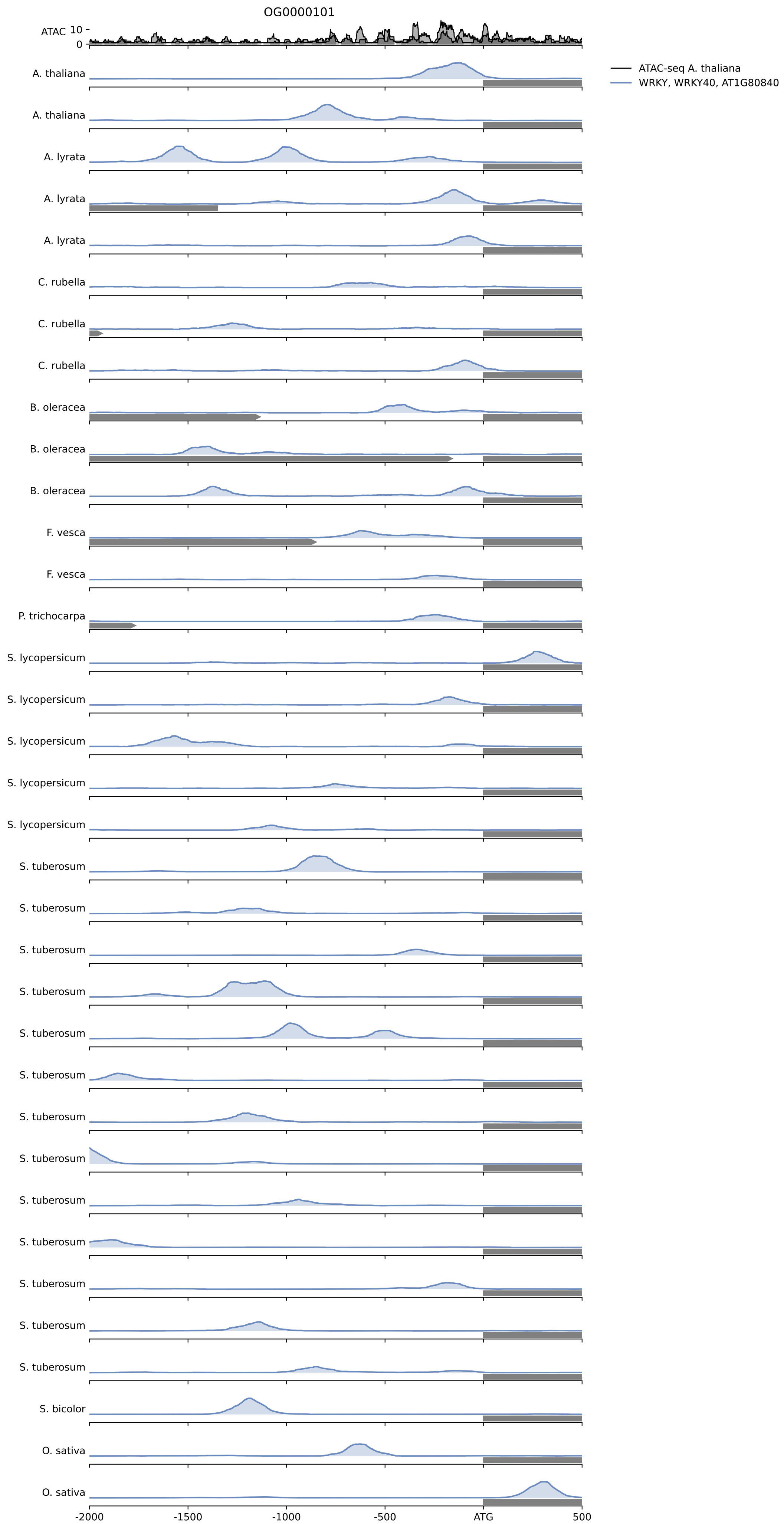
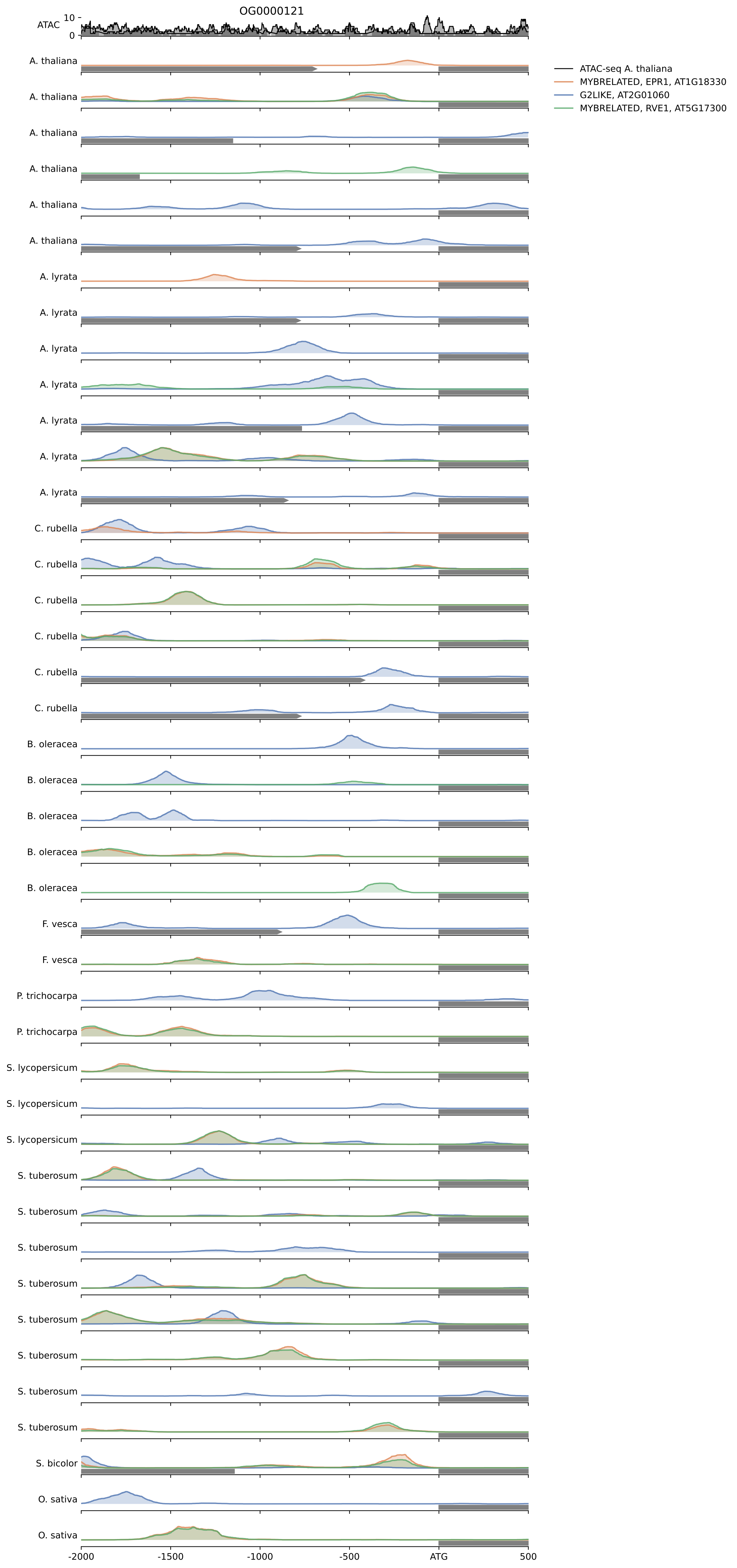


A. thaliana target: AT3G25490, Protein kinase family protein;(source:Araport11)

A. thaliana target: AT1G21270, WAK2, cytoplasmic serine/threonine protein kinase induced by salicylic acid. mutant plants exhibit a loss of cell expansion and dependence on sugars and salts for seedling growth, affecting the expression and activity of vacuolar invertase.



A. thaliana target: AT5G54010, Encodes a flavonoid 3-O-glucoside:2″-O-glucosyltransferase that determines pollen-specific flavonol structure.

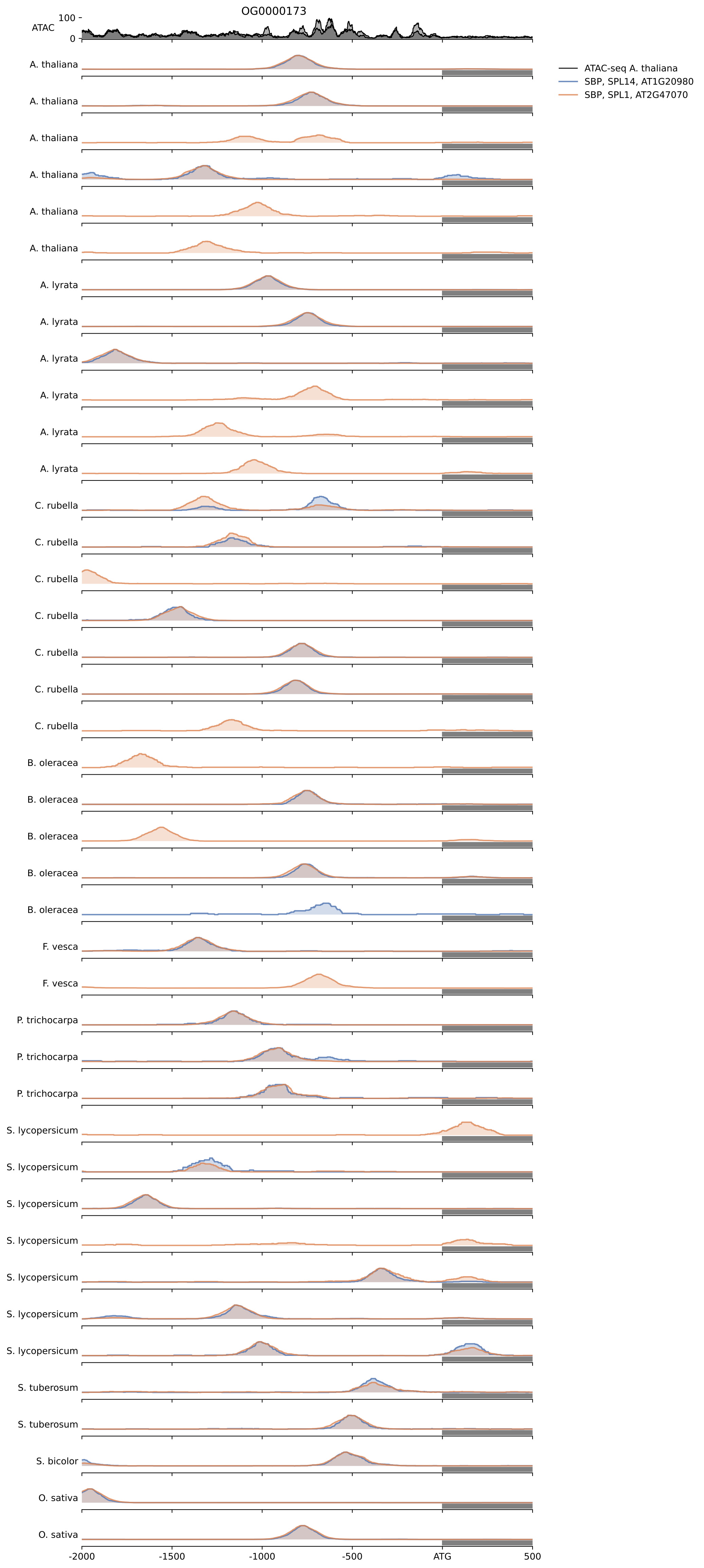
A. thaliana target: AT2G22930, UDP-Glycosyltransferase superfamily protein;(source:Araport11)

A. thaliana target: AT4G27560, Encodes a UDP-glycosyltransferase that contributes to cold, salt and drought stress tolerance via modulating anthocyanin accumulation.

