500715528	0.407827371	8.32285762	0.985149606	1.053035433	0.695329449
252570_at	AT3G45300	2.803885743	1.81697138	5.928903343	3.064232238	2.179285732	2.309204882
252537_at	AT3G45710	1.869000514	0.586160181	4.606009687	0.973038717	1.277365137	0.903439519
252430_at	AT3G47470	0.486306255	0.983525775	2.845424946	1.533050542	1.021233999	0.77255356
252397_at	AT3G47980	0.843144563	0.780586005	2.48858078	1.17751876	0.959460121	1.0473664
252123_at	AT3G51240	4.200997034	11.39649526	34.37580776	13.78245856	6.455338809	4.100865445
246302_at	AT3G51860	0.724866694	0.640200424	3.037851443	1.187940843	0.849938142	0.751793766
251827_at	AT3G55120	1.624399587	1.346340497	11.80700383	2.329539304	1.659242492	1.335801405
251713_at	AT3G56080	0.457045755	0.394648529	0.907155293	0.519365015	0.522118007	0.503972546
251722_at	AT3G56200	2.138852137	1.309328999	6.457500937	2.184228467	1.274662677	1.621437226
251664_at	AT3G56940	1.001171405	0.70492436	2.586937521	1.103413716	1.108029269	1.075398987
251503_at	AT3G59140	0.943210129	1.089488182	4.661612832	1.572705633	0.879318524	0.627142301
251309_at	AT3G61220	2.156416177	0.668230725	3.883029592	1.718117272	1.211080154	1.977362499
251287_at	AT3G61820	2.728155667	0.9344278	5.378611696	2.155597328	1.707796526	1.458130299
251272_at	AT3G61890	0.459072584	0.446373398	2.274337474	1.314638631	0.572440032	0.788958492
251146_at	AT3G63520	1.611974919	1.102752982	6.020767502	3.210264561	1.2985248	1.372813022
255674_at	AT4G00430	11.44032355	11.69859495	20.82051136	12.15689023	7.963458362	4.674411957
255630_at	AT4G00700	1.353675553	0.594369096	3.294617935	0.968730339	0.984776143	0.867762224
255502_at	AT4G02410	0.842441175	0.478298055	1.823070613	0.706029529	0.61705555	0.580330562
255413_at	AT4G03140	0.986783538	0.909938742	2.87345199	1.345478721	1.200529532	0.896902953
255435_at	AT4G03280	0.43092088	0.425834992	1.108477158	0.561387936	0.619722344	0.536287874
255428_at	AT4G03390	2.066216324	2.821789456	6.34596598	2.575950147	2.58950171	3.082631547
255290_at	AT4G04640	0.627180515	0.60992837	3.116051034	1.3006218	1.001263775	1.041623008
255294_at	AT4G04750	0.570595262	0.46953772	1.808905151	0.557809379	0.589072185	0.561360467
255310_at	AT4G04955	1.793037802	1.846352199	5.186833952	1.551844744	1.052198938	0.855673311
255103_at	AT4G08690	3.179464187	2.315551856	6.622282719	3.175373615	1.601286359	1.058320979
254998_at	AT4G09760	0.444358528	0.39812369	1.781357876	0.60477217	0.547179727	0.503687063
254970_at	AT4G10340	0.816008905	0.654123248	2.568082238	1.335566664	1.014971793	1.006806346

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254996_at	AT4G10390	0.793552696	0.59000051	4.367346089	1.694749047	1.018964454	1.759377938
254924_at	AT4G11330	0.871143427	0.810288342	1.571494339	0.829590674	0.75659671	0.582104854
254848_at	AT4G11960	0.811304927	0.541949017	1.643704588	0.920365074	0.865155258	0.846866811
254816_at	AT4G12440	0.425045674	0.416307284	1.808128812	0.745792654	0.781142446	0.578346665
254818_at	AT4G12470	1.171825722	0.973035326	5.807703714	1.291303903	0.869535307	0.680345135
254795_at	AT4G12990	0.856102191	0.583122852	1.78375825	0.84740254	0.855100069	0.876428849
245274_at	AT4G14360	3.499391618	3.336129291	6.838598982	3.660512262	3.987210818	2.372299844
245555_at	AT4G15390	1.359321572	3.004604255	20.95164164	4.731138149	2.580138936	1.88676167
245560_at	AT4G15480	0.605787119	0.658675187	2.901730316	0.711118799	0.631468393	0.531561253
245439_at	AT4G16670	0.799012425	1.665231617	3.323027134	0.747267114	0.917597733	0.938840733
254651_at	AT4G18160	1.613072296	1.255328228	5.638630859	2.579975701	1.516599155	1.756575611
254630_at	AT4G18360	0.576257218	0.527075562	5.065594153	2.646667624	1.312830113	0.655002869
254430_at	AT4G20820	0.39926989	0.376902171	1.089928905	0.447274485	0.506637135	0.512145208
254225_at	AT4G23670	0.355026665	0.340376958	12.50339102	2.665148018	3.228182024	1.165990829
254187_at	AT4G23890	0.532306517	0.484309195	1.594001139	0.605081729	0.69606383	0.715016607
254098_at	AT4G25100	1.203020841	0.459043616	5.991879297	2.582019206	0.992577185	0.642829159
254077_at	AT4G25640	2.902819511	2.887716407	5.650059052	2.178627262	1.15586583	0.848207209
254041_at	AT4G25830	1.361239386	1.16617595	3.643981425	1.545474809	1.218265677	0.590881114
253985_at	AT4G26220	2.20320456	0.632521948	5.0652326	1.327349662	1.397473322	1.51447243
253925_at	AT4G26690	2.563950545	2.595984962	4.575011234	2.344163749	1.421994569	1.880742464
253872_at	AT4G27410	4.090311878	0.845306227	11.14124399	5.45962981	3.162904945	3.217253517
253825_at	AT4G28025	2.265075168	1.415571526	4.226999151	2.441233347	1.934301074	2.391528053
253829_at	AT4G28040	3.190648807	1.181712395	12.26114733	2.190903337	1.30711066	0.936171566
253720_at	AT4G29270	4.108972103	3.838760598	8.246197306	2.28219531	1.507035148	0.903031714
253697_at	AT4G29700	0.444892999	0.571018052	3.891843818	1.710586866	0.662093741	0.5824772
253702_at	AT4G29900	3.509218264	2.205229123	6.0741352	3.352678605	1.707911284	2.948160349
253666_at	AT4G30270	0.719905029	0.511302058	7.86529191	3.769603634	0.835654449	0.631473406
253618_at	AT4G30420	0.783858924	0.781455153	11.93551126	2.178121473	1.037546112	0.80400246
253601_at	AT4G30900	1.731915139	1.422705227	4.626716434	2.031926399	2.014004638	1.572174705
253437_at	AT4G32460	2.717529346	4.274189908	15.62432832	4.092833801	7.59837955	1.608788735
253358_at	AT4G32940	4.121400765	1.918608111	7.803208986	4.080856053	2.292341693	3.700767143

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
253387_at	AT4G33010	1.491235506	2.024087845	6.028427005	3.415629369	2.10085724	1.273654203
253414_at	AT4G33050	0.610046355	0.43444913	1.631023771	0.729033502	0.661761417	0.562767767
253373_at	AT4G33150	1.019518077	0.70372866	9.003011675	3.7882858	1.140265036	3.78190707
253172_at	AT4G35060	2.281249957	1.907496088	9.657649975	5.33752315	2.279436606	1.035130635
253197_at	AT4G35250	0.594619432	0.661316165	1.510960779	0.848618055	0.718681166	0.755452054
253139_at	AT4G35450	5.428911318	5.411211786	10.04543815	5.45138129	4.682918491	3.812108874
253104_at	AT4G36010	3.80304823	1.437332144	9.635091747	4.050674405	1.541865366	3.866162576
246238_at	AT4G36670	0.568200318	0.559041037	3.442770502	0.703754563	0.756127171	0.613113909
246197_at	AT4G37010	1.173471147	0.520990434	2.319107169	0.977106549	0.54866939	0.381916443
253052_at	AT4G37310	0.992299642	0.581776267	1.870099609	0.75844364	0.785961033	0.625060194
253039_at	AT4G37760	1.260776439	0.682391659	2.807832756	0.865628615	0.850126448	1.098234093
252921_at	AT4G39030	1.218514007	1.407389315	7.003809936	4.019416142	1.290760324	1.387069953
252886_at	AT4G39350	3.554298594	2.497285798	13.55298221	7.854158732	4.56530183	3.686884442
251108_at	AT5G01620	1.704538009	2.204392437	6.562049992	3.123667585	2.473395123	1.706030449
251079_at	AT5G02000	1.089982119	1.29420032	2.59661036	0.841602594	0.925023594	1.035250186
251026_at	AT5G02200	0.714579934	0.684301731	1.548364258	0.835636818	0.762263092	0.800217622
251012_at	AT5G02580	0.504103425	0.903653766	1.821868389	0.637654293	0.619419796	0.536058942
250967_at	AT5G02790	0.646446423	0.602205388	4.423474693	1.302042408	0.802731987	1.535753845
250952_at	AT5G03570	0.795446755	0.547953739	3.17558234	0.758990688	0.777163229	0.727569935
250892_at	AT5G03760	3.079026346	3.390364747	6.951849389	1.319919456	1.794723343	1.309648745
250868_at	AT5G03860	0.496188472	0.573808707	3.087789526	0.815536156	0.826471808	0.725850922
245706_at	AT5G04310	1.035662732	0.520743589	2.045141273	1.032333476	1.175797406	1.017236513
250842_at	AT5G04490	0.719598301	0.550199912	1.474619116	0.750926539	0.657407755	0.61692438
250794_at	AT5G05270	3.069043192	5.126667154	19.02552963	4.469938742	5.649868792	2.396865144
250747_at	AT5G05900	2.244598063	0.845706006	4.254650906	0.82345117	0.6585501	0.914946869
250620_at	AT5G07190	0.557591922	0.493693523	5.532789409	0.519805563	0.618963367	0.601467993
250558_at	AT5G07990	0.817240809	0.621390615	5.537829487	0.927530283	0.703498577	0.630117798
250533_at	AT5G08640	5.697377688	5.483939799	20.16961378	7.064411954	3.828712111	2.090230529
245895_at	AT5G09230	1.9755525	1.276627682	3.746682923	2.17310125	1.692114522	1.435730366
250505_at	AT5G09870	3.091843608	2.22142498	5.805584102	1.879344731	1.672442511	1.58490765
250480_at	AT5G10290	1.579830831	0.931452756	2.793790834	1.547568977	1.012536538	1.376206309

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
250366_at	AT5G11420	1.134856794	0.96292213	10.07281927	0.735457235	1.165499993	0.776905949
245980_at	AT5G13140	0.612394865	0.445352096	1.430677029	0.610055084	0.694897283	0.75905667
250243_at	AT5G13630	0.540494661	0.596113404	4.754373933	1.752856234	0.952715019	0.634612354
250207_at	AT5G13930	9.300064835	9.359752947	49.91365045	24.94674102	13.9821612	6.114794907
250157_at	AT5G15180	2.046703278	0.595926653	6.413619146	1.352173854	1.311270246	1.012203765
246510_at	AT5G15410	0.968505086	0.788216969	2.82287564	1.116763255	0.937535215	0.787533399
246466_at	AT5G17010	2.010893533	1.509030319	4.361505523	2.523777957	1.776894206	1.396664904
246468_at	AT5G17050	4.225996321	3.499423542	9.330022711	4.080543881	2.317333195	2.104542225
246432_at	AT5G17490	0.501675556	0.53131599	1.694261964	0.757419867	0.745728639	0.836959816
249955_at	AT5G18840	0.663222418	0.558529854	1.744949075	0.623656963	0.691782209	0.687669583
249964_at	AT5G19010	3.009997229	2.450217973	7.39410655	2.917302093	2.555544693	3.38891821
246144_at	AT5G20110	2.231492801	1.851231006	4.403221884	2.378429197	0.890218996	2.550171567
249942_at	AT5G22300	0.655383118	0.881816625	2.99827689	0.717143893	0.756678361	0.765795299
249848_at	AT5G23220	1.659449964	0.679492696	3.060237541	1.71626304	0.719350893	0.687682194
249765_at	AT5G24030	1.373544583	1.396952623	2.516158936	1.31886434	1.310380649	1.447498451
246977_at	AT5G24930	5.143708525	4.376127519	10.71272472	6.142180138	2.816034742	2.970005614
246919_at	AT5G25460	11.16160909	8.77162943	20.63133222	8.494448001	2.946450635	1.090401842
246831_at	AT5G26340	3.216815436	0.877540927	6.435360154	1.154155426	0.940253978	0.795110068
246781_at	AT5G27350	0.829787681	0.47493865	2.308790255	0.860832902	0.679546995	0.584848894
246778_at	AT5G27450	4.771760699	4.100219201	10.71439269	4.283248654	2.682740189	1.705503452
246756_at	AT5G27930	1.906412665	0.964006262	4.254888559	1.256337813	0.882471435	0.798935489
249567_at	AT5G38020	1.010526428	0.626481926	4.71284127	0.904116617	1.165007997	0.951059627
249545_at	AT5G38030	0.637458984	0.50689125	2.49089514	0.745778851	0.70117342	0.517737262
249393_at	AT5G40170	0.800327386	0.474794847	1.721389224	0.666204341	0.583218021	0.577249048
249235_at	AT5G42100	0.976040027	2.203564533	4.551996787	1.986046147	2.383147134	2.358720477
249242_at	AT5G42250	1.845044357	0.744966702	16.90788213	3.506068963	1.974847647	1.042605421
249244_at	AT5G42270	1.976139884	1.286632764	4.656806482	2.295613199	1.549796542	1.545750143
249203_at	AT5G42590	3.435985794	3.83286943	14.13659528	3.051552934	2.247653574	2.933618155
249205_at	AT5G42600	1.931690787	2.551463971	11.86896933	3.096468306	2.83559183	1.176261319
249103_at	AT5G43600	1.45051364	1.149183091	5.262393229	2.102404475	1.347563472	1.106460077
249037_at	AT5G44130	2.132547719	0.921515028	6.24094774	2.122661837	1.985625531	1.084080766

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
249034_at	AT5G44160	0.43816626	0.430684946	2.275509032	0.754502579	0.891342353	0.582225762
249035_at	AT5G44190	0.577646999	0.583526784	1.621380467	0.810497196	0.845417595	0.824134877
248932_at	AT5G46050	0.767504216	0.533285686	2.318680461	0.687909979	0.700593946	0.629634999
248886_at	AT5G46110	0.866046175	0.613972625	1.635685609	0.658368349	0.668442712	0.840708411
248828_at	AT5G47110	0.730382051	1.38093279	5.203136127	1.758700235	1.637598696	1.430988834
248793_at	AT5G47240	0.606676641	0.519557356	3.51390429	1.60074753	0.690628437	0.599591632
248756_at	AT5G47560	0.810659998	0.678149934	1.560908953	0.846619824	0.760995431	0.684557227
248769_at	AT5G47730	1.873276181	1.54533299	3.540497902	2.006353793	1.141848509	1.678115326
248721_at	AT5G47780	4.025603692	3.75709252	9.13445452	3.964206144	4.895757928	4.50974499
248727_at	AT5G47990	6.029509297	5.543670779	17.91563173	4.243748523	3.50497808	3.256296316
248728_at	AT5G48000	3.608589407	5.327649406	19.25690779	3.933805252	3.561083799	2.209323522
248729_at	AT5G48010	4.693808184	3.117617073	15.69713737	3.01029334	2.53981818	1.240439942
248625_at	AT5G48880	0.559471197	0.586753866	13.47556429	1.836359331	1.593518704	0.84012408
248622_at	AT5G49360	0.878638782	5.681645661	16.05268241	3.052716898	2.54932879	1.204622448
248371_at	AT5G51810	0.538149099	0.471894985	1.762515317	0.553633008	0.65103063	0.578608417
248335_at	AT5G52450	0.796807275	0.632398262	3.499261509	0.953432198	1.134206132	0.93409331
248263_at	AT5G53370	1.593318603	0.704387463	11.77747362	2.671438623	1.882051089	0.99679307
248232_at	AT5G53760	1.979333422	3.167398477	5.541427887	1.356166726	0.940186744	2.722494216
247954_at	AT5G56870	6.324137987	0.8737201	23.97994544	5.129911415	4.386951143	3.015195937
247813_at	AT5G58330	0.670614016	0.561880614	1.646323761	0.664300817	0.704414368	0.689398253
247774_at	AT5G58660	0.506873234	0.454840323	1.479543675	0.574148488	0.565239204	0.577818919
247729_at	AT5G59530	0.448417117	0.349756413	1.066221558	0.420287899	0.41014099	0.372135622
247679_at	AT5G59540	0.811025267	0.515604376	7.331189108	1.876244302	1.246997613	0.861257479
247628_at	AT5G60400	0.42212126	0.437006928	1.282977226	0.717728007	0.675613021	0.429879166
247586_at	AT5G60660	11.61316747	12.06920032	26.50731566	11.42079467	8.764706916	9.880465229
247577_at	AT5G61290	0.632969187	0.507628832	1.48591944	0.697217448	0.716578758	0.725704911
247463_at	AT5G62210	0.62724778	0.816066861	8.356162566	0.605821194	0.93511104	0.901398295
247288_at	AT5G64330	0.391748722	0.491739374	6.536666355	1.635139925	2.087908793	0.872846172
247246_at	AT5G64620	1.23836272	0.691085923	8.398271328	1.578637163	1.559139233	1.769672235
247193_at	AT5G65380	1.438931414	0.909419571	11.77111884	1.208310742	1.174031958	0.828526261
247107_at	AT5G66040	1.421811696	0.694020661	3.704976495	1.498156419	1.242150676	0.956055677

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Cortex (CORTEX) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
247085_at	AT5G66310	1.217699395	1.366353905	3.92249461	1.794836815	1.217321453	1.466218942
247073_at	AT5G66570	0.725896012	0.631093653	1.577160684	0.876082446	0.887836359	0.754461479
246992_at	AT5G67430	0.549205984	0.490807116	1.284054337	0.6349561	0.650604879	0.594439644

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
261570_at	AT1G01120	3.534819684	0.66148798	1.63515887	18.18279182	1.543182008	0.894852168
261027_at	AT1G01340	0.67469246	0.516004776	1.009846346	1.846024088	0.716621904	0.727804709
259439_at	AT1G01480	1.092234102	0.872007756	0.917070533	6.87229871	1.167099495	1.029479358
264146_at	AT1G02205	0.733316824	0.570881836	0.633230261	1.58085201	0.738467635	0.803963188
262131_at	AT1G02900	3.639268038	0.748432845	5.489194085	16.70848855	3.41676537	1.579225171
264416_at	AT1G02980	0.531867055	0.703332657	0.624480761	2.928843953	0.812918056	0.736331163
263117_at	AT1G03040	0.479970422	0.634713895	1.218542251	2.252338423	0.936044082	0.93543315
265038_at	AT1G03920	0.839665417	0.698522714	0.745227452	18.02192738	1.342498382	1.349355982
264606_at	AT1G04660	0.792632912	0.679298364	0.751438161	3.71930566	0.981478137	1.042022723
264577_at	AT1G05260	0.564368249	0.560940597	2.659246989	40.82502385	5.410111954	2.730636285
262635_at	AT1G06570	1.447364986	0.65157245	1.861733094	4.397316498	1.249620797	1.077713165
256053_at	AT1G07260	0.677741803	0.588642399	0.539987023	2.586785134	1.466633461	0.742987713
261815_at	AT1G08320	1.669307478	0.867218111	2.726123648	4.98506066	1.331364617	1.015699154
264794_at	AT1G08670	0.395801076	0.36819443	0.406090232	5.448707531	0.728761343	0.430453214
264648_at	AT1G09080	0.436896383	0.375713223	0.600268969	1.682396888	0.475670217	0.664605421
264647_at	AT1G09090	0.375951847	0.35734333	3.83001105	11.17383152	0.806006425	0.507661831
264462_at	AT1G10200	1.907887458	2.507989504	3.226945323	6.336914595	3.524692315	1.6596584
262478_at	AT1G11170	0.629324364	0.557530558	0.734008613	1.653840804	0.72885868	0.951867602
262819_at	AT1G11600	0.529071602	0.461036554	0.478774763	2.337332107	0.60251612	0.515989417
262807_at	AT1G11740	0.56517219	0.637793398	0.815430122	2.167279471	0.978365462	0.913982022
259410_at	AT1G13340	0.620709624	0.440334937	0.958843099	1.810079132	0.817745066	0.891743417
256131_at	AT1G13600	0.386662424	0.381218809	0.359668322	1.200399443	0.458594705	0.437504248
259424_at	AT1G13830	0.705653826	0.492580853	1.45190542	2.530476863	0.789551641	0.852299132
262649_at	AT1G14040	0.758715901	0.831184118	2.908313186	11.62771623	2.489204341	1.714595712
261479_at	AT1G14380	0.87817064	0.917267165	1.282621935	4.228122738	1.629998651	1.554398167
262730_at	AT1G16390	0.559114344	0.468603778	0.827972874	8.433294345	1.485318161	1.019546695
262512_at	AT1G17145	1.576815478	0.854905629	2.598670392	5.693095145	1.237050317	1.840776273
255899_at	AT1G17970	0.605907594	0.549807755	1.369416212	2.95130298	0.764187367	0.60803857
261674_at	AT1G18270	3.109425186	0.947317989	3.239610419	6.003637171	2.084712558	2.032983076
261669_at	AT1G18490	1.408751755	1.082477307	1.290872329	7.00908711	2.003062319	1.549556553
261378_at	AT1G18890	2.100593995	0.829324854	2.18834404	7.772495019	1.788896192	1.801717363

