

Table 1 Suppl. Primers for reverse transcription quantitative PCR.

#ID	Gene	Primer sequence (forward)	Primer sequence (reverse)
Glyma18g52780.1	cytoskeletal structural protein(ActII)	Act11L:CGGTGGTTCATCTTGGCATCTC	Act11R:GTCTTTCGCTTCAATAACCCTATC
Glyma02g44460.1	eukaryotic elongation factor 1(LF1B)	LF1BL:TTGTTGAAAAGCCAGGGGACA	LF1BR:AATCTTACCCTTGAGCGTGG
Glyma.18G061300	gibberellin 2betadixygenase(GA2OX8)	GA2OX8L:AACATAGAGTCCACCCTCC	GA2OX8R:CTTGTGGTGCATGGTCTA
Glyma.06G043400	Fbox protein (GID2)	GID2L:CTCTCTCCAAACCTCAACAA	GID2R:ATAGAGAGGAGCGAAAGAGA
Glyma.12G022600	scarecrowlike protein 23(SCL23)	SCL23L:TTTCATCGAAACCTGGACTT	SCL23R:AGCTATTACGTGCTCTTGAG
Glyma.08G147900	pectinesterase 51 (F17I14.50)	Pectinesterase1L:ACAACAAGGGATGACA ACTT	Pectinesterase1R:AGTGAGTGAGCATAGA GAGT
Glyma.13G189800	gibberellin receptor (GID1C)	GID1CL:GCCAGAAGAGAAGCTACCCA	GID1CR:AAGAAGCCGTCATCAATCGC
Glyma.15G049000	Gboxbinding factor 4(F21M11.10)	Gbox4L:CCAGGATTTGTTGGGCTCTC	Gbox4R:AACTGTGTATGCCTGCTTGC
Glyma.16G063700	mybrelated protein 315 (MYB315)	Myb315L:AGGCTGAAACTCCTTGGTCT	Myb315R:GTGCCACCATTTTCCAAGGA
Glyma.02G067600	ethyleneresponsive transcription factor (LEP)	LEPL:CCAAACCCAAATCCACCAGG	LEPR:GCAATTCTTCGGTGCGAGA
Glyma.U038900	transcription factor (RAX3)	RAX3L:AGTTGTCGTCTTAGTGGCT	RAX3R:TCAGCCTCGTGTCCAGTAG
Glyma.12G238700	transcription factor (bHLH130)	bHLH130L:CCACTGACTTCTGGGATGGT	bHLH130R:ACTAGAAGAGCCAGGCAGAC
Glyma.04G101900	transcription factor (MYB39)	MYB39L:AAGGGGATCACACGGTTGAT	MYB39R:ATGCAAGATGGGGTCCCTCAA
Glyma.14G089800	extensinlike protein(EXTs)	EXTs1L:GAGGACACCAACTGGGTCAG	EXTs1R:ACGGTATGGCGATGCTTCTT
Glyma.08G069100	extensinlike protein(EXTs)	EXTs3L:ATTGCCAACTTTGCTCAGG	EXTs3R:GGTGAAGGTGGTGGAGAGA
Glyma.06G043400	extensinlike protein(EXTs)	EXTs2L:TTTCATCGAAACCTGGACTT	EXTs2R:AGCTATTACGTGCTCTTGAG
Glyma.16G173000	acidic endochitinase(Chitinase)	CHIL:TGCAAACCTCTGGCAGA	CHIR:GATTATGCACTGTGGGCTG
Glyma.19G062800	gibberellin 20 oxidase 1 (GA20 OX1)	GA20OX1L:CTGTCAATTGGTGCGGAGA G	GA20OX1R:TGTCCAGTGTAGCCATGGT T
Glyma.19G062600	gibberellin 20 oxidase 1 (GA20 OX1)	GA20OX2L:GTGGGTGAGAGCAATTTGG G	GA20OX2R:TGTTACAAGCGGGTATCC T
Glyma.10G122300	expansinB2(EXPs)	EXPL:GGTGGTGTCTGTGGTTATGG	EXPR:CACACCCAGGACAGCTATCA
Glyma.03G215800	pectinesterase(PEs)	PEsL:CGTAGTGTCTGTGATGGCTG	PEsR:TGGTATCCCTCAAAGCTGCA
Glyma.07G148900	RINGH2 finger protein RHC1a(PLs)	PLsL:AGGAGAAGGAAAGATGCGCA	PLsR:GGAAGAATTGAGCAGCTGGG
Glyma.17G22300	probable WRKY transcription factor 40 (WRKY40)	WRKY40L:ACATGGATGGGGCTTTGGT A	WRKY40R:ACTCTCGGCAGCTTTTCTCT C
Glyma.16G057400	26S protease regulatory subunit 7 (RPT1)	RPT1L:GGGACTGGCAAAACACTTTT	RPT1R:TTGAGTGGGCCATCTGAAAT
Glyma.08G339200	B3 domaincontaining transcription factor (VRN1)	VRN1L:CTTCTGGTTGGGGAGAGATC	VRN1R:TAGGAGTTGGAACCAGCAAG
Glyma.10G168900	germinlike protein subfamily 1 member 7 (At3g05950)	GerminL:CACTTCCAGCAAAACGTAGG	GerminR:TGCTTCTGAAGGTAGTCGAC
Glyma.18G195200	LRR receptorlike serine/threonineprotein kinase GSO2LRRL (K23L20.3)	LRRL:TAATGACATCTGCCATCCC	LRRLR:TTCCCGCAGATCAAGTTCTT
Glyma.17G224300	Ltype lectindomain containing receptor kinase IX.1(LECRK91)	LECRK91L:GGACTATGATTTCCGCGTT G	LECRK91R:GCTATGTAGAACCGGAAAC C
Glyma.08G367000	hydroquinone glucosyltransferase (AS)	ASL:CAGGAACATTGCAAAGGGAG	ASR:CATCCACTTCCAACCGACAC
Glyma.12G104800	mybrelated protein (Myb4)	Myb4L:GACATTTCTTTGATGCCCC	Myb4R:GTGTATGCATCGAGAAAGCC
Glyma.16G043200	NAC domaincontaining protein 18 (F14G24.15)	NACL:GGATGATTGGGTTCTTTGCC	NACR:ATGTGTTTTGAGGTGGAGGT
Glyma.20G057500	UDPglycosyltransferase 85A2 (UGT85A2)	UDPL:CACACAATTGCCACAAGACT	UDPR:TTCAGCAAAGAAAGGCCAAC
Glyma.09G027900	putative wallassociated receptor kinaselike 11 (WAKL11)	WAKL11L:AGACTTTGGGGCATCAAGA A	WAKL11R:CAAGAACCCTCAAAGCT G
Glyma.05G192300	proline rich extensinlike protein (EPR1)	EPR1L:CAAAGAAACCACCAACAGCA	EPR1R:GGAGCAGATGATGTTGGAGA
Glyma.05G101300	probable indole3acetic acidamido synthetase(GH3.1)	GH3.1L:CGTGATTTACTGGGAGCTCT	GH3.1R:GTTCCATTCTTACCACACG
Glyma.03G131200	gibberellin 20 oxidase 2 (GA20 OX2)	GA20OX2L:AGCGCAAAAGACTAGTGA GA	GA20OX2R:AGAAAACGATGATTTCCCTC C

Table 2 Suppl. The summary of RNA sequencing data from roots of gibberellic acid treatment and the control.

Sample	Treatment	Clean base pairs	Q30 ≥	Average clean reads	Average mapped reads	Percentage of mapped	Average unique match	Unique match percentage
T01	control	5323114736	96 %	42360478	36009952	85.01 %	30410151.33	78.9 %
T02	control	4855253956	97 %	38627284	33609514	87.01 %		
T03	control	4358489192	96 %	34647874	30279720	87.39 %		
T07	GA ₃	5774458790	96 %	45921796	40185675	87.51 %	30630844.67	78.1 %
T08	GA ₃	4461192586	96 %	35486606	30313304	85.42 %		
T09	GA ₃	5404817946	96 %	42983674	37307548	86.79 %		

Table 3 Suppl. Control vs gibberellic acid 3 differentially expressed genes (log₂FC > 3).

