Supplementary Materials

Table S1. List of genes that were identified as principal contributors to the deviation observed in B over Q and W, in the PCA analysis.

24528 at J4568 at J4568 18 At J25270	Affy ID	AGI ID	Annotation (Lookup from 2010-12-20)—for multiple identifier mappings only the annotation for the first identifier is shown, except in the case of the multi-line output option				
24565_8_II A1g28270 RA1_FIA_mil-like 4 24590_8_II A2g94180 CA3_ATACA3_apha carbonic anhydrase 3 246123_81 A5g1800 Qioxoyl hydrolose superfamily protein 24621_81 A45g23980 MRG family protein 2463_181 A45g21780 MRG family protein 24641_81 A5g16100 MRG family protein 24641_81 A5g15110 Pectatel yase family protein 24751_81 A5g15100 MRC like cupins superfamily protein 24751_81 A5g15100 Protein of unknown function (DUF1216) 24751_81 A5g58170 GDPPD_T-SVL5_SHY-3-like 5 24870_81 A5g59030 MRC like cupins superfamily protein 24871_81 A45g19000 Potein of unknown function (DUF1216) 24872_81 A45g19030 Plant invertises pectrin methylesterase inhibitor superfamily protein 24872_81 A45g19030 Plant invertises pectrin methylesterase inhibitor superfamily protein 24882_81_81 A45g19030 Pectra lyase-siles superfamily protein 24892_81_81 A45g19300 Pectra lyase-siles superfamily protein 24993_81 A	245053_at		Plant invertase/pectin methylesterase inhibitor superfamily				
45700 at Jay 180 at Joseph 180 at J							
246749_st ATS_18580 glyoxal oxidase-related protein 246123_st ATS_20390 (Gycosyl hydrolase superfamily protein 24639_st ATS_20390 (Gycosyl hydrolase superfamily protein 24649_st ATS_26100 Miscow protein, Has 30201 Blast hits to 17322 proteins in 780 species: Archae, 12; Bacteria, 1396; McHazoa, 17338; Fungi, 3422; Plants, 5037; Viruses, 0; Other Eukaryotes, 2996 (source: NCBI BLink). 246545_at J ATS_261700 Protein of unknown function (DUPL1216) 247804_at J ATS_261700 Protein of unknown function (DUPL1216) 247843_at J ATS_261700 Protein of unknown function (DUPL1216) 2487470_at J ATS_260030 Plant invertase/pectrin methylesterase inhibitor superfamily protein 248751_at J ATS_260030 Plant invertase/pectrin methylesterase inhibitor superfamily protein 24872_at J ATS_260030 Plant invertase/pectrin methylesterase inhibitor superfamily protein 24872_at J ATS_260030 Plant invertase/pectrin methylesterase inhibitor superfamily protein 24872_at J ATS_260030 ATS_260030 ATS_260030 24872_at J ATS_260030 ATS_260030 ATS_260030 24872_at J ATS_260030							
24623.at A15g23900 Glycosyl hydrolase superfamily protein 24624.at A18g37280 MiRG family protein 246491_BL A15g16100 MiRG family protein 24654_at A15g16100 MiRG family protein 24654_at A15g26700 MiRC jack 24752_at A15g26702 Mirc like cupins superfamily protein 247804_at A15g8170 Pectate lysse family protein 24870_at A15g81800 Mirc like cupins superfamily protein 248740_at A15g80500 DGPDL7_SVL5_SHV3-like 5 248741_at A15g80500 DGPDL7_SVL5_SHV3-like 4 248742_at A15g80500 Derel julyse-like see inhibitor superfamily protein 24875_at A15g81400 A15g81400 24870_at A15g4700 Perxidase superfamily protein 24872_at A15g4700 A15g4400 24942_at A15g4700 A15g4400 24942_at A15g4700 A15g4400 24942_at A15g4740 A15g47400 24942_at A15g48380 DURING: L mature pollen stage, a large similarge particular protein </td <td>_</td> <td></td> <td colspan="5"></td>	_						
Add							
Ads							
Ads	246234_at	At4g37280					
246841 at January 247512	246491_at						
247804 at 247804 at 345g8170 at 247843 at 2	_						
24784d_at A5g58170 A5g58050 GDPDL6_SVL_SIVA_SIVA_Sike 4 unknown protein; Ha. 4750 Blast hits to 3160 proteins in 341 species; Archae, 14; Bacteria, 239; Metazoa, 1329; Fungl, 394; Plants, 197; Viruses, 79; Other Eukaryotes, 2498 (source; NCBI BLink). 248534_nt A5g58050 A15g58030 A5g58050 Plant invertuses pectin methylesterase inhibitor superfamily protein 248534_nt A5g58030 A15g480900 Beta-glucosidase, GBA2 type family protein 24852_at A15g48140 A15g48140 Pectin Jyase-Fise superfamily protein 249402_at A5g43480 A5g43430 Defensin-like (DFEL) family protein 249402_at A15g39880 Defensin-like (DFEL) family protein unknown protein; FUNCTIONS IN: molecular, function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein; FUNCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein; FUNCATED IN: Arabidopsis thaliana protein match is: unknown protein; FUNCATED IN: Arabidopsis thaliana protein match is: unknown protein 250154_at A13g52100 A3g52100 A3g52100 A3g525010 A3g525010 A13g52							