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
255940_at	AT1G20380	0.999041729	0.886353013	1.224018288	5.553717893	1.513491846	1.315129171
259544_at	AT1G20620	0.662969471	0.695288174	1.360434342	3.453460376	1.129601858	1.163802285
259517_at	AT1G20630	0.983941277	0.829677746	1.462199902	2.936794052	1.445726016	1.679483448
264210_at	AT1G22640	6.429715066	3.403401192	5.66863248	11.36247574	4.139054515	4.798623698
264898_at	AT1G23205	0.628776046	0.51511623	0.896664944	2.469924781	0.82509314	0.780272995
262986_at	AT1G23390	2.275902632	0.663784312	2.04784769	6.549813563	1.172342565	1.467700297
265172_at	AT1G23820	2.347425998	6.217915582	7.477839005	13.958126	5.527718412	5.878637176
265023_at	AT1G24440	2.009508692	1.168007026	3.193431724	9.50079684	1.961131302	2.864066245
265028_at	AT1G24530	1.025412766	0.583432195	0.976893819	2.845172894	1.507668776	1.417562691
253397_at	AT1G26150	0.474629266	0.525362207	0.544517772	4.212921543	1.027498126	0.706822908
262750_at	AT1G28710	0.511021665	0.596234459	0.572638148	3.571035696	0.834206933	0.700042065
259788_at	AT1G29670	0.466400187	0.388999256	0.398049882	1.535099554	0.483587342	0.501098181
255999_at	AT1G29860	0.546896602	0.496430417	0.483357288	1.006244553	0.559943096	0.540838863
261801_at	AT1G30520	0.579291628	0.647725933	0.721024772	3.665997167	0.813915726	0.668641099
263227_at	AT1G30750	1.191875392	0.699708274	1.325113834	38.57506245	4.143847107	1.70038073
246635_at	AT1G31720	0.573237882	0.47127653	0.50281167	4.281785773	1.121201291	1.79093792
245792_at	AT1G32100	0.647761596	0.588771685	1.77261889	23.24775515	8.387159992	12.12782782
261708_at	AT1G32740	0.463048004	0.482477728	0.545291529	2.659580902	0.90912074	0.821069962
262408_at	AT1G34750	1.606617168	1.257622693	1.356101716	2.787768453	0.854792536	1.125582397
245757_at	AT1G35140	0.596614951	0.622070357	1.849224827	4.572391022	0.733128109	0.621276496
259548_at	AT1G35260	0.378705306	0.404740986	0.564154228	2.920336718	0.62158101	0.550356941
259624_at	AT1G43020	0.473669563	0.422421401	0.522733292	14.14869965	1.276926943	0.581663632
260813_at	AT1G43700	0.836036824	0.941994439	1.459297427	4.221320846	1.260786892	1.135552158
259506_at	AT1G43900	3.081943519	1.883305171	3.1201942	5.569709576	2.837344575	2.059778409
260941_at	AT1G44970	0.639465983	0.526791997	0.701992004	21.85014161	2.791036569	0.87959773
261308_at	AT1G48480	0.456906179	0.540073703	1.331889095	4.294935233	1.043165395	0.61205621
261307_at	AT1G48520	0.853407865	0.91373809	0.951346228	2.394489549	1.100153262	1.082205186
262393_at	AT1G49490	0.375507429	0.412533741	0.406648752	1.30520247	0.464589853	0.44810682
261605_at	AT1G49580	0.716619233	1.261901536	1.457307037	6.17520823	1.27112259	1.140361791
261866_at	AT1G50420	0.582453158	0.541228182	1.073643194	2.746968727	1.058269079	0.774045337
246631_at	AT1G50740	4.995524532	3.776161386	5.370481234	16.62720345	1.948083695	9.094913275

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
260490_at	AT1G51500	1.094182196	0.61002403	1.014996052	1.964908563	0.88802558	1.014857843
256186_at	AT1G51680	0.989632155	0.625870781	5.776820479	17.45294077	5.093933415	3.12811044
260643_at	AT1G53270	0.579209872	0.481444301	0.564729499	2.285891608	0.763199079	0.697995682
263005_at	AT1G54540	0.476571313	0.425054213	0.514300146	4.428244086	0.609975624	0.576856691
264186_at	AT1G54570	0.5358364	0.55913501	1.473377343	2.71993392	0.905125045	0.855490194
256220_at	AT1G56230	0.570891009	0.485482207	1.539597258	6.10066296	2.955597081	1.315764146
256217_at	AT1G56320	1.16552131	0.791294634	0.91192899	2.547935849	0.982378263	1.289852199
264941_at	AT1G60680	0.719280946	0.501375225	0.689984291	5.722816639	1.121083554	1.224160159
264911_at	AT1G60690	0.610871998	0.601145834	0.709254472	3.523259527	0.902802878	0.692510518
264912_at	AT1G60730	0.522303958	0.466032122	0.708059316	1.298768647	0.65985893	0.65728707
264930_at	AT1G60800	0.488631666	0.518677381	0.948367593	2.601900198	1.140134875	1.172018086
264932_at	AT1G61240	0.601748633	0.652655885	0.63085274	7.886160814	1.138728088	0.797504637
265031_at	AT1G61590	0.571250517	0.48588654	0.917195414	23.12610001	1.393109873	0.79578176
264280_at	AT1G61820	3.343527001	0.623723104	8.508118458	14.94736716	4.093805623	7.565925623
265116_at	AT1G62480	1.542440192	1.388773875	7.575236838	23.11987074	12.74839299	4.904188845
259694_at	AT1G63180	0.476428908	0.399415514	0.434223756	4.32288722	0.807201564	1.242374716
259737_at	AT1G64400	0.680575707	0.554414772	0.590067846	1.404511573	0.722731668	0.567115727
261973_at	AT1G64610	0.572524858	0.552013279	1.181863332	2.634255648	0.993432725	0.896542146
264181_at	AT1G65350	0.661019534	0.616180757	0.778912765	2.047712069	0.751071306	0.658224785
262930_at	AT1G65690	0.84782245	0.470847389	0.706922385	2.136002693	0.515588732	0.996173661
261921_at	AT1G65900	0.466834701	0.447829805	0.528691694	2.178918286	0.778455513	0.596064187
257583_at	AT1G66480	1.315215333	1.015121144	0.789447272	3.891994213	0.830724903	0.999384713
255854_at	AT1G67050	0.924458077	0.520575437	1.273942398	2.519349246	1.337991408	1.090033843
255857_at	AT1G67080	0.543267406	0.765264368	1.171879023	2.678984994	1.321975039	1.095076815
245193_at	AT1G67810	1.027705825	1.016607293	1.458426981	2.991465393	1.30315497	1.130468322
256300_at	AT1G69490	0.808270634	0.629184347	1.120584218	3.123389239	1.381957853	1.260839483
259832_at	AT1G69580	0.418109294	0.379633863	0.382242369	2.738188248	1.167236674	0.572633832
260406_at	AT1G69920	0.672816836	0.475649643	0.56769271	2.037317749	0.557129249	0.648382111
260405_at	AT1G69930	1.175856655	0.785430023	2.90324761	6.999112461	0.969701888	1.118008959
264718_at	AT1G70130	0.494523486	0.42386786	0.793729174	3.753693947	1.208435818	1.295013603
264717_at	AT1G70140	1.948865136	0.716057943	0.948582288	13.7438398	1.29616654	7.404419524

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
260206_at	AT1G70740	1.066866598	0.769877963	1.744514712	2.966141708	0.937060781	1.460084939
261522_at	AT1G71710	0.491100165	0.522154242	0.860639749	1.776793217	0.744777586	0.652051243
261509_at	AT1G71740	0.902382124	0.68927387	0.974291382	31.09902664	2.676149567	1.148207979
259801_at	AT1G72230	0.475704329	0.511515753	0.663972038	11.35155894	2.447273828	1.086306391
260454_at	AT1G72310	0.791240138	1.122495139	1.232244524	12.54968902	2.496119678	3.896133525
260451_at	AT1G72360	0.685875469	0.503033719	0.694832454	2.49830391	0.76320922	0.658309906
260427_at	AT1G72430	0.731205387	0.627898793	1.105072988	6.464339173	1.781639657	1.05621963
260399_at	AT1G72520	1.730271731	0.786655766	3.479932737	6.692832676	1.659702005	2.697423399
259863_at	AT1G72630	1.293601497	0.72225581	0.87760716	2.388184206	0.616587002	0.526190902
259865_at	AT1G72710	3.505890449	4.142655816	4.706523891	10.03133964	3.27493563	3.539581302
262382_at	AT1G72920	0.629883266	0.533473787	0.970311364	1.875437345	0.464585371	0.445446188
262383_at	AT1G72940	0.92276654	0.67270466	2.010937456	4.026744973	0.873151001	0.93731919
260074_at	AT1G73640	0.710150612	0.564989688	1.332943548	10.09169446	1.476751973	1.403802613
260394_at	AT1G74080	0.503455377	0.453773514	0.835676855	2.317526735	0.650668019	0.61352727
260234_at	AT1G74460	0.715300495	0.547911673	0.57529738	1.265123881	0.647104945	0.650144163
256455_at	AT1G75190	0.369759331	0.454542141	0.591281559	1.741206182	0.947899572	0.520885654
262947_at	AT1G75750	3.168595096	1.275164172	18.39837898	55.55371447	22.0987712	14.36460238
262682_at	AT1G75900	0.46620721	0.429807197	0.465211861	1.676380181	0.55639383	0.52319476
261777_at	AT1G76210	0.958222114	0.477477246	0.588786194	3.816849759	0.576395601	0.5136891
263127_at	AT1G78610	1.096149195	0.99034947	1.932197621	3.433220936	1.708332468	1.77283592
264137_at	AT1G78960	0.775634643	0.591589791	0.89622097	3.802919074	0.851648814	0.949764755
259860_at	AT1G80640	1.041884864	0.931875521	0.886975649	3.400356679	1.140503883	1.443461865
261899_at	AT1G80820	0.5453181	0.422767791	0.880703513	9.209430117	0.69836858	0.545434753
266234_at	AT2G02350	0.742307869	0.688524855	0.759630937	1.579718336	0.884565766	0.812714265
266235_at	AT2G02360	0.8190185	0.65445158	0.861449986	1.481279354	0.760560344	0.833885657
266182_at	AT2G02370	0.922637582	0.781474205	1.172651076	2.783000878	1.18071315	1.284532128
267472_at	AT2G02850	0.525151513	0.498665044	0.539556005	1.470555347	0.628274296	0.669258545
263046_at	AT2G05380	0.825535765	0.588736614	0.857038565	2.151883417	0.719165114	0.59571777
265511_at	AT2G05540	0.670615178	0.627030041	0.634244922	1.780237267	0.831166777	0.631709276
266428_at	AT2G07180	1.480668	0.900125865	1.971511255	4.0247689	1.001542416	1.418287621
266613_at	AT2G14900	0.569163243	0.521765915	1.558687448	20.68031334	3.136609922	1.730655887

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
263327_at	AT2G15300	0.667069783	0.507543315	0.572311072	8.12703585	1.071391498	0.806509398
265359_at	AT2G16720	2.471933289	0.830746009	5.614091564	11.7252536	3.203200183	3.86567584
265405_at	AT2G16750	0.481745902	0.398138436	1.064714528	1.920127516	0.7040423	0.520330157
266526_at	AT2G16980	2.054152273	0.671918867	4.178988438	7.104913041	1.776548039	1.46885637
264594_at	AT2G17640	0.540388713	0.496477016	0.828457694	1.48974871	0.750481439	0.819515319
265807_at	AT2G17990	2.325907634	1.541038659	2.258579154	5.294655163	2.773569814	2.500902715
265336_at	AT2G18290	0.839522344	1.002611376	0.939948986	2.721234188	1.161955843	1.165018276
265309_at	AT2G20290	0.645285692	0.717310518	0.555088169	6.029072839	0.977954944	1.507187276
264010_at	AT2G21100	0.459310565	0.406684709	0.476674737	21.04085868	1.452465916	0.672629085
264052_at	AT2G22330	0.664301314	0.564532835	0.961769761	2.365324713	1.287409555	1.056163484
265350_at	AT2G22620	0.429348317	0.369275285	0.398934693	12.54244024	1.13387458	0.616208486
266798_at	AT2G22850	0.622380647	0.510717949	1.10354643	2.381213508	0.936625132	1.007125141
267265_at	AT2G22980	0.415496014	0.379209238	0.417218034	1.349654297	0.48068037	0.44091122
245084_at	AT2G23290	1.073703728	0.788711304	1.119962611	3.178355796	1.156888915	1.067056347
267121_at	AT2G23540	0.359904924	0.379582802	0.486300114	1.185457337	0.447641256	0.419659642
267123_at	AT2G23560	0.738336502	0.58561471	0.746665251	4.895349807	1.289631319	1.204810814
265987_at	AT2G24240	1.206514273	0.641614453	1.035429917	8.091003298	1.698575094	2.692603967
266655_at	AT2G25880	0.416375823	1.346120029	0.533454124	2.997972846	1.200154833	0.950053688
267380_at	AT2G26170	0.531161598	0.430940505	0.721752042	2.75630922	1.163096911	1.024504405
245028_at	AT2G26570	2.190794755	1.045085618	1.583949372	5.359917683	1.285527605	1.13677962
265645_at	AT2G27370	0.863491424	0.750999985	1.174644025	25.82279644	3.236886255	1.274423274
265547_at	AT2G28305	0.459341688	0.431316258	0.44664834	1.050382084	0.541651846	0.476870951
263439_at	AT2G28650	0.807754947	0.568545358	0.712708535	10.47584334	1.605936362	1.422874166
263437_at	AT2G28670	0.952832703	0.801732867	1.932909334	44.42672904	5.511548674	1.704445177
266276_at	AT2G29330	0.523631012	0.430025631	0.671322149	1.680631467	0.575203595	0.468191088
266273_at	AT2G29410	0.448595409	0.421411711	0.435511765	1.761969041	0.536231071	0.513105994
267307_at	AT2G30210	0.532896918	0.529858248	0.698328105	28.99433854	3.503031106	1.011188771
267564_at	AT2G30740	2.834352288	2.327140064	2.177753048	5.096207928	1.773213664	1.517544196
267153_at	AT2G30860	6.712739807	12.78535164	16.42248361	31.89067542	12.86942743	15.58484106
263467_at	AT2G31730	0.654221848	0.539976356	0.924219619	2.42042441	0.757626836	0.68057749
266356_at	AT2G32300	0.446366774	0.495459129	0.761489445	26.44651899	2.456606631	0.912280068

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
267544_at	AT2G32720	2.158046747	3.465961011	4.419135017	7.63640841	3.438476809	2.641823315
267595_at	AT2G32990	0.449744902	0.78362305	0.510641471	2.354180023	0.925273789	1.281058236
267000_at	AT2G34310	0.836216518	1.190274218	1.533129349	4.824677857	1.335976858	1.040101594
266904_at	AT2G34590	7.2034322	9.165766128	11.461049	25.23156058	10.38314859	6.03565024
263284_at	AT2G36100	1.150373744	0.862616116	2.831881793	55.50674924	7.517020204	2.339816519
263920_at	AT2G36410	0.568379048	1.147245898	1.47493414	4.605304179	2.212409298	0.942794765
263892_at	AT2G36890	0.752551645	0.572140621	0.828104627	1.538561129	0.550963499	0.462053443
257381_at	AT2G37950	0.543268324	0.490287915	0.518732126	12.87418414	1.306139284	0.66561747
267096_at	AT2G38180	0.616967816	0.604532319	0.675756793	3.990084383	1.100826056	1.005455467
267054_at	AT2G38370	0.436719138	0.683572611	0.679940476	3.356541384	1.656807378	1.942836816
267035_at	AT2G38400	1.730195313	1.334783093	1.100980273	12.69739183	1.821383598	5.579255273
266415_at	AT2G38530	0.620675316	0.546036143	0.549858916	13.36261484	0.732376613	0.588795098
266421_at	AT2G38540	0.680255946	0.535507626	0.585524391	5.076484668	0.863309071	0.62295464
263296_at	AT2G38800	0.723577513	0.554236352	2.737501799	6.689644104	1.669692644	2.904435206
266968_at	AT2G39360	0.902925887	0.426345272	1.311118144	3.47938149	0.862762041	0.531081304
266978_at	AT2G39430	1.066821646	0.722415734	1.154194693	30.59117432	2.635843376	1.177273659
267360_at	AT2G40060	1.925765703	3.29731506	5.024534903	10.81719966	4.43414294	3.814486923
263387_at	AT2G40160	0.478231793	0.479476486	0.715976641	9.231394593	1.054266234	0.69183251
245101_at	AT2G40890	2.397815257	1.019663666	10.36799757	21.6225121	10.35264227	5.644626697
265856_at	AT2G42430	0.850918999	0.571885297	1.075945566	2.162169453	0.954860651	1.059288878
263979_at	AT2G42840	0.589778312	0.632343422	0.581580567	2.654343025	0.74413624	0.745182902
260563_at	AT2G43840	0.727581305	0.479901722	0.640728858	2.046160146	0.852253851	0.904775579
267344_at	AT2G44230	0.824086543	0.573052234	0.529061581	1.413490434	0.635147665	0.584980126
267391_at	AT2G44480	0.451465215	0.403325261	0.434922921	5.9699292	0.689477408	0.538699362
266126_at	AT2G45040	0.605333876	0.663204896	0.542352035	3.307977648	0.870611225	0.735103804
263783_at	AT2G46400	4.046950039	0.895634408	2.785883089	7.119964395	1.624206926	3.368829597
266485_at	AT2G47630	0.847130479	0.74025269	1.31686987	7.983949527	1.000322308	0.866174158
257371_at	AT2G47810	0.90633389	0.609380482	0.831168243	6.013123254	1.102216556	1.145595455
266486_at	AT2G47950	1.456344156	0.656481147	1.505688555	3.076579436	1.260141061	1.23451637
265771_at	AT2G48030	0.895407277	0.951057015	1.262479474	6.909576344	0.958926046	0.982142032
262349_at	AT2G48130	0.539532926	0.55425416	0.581582616	6.716031893	0.941593902	0.72608467