#ID	FDR	log ₂ FC	Regulation	Swissprot_annotation
20G062000.	8.7E-08	-	down	Nudix hydrolase 2 GN=MNJ7.24 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
13G104100.	8.3E-04	-	down	Probable polyamine oxidase 5 GN=PAO5 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
14G051600.	4.7E-14	-	down	--
15G222200.	1.5E-06	-	down	Histone H3.2 OS=Triticum aestivum (Wheat) PE=1 SV=2
07G187700.	5.9E-06	-	down	(3S,6E)-nerolidol synthase 1 OS=Fragaria ananassa (Strawberry) PE=1 SV=1
09G027900.	2.0E-10	-	down	Putative wall-associated receptor kinase-like 11 (Precursor) GN=WAKL11 OS=Arabidopsis thaliana (Mouse-ear cress) PE=3 SV=2
17G173200.	3.8E-07	-	down	Dihydroflavonol-4-reductase GN=DFR OS=Vitis vinifera (Grape) PE=1 SV=1
19G220800.	1.0E-07	-	down	Protein RADIALIS-like 6 GN=F22H5.3 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
17G214100.	2.4E-09	-	down	Probable receptor-like protein kinase At5g39020 (Precursor) GN=At5g39020 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
16G065000.	3.9E-05	-	down	Probable leucine-rich repeat receptor-like protein kinase At1g35710 (Precursor) GN=At1g35710 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
U024800.	8.7E-07	-	down	Probable LRR receptor-like serine/threonine-protein kinase At4g08850 (Precursor) GN=At4g08850 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=3
09G216400.	5.0E-20	-	down	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 (Precursor) GN=At3g47570 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
20G034200.	1.8E-04	-	down	Probable calcium-binding protein CML45 GN=CML45 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
05G192300.	3.0E-08	-	down	Proline-rich extensin-like protein EPR1 (Precursor) GN=EPR1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
18G270000.	2.6E-78	-	down	--
10G081800.	4.5E-03	-	down	Protein VAC14 homolog GN=VAC14 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
16G159300.	1.3E-06	-	down	TMV resistance protein N GN=N OS=Nicotiana glutinosa (Tobacco) PE=1 SV=1
16G064400.	1.9E-06	-	down	Probable LRR receptor-like serine/threonine-protein kinase At4g08850 (Precursor) GN=At4g08850 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=3
12G198200.	1.3E-06	-	down	G-type lectin S-receptor-like serine/threonine-protein kinase At4g03230 (Precursor) GN=At4g03230 OS=Arabidopsis thaliana (Mouse-ear cress) PE=3 SV=3
04G114500.	1.3E-03	-	down	--
18G218200.	5.6E-36	-	down	E3 ubiquitin-protein ligase RING1 GN=RING1 OS=Gossypium hirsutum (Upland cotton) PE=2 SV=1
09G254400.	8.5E-09	-	down	Probable WRKY transcription factor 24 GN=WRKY24 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
16G169200.	1.3E-11	-	down	Receptor-like protein 12 (Precursor) GN=RPL12 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
10G285300.	1.2E-06	-	down	E3 ubiquitin-protein ligase RING1 GN=RING1 OS=Gossypium hirsutum (Upland cotton) PE=2 SV=1
18G082300.	4.6E-03	-	down	Disease resistance protein RPM1 GN=F17A9.20 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
16G098100.	9.2E-08	-	down	Leucine aminopeptidase 3, chloroplastic (Precursor) GN=At4g30920 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
14G067200.	8.8E-17	-	down	Glycerol-3-phosphate acyltransferase 5 GN=GPAT5 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
20G057500.	3.9E-11	-	down	UDP-glycosyltransferase 85A2 GN=UGT85A2 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
18G082200.	2.0E-05	-	down	Disease resistance protein RPM1 GN=F17A9.20 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
08G339600.	3.2E-07	-	down	--
19G069300.	4.9E-37	-	down	Probable receptor-like protein kinase At5g39020 (Precursor) GN=At5g39020 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G367000.	6.8E-03	-7.70	down	Hydroquinone glucosyltransferase GN=AS OS=Rauvolfia serpentina (Serpentwood) PE=1 SV=1
14G136300.	2.4E-08	-7.13	down	Phytochromobilin:ferredoxin oxidoreductase, chloroplastic (Precursor) GN=HY2 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G339400.	1.8E-40	-6.60	down	--
02G054200.	3.7E-31	-6.49	down	Salicylate O-methyltransferase GN=SAMT OS=Clarkia breweri (Fairy fans) PE=1 SV=1
01G016700.	3.8E-03	-6.38	down	Inositol-tetrakisphosphate 1-kinase 1 GN=ITPK1 OS=Zea mays (Maize) PE=2 SV=1
06G187300.	9.6E-77	-6.26	down	--
08G339200.	2.1E-09	-6.11	down	B3 domain-containing transcription factor VRN1 GN=VRN1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
15G143900.	1.5E-08	-5.99	down	Sulfated surface glycoprotein 185 (Precursor) OS=Volvox carteri (Green alga) PE=1 SV=1
14G054100.	5.1E-05	-5.88	down	Probable amino acid permease 7 GN=AAP7 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
12G176200.	3.9E-09	-5.87	down	--
10G266500.	1.6E-40	-5.86	down	UPF0481 protein At3g47200 GN=At3g47200 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
10G028300.	2.8E-06	-5.66	down	Sucrose-binding protein (Precursor) GN=SBP OS=Glycine max (Soybean) PE=1 SV=1
08G339300.	1.3E-19	-5.53	down	--
17G222300.	1.6E-30	-5.29	down	Probable WRKY transcription factor 40 GN=WRKY40 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
13G243500.	5.1E-04	-5.27	down	Serine carboxypeptidase-like 31 (Precursor) GN=SCPL31 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
03G025200.	4.6E-03	-5.22	down	RuBisCO-associated protein OS=Glycine max (Soybean) PE=2 SV=1
16G218300.	5.6E-20	-5.20	down	Probable cyclic nucleotide-gated ion channel 20, chloroplastic (Precursor) GN=MKP6.28 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
10G005800.	5.8E-11	-4.99	down	--

#ID	FDR	log2FC	Regulation	Swissprot_annotation
18G293100.	5.6E-11	-4.86	down	MATE efflux family protein DTX1 GN=F3L12.13 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
12G198100.	3.7E-06	-4.85	down	G-type lectin S-receptor-like serine/threonine-protein kinase At4g03230 (Precursor) GN=At4g03230 OS=Arabidopsis thaliana (Mouse-ear cress) PE=3 SV=3
05G026100.	1.4E-09	-4.78	down	GDSL esterase/lipase At1g74460 (Precursor) GN=At1g74460 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
03G003000.	5.9E-10	-4.75	down	Putative receptor protein kinase ZmPK1 (Precursor) GN=PK1 OS=Zea mays (Maize) PE=2 SV=2
12G030300.	2.6E-09	-4.58	down	Dirigent protein 23 (Precursor) GN=DIR23 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
14G103100.	1.7E-17	-4.56	down	Probable WRKY transcription factor 40 GN=WRKY40 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
02G001500.	3.6E-08	-4.54	down	3-ketoacyl-CoA synthase 11 GN=KCS11 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
18G205600.	3.6E-08	-4.54	down	Receptor-like protein 12 (Precursor) GN=RLP12 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
13G267500.	3.6E-25	-4.44	down	Probable WRKY transcription factor 70 GN=WRKY70 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
16G144900.	7.1E-06	-4.38	down	GDSL esterase/lipase At2g23540 (Precursor) GN=At2g23540 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
14G003800.	1.1E-27	-4.37	down	Protein FANTASTIC FOUR 1 GN=FAF1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
06G213600.	3.3E-03	-4.35	down	Phosphatidylinositol 4-phosphate 5-kinase 3 GN=PIP5K3 OS=Arabidopsis thaliana (Mouse-ear cress) PE=4 SV=1
06G247100.	4.1E-10	-4.34	down	Protochlorophyllide reductase, chloroplastic (Precursor) GN=PORA OS=Cucumis sativus (Cucumber) PE=2 SV=1
12G224000.	1.1E-31	-4.32	down	--
18G195200.	7.3E-28	-4.29	down	LRR receptor-like serine/threonine-protein kinase GSO2 (Precursor) GN=K23L20.3 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
16G090000.	5.8E-35	-4.27	down	Cytochrome P450 82C4 GN=CYP82C4 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
03G002300.	5.2E-14	-4.20	down	Probable WRKY transcription factor 67 GN=WRKY67 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
16G176600.	4.4E-08	-4.19	down	Probable LRR receptor-like serine/threonine-protein kinase At4g36180 (Precursor) GN=At4g36180 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
13G113100.	9.6E-03	-4.12	down	Probable flavin-containing monooxygenase 1 GN=FMO1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
06G214400.	1.9E-07	-4.11	down	--
14G192500.	1.4E-17	-4.11	down	Cytochrome P450 86A1 GN=K19M22.6 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=2
12G069800.	3.9E-05	-4.08	down	Fasciclin-like arabinogalactan protein 12 (Precursor) GN=FLA12 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
04G168500.	2.1E-13	-4.07	down	GDSL esterase/lipase At1g74460 (Precursor) GN=At1g74460 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
11G130200.	1.2E-04	-3.90	down	Linoleate 13S-lipoxygenase 2-1, chloroplastic (Precursor) GN=LOX2.1 OS=Solanum tuberosum (Potato) PE=1 SV=1
13G190700.	9.9E-03	-3.88	down	--
17G224300.	1.4E-15	-3.84	down	L-type lectin-domain containing receptor kinase IX.1 (Precursor) GN=LECRK91 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
04G230000.	7.9E-14	-3.83	down	--
17G139900.	2.6E-46	-3.81	down	14 kDa proline-rich protein DC2.15 (Precursor) OS=Daucus carota (Carrot) PE=2 SV=1
09G016400.	1.9E-40	-3.78	down	--
19G176000.	5.3E-17	-3.70	down	ABC transporter G family member 20 GN=F4P12.210 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
14G028300.	7.3E-08	-3.69	down	Glycerol-3-phosphate acyltransferase 1 GN=GPAT1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
15G244200.	1.0E-04	-3.67	down	Secologanin synthase GN=CYP72A1 OS=Catharanthus roseus (Madagascar periwinkle) PE=2 SV=1
05G170900.	1.2E-08	-3.65	down	CASP-like protein 9 OS=Glycine max (Soybean) PE=2 SV=1
18G061300.	2.1E-04	-3.61	down	Gibberellin 2-beta-dioxygenase 8 GN=GA2OX8 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=2
06G103300.	4.2E-09	-3.60	down	Transcription factor MYB39 GN=dl4925c OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
15G077600.	1.6E-03	-3.60	down	Protein E6 GN=E6 OS=Gossypium hirsutum (Upland cotton) PE=2 SV=1
04G121000.	1.8E-20	-3.58	down	Derlin-1 GN=DER1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
02G062600.	5.3E-08	-3.54	down	GDSL esterase/lipase At2g23540 (Precursor) GN=At2g23540 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
07G161900.	2.4E-25	-3.53	down	Long chain acyl-CoA synthetase 2 GN=F13F21.14 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
02G249300.	1.6E-06	-3.52	down	Glycerol-3-phosphate acyltransferase 5 GN=GPAT5 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
06G194500.	1.6E-06	-3.52	down	GDSL esterase/lipase At1g74460 (Precursor) GN=At1g74460 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
U038200.	4.1E-08	-3.51	down	Pollen-specific leucine-rich repeat extensin-like protein 1 (Precursor) GN=PEX1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
11G175900.	3.1E-05	-3.50	down	Cytochrome P450 86A1 GN=K19M22.6 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=2
06G061900.	6.9E-08	-3.50	down	Probable WRKY transcription factor 40 GN=WRKY40 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
11G192400.	1.4E-07	-3.50	down	Protein SENSITIVE TO PROTON RHIZOTOXICITY 1 GN=STOP1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
03G061300.	1.1E-04	-3.49	down	--
03G113600.	2.2E-25	-3.47	down	--
12G104800.	2.8E-09	-3.42	down	Myb-related protein Myb4 GN=OSJNBa0073E02.6 OS=Oryza sativa subsp. japonica (Rice) PE=2 SV=2

