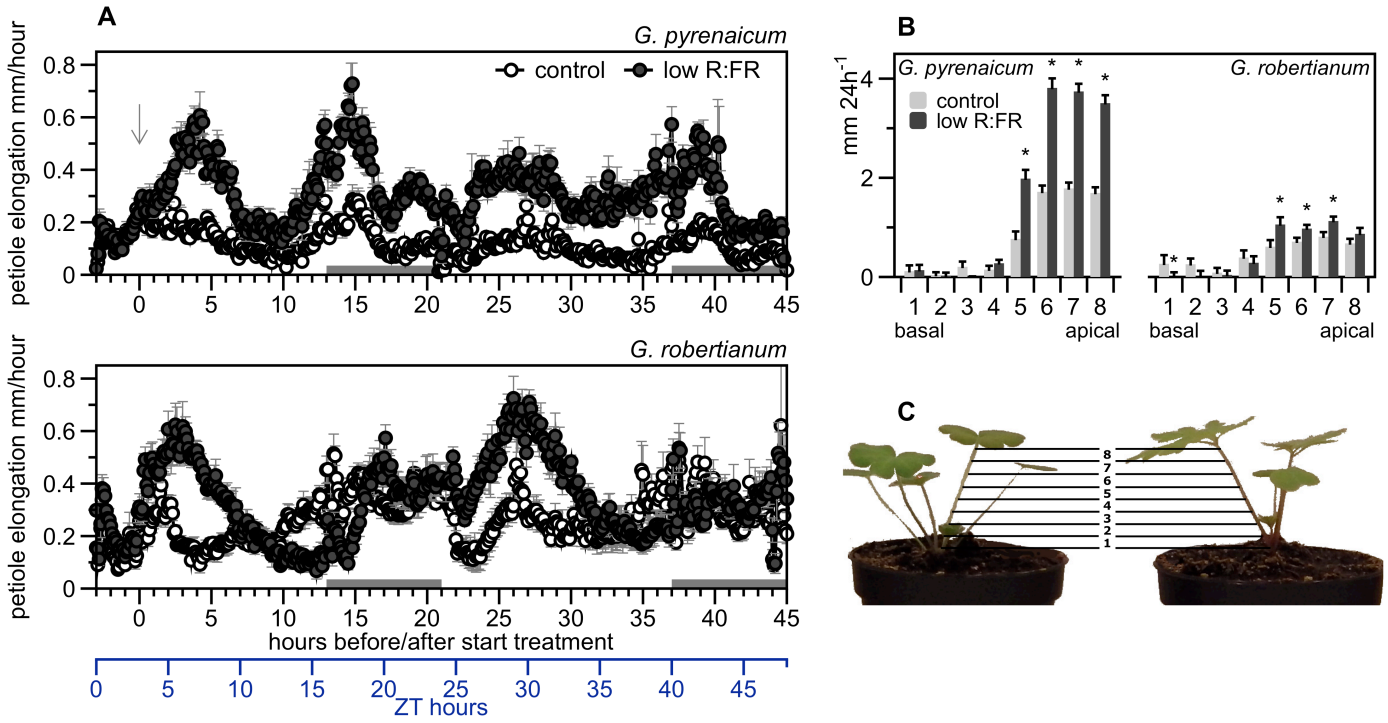
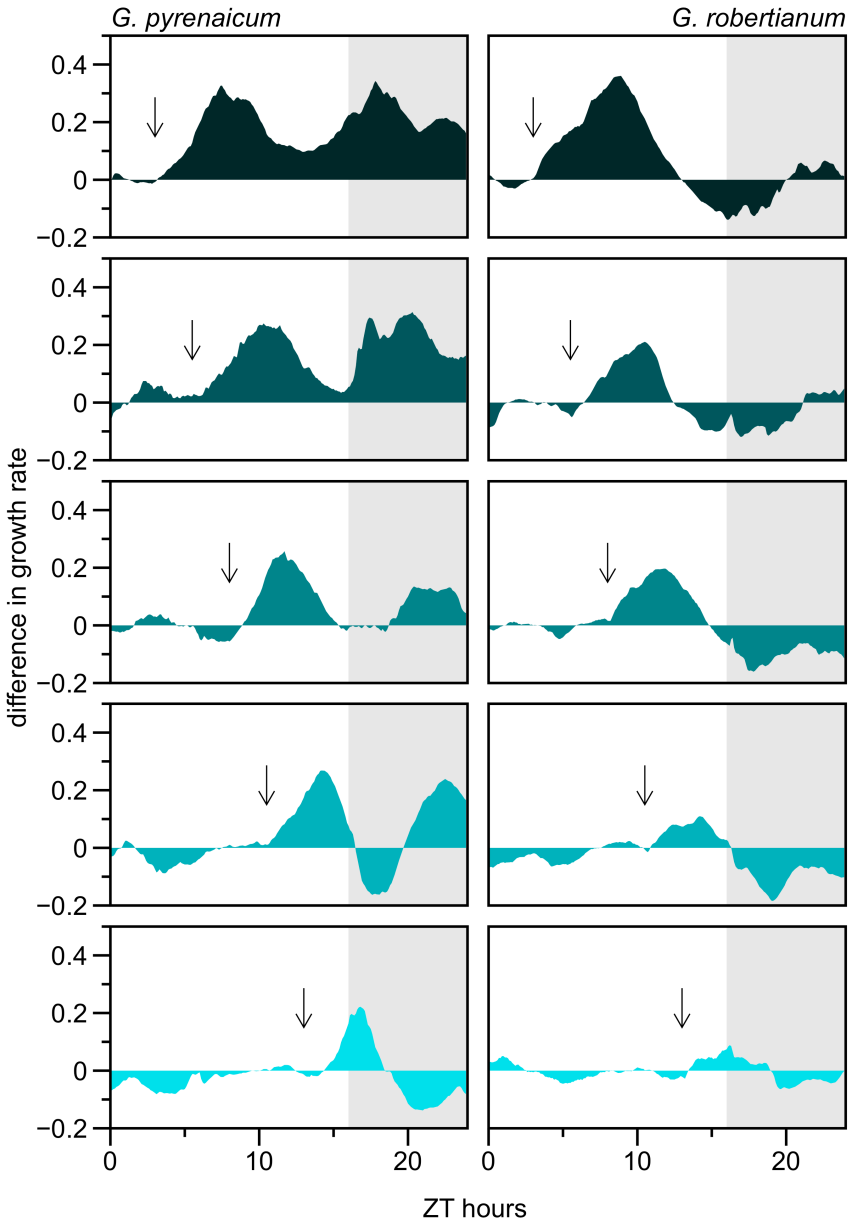
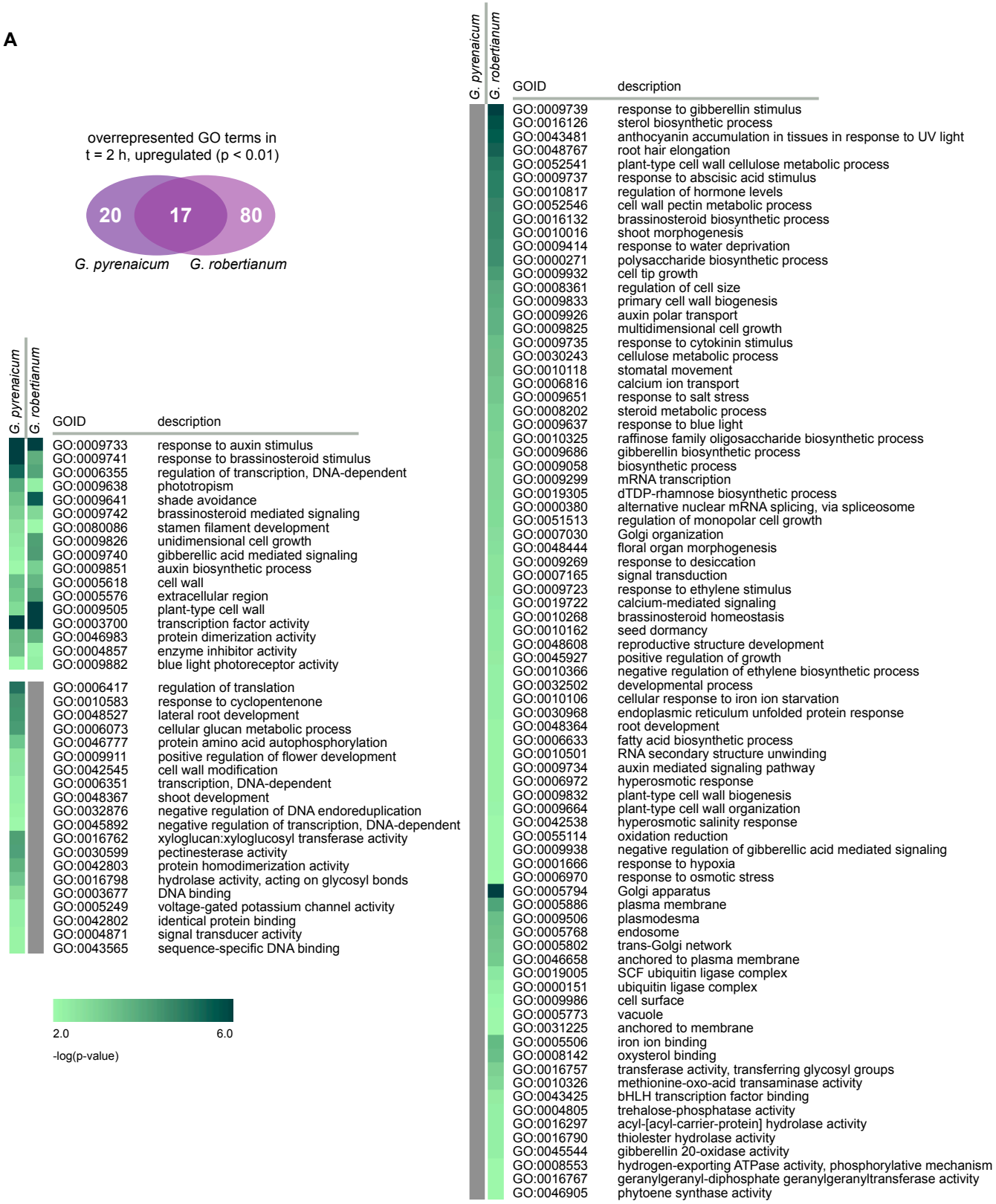


Supplemental Figure 1. A detailed analysis of low R:FR-induced growth over the time of day and in *Geranium* petioles. (Supports Figure 1.) (*A*) Growth rates of *G. pyrenaicum* and *G. robertianum* petioles (mm h^{-1}) over 48 h, data for every 6 minutes. Plants grown in either control white light (open circles, R:FR = 1.8) or a low R:FR treatment (dark circles R:FR = 0.2), starting at time point 0 (ZT = 3 h, indicated by an arrow). Error bars represent SEM, n = 6. The grey bars at the x-axis indicate the night periods. (*B*) Detailed elongation (mm 24 h^{-1}) of putative segments (1 to 8) of the *G. pyrenaicum* and *G. robertianum* petioles in control and low R:FR conditions. Data represent means ± SEM, n = 10, asterisks represent significant differences between control and low R:FR (Student's *t*-test, $p < 0.05$). (*C*) Representation of the 'segment' distribution over the *Geranium* petioles, of which elongation data are shown in (*B*).



