

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.

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
245053_at	At2g26450	Plant invertase/pectin methylesterase inhibitor superfamily
245528_at	At4g15530	PPDK__pyruvate orthophosphate dikinase
245658_at	At1g28270	RALFL4__ralf-like 4
245700_at	At5g04180	ACA3_ATACA3__alpha carbonic anhydrase 3
245946_at	At5g19580	glyoxal oxidase-related protein
246123_at	At5g20390	Glycosyl hydrolase superfamily protein
246234_at	At4g37280	MRG family protein
246491_at	At5g16100	unknown protein; 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).
246545_at	At5g15110	Pectate lyase family protein
246841_at	At5g26700	RmlC-like cupins superfamily protein
247512_at	At5g61720	Protein of unknown function (DUF1216)
247804_at	At5g58170	GDPDL7_SVL5__SHV3-like 5
247843_at	At5g58050	GDPDL6_SVL4__SHV3-like 4
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).
248534_at	At5g50030	Plant invertase/pectin methylesterase inhibitor superfamily protein
248581_at	At5g49900	Beta-glucosidase, GBA2 type family protein
248714_at	At5g48140	Pectin lyase-like superfamily protein
248822_at	At5g47000	Peroxidase superfamily protein
248926_at	At5g45880	Pollen Ole e 1 allergen and extensin family protein
249049_at	At5g44340	TUB4__tubulin beta chain 4
249402_at	At5g40155	Defensin-like (DEFL) family protein
249429_at	At5g39880	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).
250154_at	At5g15140	Galactose mutarotase-like superfamily protein
250606_s_at	At1g69940 At5g07410	ATPME1_PPME1__Pectin lyase-like superfamily protein
251250_at	At3g62180	Plant invertase/pectin methylesterase inhibitor superfamily protein
251252_at	At3g62230	DAF1__F-box family protein
251258_at	At3g62170	VGDH2__VANGUARD 1 homolog 2
251358_at	At3g61160	Protein kinase superfamily protein
251590_at	At3g57690	AGP23_ATAGP23__arabinogalactan protein 23
251804_at	At3g55430	O-Glycosyl hydrolases family 17 protein
252052_at	At3g52600	AtcwINV2_CWINV2__cell wall invertase 2
252085_s_at	At3g52000 At3g52010	scpl36__serine carboxypeptidase-like 36
252212_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
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	At4g02380	AtLEA5_SAG21__senescence-associated gene 21
256277_at	At3g12120	FAD2__fatty acid desaturase 2
256285_at	At3g12510	MADS-box family protein
256584_at	At3g28750	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
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 the first identifier is shown, except in the case of the multi-line output option
257469_at	At1g49290	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13620.1); Has 99 Blast hits to 93 proteins in 11 species: Archae, 0; Bacteria, 0; Metazoa, 2; Fungi, 0; Plants, 97; Viruses, 0; Other Eukaryotes, 0 (source: NCBI BLink).
257809_at	At3g27060	ATTSO2_TSO2__Ferritin/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
258748_at	At3g05930	GLP8__germin-like protein 8
258889_at	At3g05610	Plant invertase/pectin methylesterase inhibitor superfamily
259044_at	At3g03430	Calcium-binding EF-hand family protein
259189_at	At3g01700	AGP11_ATAGP11__arabinogalactan protein 11
259266_at	At3g01240	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 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
260847_s_at	At1g17290 At1g72330	AlaAT1__alanine 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)
262620_at	At1g06540	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30930.1); 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_SKP1_SKP1A_UIP1__S 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_ORC6__origin 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
266750_s_at	At2g47030 At2g47040	VGDH1__Plant invertase/pectin methylesterase inhibitor superfamily
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_EXPA4__expansin 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_BCB_SAG14__blue-copper-binding protein
246208_at	At4g36490	ATSFH12_SF12__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_OPT1__oligopeptide 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_PTEN1__Calcium/lipid-binding (CaLB) phosphatase
249536_at	At5g38760	Late embryogenesis abundant protein (LEA) family protein
250358_at	At5g11740	AGP15_ATAGP15__arabinogalactan 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_GH9A4__glycosyl hydrolase 9A4
252820_at	At3g42640	AHA8_HA8__H(+)-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_SAG24__senescence 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_DELTAVPE__delta 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_S6K1__protein-serine kinase 1
258680_at	At3g08580	AAC1__ADP/ATP carrier 1
259064_at	At3g07490	AGD11_AtCML3_CML3__ARF-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	scpl38__serine carboxypeptidase-like 38
266428_at	At2g07180	Protein kinase superfamily protein
266592_at	At2g46210	AtSLD2_SLD2__Fatty acid/sphingolipid desaturase
266765_at	At2g46860	AtPPa3_PP3__pyrophosphorylase 3
266918_at	At2g45800	PLIM2a__GATA type zinc finger transcription factor family protein
267590_at	At2g39700	ATEXP4_ATEXPA4_ATHXP ALPHA 1.6_EXPA4__expansin A4