A5g8050							
28870_at							
Adsgo. Adsgo. Adsgo. Beta-glucosidase, GBA2 type family protein Adsgo. Adsgo. Beta-glucosidase, GBA2 type family protein Adsg. Adsgo. Beta-glucosidase, GBA2 type family protein Adsgo. Alsgo. Beta-glucosidase, GBA2 t	247843_at	At5g58050					
24881 at A5g49900 Beta-glucosidase, GBA2 type family protein 24872 at A5g4880 A5g48480 Pectin Ivasce-like superfamily protein 249049 at A9900 A15g48880 Perion Ivasce-like superfamily protein 249429 at A15g4905 A15g49155 Defensin-like (DELT) family protein unknown; Invol.VED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28750.1); Has 25 Blast hits to 25 proteins in 3 species: Archae, 0; Bacteria, 2; Metazoa, 0; Fungi, 0; Plants, 23; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink). 251250 at A15g5130 A15g62300 A3g62130 A7g62230 DAFI_E-box family protein 251383 at A15g57690 A15g52600 A15g52600 A17g52300 A17g5230	248470_at	At5g50830					
24872_at Af5g4580 Pectin Vase-like superfamily protein 24892_at Af5g4430 TUB4_tubulin beta chain 4 Af5g4434 Af5g4435 24949_at Af5g4435 24949_at Af5g4434 24949_at Af5g4434 24949_at Af5g4368 24949_at Af5g39880 24949_at Af5g4368 24949_at Af5g39880 24949_at Af5g43980 24949_at Af5g43980 24949_at Af5g43980 24949_at Af5g439880 24949_at Af5g43980 24949_at Af5g439880 24949_at Af5g43980 24949_at Af5g43980 24949_at Af5g439880 24949_at Af5g43980 24949_at Af5g43980 24949_at Af5g439880 24949_at Af5g43980 24949_at Af5g439880 2494	248534_at						
248822 at A5g47000 A75g45880 Pollen Ole e I allergen and extensin family protein 249049 at A15g45880 A15g45880 Pollen Ole e I allergen and extensin family protein 249402 at A15g40155 A15g40155 Defensin-like (DEFL) family protein unknown; involved in unknown protein; PINOTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system: EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28750.1); Has 25 Blast hits to 25 proteins in 3 species: Archae, 0; Bacteria, 2; Metazoa, 0; Fungi, 0; Plants, 23; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink). 250154 at A15g1540 A15g6180 Galactose mutarotase-like superfamily protein 251252 at A13g62180 A13g6180 Plant invertase/pectin methylesterase inhibitor superfamily protein 251252 at A13g62180 A13g6180 VOIGHE VNNGUARD I homolog 2 251253 at A13g62190 A13g57600 ACP23 ATAGP23 _ arabinogalactan protein 23 25208.5 s. at A13g52000 Atcs WNV2 _ CWINV2 _ Cell wall invertase 2 25240 at A13g43031 A13g43860 ACP23 ATAGP23 _ arabinogalactan protein 5:1 25210 at A13g43030 A2g41840 AVERIA GALACTION GA	248581_at	At5g49900	Beta-glucosidase, GBA2 type family protein				
249429_at 249429	248714_at						
At5g405							
Af5g40155							
Unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage: BEST Arabidopsis thaliana protein match is: unknown protein (TAIR: AT3G28750.1); Has 25 Blast hits to 25 proteins in 3 species: Archae, 0; Bacteria, 2; Metazoa, 0; Fungi, 0, Plants, 23; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink). At5g15140	249049_at		TUB4tubulin beta chain 4				
	249402_at	At5g40155					
At At At At At At At At	249429_at	At5g39880	unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G28750.1); Has 25 Blast hits to 25 proteins in 3 species: Archae, 0; Bacteria, 2; Metazoa, 0;				
At At At At At At At At	250154_at						
At3g62180	250606_s_at		ATPPME1_PPME1Pectin lyase-like superfamily protein				
At3g62230	251250_at		Plant invertase/pectin methylesterase inhibitor superfamily protein				
A3 A3 A3 A3 A3 A3 A3 A3							
According to the color of the	251258_at	At3g62170	VGDH2_VANGUARD 1 homolog 2				