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
262317_at	AT2G48140	0.529719126	0.448544365	0.524865069	2.324064695	0.571283183	0.553511856
259188_at	AT3G01510	1.377674182	1.357574868	1.052316108	3.826125394	0.847892651	1.716087762
258487_at	AT3G02550	0.708812537	0.750366853	0.575849107	1.544723389	0.806602142	0.765004297
258614_at	AT3G02770	1.489663771	0.911817263	5.853336843	12.19124457	3.569316291	2.003166586
258599_at	AT3G04520	0.821334497	0.552455686	0.979868036	7.145580645	1.511893769	0.755172685
259309_at	AT3G05050	2.063746817	1.220000192	1.036565804	3.516248528	1.388684498	1.648746973
258511_at	AT3G06590	0.697567766	0.906588272	1.016443776	2.288957799	1.285551512	1.089744454
258675_at	AT3G08770	0.561985758	0.547340282	0.570614734	2.091793381	0.597668563	0.58304494
258719_at	AT3G09540	0.455932213	0.464315143	0.949249572	4.371628176	0.770186827	0.669508923
258757_at	AT3G10910	0.618525715	0.499669958	0.812263363	5.830755003	0.859736421	0.764459886
259291_at	AT3G11550	0.526712961	0.499172577	0.935348512	38.2794723	2.694264067	0.953177696
256659_at	AT3G12020	0.563686459	0.562726046	0.461448285	2.548845983	0.580387614	0.580755433
257280_at	AT3G14440	0.484861392	0.625271382	0.853925692	1.663558231	0.618628169	0.660378144
257105_at	AT3G15300	2.883606494	1.715718097	1.222303449	5.449602262	1.67607154	1.797878712
258287_at	AT3G15990	0.510983923	0.476385779	0.603006783	1.345061387	0.626124329	0.512140876
259380_at	AT3G16340	0.820431327	0.579888079	1.016662176	10.8363483	2.686545927	1.933950998
259375_at	AT3G16370	0.626862308	0.86082817	0.595090977	1.499631051	0.688447117	0.696283232
258377_at	AT3G17690	0.482213441	0.383471287	0.619767149	3.817659219	1.309048708	1.639925546
256948_at	AT3G18930	0.65032347	0.448792867	0.558927027	1.375121469	0.648206164	0.68011132
257672_at	AT3G20300	1.040400539	0.676682312	0.546496124	1.821111023	0.662167832	0.81239067
256970_at	AT3G21090	0.686393154	0.692829904	0.625195466	1.755060074	0.691724639	0.885468913
258047_at	AT3G21240	1.637145448	0.950169325	8.926883047	18.90766973	6.548042909	3.525076943
256825_at	AT3G22120	0.54715052	0.484978324	0.602792485	1.160012756	0.681284456	0.616298441
258445_at	AT3G22400	0.432300479	0.461303904	0.480023386	2.922808081	1.12869588	0.745845755
256926_at	AT3G22540	0.771819476	1.19893695	4.296920832	7.757608614	1.404080508	0.734836797
256933_at	AT3G22600	0.896410586	0.806559191	3.141969458	45.70831607	5.754916755	2.807674214
256937_at	AT3G22620	0.716046306	1.014911708	1.08331096	32.69600588	4.253574314	1.382503068
256929_at	AT3G22620	0.609903733	0.547633427	0.600132899	1.988772493	0.689887575	0.552101121
258321_at	AT3G22840	0.720747624	0.7904645	3.590079481	8.960345033	1.761547948	4.500032326
257923_at	AT3G23160	0.493781561	0.656145142	0.79467029	12.74371097	1.670980151	0.847429049
257919_at	AT3G23250	0.789233987	0.425888925	1.588392209	2.813583322	0.873614699	1.030766823

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
258291_at	AT3G23310	0.563197202	0.828775968	0.737869876	2.037159768	1.066032111	0.761617138
257203_at	AT3G23730	0.441902157	0.398387768	0.587203973	4.055297218	1.039233961	0.613699904
256889_at	AT3G24010	2.290794281	1.903002579	2.014108361	5.279810696	2.481301027	2.498430735
256759_at	AT3G25640	0.592912754	0.476482372	0.596097642	1.675677791	0.875267849	0.854154637
258060_at	AT3G26030	2.477130978	2.858333232	3.131049691	5.994777384	3.104207645	1.963150732
257784_at	AT3G26980	1.197676927	0.957837185	2.217925559	4.503364799	1.350570295	1.463334522
257147_at	AT3G27270	0.769944307	0.608054851	0.794389823	3.148592951	1.144290929	0.832307532
256991_at	AT3G28600	0.465664987	0.36274483	0.446483188	1.879083624	0.942841037	0.843513577
256598_at	AT3G30180	0.623626072	0.511443131	1.458228407	3.613024768	1.492109512	0.69230728
252557_at	AT3G45960	0.453478547	0.425264475	0.671048741	2.473246074	0.535584939	0.480961992
252282_at	AT3G49360	0.589485877	0.511086419	0.631155475	1.900425968	1.097612491	0.606646918
252233_at	AT3G49690	0.584508018	0.461783153	0.651530297	3.156790418	0.785664368	1.345715479
252251_at	AT3G49820	0.542836548	0.477500103	0.549727411	1.127562847	0.535528816	0.546679951
252195_at	AT3G50190	0.425476701	0.524118481	0.543253351	2.680984098	0.548584408	0.548707267
252202_at	AT3G50300	1.902859007	1.167957292	4.477877388	10.00936182	2.049391828	1.181740379
252131_at	AT3G50930	3.890109697	2.162928291	1.543605909	9.242586782	1.742854312	4.027648937
252101_at	AT3G51300	0.703082034	0.691249691	0.727612847	3.195116478	1.106040443	1.371678208
252053_at	AT3G52400	5.761965362	1.262185852	3.791842491	11.06381269	1.741938921	2.509044028
252060_at	AT3G52430	0.979566632	0.411643451	0.868432661	2.660958804	0.667298796	0.761421245
252023_at	AT3G52920	0.394976978	0.986898599	0.793115455	4.917579325	2.792193573	1.818237429
251984_at	AT3G53260	2.870847939	1.34248962	11.24079155	32.81899625	6.97459614	4.25188268
251890_at	AT3G54220	0.839925862	1.011587758	2.571999211	8.143595605	1.61257894	0.794116398
251824_at	AT3G55090	0.582169267	0.409774058	0.477654697	1.159665647	0.522177944	0.546196337
251795_at	AT3G55390	0.873878327	0.839199909	0.908083789	6.309410951	1.13001694	0.976416474
251723_at	AT3G56230	2.964180467	2.015809258	3.757753193	9.100735065	2.024332118	2.47667803
251733_at	AT3G56240	5.748443411	1.683988537	3.106430917	24.22010455	9.435113207	6.982205855
251563_at	AT3G57880	0.724065469	0.932548129	2.036996275	9.519565065	2.478126685	1.225655733
251494_at	AT3G59350	2.933561661	1.151457725	4.295959314	7.630058509	3.531694713	2.679957763
251259_at	AT3G62260	2.050054995	1.09439462	4.643481567	9.48999145	2.178378361	4.738899193
251162_at	AT3G63300	0.546035539	0.481412574	0.756203753	3.204008015	1.606628598	0.988569975
251166_at	AT3G63350	0.464700411	0.53350714	0.649509731	2.145559021	0.834555977	0.786547358

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
255692_at	AT4G00400	0.557377467	0.901437169	0.473380261	2.151640304	0.62934666	0.499736549
255622_at	AT4G01070	2.895883788	0.74679086	4.612540211	11.42954234	2.692267274	1.952367887
255528_at	AT4G02090	0.972106234	0.688878492	1.041412753	33.04387511	3.341761407	1.299605934
255250_at	AT4G05100	0.488734638	0.407615165	1.470420927	3.03211598	0.708591883	0.999589337
255264_at	AT4G05170	0.576573797	0.480203775	0.748793115	16.66711564	1.203908323	0.654889884
255110_at	AT4G08770	0.659037649	0.517431006	0.659598587	6.263689335	1.273335797	0.641636954
255080_at	AT4G09030	3.979165872	5.706491448	8.337437667	16.75824724	9.079404159	6.448741886
255047_at	AT4G09670	0.81292646	1.136050971	1.510416845	3.274387775	1.689484709	1.533522236
255028_at	AT4G09890	0.302584384	0.322830103	0.34143014	4.778011909	1.191324112	0.576436915
254907_at	AT4G11190	0.536860386	0.468093494	0.636321985	5.612953137	1.718450002	0.857615483
254914_at	AT4G11290	0.565817953	0.545293347	1.859108996	27.61945523	3.294022124	1.811716645
254849_at	AT4G11970	0.764726551	0.766261591	0.714800041	2.250963455	1.043988305	1.003421907
254803_at	AT4G13100	0.487931086	0.517533847	0.897120464	2.757609825	0.893640314	0.775276115
254726_at	AT4G13660	3.117443083	1.592242724	9.378509969	15.98260102	3.230751201	1.871321325
245386_at	AT4G14010	0.492646841	0.907012604	0.593810436	4.499747655	2.067374608	1.680685537
245612_at	AT4G14440	0.630260852	0.527003652	0.556695808	1.406564159	0.601376002	0.660915346
245563_at	AT4G14580	0.609431264	0.573288106	0.843849182	2.042916146	1.037363809	1.128296186
245363_at	AT4G15120	0.931895049	0.519079841	1.048735869	2.359948789	0.743979202	0.739967279
245550_at	AT4G15330	0.510450589	0.446702516	0.621427171	5.969646307	0.869073891	0.900661871
245486_x_at	AT4G16240	0.930847194	0.888669928	1.056880836	3.273862909	1.259248372	0.843107805
245488_at	AT4G16270	0.671861503	0.519248429	0.682183597	3.664095984	1.058659058	0.776194545
245341_at	AT4G16447	0.472825873	0.434321945	0.451902744	1.513435189	0.615821017	0.523302043
245305_at	AT4G17215	0.656497039	0.474536135	0.936740664	22.85803829	2.155394947	0.907453977
245410_at	AT4G17220	0.398697902	0.429368654	0.998345191	5.646187741	1.302922081	1.520338923
245412_at	AT4G17280	0.93171194	2.262510017	3.275809604	17.92867072	2.154656746	1.128959473
245413_at	AT4G17300	1.393044822	1.159457976	1.362325588	4.763091966	1.525937187	1.304179258
245423_at	AT4G17483	0.710891325	0.574290968	0.616873388	3.807909512	0.998238073	2.130142817
245382_at	AT4G17800	2.538779604	2.318038614	2.27624268	5.855524668	2.834002595	1.500800901
254697_at	AT4G17970	0.591771843	0.550161741	0.520052722	1.700747051	0.712526968	0.640930338
254646_at	AT4G18530	0.570750781	0.48800415	0.574678708	1.65265306	0.967825024	0.722706423

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254580_at	AT4G19390	0.682524784	0.598586803	0.896792845	1.999009359	0.765359109	1.021662358
254536_at	AT4G19720	0.575694786	0.461861031	0.529493528	1.574536826	0.59417176	0.607606704
254506_at	AT4G20140	0.68889663	0.563550786	3.161381225	19.39275024	1.829886981	0.923912863
254404_at	AT4G21340	0.555602346	0.474573358	0.570642871	5.487571492	0.788947677	0.630147412
254408_at	AT4G21390	0.420270935	0.383246909	0.530932117	7.159868927	0.626858444	0.515292731
254372_at	AT4G21620	0.655022652	0.529075081	0.605422527	3.036760506	0.730922498	0.633101156
254344_at	AT4G22110	0.83227274	0.492149299	2.10268795	8.270853986	1.286827374	0.822529489
254340_at	AT4G22120	0.806603827	0.890054402	2.328454812	6.927420219	3.167425147	1.635415119
254300_at	AT4G22780	0.570493091	0.485408449	0.921377636	2.879825974	1.137749939	0.928289758
254256_at	AT4G23180	0.505231647	0.474185418	1.711400924	5.913147039	0.579081324	0.925625533
254201_at	AT4G24130	0.469915754	0.469627705	0.488042406	9.207101201	0.843754367	0.581310808
254063_at	AT4G25390	4.048397086	2.457706675	5.537074008	10.73639628	1.3966015	2.137894646
254081_at	AT4G25660	3.613373207	1.749871228	2.985105973	7.922638092	2.27548819	2.308982875
254048_at	AT4G25680	2.274284961	1.824539729	2.08717962	10.57799498	2.187110045	2.299619281
254042_at	AT4G25810	1.339047316	0.63142688	0.941232802	26.06861798	4.748493146	4.806211912
254015_at	AT4G26140	0.577464658	0.703004765	0.850334907	18.29190886	1.463971393	1.046917441
253999_at	AT4G26200	1.250641234	0.678170818	1.264697055	2.6281912	0.77755071	0.670803443
253957_at	AT4G26320	0.678230406	1.025230461	3.501085549	26.37544333	11.1042297	5.936814547
253828_at	AT4G27970	0.95724175	0.615069995	1.47218674	3.75677951	1.046998416	0.951258612
253827_at	AT4G28085	2.174151365	2.922255874	2.041958833	5.655583713	0.848795773	0.737892953
253819_at	AT4G28350	0.858748278	0.452650422	0.919112031	1.666443365	0.609504294	0.617888249
253741_at	AT4G28890	1.606939188	1.077194684	1.259420809	3.178414897	0.820958222	0.590553837
253754_at	AT4G29020	1.131898011	0.906641002	0.808433781	7.77777516	1.464079833	1.059891718
253614_at	AT4G30350	0.903978889	0.529874365	1.368981124	4.647103277	1.509731902	2.029455692
253478_at	AT4G32350	0.605716403	0.667084251	0.525313871	1.881322837	0.860021422	0.935017535
253332_at	AT4G33420	0.687917663	0.434988014	0.794945709	6.857645377	1.456629803	2.036864253
253276_at	AT4G34050	7.98361503	2.723526317	25.51166678	46.36201844	20.10033394	15.01884882
253278_at	AT4G34220	0.58983914	0.498391324	0.554537663	3.776445219	0.791523003	0.696212068
253239_at	AT4G34500	2.156160021	0.878642768	2.327076897	4.304586655	1.40920528	1.67175431
253195_at	AT4G35420	0.644612086	0.518613755	0.531300901	1.613562483	0.614238419	0.631707519
253120_at	AT4G35790	4.93875729	2.459365216	4.557016356	9.490980602	3.046995527	2.718759009

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
253084_at	AT4G36260	0.406019476	0.418073276	0.430049453	1.221454242	0.512563729	0.504843469
246228_at	AT4G36430	0.838847477	0.462048041	0.513224111	3.11853901	0.550127995	0.489117251
246203_at	AT4G36610	0.588935665	0.483721162	0.619961505	1.339371502	0.6968622	0.694340087
246214_at	AT4G36990	2.351865638	0.762643467	9.018689322	17.18893244	2.416585823	3.493341617
253038_at	AT4G37790	1.778980521	0.75638621	2.363179858	4.683590211	1.256098023	1.901348618
253024_at	AT4G38080	0.406276491	0.411012464	0.573863476	1.468980012	0.505938046	0.483763914
252958_at	AT4G38620	1.147214708	0.503435883	5.794174824	13.02631097	2.208158318	3.102641423
252950_at	AT4G38690	0.506474127	0.457433524	0.453263042	3.336626638	0.677325366	0.532009168
252943_at	AT4G39330	1.056852428	0.663316293	0.747195957	4.837508572	1.011718778	0.916045112
252862_at	AT4G39830	0.601783534	0.769612812	0.735999824	1.715149914	0.689545142	0.806940874
251109_at	AT5G01600	4.425562013	1.289948589	5.515685321	14.75297434	4.627091971	6.411896637
251061_at	AT5G01830	1.800551973	1.215453506	1.310730868	4.020311972	1.30079021	0.94334544
251065_at	AT5G01870	0.656965295	0.58560875	0.54042122	10.70875748	0.668660842	0.618272221
251042_at	AT5G02310	1.880803041	1.074556506	1.560481918	3.66536952	1.793273899	1.68761218
245689_at	AT5G04120	0.822918105	3.256335188	7.470428615	13.71306493	1.63019078	0.804463646
250823_at	AT5G05180	0.33065935	0.421308604	0.375727176	0.988949336	0.475206621	0.430561002
250741_at	AT5G05790	0.492256294	0.459651946	0.517629349	4.357348057	1.462739773	1.794173116
250717_at	AT5G06200	0.857169866	0.689675953	0.912722012	22.38225717	2.174735566	0.996701912
250702_at	AT5G06730	0.440783206	0.396189446	0.442593506	1.411233615	0.603945508	0.54719485
250701_at	AT5G06839	1.466670417	0.666888084	1.72420853	3.276325999	0.909295506	0.837980555
250629_at	AT5G07390	1.329199319	0.550144371	0.589789068	2.503243846	0.721438682	0.648218782
250597_at	AT5G07680	0.489425339	0.433920968	0.507528636	1.108762929	0.601802046	0.566778963
250604_at	AT5G07830	1.67561084	0.699925114	3.229502153	8.583899803	4.312464962	2.253795174
250500_at	AT5G09530	0.436241606	0.441015955	0.766600609	2.608854218	0.574731891	0.532869885
250450_at	AT5G10280	0.576265682	0.459356413	1.004856249	4.562006015	0.796711402	2.280244981
250443_at	AT5G10520	0.763904931	0.525157452	0.733045549	8.237398248	1.137250266	1.099443769
250449_at	AT5G10830	9.712391304	7.67731793	8.610705502	18.50518481	3.794203076	8.754553528
245898_at	AT5G11020	0.564708022	0.656727642	2.006880827	3.907066659	0.901692547	0.624708092
250378_at	AT5G11570	0.549927353	0.438175222	0.577557839	1.550002013	0.649228461	0.613143974
245181_at	AT5G12420	0.418551615	0.37388998	0.454989495	0.873907702	0.493743668	0.501801912
250265_at	AT5G12900	0.429582503	0.393366313	0.467036475	3.845864961	0.947955512	0.730473255

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, $p <0.5$)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
250230_at	AT5G13900	0.827076676	0.487897625	0.494795301	2.063064447	0.58075655	0.613652203
250165_at	AT5G15290	0.590029713	0.528736499	0.966889224	28.10461027	3.358604125	1.091868904
246516_at	AT5G15740	1.190392125	2.569563116	0.964031633	5.197001296	1.363931452	1.315447744
246535_at	AT5G15900	0.515504852	0.452583281	0.577466544	3.085167523	1.001503986	0.708708908
250001_at	AT5G18680	5.544249153	1.702083457	3.71343386	18.05958387	2.441828501	2.73822729
246041_at	AT5G19290	1.107996406	2.63203076	2.022488289	10.10022719	3.201944766	2.583761293
245965_at	AT5G19730	0.768478529	0.559702096	0.64435671	2.927203395	1.096255447	1.442334311
246000_at	AT5G20820	0.515436327	0.439868443	1.287503719	2.715865607	0.899955247	0.726978785
249941_at	AT5G22270	0.737482773	0.619523426	0.684244585	1.699347334	0.708011871	0.84033902
249914_at	AT5G22850	2.093913106	1.346862458	3.417243812	7.805886719	3.972043973	2.943667223
249811_at	AT5G23760	0.377068473	0.420897083	0.588385943	2.798143248	0.686682977	0.639559828
249791_at	AT5G23810	0.625233515	0.53436429	0.648635841	1.625475959	0.831498163	0.788825217
249810_at	AT5G23920	1.17206127	0.796242057	1.314750773	11.08591505	2.123311345	1.532325506
246970_at	AT5G24900	0.537419203	0.475360966	0.500408931	1.297521019	0.70503784	0.684303098
246908_at	AT5G25610	0.647388031	0.459568386	0.5154901	1.875637963	0.61693295	0.62035258
246909_at	AT5G25770	3.55469754	0.856059555	4.866908389	12.27543393	2.822087061	2.580078219
246826_at	AT5G26310	0.635757596	0.523918753	1.425486153	12.98746208	1.088820238	0.718177368
255945_at	AT5G28610	0.51057205	0.386386111	0.580834153	0.99238167	0.465266304	0.474817125
246608_at	AT5G35380	0.437551407	0.444514311	0.401632197	1.536804057	0.491844267	0.487802454
249705_at	AT5G35580	1.27681523	0.498062938	0.593685196	7.938895844	1.846090661	1.398549603
249626_at	AT5G37540	1.052340049	0.644096089	5.2065942	15.32526764	2.784941167	3.332818754
249622_at	AT5G37550	0.792262721	0.459334289	1.172741062	5.797557927	1.175982837	0.864336247
249403_at	AT5G40270	0.643695089	0.480581208	0.427543008	3.471830233	0.740148067	0.62248739
249289_at	AT5G41040	0.559688368	0.476142018	0.608489452	5.413961354	0.921115772	0.648054728
249279_at	AT5G41920	0.824936325	0.574596945	1.034119614	2.283722713	0.925558375	0.925823371
249231_at	AT5G42030	0.548726735	0.460705721	1.133612542	2.426693246	0.849565667	0.765590417
249227_at	AT5G42180	0.584900583	0.541517299	1.466686152	44.93166719	4.66829358	1.384994747
249208_at	AT5G42650	5.28536655	1.762780485	12.13284016	20.83813338	6.020671021	8.880580627
249148_at	AT5G43260	1.630814862	0.828715056	1.930654554	4.741409323	1.228528962	1.174411238
249123_at	AT5G43760	1.628826261	2.020926375	4.440951328	9.423170941	2.401764202	1.00061519
249093_at	AT5G43880	1.193065429	0.974111795	1.623031786	6.250557529	1.37446	1.114925491