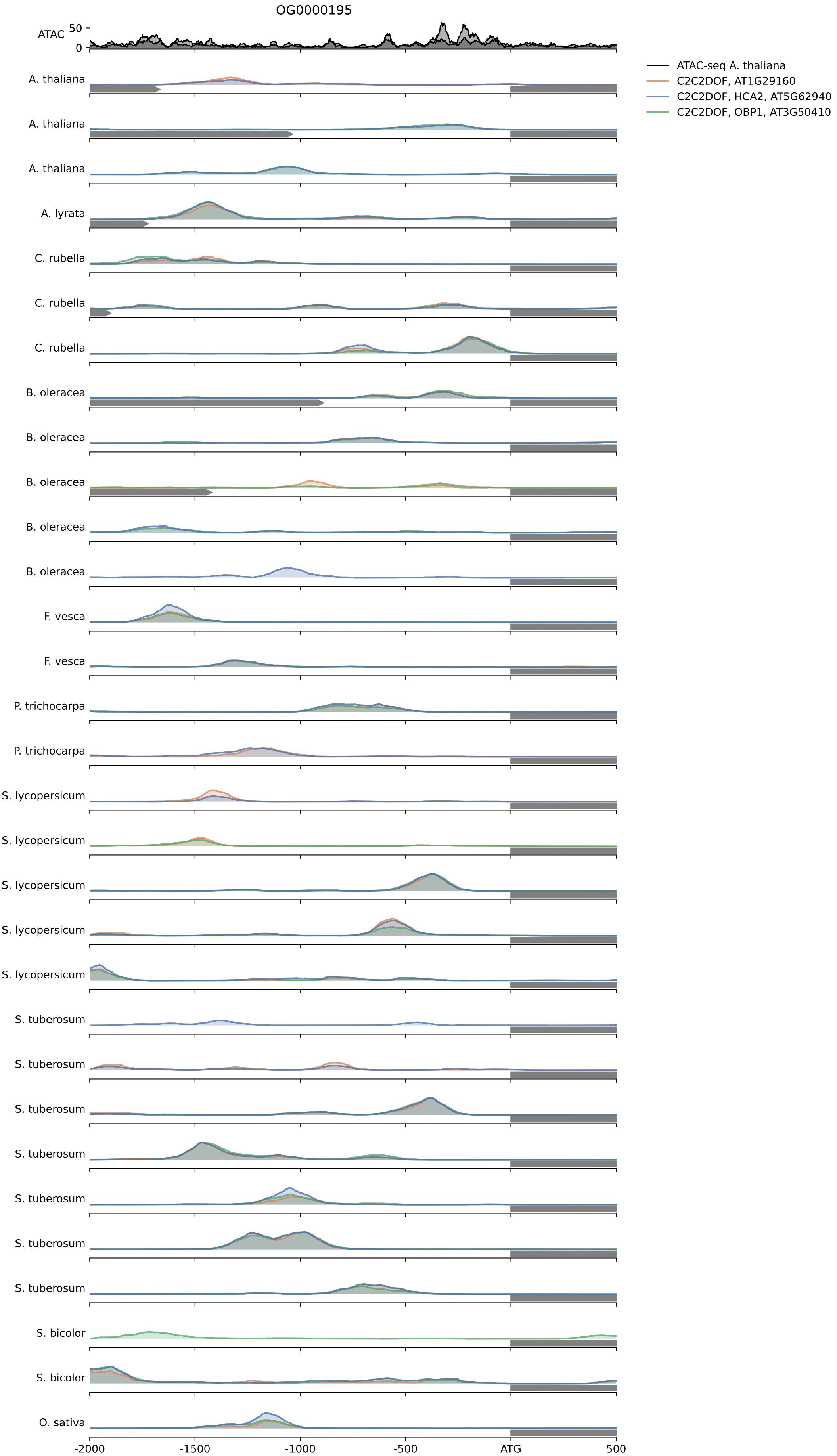
A. thaliana target: AT4G09500, Putative glycosyltransferase.

A. thaliana target: AT3G29630, UDP-Glycosyltransferase superfamily protein;(source:Araport11)

A. thaliana target: AT1G64910, UDP-Glycosyltransferase superfamily protein;(source:Araport11)



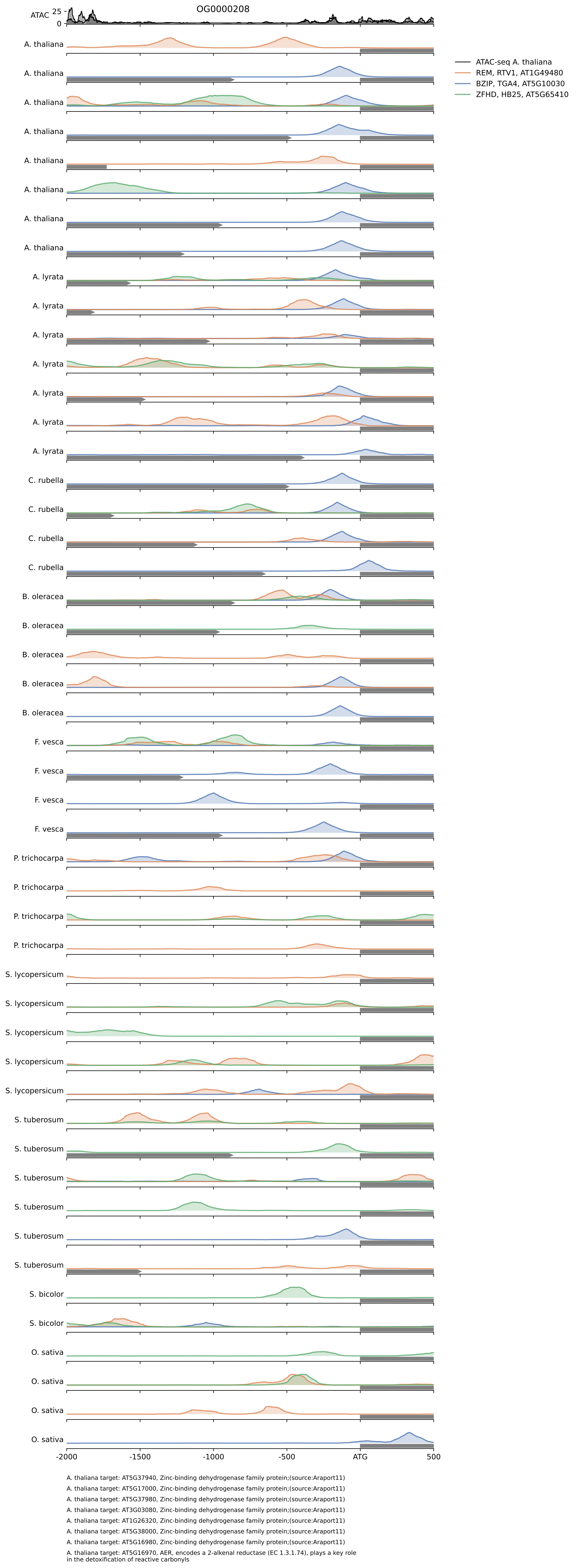
A. thaliana target: AT4G38860, SAUR-like auxin-responsive protein family;(source:Araport11)
A. thaliana target: AT2G21220, SAUR-like auxin-responsive protein family;(source:Araport11)
A. thaliana target: AT4G34760, SAUR-like auxin-responsive protein family;(source:Araport11)
A. thaliana target: AT1G75580, SAUR-like auxin-responsive protein family;(source:Araport11)
A. thaliana target: AT2G16580, SAUR-like auxin-responsive protein family;(source:Araport11)
A. thaliana target: AT1G19830, SAUR-like auxin-responsive protein family;(source:Araport11)



A. thaliana target: AT2G36790, UGT73C6, The At2g36790 gene encodes a UDP-glucose:flavonol-3-O-glycoside-7-O-glucosyltransferase (UGT73C6)attaching a glucosyl residue to the 7-O-position of the flavonols kaempferol, quercetin and their 3-O-glycoside derivatives.

A. thaliana target: AT2G36750, UGT73C1, UDP-glucosyl transferase 73C1;(source:Araport11)

A. thaliana target: AT3G53150, UGT73D1, UDP-glucosyl transferase 73D1;(source:Araport11)



A. thaliana target: AT5G37940, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT5G17000, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT5G37980, Zinc-binding dehydrogenase family protein;(source:Araport11)

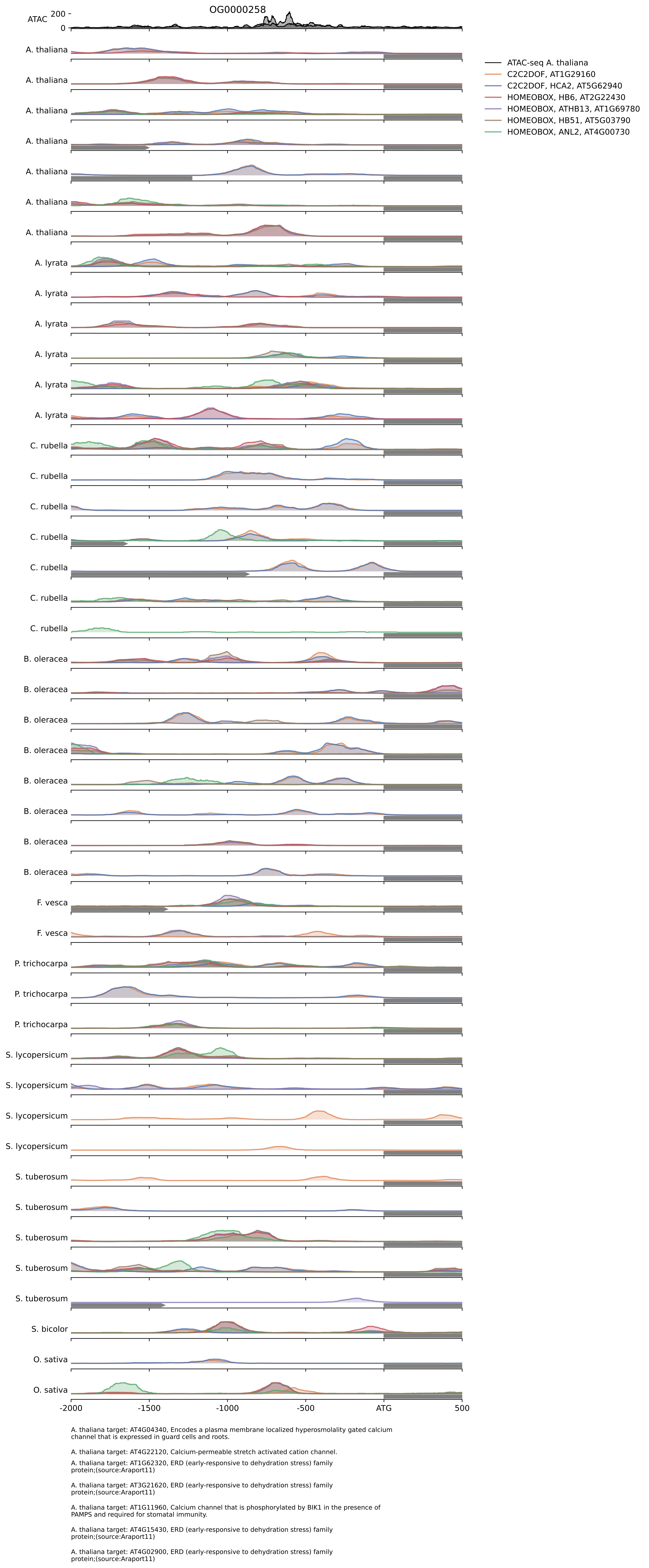
A. thaliana target: AT3G03080, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT1G26320, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT5G38000, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT5G16980, Zinc-binding dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT5G16970, AER, encodes a 2-alkenal reductase (EC 1.3.1.74), plays a key role in the detoxification of reactive carbonyls



A. thaliana target: AT4G04340, Encodes a plasma membrane localized hyperosmolality gated calcium channel that is expressed in guard cells and roots.

A. thaliana target: AT4G22120, Calcium-permeable stretch activated cation channel.

A. thaliana target: AT1G62320, ERD (early-responsive to dehydration stress) family protein;(source:Araport11)

A. thaliana target: AT3G21620, ERD (early-responsive to dehydration stress) family protein;(source:Araport11)

A. thaliana target: AT1G11960, Calcium channel that is phosphorylated by BIK1 in the presence of PAMPS and required for stomatal immunity.