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_ATACA3__alpha 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_BCB_SAG14__blue-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_ATAGP24__arabinogalactan protein 24
249584_s_at	At5g37810 At5g37820	NIP4;1_NLM4__NOD26-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	BGAL11__beta-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	FAD2__fatty 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_TRX5__thioredoxin 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

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

AGI ID	Primer ID	Forward primer	Reverse primer
At4g27960	UBC9	GTTTCACCACCCTTTCTTC	AAATCCCACGATCAAATTCC
At5g59370	ACT4	CACCAAACGAAGACGGAAGT	CATTGGGAGTGGAAAATTGTTT
At1g71380	CEL3	TCTCCAAGTCATTGCTCTTCTTC	CGTTGTCTCCTGCGTCATAGTAC
At3g60570	EXPB5	GCAAACGGTGATGGAACTTCG	GGACACGGCGGAGGTAAGC
At5g11110	SPS2F	TGGTGGTGTTCGTGGGAGATTGAG	TTAGCCTCGGTGATGTTGGGACTG
At5g42260	BGLU13	CCATTGGGACACACCGCAAAGC	ACACCTTCTGGAGCCATTACACC
At3g02870	VTC4	GAGACATTCTGATGGACCTTACG	TCCGAGACTTAACGATTGATTGG
At5g14380	AGP6	TTCTAAGTTAAGTCGTCCAC	GACATTTAGGTTTATATTTACTCC
At3g01700	AGP11	CCACGTAATGTCAAGC	CAACAGGGGATGATGCTTTTC
At3g57690	AGP23	AATGGAGATGAAGAAGATTG	TGCAAGTAGTAGCTGAAG
At5g40730	AGP24	CGGTTACAGATGGAGGAGGCACTC	AGGACACCACACGTAGCCACAATC
At3g20865	AGP40	GCGGCTACAATGGAGTCTC	CAAGAAGGCGGAGAGTGATG
AT4G35010	BGAL11	GGAATGGGAAAAGGGTTGAT	GCTCAGGCTTCACATTAGGC
AT2G16730	BGAL13	AAACAAGGCGGTTGAACAC	GGAACTCTCCATTGCTCCA
AT3G01040	GAUT13	GAATTTTGTGGTGTCTGT	ACAACATCACCTCCCTACGC
AT1G06780	GAUT6	CGGCTTAAGAGCATCACTCC	CCATCACTTTTACGACAGACGA
At3g18780	ACT2	GTGCTGGATTCTGGTGATGGTGTG	CGTTGTCTCCTGCGTCATAGTAC
At4g33240	PI4K	TCCTCCAGCCACACGCAGAATTG	GAAGCATAGCGGAAGCAAGCAACC
At5g60250	C3HC4-Type ring	CCATTGGGACACACCGCAAAGC	ACACCTTCTGGAGCCATTACACC
AT5G12030	HSP17.6C-CL	GGCAAACGACCCCGTATG	TTCACCTTTCCTTCTCAGTCC
At2g39890	PROT1	ATGGCCAGAGGCGGGTAC	GTGGTTGGCTAGAATGAATGTGAG
At1g50490	UBC20	AGATCCTCCGGCTCTAATGG	TGCTTCTGTTATTGCTCCCTTTC
At1g50490	UBQ10	GCTCCGACACCATTGACAAC	ACGCAGGACCAAGTGAAGAG
AT1G69940	PPME1	ATGCCTACACCGAGATGACC	AGTTTACAAAGCGGGTGGTG
AT2G47040	VGD1	ACTGGCCCAAGTCATTCAAC	CCACCGAGACCACAACCTTTT

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.