251804_at At3g55430 O-Glycosyl hydrolases family 17 protein 252052_at At3g52600 AtcwINV2_CWINV2_cell wall invertase 2 252085_s_at At3g52000 At3g52000 At3g52010 At3g5301 MAPKKK20_MKKK20_mitogen-activated protein kinase kinase kinase 20 252440_at At3g47440 TIP5;1_tonoplast intrinsic protein 5;1 253153_at At3g43860 At4H9A4_GH9A4_glycosyl hydrolase 9A4 253153_at At4g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at At4g31420 Zinc finger protein 622 25360_at At4g30860 ASHR3_SDG4_SET domain group 4 254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein 25477_at At3g12120 ALEA5_SAG21_senescence-associated gene 21 256285_at At3g1210 MADS-box family protein 256584_at At3g28750 25666_at At3g13400 Ak1sg28750 At3g28750	251358_at	At3g61160	Protein kinase superfamily protein				
252052_at At3g52600 AtcwINV2_CWINV2_cell wall invertase 2 252085_s_at At3g52000 At3g52010 scpl36_serine carboxypeptidase-like 36 25212_at At3g50310 MAPKKK20_MKKK20_mitogen-activated protein kinase kinase kinase 20 252440_at At3g47440 TIP5;1_tonoplast intrinsic protein 5;1 252710_at At3g43860 AtGH9A4_GH9A4_glycosyl hydrolase 9A4 253526_at At4g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at At4g31420 Zinc finger protein 622 253600_at At4g3040 ASHR3_SDG4_SET domain group 4 254024_at At4g25780 CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein 254123_at At4g25780 At4g2580 ALEA5_SAG21_senescence-associated gene 21 25427_at At3g1210 ALEA5_SAG21_senescence-associated gene 21 256277_at At3g12510 AADS-box family protein 256285_at At3g12510 AADS-box family protein 256584_at At3g28750 At3g28750 ALGHAMAS-box family protein 256584_at At3g1340 At3g1340 ALGHAMAS-box family protein ALGHAMAS-box family protein	251590_at	At3g57690	AGP23_ATAGP23arabinogalactan protein 23				
25212_at At3g52010	251804_at	At3g55430	O-Glycosyl hydrolases family 17 protein				
25212_at At3g52010 MAPKKK20_MKKK20_mitogen-activated protein kinase kinase 20 252440_at At3g47440 TIP5;1_tonoplast intrinsic protein 5;1 252710_at At3g43860 AtGH9A4_glycosyl hydrolase 9A4 253153_at At4g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at At4g31420 Zinc finger protein 622 253599_at At4g30860 ASHR3_SDG4_SET domain group 4 253660_at At4g30140 CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein 254123_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g02380 ALEA5_SAG21_senescence-associated gene 21 256285_at At3g12120 FAD2_fatty acid desaturase 2 256285_at At3g12510 MADS-box family protein 256275 At3g28750 MADS-box family protein 256285_at At3g28750 MADS-box family protein 256285_at At3g12510 MADS-box family protein 256285_at At3g28750 MADS-box family protein 256286_at At3g28750 MADS-box family protein 256286_at At3g28750 MADS-	252052_at	At3g52600	AtcwINV2_CWINV2cell wall invertase 2				
252212_at A13g50310 MAPKKK20_MKKK20_mitogen-activated protein kinase kinase 20 252440_at A13g43460 TIP5;1_tonoplast intrinsic protein 5;1 252710_at A13g43860 AtGH9A4_GH9A4_glycosyl hydrolase 9A4 253153_at A14g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at A14g31420 Zinc finger protein 622 253599_at A14g30860 ASHR3_SDG4_SET domain group 4 253660_at A14g30140 CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein 254024_at A14g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at A14g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein 255479_at A13g12120 FAD2_fatty acid desaturase 2 256277_at A13g12120 FAD2_fatty acid desaturase 2 256285_at A13g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink).	252085 c of	At3g52000	son 26 sarina carbovy pantidasa lika 26				
252440_at	252065_s_at						
252710_at At3g43860 AtGH9A4_GH9A4_glycosyl hydrolase 9A4 253153_at At4g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at At4g31420 Zinc finger protein 622 253599_at At4g30860 ASHR3_SDG4_SET domain group 4 253660_at At4g30140 CDEFI_GDSL-like Lipase/Acylhydrolase superfamily protein 254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g24640 APPBI_Plant invertase/pectin methylesterase inhibitor superfamily protein 255479_at At3g12120 FAD2_fatty acid desaturase 2 256277_at At3g12120 FAD2_fatty acid desaturase 2 256285_at At3g12510 MADS-box family protein 256584_at At3g28750 EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown protein; (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 sks13_SKU5 similar 13	252212_at	At3g50310					