#ID	FDR	log2FC	Regulation	Swissprot_annotation
15G202700.	3.8E-26	-3.39	down	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 (Precursor) GN=At3g47570 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
01G069000.	8.7E-15	-3.39	down	--
03G016300.	1.1E-06	-3.38	down	BON1-associated protein 2 GN=F4I18.26 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
08G087400.	3.3E-23	-3.37	down	--
10G179400.	2.9E-05	-3.36	down	3-ketoacyl-CoA synthase 19 GN=KCS19 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
06G263700.	1.6E-12	-3.36	down	Toll/interleukin-1 receptor-like protein GN=TIR OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
13G185200.	1.7E-11	-3.34	down	PAP-specific phosphatase HAL2-like GN=AHL OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
18G219700.	6.3E-11	-3.29	down	Cysteine-rich receptor-like protein kinase 10 (Precursor) GN=F21P8.70 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=3
02G186900.	1.0E-20	-3.28	down	Probable calcium-binding protein CML50 GN=CML50 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
01G200400.	9.8E-09	-3.26	down	Peroxidase 20 (Precursor) GN=T32F12.24 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
03G024500.	1.8E-05	-3.25	down	RuBisCO-associated protein OS=Glycine max (Soybean) PE=2 SV=1
13G029200.	5.9E-16	-3.24	down	Serine carboxypeptidase-like 40 (Precursor) GN=SCPL40 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
14G100600.	3.9E-05	-3.24	down	L-type lectin-domain containing receptor kinase IX.1 (Precursor) GN=LECRK91 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
09G099900.	4.7E-36	-3.22	down	Probable LRR receptor-like serine/threonine-protein kinase At1g56130 (Precursor) GN=At1g56130 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=2
05G005800.	1.5E-04	-3.20	down	Polygalacturonase At1g48100 (Precursor) GN=At1g48100 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G169300.	1.9E-05	-3.19	down	Feruloyl CoA ortho-hydroxylase 1 GN=F'H1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
17G187300.	1.9E-05	-3.19	down	--
15G057500.	3.9E-07	-3.18	down	Proline-rich receptor-like protein kinase PERK2 GN=PERK2 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=3
04G223300.	9.5E-39	-3.18	down	Probable WRKY transcription factor 70 GN=WRKY70 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
15G178300.	5.8E-12	-3.17	down	Protein LURP-one-related 6 GN=At2g05910 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G069100.	1.3E-04	-3.16	down	Leucine-rich repeat extensin-like protein 5 (Precursor) GN=LRX5 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=2
10G036800.	5.4E-21	-3.13	down	Inorganic phosphate transporter 1-4 GN=T7F6.11 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
15G164800.	3.6E-04	-3.11	down	--
06G264100.	3.6E-04	-3.11	down	TMV resistance protein N GN=N OS=Nicotiana glutinosa (Tobacco) PE=1 SV=1
15G191800.	3.1E-07	-3.08	down	CASP-like protein 9 OS=Glycine max (Soybean) PE=2 SV=1
16G137200.	3.1E-25	-3.08	down	TMV resistance protein N GN=N OS=Nicotiana glutinosa (Tobacco) PE=1 SV=1
03G165800.	6.1E-26	-3.06	down	Probable leucine-rich repeat receptor-like protein kinase At1g35710 (Precursor) GN=At1g35710 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
09G022800.	6.1E-43	-3.05	down	Peroxidase 54 (Precursor) GN=MPH15.9 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
15G140200.	1.2E-04	-3.04	down	ATP-citrate synthase beta chain protein 1 OS=Oryza sativa subsp. japonica (Rice) PE=2 SV=1
05G184500.	5.0E-23	-3.03	down	Probable WRKY transcription factor 51 GN=WRKY51 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G129300.	7.2E-06	-3.03	down	CASP-like protein 9 OS=Glycine max (Soybean) PE=2 SV=1
02G156100.	2.5E-05	3.17	up	Cytochrome P450 71D8 GN=CYP71D8 OS=Glycine max (Soybean) PE=2 SV=1
16G057400.	5.4E-10	3.21	up	26S protease regulatory subunit 7 GN=RPT1 OS=Prunus persica (Peach) PE=1 SV=1
03G226800.	9.3E-03	3.37	up	Secologanin synthase GN=CYP72A1 OS=Catharanthus roseus (Madagascar periwinkle) PE=2 SV=1
17G092800.	2.0E-03	3.43	up	Snakin-2 (Precursor) GN=SN2 OS=Solanum tuberosum (Potato) PE=1 SV=1
19G199900.	2.9E-06	3.48	up	Aluminum-activated malate transporter 8 GN=ALMT8 OS=Arabidopsis thaliana (Mouse-ear cress) PE=3 SV=1
17G023100.	3.5E-09	3.69	up	CASP-like protein 5 OS=Glycine max (Soybean) PE=2 SV=1
17G127900.	1.2E-16	3.74	up	Proline-rich receptor-like protein kinase PERK8 GN=PERK8 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
09G183500.	2.9E-11	3.76	up	Transcription factor BEE 1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
16G043200.	6.3E-09	3.83	up	NAC domain-containing protein 18 GN=F14G24.15 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
19G046000.	5.9E-04	4.01	up	O-acyltransferase WSD1 GN=WSD1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
05G101300.	3.8E-33	4.04	up	Probable indole-3-acetic acid-amido synthetase GH3.1 GN=GH3.1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
10G168900.	5.4E-12	4.24	up	Germin-like protein subfamily 1 member 7 (Precursor) GN=At3g05950 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
02G239400.	5.8E-15	4.37	up	Probable acyl-activating enzyme 5, peroxisomal GN=MQK4.9 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
10G215700.	2.0E-15	4.41	up	Isoliquiritigenin '-O-methyltransferase OS=Medicago sativa (Alfalfa) PE=1 SV=1
01G050700.	8.0E-07	5.94	up	CASP-like protein 1 OS=Glycine max (Soybean) PE=2 SV=1
03G202200.	7.3E-05	6.13	up	Aluminum-activated malate transporter 8 GN=ALMT8 OS=Arabidopsis thaliana (Mouse-ear cress) PE=3 SV=1
12G194600.	3.3E-07	6.36	up	--
08G174900.	6.1E-03	9.39	up	Glutathione S-transferase 3 GN=GST3 OS=Glycine max (Soybean) PE=1 SV=1
13G278000.	3.8E-03	+	up	Defensin-like protein (Precursor) OS=Vigna unguiculata (Cowpea) PE=3 SV=1
10G103200.	3.7E-03	+	up	Polygalacturonase (Precursor) OS=Actinidia deliciosa (Kiwi) PE=2 SV=1
10G061800.	3.0E-03	+	up	Thaumatococin-like protein 1a (Precursor) GN=TL1 OS=Malus domestica (Apple) PE=1 SV=1
11G021100.	5.5E-03	+	up	Endoglucanase (Precursor) OS=Phaseolus vulgaris (Kidney bean) PE=2 SV=2