Supplemental Figure 2. Low R:FR light suppresses petiole growth in *G. robertianum*, but not *G. pyrenaicum*, at a fixed time of the day. (Supports Figure 1.) The difference between petiole growth rates (mm h^{-1}) in control and low R:FR treatments with a different starting point during the photoperiod, in *G. pyrenaicum* (left) and *G. robertianum* (right). Starting point of the low R:FR light treatment is indicated by an arrow (top down ZT 3 h, 5.5 h, 8 h, 10.5 h and 13 h). Data are the same as presented in Figure 1D. Differences between the means of the two treatments are smoothed using exponential smoothing, n = 6. The grey area represents the night period.



Supplemental Figure 3. Gene ontology analysis on low R:FR induced and repressed *Geranium* OMCL groups. (Supports Figure 3.) Venn diagrams showing the overlap in significantly overrepresented gene ontology (GO) terms ($p < 0.01$) among *Geranium* OMCL groups significantly ($p < 0.01$) up- (*A*, *B*) or down-regulated (*C*, *D*) by the low R:FR light treatment at the first (t= 2 h, *A*, *C*) or second time point (t = 11.5 h, *B*, *D*). Heat maps present these defined GO terms with description, sorted by domain (biological process, cellular component and molecular function) and -log p-values (green for up-regulated OMCL groups, blue for down-regulated OMCL groups in low R:FR). Grey areas represent non-enriched GO terms in the specific species.

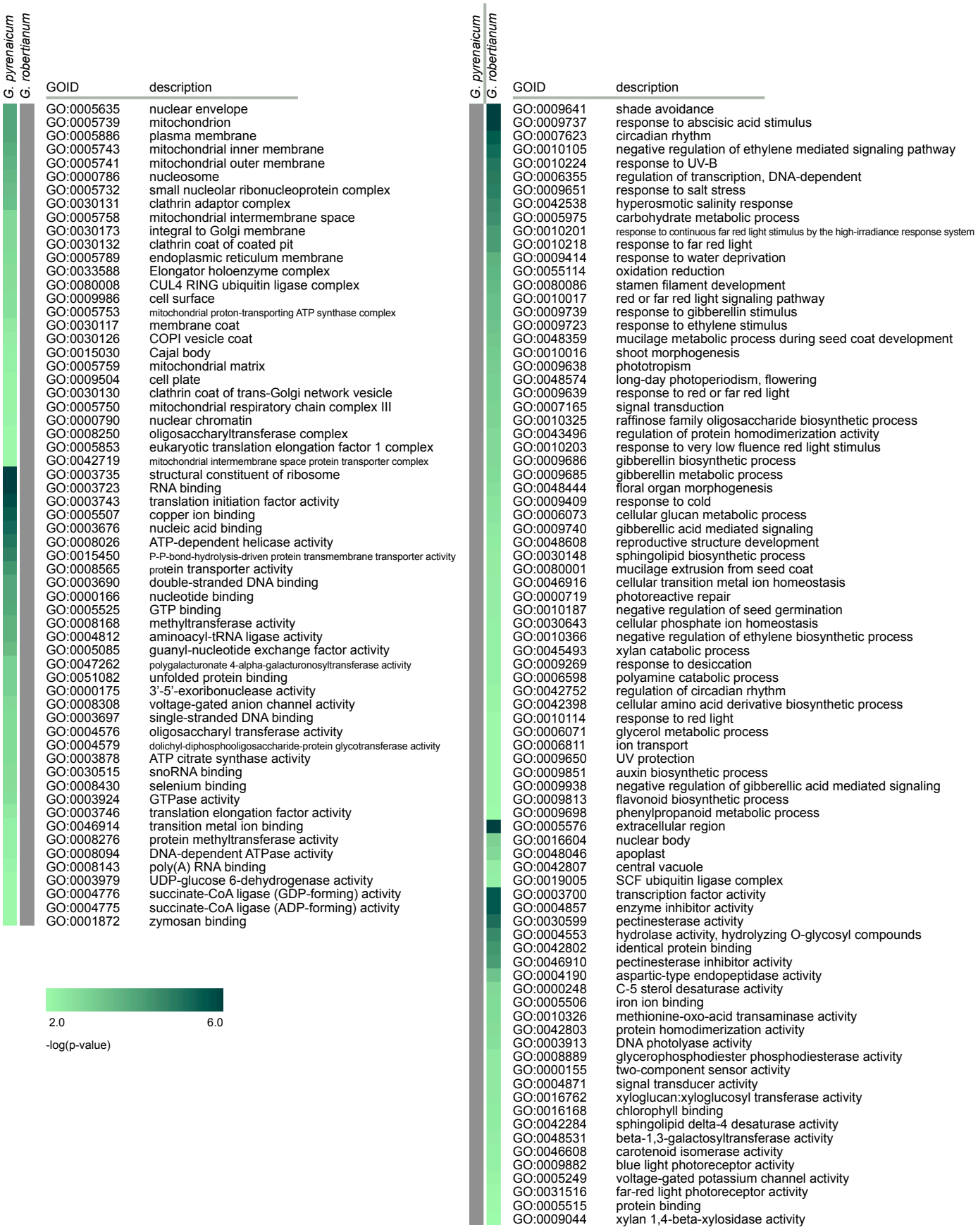
B

overrepresented GO terms in
t = 11.5 h, upregulated (p < 0.01)