A. thaliana target: AT4G15430, ERD (early-responsive to dehydration stress) family protein;(source:Araport11)

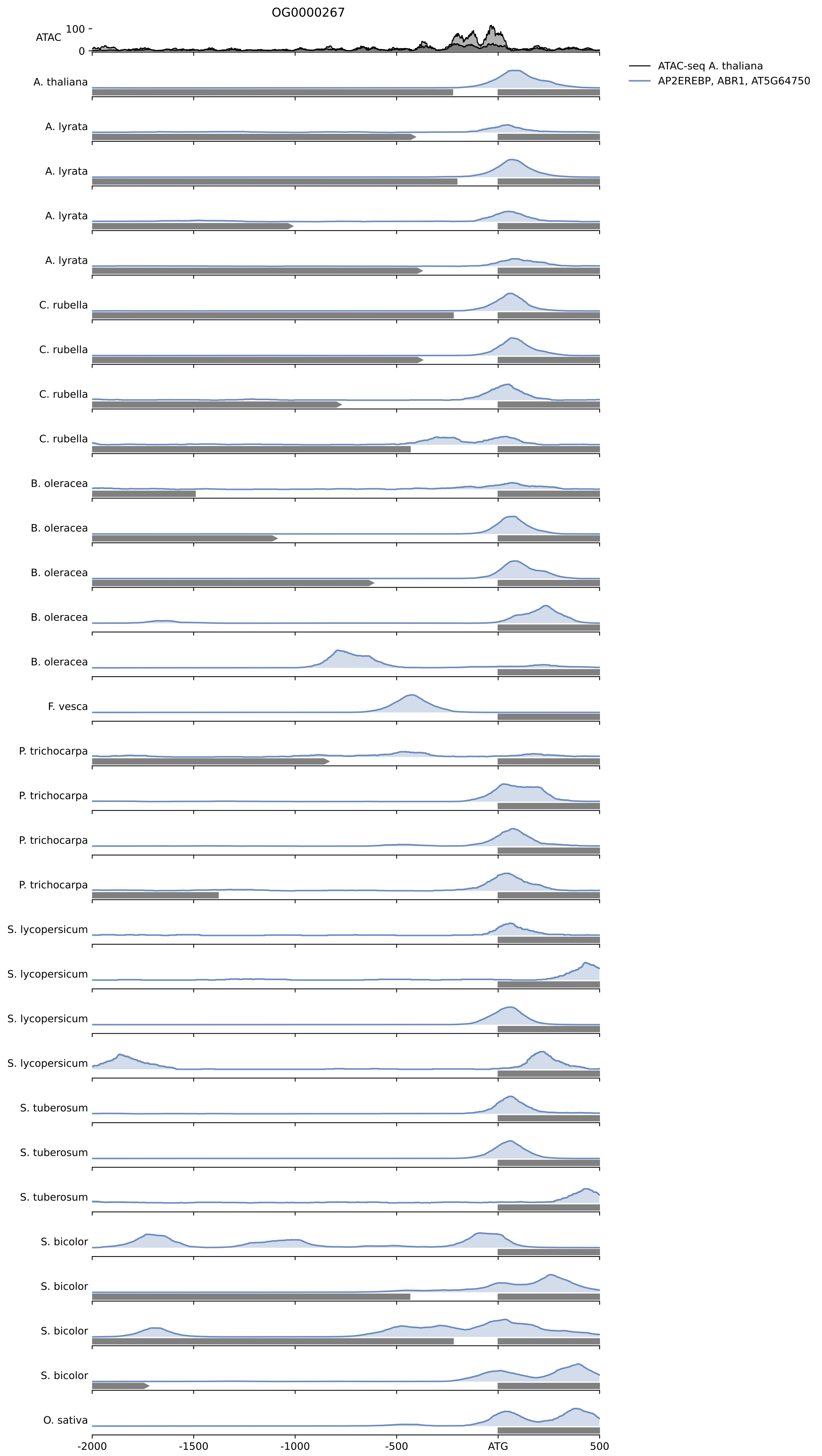
A. thaliana target: AT4G02900, ERD (early-responsive to dehydration stress) family protein;(source:Araport11)

A. thaliana target: AT1G23710, hypothetical protein (DUF1645);(source:Araport11)

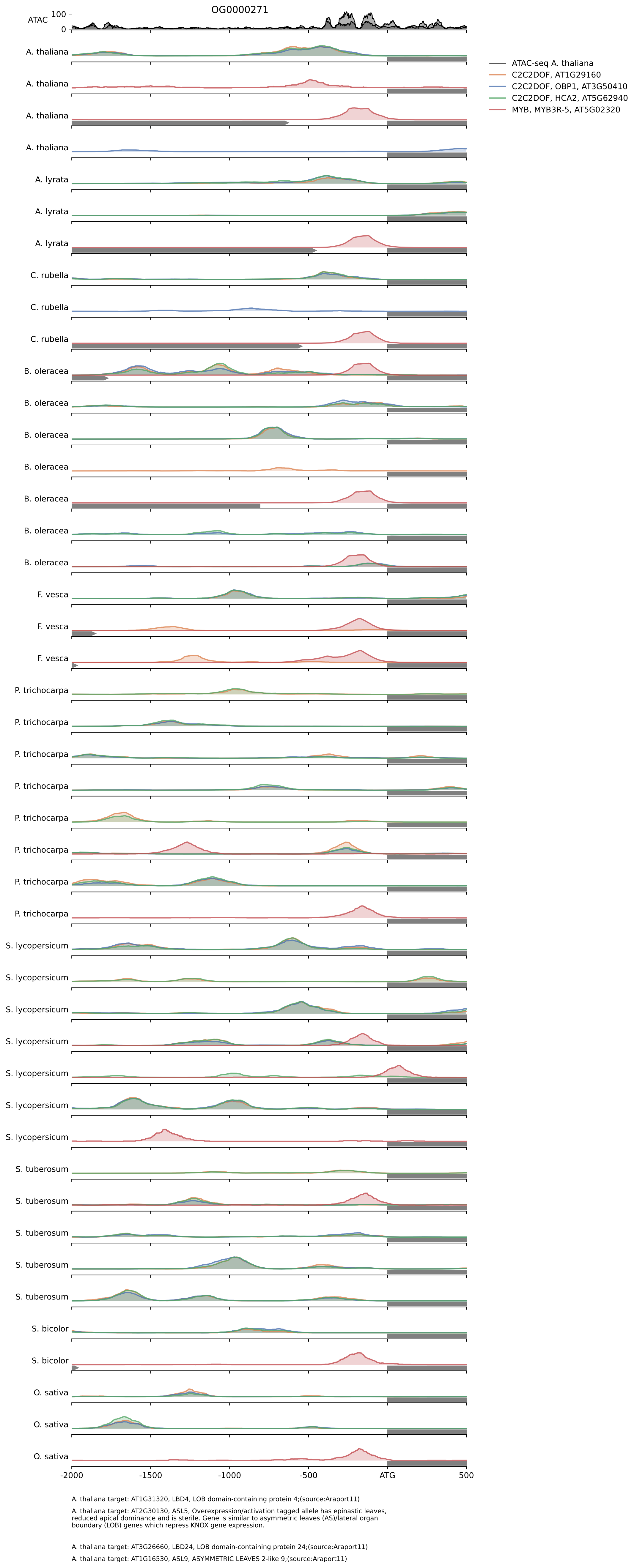
A. thaliana target: AT5G62770, membrane-associated kinase regulator, putative (DUF1645);(source:Araport11)

A. thaliana target: AT3G27880, hypothetical protein (DUF1645);(source:Araport11)

A. thaliana target: AT1G70420, DNA ligase-like protein, putative (DUF1645);(source:Araport11)



A. thaliana target: AT1G55890, Ribosomal pentatricopeptide repeat protein

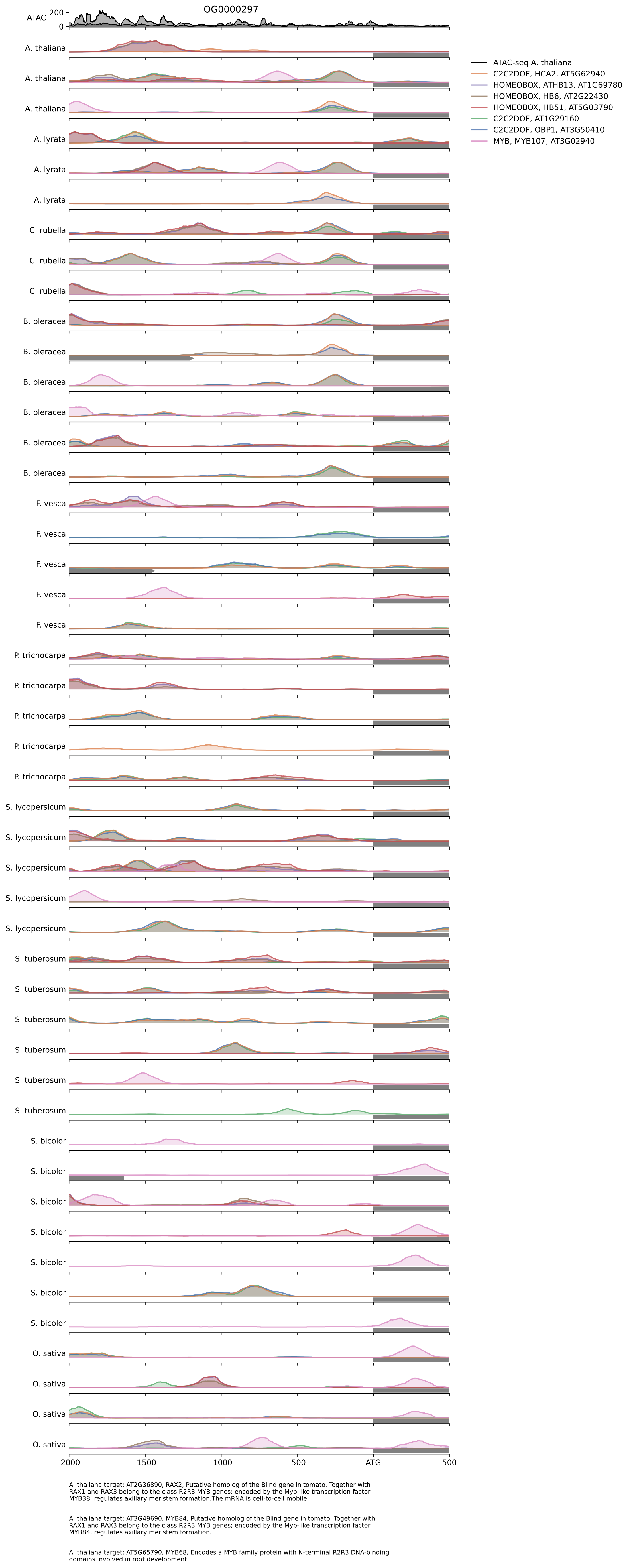


A. thaliana target: AT1G31320, LBD4, LOB domain-containing protein 4;(source:Araport11)

A. thaliana target: AT2G30130, ASL5, Overexpression/activation tagged allele has epinastic leaves, reduced apical dominance and is sterile. Gene is similar to asymmetric leaves (AS)/lateral organ boundary (LOB) genes which repress KNOX gene expression.

A. thaliana target: AT3G26660, LBD24, LOB domain-containing protein 24;(source:Araport11)

A. thaliana target: AT1G16530, ASL9, ASYMMETRIC LEAVES 2-like 9;(source:Araport11)



A. thaliana target: AT2G36890, RAX2, Putative homolog of the Blind gene in tomato. Together with RAX1 and RAX3 belong to the class R2R3 MYB genes; encoded by the Myb-like transcription factor MYB38, regulates axillary meristem formation.The mRNA is cell-to-cell mobile.

A. thaliana target: AT3G49690, MYB84, Putative homolog of the Blind gene in tomato. Together with RAX1 and RAX3 belong to the class R2R3 MYB genes; encoded by the Myb-like transcription factor MYB84, regulates axillary meristem formation.

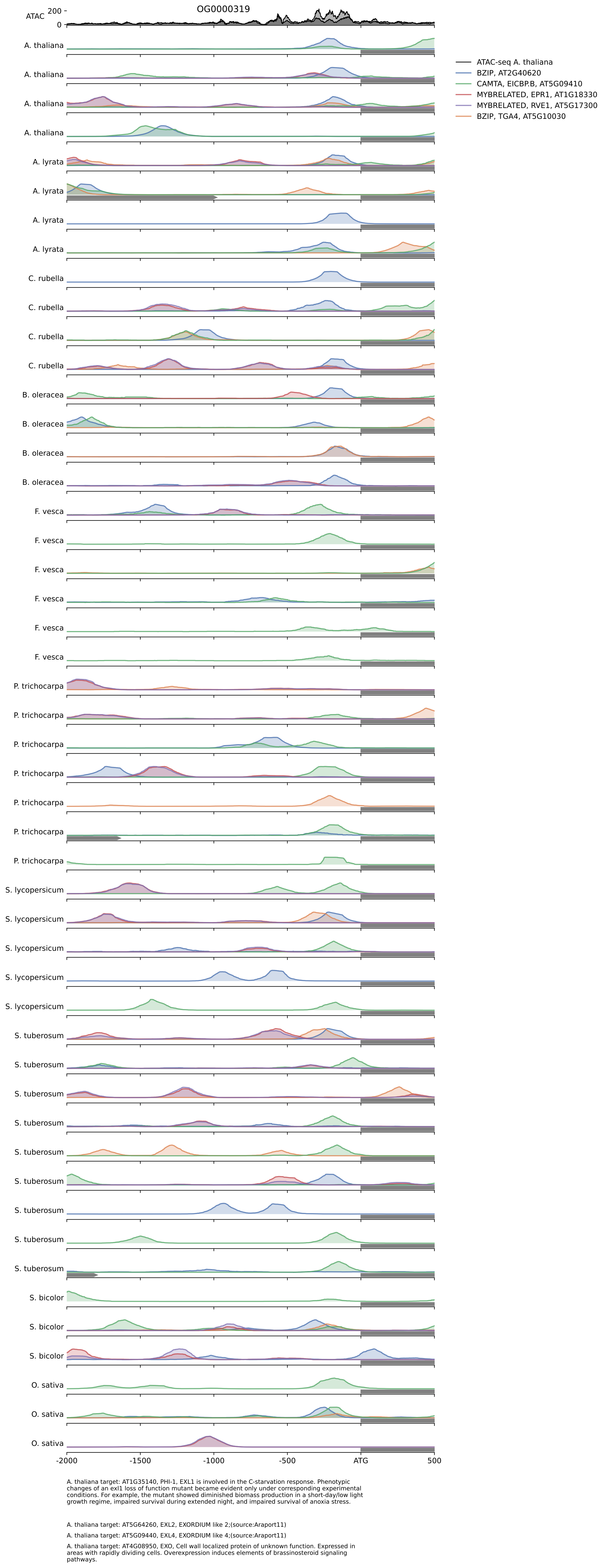
A. thaliana target: AT5G65790, MYB68, Encodes a MYB family protein with N-terminal R2R3 DNA-binding domains involved in root development.