#ID	FDR	log2FC	Regulation	Swissprot_annotation
07G124400.	1.9E-08	+	up	Feruloyl CoA ortho-hydroxylase 1 GN=F6'H1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1
18G190200.	1.3E-06	+	up	Probable glutathione S-transferase GN=HSP26-A OS=Glycine max (Soybean) PE=2 SV=1
12G234600.	6.0E-03	+	up	Probable sodium/metabolite cotransporter BASS1, chloroplastic (Precursor) GN=T30F21.11 OS=Arabidopsis thaliana (Mouse-ear cress) PE=2 SV=1
08G179600.	7.7E-03	+	up	Cationic peroxidase 2 (Precursor) GN=PNC2 OS=Arachis hypogaea (Peanut) PE=2 SV=1
03G096500.	5.5E-03	+	up	Feruloyl CoA ortho-hydroxylase 1 GN=F6'H1 OS=Arabidopsis thaliana (Mouse-ear cress) PE=1 SV=1

Table 4 Suppl. Kyoto encyclopedia of genes and genomes (KEGG) statistics data. #KEGG_n: 149;KEGG_N: 7654.

#Pathway	ko_ID	Unigene	Gene	Gene ID	KO
Glycolysis / gluconeogenesis	ko00010	4	279	01G019200;03G046100;04G008300;13G170600	K01610+K01835+K01623+K00128
Citrate cycle (TCA cycle)	ko00020	2	114	01G019200;15G140200	K01610+K01648
Pentose phosphate pathway	ko00030	2	115	03G046100;04G008300	K01835+K01623
Pentose and glucuronate interconversions	ko00040	10	142	02G016500;03G215800;05G114000;06G314200;13G170600;13G186000;15G223500;18G044400;19G053800;20G023200	K01051+K01051+K01728+K01051+K00128+K01051+K01051+K00963+K01728+K01184
Fructose and mannose metabolism	ko00051	1	116	04G008300	K01623
Galactose metabolism	ko00052	4	95	01G211000;03G046100;09G028000;18G044400	K01193+K01835+K01187+K00963
Ascorbate and aldarate metabolism	ko00053	1	77	13G170600	K00128
Fatty acid biosynthesis	ko00061	2	63	08G024700;13G038600	K09458+K03921
Fatty acid metabolism	ko00071	4	106	07G161900;12G047400;13G170600;20G007900	K01897+K01897+K00128+K01897
Oxidative phosphorylation	ko00190	2	299	12G231900;19G019200	K02109+K01535
Photosynthesis	ko00195	5	139	01G180800;04G020300;10G249000;12G231900;16G143600	K02716+K02638+K02692+K02109+K02716
Photosynthesis - antenna proteins	ko00196	5	40	03G060300;03G262300;05G128000;16G145800;18G028400	K08915+K08908+K08912+K08907+K08915
Purine metabolism	ko00230	3	304	03G046100;16G037200;16G043300	K01835+K00601+K14641
Pyrimidine metabolism	ko00240	1	243	16G043300	K14641
Alanine, aspartate and glutamate metabolism	ko00250	3	119	11G170300;11G171400;18G061100	K01953+K01953+K01953
Cysteine and methionine metabolism	ko00270	5	186	02G268000;04G245900;05G036300;08G050400;09G258000	K05933+K05933+K00797+K05933+K13034
Valine, leucine and isoleucine degradation	ko00280	1	97	13G170600	K00128
Lysine degradation	ko00310	1	37	13G170600	K00128
Arginine and proline metabolism	ko00330	3	175	04G020200;05G036300;13G170600	K01581+K00797+K00128
Histidine metabolism	ko00340	1	55	13G170600	K00128
Phenylalanine metabolism	ko00360	12	158	02G234200;06G302700;09G023000;09G109800;11G161600;13G307000;14G221400;15G163500;16G055900;18G055300;20G114200;20G169200	K00430+K00430+K00430+K00430+K00430+K00430+K00430+K00430+K00430+K00430+K00430+K00430
Tryptophan metabolism	ko00380	4	55	04G079700;05G231100;07G086200;13G170600	K11816+K11816+K11816+K00128
beta-Alanine metabolism	ko00410	2	80	05G036300;13G170600	K00797+K00128
Taurine and hypotaurine metabolism	ko00430	3	34	09G240100;15G207700;17G187300	K10712+K10712+K10712
Selenocompound metabolism	ko00450	2	33	12G018300;13G000200	K01874+K01874
Cyanoamino acid metabolism	ko00460	1	48	09G258000	K13034
Glutathione metabolism	ko00480	6	143	02G024800;04G020200;05G036300;06G060500;16G098100;18G111300	K00799+K01581+K00797+K01256+K01255+K00799
Starch and sucrose metabolism	ko00500	11	288	01G211000;02G016500;03G046100;03G215800;03G216300;06G314200;09G028000;13G186000;15G223500;18G044400;20G023200	K01193+K01051+K01835+K01051+K00695+K01051+K01187+K01051+K01051+K00963+K01184
N-Glycan biosynthesis	ko00510	1	86	11G243000	K00737
Amino sugar and nucleotide sugar metabolism	ko00520	2	229	03G046100;18G044400	K01835+K00963
Glycerolipid metabolism	ko00561	6	110	02G249300;07G069700;07G146800;13G170600;14G028300;14G067200	K13508+K13508+K13508+K00128+K13508+K13508
Inositol phosphate metabolism	ko00562	3	112	01G016700;03G092800;08G138200	K00913+K01114+K01858
Glycerophospholipid metabolism	ko00564	6	129	02G249300;03G092800;07G069700;07G146800;14G028300;14G067200	K13508+K01114+K13508+K13508+K13508+K13508
Ether lipid metabolism	ko00565	1	35	03G092800	K01114
Glycosphingolipid biosynthesis - globo series	ko00603	1	20	01G114900	K01988
Pyruvate metabolism	ko00620	2	194	01G019200;13G170600	K01610+K00128
Glyoxylate and dicarboxylate metabolism	ko00630	1	73	19G046800	K01602
Propanoate metabolism	ko00640	1	71	13G170600	K00128
One carbon pool by folate	ko00670	1	42	16G037200	K00601
Carbon fixation in photosynthetic organisms	ko00710	3	164	01G019200;04G008300;19G046800	K01610+K01623+K01602
Lipoic acid metabolism	ko00785	1	10	08G314300	K03801
Folate biosynthesis	ko00790	1	27	03G085500	K01495

Table 5 Suppl. Differentially expressed genes information in plant hormone signal transduction.

Gene name	ko_ID, ID, log2FC
	K13447
Rboh	Glyma.03G236300.Wm82.a2.v1;Glyma.10G152200.Wm82.a2.v1;Glyma.19G233900.Wm82.a2.v1;Glyma.20G236200.Wm82.a2.v1 (-1.16947218981932;-1.27516278907062;-1.06998555490937;-1.10886196632517)
	K13448
CaMCML	Glyma.02G186900.Wm82.a2.v1;Glyma.02G245700.Wm82.a2.v1;Glyma.04G245000.Wm82.a2.v1;Glyma.06G034700.Wm82.a2.v1 ;Glyma.13G035100.Wm82.a2.v1;Glyma.14G156300.Wm82.a2.v1 (-3.2841993117944;-1.0746296289184;-1.97470671523417;-1.8559818560161;-1.84798282967927;-1.30807347303143)
BAK1	K13416 Glyma.05G119500.Wm82.a2.v1 (-1.34959507387288)
MAP2K1	K04368 Glyma.15G172600.Wm82.a2.v1 (-1.06293892595367)
WRKY29	K13424 Glyma.09G280200.Wm82.a2.v1 (-1.1339768007554)
WRKY33	K13426 Glyma.05G211900.Wm82.a2.v1 (-1.16050368060781)
SGT1	K12795 Glyma.10G230000.Wm82.a2.v1 (-1.31628006797866)
GH3	K14487 Glyma.05G101300.Wm82.a2.v1 (4.04426964418934);K14487 Glyma.06G260800.Wm82.a2.v1 (-1.08939388652773) K14488 Glyma.04G025500.Wm82.a2.v1;Glyma.08G010400.Wm82.a2.v1;Glyma.14G217800.Wm82.a2.v1
SAUR	(1.37391243192958;2.0357707403275;1.16541301985044); K14488 Glyma.06G079200.Wm82.a2.v1;Glyma.10G056000.Wm82.a2.v1 (-1.26643033136478;-2.55397973276383)
AHP4	K14490 Glyma.13G354700.Wm82.a2.v1 (-2.65405704713969)
ERF1/2	K14516 Glyma.20G203700.Wm82.a2.v1 (-1.6249261621763)
JAZ	K13464 Glyma.13G116100.Wm82.a2.v1 (1.99167488478208)
ABF	K14432 Glyma.15G049000.Wm82.a2.v1 (1.89677638734186)
BKI1	K14499 Glyma.14G082300.Wm82.a2.v1 (-1.60168833388679)

Table 6 Suppl. Effects of gibberellic acid 3 on the expressions of cell wall biogenesis/degradation related genes.