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
249013_at	AT5G44700	0.435332431	0.402251264	0.490109342	2.134688301	0.589149959	0.48722492
248989_at	AT5G45200	0.451731664	0.414443785	0.452627641	1.143787975	0.58140065	0.495969656
248990_at	AT5G45210	0.401640177	0.413228897	0.439237162	2.551278061	0.772304276	0.505534512
248912_at	AT5G45670	0.460726113	0.415525348	0.414595861	1.494307165	0.516239196	0.49068298
248908_at	AT5G45800	0.508190344	0.57400639	0.57553437	10.98442653	1.5023555	0.768474763
248838_at	AT5G46800	3.342316366	3.660265083	6.03348541	15.56737082	5.103109144	2.903139572
248794_at	AT5G47220	2.603550824	0.619358421	1.414896835	4.945198702	1.167305208	2.507903518
248750_at	AT5G47530	0.757181311	0.628921246	0.759660892	10.16682806	1.281965945	1.208432959
248761_at	AT5G47635	0.52417601	0.519090137	0.493940282	2.153722568	0.671634747	0.842686728
248639_at	AT5G48930	4.042212458	1.436478827	4.647175963	19.40978676	6.352591891	4.619889518
248428_at	AT5G51760	0.712982062	0.585530764	0.609485536	1.869685431	0.765112212	0.729856394
248316_at	AT5G52670	0.393609087	0.380261266	0.414875719	1.065089457	0.433985462	0.4040314
248327_at	AT5G52750	0.575269502	0.463028552	0.518861417	1.342366806	0.672346285	0.628595343
248254_at	AT5G53320	0.392161624	0.427858254	0.493379454	6.339821186	0.806415547	0.57724516
248218_at	AT5G53710	0.622597597	0.440448826	0.59242081	1.68955368	0.719150646	0.605712419
248209_at	AT5G53990	0.536477898	0.60436786	0.715312711	1.778622567	0.657595118	0.603768057
248108_at	AT5G55130	2.577118074	2.906353842	2.647202128	10.87209244	4.455130315	2.846883844
248025_at	AT5G55850	4.442835644	2.423729475	3.260997316	7.835344	2.241304416	2.480259135
248004_at	AT5G56230	1.558722489	0.687355365	1.354304329	4.870612369	1.221947687	1.204723656
247925_at	AT5G57560	7.215903535	2.829922162	5.499273604	29.66455219	9.948683992	8.701098904
247868_at	AT5G57620	0.548306055	0.491486893	0.735407547	10.73994375	1.181321003	0.776562569
247884_at	AT5G57800	1.41183538	2.226010562	0.912585113	3.830698676	0.976647044	1.160092606
247795_at	AT5G58620	0.825107251	0.710190468	0.663346527	2.213491693	0.805850154	0.73665462
247717_at	AT5G59320	0.614202387	0.438581903	0.463471426	8.530994709	0.636364539	0.621982661
247707_at	AT5G59450	0.989943478	1.613866983	2.168451157	4.126890524	0.851242891	1.237444032
247727_at	AT5G59490	5.125431697	1.187736539	7.023225493	19.71094939	3.283909043	3.866332973
247522_at	AT5G61340	1.745786413	1.383677714	4.483865118	12.88205914	3.098533737	3.603180916
247493_at	AT5G61900	2.161973647	1.009433508	3.579820901	6.12846461	1.444463539	2.801023449
247464_at	AT5G62070	0.742387375	0.534981019	1.165338952	3.023855015	1.171058341	0.983241345
247354_at	AT5G63590	0.997403176	0.600646949	1.447830472	5.585707599	1.013514754	0.822504959
247337_at	AT5G63660	0.448230807	0.523829191	2.530530682	9.504412877	4.889378606	0.712871409

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Endodermis/Quiescent Center (SCR) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
247261_at	AT5G64460	1.336053376	1.757556143	3.531172312	6.298579201	2.95056846	2.273606481
247266_at	AT5G64570	0.484675556	0.399103647	4.390107257	8.608475839	3.449591427	1.210048251
247169_at	AT5G65520	0.809582171	1.154265843	0.892147805	2.313744995	1.032562244	0.806123671
247170_at	AT5G65530	0.574238029	0.482144351	0.851478402	31.9424287	2.556019347	0.917260146
247149_at	AT5G65660	8.410872753	4.944022529	6.719014472	20.89233456	4.463871269	5.867642227
247165_at	AT5G65790	0.403104289	0.394118735	0.460975906	3.154572851	0.612072009	0.502585332
247091_at	AT5G66390	0.410058024	0.411519753	0.896197851	43.3199995	3.50415951	1.017161239
247095_at	AT5G66400	0.570880756	0.468692477	0.436448928	1.330803455	0.563538416	0.499738125
247072_at	AT5G66490	0.543166308	0.394974691	0.795108312	1.575364401	0.540444752	0.512116636
247048_at	AT5G66560	0.733934517	1.112027524	1.503135355	2.737081961	1.482416987	1.262996657
246988_at	AT5G67340	0.666026385	0.500505566	0.739543111	7.154787935	0.713143394	0.626053709
246998_at	AT5G67370	0.468562851	0.479469498	1.239311703	2.870523359	0.683046653	0.619486178

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Vasculature (WOL) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
261559_at	AT1G01780	1.372885701	1.246358915	0.636122139	0.956010811	2.719128617	1.233922443
264605_at	AT1G04550	0.339633787	0.392053334	0.461659948	0.643038282	1.261664576	0.573866727
261256_at	AT1G05760	0.55841606	0.57320544	0.612988304	0.667918721	1.335017049	0.586295676
264342_at	AT1G12080	2.031368935	0.543397081	0.543735386	2.4452331	8.175110367	1.873321589
262802_at	AT1G20930	0.571592345	1.208686713	0.687516089	1.053627043	2.167362205	0.82838451
261500_at	AT1G28400	0.399866355	0.359837524	0.523246251	1.613388956	3.168086433	1.213895802
260027_at	AT1G29950	0.488750942	0.554784237	0.659313175	0.965246706	4.082156611	1.27498335
261239_at	AT1G32930	1.33052134	1.168241644	1.151045497	1.54461168	2.934606647	1.581506462
245739_at	AT1G44110	0.864059665	1.411372479	0.822976679	1.239293953	2.481464851	1.065622998
265144_at	AT1G51170	0.560491488	0.485635147	0.688382689	0.845580534	1.574662806	0.910531529
265060_at	AT1G52150	0.52614825	0.54640729	0.736720981	0.90155852	5.171015146	1.237850461
264277_at	AT1G60390	0.8516799	0.560232939	0.723091818	1.926910708	3.357865037	1.878389994
261957_at	AT1G64660	0.493652344	0.495947218	1.23122912	2.254753492	6.53002661	1.072746574
260460_at	AT1G68230	0.441261565	0.422197925	0.463294519	0.514940147	1.12704211	0.505238729
260034_at	AT1G68810	0.44228112	0.446105421	0.55242029	0.757251669	5.084891847	1.512110595
259371_at	AT1G69080	0.682145917	0.641395453	0.662934549	1.121510519	1.927692924	1.064303657
261521_at	AT1G71830	1.145934828	1.318356793	2.744725406	1.994856856	5.453186722	2.456076587
262380_at	AT1G72810	0.701864229	0.678631721	0.828034366	1.445190427	2.955011018	1.241174048
245725_at	AT1G73370	0.949213035	0.699955942	0.987874499	1.34786552	2.930927167	1.176026024
259845_at	AT1G73590	0.487984325	0.703257517	0.639713019	1.355269884	3.610757418	1.306435661
260067_at	AT1G73780	0.398622644	0.44196284	0.437747118	0.527163212	3.601730811	0.86255075
259904_at	AT1G74150	0.446518275	0.455290823	0.434970821	0.501958796	0.92120851	0.487112831
260250_at	AT1G74260	1.253318447	3.694789119	2.2338839	3.779412714	6.662666609	2.07089803
262951_at	AT1G75500	0.642480274	0.527995986	1.281244652	3.225088546	10.80759749	2.067526458
264947_at	AT1G77020	0.355887272	0.364029578	0.493888802	0.968102885	2.232159774	0.987244099
259759_at	AT1G77550	0.857038431	2.494774279	1.083088922	2.056578292	4.311988354	1.852236969
259680_at	AT1G77690	0.550452613	0.623746361	1.563508068	2.679527885	14.56382511	3.753424307
259674_at	AT1G77700	0.634381292	0.529202954	0.628241233	0.812668848	1.50446101	0.678871383
260801_at	AT1G78430	0.469747345	0.491269437	0.479158609	0.724098494	1.410404648	0.591837616
261345_at	AT1G79760	0.57346788	0.433009905	0.484109594	0.580726087	1.118088097	0.543960142
262041_at	AT1G80100	0.749600531	0.546011108	0.624816034	0.714254651	1.439843442	0.694545994

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Vasculature (WOL) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
265249_at	AT2G01940	0.444069427	0.411051606	0.453853085	0.586348258	2.795869161	0.721772181
265250_at	AT2G01950	0.497549203	0.462928414	0.477225923	0.622016422	2.342094175	0.735028714
266770_at	AT2G03090	1.537102861	1.881019789	1.217191875	1.774788191	9.555417877	3.033321674
263629_at	AT2G04850	0.622936115	0.660869218	0.712933335	0.863929668	5.518011764	2.572628181
266038_at	AT2G07680	0.621095876	0.529648882	0.60132802	0.889484169	1.742497132	0.838882691
265656_at	AT2G13820	0.730041301	0.701500496	1.310315529	3.540697433	11.33284634	4.548500653
263017_at	AT2G17620	0.58207466	0.781967488	0.706265335	0.810073455	1.56006712	0.748180163
265813_at	AT2G18060	0.427244939	0.4019176	0.436593929	0.490342206	1.55136988	0.747766841
265378_at	AT2G18380	0.665296309	0.539979495	0.571092716	0.608682928	1.299764499	0.616935728
264377_at	AT2G25060	1.071197708	2.887315062	1.561163423	2.339116826	5.69867304	1.299943428
267613_at	AT2G26700	0.37845967	0.405168426	0.400518301	0.452790426	0.865179703	0.453806731
267619_at	AT2G26730	0.559910072	0.565351177	1.689281303	2.233293272	4.662284992	1.618735746
265277_at	AT2G28410	0.70887806	0.587832807	0.690932971	1.008783224	3.925298151	1.268321586
267299_at	AT2G30150	0.713281614	0.897827625	1.020475265	1.218052144	2.870304078	1.124316232
263470_at	AT2G31900	0.527798961	0.462850964	0.471324441	0.577487295	1.530991218	0.775608321
266358_at	AT2G32280	0.863727921	0.658381482	2.509730956	1.76696411	4.912194998	1.185901146
256713_at	AT2G34060	0.919391167	0.633164032	0.760968197	0.69627476	2.242633798	1.026513708
267316_at	AT2G34710	0.60912818	0.66091305	0.866048416	1.311081046	5.148852117	2.540154419
263913_at	AT2G36570	0.551055391	0.522365179	0.500731401	0.642019628	1.418806655	0.675135881
265468_at	AT2G37210	0.632025266	0.545806369	0.644202161	0.740341393	1.990823645	0.763039956
266007_at	AT2G37380	0.57812032	0.662886105	0.691525187	1.020155888	1.81583199	0.7482854
266187_at	AT2G38970	0.505707387	0.67100104	1.063647155	1.029890841	2.288831941	1.245731347
255876_at	AT2G40480	0.477002699	0.497835033	0.530557528	0.66337822	1.712474505	0.859267623
251395_at	AT2G45470	0.753580807	3.056432076	1.473096861	2.912933526	8.089152484	3.344782803
258952_at	AT3G01410	0.908762944	1.162716014	0.807466375	1.123229048	2.005574634	1.118250877
259308_at	AT3G05180	0.442089181	0.420552728	0.461317056	0.518517147	1.238099538	0.723753334
259022_at	AT3G07420	0.666839027	0.527394741	0.653276235	0.932850659	1.712709559	0.719118134
258672_at	AT3G08570	0.66842709	0.607021292	0.613080341	0.766738561	1.52245296	0.883872524
258938_at	AT3G10080	0.600156101	0.487607701	0.545482361	0.847472959	4.931823317	2.056106459
259290_at	AT3G11520	0.878070364	1.283067003	0.858242104	1.545130143	2.627805267	1.042631573
256275_at	AT3G12110	1.615390329	2.099783026	2.300072948	2.502932284	6.792634662	2.936291309

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Vasculature (WOL) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
258222_at	AT3G15680	0.582511269	0.454694216	0.571030904	0.804607473	1.928199469	0.579889394
258252_at	AT3G15720	0.425988819	0.527385428	0.469583805	0.802378415	1.37134679	0.466098984
257229_at	AT3G16490	0.50108231	0.77830343	0.661420632	0.665254757	1.369702487	0.680784311
258414_at	AT3G17380	0.404669035	0.405137997	0.412864889	0.572856232	1.079348408	0.446127304
258010_at	AT3G19300	0.641481227	0.745403645	0.708018903	0.996680097	1.822850126	0.999093863
256818_at	AT3G21420	0.813860373	0.606872369	0.696156907	0.71065703	1.773111308	0.867452453
256899_at	AT3G24660	0.435789107	0.676915935	0.561104378	1.84609629	4.876782068	1.711329307
257642_at	AT3G25710	0.401684006	0.408724261	0.427366832	0.576819014	2.200280373	0.61330307
257613_at	AT3G26610	0.767654688	0.50472096	0.69358975	2.02230029	4.036102336	1.446004651
256564_at	AT3G29770	0.604172568	0.593752279	0.880148108	0.951789008	2.804814748	1.233037019
252765_at	AT3G42800	0.472340061	0.406437755	0.456291078	0.462098486	3.457657793	0.624567804
252691_at	AT3G44050	0.317994525	0.709683705	0.401639168	0.687867493	1.210030447	0.442249408
252425_at	AT3G47620	0.514216619	0.505182565	0.698246657	1.100633629	2.597735299	1.062214949
252352_at	AT3G48185	0.586543543	0.427295081	0.639625806	0.808797059	4.022802109	0.90274202
252322_at	AT3G48550	0.466072279	0.430068224	0.435297639	0.528924859	1.488537243	0.557115331
252296_at	AT3G48970	0.553157621	0.439839774	0.577428098	1.159813303	2.208052641	0.969054942
252119_at	AT3G51030	0.711112556	0.667267198	0.93909198	1.191786796	6.808987529	2.362524737
252080_at	AT3G51670	0.75454331	1.483261543	1.020834087	1.359294791	13.41430964	3.039716489
251982_at	AT3G53190	1.071619052	1.7692288	2.161619395	4.136107673	9.430565911	1.933353473
251920_at	AT3G53900	0.741197759	1.105605075	0.84410575	1.52884639	2.693868601	0.980780038
251889_at	AT3G54080	1.190967767	1.483567963	1.486612212	1.637785098	3.496531285	1.987787456
251886_at	AT3G54260	0.872792436	1.055894476	0.853060393	2.173632109	6.803234846	1.75340479
251688_at	AT3G56480	0.610288376	0.530715261	0.646526552	1.570504674	3.190343613	0.922088646
246346_at	AT3G56810	0.449126572	0.419802571	0.515368774	0.740338	1.689735708	0.572470167
251574_at	AT3G58100	0.742912667	0.886360584	1.19136634	1.069763612	2.258050392	0.978480822
251556_at	AT3G58840	1.448085931	2.46245383	1.59328948	1.968546935	4.403312835	2.136321201
251517_at	AT3G59370	0.301261782	0.364026484	0.371930277	1.234818917	3.053757979	0.614789259
251244_at	AT3G62060	0.647502698	0.877816085	0.89672204	1.056532531	2.077346303	1.023527471
255664_at	AT4G00440	0.994011645	0.730305564	0.734033679	1.380337661	4.198203586	1.432428183
255433_at	AT4G03210	0.522199644	0.510059423	0.674501972	1.164867042	2.166994417	0.830541305
255003_at	AT4G09950	0.466242901	0.45199291	0.406117247	0.578639937	1.203075768	0.485049705

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Vasculature (WOL) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
254810_at	AT4G12390	0.823470036	0.58461502	0.988969817	3.448243861	8.228620046	2.044775919
254823_at	AT4G12580	0.399039671	0.347187053	0.403963681	0.523016389	1.125603252	0.579370168
245568_at	AT4G14650	0.562590732	0.553618552	0.682328756	0.899734023	1.548716081	0.832441194
245576_at	AT4G14770	0.803369611	1.212996819	0.808806425	1.029523468	2.713621354	0.999948272
245584_at	AT4G14940	0.566319463	1.399919368	0.575850967	2.042868792	6.701824751	3.295618556
245343_at	AT4G15830	0.510916654	1.54558859	0.70187051	1.428957495	3.043677496	0.773635868
254515_at	AT4G20270	0.553805022	0.412584539	0.48431986	0.976930706	1.877981703	0.798665185
254466_at	AT4G20430	0.60547349	0.523436194	0.579583456	0.693023757	3.030059091	0.797970054
254402_at	AT4G21310	0.757852195	0.74230991	0.710707214	0.782882099	1.952192111	1.011010068
254328_at	AT4G22570	0.596138163	0.516141545	1.298262159	2.228927671	5.958363985	1.688914181
254119_at	AT4G24780	1.068660005	6.109534848	2.962900879	4.240523013	14.08239518	6.250543056
253818_at	AT4G28330	0.534894143	0.450833376	0.502805777	0.564628392	1.093684259	0.622578069
253620_at	AT4G30520	0.68864589	0.590688231	0.635137961	0.783136978	2.303010424	0.72185411
253498_at	AT4G31890	0.695969406	0.716313418	0.71713024	0.649735801	1.524674437	0.83247349
253076_at	AT4G36160	0.506518109	0.404896373	0.493794647	0.544507122	2.135518164	1.201084733
246274_at	AT4G36620	0.611910345	0.702447651	0.617191204	0.868080149	1.613587979	0.74717874
253045_at	AT4G37445	0.56748852	0.512143776	0.54112376	0.782710764	1.420261704	0.647381258
253056_at	AT4G37650	0.600895086	0.508301734	0.656900386	1.885985497	6.183999133	1.052966914
252954_at	AT4G38660	0.633938535	2.531534342	1.158422452	2.102667	6.122557643	2.953332441
251113_at	AT5G01370	0.507536887	0.426950077	0.48428533	0.5511047	1.250193012	0.585646464
251075_at	AT5G01890	7.619161016	5.043728946	1.753831172	2.194537529	14.67295108	5.751847682
251021_at	AT5G02140	0.565745444	0.548705329	0.549356756	0.615919084	1.706036742	0.598140421
251009_at	AT5G02640	1.130621534	0.623201946	0.796478204	0.957988152	6.450447141	2.514404878
250872_at	AT5G03960	0.506325651	0.525269506	0.581637862	0.713523887	3.254712267	0.936849486
246956_at	AT5G04890	0.663303752	0.553246945	0.820854175	1.305692185	3.348469427	0.713065202
250752_at	AT5G05690	0.498687082	0.455701464	1.084214274	1.184458522	9.572112938	2.149987175
250661_at	AT5G07030	0.521544891	0.643130654	0.731484646	1.906462545	4.773493435	1.603303568
250517_at	AT5G08260	0.889598779	0.828806586	0.887719471	1.500603165	4.947843795	1.372579279
245883_at	AT5G09500	0.774771037	0.916667943	0.612501186	0.697264732	1.623197669	0.678889843
245903_at	AT5G11100	0.568972824	0.578317945	0.515801146	0.624275182	1.671244474	0.707161595
250333_at	AT5G11690	0.732131975	1.061774479	0.845770822	1.058460233	2.093442783	0.961727549