253153_at At4g35700 DAZ3_zinc finger (C2H2 type) family protein 253526_at At4g31420 Zinc finger protein 622 253599_at At4g30860 ASHR3_SDG4_SET domain group 4 253660_at At4g30140 CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein 254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein 255479_at At3g12120 FAD2_fatty acid desaturase 2 256277_at At3g12120 FAD2_fatty acid desaturase 2 256285_at At3g12510 MADS-box family protein 256285_at At3g28750 MADS-box family protein 256285_at At3g28750 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink).							
253526_at At4g31420 Zinc finger protein 622 253599_at At4g30860 ASHR3_SDG4_SET domain group 4 253660_at At4g30140 CDEF1_GDSL-like Lipase/Acylhydrolase superfamily protein 254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein 25427_at At3g12120 FAD2_fatty acid desaturase 2 256285_at At3g12510 MADS-box family protein 256285_at At3g28750 At3g28750 256584_at At3g28750 At3g28750 At3g28750 At3g28750 At3g28750 At3g13400 Secretary protein function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink).							
25369_at At4g30860 ASHR3_SDG4SET domain group 4 253660_at At4g30140 CDEF1GDSL-like Lipase/Acylhydrolase superfamily protein 254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein 254123_at At4g24640 APPB1Plant invertase/pectin methylesterase inhibitor superfamily protein 255479_at At3g12120 FAD2fatty acid desaturase 2 256277_at At3g12510 MADS-box family protein 256285_at MADS-box family protein 25628							
254024_at At4g30140 At4g25780 At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein At4g25780 At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein At4g02380 AtLEA5_SAG21_senescence-associated gene 21 At3g12120 FAD2_fatty acid desaturase 2 At3g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein attemption of the protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein of the protein							
254024_at At4g25780 CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein At4g24640 APPB1Plant invertase/pectin methylesterase inhibitor superfamily protein At4g02380 AtLEA5_SAG21senescence-associated gene 21 At3g12120 FAD2fatty acid desaturase 2 At3g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 At4g24640 At4g25780 At4g24640 At4g24640 At4g25780 At4g02380 AtLEA5_SAG21senescence-associated gene 21 EAD2fatty acid desaturase 2 MADS-box family protein unknown protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein; (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink).							
254123_at At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein At4g02380 AtLEA5_SAG21_senescence-associated gene 21 At3g12120 FAD2_fatty acid desaturase 2 At3g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 At4g24640 At4g24640 APPB1_Plant invertase/pectin methylesterase inhibitor superfamily protein at4g28750 FAD2_fatty acid desaturase 2 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink).	_						
256277_at At3g12120 FAD2fatty acid desaturase 2 256285_at At3g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 Sks13SKU5 similar 13							
256285_at At3g12120 At3g12510							
256285_at At3g12510 MADS-box family protein unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 At3g13400 At3g13400							
unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 28; Viruses, 0; Other Eukaryotes, 9 (source: NCBI BLink). 256966_at At3g13400 sks13_SKU5 similar 13			•				
256966_at At3g13400 sks13SKU5 similar 13			unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1216 (InterPro:IPR009605); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G39880.1); Has 37 Blast hits to 31 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0;				
	256966 at	At3g13400					
CALLAC ALL MICY/44 III FLAA FAA II LIN-IIKE SISDIIIIOSISCISII DIDIENIA ORDENIA	250900_at 257392_at	At2g24450	FLA3_FASCICLIN-like arabinogalactan protein 3 precursor				