	Gene	Gene ID(Wm82.a2.v1)	log ₂ FC
EXP(s)	expansin-B2	Glyma.10G122300	-1.70
EGases	endoglucanase	Glyma.11G021100	
β-galactosidases	β-galactosidase 8	Glyma.11G147900	-1.01
glucosidases	β-glucosidase activity	Glyma.20G133900	-1.93
glucosidases	β-glucosidase activity	Glyma.08G180900	-1.47
glucosidases	α-glucosidase	Glyma.09G028000	-1.60
glucosidases	sucrose α-glucosidase activity	Glyma.17G227900	-1.69
glucosidases	sucrose α-glucosidase activity	Glyma.17G227800	-1.12
glucosidases	β-glucosidase	Glyma.12G130200	-1.33
glucosidases	β-glucosidase	Glyma.11G129600	-1.47
glucosidases	β-glucosidase	Glyma.12G053900	-1.60
glucosidases	β-glucosidase	Glyma.11G129500	-1.68
glucosidases	β-glucosidase	Glyma.12G054100	-1.86
glucosidases	β-glucosidase	Glyma.11G129900	-1.19
glucosidases	β-glucosidase	Glyma.11G129700	-1.33
glucosidases	glucan endo-1,3-β-glucosidase 14	Glyma.20G018200	2.76
PLs	pectate lyase	Glyma.05G114000	-1.38
PLs	pectate lyase	Glyma.19G053800	-1.77
PEs	pectinesterase	Glyma.15G223500	-1.97
PEs	pectinesterase	Glyma.06G314200	-1.22
PEs	pectinesterase	Glyma.03G028500	-1.65
PEs	pectinesterase	Glyma.06G152400	-1.18
PEs	pectinesterase	Glyma.09G232000	-1.48
PEs	pectinesterase	Glyma.13G186000	-1.65
PEs	pectinesterase	Glyma.17G180500	-1.13
PEs	pectinesterase	Glyma.03G215800	-2.09
PEs	pectinesterase	Glyma.05G236800	1.29
PEs	pectinesterase	Glyma.08G147900	1.01
PEs	pectinesterase	Glyma.03G103400	-1.16
PEs	pectinesterase	Glyma.02G016500	-1.77
β-1,3-glucanases	glucan endo-1,3-β-glucanase activity	Glyma.18G266900	-1.55
β-1,3-glucanases	acid β-fructofuranosidase	Glyma.01G211000	-1.54
PGs	polygalacturonase	Glyma.16G179000	2.52
PGs	polygalacturonase	Glyma.10G103200	
PGs	polygalacturonase	Glyma.19G006200	-1.57
PGs	polygalacturonase	Glyma.01G027900	1.27
PGs	polygalacturonase	Glyma.10G010000	1.09
PGs	polygalacturonase	Glyma.05G005800	-3.2
PGs	polygalacturonase	Glyma.13G364700	-1.58
PGs	polygalacturonase	Glyma.20G023200	1.20
PGs	polygalacturonase	Glyma.15G008900	-1.42
PGs	polygalacturonase	Glyma.19G145200	1.31
PGs	polygalacturonase	Glyma.19G032600	-1.98
	glycogenin glucosyltransferase	Glyma.13G053000	-1.64
EXTs	extensin-like protein	Glyma.08G032100	-1.38
EXTs	extensin-like protein	Glyma.05G192300	
EXTs	extensin-like protein	Glyma.14G121800	-1.24
EXTs	extensin-like protein	Glyma.19G125300	-1.03
EXTs	extensin-like protein	Glyma.08G069100	-3.16
EXTs	extensin-like protein	Glyma.14G089800	-2.77
EXTs	extensin-like protein	Glyma.06G034300	-1.48
EXTs	extensin-like protein	Glyma.U038200	-3.51
Cellulose synthase	cellulose synthase	Glyma.04G255400	1.30
Cellulose synthase	cellulose synthase	Glyma.10G145300	-1.47
Chitinase	acidic endochitinase	Glyma.16G173000	-2.14

Table 7 Suppl. Reverse transcription quantitative PCR (RT-qPCR) validation of differentially expressed genes from RNA sequencing. FPKM - fragments per kilobase of transcripts per million mapped fragments.

#ID	Gene	RT-qPCR /log2 $\Delta\Delta$ Ct	log2FC	Control_FPKM	MGA_FPKM
Glyma18g52780.1	cytoskeletal structural protein(ActII)				
Glyma02g44460.1	eukaryotic elongation factor 1(LF1B)				
Glyma.18G061300	gibberellin 2-beta-dioxygenase(GA2OX8)		-3.61	2.9462	0.2757
Glyma.06G043400	F-box protein (GID2)	-2.9	-1.59	22.7750	7.5280
Glyma.12G022600	scarecrow-like protein 23(SCL23)		1.14	1.0353	2.2040
Glyma.08G147900	pectinesterase 51 (F17114.50)	1.23	1.01	2.6172	5.2799
Glyma.13G189800	gibberellin receptor (GID1C)	1.54	2.04	2.4739	9.7250
Glyma.15G049000	G-box-binding factor 4(F21M11.10)	1.52	1.90	0.4533	1.5708
Glyma.16G063700	Myb-related protein 315 (MYB315)	1.32	1.85	0.6974	2.5536
Glyma.02G067600	ethylene-responsive transcription factor (LEP)	1.02	1.20	1.9317	4.4729
Glyma.U038900	transcription factor (RAX3)	1.25	1.04	1.6436	3.4610
Glyma.12G238700	transcription factor (bHLH130)	-2.34	-1.03	3.0078	1.5683
Glyma.04G101900	transcription factor (MYB39)	-2.58	-2.07	3.0697	0.8050
Glyma.14G089800	extensin-like protein(EXTs)	-3.12	-2.77	0.8636	0.0000
Glyma.08G069100	extensin-like protein(EXTs)	-2.15	-3.16	4.0135	0.6048
Glyma.06G043400	extensin-like protein(EXTs)	-3.68	-1.48	4.5191	0.4550
Glyma.16G173000	acidic endochitinase(Chitinase)	-3.05	-2.14	34.4029	7.9507
Glyma.19G062800	gibberellin 20 oxidase 1 (GA20 OX1)	-0.5	-1.19	29.4101	13.7217
Glyma.19G062600	gibberellin 20 oxidase 1 (GA20 OX1)	-2.31	-1.48	29.6404	11.2149
Glyma.10G122300	expansin-B2(EXPs)	0.64	-1.70	13.1341	4.0687
Glyma.03G215800	pectinesterase(PEs)		-2.09	9.4007	2.2407
Glyma.07G148900	RING-H2 finger protein RHC1a(PLs)		-2.27	2.6227	0.6071
Glyma.17G222300	probable WRKY transcription factor 40 (WRKY40)	-2.59	-5.29	4.0564	0.1408
Glyma.16G057400	26S protease regulatory subunit 7 (RPT1)	2.14	3.21	0.2231	1.8007
Glyma.08G339200	B3 domain-containing transcription factor (VRN1)	-2.1	-6.11	1.2876	0.0468
Glyma.10G168900	germin-like protein subfamily 1 member 7 (At3g05950)	3.21	4.24	0.9344	16.9924
Glyma.18G195200	LRR receptor-like serine/threonine-protein kinase GSO2 (K23L20.3)	-1.54	-4.29	1.7012	0.1088
Glyma.17G224300	L-type lectin-domain containing receptor kinase IX.1(LECRK91)	-1.43	-3.84	4.2674	0.3141
Glyma.08G367000	hydroquinone glucosyltransferase (AS)	-3.67	-7.70	2.3586	0.0285
Glyma.12G104800	Myb-related protein (Myb4)	-2.96	-3.42	2.1612	0.2361
Glyma.16G043200	NAC domain-containing protein 18 (F14G24.15)		3.83	0.1101	1.3073
Glyma.20G057500	UDP-glycosyltransferase 85A2 (UGT85A2)	-1.58		0.9556	0.0000
Glyma.09G027900	putative wall-associated receptor kinase-like 11 (WAKL11)	-3.67		0.7522	0.0000
Glyma.05G192300	proline-rich extensin-like protein (EPR1)			0.8636	0.0000
Glyma.05G101300	probable indole-3-acetic acid-amido synthetase(GH3.1)	1.81	4.04	0.2279	3.5235
Glyma.03G131200	gibberellin 20 oxidase 2 (GA20 OX2)	-2.35	-1.01	3.9844	2.0343