A. thaliana target: AT4G22010, sks4, SKU5 similar 4;(source:Araport11)

A. thaliana target: AT1G76160, sks5, SKU5 similar 5;(source:Araport11)

A. thaliana target: AT4G38420, sks9, SKU5 similar 9;(source:Araport11)

A. thaliana target: AT1G41830, SKS6, SKU5-similar 6;(source:Araport11)

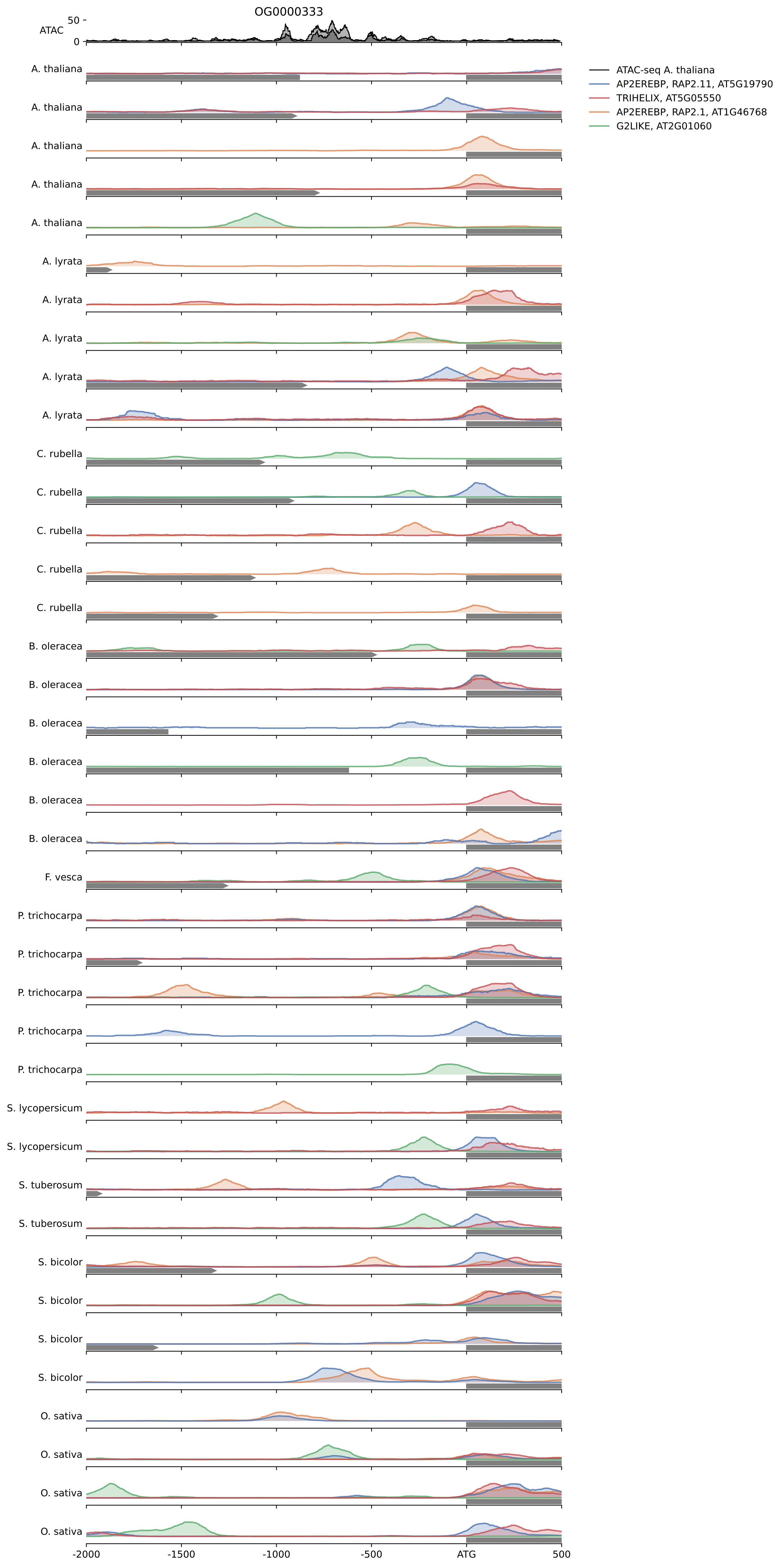


A. thaliana target: AT1G35140, PHI-1, EXL1 is involved in the C-starvation response. Phenotypic changes of an exl1 loss of function mutant became evident only under corresponding experimental conditions. For example, the mutant showed diminished biomass production in a short-day/low light growth regime, impaired survival during extended night, and impaired survival of anoxia stress.

A. thaliana target: AT5G64260, EXL2, EXORDIUM like 2;(source:Araport11)

A. thaliana target: AT5G09440, EXL4, EXORDIUM like 4;(source:Araport11)

A. thaliana target: AT4G08950, EXO, Cell wall localized protein of unknown function. Expressed in areas with rapidly dividing cells. Overexpression induces elements of brassinosteroid signaling pathways.



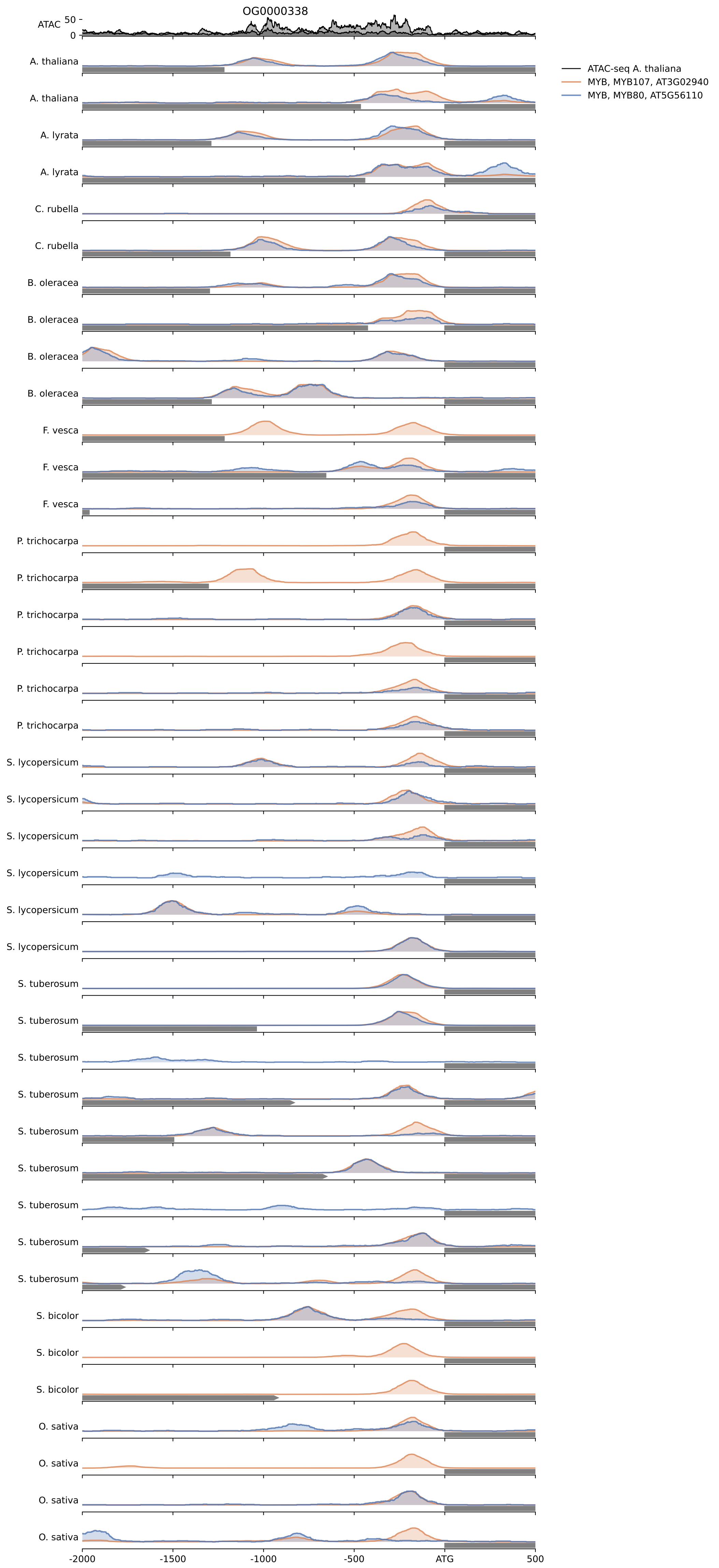
A. thaliana target: AT4G32420, Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein;(source:Araport11)

A. thaliana target: AT4G38740, ROC1, Encodes cytosolic cyclophilin ROC1.

A. thaliana target: AT2G21130, Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein;(source:Araport11)

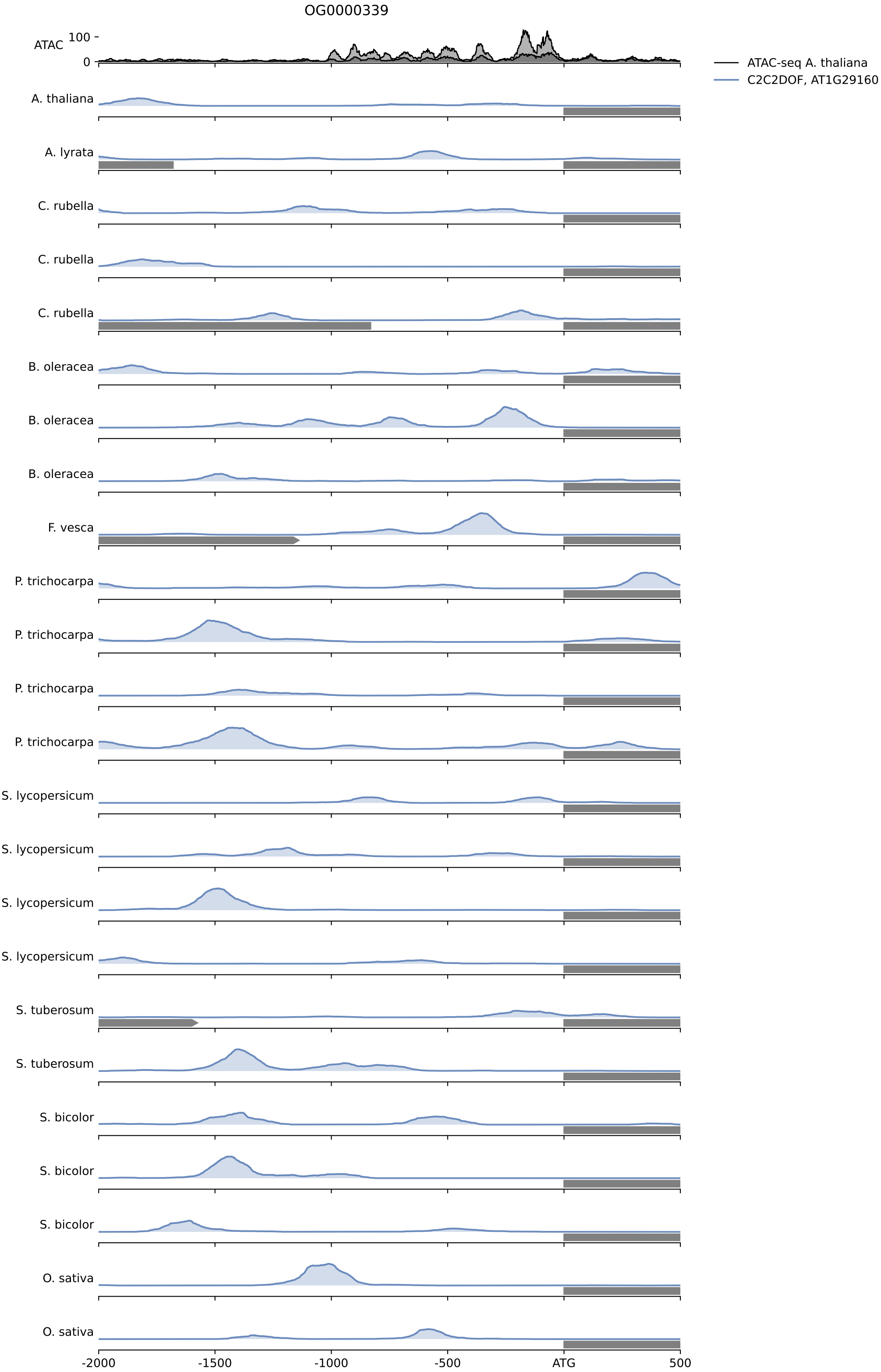
A. thaliana target: AT2G16600, ROC3, Encodes cytosolic cyclophilin ROC3. The mRNA is cell-to-cell mobile.