Supplementary Tables pertaining to Figure 3
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245947_at	AT5G19530	0.531217875	0.458686641	0.518623642	0.639615403	4.131345551	0.825292776
249832_at	AT5G23400	0.42136482	0.526211669	0.545339799	0.702464956	2.001683811	1.12626106
249780_at	AT5G24240	0.694025549	0.552495086	0.505296829	0.514361315	1.391950484	0.543612874
246891_at	AT5G25490	0.697481626	0.556657051	0.59448348	0.733073151	2.106360845	0.676987665
246860_at	AT5G25840	0.440395701	0.39734769	0.396754982	0.482391874	1.607899789	0.61104363
246802_at	AT5G27000	0.458317385	0.453830767	0.501320362	0.957075488	2.106119251	0.879010045
249115_at	AT5G43810	0.485797097	0.406308385	0.493968344	0.818519208	3.481518071	1.119909915
249118_at	AT5G43870	0.673342158	0.563399055	0.569303125	0.649255519	3.01735332	1.032285368
248807_at	AT5G47500	0.67689132	0.474518844	0.621890562	0.870715785	1.946287277	0.819996806
248731_at	AT5G48060	0.634344043	0.606075019	0.634580238	0.774818977	1.343955661	0.704246825
248656_at	AT5G48460	0.556983635	0.781964726	1.156996214	1.119406754	2.206790719	0.821059208
248710_at	AT5G48480	0.768893903	0.758998579	1.008811405	3.941432389	7.391342609	3.055191502
248435_at	AT5G51210	0.637573252	0.534763005	0.611136648	0.701912483	1.769848856	0.767166218
247879_at	AT5G57770	0.606197605	0.536030815	0.508753967	0.645180382	1.90132301	0.682092343
247589_at	AT5G60690	0.741653041	0.765347125	0.931040628	1.293069613	5.260757031	2.814163459
247264_at	AT5G64530	0.426149524	0.403264149	0.412686833	0.426815618	1.348406899	0.582214641
247084_at	AT5G66300	0.581658268	0.445101639	0.562800579	0.626298516	1.758433748	1.002353386
247034_at	AT5G67260	1.162026005	2.688163044	2.626357112	3.138297369	5.425939927	1.905872565
246999_at	AT5G67440	0.613528169	0.741807189	0.52585299	0.628077976	2.067949861	1.085483115
246994_at	AT5G67460	0.781933137	0.783701391	0.737082908	0.813957573	1.756527403	0.886391583

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
261586_at	AT1G01640	0.739323691	0.528576061	0.769074472	0.924158917	0.897042069	2.676275585
262108_at	AT1G02740	0.855108304	0.800395549	0.869641226	0.925584187	0.859726872	1.622383617
262105_at	AT1G02810	5.597292921	5.568987399	5.134262622	2.229906589	2.022620495	12.74490538
264352_at	AT1G03270	0.429642583	0.687644617	0.494993037	0.593927952	0.663588498	1.441722621
264360_at	AT1G03310	0.718622533	0.642293351	0.765993917	0.626224736	0.712080109	1.974551887
264328_at	AT1G04100	1.33206405	0.80346834	0.987927208	1.099249054	1.118300867	2.424451059
264323_at	AT1G04180	1.704990115	1.521709112	0.636727823	0.879166586	0.930799672	10.43991888
264598_at	AT1G04610	1.34046374	3.241614952	1.203299016	3.032169861	2.126918504	27.12652783
265194_at	AT1G05010	2.858919854	3.366300176	1.687741599	1.190808584	1.2312319	21.61144998
264587_at	AT1G05200	0.577020236	0.526473486	0.668451944	0.636204906	0.655988729	1.223592923
259394_at	AT1G06420	0.607107751	0.593870065	0.530145224	0.884163831	0.692270492	2.241868937
262629_at	AT1G06460	0.444271532	0.406985951	0.492737542	0.45366367	0.519416149	1.100152392
256066_at	AT1G06980	0.843014326	0.947472003	0.599218093	0.671422395	0.792278515	2.725472285
256059_at	AT1G06990	0.431792131	0.463871215	0.447168955	0.509088293	0.501943424	2.152030767
261075_at	AT1G07280	0.640319377	0.946868706	0.904497214	0.752184922	0.562777197	4.775347327
261074_at	AT1G07290	1.172995415	1.72179658	1.014473772	0.81633859	0.858346648	7.700280301
261809_at	AT1G08340	3.343579753	1.346764647	0.608205107	1.160435277	2.675151826	7.499315497
261747_at	AT1G08350	5.603252047	2.981446319	2.880474604	1.528713942	1.886476101	9.901873062
264549_at	AT1G09440	0.40427588	0.378114852	0.43853219	0.528715926	0.783914279	1.661016611
264510_at	AT1G09530	0.648705831	0.687227646	0.758455792	1.117226425	0.954611371	2.26907782
264508_at	AT1G09570	2.135233836	2.084786273	6.603546603	3.478747968	3.676853376	14.71115038
257450_at	AT1G10530	0.625138379	2.89518917	0.542769615	0.56798421	0.607239213	6.97752032
263258_at	AT1G10540	0.567730323	0.513263841	0.503070764	0.552353658	0.608318133	1.152513156
262784_at	AT1G10760	1.276047673	1.879306645	2.72946462	1.816480449	2.448854436	16.99646918
262759_at	AT1G10800	0.809391943	0.680433381	0.707883287	0.999193567	1.340858555	2.632304625
262454_at	AT1G11190	0.970448958	0.775799827	0.520380592	0.832573363	0.976227967	2.130086606
264389_at	AT1G11960	1.37289248	1.109165583	2.69991244	2.321448185	1.008183766	4.766728089
264385_at	AT1G12020	0.838844161	0.845746171	0.657268871	0.724785726	0.901790977	1.836605914
259520_at	AT1G12320	0.443203368	0.450326743	0.407191847	0.803216838	0.709596616	1.492120083
259527_at	AT1G12600	0.931927577	0.937832927	0.645462273	0.653091344	0.755608681	5.539670343
261211_at	AT1G12780	0.714884286	1.035268127	0.852869812	1.201169115	2.743549879	8.769272566

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
262842_at	AT1G14720	0.6510025	0.863312042	0.637282456	1.931525273	0.977948159	5.003187097
257463_at	AT1G14820	1.260739414	1.691001174	1.119183644	1.36327365	1.157971013	5.376355233
262580_at	AT1G15330	1.044526635	1.058911275	0.895074035	1.063191799	0.957179486	2.304081255
261763_at	AT1G15520	2.118376179	0.782365464	1.06054423	2.705185969	0.928333199	5.176036727
261787_at	AT1G16020	2.385635361	1.505275561	1.612193906	2.053447751	1.429203745	4.218466231
255893_at	AT1G17960	0.681498528	0.492959524	0.586206886	0.732832991	0.60786059	1.984163932
260666_at	AT1G19300	1.049041316	0.706600965	1.231387399	0.730653282	1.21269894	3.78845171
255782_at	AT1G19850	0.704194818	1.299223767	0.5130332	0.994491595	2.005952967	5.376219699
260925_at	AT1G21340	0.682323566	0.988552481	0.557678078	0.589888105	0.668565155	6.624278992
255955_at	AT1G22030	0.633323459	0.548616466	0.648426312	0.81097567	1.446758794	3.323349423
255926_at	AT1G22190	7.96104276	6.462778868	5.856178675	6.524374847	2.692868815	17.66779481
261934_at	AT1G22400	1.960822631	3.596327077	4.540834102	0.967380915	1.194463348	11.19024208
264204_at	AT1G22710	0.9411697	0.714042312	0.924371721	1.651923046	1.802322887	3.952692916
264775_at	AT1G22880	3.87354623	8.179488066	1.171054988	1.197577215	0.8119692	32.12007795
264894_at	AT1G23040	3.035024288	2.681368709	5.418369639	3.915786335	3.02318922	12.04163537
264900_at	AT1G23080	0.48947759	0.451755406	0.537855108	0.990083663	1.793887731	3.388505135
264892_at	AT1G23160	0.439542208	3.092243234	0.533896456	0.619810065	0.47584937	10.4064249
264896_at	AT1G23210	0.840585018	0.67055579	0.520121336	0.523137223	0.556258818	9.752389871
263028_at	AT1G24030	0.456027426	0.440537231	0.476176759	0.880635429	1.467971858	3.751310741
264868_at	AT1G24090	1.026986468	1.297623136	0.660953725	0.675622749	0.862376349	3.162785539
245871_at	AT1G26290	0.364527458	0.344520286	0.346118545	0.37826778	0.414321924	0.752218581
261260_at	AT1G26680	0.569845926	0.664939743	0.594652289	0.627847868	0.818932427	10.3647881
263689_at	AT1G26820	3.928742339	3.161238758	0.675271209	1.318777885	3.213733721	8.731624831
263683_at	AT1G26870	0.520868629	1.055995563	0.512720549	0.517974976	0.551760045	4.537579217
264493_at	AT1G27440	1.135191096	0.814072191	0.737311483	0.805716827	1.246308958	3.263378112
259606_at	AT1G27920	0.370217518	0.35096279	0.380146998	0.553840881	0.95763181	1.808123498
259596_at	AT1G28130	0.922299228	4.252448464	6.137153328	0.97269172	0.783271009	14.55181411
261441_at	AT1G28470	0.656814222	0.629682211	0.601298826	0.658569914	0.980235587	3.312894873
260884_at	AT1G29240	0.657660897	0.616249721	0.927526616	0.593187016	0.675254119	1.912223333
256190_at	AT1G30100	0.37334631	0.419679673	0.375256525	0.441384229	0.491544717	1.035076743
256311_at	AT1G30330	0.848748152	1.818985153	1.259379395	1.099140596	1.589421501	3.718961823

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
257467_at	AT1G31320	0.434080554	0.454064177	0.520991423	0.504997523	0.642540864	1.104275376
261187_at	AT1G32860	0.912792104	1.375934628	0.795803908	0.777149765	3.30514379	5.790700611
261191_at	AT1G32900	0.498713533	0.636174092	0.494302892	0.765150666	0.574659852	6.074222165
256534_at	AT1G33270	1.411458905	1.276549576	1.280649477	1.267676103	1.181117168	2.514705144
256535_at	AT1G33280	0.775976918	2.458011937	0.521570911	0.567794633	0.569795485	5.559591573
262542_at	AT1G34180	0.602158247	0.579037043	0.592982813	0.576814066	0.581839159	1.048573684
259550_at	AT1G35230	0.527917706	0.564565235	0.530285529	0.760797882	0.694175078	5.866417663
256319_at	AT1G35910	0.371220539	0.357758534	0.396201611	0.739774104	0.636302831	1.971297309
260867_at	AT1G43790	0.792995056	0.652995377	0.8216928	1.726930465	3.592274396	9.347461993
245245_at	AT1G44318	0.773231118	2.869327182	0.665601649	0.675447982	0.669494967	7.365711905
260502_at	AT1G47270	0.784907573	1.032389599	0.905902796	1.78792464	1.60113908	9.62018837
260723_at	AT1G48070	0.662834147	1.150533133	0.478882786	0.541935386	0.509265996	6.756925484
262244_at	AT1G48260	1.091238011	0.805725436	0.777502879	0.734501021	0.95032327	2.524079059
260769_at	AT1G49010	0.867794465	0.77531328	0.690405451	0.735523337	0.914035163	2.313653583
262416_at	AT1G49390	0.630570796	0.760387042	0.77078285	0.595293355	0.535444196	1.349688668
257483_at	AT1G49620	0.711183752	0.906457144	0.752424896	0.966239416	1.164874367	3.378547401
261691_at	AT1G50060	6.309542851	9.603673861	1.090876616	1.30047409	0.633617664	31.28930313
257582_at	AT1G50720	0.420026909	1.360136138	0.421379377	0.414025544	0.412192513	2.472140774
265145_at	AT1G51190	0.721213923	1.358090701	0.593909006	1.003007798	0.702332383	3.33490468
262128_at	AT1G52690	0.484523303	2.473389375	0.599942495	1.29325274	0.567627841	4.524430856
261369_at	AT1G53060	0.952937853	1.004047781	0.609304045	0.588756822	0.7889069	2.512994019
261368_at	AT1G53070	0.559766562	1.220640523	0.568898646	0.808129669	1.279723244	5.452741631
261315_at	AT1G53170	1.046114679	2.90277848	3.2299569	3.713408703	2.206163712	7.261835107
260589_at	AT1G53400	2.037908349	1.632316552	2.477189283	3.158763356	1.674575155	7.764686079
260973_at	AT1G53490	0.615638814	0.730505258	0.642607572	0.631910097	0.771257994	1.539535978
259961_at	AT1G53700	3.080487497	2.755006973	0.649719312	0.953894019	0.940586987	8.660900457
262257_at	AT1G53860	0.569073256	0.623878976	0.546218684	0.699364897	0.690943526	3.665945953
264184_at	AT1G54790	0.52269447	0.394312029	0.459241197	0.646297316	1.122164761	3.185194228
245674_at	AT1G56680	0.677599499	5.077248952	0.733706712	0.858263832	0.681230477	11.94499595
256025_at	AT1G58370	0.726809702	0.563110432	0.66087189	1.231223839	3.013871217	5.140227735
262905_at	AT1G59730	0.469748271	0.381054423	0.428579489	0.582757451	0.51311313	1.152038679

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
263732_at	AT1G59980	0.807409247	0.736481684	0.678673976	0.553988901	0.635313938	1.798391908
260632_at	AT1G62360	0.687843757	0.539582349	0.60696623	0.586641967	0.657078664	1.306911406
260637_at	AT1G62380	0.831032234	0.598311873	1.522021801	7.340247048	6.484404869	18.77727985
261100_at	AT1G63020	0.575052449	0.568865105	0.575879568	0.643266731	0.635691448	2.575779326
259688_at	AT1G63120	1.512164989	1.141305915	1.476234703	2.143773108	5.361715462	12.76612223
262003_at	AT1G64460	3.251031169	2.044606408	1.580255504	3.205739181	2.550478176	7.087119694
264682_at	AT1G65570	2.46770682	1.376292216	0.638327621	0.859948056	0.647636782	20.23881795
264626_at	AT1G65620	0.827203854	0.894198068	0.674414054	0.736909201	0.793902504	6.353680904
260141_at	AT1G66350	0.611550152	0.76325515	0.727762878	0.598867236	0.633521134	1.851019187
255851_at	AT1G67040	0.482937872	0.527821928	0.450446204	0.613947081	0.641867723	1.265582327
255881_at	AT1G67070	2.125416792	1.031615441	0.961305527	0.875608906	0.860257402	7.452526304
264942_at	AT1G67340	1.00387915	0.920728071	1.224077811	1.534402999	2.147825386	5.199574315
264227_at	AT1G67500	1.611659011	1.122541724	1.326491279	1.31805995	1.465175291	2.909451416
245200_at	AT1G67850	1.442825273	1.834116749	0.647329363	0.764456889	0.747596582	5.214628172
260412_at	AT1G69830	1.095360705	1.082380349	1.018447804	1.502215975	0.981259354	10.20923026
260414_at	AT1G69850	1.015898706	1.286704329	0.906512749	1.157757686	1.007208837	2.534808194
260407_at	AT1G69910	0.896899855	1.111563409	1.488645252	1.139688496	1.544471421	3.376182564
264714_at	AT1G69990	0.5183672	0.490029892	0.467173435	0.507137558	0.573312636	1.242340622
264314_at	AT1G70420	1.639895271	1.646120333	1.194427038	1.996327881	0.93620468	4.894744153
260333_at	AT1G70500	0.406063195	0.417021495	0.487417078	0.817118631	1.439534385	3.807817679
262263_at	AT1G70940	0.707884827	0.546792208	0.723203581	1.363499065	2.345246381	4.870658555
259897_at	AT1G71380	0.680698624	1.13541495	0.450696388	0.516204367	0.54888694	3.989072692
261514_at	AT1G71870	0.607689266	0.541859123	0.593237189	0.93902317	0.853188569	2.503560451
256338_at	AT1G72100	0.501179399	0.50937284	0.454571553	0.531411529	0.55007716	1.361456332
259848_at	AT1G72180	0.852712134	0.778430574	0.874545253	1.438123458	1.517466949	9.377000442
245734_at	AT1G73480	1.634548908	1.456875317	1.328841018	1.508766363	1.2194778	5.670931399
245779_at	AT1G73510	0.736355615	0.728891192	0.649812515	0.822025238	0.507522751	2.051915178
245778_at	AT1G73530	1.796911361	1.486419505	1.257592179	1.668879567	1.039560976	3.533757027
260076_at	AT1G73630	0.48519937	0.394566616	0.399064688	0.565526058	0.572937358	1.070697462
260373_at	AT1G73970	0.985717482	0.987393071	1.08789305	0.962534022	1.080258048	2.854444975
260386_at	AT1G74010	2.403583835	0.872550548	0.666435076	0.729982204	0.690225814	4.992409352

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
260211_at	AT1G74440	1.382325985	0.673864363	0.89519324	0.767708866	0.77441778	2.999617579
256454_at	AT1G75280	0.760169245	0.743443747	2.305836124	2.632047211	5.543806158	12.21303988
262969_at	AT1G75710	4.367804362	5.465089101	2.109425179	1.461429156	4.10574762	10.01277907
262967_at	AT1G75730	0.562179605	0.742161253	0.763049573	0.603017695	0.941325302	1.806623794
262728_at	AT1G75820	0.785610028	0.655463611	0.718580235	1.033465822	1.098543002	2.60624945
259979_at	AT1G76600	12.59021713	11.82732525	10.15388721	14.23723804	4.944246471	25.92982772
264961_at	AT1G76950	1.53995176	1.388259134	1.285708097	1.181494523	1.120425699	2.839919073
264957_at	AT1G77000	1.650701372	1.098013614	1.015200926	1.257277739	1.014990111	5.093709942
264485_at	AT1G77220	1.022882275	1.070719361	0.961924595	1.031640314	1.155861919	2.633451688
259707_at	AT1G77490	0.839581038	0.78873378	0.906979096	0.835789037	0.767859752	3.070962163
260053_at	AT1G78120	1.35709589	0.742680167	1.566376817	1.770661388	2.837571311	5.725534014
261393_at	AT1G79580	0.416111085	1.963080604	0.481349881	0.447945802	0.476247515	3.597770029
262061_at	AT1G80110	1.460274185	1.521260584	0.871789653	0.919794149	1.078326281	6.099961581
260276_at	AT1G80450	0.557909125	0.459044798	0.553819537	0.614324993	0.496155421	1.728023188
260288_at	AT1G80530	0.802310156	1.989711166	1.11713773	1.939454534	2.160721383	6.169369176
261881_at	AT1G80760	0.636581357	0.562619666	0.68399294	0.77690376	0.783295767	1.506244136
262205_at	AT2G01080	1.395575241	0.947155467	0.956255664	0.942502923	1.133198531	2.497804653
266300_at	AT2G01420	0.727472478	1.569378096	4.205793636	2.628160785	3.86304651	19.52480546
266708_at	AT2G03200	0.713046134	0.646712801	0.691052215	1.009600057	1.24607442	2.145026503
263481_at	AT2G04025	0.327207465	1.480564222	0.472514934	1.980121713	0.48628285	22.90738086
266381_at	AT2G14670	0.687991321	0.528366915	0.573811515	0.594192898	0.687172689	1.461048247
263096_at	AT2G16060	1.217667396	1.829240414	0.780784876	0.906712445	1.299067203	4.403115294
265354_at	AT2G16700	0.490991259	0.523778949	0.889257162	2.300187802	0.883921007	7.208267192
265358_at	AT2G16710	3.740964086	2.317072941	3.731103822	4.289683504	3.867598772	8.484170151
265357_at	AT2G16740	0.964963161	0.799278874	0.765929067	1.266670059	1.2499238	3.315638649
265339_at	AT2G18230	0.905484121	2.214958552	0.94334052	1.268431038	2.067148368	10.13001601
265948_at	AT2G19590	1.553468794	1.175075429	1.840360413	1.183354252	1.168349677	8.971790177
266695_at	AT2G19810	1.439510255	1.518554193	1.1736932	1.734496384	1.667777587	5.133965338
265577_at	AT2G20100	0.346118608	0.325488873	0.343776157	0.60650342	0.547497598	1.065591512
264019_at	AT2G21130	5.921420648	4.627509082	3.718790739	3.910783843	2.670257455	10.33951842
263544_at	AT2G21590	0.361028405	0.374044187	0.350489549	0.408029724	0.414706508	1.675974802