Table 8 Suppl. Correlation of reverse transcription quantitative PCR (RT-qPCR) and RNA sequencing data of differentially expressed genes.

		log2FC	RT-qPCR/log2 $\Delta\Delta$ Ct
log2FC	Pearson coefficient	1	.853
	Sig.(2-tailed)		.000
	N	24	24
RT-qPCR/log2 $\Delta\Delta$ Ct	Pearson coefficient	0.853	1
	Sig.(2-tailed)	0.000	
	N	24	24

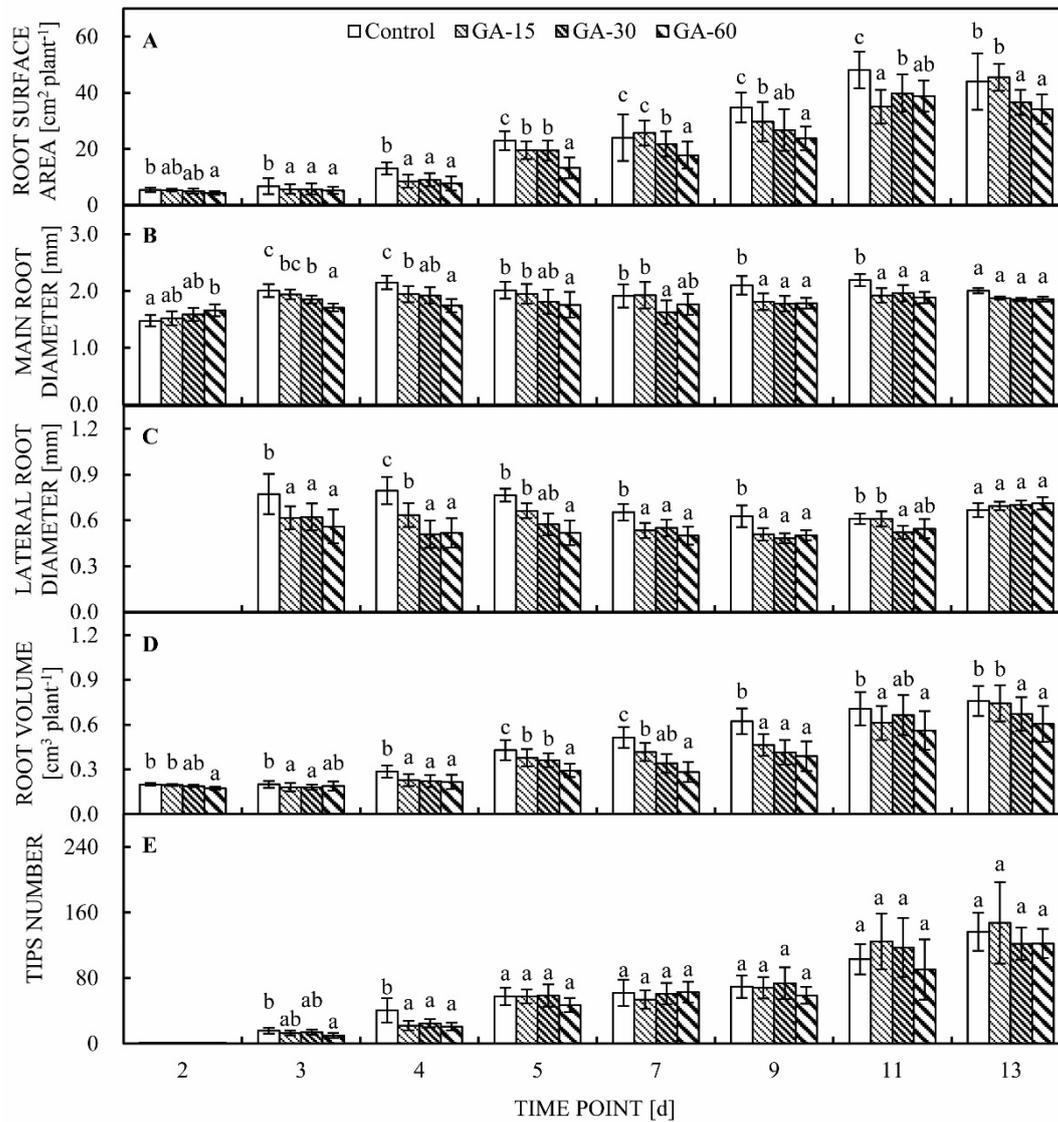


Fig. 1 Suppl. Gibberellic acid 3 (GA₃) treatment modulates different morphophysiological parameters of roots measured at different time points. Soybean seeds were soaked in 0.43, 0.87, and 1.74 mM GA₃ for 12 h (corresponding to three different treatments GA-15, GA-30, and GA-60) and then cultivated in sand moistened with a nutrient solution for 13 d. Means ± SEs, $n \geq 20$, different letters indicate significant differences ($P \leq 0.05$) according to analysis of variance (one way ANOVA) with the Tukey's multiple comparison posttest.

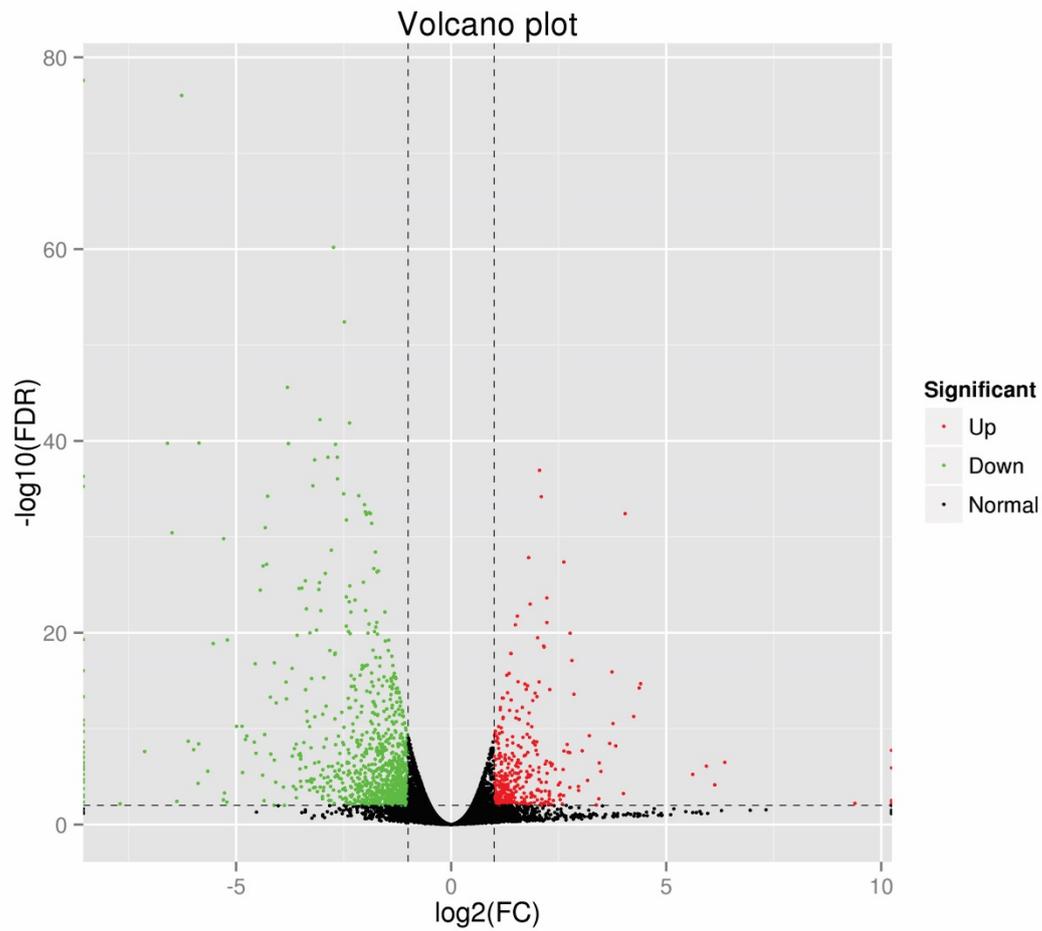


Fig. 2 Suppl. Cufflinks volcano plots of differentially expressed genes under various gibberellic acid 3 treatments. Each dot represents an individual gene. *Black dots* represent genes that were not differentially expressed, whereas *red dots* represent genes that had significantly higher expressions, and *green dots* represent genes that had significantly lower expressions.