A. thaliana target: AT4G34870, ROC5, belongs to cyclophilin family

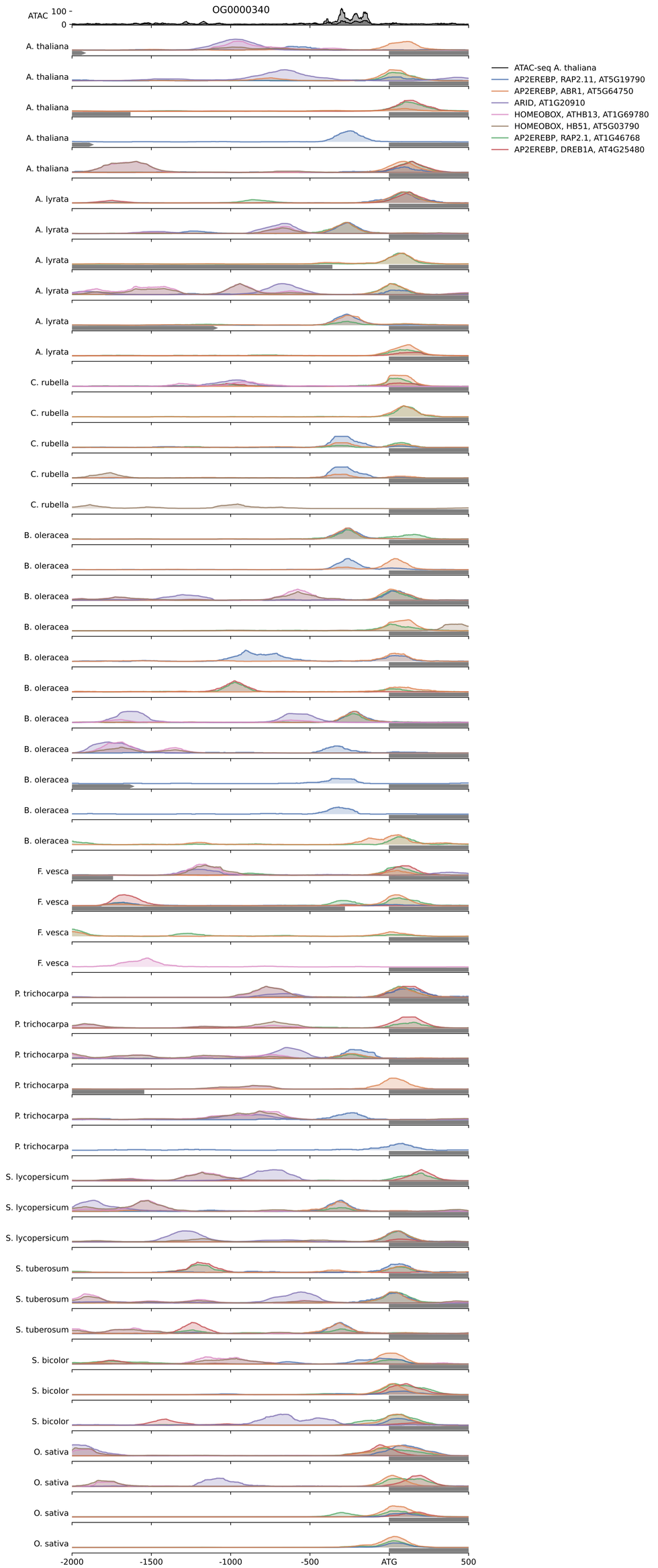


A. thaliana target: AT3G22600, Glycosylphosphatidylinositol (GPI)-anchored LTPg protein, downregulated in syncytia induced by the beet cyst nematode Heterodera schachtii and root knot nematode Meloidogyne incognita. Infection with bacteria (Pseudomonas syringae) and fungi (Botrytis cinerea) leads to the induction of the gene in leaves.

A. thaliana target: AT2G48130, Encodes a plasma membrane-localized glycosylphosphatidylinositol-anchored lipid transfer protein expressed in root endodermis and seed coats that is involved in very long chain fatty acid (and their derivatives) transport.



A. thaliana target: AT2G24170, Endomembrane protein 70 protein family;(source:Araport11)



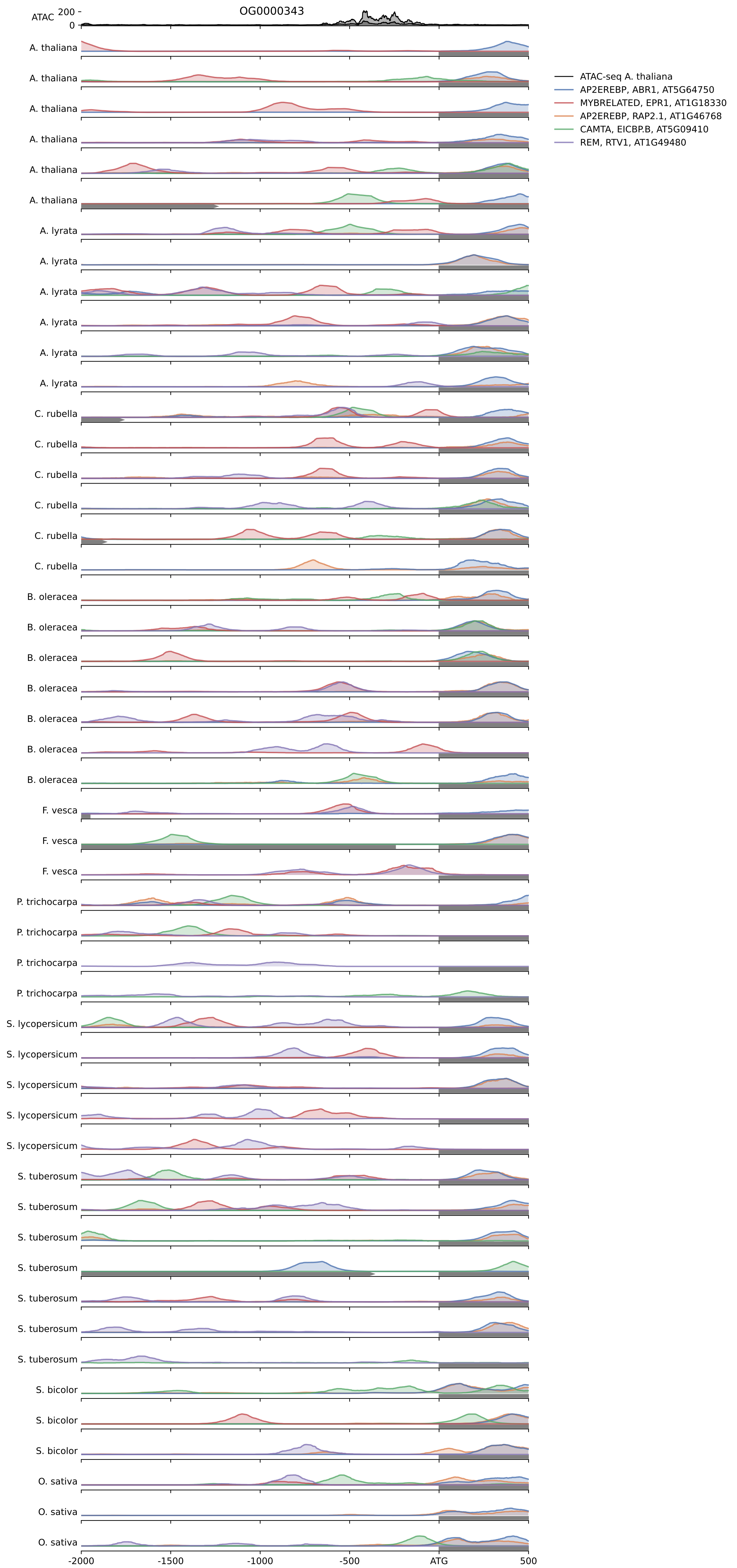
A. thaliana target: AT1G71770, PAB5, Encodes a Class I polyA-binding protein. Expressed in floral organs. Binds polyA sepharose in vitro.

A. thaliana target: AT1G22760, PAB3, Putative poly(A) binding protein May there fore function in posttranscriptional regulation, including mRNA turnover and translational initiation. Expression detected only in floral organs.

A. thaliana target: AT2G23350, PAB4, polyadenylate-binding protein, putative / PABP, putative.Member of the Class II family of PABP proteins. Highly and ubiquitously expressed. The mRNA is cell-to-cell mobile.

A. thaliana target: AT4G34110, PAB2, Putative poly-A binding protein. Member of a gene family .Expressed in stele and root meristem and post-fertilization ovules.Member of the class II family of PABP proteins. The mRNA is cell-to-cell mobile.

A. thaliana target: AT1G49760, PAB8, polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum). Highly and ubiquitously expressed. Member of the class II PABP family.



A. thaliana target: AT4G25480, DREB1A, Encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF3). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to low temperature and abscisic acid.

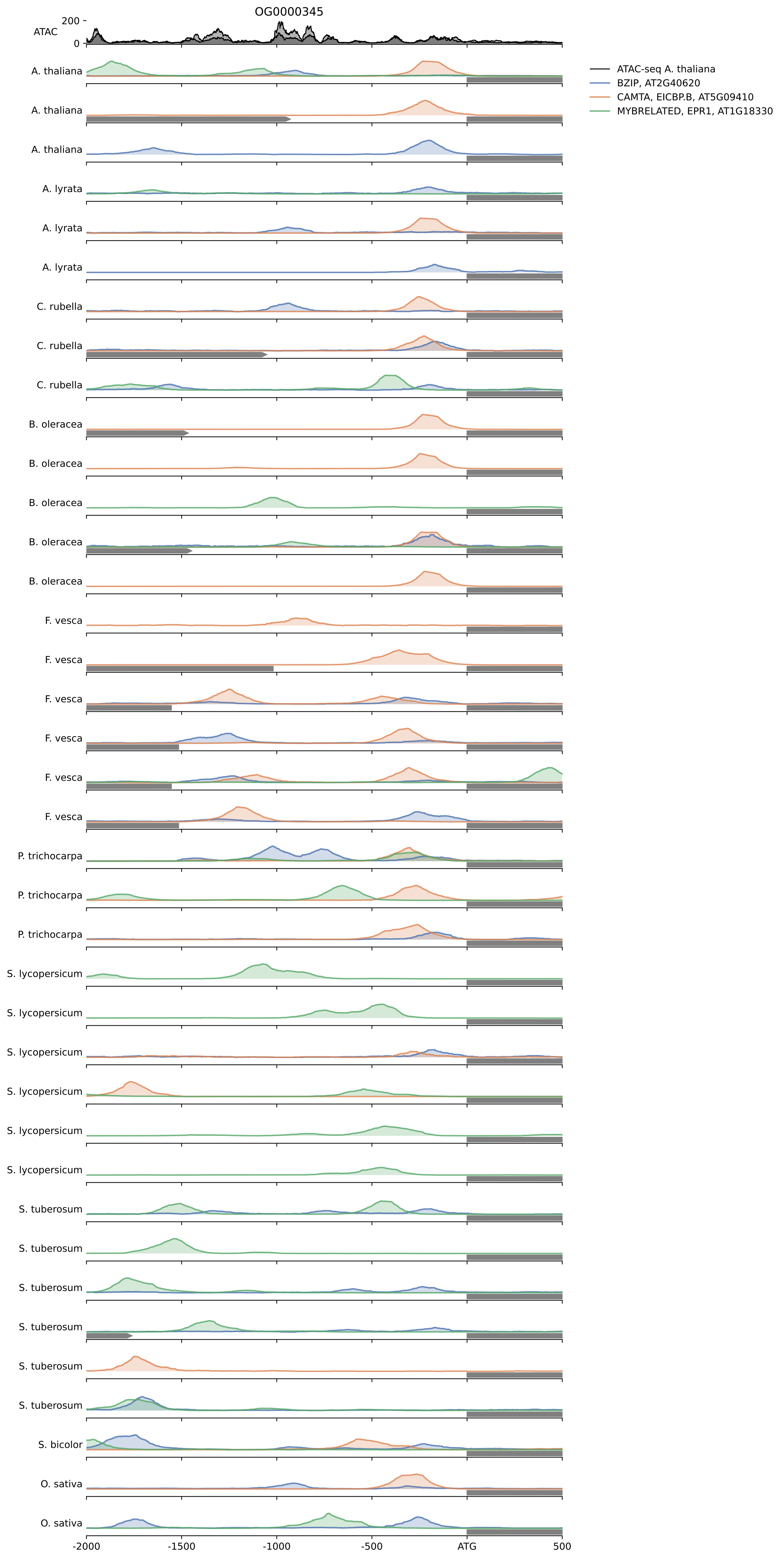
A. thaliana target: AT1G12610, DDF1, Encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (DDF1). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. Overexpression of this gene results in delayed flowering and dwarfism, reduction of gibberellic acid biosynthesis, and increased tolerance to high levels of salt. This gene is expressed in all tissues examined, but most abundantly expressed in upper stems. Overexpression of this gene is also correlated with increased expression of GA biosynthetic genes and RD29A (a cold and drought responsive gene). Under salt stress it induces the expression of GAOX7, which encodes ad C20-GA inhibitor.