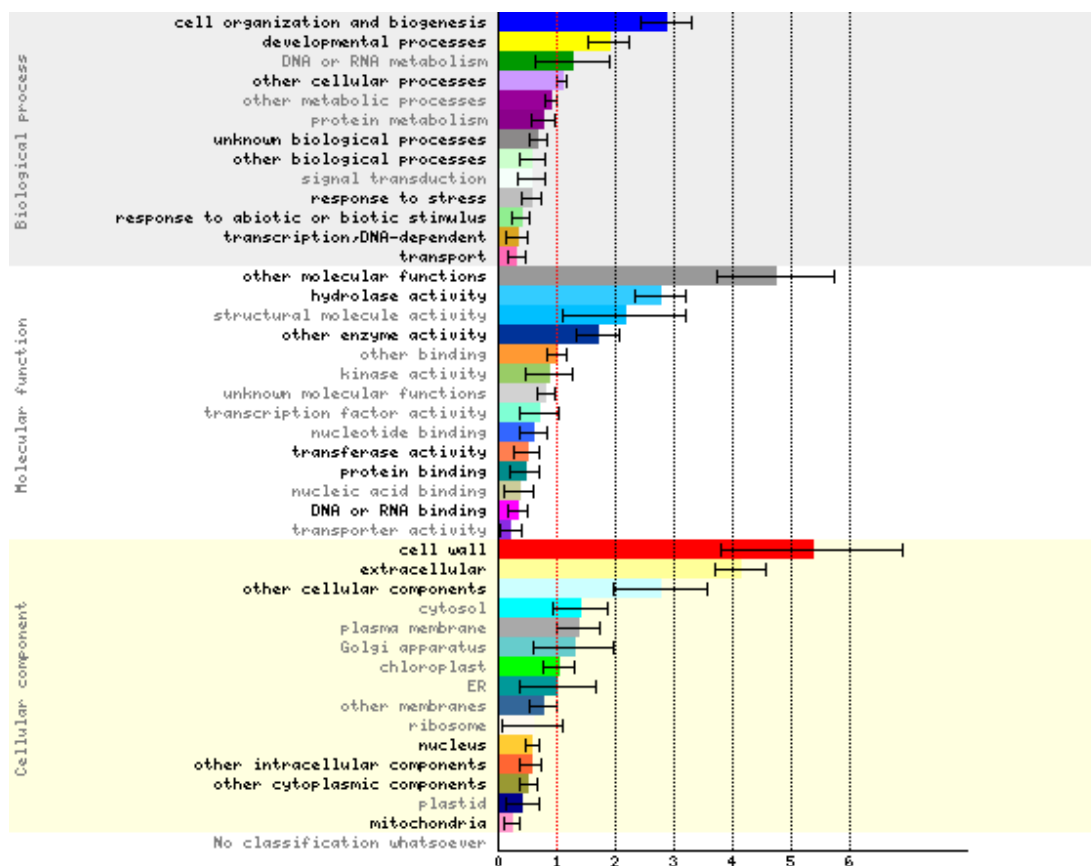


Figure 2. Functional classification of the genes listed in Table 2 that produced the most diverging transcript levels. Most of the genes are associated to cell organization and biogenesis, protein metabolism and developmental processes, most of them are located at the cell wall or are extracellular,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