Table S1. Cont.

Affy ID	AGI ID	Annotation (Lookup from 2010-12-20)—for multiple identifier mappings only the annotation for			
1111y 120	the first identifier is shown, except in the case of the multi-line output option				
		unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13620.1);			
257469_at	At1g49290	Has 99 Blast hits to 93 proteins in 11 species: Archae, 0; Bacteria, 0; Metazoa, 2; Fungi, 0; Plants, 97;			
	1.2.25060	Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).			
257809_at	At3g27060	ATTSO2_TSO2Ferritin/ribonucleotide reductase-like family protein			
257819_at	At3g25165	RALFL25_ralf-like 25			
257886_at	At3g17060	Pectin lyase-like superfamily protein			
257981_at	At3g20770	AtEIN3_EIN3_Ethylene insensitive 3 family protein			
257986_at	At3g20865	AGP40_arabinogalactan protein 40			
258077_at	At3g26110	Anther-specific protein agp1-like			
258092_at	At3g14595	Ribosomal protein L18ae family			
258279_at	At3g26870	Plant self-incompatibility protein S1 family			
258280_at	At3g26880	Plant self-incompatibility protein S1 family			
258326_at	At3g22760	SOL1_Tesmin/TSO1-like CXC domain-containing protein			
258639_at	At3g07820	Pectin lyase-like superfamily protein GLP8germin-like protein 8			
258748_at	At3g05930 At3g05610	Plant invertase/pectin methylesterase inhibitor superfamily			
258889_at 259044_at	At3g03430	Calcium-binding EF-hand family protein			
259189_at	At3g01700	AGP11_ATAGP11arabinogalactan protein 11			
239109_at	Alagoi700	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process			
		unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED			
		DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal			
259266_at	At3g01240	differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein			
		(TAIR:AT3G01230.1); Has 12 Blast hits to 12 proteins in 3 species: Archae, 0; Bacteria, 0; Metazoa, 0;			
		Fungi, 0; Plants, 11; Viruses, 0; Other Eukaryotes, 1 (source: NCBI BLink).			
259269_at	At3g01270	Pectate lyase family protein			
260386_at	At1g74010	Calcium-dependent phosphotriesterase superfamily protein			
200300_at	At1g17290	Carcium-dependent phosphothesicrase superranning protein			
260847_s_at	At1g17230 At1g72330	AlaAT1alanine aminotransferase			
260888_at	At1g29140	Pollen Ole e 1 allergen and extensin family protein			
261511_at	At1g71770	PAB5_poly(A)-binding protein 5			
261623_at	At1g01980	FAD-binding Berberine family protein			
262122_at	At1g02790	PGA4_polygalacturonase 4			
262282_at	At1g68610	PCR11_PLANT CADMIUM RESISTANCE 11			
262291_at	At1g70790	Calcium-dependent lipid-binding (CaLB domain) family protein			
262393_at	At1g49490	Leucine-rich repeat (LRR) family protein			
262571_at	At1g15430	Protein of unknown function (DUF1644)			
		unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30930.1);			
262620_at	At1g06540	Has 16 Blast hits to 16 proteins in 3 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 16;			
		Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).			
262676_at	At1g75950	ASK1_ATSKP1_SKP1A_UIP1S phase kinase-associated protein 1			
262696_at	At1g75870	unknown protein; Has 10 Blast hits to 10 proteins in 5 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi,			
		0; Plants, 10; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).			
262760_at	At1g10770	Plant invertase/pectin methylesterase inhibitor superfamily protein			
262885_at	At1g64740	TUA1_alpha-1 tubulin			
263043_at	At1g23350	Plant invertase/pectin methylesterase inhibitor superfamily protein			
263215_at	At1g30710	FAD-binding Berberine family protein			
263681_at	At1g26840	ATORC6_ORC6origin recognition complex protein 6			
265007_s_at	At1g61563 At1g61566	RALFL8_ralf-like 8			
265022_at	At1g24520	BCP1_homolog of Brassica campestris pollen protein 1			
265080_at	At1g55570	sks12_SKU5 similar 12			
265127_at	At1g55560	sks14_SKU5 similar 14			
265960_at	At2g37470	Histone superfamily protein			
	At2g47030	VGDH1_Plant invertase/pectin methylesterase inhibitor superfamily			
266750_s_at	At2g47040				
266764_at	At2g47050	Plant invertase/pectin methylesterase inhibitor superfamily protein			
266977_at	At2g39420	alpha/beta-Hydrolases superfamily protein			
267590_at	At2g39700	ATEXP4_ATEXPA4_ATHEXP ALPHA 1.6_EXPA4expansin A4			