A. thaliana target: AT4G25490, CBF1, Transcriptional activator that binds to the DRE/CRT regulatory element and induces COR (cold-regulated) gene expression increasing plant freezing tolerance. It encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF1). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to low temperature and abscisic acid.

A. thaliana target: AT1G63030, ddf2, encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (DDF2). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. Overexpression of this gene results in the reduction of gibberellic acid biosynthesis. This gene is expressed in all tissues examined, but most abundantly expressed in rosette leaves and stems. Overexpression of DDF1, a putative paralog of this gene, also reduces gibberellic acid biosynthesis and makes the plants more tolerant to high-salinity levels.

A. thaliana target: AT4G25470, CBF2, Encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF2). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to low temperature, abscisic acid, and circadian rhythm. Overexpressing this gene leads to increased freeze tolerance and induces the expression level of 85 cold-induced genes and reduces the expression level of 8 cold-repressed genes, which constitute the CBF2 regulon. Mutations in CBF2 increases the expression level of CBF1 and CBF3, suggesting that this gene may be involved in a negative regulatory or feedback circuit of the CBF pathway.

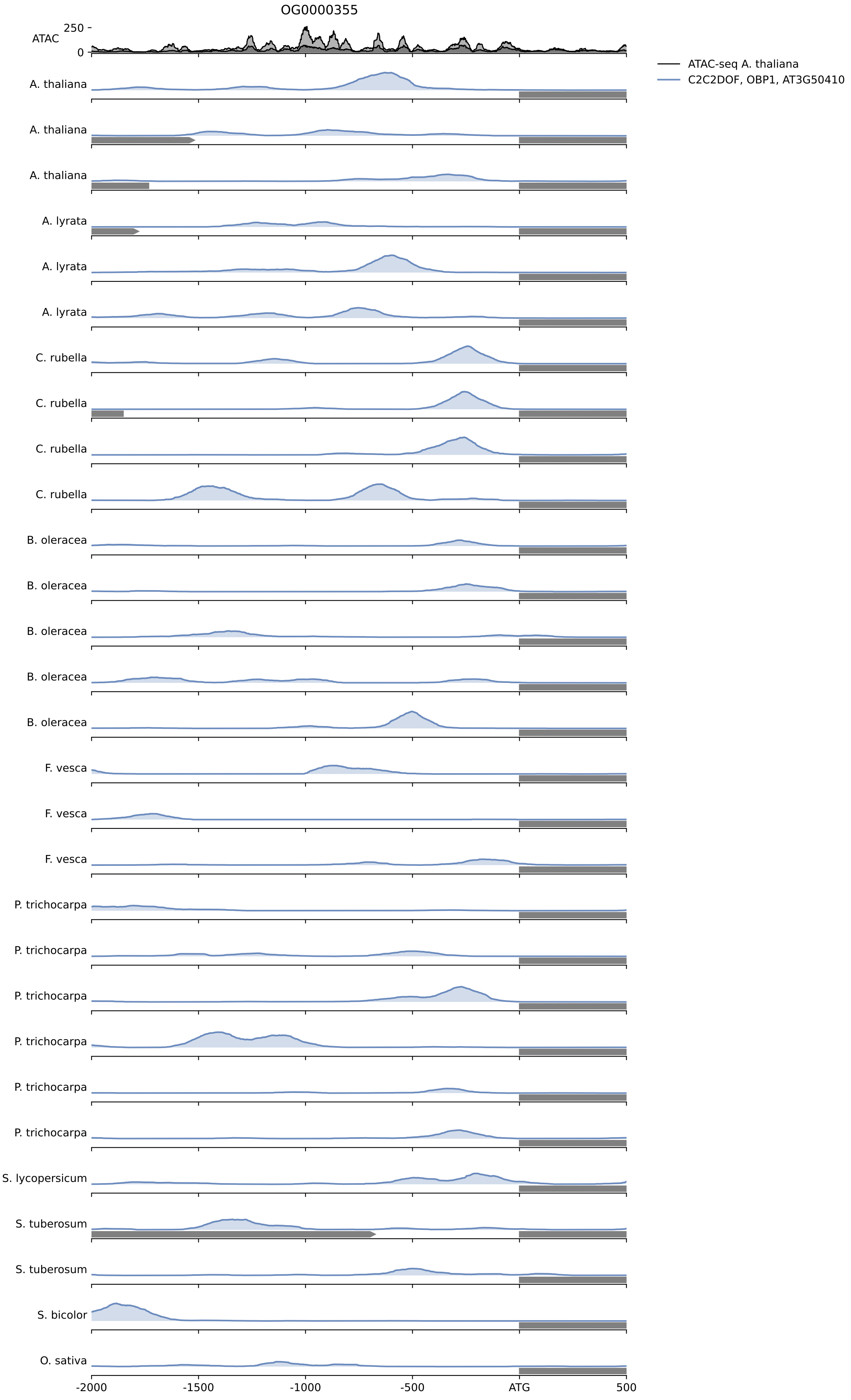
A. thaliana target: AT5G51990, CBF4, encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF4). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to drought stress and abscisic acid treatment, but not to low temperature.



A. thaliana target: AT5G57560, TCH4, Encodes a cell wall-modifying enzyme, rapidly upregulated in response to environmental stimuli.

A. thaliana target: AT4G25810, XTR6, xyloglucan endotransglycosylase-related protein (XTR6)

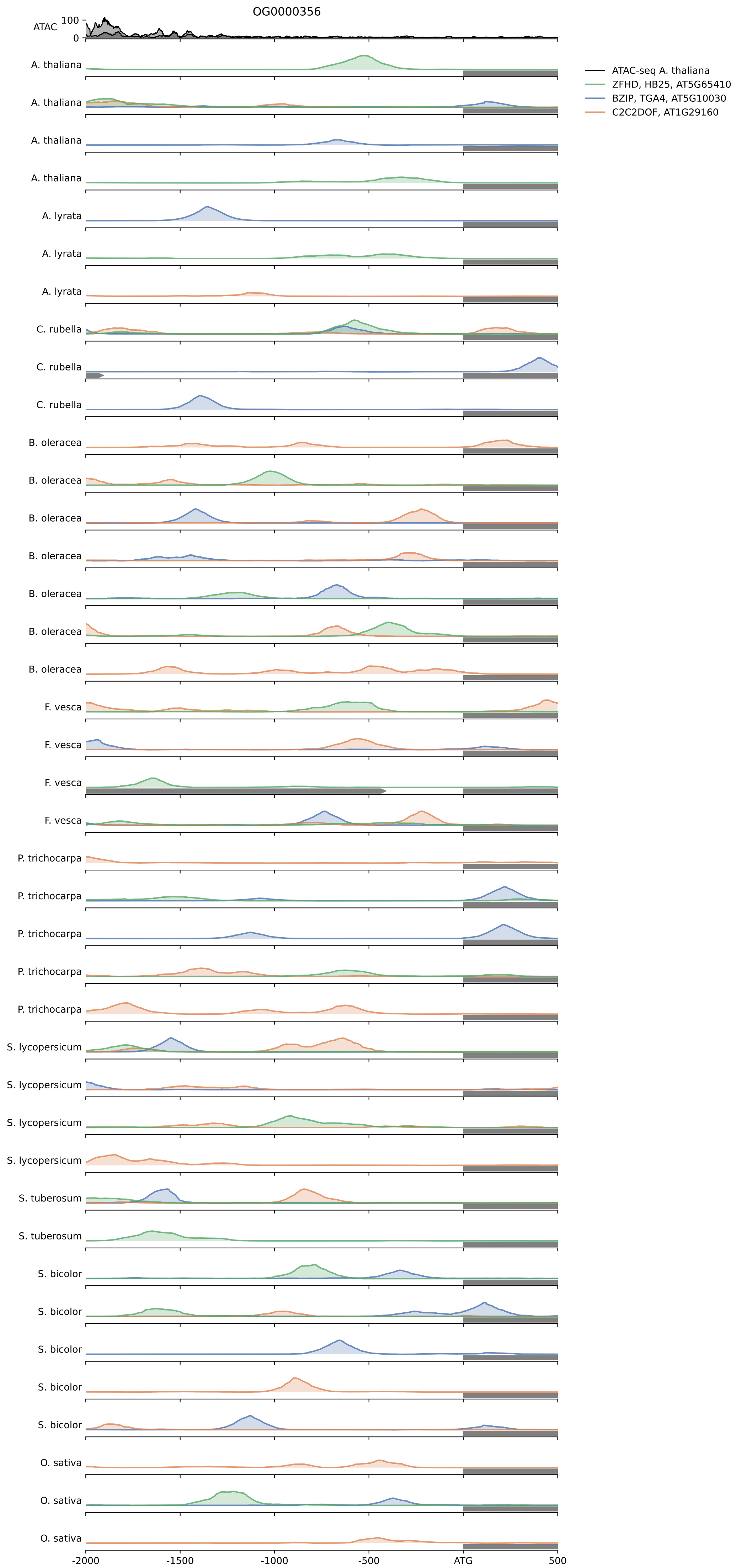
A. thaliana target: AT4G30270, XTH24, encodes a protein similar to endo xyloglucan transferase in sequence. It is also very similar to BRU1 in soybean, which is involved in brassinosteroid response.



A. thaliana target: AT1G55210, Disease resistance-responsive (dirigent-like protein) family protein;(source:Araport11)

A. thaliana target: AT3G13660, Disease resistance-responsive (dirigent-like protein) family protein;(source:Araport11)

A. thaliana target: AT3G13650, Disease resistance-responsive (dirigent-like protein) family protein;(source:Araport11)

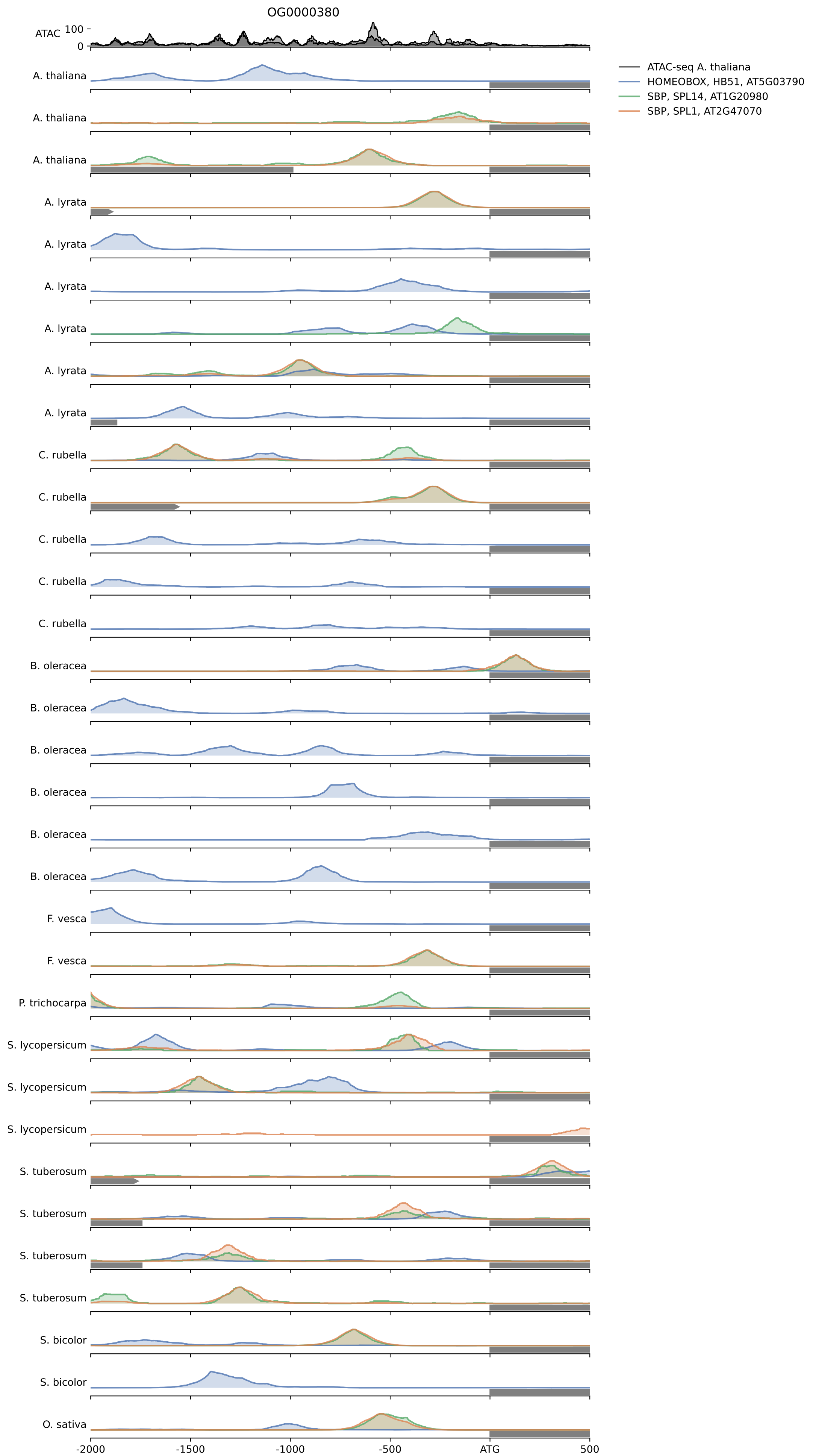


A. thaliana target: AT1G62700, ANAC026, Encodes a NAC-domain transcription factor. Expressed in the vascular tissue.

A. thaliana target: AT2G18060, VND1, Encodes a NAC-domain transcription factor that is expressed in developing vessels and protoxylem. Along with other members of this family, VND1 appears to regulate the development of genes required for secondary cell wall biosynthesis.