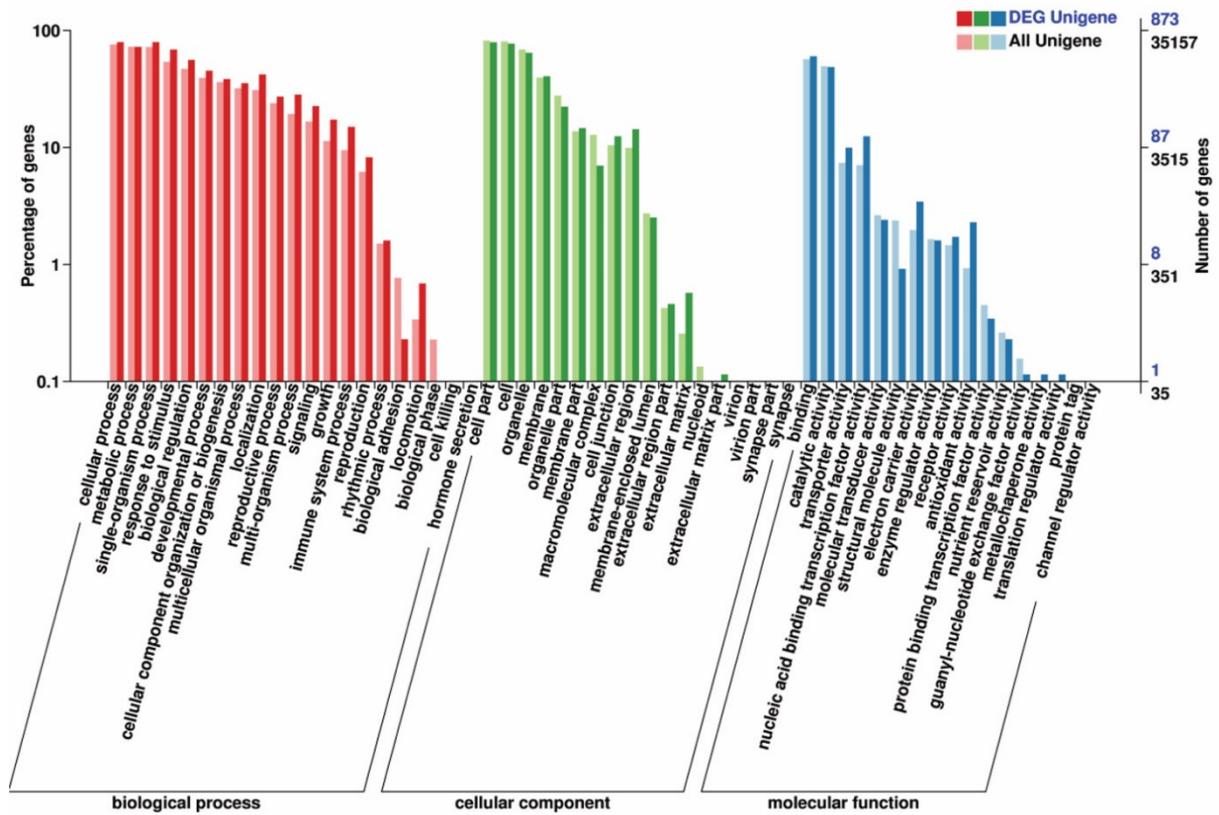


Fig. 3 Suppl. Gene ontology classification of the differentially expressed genes (DEGs) between gibberellic acid 3 treatments and the control. Differentially expressed genes were classified into three *GO* categories: biological processes, cellular components, and molecular functions.

COG Function Classification of Consensus Sequence

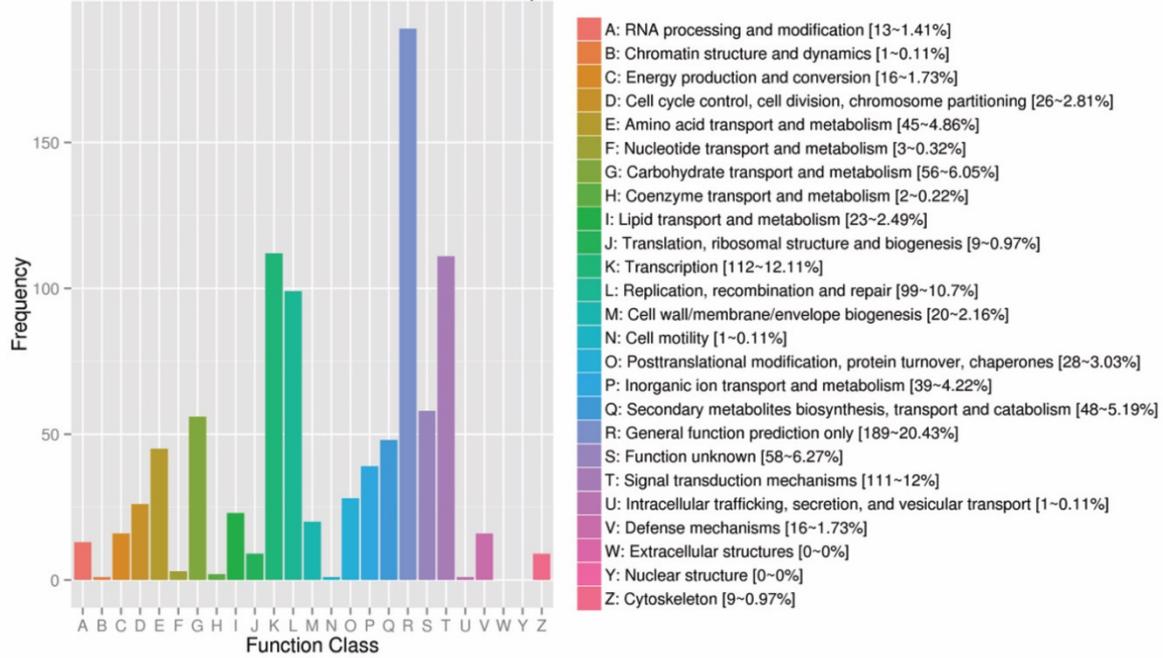


Fig. 4 Suppl. Clusters of orthologous group (COG) classifications of putative proteins. All putative proteins were aligned to the COG database and can be classified functionally into at least 25 molecular families.

PLANT HORMONE SIGNAL TRANSDUCTION

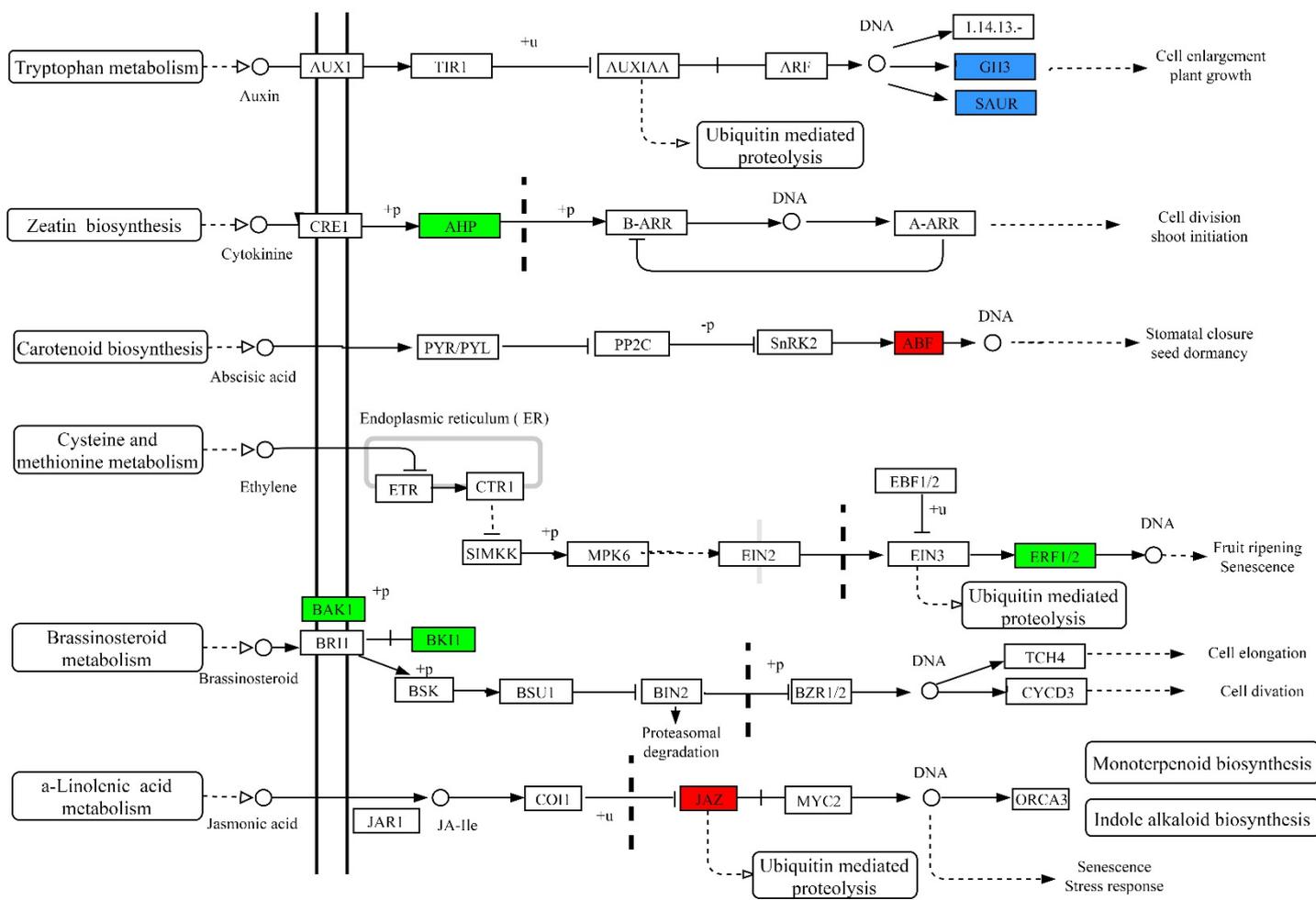


Fig. 5 Suppl. Differentially expressed genes in plant hormone signal transduction. Red blocks - up-regulated; green blocks - down-regulated; blue blocks - some genes up-regulated and some genes down-regulated.