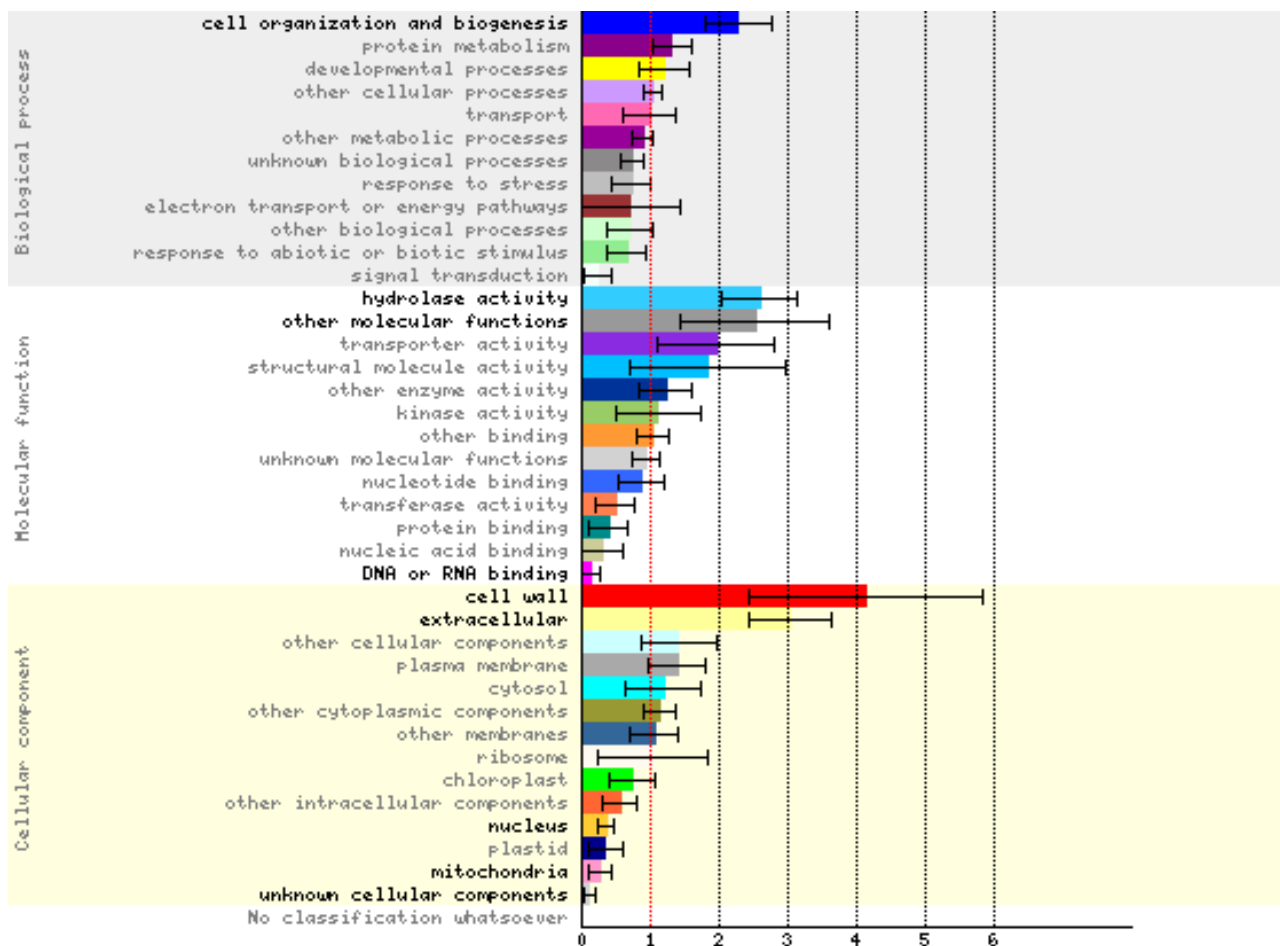


Figure 3. Functional classification of the genes listed in Table 3 that produced the most diverging transcript levels. Most of the genes are associated with cell organization and biogenesis, response to biotic and abiotic stimulus, response to stress and transport, most of them are extracellular or located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