A. thaliana target: AT5G66300, NAC105, Encodes a NAC-domain transcription factor. Expressed in the vascular tissue.

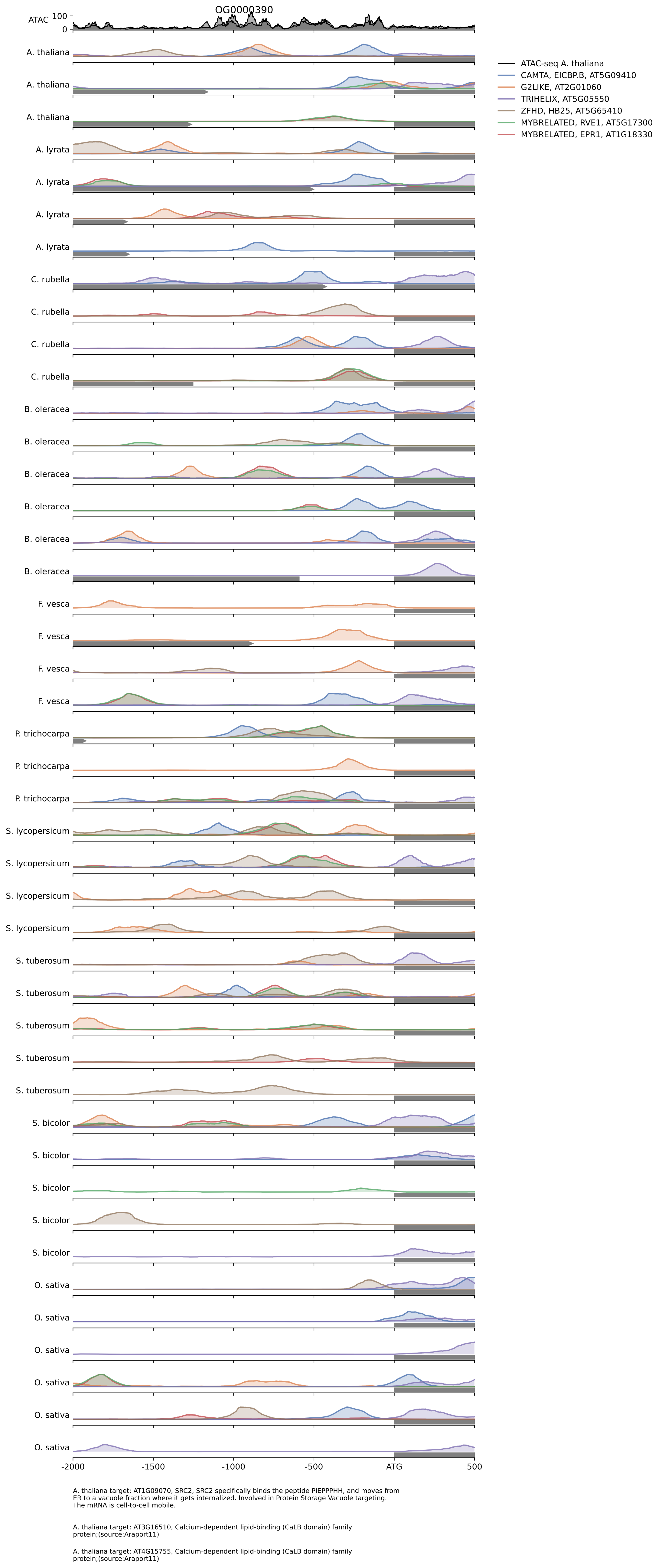
A. thaliana target: AT1G12260, NAC007, Encodes a NAC-domain transcription factor that is expressed in developing xylem. Over expression of this protein causes ectopic secondary cell wall growth. Complements some of the cell wall defects seen in SND1/NST1 double mutants.



A. thaliana target: AT4G19680, IRT2, encodes an iron transporter whose expression is induced by iron and zinc deficiency. Gene is specifically expressed in the external cell layers of the root subapical zone.

A. thaliana target: AT2G04032, ZIP7, zinc transporter 7 precursor;(source:Araport11)

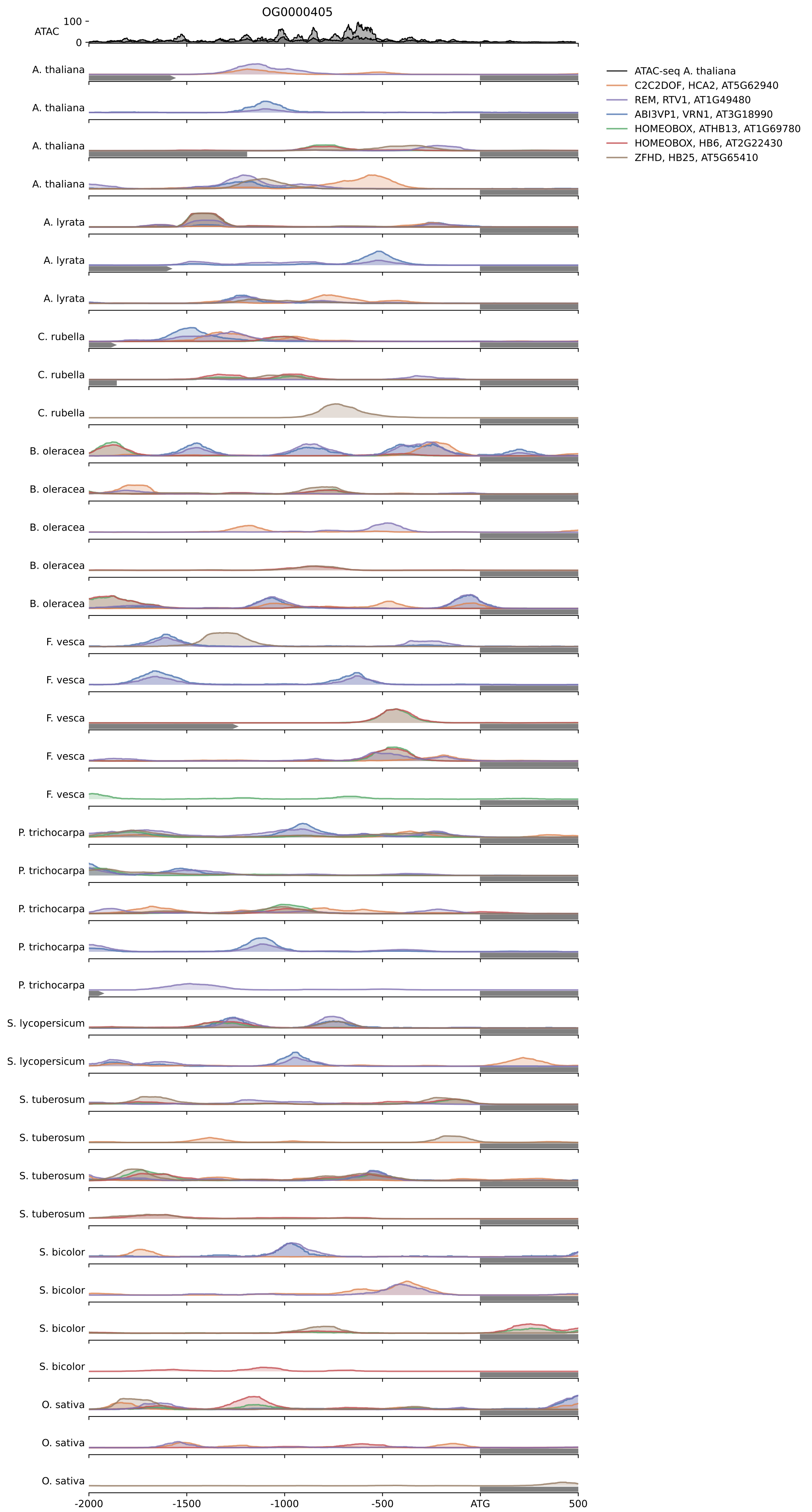
A. thaliana target: AT1G31260, ZIP10, member of Fe(II) transporter isolog family



A. thaliana target: AT1G09070, SRC2, SRC2 specifically binds the peptide PIEPPPHH, and moves from ER to a vacuole fraction where it gets internalized. Involved in Protein Storage Vacuole targeting. The mRNA is cell-to-cell mobile.

A. thaliana target: AT3G16510, Calcium-dependent lipid-binding (CaLB domain) family protein;(source:Araport11)

A. thaliana target: AT4G15755, Calcium-dependent lipid-binding (CaLB domain) family protein;(source:Araport11)

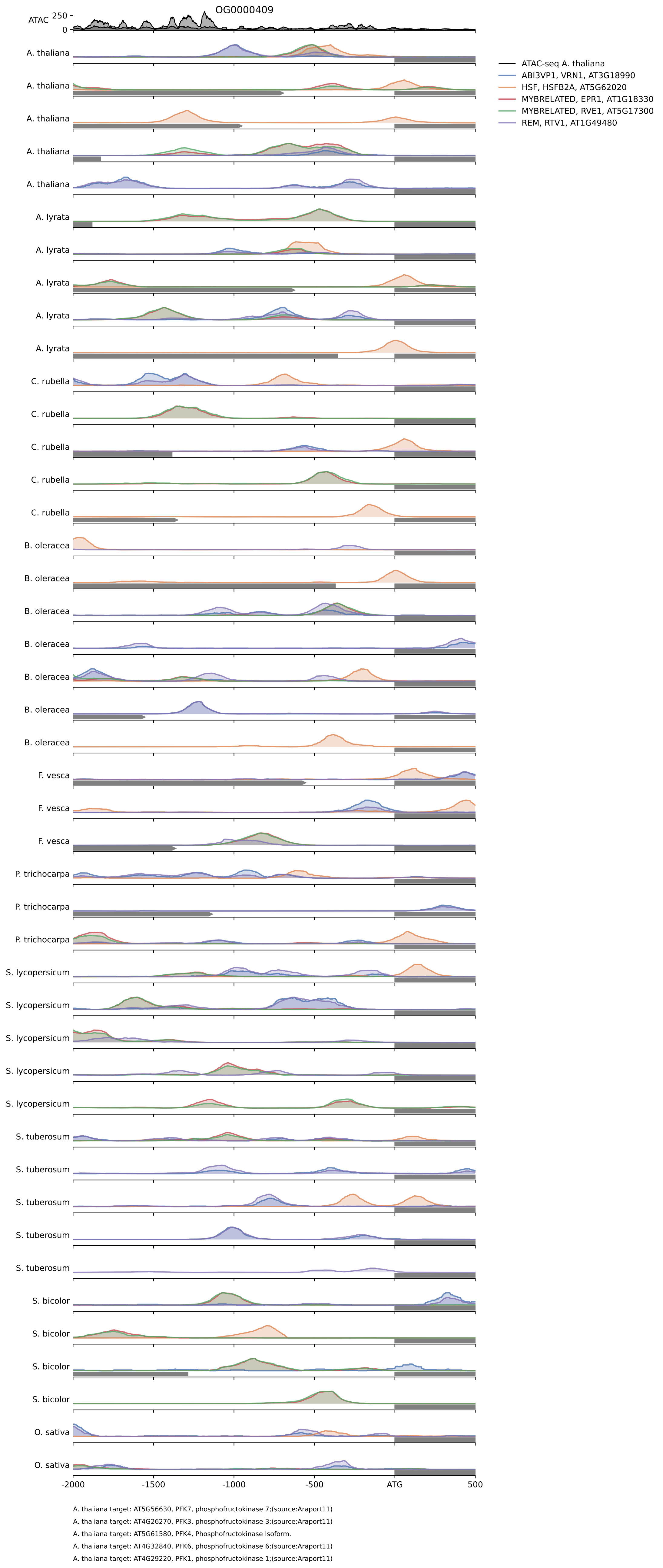


A. thaliana target: AT1G11950, Transcription factor jumonji (jmjC) domain-containing protein;(source:Araport11)

A. thaliana target: AT4G00990, jJumonji-domain-containing H3K9 histone demethylase. Loss of function mutants are susceptible to bacterial infection and early flowering.