Table 2. List of genes that were identified as principal contributors to the deviation observed in Q over B and W, in the PCA analysis.

Affy ID	AGI ID	Annotation (Lookup from 2010-12-20)—for multiple identifier mappings only the annotation for the first identifier is shown, except in the case of the multi-line output option			
246099_at	At5g20230	ATBCB_BCB_SAG14blue-copper-binding protein			
246208_at	At4g36490	ATSFH12_SFH12_SEC14-like 12			
246751_at	At5g27870	Plant invertase/pectin methylesterase inhibitor superfamily			
246761_at	At5g27980	Seed maturation protein			
247512_at	At5g61720	Protein of unknown function (DUF1216)			
248037_at	At5g55930	ATOPT1_OPT1oligopeptide transporter 1			
248194_at	At5g54095	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27580.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae, 12; Bacteria, 1396; Metazoa, 17338; Fungi, 3422; Plants, 5037; Viruses, 0; Other Eukaryotes, 2996 (source: NCBI BLink).			
248758_at	At5g47620	RNA-binding (RRM/RBD/RNP motifs) family protein			
249447_at	At5g39400	ATPTEN1_PTEN1Calcium/lipid-binding (CaLB) phosphatase			
249536_at	At5g38760	Late embryogenesis abundant protein (LEA) family protein			
250358_at	At5g11740	AGP15_ATAGP15arabinogalactan protein 15			
250608_at	At5g07420	Pectin lyase-like superfamily protein			
250917_at	At5g03690	Aldolase superfamily protein			
251228_at	At3g62710	Glycosyl hydrolase family protein			
251258_at	At3g62170	VGDH2_VANGUARD 1 homolog 2			
252085_s_at	At3g52000 At3g52010	scpl36_serine carboxypeptidase-like 36			
252710_at	At3g43860	AtGH9A4_GH9A4glycosyl hydrolase 9A4			
252820_at	At3g42640	AHA8_HA8H(+)-ATPase 8			
254001_at	At4g26260	MIOX4_myo-inositol oxygenase 4			
254716_at	At4g13560	UNE15_Late embryogenesis abundant protein (LEA) family protein			
256385_at	At1g66580	RPL10C_SAG24senescence associated gene 24			
256580_s_at	At3g28810 At3g28820	Protein of unknown function (DUF1216)			
256581_at	At3g28830	Protein of unknown function (DUF1216)			
256588_at	At3g28790	Protein of unknown function (DUF1216)			
256955_at	At3g13390	sks11_SKU5 similar 11			
257077_at	At3g19690	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein			
257090_at	At3g20530	Protein kinase superfamily protein			
257121_at	At3g20210 At3g20220	DELTA-VPE_DELTAVPEdelta vacuolar processing enzyme			
257532_at	At3g04700 At3g04710	Protein of unknown function (DUF1685)			
257736_at	At3g27410	unknown protein; Has 10 Blast hits to 10 proteins in 2 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 10; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).			
257821_at	At3g25170	RALFL26_ralf-like 26			
258058_at	At3g28980	Protein of unknown function (DUF1216)			
258498_at	At3g02480	Late embryogenesis abundant protein (LEA) family protein			
258639_at	At3g07820	Pectin lyase-like superfamily protein			
258645_s_at	At3g07850 At3g14040	Pectin lyase-like superfamily protein			
258677_at	At3g08730	ATPK1_ATPK6_ATS6K1_PK1_PK6_S6K1protein-serine kinase 1			
258680_at	At3g08580	AAC1_ADP/ATP carrier 1			
259064_at	At3g07490	AGD11_AtCML3_CML3ARF-GAP domain 11			
262664_at	At1g13970	Protein of unknown function (DUF1336)			
262885_at	At1g64740	TUA1_alpha-1 tubulin			
263062_at	At2g18180	Sec14p-like phosphatidylinositol transfer family protein			
263144_at	At1g54070	Dormancy/auxin associated family protein			
264923_s_at	At1g60740 At1g65970	Thioredoxin superfamily protein			
264993_at	At1g67290	GLOX1_glyoxal oxidase-related protein			
265404_at	At2g16730	BGAL13_glycosyl hydrolase family 35 protein			
266029_at	At2g05850	scpl38serine carboxypeptidase-like 38			
266428_at	At2g07180	Protein kinase superfamily protein			
266592_at	At2g46210	AtSLD2_SLD2_Fatty acid/sphingolipid desaturase			
266765_at	At2g46860	AtPPa3_PPa3_pyrophosphorylase 3			
266918_at	At2g45800	PLIM2a_GATA type zinc finger transcription factor family protein			
267590_at	At2g39700	ATEXP4_ATEXPA4_ATHEXP ALPHA 1.6_EXPA4_expansin A4			
at	1112537100	TITEM I_TITEMITITIEM TIEFTIN TO_EMITIT_CAPUIISIII TIT			

Table 3. List of genes that were identified as principal contributors to the deviation observed in W over B and Q, in the PCA analysis.