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
263543_at	AT2G21610	1.544574247	1.629091053	0.774621019	0.831786748	0.697989355	12.46143581
267182_at	AT2G23360	0.578236303	1.050998839	1.00208614	0.645272433	0.934995044	4.535979671
267290_at	AT2G23750	0.77028885	1.088524025	0.755595521	0.813396702	1.117130257	2.831709247
266568_at	AT2G24070	0.652529791	0.807170317	0.862374524	0.641260756	1.073075234	1.845904668
265609_at	AT2G25420	0.549802562	0.780015488	0.826593085	0.744603079	0.866601549	1.615091344
266893_at	AT2G26070	1.322919519	1.656772944	1.570458258	1.909865788	2.169026026	4.768133565
267376_at	AT2G26330	0.602056767	0.676335622	0.621998114	0.683841203	0.764230693	2.070010838
267614_at	AT2G26710	1.623627242	1.98013746	0.591232	0.669670508	0.678525874	3.423316334
266209_at	AT2G27550	0.786181541	0.840230794	0.877812354	1.63123801	1.40176429	7.442701474
266244_at	AT2G27740	0.468773066	0.445109551	0.459664555	0.995173344	3.468662664	6.541794226
266163_at	AT2G28130	0.645830159	0.83087634	0.919982004	0.949217805	0.903153194	1.636405531
265272_at	AT2G28350	1.478449276	1.697744459	1.294508174	1.175897186	1.20353626	8.06192315
265276_at	AT2G28400	4.16916606	3.7023391	2.42956654	2.886517657	1.11686096	7.660103021
266221_at	AT2G28760	3.071895916	4.293910444	0.949992378	1.297223548	2.313995376	10.33180752
266227_at	AT2G28870	0.444450392	0.433124993	0.395856442	0.464044202	0.657209601	4.673275213
266225_at	AT2G28900	0.692390402	1.401759043	0.697178382	1.842415061	0.986624111	11.48191735
266783_at	AT2G29130	0.600153947	0.494528029	0.56330165	0.543492502	0.709845994	1.336124756
266274_at	AT2G29380	0.685668619	0.755330324	0.590311843	0.657945954	0.680847296	1.715787351
266805_at	AT2G30010	0.579869245	0.607839078	0.613558852	1.051956475	0.947569046	2.041591999
267300_at	AT2G30140	1.964115999	1.436415581	1.639504162	1.350985817	1.381469752	4.666337403
263465_at	AT2G31940	0.600020912	0.743257949	0.628447856	0.853811616	0.829758799	3.478489244
266362_at	AT2G32430	0.899773328	1.348123349	1.134841533	3.71815128	1.104249781	7.822223206
267116_at	AT2G32560	0.850990315	1.060356224	0.841894365	1.056284523	0.905877962	2.09258113
245163_at	AT2G33230	0.654986121	0.474167376	0.514742354	0.581310179	0.670968975	3.341866541
256714_at	AT2G34080	0.986100686	1.199497697	0.836798578	0.586538335	0.690002939	2.13411028
256720_at	AT2G34140	0.809866406	1.328450559	0.736456184	1.441037357	1.661635196	4.509543744
267414_at	AT2G34790	0.483967816	0.399359582	0.369612966	0.681950554	1.298875088	3.025411611
263912_at	AT2G36390	2.384596451	1.797727306	3.103097261	2.406045566	1.675965898	5.705296454
263866_at	AT2G36950	2.784163819	4.876728898	4.480687877	15.27938471	2.564884295	29.45097843
265463_at	AT2G37090	0.702175585	0.484312972	0.847016646	1.196015842	2.922808287	7.406216851
267094_at	AT2G38080	0.549394268	0.459020227	0.488286332	1.183568846	2.550858875	7.963626656

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
263265_at	AT2G38820	0.987604857	0.835764644	1.567754102	2.173164242	1.426867784	4.079337228
267591_at	AT2G39705	3.280986798	2.063187719	3.881489127	2.127015604	2.935693901	7.011349614
267356_at	AT2G39930	0.597869338	0.915858883	1.34536419	1.074566116	1.385936273	2.419127868
267337_at	AT2G39980	1.269911463	1.138263056	1.005459683	0.847849479	1.213741348	3.272375261
255823_at	AT2G40470	0.639473085	2.226065268	0.57645069	0.574563722	0.695658061	7.155491381
245094_at	AT2G40840	1.863133068	2.878919988	4.896346464	1.924439939	2.163536117	10.08732161
267075_at	AT2G41070	0.52863109	0.780275264	0.516257497	0.57245066	1.083045055	2.246839853
267082_at	AT2G41140	1.177490447	0.906822861	1.066375627	1.444100204	1.321705336	2.498741297
266391_at	AT2G41290	4.41567955	3.654217103	2.032261867	0.916714708	1.192675805	11.67013715
245105_at	AT2G41610	0.754647265	0.593020855	0.62672851	0.857502102	1.409391225	3.309037464
245140_at	AT2G45420	0.466247379	0.400156174	0.46257447	0.775293307	1.121352335	2.060306272
266925_at	AT2G45740	1.086127975	0.822001584	1.048094126	0.789069392	0.787684043	2.721555455
266917_at	AT2G45830	0.69924413	0.965377654	1.420777847	1.531626292	1.146582606	3.205391498
266710_at	AT2G46850	0.468078921	1.061861749	0.536812624	0.611176479	0.667279326	5.866974357
266756_at	AT2G46950	1.011478446	1.453947554	0.893357388	0.840017681	1.032333727	2.908357152
266753_at	AT2G46990	0.485719741	0.522650873	0.464246502	0.558269971	0.749648126	3.371192284
260528_at	AT2G47260	1.14913215	1.204876146	0.88001844	1.232612605	0.736838261	3.32642718
259268_at	AT3G01070	0.538753217	1.716513047	0.611459263	0.658316906	0.797618376	3.632291623
259181_at	AT3G01690	0.746831803	1.401952982	1.806945073	1.386984914	1.386939089	7.221372944
259182_at	AT3G01750	0.599009086	0.559532086	0.574976074	0.666282971	1.170565675	2.973577361
259000_at	AT3G01860	0.996495795	0.793837764	0.835287097	1.151227752	1.107848596	6.240508407
258857_at	AT3G02110	1.024949367	1.082209108	0.630604354	1.204546363	0.798861929	2.405850662
259122_at	AT3G02210	2.294805656	1.212397685	2.011125781	2.682864313	3.163071264	6.523921491
258603_at	AT3G02990	0.934151154	0.75925257	0.999958001	0.904267731	0.78745992	1.921639666
259043_at	AT3G03440	0.651460644	0.545952529	0.73600364	0.720120675	0.826447221	1.647880205
259042_at	AT3G03450	0.549769215	1.373327617	0.674050599	0.593584619	1.132382644	2.65275757
259058_at	AT3G03470	0.676105416	0.63848057	0.634693694	0.739818848	1.277864355	2.515826199
259339_at	AT3G03900	1.460801036	1.201692948	1.118047403	1.157616259	1.924953684	4.544444528
258591_at	AT3G04360	0.53024092	0.630985738	0.538752213	0.528550135	0.548522771	1.241820759
259081_at	AT3G05030	0.888379903	0.851936617	1.236865253	1.081103203	1.244825205	3.445620149
258901_at	AT3G05640	0.4782973	0.479699	0.537260024	0.632107638	0.642375108	1.126240656

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
259061_at	AT3G07410	5.459209637	3.074651603	0.961202609	1.71293878	1.479790391	13.11639019
257522_at	AT3G08990	0.683417126	0.880469472	0.795697561	1.073444209	0.952683168	2.087879839
259142_at	AT3G10200	0.496848828	0.486751121	0.49447496	0.578648971	0.670238869	1.8391617
259150_at	AT3G10320	0.551001178	0.434154688	0.464637957	0.453300679	0.459134325	2.53004501
258959_at	AT3G10600	0.857433316	0.617479362	0.610140039	0.676841244	0.675261357	3.03716877
258760_at	AT3G10780	0.379749498	0.601098286	0.425819153	0.544940632	0.461134987	4.016914973
256441_at	AT3G10940	0.694925797	1.833408435	1.760496051	1.441422438	1.39236993	5.518156847
259235_at	AT3G11600	0.782854023	0.806309333	0.592312507	0.737983035	0.573473012	2.473228859
259102_at	AT3G11660	0.846429256	0.744359197	1.07708155	3.303106807	1.054638677	6.101256544
256660_at	AT3G12060	0.410703846	0.448718338	0.428105039	0.5014079	0.656790575	2.833448069
256235_at	AT3G12490	6.287081144	5.167505095	4.023685452	4.726158097	3.232869156	15.07387072
257054_at	AT3G15353	0.403352669	0.427119847	0.504823281	0.853536028	0.947282403	3.433616611
258270_at	AT3G15650	0.573312042	0.475105966	0.580923438	0.794987845	1.010254026	2.289033583
258434_at	AT3G16770	1.222052251	1.128073697	4.664150124	1.835295704	1.848647522	10.03969971
257896_at	AT3G16920	0.456744639	0.469034362	0.505303031	1.021016436	2.762956565	9.007360043
257060_at	AT3G18230	2.127842352	2.954827554	1.226858735	1.578909365	1.092111883	15.96315552
257718_at	AT3G18400	0.469898269	0.426163663	0.456528228	0.529526709	0.522592339	0.957836064
257722_at	AT3G18490	1.421152988	2.898608346	2.355675647	2.938719089	3.57125364	9.292028812
257750_at	AT3G18800	0.570946312	0.90658967	0.662063941	0.73724358	0.763959041	1.697357882
256652_at	AT3G18850	0.866623656	0.911588374	0.717192338	0.70858393	0.824860607	1.754525367
258021_at	AT3G19380	0.600437882	0.965585152	0.802685843	1.299269766	1.066497521	3.539915473
258008_at	AT3G19430	7.794198285	9.708857284	1.04270325	1.517235831	0.947008273	40.64884721
257962_at	AT3G19790	1.198962587	2.302570558	1.411326478	1.458660082	1.762230866	4.137350182
257976_at	AT3G20840	0.663121389	0.899554163	0.65008051	0.706000312	0.884605814	2.156009391
257544_at	AT3G20880	0.962326272	0.671356591	0.72448532	1.021175339	0.708949452	2.613448967
258183_at	AT3G21550	0.699869689	0.552403843	0.65987565	1.240448711	2.301993886	6.403479329
257262_at	AT3G21890	1.295025023	1.496124062	1.027651429	0.870693525	0.910909264	3.113035548
257264_at	AT3G22060	0.603351593	1.091636756	0.453650531	0.449235066	0.489641698	2.051857892
257260_at	AT3G22104	0.877398066	0.878288136	1.002444272	0.954362907	0.902126507	1.974659073
256833_at	AT3G22910	2.15243304	0.707313286	0.674670779	1.838059125	0.708067181	5.043807391
257769_at	AT3G23050	6.30173704	7.878960654	5.672993041	3.085502879	1.719929082	20.22766268

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
257926_at	AT3G23280	7.162227239	2.747858847	6.685023578	7.741135736	3.790138984	17.88000269
258299_at	AT3G23410	1.494240783	4.572437153	1.389050077	1.065358726	0.862667447	9.466957171
258139_at	AT3G24520	1.317509943	1.285231527	3.025257657	4.841518073	2.711870924	11.32469124
256762_at	AT3G25655	1.965975421	1.171300155	1.74990497	0.834442401	0.705963728	4.22634706
257637_at	AT3G25810	0.513716938	0.472559249	0.514513425	0.579284875	0.541688516	1.16900258
258072_at	AT3G26090	1.804705395	1.409744306	1.630407292	0.95148049	0.943449601	3.303061521
257633_at	AT3G26125	0.578995898	0.434737305	0.504175667	0.586299459	0.756388722	1.425002996
258029_at	AT3G27580	1.236233792	1.913421112	1.722552037	0.964015557	0.934987228	3.604150134
257226_at	AT3G27880	3.527127689	3.719629468	1.420224025	1.54003709	0.986170397	6.696973028
256596_at	AT3G28540	0.47671498	0.446525821	0.458267926	0.476494299	0.514283217	2.70585986
245228_at	AT3G29810	0.689209064	0.725465356	0.612370723	0.749490438	0.689220206	2.446686635
252786_at	AT3G42670	0.537503707	0.49702969	0.509398508	0.760191222	0.756946521	2.62824279
252746_at	AT3G43190	0.574931154	0.460914929	0.603112603	0.885729951	1.514842272	2.636463078
252736_at	AT3G43210	0.592284838	0.79518145	0.650360391	0.851743652	0.999723105	1.922367695
252673_at	AT3G44240	0.528368513	0.413140963	0.442911549	0.507623174	0.519860849	0.978229718
252606_at	AT3G45010	4.294368152	2.890508441	1.857316873	10.14554207	5.953386304	23.30698903
252615_at	AT3G45230	2.114286432	3.831132243	3.449498443	1.719373553	3.084167325	7.802098675
252550_at	AT3G45870	0.592367224	0.491375565	0.585452701	0.659516632	0.862719303	1.698533711
252505_at	AT3G46170	0.439690329	0.540317128	0.586242605	0.46758457	0.556112789	1.016690238
252527_at	AT3G46440	8.86063735	7.009311109	5.332749993	3.121326148	3.94418131	17.64368885
252504_at	AT3G46590	1.055071153	1.18972896	1.021954893	0.984762376	1.118311621	2.279839318
252468_at	AT3G46970	1.616089946	1.870662547	1.880926271	1.341811014	1.368275425	12.78257965
252359_at	AT3G48440	0.854726627	0.693767952	0.710579067	0.886315309	1.03676905	2.304202334
252286_at	AT3G49070	0.86279663	0.610140647	0.695913673	0.667862164	0.862569985	1.646136182
252189_at	AT3G50070	0.881074106	2.310995233	2.704177633	1.517618832	1.946937317	6.637759637
252211_at	AT3G50220	0.478963935	0.433407349	0.45801231	0.67182061	0.875954939	2.415581466
252215_at	AT3G50240	0.462782125	0.699222695	0.517042029	0.603545097	0.803236958	3.623575386
252212_at	AT3G50310	0.592078014	0.50902096	0.552577895	0.569489517	0.618097695	2.660997326
252204_at	AT3G50340	0.863174072	1.608887524	1.38026761	1.845413492	2.673709748	7.537475215
252158_at	AT3G50530	4.636622354	3.480931885	3.099796342	1.306710304	2.103983509	10.91077503
256676_at	AT3G52180	0.58302275	0.68056289	0.61532351	0.755531341	0.602919664	3.310993288

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
251994_at	AT3G52890	1.198396603	1.330347922	1.726565332	1.457132312	1.364659519	3.213442993
252019_at	AT3G53040	0.496477707	0.444254258	0.396010003	0.498816625	0.537669248	3.70425603
251937_at	AT3G53400	1.199519329	1.570442795	2.246744511	1.617115182	0.99754226	8.854162502
251961_at	AT3G53620	1.739620191	1.772530242	1.148996214	1.332000788	2.986161934	7.733918945
251906_at	AT3G53720	0.580460593	0.590228019	0.510369729	0.573921964	0.522095963	1.534999757
251912_at	AT3G53840	0.689484229	0.636667842	0.625969371	0.554885917	0.603841122	1.901677518
251900_at	AT3G54430	0.459159369	0.449500373	0.479439247	0.562723937	0.592224516	1.113563634
251835_at	AT3G55180	0.522597467	0.797273003	0.541777647	0.574383931	0.57656253	7.364575193
251792_at	AT3G55550	0.469116378	0.479644544	0.498705673	0.683964371	0.58078896	6.93125324
251753_at	AT3G55760	0.537714241	1.100573952	0.675903176	0.916929226	0.90924921	4.771614022
251768_at	AT3G55940	1.081983695	0.57952976	0.545276404	0.642834983	0.903608423	2.044173645
251770_at	AT3G55970	1.497171611	0.683712168	0.671614331	0.746874144	0.56051756	8.814273688
251739_at	AT3G56170	5.845221332	2.745583313	2.181478123	1.524059174	2.033775031	13.68958577
246293_at	AT3G56710	2.122960477	0.869829328	0.397189922	0.629976129	0.574026599	7.103895516
251660_at	AT3G57160	0.742021478	1.153045281	0.737137557	0.97349087	0.951129561	4.279634904
251592_at	AT3G57670	0.500962641	0.429277034	0.528991353	0.559566257	0.713251829	1.709974976
251533_at	AT3G58460	2.969260969	2.589710089	2.356308294	1.621779211	1.86489356	5.096091433
251521_at	AT3G59420	0.463033574	0.654733243	0.52591498	0.609181405	0.609109225	1.157200954
251436_at	AT3G59900	1.789331327	1.159509625	0.927811815	0.630568304	1.047232443	3.255744311
251393_at	AT3G60640	1.408879336	1.084432777	0.769521902	1.521380923	0.856535269	2.775005421
251377_at	AT3G60650	0.289488775	0.304211592	0.283433584	0.428527261	0.342933541	2.455450025
251342_at	AT3G60690	1.093965204	0.607842117	1.023411163	1.203737533	0.876977594	4.448814708
251321_at	AT3G61460	1.390443603	1.282974414	1.23583116	1.509831175	1.652495466	3.870344337
251326_at	AT3G61590	0.785378866	1.015403596	1.20767158	1.80902141	1.562739725	3.205998461
251282_at	AT3G61630	0.69690026	0.750141302	0.905630816	0.782091326	0.711395259	1.763857007
251293_at	AT3G61930	2.491962284	2.622812639	0.565084989	0.960619507	0.863289103	23.07389533
251297_at	AT3G62020	0.620322794	0.729620549	0.538397375	1.066458651	3.053444305	8.932660515
251249_at	AT3G62160	0.775481667	0.700257916	0.581726149	1.323440479	2.270361094	5.186434559
251266_at	AT3G62320	0.91219653	0.673335188	0.884715671	0.836667197	0.98551567	4.080372232
251160_at	AT3G63240	0.841595988	1.030951395	0.964430085	0.924974647	0.989811909	2.763227842
255701_at	AT4G00220	1.196382715	0.789148039	0.810090182	0.932956571	1.18782616	2.893682521

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
255702_at	AT4G00230	0.775874093	0.637245047	0.668372056	0.774829025	0.862779948	1.586694555
255676_at	AT4G00490	1.914745784	2.069399645	1.400827258	1.059871385	0.938010321	12.37770473
255637_at	AT4G00750	0.582515324	0.694335317	0.47951693	0.582449225	0.540809493	6.041932073
255639_at	AT4G00760	0.773477376	0.742445572	0.629305297	0.824894095	0.825513143	1.405348282
255645_at	AT4G00880	0.54515625	0.477516084	0.476591832	0.538724237	0.588637279	1.426968366
255612_at	AT4G01240	0.979768668	2.999597225	0.525421479	0.475953246	0.629311098	6.981851652
255568_at	AT4G01250	2.293608701	1.851019767	1.601168362	1.435976593	0.765670255	4.586720175
255448_at	AT4G02810	0.570364081	0.618283956	0.714924597	0.844490181	0.84661686	2.212700953
255332_at	AT4G04340	1.724820173	2.548191526	2.823531737	1.380945611	2.138520083	6.158765452
255150_at	AT4G08160	0.580363327	0.483516077	0.694120854	1.526096974	2.743233593	5.880637413
255064_at	AT4G08950	0.869421184	3.426794588	5.774096815	4.725495861	1.949048598	10.15770331
255070_at	AT4G09020	1.077269431	1.559445957	1.839736423	1.646634055	1.00688771	12.2859814
255014_at	AT4G09960	0.517289634	0.399611792	0.411655022	0.45711512	0.472565419	2.72841582
254975_at	AT4G10500	1.111419415	0.610349427	0.578653936	0.730770131	0.679372488	5.655045118
254933_at	AT4G11130	0.468994673	0.527520281	0.482483738	0.646616094	0.683405324	1.67626919
254917_at	AT4G11350	1.434415061	1.464419963	0.670237724	0.929732107	0.954279041	4.357884693
254897_at	AT4G11470	0.433410052	0.38598225	0.382253516	0.46598379	0.448218386	0.897619943
254781_at	AT4G12840	0.590722943	1.57577779	0.963564721	0.754318496	1.027160378	3.805385419
254791_at	AT4G12910	1.109324779	1.561038384	0.768759856	0.903230982	1.454446738	11.42871006
254754_at	AT4G13210	0.947394739	0.839324559	0.563161369	0.583325553	0.625080954	4.404683313
254764_at	AT4G13250	0.942724118	0.845495729	0.999165901	1.012321726	1.063823574	5.670565782
254728_at	AT4G13690	0.436582174	0.609127983	0.477100143	0.599104369	0.715980174	1.481036366
245619_at	AT4G13990	0.664560057	1.423455198	0.607397063	0.607758193	0.7572962	3.55394287
245385_at	AT4G14020	0.605909968	0.488080472	0.536506728	0.770906693	0.65971259	1.346655363
245545_at	AT4G15280	0.579792518	0.700721346	0.55987508	0.607139896	0.579844435	3.269872086
245528_at	AT4G15530	1.28820571	0.802014068	0.735714006	0.558899314	0.609031604	7.721086434
245517_at	AT4G15840	2.143239433	1.171468394	2.09126459	1.857027652	1.631724954	3.836068051
245276_at	AT4G16780	1.465578003	1.230108416	0.946813725	1.156055812	2.045806268	4.043112271
245405_at	AT4G17150	0.845078611	1.212454607	2.289678821	1.644077235	0.970781656	4.434500773
254702_at	AT4G17940	5.469494548	4.785564404	3.666099508	2.74937935	2.165322564	13.23751168
254668_at	AT4G18350	0.518362294	0.454642558	0.474924015	0.56302025	0.555959799	3.256530125