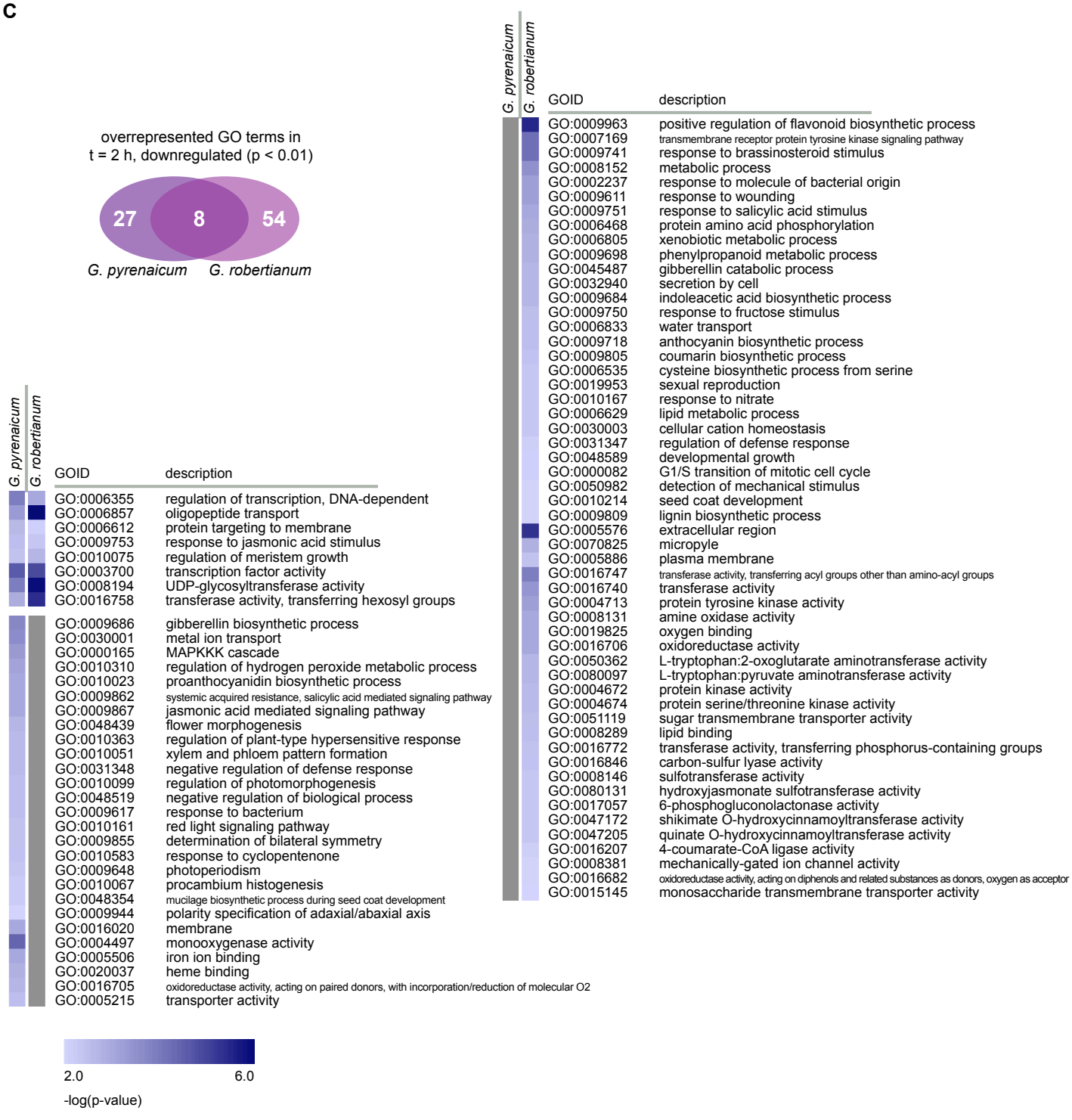
GOID	description
GO:0052546	cell wall pectin metabolic process
GO:0006084	acetyl-CoA metabolic process
GO:0016126	sterol biosynthetic process
GO:0052541	plant-type cell wall cellulose metabolic process
GO:0016132	brassinosteroid biosynthetic process
GO:0019745	pentacyclic triterpenoid biosynthetic process
GO:0009826	unidimensional cell growth
GO:0006633	fatty acid biosynthetic process
GO:0009733	response to auxin stimulus
GO:0006816	calcium ion transport
GO:0009741	response to brassinosteroid stimulus
GO:0046658	anchored to plasma membrane
GO:0005618	cell wall
GO:0009505	plant-type cell wall
GO:0031225	anchored to membrane
GO:0001510	RNA methylation
GO:0006412	translation
GO:0009220	pyrimidine ribonucleotide biosynthetic process
GO:0006606	protein import into nucleus
GO:0042254	ribosome biogenesis
GO:0006626	protein targeting to mitochondrion
GO:0006406	mRNA export from nucleus
GO:0009560	embryo sac egg cell differentiation
GO:0009909	regulation of flower development
GO:0009640	photomorphogenesis
GO:0009165	nucleotide biosynthetic process
GO:0010388	cullin deneddylation
GO:0000741	karyogamy
GO:0006164	purine nucleotide biosynthetic process
GO:0006094	gluconeogenesis
GO:0051604	protein maturation
GO:0034968	histone lysine methylation
GO:0006261	DNA-dependent DNA replication
GO:0006886	intracellular protein transport
GO:0000398	nuclear mRNA splicing, via spliceosome
GO:0010162	seed dormancy
GO:0007010	cytoskeleton organization
GO:0019915	lipid storage
GO:0042545	cell wall modification
GO:0009933	meristem structural organization
GO:0006260	DNA replication
GO:0010498	proteasomal protein catabolic process
GO:0009664	plant-type cell wall organization
GO:0006414	translational elongation
GO:0009845	seed germination
GO:0006007	glucose catabolic process
GO:0051567	histone H3-K9 methylation
GO:0010182	sugar mediated signaling
GO:0050826	response to freezing
GO:0009553	embryo sac development
GO:0000478	endonucleolytic cleavages during rRNA processing
GO:0048767	root hair elongation
GO:0016192	vesicle-mediated transport
GO:0042991	transcription factor import into nucleus
GO:0045039	protein import into mitochondrial inner membrane
GO:0006913	nucleocytoplasmic transport
GO:0006354	RNA elongation
GO:0034976	response to endoplasmic reticulum stress
GO:0006270	DNA replication initiation
GO:0009086	methionine biosynthetic process
GO:0044267	cellular protein metabolic process
GO:0006334	nucleosome assembly
GO:0008283	cell proliferation
GO:0006446	regulation of translational initiation
GO:0006096	glycolysis
GO:0006413	translational initiation
GO:0006418	tRNA aminoacylation for protein translation
GO:0051301	cell division
GO:0046686	response to cadmium ion
GO:0044070	regulation of anion transport

GOID	description
GO:0009853	photorespiration
GO:0048825	cotyledon development
GO:0015031	protein transport
GO:0000059	protein import into nucleus, docking
GO:0010074	maintenance of meristem identity
GO:0009846	pollen germination
GO:0006457	protein folding
GO:0006275	regulation of DNA replication
GO:0009113	purine base biosynthetic process
GO:0045489	pectin biosynthetic process
GO:0048193	Golgi vesicle transport
GO:0048366	leaf development
GO:0009561	megagametogenesis
GO:0032508	DNA duplex unwinding
GO:0007030	Golgi organization
GO:0055072	iron ion homeostasis
GO:0000902	cell morphogenesis
GO:0000724	double-strand break repair via homologous recombination
GO:0006351	transcription, DNA-dependent
GO:0051788	response to misfolded protein
GO:0051726	regulation of cell cycle
GO:0009831	plant-type cell wall modification during multidimensional cell growth
GO:0019932	second-messenger-mediated signaling
GO:0032259	methylation
GO:0006396	RNA processing
GO:0016458	gene silencing
GO:0016051	carbohydrate biosynthetic process
GO:0009736	cytokinin mediated signaling
GO:0010082	regulation of root meristem growth
GO:0010107	potassium ion import
GO:0006268	DNA unwinding during replication
GO:0006189	'de novo' IMP biosynthetic process
GO:0032875	regulation of DNA endoreduplication
GO:0030244	cellulose biosynthetic process
GO:0016049	cell growth
GO:0016579	protein deubiquitination
GO:0010197	polar nucleus fusion
GO:0006571	tyrosine biosynthetic process
GO:0006065	UDP-glucuronate biosynthetic process
GO:0051510	regulation of unidimensional cell growth
GO:0006269	DNA replication, synthesis of RNA primer
GO:0015946	methanol oxidation
GO:0019415	acetate biosynthetic process from carbon monoxide
GO:0042274	ribosomal small subunit biogenesis
GO:0031538	negative regulation of anthocyanin metabolic process
GO:0031120	snRNA pseudouridine synthesis
GO:0000380	alternative nuclear mRNA splicing, via spliceosome
GO:0010501	RNA secondary structure unwinding
GO:0016567	protein ubiquitination
GO:0009958	positive gravitropism
GO:0009793	embryonic development ending in seed dormancy
GO:0005840	ribosome
GO:0005730	nucleolus
GO:0005829	cytosol
GO:0022625	cytosolic large ribosomal subunit
GO:0022627	cytosolic small ribosomal subunit
GO:0005794	Golgi apparatus
GO:0022626	cytosolic ribosome
GO:0005622	intracellular
GO:0009506	plasmodesma
GO:0005802	trans-Golgi network
GO:0005774	vacuolar membrane
GO:0015934	large ribosomal subunit
GO:0005768	endosome
GO:0005737	cytoplasm
GO:0005783	endoplasmic reticulum
GO:0016020	membrane
GO:0015935	small ribosomal subunit
GO:0005852	eukaryotic translation initiation factor 3 complex
GO:0005773	vacuole
GO:0005643	nuclear pore

B (continued)