Affy ID	AGI ID	Annotation (Lookup from 2010-12-20)—for multiple identifier mappings only the annotation for the first identifier is shown, except in the case of the multi-line output option		
245700_at	At5g04180	ACA3_ATACA3alpha carbonic anhydrase 3		
245946_at	At5g19580	glyoxal oxidase-related protein		
245956_s_at	At5g28540 At5g42020	BIP1_heat shock protein 70 (Hsp 70) family protein		
246099_at	At5g20230	ATBCB_BCB_SAG14blue-copper-binding protein		
246118_at	At5g20340	BG5_beta-1,3-glucanase 5		
246631_at	At1g50740	Transmembrane proteins 14C		
248038_at	At5g55980	serine-rich protein-related		
248470_at	At5g50830	unknown protein; Has 4750 Blast hits to 3160 proteins in 341 species: Archae, 14; Bacteria, 239; Metazoa, 1329; Fungi, 394; Plants, 197; Viruses, 79; Other Eukaryotes, 2498 (source: NCBI BLink).		
249049_at	At5g44340	TUB4_tubulin beta chain 4		
249187_at	At5g43060	Granulin repeat cysteine protease family protein		
249243_s_at	At5g42260 At5g44640	BGLU12_beta glucosidase 12		
249375_at	At5g40730	AGP24_ATAGP24arabinogalactan protein 24		
249584_s_at	At5g37810 At5g37820	NIP4;1_NLM4NOD26-like intrinsic protein 4;1		
250174_at	At5g14380	AGP6_arabinogalactan protein 6		
250631_at	At5g07430	Pectin lyase-like superfamily protein		
251250_at	At3g62180	Plant invertase/pectin methylesterase inhibitor superfamily protein		
253226_at	At4g35010	BGAL11beta-galactosidase 11		
253814_at	At4g28290	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 45 Blast hits to 45 proteins in 11 species: Archae, 0; Bacteria, 0; Metazoa, 0; Fungi, 0; Plants, 45; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).		
253831_at	At4g27580	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, cell wall; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae, 12; Bacteria, 1396; Metazoa, 17338; Fungi, 3422; Plants, 5037; Viruses, 0; Other Eukaryotes, 2996 (source: NCBI BLink).		
255515_at	At4g02250	Plant invertase/pectin methylesterase inhibitor superfamily protein		
256277_at	At3g12120	FAD2fatty acid desaturase 2		
259866_at	At1g76640	Calcium-binding EF-hand family protein		
260401_at	At1g69840	SPFH/Band 7/PHB domain-containing membrane-associated protein family		
260943_at	At1g45145	ATH5_ATTRX5_LIV1_TRX5thioredoxin H-type 5		
262022_at	At1g35490	bZIP family transcription factor		
263126_at	At1g78460	SOUL heme-binding family protein		
263950_at	At2g36020	HVA22J_HVA22-like protein J		
264655_at	At1g09070	(AT)SRC2_SRC2_soybean gene regulated by cold-2		
266428_at	At2g07180	Protein kinase superfamily protein		

AGI ID	Primer ID	Forward primer	Reverse primer
At4g27960	UBC9	GTTTCACCACCCTTTCTTC	AAATCCCACGATCAAATTCC
At5g59370	ACT4	CACCAAACGAAGACGGAAGT	CATTGGGAGTGGAAATTGTTT
At1g71380	CEL3	TCTCCAAGTCATTGCTCTTCTTCC	CGTTGTCTCCTGCGTCATAGTAC
At3g60570	EXPB5	GCAAACGGTGATGGGAACTTCG	GGACACGGCGGAGGTAAGC
At5g11110	SPS2F	TGGTGGTGTTCGTGGGAGATTCAG	TTAGCCTCGGTGATGTTGGGACTG
At5g42260	BGLU13	CCATTGGGACACACCGCAAAGC	ACACCTTCCTGGAGCCATTACACC
At3g02870	VTC4	GAGACATTCTGATGGACCTTACG	TCCGAGACTTAACGATTGATTGG
At5g14380	AGP6	TTCTAAGTTAAGTCGTCCAC	GACATTTAGGTTTATATTTACTCC
At3g01700	AGP11	CCACGTAATGTCAAGC	CAACAGGGGATGATGCTTTC
At3g57690	AGP23	AATGGAGATGAAGAAGATTG	TGCAAGTAGTAGCTGAAG
At5g40730	AGP24	CGGTTACAGATGGAGGAGGCACTC	AGGACACCACACGTAGCCACAATC
At3g20865	AGP40	GCGGCTACAATGGAGTCTC	CAAGAAGGCGGAGAGTGATG
AT4G35010	BGAL11	GGAATGGGAAAAGGGTTGAT	GCTCAGGCTTCACATTAGGC
AT2G16730	BGAL13	AAACAAGGCGGTTTGAACAC	GGAAGTCCTCCATGAGTCCA
AT3G01040	GAUT13	GAATTTTGCTGGGTTGTCGT	ACAACATCACCTCCCTACGC
AT1G06780	GAUT6	CGGCTTAAGAGCATCACTCC	CCATCACTTTCAGCAGACGA
At3g18780	ACT2	GTGCTGGATTCTGGTGATGGTGTG	CGTTGTCTCCTGCGTCATAGTAC
At4g33240	PI4K	TCCTCCAGCCACACGCAGAATTG	GAAGCATAGCGGAAGCAAGCAACC
At5g60250	C3HC4-Type ring	CCATTGGGACACACCGCAAAGC	ACACCTTCCTGGAGCCATTACACC
AT5G12030	HSP17.6C-CL	GGCAAACGCACCCGCTATG	TTCACCTCTTCCTTCAGTCC
At2g39890	PROT1	ATGGCGAGAGGCGGGTAC	GTGGTTGGCTAGAATGAATGTGAG
At1g50490	UBC20	AGATCCTCCGGCGTCTAATGG	TGCTTCCTGTTATTGTCCCTTTCC
At1g50490	UBQ10	GCTCCGACACCATTGACAAC	ACGCAGGACCAAGTGAAGAG
AT1G69940	PPME1	ATGCCTACACCGAGATGACC	AGTTTACAAAGCGGGTGGTG
AT2G47040	VGD1	ACTGGCCCAAGTCATTCAAC	CCACCGAGACCACAACTTTT