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254629_at	AT4G18425	1.184739614	0.794800168	0.555657787	1.31331781	2.422493683	5.135165273
254674_at	AT4G18450	0.758485618	0.60703842	0.467680017	0.567545523	0.618946767	3.74772972
254605_at	AT4G18950	5.758792699	4.33779384	4.53447945	4.086298274	1.674250875	10.84896754
254575_at	AT4G19460	0.784913493	1.409862697	0.438068982	0.63367758	0.517573267	8.438997229
254551_at	AT4G19840	0.667540317	0.582289674	0.686143864	1.213708718	0.997795475	4.383489486
254349_at	AT4G22250	0.640995046	1.825675406	0.746675442	0.545884062	0.854849771	3.414572882
254304_at	AT4G22270	0.717006115	0.617918813	1.138092072	1.120343915	0.854619474	2.856459724
254299_at	AT4G22920	0.707087569	0.635076601	0.838221333	0.976206192	1.283890678	2.341911872
254293_at	AT4G23060	1.059854832	0.790206457	2.798013433	1.870144271	0.831363929	7.040374209
254188_at	AT4G23920	0.764948919	0.992165921	0.85050841	0.810010032	0.761858326	5.65960925
254115_at	AT4G24710	0.557063584	0.866906835	0.723606839	0.7823132	0.910653103	2.911801787
254068_at	AT4G25450	0.86901689	1.077505354	1.307370721	1.513541724	1.763198555	3.537169365
253956_at	AT4G26700	0.516855723	1.186757937	1.586305028	0.730543009	0.568309696	7.282314161
253936_at	AT4G26880	1.160351865	2.852178106	0.570860401	0.670873294	0.546156233	15.13774755
253908_at	AT4G27260	1.825740535	0.859706711	1.023634587	1.741403579	1.548541546	3.608839775
253914_at	AT4G27400	3.940805244	5.66465752	1.107604774	1.397434396	0.974307366	24.31015063
253875_at	AT4G27520	0.896983361	0.786655055	0.695082345	0.906299677	0.827214689	10.38667226
253801_at	AT4G28170	0.559093488	0.590519233	0.568691323	0.647765473	0.598271008	1.162074136
253806_at	AT4G28270	1.204177325	0.604549367	1.258593465	1.918585919	1.367866369	3.909267145
253814_at	AT4G28290	2.6592563	1.096716157	1.883987916	3.944527349	2.032229622	10.55557382
253791_at	AT4G28640	0.751011081	0.594189563	0.599869429	0.660305581	0.96317004	2.107150499
253794_at	AT4G28720	0.797578155	1.698835676	0.552736504	1.036833203	1.474441192	13.49733603
253696_at	AT4G29740	0.732908065	0.522986545	0.622839388	0.612997145	0.68068838	1.526985121
253650_at	AT4G30020	0.793790254	2.239405748	1.915601023	1.57299533	2.259031741	4.684132876
253501_at	AT4G32010	1.039314567	0.978991241	0.865843912	0.851207743	1.595904531	2.808831484
253475_at	AT4G32290	0.6981919	1.281433769	0.812219996	1.247447771	1.176761614	2.624613252
253382_at	AT4G33040	0.785341382	0.843499059	0.769188083	1.119300986	0.76504856	2.7138548
253299_at	AT4G33800	0.542787485	1.194414803	0.619801001	0.764523642	0.886873215	3.62120818
253215_at	AT4G34950	0.764209017	0.61317408	0.711439483	0.778096843	2.353990897	5.862766834
253217_at	AT4G34970	0.438609892	0.567325745	0.673278118	1.027390094	0.606466938	31.26792361
253155_at	AT4G35720	0.544205271	0.66248831	0.496311974	0.584895657	0.543764212	5.212393745

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
253126_at	AT4G36050	0.675695558	0.6570104	0.737060483	0.8313574	0.892562612	1.788965452
246195_at	AT4G36410	0.554214221	0.487150407	0.555934776	0.750254202	0.787053975	1.380138374
246235_at	AT4G36830	1.333007834	0.780417814	1.499448139	1.036838292	0.825946909	3.889680099
246212_at	AT4G36930	0.559123208	1.040378121	0.660169772	0.852105508	1.210073511	2.866827404
253043_at	AT4G37540	1.720362591	1.40816851	1.509435404	1.452110545	1.767184079	3.872536883
253066_at	AT4G37770	1.077637437	1.33369924	0.794242372	0.964342826	0.919902496	3.577688233
253041_at	AT4G37870	7.537916128	9.97938133	4.447365503	8.763187472	2.247581486	22.3507648
253011_at	AT4G37890	0.585751582	0.655241857	0.631972013	1.33736574	1.063731082	6.185022939
253014_at	AT4G37940	0.947091397	1.577845314	1.237725848	1.199093985	1.540377886	6.462853956
253008_at	AT4G38210	0.620157904	0.708683516	0.902660061	0.98440474	0.755124689	1.797619959
252988_at	AT4G38410	0.699330679	1.446998836	0.64742928	3.297380112	0.959505604	14.01341893
252956_at	AT4G38580	0.660016776	0.654422323	0.648822431	1.151286819	1.875238908	3.502544232
252944_at	AT4G39320	0.471874739	0.435983324	0.722200708	0.603254148	0.800901767	1.466650824
252860_at	AT4G39790	0.585100471	0.615273355	0.560303565	0.754317757	0.78462028	1.439033382
251123_at	AT5G01030	0.957319275	0.946220693	1.051869323	1.067823813	1.123370081	6.824614582
251131_at	AT5G01190	0.855651199	0.667039464	0.587205123	0.599914878	1.412686766	2.444735372
251081_at	AT5G02070	0.425524058	0.516762277	0.391179132	0.455594915	0.446244677	6.908253358
250991_at	AT5G02380	5.686911269	11.10016314	4.147878445	10.92918398	13.21379315	40.13904887
250958_at	AT5G03260	0.709866731	0.629133206	0.923757156	1.466552665	3.153410459	7.747603065
250906_at	AT5G03650	0.681058619	1.125368942	1.271657887	1.148177732	1.22582448	3.666116405
250881_at	AT5G04080	0.360441122	0.350348368	0.354795591	0.48689885	0.498576845	0.897243882
245697_at	AT5G04200	1.135291414	1.840259495	0.543594787	0.787330505	1.264724587	3.22058506
250848_at	AT5G04510	1.650606012	1.482018357	2.095451108	1.334465863	1.836310145	3.953630208
250803_at	AT5G04980	0.589938708	0.618054895	0.659120979	0.627502279	0.656812956	2.021853202
250811_at	AT5G05110	1.022433048	0.794081256	1.022439105	1.096344857	0.946941995	3.093028677
250738_at	AT5G05730	3.337589361	2.466662848	3.047625947	4.199868601	2.621611485	10.85788307
250753_at	AT5G05860	0.769737928	0.630252875	1.641188798	1.363813266	1.406018116	3.050593879
250724_at	AT5G06330	0.846510873	0.755666112	1.074023265	1.620902052	0.922245969	4.232520866
250737_at	AT5G06370	2.226879082	1.329012622	2.248939749	2.542420333	2.618246278	4.488117005
250728_at	AT5G06440	0.634382184	0.4978804	0.713176063	0.750299822	0.500082656	2.142713661
250610_at	AT5G07550	0.456446995	0.497642759	0.443666109	0.470484536	0.53505752	1.674502172

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
245891_at	AT5G09220	0.806051504	0.651750176	1.130147331	3.579533394	1.684735385	10.60277697
250511_at	AT5G09960	1.909746873	2.090943333	2.616941276	1.923860912	1.443210931	13.97548729
250435_at	AT5G10380	0.494075743	0.462147752	0.51103359	0.62000391	0.578910008	1.306982064
250426_at	AT5G10510	0.668176262	1.862268333	0.738333905	1.11206236	1.086969056	3.860872823
250322_at	AT5G12870	0.738645377	0.510825421	0.658075669	0.754672015	1.498003406	2.851190175
250205_at	AT5G14020	2.557176354	4.104953746	4.527073255	1.0349707	0.964414086	8.449370311
250194_at	AT5G14550	1.34871483	1.519550642	1.841086359	1.111983117	1.604031897	3.851620469
250149_at	AT5G14700	1.533845791	1.194253396	1.607370065	2.366153464	0.823944576	5.23823574
246600_at	AT5G14930	0.781630889	0.690001849	0.791410719	0.531192598	0.512629937	1.902821385
250155_at	AT5G15160	0.539725031	1.148603288	0.401279464	0.451711136	0.492528703	4.549563732
246554_at	AT5G15450	0.859494316	1.225902724	1.286626429	1.798980103	1.382292504	4.178516501
246511_at	AT5G15490	11.26141053	10.01382887	7.129351902	3.732729143	11.74420033	20.21091684
246512_at	AT5G15630	0.96913106	0.715504177	0.742665659	0.925994676	2.067467693	4.257975042
246493_at	AT5G16180	0.508006797	0.500070388	0.625887305	0.617110326	0.631211024	1.248232949
246502_at	AT5G16240	0.810559418	0.927881435	0.742501365	0.700861517	0.875851047	1.660640452
250120_at	AT5G16490	0.683562012	0.63883128	0.693723218	0.969508085	2.007670068	3.862189094
246434_at	AT5G17520	1.14858156	2.481361567	1.757371851	1.137593967	1.233820211	10.84250762
249986_at	AT5G18460	0.905095015	2.545598976	0.708202824	0.674954671	1.429034398	6.474347149
249983_at	AT5G18470	2.195443782	0.694286069	2.298939357	1.048376672	0.758143541	7.927864673
246138_at	AT5G19870	0.445141795	0.401943505	0.434766622	0.613541087	0.894129989	2.019339144
246097_at	AT5G20270	0.697775871	0.78487996	0.643050086	1.640795164	0.695895842	3.073895348
246117_at	AT5G20320	1.001669937	0.868123893	0.898799753	1.012530374	0.983544325	1.73355434
245998_at	AT5G20830	0.574777093	0.755190259	0.543545537	0.964653931	0.736019147	2.289918084
249897_at	AT5G22550	0.894948204	0.688443661	0.665960611	0.585331881	0.429490515	2.227676349
249879_at	AT5G23170	0.655233105	0.566424801	0.621682127	0.869495752	1.133977027	2.843420346
249752_at	AT5G24660	0.570769115	0.789685322	1.031549613	0.964799305	0.765154652	4.568933606
246922_at	AT5G25110	0.695556683	0.602064316	1.412392302	0.807445616	1.100902095	4.543991319
246829_at	AT5G26570	0.79953071	0.95868115	0.852413263	1.10588302	1.034037888	6.229702577
246820_at	AT5G26910	0.87915415	0.825842129	1.226506115	1.030944559	1.137358722	2.877694935
246822_at	AT5G26960	0.935690665	0.886664971	0.761527381	0.990046011	1.137192764	2.186858625
246814_at	AT5G27200	0.660973845	0.654116901	0.736170604	0.660713765	0.65821436	1.524119241

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
246682_at	AT5G33290	1.116779422	0.960511096	0.819910116	0.605586938	0.726155817	2.360702268
249719_at	AT5G35735	6.857109139	7.521765978	6.322074785	11.02987034	2.966954676	23.63065699
249631_at	AT5G37160	0.489308017	0.412584971	0.451141211	0.453800583	0.527752022	1.998935241
249574_at	AT5G37660	0.675059521	0.582537288	0.60270507	0.810761426	1.083956604	3.221560596
249532_at	AT5G38780	0.414585949	0.525784377	0.387226261	0.422973867	0.490061633	1.350745081
249420_at	AT5G39820	0.52732977	0.760410642	0.467592786	0.475974444	0.499355338	6.433625418
249432_at	AT5G39930	0.43749783	0.463313808	0.411921672	0.471942348	0.477148354	0.926599038
249439_at	AT5G40020	0.538366003	0.483933386	0.56823499	1.649937755	2.757445933	8.16526008
249202_at	AT5G42580	1.332205567	0.950723308	4.617341408	1.338114841	1.337921256	8.897609397
249174_at	AT5G42900	0.614852083	0.419328472	0.464752029	0.81617361	0.701040755	1.450017994
249126_at	AT5G43380	0.699582889	0.517451706	0.748738044	1.394584032	1.103454827	2.423601419
248964_at	AT5G45340	3.716722699	3.158281808	4.309841865	5.315920739	1.557321065	12.84361996
248961_at	AT5G45650	0.991228181	0.682456611	1.128175159	0.812500647	0.859792466	2.317309433
248909_at	AT5G45810	1.607369652	1.087312079	0.659510776	1.073978521	0.896802631	5.058460145
248926_at	AT5G45880	0.715364743	1.014789881	0.657441559	0.677444572	0.661035933	2.609302678
248928_at	AT5G45970	0.531592688	0.43243053	0.488918533	0.584377657	0.933735239	1.595326793
248887_at	AT5G46115	0.380589204	0.421358935	0.388242545	0.44895673	0.617778031	1.180374445
248819_at	AT5G47050	2.886134524	2.132430401	4.418930996	4.380353075	1.854452651	7.959267711
248789_at	AT5G47440	0.819083045	0.545557916	0.563514421	0.793801364	0.885363017	1.860920699
248740_at	AT5G48130	0.663353486	0.727133188	0.583341817	0.640896847	0.676022638	6.627058352
248687_at	AT5G48300	0.916413298	2.059851324	2.848184557	1.453096003	1.181467552	7.929884872
248642_at	AT5G49120	0.399587563	0.613886596	0.39821361	0.445067359	0.546093036	1.058165734
248590_at	AT5G49660	0.650509556	0.51482862	0.601068064	0.898435274	0.910018374	1.774110957
248558_at	AT5G49990	0.602949138	0.705941284	0.919294148	0.868597093	0.908532032	1.721949703
248476_at	AT5G50890	0.665946829	0.616019595	0.616136101	0.699230107	0.797178163	1.586927629
248431_at	AT5G51470	0.64112711	1.161951654	0.544975214	0.510783677	0.537598071	12.3520676
248419_at	AT5G51550	0.60123313	0.852453186	0.774867244	1.652650134	1.595085808	10.46652041
248380_at	AT5G51820	0.609665588	1.240640798	1.254356105	1.185377184	1.389474153	3.307224682
248382_at	AT5G51890	0.645501438	0.568550404	0.86865237	3.393877245	9.054448674	21.23891141
248286_at	AT5G52870	0.543759866	0.428121937	0.417796932	0.5626026	0.533440949	1.005167944
248273_at	AT5G53500	1.159342846	1.254724904	0.907760303	0.890425733	0.933703704	2.439402732

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
248237_at	AT5G53890	0.414354827	1.649067209	0.637678233	0.693032809	0.762995496	4.992243001
248178_at	AT5G54370	18.48790635	23.28176478	4.296540418	5.09936747	3.98019371	39.72959186
248121_at	AT5G54690	0.725626103	0.653840628	0.691223509	1.063336047	2.683894152	7.263942264
248128_at	AT5G54770	0.843382955	0.635837461	0.745897328	0.827622461	0.905816157	2.00945696
248112_at	AT5G55350	0.732159085	0.761046333	0.618035457	0.684472922	0.759613347	1.381379995
248039_at	AT5G55950	1.11045917	0.617584526	0.5757121	0.63452781	0.908094048	4.102639036
247985_at	AT5G56790	0.584552573	1.558928726	0.702256958	1.840669528	1.489713442	5.557715459
247902_at	AT5G57350	0.391818645	0.389178958	0.50844213	0.954182909	1.236064058	2.115044224
247904_at	AT5G57390	0.687628278	0.79024362	0.545933011	0.695999708	0.757795431	1.53431071
247906_at	AT5G57420	0.529294152	0.965101974	0.535595561	0.598004156	0.578934239	7.133839124
247922_at	AT5G57500	1.653706362	2.641620634	0.594456799	0.534786159	0.554297975	10.46591799
247874_at	AT5G57710	2.74115951	0.801775378	2.430591658	1.217427689	1.14768196	6.623166452
247802_at	AT5G58580	0.604900239	0.58306803	0.524489093	0.567920904	0.633695384	4.820230919
247657_at	AT5G59845	0.413615018	0.402336988	0.430311203	0.720401675	1.02339283	2.313975711
247648_at	AT5G60020	0.813210685	0.620237503	0.847322453	1.870649392	3.835543361	11.9749517
247645_at	AT5G60530	12.00702679	17.29816401	1.59701466	2.064784359	2.030307417	35.49825113
247640_at	AT5G60610	0.480573566	0.47656389	0.450237807	0.549668026	0.540177965	1.055521737
247610_at	AT5G60630	0.886071592	1.822479086	0.714313476	0.802855126	0.770288438	11.9491666
247611_at	AT5G60710	2.03286624	1.847249134	0.902368894	1.243596081	1.205812586	4.412537908
247590_at	AT5G60720	0.50953244	0.465960172	0.490389869	0.823727899	1.864411722	4.312054673
247601_at	AT5G60850	0.675104404	0.811581132	1.249027808	1.284098285	1.529862526	2.800941461
247452_at	AT5G62430	0.808871615	0.775539721	0.868457047	1.267555883	0.974201478	3.558718677
247437_at	AT5G62490	0.597450018	0.547807389	0.539498523	0.605550068	0.649154332	1.137315977
247331_at	AT5G63530	1.358353438	1.237046515	1.212913341	1.679973281	2.100226126	4.613528631
247304_at	AT5G63850	0.613649876	0.669684968	0.681963023	0.941945753	0.951465474	3.240742222
247282_at	AT5G64240	0.808492614	0.632255481	0.851121819	1.181370955	1.112640031	2.689984388
247216_at	AT5G64860	0.460017798	0.985349685	0.889777062	0.970378999	1.083707703	3.164627385
247208_at	AT5G64870	1.585871321	0.565475387	0.766433974	2.145436517	1.194140582	3.858925995
247153_at	AT5G65700	1.897998499	3.837805391	2.520141344	3.845329843	4.163937074	7.658920779
247094_at	AT5G66280	11.74170366	12.19740175	6.372605076	1.992078755	1.794353315	26.8203055
247038_at	AT5G67160	0.723109343	0.637300244	0.954726703	1.167513324	1.140562744	2.267031087

Supplementary Tables pertaining to Figure 3
Supplementary Table S19. Loci enriched in individual cell types from microarray data

Loci enriched in Columella (PET111) from micorarray expression data analysis (1.7 fold, p <0.5)

		Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
247031_at	AT5G67230	0.667415395	0.534395919	0.578653785	0.70109185	1.49277047	2.661167414
246986_at	AT5G67280	0.592058775	0.721559269	0.982531056	1.122682834	1.130857144	2.815581723