G. pyrenaicum
G. robertianum
GOID
description
GO:0005635 nuclear envelope
GO:0005739 mitochondrion
GO:0005886 plasma membrane
GO:0005743 mitochondrial inner membrane
GO:0005741 mitochondrial outer membrane
GO:0000786 nucleosome
GO:0005732 small nucleolar ribonucleoprotein complex
GO:0030131 clathrin adaptor complex
GO:0005758 mitochondrial intermembrane space
GO:0030173 integral to Golgi membrane
GO:0030132 clathrin coat of coated pit
GO:0005789 endoplasmic reticulum membrane
GO:0033588 Elongator holoenzyme complex
GO:0080008 CUL4 RING ubiquitin ligase complex
GO:0009986 cell surface
GO:0005753 mitochondrial proton-transporting ATP synthase complex
GO:0030117 membrane coat
GO:0030126 COPI vesicle coat
GO:0015030 Cajal body
GO:0005759 mitochondrial matrix
GO:0009504 cell plate
GO:0030130 clathrin coat of trans-Golgi network vesicle
GO:0005750 mitochondrial respiratory chain complex III
GO:0000790 nuclear chromatin
GO:0008250 oligosaccharyltransferase complex
GO:0005853 eukaryotic translation elongation factor 1 complex
GO:0042719 mitochondrial intermembrane space protein transporter complex
GO:0003735 structural constituent of ribosome
GO:0003723 RNA binding
GO:0003743 translation initiation factor activity
GO:0005507 copper ion binding
GO:0003676 nucleic acid binding
GO:0008026 ATP-dependent helicase activity
GO:0015450 P-P-bond-hydrolysis-driven protein transmembrane transporter activity
GO:0008565 protein transporter activity
GO:0003690 double-stranded DNA binding
GO:0000166 nucleotide binding
GO:0005525 GTP binding
GO:0008168 methyltransferase activity
GO:0004812 aminoacyl-tRNA ligase activity
GO:0005085 guanyl-nucleotide exchange factor activity
GO:0047262 polygalacturonate 4-alpha-galacturonosyltransferase activity
GO:0051082 unfolded protein binding
GO:0000175 3'-5'-exoribonuclease activity
GO:0008308 voltage-gated anion channel activity
GO:0003697 single-stranded DNA binding
GO:0004576 oligosaccharyl transferase activity
GO:0004579 dolichyl-diphosphooligosaccharide-protein glycotransferase activity
GO:0003878 ATP citrate synthase activity
GO:0030515 snoRNA binding
GO:0008430 selenium binding
GO:0003924 GTPase activity
GO:0003746 translation elongation factor activity
GO:0046914 transition metal ion binding
GO:0008276 protein methyltransferase activity
GO:0008094 DNA-dependent ATPase activity
GO:0008143 poly(A) RNA binding
GO:0003979 UDP-glucose 6-dehydrogenase activity
GO:0004776 succinate-CoA ligase (GDP-forming) activity
GO:0004775 succinate-CoA ligase (ADP-forming) activity
GO:0001872 zymosan binding
2.0
6.0
-log(p-value)
G. pyrenaicum
G. robertianum
GOID
description
GO:0009641 shade avoidance
GO:0009737 response to abscisic acid stimulus
GO:0007623 circadian rhythm
GO:0010105 negative regulation of ethylene mediated signaling pathway
GO:0010224 response to UV-B
GO:0006355 regulation of transcription, DNA-dependent
GO:0009651 response to salt stress
GO:0042538 hyperosmotic salinity response
GO:0005975 carbohydrate metabolic process
GO:0010201 response to continuous far red light stimulus by the high-irradiance response system
GO:0010218 response to far red light
GO:0009414 response to water deprivation
GO:0055114 oxidation reduction
GO:0080086 stamen filament development
GO:0010017 red or far red light signaling pathway
GO:0009739 response to gibberellin stimulus
GO:0009723 response to ethylene stimulus
GO:0048359 mucilage metabolic process during seed coat development
GO:0010016 shoot morphogenesis
GO:0009638 phototropism
GO:0048574 long-day photoperiodism, flowering
GO:0009639 response to red or far red light
GO:0007165 signal transduction
GO:0010325 raffinose family oligosaccharide biosynthetic process
GO:0043496 regulation of protein homodimerization activity
GO:0010203 response to very low fluence red light stimulus
GO:0009686 gibberellin biosynthetic process
GO:0009685 gibberellin metabolic process
GO:0048444 floral organ morphogenesis
GO:0009409 response to cold
GO:0006073 cellular glucan metabolic process
GO:0009740 gibberellic acid mediated signaling
GO:0048608 reproductive structure development
GO:0030148 sphingolipid biosynthetic process
GO:0080001 mucilage extrusion from seed coat
GO:0046916 cellular transition metal ion homeostasis
GO:0000719 photoreactive repair
GO:0010187 negative regulation of seed germination
GO:0030643 cellular phosphate ion homeostasis
GO:0010366 negative regulation of ethylene biosynthetic process
GO:0045493 xylan catabolic process
GO:0009269 response to desiccation
GO:0006598 polyamine catabolic process
GO:0042752 regulation of circadian rhythm
GO:0042398 cellular amino acid derivative biosynthetic process
GO:0010114 response to red light
GO:0006071 glycerol metabolic process
GO:0006811 ion transport
GO:0009650 UV protection
GO:0009851 auxin biosynthetic process
GO:0009938 negative regulation of gibberellic acid mediated signaling
GO:0009813 flavonoid biosynthetic process
GO:0009698 phenylpropanoid metabolic process
GO:0005576 extracellular region
GO:0016604 nuclear body
GO:0048046 apoplast
GO:0042807 central vacuole
GO:0019005 SCF ubiquitin ligase complex
GO:0003700 transcription factor activity
GO:0004857 enzyme inhibitor activity
GO:0030599 pectinesterase activity
GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds
GO:0042802 identical protein binding
GO:0046910 pectinesterase inhibitor activity
GO:0004190 aspartic-type endopeptidase activity
GO:0000248 C-5 sterol desaturase activity
GO:0005506 iron ion binding
GO:0010326 methionine-oxo-acid transaminase activity
GO:0042803 protein homodimerization activity
GO:0003913 DNA photolyase activity
GO:0008889 glycerophosphodiester phosphodiesterase activity
GO:0000155 two-component sensor activity
GO:0004871 signal transducer activity
GO:0016762 xyloglucan:xyloglucosyl transferase activity
GO:0016168 chlorophyll binding
GO:0042284 sphingolipid delta-4 desaturase activity
GO:0048531 beta-1,3-galactosyltransferase activity
GO:0046608 carotenoid isomerase activity
GO:0009882 blue light photoreceptor activity
GO:0005249 voltage-gated potassium channel activity
GO:0031516 far-red light photoreceptor activity
GO:0005515 protein binding
GO:0009044 xylan 1,4-beta-xylosidase activity

C


overrepresented GO terms in
t = 2 h, downregulated (p < 0.01)
27
8
54
G. pyrenaicum
G. robertianum
G. pyrenaicum
G. robertianum
GOID
description
GO:0006355 regulation of transcription, DNA-dependent
GO:0006857 oligopeptide transport
GO:0006612 protein targeting to membrane
GO:0009753 response to jasmonic acid stimulus
GO:0010075 regulation of meristem growth
GO:0003700 transcription factor activity
GO:0008194 UDP-glycosyltransferase activity
GO:0016758 transferase activity, transferring hexosyl groups
GO:0009686 gibberellin biosynthetic process
GO:0030001 metal ion transport
GO:0000165 MAPKKK cascade
GO:0010310 regulation of hydrogen peroxide metabolic process
GO:0010023 proanthocyanidin biosynthetic process
GO:0009862 systemic acquired resistance, salicylic acid mediated signaling pathway
GO:0009867 jasmonic acid mediated signaling pathway
GO:0048439 flower morphogenesis
GO:0010363 regulation of plant-type hypersensitive response
GO:0010051 xylem and phloem pattern formation
GO:0031348 negative regulation of defense response
GO:0010099 regulation of photomorphogenesis
GO:0048519 negative regulation of biological process
GO:0009617 response to bacterium
GO:0010161 red light signaling pathway
GO:0009855 determination of bilateral symmetry
GO:0010583 response to cyclopentenone
GO:0009648 photoperiodism
GO:0010067 procambium histogenesis
GO:0048354 mucilage biosynthetic process during seed coat development
GO:0009944 polarity specification of adaxial/abaxial axis
GO:0016020 membrane
GO:0004497 monooxygenase activity
GO:0005506 iron ion binding
GO:0020037 heme binding
GO:0016705 oxidoreductase activity, acting on paired donors, with incorporation/reduction of molecular O2
GO:0005215 transporter activity
2.0
6.0
-log(p-value)
G. pyrenaicum
G. robertianum
GOID
description
GO:0009963 positive regulation of flavonoid biosynthetic process
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway
GO:0009741 response to brassinosteroid stimulus
GO:0008152 metabolic process
GO:0002237 response to molecule of bacterial origin
GO:0009611 response to wounding
GO:0009751 response to salicylic acid stimulus
GO:0006468 protein amino acid phosphorylation
GO:0006805 xenobiotic metabolic process
GO:0009698 phenylpropanoid metabolic process
GO:0045487 gibberellin catabolic process
GO:0032940 secretion by cell
GO:0009684 indoleacetic acid biosynthetic process
GO:0009750 response to fructose stimulus
GO:0006833 water transport
GO:0009718 anthocyanin biosynthetic process
GO:0009805 coumarin biosynthetic process
GO:0006535 cysteine biosynthetic process from serine
GO:0019953 sexual reproduction
GO:0010167 response to nitrate
GO:0006629 lipid metabolic process
GO:0030003 cellular cation homeostasis
GO:0031347 regulation of defense response
GO:0048589 developmental growth
GO:0000082 G1/S transition of mitotic cell cycle
GO:0050982 detection of mechanical stimulus
GO:0010214 seed coat development
GO:0009809 lignin biosynthetic process
GO:0005576 extracellular region
GO:0070825 micropyle
GO:0005886 plasma membrane
GO:0016747 transferase activity, transferring acyl groups other than amino-acyl groups
GO:0016740 transferase activity
GO:0004713 protein tyrosine kinase activity
GO:0008131 amine oxidase activity
GO:0019825 oxygen binding
GO:0016706 oxidoreductase activity
GO:0050362 L-tryptophan:2-oxoglutarate aminotransferase activity
GO:0080097 L-tryptophan:pyruvate aminotransferase activity
GO:0004672 protein kinase activity
GO:0004674 protein serine/threonine kinase activity
GO:0051119 sugar transmembrane transporter activity
GO:0008289 lipid binding
GO:0016772 transferase activity, transferring phosphorus-containing groups
GO:0016846 carbon-sulfur lyase activity
GO:0008146 sulfotransferase activity
GO:0080131 hydroxyjasmonate sulfotransferase activity
GO:0017057 6-phosphogluconolactonase activity
GO:0047172 shikimate O-hydroxycinnamoyltransferase activity
GO:0047205 quinate O-hydroxycinnamoyltransferase activity
GO:0016207 4-coumarate-CoA ligase activity
GO:0008381 mechanically-gated ion channel activity
GO:0016682 oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor
GO:0015145 monosaccharide transmembrane transporter activity