Table 4. List of primers used in the qPCR assay.

Figure 1. Functional classification of the genes listed in Table S1 that produced the most diverging transcript levels. Most of the genes are associated to cell organization and biogenesis, and developmental processes. Most of them are extracellular or located at the cell wall, and the most conspicuous functional annotation relates to hydrolase activity.

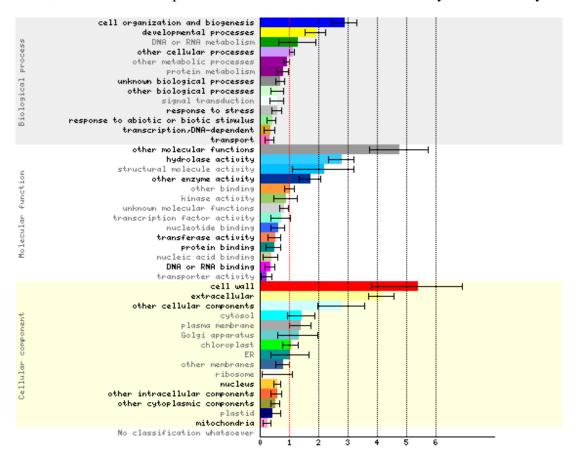


Figure 2. Functional classification of the genes listed in Table 2 that produced the most diverging transcript levels. Most of the genes are associated to cell organization and biogenesis, protein metabolism and developmental processes, most of them are located at the cell wall or are extracellular, and the most conspicuous functional annotation relates to hydrolase activity, transporter and other molecular functions.

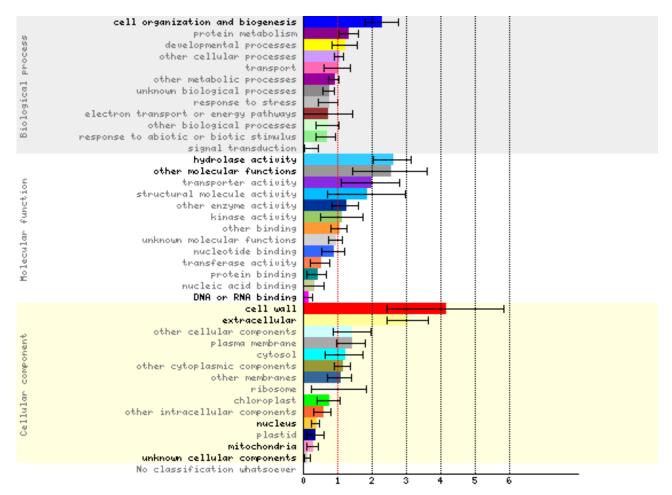


Figure 3. Functional classification of the genes listed in Table 3 that produced the most diverging transcript levels. Most of the genes are associated with cell organization and biogenesis, response to biotic and abiotic stimulus, response to stress and transport, most of them are extracellular or located at the Endoplasmic reticulum and cell wall, and the most conspicuous functional annotation relates to hydrolase activity.