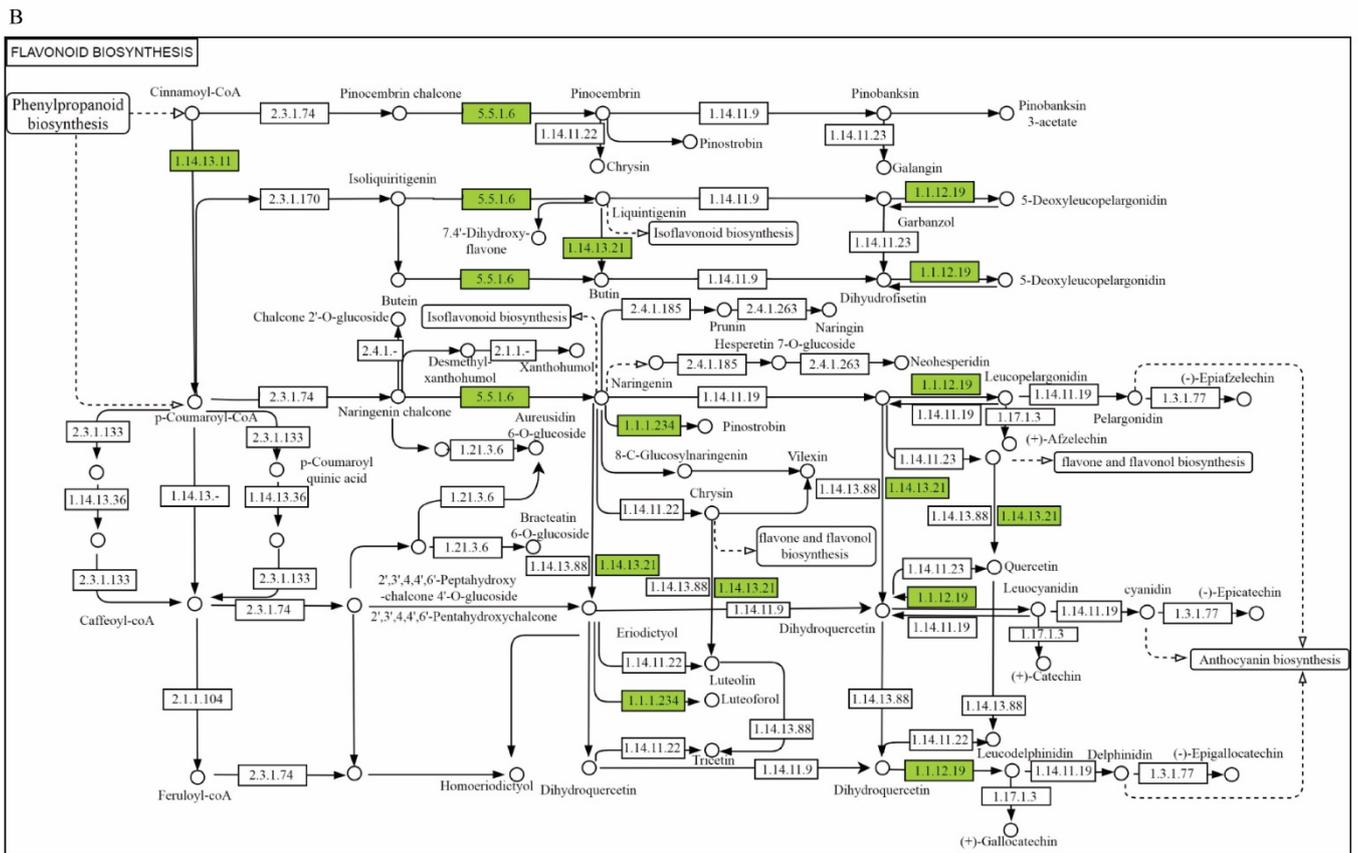
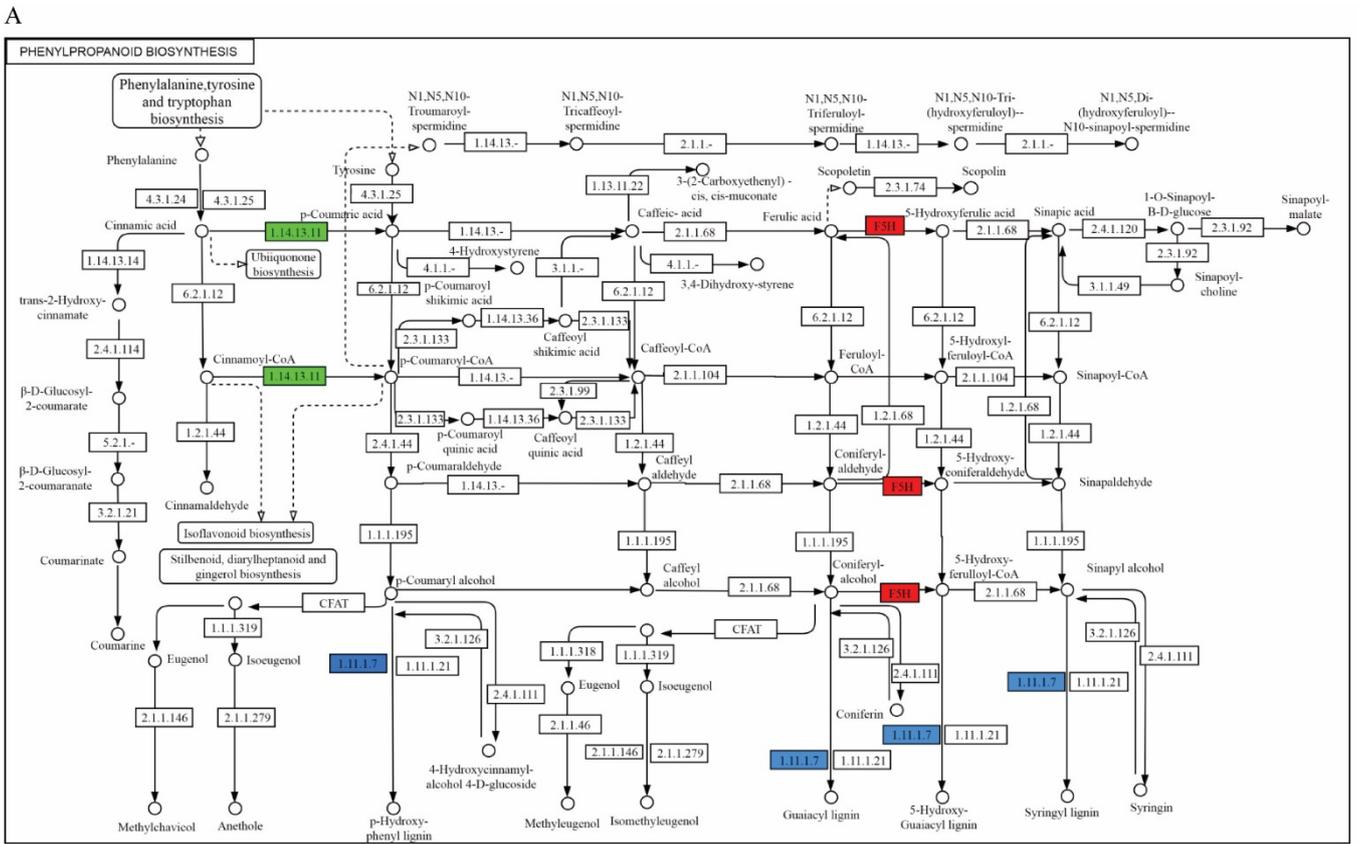


Fig. 6 Suppl. Differentially expressed genes in the flavonoid biosynthesis pathway and the phenylpropanoid biosynthesis pathway. Red blocks - up-regulated; green blocks - down-regulated; blue blocks - some genes up-regulated and some genes down-regulated.