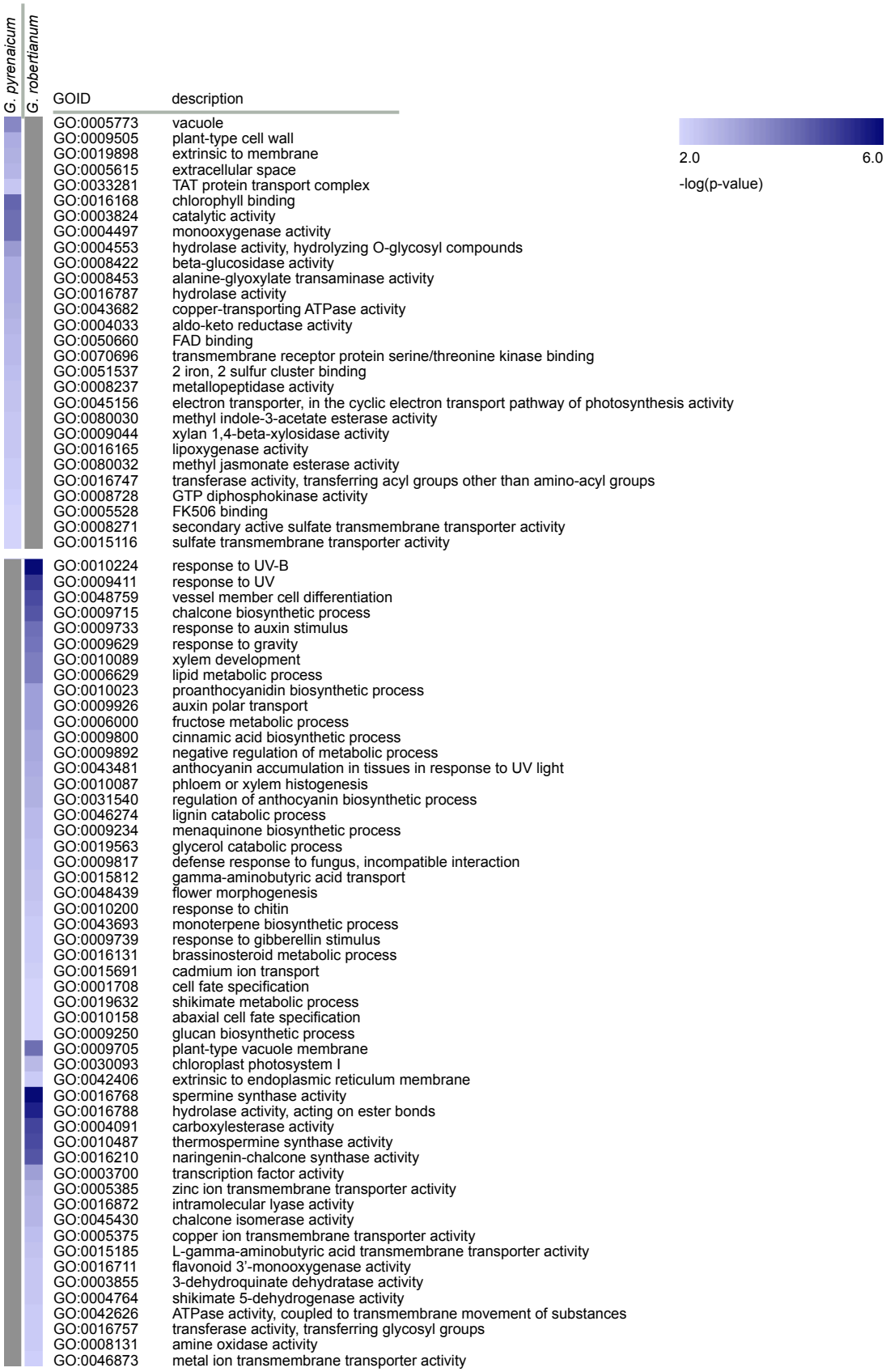
D

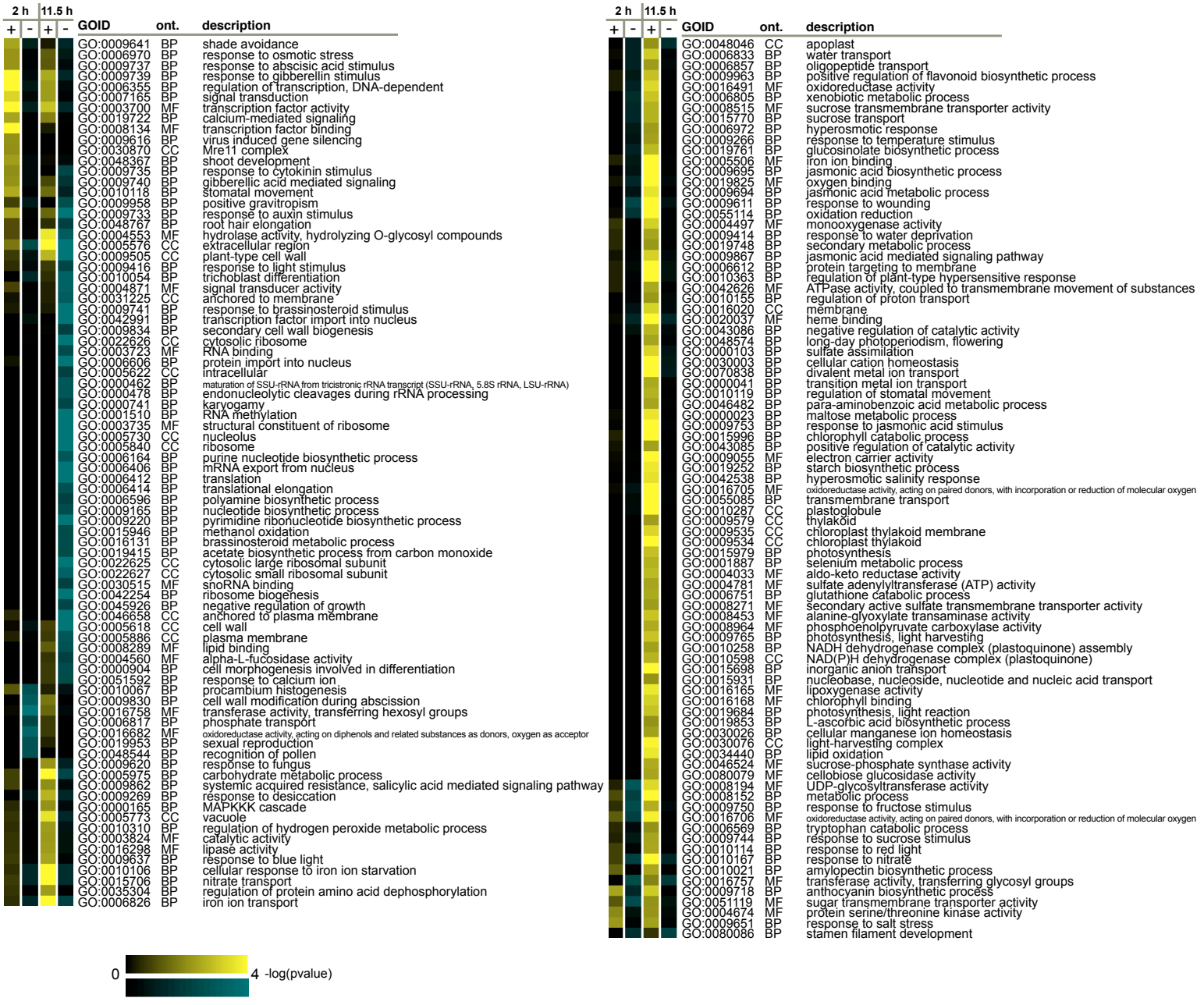
overrepresented GO terms in
t = 11.5 h, downregulated (p < 0.01)

GOID	description
GO:0019684	photosynthesis, light reaction
GO:0015979	photosynthesis
GO:0006098	pentose-phosphate shunt
GO:0055114	oxidation reduction
GO:0019252	starch biosynthetic process
GO:0043085	positive regulation of catalytic activity
GO:0008152	metabolic process
GO:0010218	response to far red light
GO:0009744	response to sucrose stimulus
GO:0010310	regulation of hydrogen peroxide metabolic process
GO:0009718	anthocyanin biosynthetic process
GO:0042742	defense response to bacterium
GO:0043900	regulation of multi-organism process
GO:0009595	detection of biotic stimulus
GO:0009813	flavonoid biosynthetic process
GO:0006979	response to oxidative stress
GO:0015976	carbon utilization
GO:0010037	response to carbon dioxide
GO:0009830	cell wall modification during abscission
GO:0034484	raffinose catabolic process
GO:0009751	response to salicylic acid stimulus
GO:0009809	lignin biosynthetic process
GO:0030388	fructose 1,6-bisphosphate metabolic process
GO:0009579	thylakoid
GO:0005576	extracellular region
GO:0009570	chloroplast stroma
GO:0010319	stromule
GO:0048046	apoplast
GO:0016491	oxidoreductase activity
GO:0020037	heme binding
GO:0016705	oxidoreductase activity, acting on paired donors
GO:0009055	electron carrier activity
GO:0019825	oxygen binding
GO:0005506	iron ion binding
GO:0008194	UDP-glycosyltransferase activity
GO:0016706	oxidoreductase activity
GO:0016298	lipase activity
GO:0004185	serine-type carboxypeptidase activity
GO:0004089	carbonate dehydratase activity
GO:0015171	amino acid transmembrane transporter activity
GO:0008289	lipid binding
GO:0042132	fructose 1,6-bisphosphate 1-phosphatase activity
GO:0010207	photosystem II assembly
GO:0000023	maltose metabolic process
GO:0070838	divalent metal ion transport
GO:0009657	plastid organization
GO:0009773	photosynthetic electron transport in photosystem I
GO:0030003	cellular cation homeostasis
GO:0006364	rRNA processing
GO:0010027	thylakoid membrane organization
GO:0019761	glucosinolate biosynthetic process
GO:0009637	response to blue light
GO:0035304	regulation of protein amino acid dephosphorylation
GO:0019288	isopentenyl diphosphate biosynthetic process
GO:0010155	regulation of proton transport
GO:0016117	carotenoid biosynthetic process
GO:0015995	chlorophyll biosynthetic process
GO:0009902	chloroplast relocation
GO:0010114	response to red light
GO:0019344	cysteine biosynthetic process
GO:0010103	stomatal complex morphogenesis
GO:0016556	mRNA modification
GO:0015996	chlorophyll catabolic process
GO:0034660	ncRNA metabolic process
GO:0006612	protein targeting to membrane
GO:0010363	regulation of plant-type hypersensitive response
GO:0009611	response to wounding
GO:0009862	systemic acquired resistance, salicylic acid signaling pathway