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
259486_at	AT1G15710	prephenate dehydrogenase family protein, contains Pfam profile: PF02153 prephenate dehydrogenase	3.349547712	1.955732468	1.446796127	1.159425507	1.409721486	1.417230051
260899_at	AT1G21370	expressed protein	11.02950709	4.090569886	5.777314045	3.107166852	2.879492743	4.645647995
265102_at	AT1G30870	cationic peroxidase, putative, similar to cationic peroxidase (gi:1232069); similar to EST gb:AI100412	29.26649439	6.119595789	1.215674212	2.232677527	4.666007882	1.479413597
262641_at	AT1G62730	expressed protein	2.504203579	1.400996357	1.035569994	0.883670474	1.146095388	0.994338229
261550_at	AT1G63450	exostosin family protein, contains Pfam profile: PF03016	9.996851076	2.072149195	0.61475174	0.677585192	1.108367087	0.904885377

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
263565_at	AT2G15390	FUT4_ATFUT4__xyloglucan fucosyltransferase, putative (FUT4), identical to SP:Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SP:Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}	3.793711249	1.854523242	1.722786581	0.750288885	0.842964194	0.682665858
267160_at	AT2G37670	WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similiar to rab11 binding protein (GI:4512103) (Bos taurus)	1.9831187	0.821726928	0.658934544	0.527714229	0.621620215	0.839815341

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
245172_at	AT2G47540	pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family	32.96739091	9.699127898	1.158309845	1.433289202	2.356085561	1.083314431
257924_at	AT3G23190	lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum)	21.72218486	3.259058347	1.083496123	1.042912533	1.611341643	1.042869254
257144_at	AT3G27300	G6PD5__glucose-6-phosphate 1-dehydrogenase / G6PD (ACG9), identical to glucose-6-phosphate 1-dehydrogenase (acg9) (Arabidopsis thaliana) GI:5732195	6.868998452	3.307803561	0.913901483	1.479300066	1.013707473	1.064181043

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
251973_at	AT3G53180	glutamine synthetase, putative, similar to glutamine synthetase (glutamate--ammonia ligase) (Bacillus subtilis) SWISS-PROT:P12425	17.44707864	5.487026304	7.01058528	3.266296095	2.062995207	1.994137427
255005_at	AT4G09990	expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)	23.18906269	6.882259296	1.22080574	1.440892545	3.997105863	4.500734934

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
245484_at	AT4G16210	enoyl-CoA hydratase/isomerase family protein, similar to 3-hydroxybutyryl-CoA dehydratase (Crotonase) from Clostridium acetobutylicum (SP:P52046), FadB1x (enoyl-CoA hydratase) from Pseudomonas putida (GI:13310130); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein	7.255701671	3.227990117	3.411651512	1.934220883	1.75728261	1.863429591

Supplementary Tables pertaining to Figure 3

Supplementary Table S20. Root cell type biomarkers

Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254468_at	AT4G20460	NAD-dependent epimerase/dehydratase family protein, similar to UDP-galactose 4-epimerase from Cyamopsis tetragonoloba GI:3021357 (EMBL:AJ005082), Bacillus subtilis SP:P55180; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	13.0876895	4.470302291	3.746529008	3.537187832	1.671318347	1.008696536
253998_at	AT4G26010	peroxidase, putative, peroxidase ATP13a - Arabidopsis thaliana, PID:e264765; identical to cDNA class III peroxidase ATP35, GI:17530565	9.313683744	3.343634451	1.56439787	3.970742651	4.182537327	1.419425618
254521_at	AT5G44820	expressed protein, similar to unknown protein (pir::T04881)	6.841962989	1.916413575	0.980855352	0.478916603	0.663954812	0.536020969

Supplementary Tables pertaining to Figure 3

Supplementary Table S20. Root cell type biomarkers

Root Hair Biomarkers: Proteins Identified Only in Root Hairs (COBL9) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
248652_at	AT5G49270	COBL9; phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region	26.35831667	7.037165721	1.699631882	1.95741069	2.557357167	1.480283545
248562_at	AT5G49680	cell expansion protein, putative, similar to SABRE (Arabidopsis thaliana) GI:719291	4.531574955	2.098588537	0.756013934	0.716298602	0.841458557	1.624108895
248162_at	AT5G54500	FQR1__quinone reductase, putative, similar to 1,4-benzoquinone reductase (Phanerochaete chrysosporium)(GI: 4454993); contains flavodoxin domain PF00258	18.76963794	5.053339414	10.44207374	10.17027372	6.89654573	7.866507718

Supplementary Tables pertaining to Figure 3

Supplementary Table S20. Root cell type biomarkers

Root Hair Biomarkers: Proteins Identified Only in Non-Hair Epidermis (WER) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
255751_at	AT1G31950	terpene synthase/cyclase family protein, similar to sesquiterpene synthases (GI:11934937)(Lycopersicon hirsutum), (GI:11934933)(Lycopersicon esculentum); contains Pfam profile: PF01397: Terpene synthase family	1.351196296	6.825177784	3.500261546	0.822523685	0.989691043	0.963566385
264702_at	AT1G70190	ribosomal protein L12 family protein, contains similarity to ribosomal protein GI:7270590 from (Arabidopsis thaliana)	0.739737901	3.303000341	0.75827552	0.621033329	0.870659702	0.655652956
251938_at	AT3G53430	60S ribosomal protein L12 (RPL12B), 60S RIBOSOMAL PROTEIN L12, Prunus armeniaca, SWISSPROT:RL12_PRUAR	16.18203296	35.61462681	12.30807521	15.00948713	20.18923067	9.19847477

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Non-Hair Epidermis (WER) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
250992_at	AT5G02260	ATEXPA9_ATEXP9_ATHEXP ALPHA 1.10_EXP9__expansin, putative (EXP9), similar to expansin precursor GI:4138914 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069	3.221214528	13.77040078	2.588498013	0.627560987	0.801968371	5.401973136
246537_at	AT5G15940	short-chain dehydrogenase/reductase (SDR) family protein, similar to forever young oxidoreductase GI:18138083 from (Lycopersicon esculentum)	1.076284251	2.056433692	0.631369091	0.624907332	0.700810651	0.84019682

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Non-Hair Epidermis (WER) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
245937_at	AT5G19750	peroxisomal membrane 22 kDa family protein, similar to SP:P42925 22 kDa peroxisomal membrane protein {Mus musculus}; contains Pfam profile PF04117: Mpv17 / PMP22 family	1.593756009	4.494213166	2.38800243	1.481674134	2.026796007	1.103139917
248131_at	AT5G54830	DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein, contains Pfam PF03351: DOMON domain	0.977162769	2.262576459	0.880080333	0.631129624	0.853943056	0.882128914

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Cortex (CORTEX) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**

Affymetrix Probeset	Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
262626_at	AT1G06430	FTSH8__encodes a FtsH protease that is localized to the chloroplast	0.808416069	0.618892735	1.514055517	0.68734792	0.659110202	0.648147836
265768_at	AT2G48020	sugar transporter, putative, similar to ERD6 protein {Arabidopsis thaliana} GI:3123712, sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein	4.754682848	2.089936802	16.80413015	5.094057004	1.839738676	1.449043374

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Cortex (CORTEX) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254630_at	AT4G18360	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) (Spinacia oleracea) SWISS-PROT:P05414	0.576257218	0.527075562	5.065594153	2.646667624	1.312830113	0.655002869
250868_at	AT5G03860	malate synthase, putative, strong similarity to glyoxysomal malate synthase from Brassica napus (SP:P13244)	0.496188472	0.573808707	3.087789526	0.815536156	0.826471808	0.725850922

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Cortex (CORTEX) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
250558_at	AT5G07990	TT7_CYP75B1_D501_F3`H__flavonoid 3`-monooxygenase / flavonoid 3`-hydroxylase (F3`H) / cytochrome P450 75B1 (CYP75B1) / transparent testa 7 protein (TT7), identical to SP:Q9SD85 Flavonoid 3`-monooxygenase (EC 1.14.13.21) (Flavonoid 3`-hydroxylase) (AtF3`H) (Cytochrome P450 75B1) (TRANSPARENT TESTA 7 protein) {Arabidopsis thaliana}; similar to gi:10334806, gi:10334808	0.817240809	0.621390615	5.537829487	0.927530283	0.703498577	0.630117798

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Cortex (CORTEX) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
249103_at	AT5G43600	N-carbamyl-L-amino acid hydrolase, putative, similar to N-carbamoyl-L-amino acid hydrolase (Bacillus stearothermophilus) SWISS-PROT:Q53389	1.45051364	1.149183091	5.262393229	2.102404475	1.347563472	1.106460077
248625_at	AT5G48880	PKT1_PKT2_KAT5__acetyl-CoA C-acyltransferase 1 / 3-ketoacyl-CoA thiolase 1 (PKT1), identical to 3-keto-acyl-CoA-thiolase 1 (Arabidopsis thaliana) GI:3169568	0.559471197	0.586753866	13.47556429	1.836359331	1.593518704	0.84012408

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Vasculature (WOL) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
264577_at	AT1G05260	RCI3_RCI3A__peroxidase 3 (PER3) (P3) / rare cold-inducible protein (RCI3A) (PRC), identical to SP:O23044 Peroxidase 3 precursor (EC 1.11.1.7) (Atperox P3) (Rare cold inducible protein) (RCI3A) (ATPRC) {Arabidopsis thalliana}	0.564368249	0.560940597	2.659246989	40.82502385	5.410111954	2.730636285
258599_at	AT3G04520	threonine aldolase family protein, similar to L-allo-threonine aldolase SP:O07051 from (Aeromonas jandaei)	0.821334497	0.552455686	0.979868036	7.145580645	1.511893769	0.755172685
254914_at	AT4G11290	peroxidase, putative, identical to peroxidase ATP19a (Arabidopsis thaliana) gi:1546692:emb:CAA67337	0.565817953	0.545293347	1.859108996	27.61945523	3.294022124	1.811716645

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Vasculature (WOL) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values					
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
259845_at	AT1G73590	PIN1_ATPIN1__auxin efflux carrier protein, putative (PIN1), identical to putative auxin efflux carrier protein; AtPIN1 (Arabidopsis thaliana) GI:4151319; contains Pfam profile PF03547: Auxin Efflux Carrier	0.487984325	0.703257517	0.639713019	1.355269884	3.610757418	1.306435661
267619_at	AT2G26730	leucine-rich repeat transmembrane protein kinase, putative	0.559910072	0.565351177	1.689281303	2.233293272	4.662284992	1.618735746

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Vasculature (WOL) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
252080_at	AT3G51670	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) {Glycine max};; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus	0.75454331	1.483261543	1.020834087	1.359294791	13.41430964	3.039716489
250752_at	AT5G05690	CPD_CBB3_CYP90_CYP90A_CYP90A1_DWF3__cytochrome P450 90A1 (CYP90A1) (CYP90) (CPD), identical to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana)	0.498687082	0.455701464	1.084214274	1.184458522	9.572112938	2.149987175
248710_at	AT5G48480	expressed protein	0.768893903	0.758998579	1.008811405	3.941432389	7.391342609	3.055191502

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, p < 0.05) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
264868_at	AT1G24090	RNase H domain-containing protein, very low similarity to GAG-POL precursor (Oryza sativa (japonica cultivar-group)) GI:5902445; contains Pfam profiles PF00075: RNase H, PF04134: Protein of unknown function, DUF393	1.026986468	1.297623136	0.660953725	0.675622749	0.862376349	3.162785539
259596_at	AT1G28130	GH3.17__encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro. Lines carrying insertions in this gene are hypersensitive to auxin.	0.922299228	4.252448464	6.137153328	0.97269172	0.783271009	14.55181411
261191_at	AT1G32900	PRPL11__starch synthase, putative, similar to starch synthase SP:Q42857 from (Ipomoea batatas)	0.498713533	0.636174092	0.494302892	0.765150666	0.574659852	6.074222165

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
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				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
245200_at	AT1G67850	expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)	1.442825273	1.834116749	0.647329363	0.764456889	0.747596582	5.214628172
260412_at	AT1G69830	AMY3_ATAMY3__ Encodes a plastid-localized α-amylase. Expression is reduced in the SEX4 mutant. Loss of function mutations show normal diurnal pattern of starch accumulation/degradation. Expression follows circadian rhythms.	1.095360705	1.082380349	1.018447804	1.502215975	0.981259354	10.20923026
262263_at	AT1G70940	PIN3__auxin transport protein, putative (PIN3), similar to auxin transport protein (Arabidopsis thaliana) gi:5817301:gb:AAD52695	0.707884827	0.546792208	0.723203581	1.363499065	2.345246381	4.870658555

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
265339_at	AT2G18230	inorganic pyrophosphatase (soluble) (PPA) / pyrophosphate phospho-hydrolase / PPase, nearly identical to SP:P21216 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase) {Arabidopsis thaliana}	0.905484121	2.214958552	0.94334052	1.268431038	2.067148368	10.13001601
263544_at	AT2G21590	APL4__glucose-1-phosphate adenylyltransferase large subunit, putative / ADP-glucose pyrophosphorylase, putative, strong similarity to SP:P55231	0.361028405	0.374044187	0.350489549	0.408029724	0.414706508	1.675974802

Supplementary Tables pertaining to Figure 3
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Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
266221_at	AT2G28760	NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	3.071895916	4.293910444	0.949992378	1.297223548	2.313995376	10.33180752
266225_at	AT2G28900	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17	0.692390402	1.401759043	0.697178382	1.842415061	0.986624111	11.48191735

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	Locus	Annotation	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)
266925_at	AT2G45740	peroxisomal biogenesis factor 11 family protein / PEX11 family protein, contains Pfam profile PF05648: Peroxisomal biogenesis factor 11 (PEX11)	1.086127975	0.822001584	1.048094126	0.789069392	0.787684043	2.721555455
256676_at	AT3G52180	protein tyrosine phosphatase/kinase interaction sequence protein (PTPKIS1), identical to PTPKIS1 protein (Arabidopsis thaliana) GI:11595504; contains Pfam profile PF00782: Dual specificity phosphatase, catalytic domain	0.58302275	0.68056289	0.61532351	0.755531341	0.602919664	3.310993288

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
251739_at	AT3G56170	CAN__Ca(2+)-dependent nuclease, identical to Ca(2+)-dependent nuclease (Arabidopsis thaliana) GI:7684292; supporting cDNA gi:7684291:dbj:D84226.1:	5.845221332	2.745583313	2.181478123	1.524059174	2.033775031	13.68958577
255637_at	AT4G00750	dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase	0.582515324	0.694335317	0.47951693	0.582449225	0.540809493	6.041932073
254575_at	AT4G19460	glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1	0.784913493	1.409862697	0.438068982	0.63367758	0.517573267	8.438997229

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
254188_at	AT4G23920	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP:Q42605, Cyamopsis tetragonoloba GI:3021357 (AJ005082)	0.764948919	0.992165921	0.85050841	0.810010032	0.761858326	5.65960925
254068_at	AT4G25450	ATNAP8__ABC transporter family protein, similar to multidrug resistance protein 2 SP:P21440 from (Mus musculus)	0.86901689	1.077505354	1.307370721	1.513541724	1.763198555	3.537169365

Supplementary Tables pertaining to Figure 3

Supplementary Table S20. Root cell type biomarkers

Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
253914_at	AT4G27400	late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543	3.940805244	5.66465752	1.107604774	1.397434396	0.974307366	24.31015063

Supplementary Tables pertaining to Figure 3
Supplementary Table S20. Root cell type biomarkers
Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
246511_at	AT5G15490	UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	11.26141053	10.01382887	7.129351902	3.732729143	11.74420033	20.21091684

Supplementary Tables pertaining to Figure 3

Supplementary Table S20. Root cell type biomarkers

Root Hair Biomarkers: Proteins Identified Only in Columella (PET111) that were also enriched in this cell type (1.7 fold, $p < 0.05$) in RNA expression data

				Mean Microarray Expression Values				
Affymetrix Probeset	**Locus**	**Annotation**	**Root Hairs (COBL9)**	**Non-Hair Epidermis (WER)**	**Cortex (CORTEX)**	**Endodermis/ Quiescent (SCR)**	**Vasculature (WOL)**	**Columella (PET111)**
247094_at	AT5G66280	GMD1__GDP-D-mannose 4,6-dehydratase, putative, strong similarity to GDP-D-mannose-4,6-dehydratase (Arabidopsis thaliana) GI:1764100	11.74170366	12.19740175	6.372605076	1.992078755	1.794353315	26.8203055

Supplementary Tables pertaining to Figure 3

Supplementary Table S21. Proteins of the root cellular proteome with gene ontology (GO) annotations associated with the cell wall

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	GO Identifier	GO Description
AT1G04040	1	0	1	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G04980	1	0	1	0	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G11580	0	0	1	1	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G14080	1	1	0	0	1	1	GO:0042546	cell wall biosynthesis
AT1G27450	1	0	0	0	0	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G30620	0	0	0	0	1	1	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
AT1G35620	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G53840	1	1	1	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT1G55850	1	1	1	0	0	0	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
							GO:0016759	cellulose synthase activity
AT1G72730	0	0	1	0	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT2G01720	1	1	1	0	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT2G01970	1	0	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT2G15390	1	0	0	0	0	0	GO:0042546	cell wall biosynthesis
AT2G28790	0	0	0	1	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT2G30490	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT2G47470	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT3G02880	1	0	1	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT3G03220	0	0	0	0	1	0	GO:0009831	cell wall modification during multidimensional cell growth (sensu Magnoliophyta)
AT3G03050	1	0	0	0	0	0	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
							GO:0016759	cellulose synthase activity
AT3G03060	0	1	0	1	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT3G07330	0	1	0	0	0	0	GO:0016759	cellulose synthase activity

Supplementary Tables pertaining to Figure 3

Supplementary Table S21. Proteins of the root cellular proteome with gene ontology (GO) annotations associated with the cell wall

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	GO Identifier	GO Description
AT3G08550	1	0	0	0	0	0	GO:0009831	cell wall modification during multidimensional cell growth (sensu Magnoliophyta)
							GO:0030244	cellulose biosynthesis
AT3G13870	1	1	1	0	1	1	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
AT3G27280	1	1	1	1	0	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT3G57030	0	0	0	0	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT3G62360	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT4G11150	1	1	1	1	1	1	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
AT4G12420	0	1	1	0	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT4G18030	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT4G20830	1	0	0	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT4G21150	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT4G32410	1	1	1	1	1	0	GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
							GO:0009833	primary cell wall biosynthesis (sensu Magnoliophyta)
							GO:0030244	cellulose biosynthesis
							GO:0016759	cellulose synthase activity
AT5G02260	0	1	0	0	0	0	GO:0009831	cell wall modification during multidimensional cell growth (sensu Magnoliophyta)
AT5G04960	1	0	0	0	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G05170	1	1	1	1	1	0	GO:0009833	primary cell wall biosynthesis (sensu Magnoliophyta)
							GO:0016759	cellulose synthase activity
							GO:0030244	cellulose biosynthesis

Supplementary Tables pertaining to Figure 3

Supplementary Table S21. Proteins of the root cellular proteome with gene ontology (GO) annotations associated with the cell wall

Locus	Root Hairs (COBL9)	Non-Hair Epidermis (WER)	Cortex (CORTEX)	Endodermis/ Quiescent (SCR)	Vasculature (WOL)	Columella (PET111)	GO Identifier	GO Description
AT5G14430	0	1	1	0	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G16510	1	0	1	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
							GO:0030244	cellulose biosynthesis
AT5G16590	1	0	1	1	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G17770	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G17820	1	1	0	1	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G20080	1	0	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G20950	0	0	1	0	0	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G37310	1	0	0	0	0	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G49720	1	0	1	0	1	0	GO:0008810	cellulase activity
							GO:0030244	cellulose biosynthesis
AT5G60920	0	0	1	0	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
							GO:0010215	cellulose microfibril organization
AT5G61790	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G63840	1	1	1	1	1	1	GO:0030244	cellulose biosynthesis
AT5G64740	1	0	0	0	1	0	GO:0009833	primary cell wall biosynthesis (sensu Magnoliophyta)
							GO:0009832	cell wall biosynthesis (sensu Magnoliophyta)
							GO:0016759	cellulose synthase activity
							GO:0030244	cellulose biosynthesis
AT5G65430	1	0	0	1	1	0	GO:0009505	cell wall (sensu Magnoliophyta)
AT5G66680	1	1	1	1	1	1	GO:0009505	cell wall (sensu Magnoliophyta)