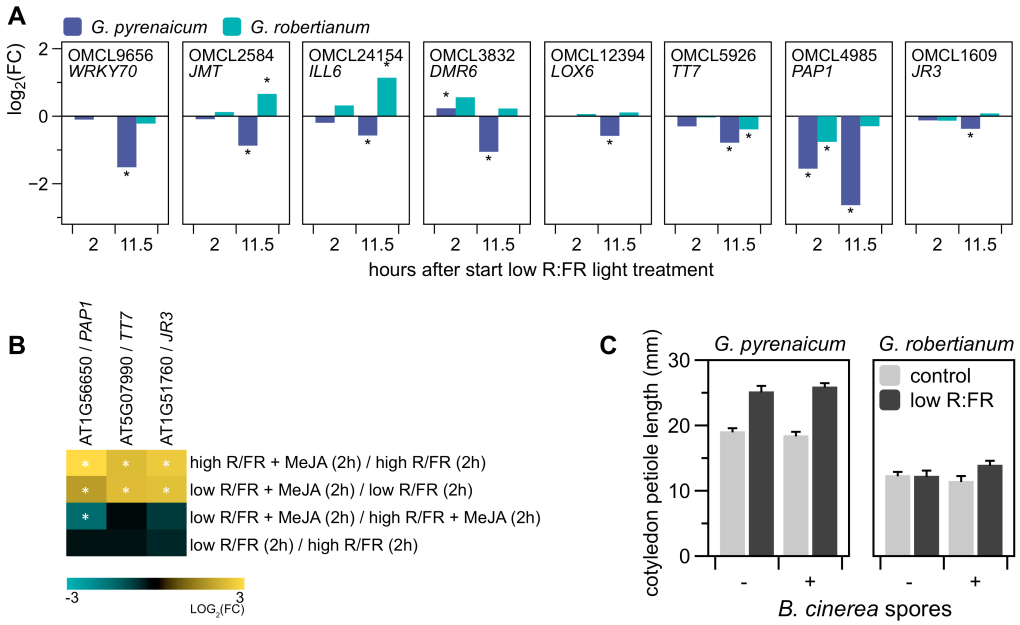
GOID	description
GO:0009765	photosynthesis, light harvesting
GO:0005975	carbohydrate metabolic process
GO:0030154	cell differentiation
GO:0010304	PSII associated light-harvesting complex II catabolic process
GO:0019760	glucosinolate metabolic process
GO:0009867	jasmonic acid mediated signaling pathway
GO:0009814	defense response, incompatible interaction
GO:0009965	leaf morphogenesis
GO:0000165	MAPKKK cascade
GO:0009409	response to cold
GO:0050832	defense response to fungus
GO:0009963	positive regulation of flavonoid biosynthetic process
GO:0006636	unsaturated fatty acid biosynthetic process
GO:0006508	proteolysis
GO:0010106	cellular response to iron ion starvation
GO:0009767	photosynthetic electron transport chain
GO:0006952	defense response
GO:0055085	transmembrane transport
GO:0009617	response to bacterium
GO:0009699	phenylpropanoid biosynthetic process
GO:0009684	indoleacetic acid biosynthetic process
GO:0010043	response to zinc ion
GO:0009750	response to fructose stimulus
GO:0042793	transcription from plastid promoter
GO:0006569	tryptophan catabolic process
GO:0009753	response to jasmonic acid stimulus
GO:0006857	oligopeptide transport
GO:0009697	salicylic acid biosynthetic process
GO:0019375	galactolipid biosynthetic process
GO:0009768	photosynthesis, light harvesting in photosystem I
GO:0015977	carbon utilization by fixation of carbon dioxide
GO:0015969	guanosine tetraphosphate metabolic process
GO:0031348	negative regulation of defense response
GO:0016036	cellular response to phosphate starvation
GO:0016120	carotene biosynthetic process
GO:0009269	response to desiccation
GO:0010264	myo-inositol hexakisphosphate biosynthetic process
GO:0042744	hydrogen peroxide catabolic process
GO:0006869	lipid transport
GO:0002238	response to molecule of fungal origin
GO:0006817	phosphate transport
GO:0009694	jasmonic acid metabolic process
GO:0046777	protein amino acid autophosphorylation
GO:0000413	protein peptidyl-prolyl isomerization
GO:0009695	jasmonic acid biosynthetic process
GO:0006655	phosphatidylglycerol biosynthetic process
GO:0010270	photosystem II oxygen evolving complex assembly
GO:0006598	polyamine catabolic process
GO:0015994	chlorophyll metabolic process
GO:0019748	secondary metabolic process
GO:0006805	xenobiotic metabolic process
GO:0010351	lithium ion transport
GO:0034440	lipid oxidation
GO:0009821	alkaloid biosynthetic process
GO:0006826	iron ion transport
GO:0019464	glycine decarboxylation via glycine cleavage system
GO:0043086	negative regulation of catalytic activity
GO:0044265	cellular macromolecule catabolic process
GO:0018208	peptidyl-proline modification
GO:0005985	sucrose metabolic process
GO:0015698	inorganic anion transport
GO:0010271	regulation of chlorophyll catabolic process
GO:0010115	regulation of abscisic acid biosynthetic process
GO:0042549	photosystem II stabilization
GO:0009698	phenylpropanoid metabolic process
GO:0009535	chloroplast thylakoid membrane
GO:0009507	chloroplast
GO:0009534	chloroplast thylakoid
GO:0009941	chloroplast envelope
GO:0010287	plastoglobule
GO:0031977	thylakoid lumen
GO:0009543	chloroplast thylakoid lumen
GO:0030095	chloroplast photosystem II
GO:0009522	photosystem I
GO:0009523	photosystem II
GO:0009654	oxygen evolving complex
GO:0010598	NAD(P)H dehydrogenase complex (plastoquinone)
GO:0030076	light-harvesting complex
GO:0005777	peroxisome
GO:0009538	photosystem I reaction center
GO:0016020	membrane

D (continued)

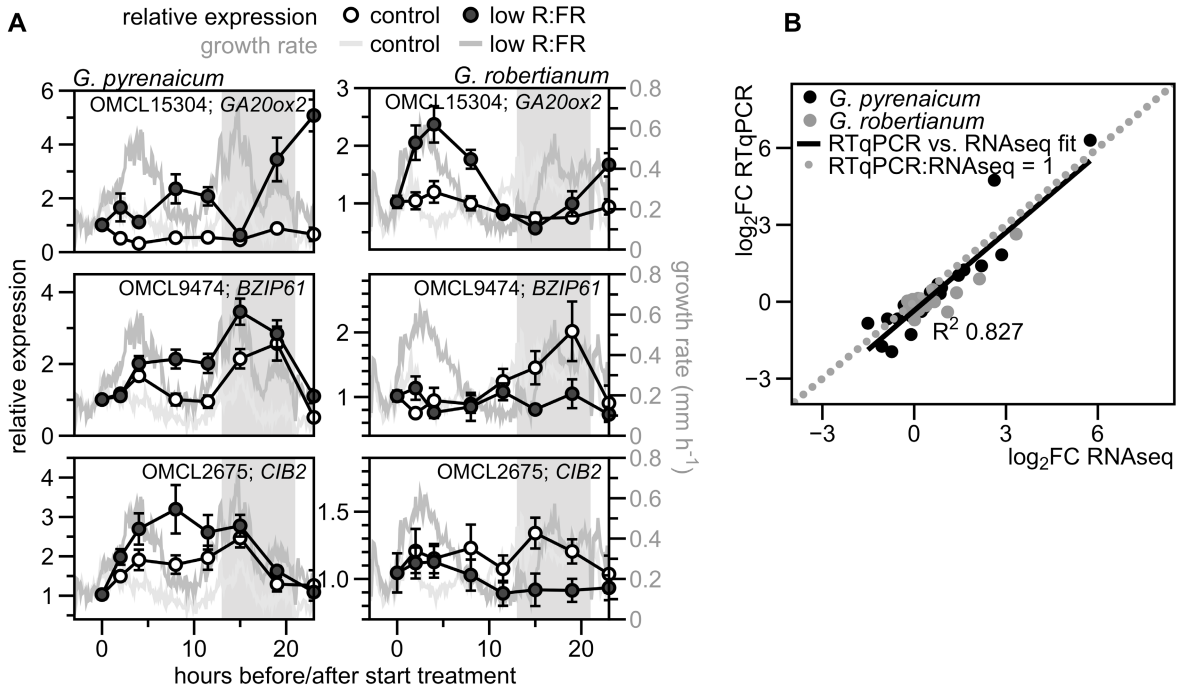

G. pyrenaicum
G. robertianum
GOID
description
2.0
6.0
-log(p-value)
GO:0005773 vacuole
GO:0009505 plant-type cell wall
GO:0019898 extrinsic to membrane
GO:0005615 extracellular space
GO:0033281 TAT protein transport complex
GO:0016168 chlorophyll binding
GO:0003824 catalytic activity
GO:0004497 monooxygenase activity
GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds
GO:0008422 beta-glucosidase activity
GO:0008453 alanine-glyoxylate transaminase activity
GO:0016787 hydrolase activity
GO:0043682 copper-transporting ATPase activity
GO:0004033 aldo-keto reductase activity
GO:0050660 FAD binding
GO:0070696 transmembrane receptor protein serine/threonine kinase binding
GO:0051537 2 iron, 2 sulfur cluster binding
GO:0008237 metallopeptidase activity
GO:0045156 electron transporter, in the cyclic electron transport pathway of photosynthesis activity
GO:0080030 methyl indole-3-acetate esterase activity
GO:0009044 xylan 1,4-beta-xylosidase activity
GO:0016165 lipoxygenase activity
GO:0080032 methyl jasmonate esterase activity
GO:0016747 transferase activity, transferring acyl groups other than amino-acyl groups
GO:0008728 GTP diphosphokinase activity
GO:0005528 FK506 binding
GO:0008271 secondary active sulfate transmembrane transporter activity
GO:0015116 sulfate transmembrane transporter activity
GO:0010224 response to UV-B
GO:0009411 response to UV
GO:0048759 vessel member cell differentiation
GO:0009715 chalcone biosynthetic process
GO:0009733 response to auxin stimulus
GO:0009629 response to gravity
GO:0010089 xylem development
GO:0006629 lipid metabolic process
GO:0010023 proanthocyanidin biosynthetic process
GO:0009926 auxin polar transport
GO:0006000 fructose metabolic process
GO:0009800 cinnamic acid biosynthetic process
GO:0009892 negative regulation of metabolic process
GO:0043481 anthocyanin accumulation in tissues in response to UV light
GO:0010087 phloem or xylem histogenesis
GO:0031540 regulation of anthocyanin biosynthetic process
GO:0046274 lignin catabolic process
GO:0009234 menaquinone biosynthetic process
GO:0019563 glycerol catabolic process
GO:0009817 defense response to fungus, incompatible interaction
GO:0015812 gamma-aminobutyric acid transport
GO:0048439 flower morphogenesis
GO:0010200 response to chitin
GO:0043693 monoterpene biosynthetic process
GO:0009739 response to gibberellin stimulus
GO:0016131 brassinosteroid metabolic process
GO:0015691 cadmium ion transport
GO:0001708 cell fate specification
GO:0019632 shikimate metabolic process
GO:0010158 abaxial cell fate specification
GO:0009250 glucan biosynthetic process
GO:0009705 plant-type vacuole membrane
GO:0030093 chloroplast photosystem I
GO:0042406 extrinsic to endoplasmic reticulum membrane
GO:0016768 spermine synthase activity
GO:0016788 hydrolase activity, acting on ester bonds
GO:0004091 carboxylesterase activity
GO:0010487 thermospermine synthase activity
GO:0016210 naringenin-chalcone synthase activity
GO:0003700 transcription factor activity
GO:0005385 zinc ion transmembrane transporter activity
GO:0016872 intramolecular lyase activity
GO:0045430 chalcone isomerase activity
GO:0005375 copper ion transmembrane transporter activity
GO:0015185 L-gamma-aminobutyric acid transmembrane transporter activity
GO:0016711 flavonoid 3'-monooxygenase activity
GO:0003855 3-dehydroquinate dehydratase activity
GO:0004764 shikimate 5-dehydrogenase activity
GO:0042626 ATPase activity, coupled to transmembrane movement of substances
GO:0016757 transferase activity, transferring glycosyl groups
GO:0008131 amine oxidase activity
GO:0046873 metal ion transmembrane transporter activity



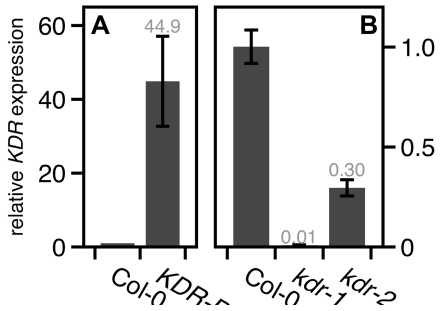
Supplemental Figure 4. Plant processes differentially regulated in low R:FR by the two *Geranium* species. (Supports Figure 3.) Heat map of the gene ontology (GO) overrepresentation analysis on the OMCL groups with a significant treatment*species interaction ($p < 0.01$, glmLRT), as presented in Fig. 3C in at least one of the time points. Colours represent the -log of the p-value, where yellow is a positive interaction (*G. pyrenaicum* < *G. robertianum*) and blue is a negative interaction (*G. pyrenaicum* > *G. robertianum*).



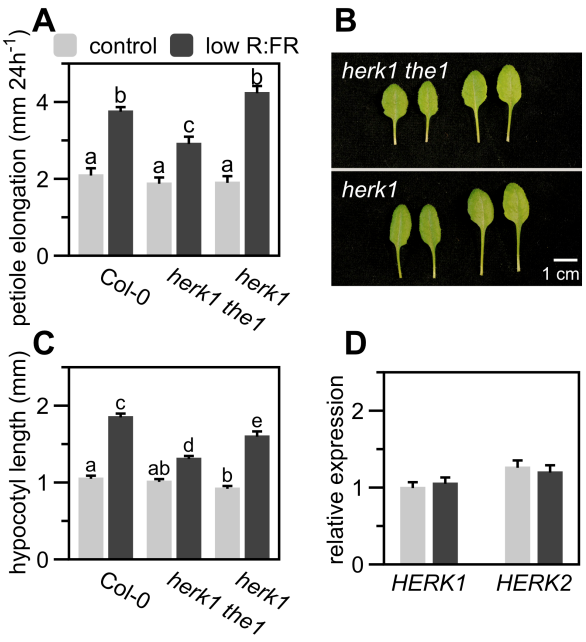
Supplemental Figure 5. Low R:FR light affects meJA-induced transcript abundance in the Geraniums and *A. thaliana*, and pathogen infection does not affect *Geranium* growth in the shade. (Supports Figure 4.) (*A*) Log_2 fold-changes of a subset of OMCL groups from the GO clusters shown in Fig. 4A. Asterisks represent significant differences between low R:FR and control ($p < 0.01$, qCML method, followed by an exact test). (*B*) Heat map representing log fold changes for *PAP1*, *TT7* and *JR3*, upon a meJA (100 µM) treatment in a control (R:FR = 1.8) or low (R:FR = 0.2) R:FR light environment in *A. thaliana*. Samples harvested 2 hours after start of the hormone and light treatment, n = 3. Asterisks represent a significant difference between the presented conditions ($p < 0.01$). Data taken from de Wit et al., 2013. (*B*) Petiole length of *G. pyernaicum* (left) and *G. robertianum* (right) cotyledons (mm), with or without *B. cinerea* infection, in a control (R:FR = 1.8) or low R:FR (R:FR = 0.2) light treatment. Data represent means + SEM, n = 28.



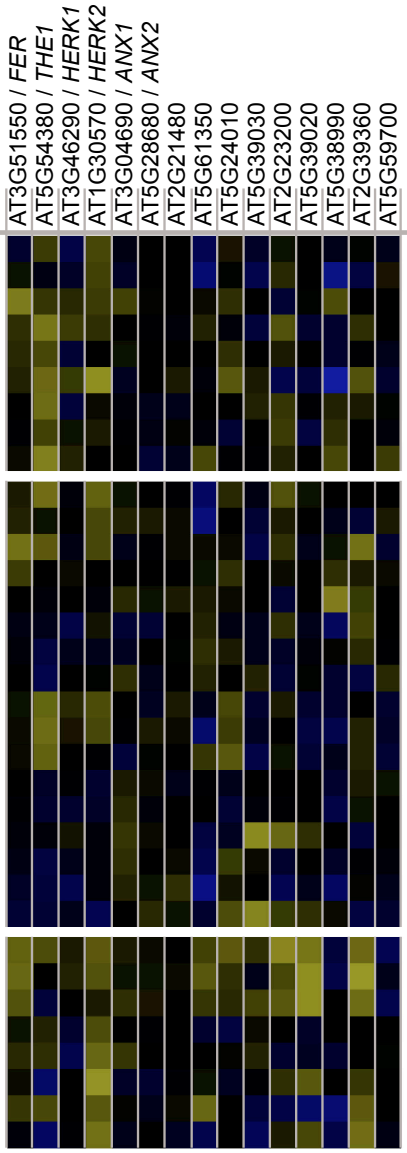
Supplemental Figure 6. RT qPCR on *Geranium* transcripts and validation of RNA sequencing. (Supports Figure 6.) (*A*) Relative OMCL group expression (orthologues of *GA20OX2*, *BZIP61* and *CIB2*) over time in *G. pyrenaicum* (left panels) and *G. robertianum* (right panels) in control (R:FR = 1.8; open circles) and low R:FR (R:FR = 0.2; dark circles) conditions, on the left y-axis. Data are relative to the reference gene (orthologue of *PDF1*) and to t = 0 (10:00 am), data represent means ± SEM, n = 5 (biological replicates are a pool of the second petiole of three individual plants). Right y-axis and grey lines represent growth rates in mm h^{-1} over the same time period in control (light grey) and low R:FR (darker grey) conditions (same data as Fig. 1C). Grey area represents the night period. (*B*) Comparison of the log2 fold-changes of several OMCL groups determined by RNAseq (x-axis) and real-time quantitative PCR (y-axis). Analyses were performed on a different set of samples, harvested under the same conditions; low R:FR vs. control light, t = 2 h and t = 11.5 h.



Supplemental Figure 7. Confirmation of *kdr* mutants. (Supports Figure 7.) (*A and B*) Relative *KDR* expression in Col-0 wild-type, *KDR* over-expressing *KDR-D* (*A*) and knock-out *kdr-1* and knock-down *kdr-2* (*B*), relative to Col-0 and reference genes *UBQ5* (*KDR-D*) and *APT* (*kdr-1* and *kdr-2*). Data represent means ± SEM, n = 2-3.



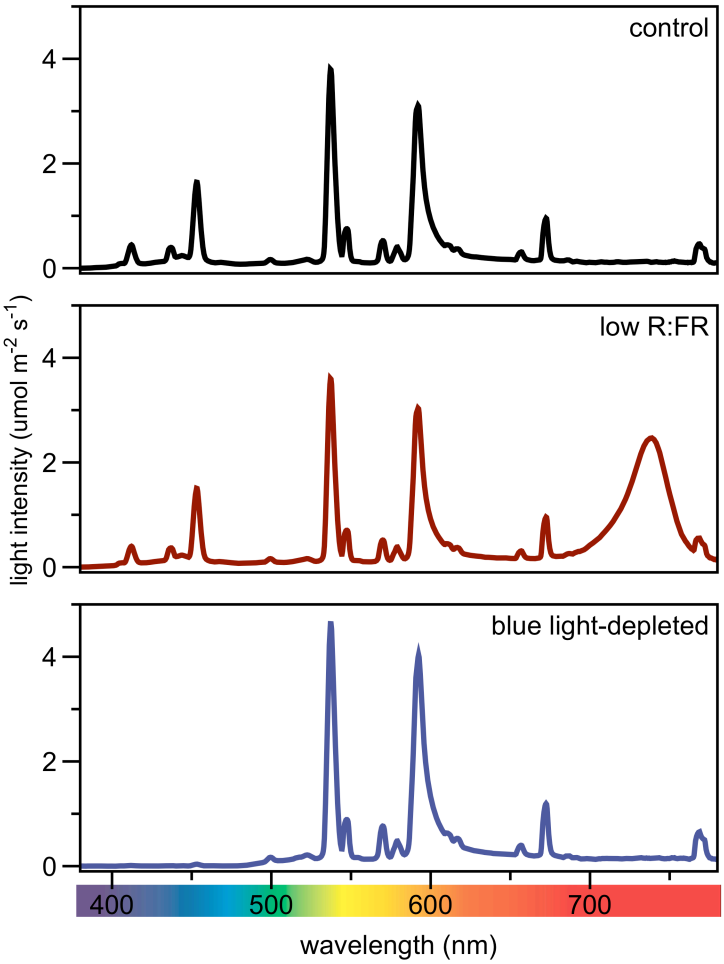
Supplemental Figure 8. HERK1 has no function in the *A. thaliana* shade avoidance syndrome. (Supports Figure 7.) (*A*) Petiole elongation (mm 24 h^{-1}) of *A. thaliana herk1the1* and *herk1* mutants, and WT control (Col-0), grown in control white light (R:FR = 1.8) or low R:FR (R:FR = 0.2) conditions. Data represent means + SEM, n = 10. Different letters indicate significant differences ($p < 0.05$, 2-way ANOVA with post-hoc Tukey test). (*B*) Pictures of representative leaves of *herk1the1* and *herk1* grown for five days in control white light (left pair) or low R:FR (right pair) conditions. (*C*) Hypocotyl length (mm) of lines shown in (*A*), after four days of control white light or low R:FR treatment. Data represent means + SEM, n = 40. Different letters indicate significant differences ($p < 0.05$, 2-way ANOVA with post-hoc Tukey test). (*D*) Relative expression of *HERK1* and *HERK2* in *A. thaliana* (Col-0) petioles exposed to control white or low R:FR light for 4 hours. Data represent means + SEM, data is relative to reference genes and control, n = 6.



Conditions	Tissue	Reference
1 h white light + far-red vs. white light	2 day old seedlings	1
3 h white light + far-red vs. white light	2 day old seedlings	1
24 h white light + far-red vs. white light	2 day old seedlings	1
2 h white light + far-red vs. white light	14 day old rosettes	2
1 h low R:FR light vs. high R:FR light	7 day old seedlings	3
2 h low R:FR light vs. high R:FR light	28 day old petioles	4
1 h continuous low R:FR light vs. contiuous high R:FR light	8 day old seedlings	5,6
1 day continuous low R:FR light vs. contiuous high R:FR light	8 day old seedlings	5,6
4 days continuous low R:FR light vs. contiuous high R:FR light	8 day old seedlings	5,6
1 h white light + far-red (*pifq*) vs. white light (*pifq*)	2 day old seedlings	1
3 h white light + far-red (*pifq*) vs. white light (*pifq*)	2 day old seedlings	1
24 h white light + far-red (*pifq*) vs. white light (*pifq*)	2 day old seedlings	1
1 h white light + far-red (*pifq*) vs. 1 h white light + far-red (Col-0)	2 day old seedlings	1
3 h white light + far-red (*pifq*) vs. 3 h white light + far-red (Col-0)	2 day old seedlings	1
24 h white light + far-red (*pifq*) vs. 24 h white light + far-red (Col-0)	2 day old seedlings	1
white light (*pifq*) vs. white light (Col-0)	2 day old seedlings	1
white light (*pifq*) vs. white light (Col-0)	3 day old seedlings	1
2 h white light + far-red (*pif5-3*) vs. white light (*pif5-3*)	14 day old rosettes	2
2 h white light + far-red (*pif4-101 pif5-3*) vs. white light (*pif4-101 pif5-3*)	14 day old rosettes	2
2 h white light + far-red (*35S:PIF5-HA*) vs. white light (*35S:PIF5-HA*)	14 day old rosettes	2
white light (*pif5*-3) vs. white light (Col-0)	14 day old rosettes	2
white light (*pif4-101 pif5-3*) vs. white light (Col-0)	14 day old rosettes	2
white light (*35S:PIF5-HA*) vs. white light (Col-0)	14 day old rosettes	2
2 h white light + far-red (*pif5-3*) vs. 2 h white light + far-red (Col-0)	14 day old rosettes	2
2 h white light + far-red (*pif4-101 pif5-3*) vs. 2 h white light + far-red (Col-0)	14 day old rosettes	2
2 h white light + far-red (*35S:PIF5-HA*) vs. 2 h white light + far-red (Col-0)	14 day old rosettes	2
30 min 1 µM IAA treatment vs. untreated	7 day old seedlings	7
1 h 1 µM IAA treatment vs. untreated	7 day old seedlings	7
3 h 1 µM IAA treatment vs. untreated	7 day old seedlings	7
30 min 1 µM IAA treatment vs. mock treatment	7 day old seedlings	8
1 h 1 µM IAA treatment vs. mock treatment	7 day old seedlings	8
3 h 1 µM IAA treatment vs. mock treatment	7 day old seedlings	8
1 h 5 µM IAA treatment vs. solvent treatment	7 day old seedlings	9
2 h 5 µM IAA treatment vs. solvent treatment	7 day old seedlings	10

1. Leivar *et al.* 2012, Plant Cell
2. Hornitschek *et al.* 2012, Plant Journal
3. Tao *et al.* 2008, Cell
4. De Wit *et al.* 2013, Plant Journal
5. Sessa *et al.* 2005, Genes & Development
6. Ciolfi *et al.* 2013, Plant Physiology
7. Delker *et al.* 2010, Plant Cell
8. Goda *et al.* 2008, Plant Journal
9. Armstrong *et al.* 2004, PNAS
10. Okushima *et al.* 2005, Plant Cell

Supplemental Figure 9. *RLK* gene expression is hardly affected by low R:FR, *pif* mutations and IAA in previous transcriptome studies. (Supports Figure 9.) Heatmap showing transcriptional Log2 fold-changes of *THE1*, *FER* and several other RLK-encoding genes in previous micro-array studies with various R:FR ratios, different *pif*-deficient and over-expressing mutants, and IAA treatments. Data were obtained via the Genevestigator programme and numbers refer to the publications of the original datasets.



Supplemental Figure 10. Light spectra of the treatments used in this study. Light spectra of control white light (R:FR = 1.8, upper), low R:FR (0.2, middle) and blue light-depleted (R:FR = 1.8, 4 µmol m^{-2} s^{-1} B, lower) treatments, given in µmol m^{-2} s^{-1} nm^{-1}.

Supplemental Table 1. List of all primers used for RT qPCR on *G. pyrenaicum*, *G. robertianum* and *A. thaliana* in this study.

Species	OMCL group	Description	Forward	Reverse
G. pyrenaicum	OMCL1609	*JR3*	TTTTGCCCCTTCACCTCGTT	ATGCCCACACTACCATGCTC
	OMCL5926	*TT7*	ATCTTCCTGAACAAGCGCCA	GAGCCAAACACGTCGCTTAC
	OMCL4985	*PAP1*	TCAACCACCTCAGTCTACAGC	TGGTGAAGGAAGATGGCACC
	OMCL14968	*KDR*	CATGATCTCCGACGACCAGA	CTTGCAACACCTTCGAAGCT
	OMCL1872	*THE1*	GGGCCACACAGCAACAATAA	TTCCTTCTTCGTCGGCAGAT
	OMCL2164	*FER*	CAGCAGGGTACGTAACAGTC	ACGGGATTGTTCAGGTCATG
	OMCL15305	*GA20OX2*	ATTACCACGCACACTCCCTT	CGGGCCTGATTTTGAACCAA
	OMCL2675	*CIB*	TTCCAAGGTTGCATCAGAGG	GCTCCAAATTGCCGTCTTTC
	OMCL9475	*BZIP61*	AGTGGTGCGTTCTGGCTAAA	TGTCACAATCTGGCCCCATC
	OMCL703	*PDF1 (ref.)*	TCTGGAGACCCTTTGCTCTG	CCACCAGATCACTCTCCCTC
G. robertianum	OMCL1609	*JR3*	CCCGACTGTGAACGATCCAA	CGGTGAAAGTTGGAGCCAGT
	OMCL5926	*TT7*	TCTCGCCCAACAACAGAGTC	GACGTCAAGCACTGTGGAGT
	OMCL4985	*PAP1*	TCGCTGTTCTTCCAAACCCA	TGATCCAGCTTTCGACCACA
	OMCL14968	*KDR*	GGATGATTTGAGCGAGCGTT	TGCGAATAATGGCTGCTTGA
	OMCL1872	*THE1*	AGGTTGAAGTTTCCGTTGCC	ACACCCGAAACAGCTCCTAA
	OMCL2164	*FER*	GTCATGTTCGGATCAGCAGT	CGGGACTGTTTAGGTCATGG
	OMCL15305	*GA20OX2*	CTGCCACTTGTTTTCGGTGA	TCAGGATTGACACTCGGGAC
	OMCL2675	*CIB*	TGCTCAACCTTCATATGCCC	TCGGGATTCTGAGACGATGA
	OMCL9475	*BZIP61*	TTACCGCCCAAAGTACCGAC	AGTCGTCCACCCAACAAGTT
	OMCL703	*PDF1 (ref.)*	CCAGAGGCGATGAAGACTGA	TTCCCCAAGTTTGATGCAGC
A. thaliana		*KDR*	CAACACCTCATCCCTGAACT	ACGGTCACTGAGGTCATCAAC
		THE1	GTTCTTTGGTTGGTGCGGTT	TTCTTGAGGACTCGTCGACC
		FER	GGTTTCTTCCCCGATTCTTCAG	AGAAGAAGAAGAGAGAGACGGAA
		IAA19	GCTGTAAGGAAGCTTCGACC	ACCATCTTTCAAGGCCACAC
		ATHB2	CGAGCAAGACAAGTGGAAGT	ATTCTCGCAGCATCTCCGTA
		HERK1	TCCTTTCATGGGACCGTTACT	CCATGGCAGATACAAAGCAAGA
		HERK2	TCGACTGGTCACTCGGTAAG	TGCTTCGCCTTTTCTTGCAT
		APT1 (ref.)	AATGGCGACTGAAGATGTGC	TCAGTGTCGAGAAGAAGCGT
		AT1G13320 (ref.)	GTAGGACCGGAGCCAACTAG	ACAGGGAAGAATGTGCTGGA
		UBQ5 (ref.)	CGGACCAGCAGCGATTGATT	CCTCTTCTTAGCACCACCACG
		AT4G26410 (ref.)	ATTGGTGTCGCTGCTAGTCT	TAAAGCCGTCCTCTCAAGCA