A. thaliana target: AT3G07610, IBM1, IBM1 likely encodes a protein with histone H3mK9 demethylation activity. It may preferentially demethylate H3mK9 at low-copy loci to protect them from silencing by nearby heterochromatin by preventing the spread of cytosine methylation. BONSAI (At1g73177) is hypermethylated in ibm1 mutants. ibm1 mutants have morphological defects that become apparent at the F3 generation, including small narrow leaves, arrested flower development, and faulty pollen development. These phenotypes cannot result solely from the BONSAI hypermethylation. Aberrant phenotypes in ibm1 mutants in both DNA methylation and plant development can be suppressed by mutations in the KYP H3K9 methyltransferase or the CMT3 non CG-cytosine methylase.

A. thaliana target: AT1G62310, Encodes a probable H3K9me2 demethylase. Functions in trichome morphogenesis via regulation of GL3.



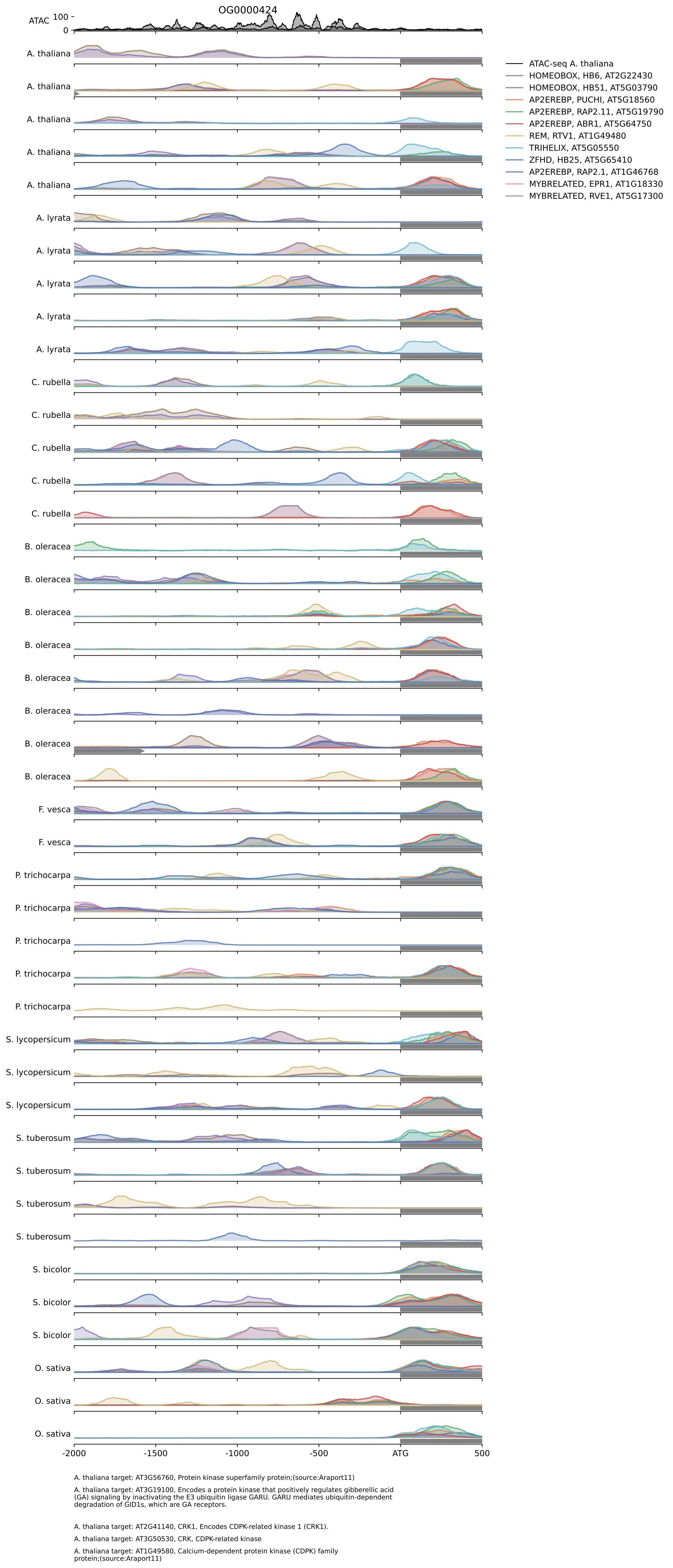
A. thaliana target: AT5G56630, PFK7, phosphofructokinase 7;(source:Araport11)

A. thaliana target: AT4G26270, PFK3, phosphofructokinase 3;(source:Araport11)

A. thaliana target: AT5G61580, PFK4, Phosphofructokinase Isoform.

A. thaliana target: AT4G32840, PFK6, phosphofructokinase 6;(source:Araport11)

A. thaliana target: AT4G29220, PFK1, phosphofructokinase 1;(source:Araport11)



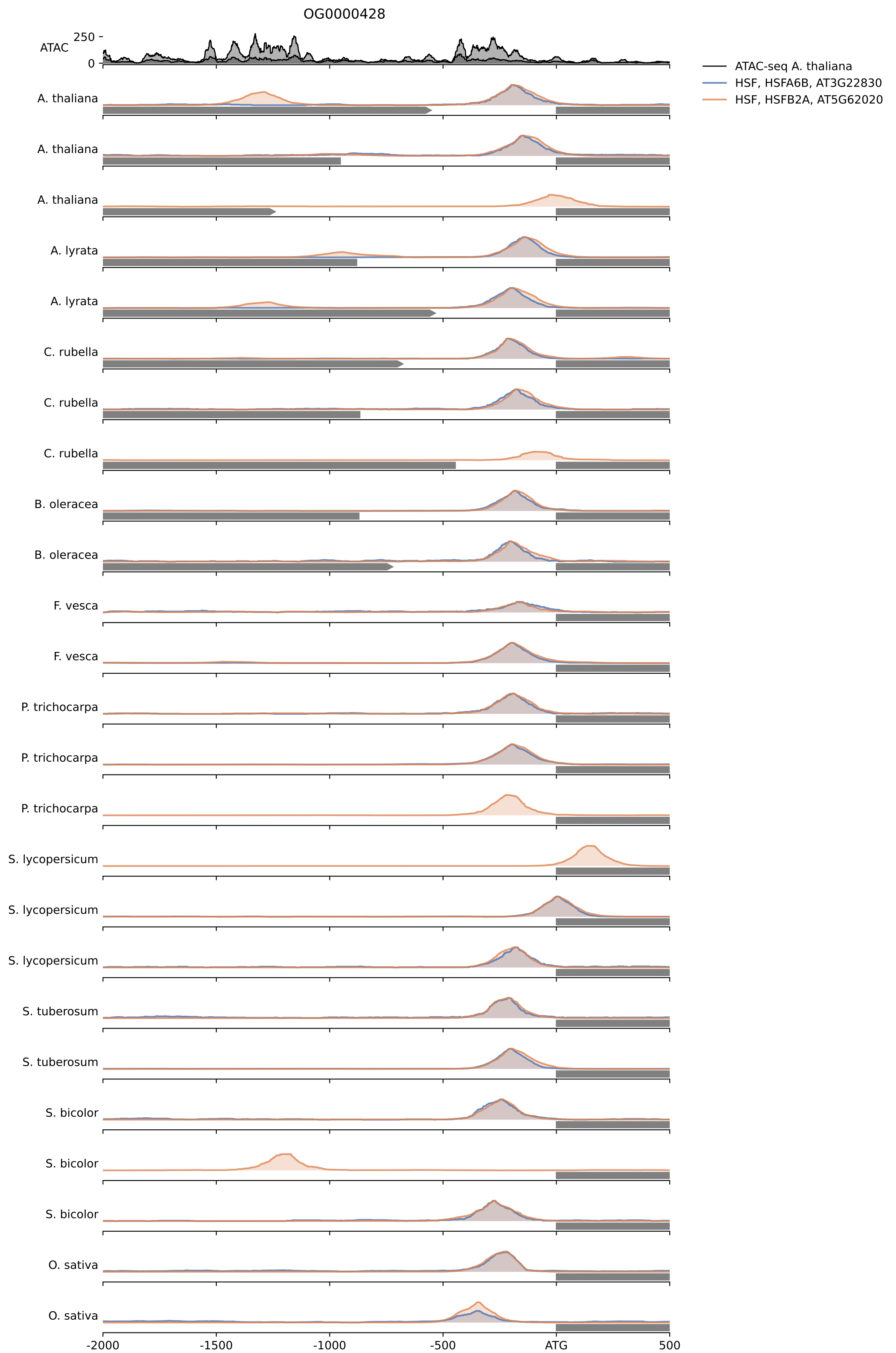
A. thaliana target: AT3G56760, Protein kinase superfamily protein;(source:Araport11)

A. thaliana target: AT3G19100, Encodes a protein kinase that positively regulates gibberellic acid (GA) signaling by inactivating the E3 ubiquitin ligase GARU. GARU mediates ubiquitin-dependent degradation of GID1s, which are GA receptors.

A. thaliana target: AT2G41140, CRK1, Encodes CDPK-related kinase 1 (CRK1).

A. thaliana target: AT3G50530, CRK, CDPK-related kinase

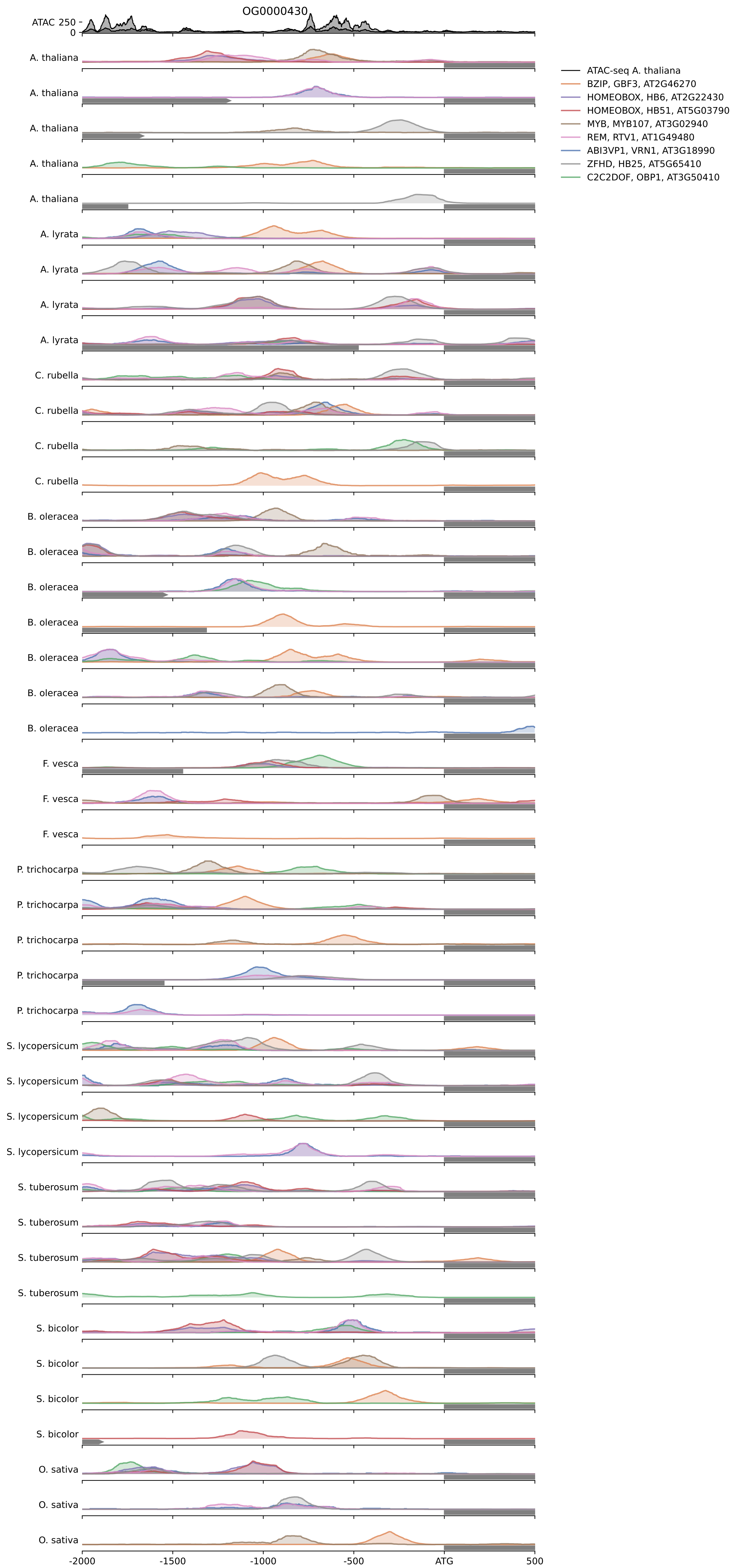
A. thaliana target: AT1G49580, Calcium-dependent protein kinase (CDPK) family protein;(source:Araport11)



A. thaliana target: AT2G20560, DNAJ heat shock family protein;(source:Araport11)

A. thaliana target: AT4G28480, DNAJ heat shock family protein;(source:Araport11)

A. thaliana target: AT2G20550, HSP40/DnaJ peptide-binding protein;(source:Araport11)



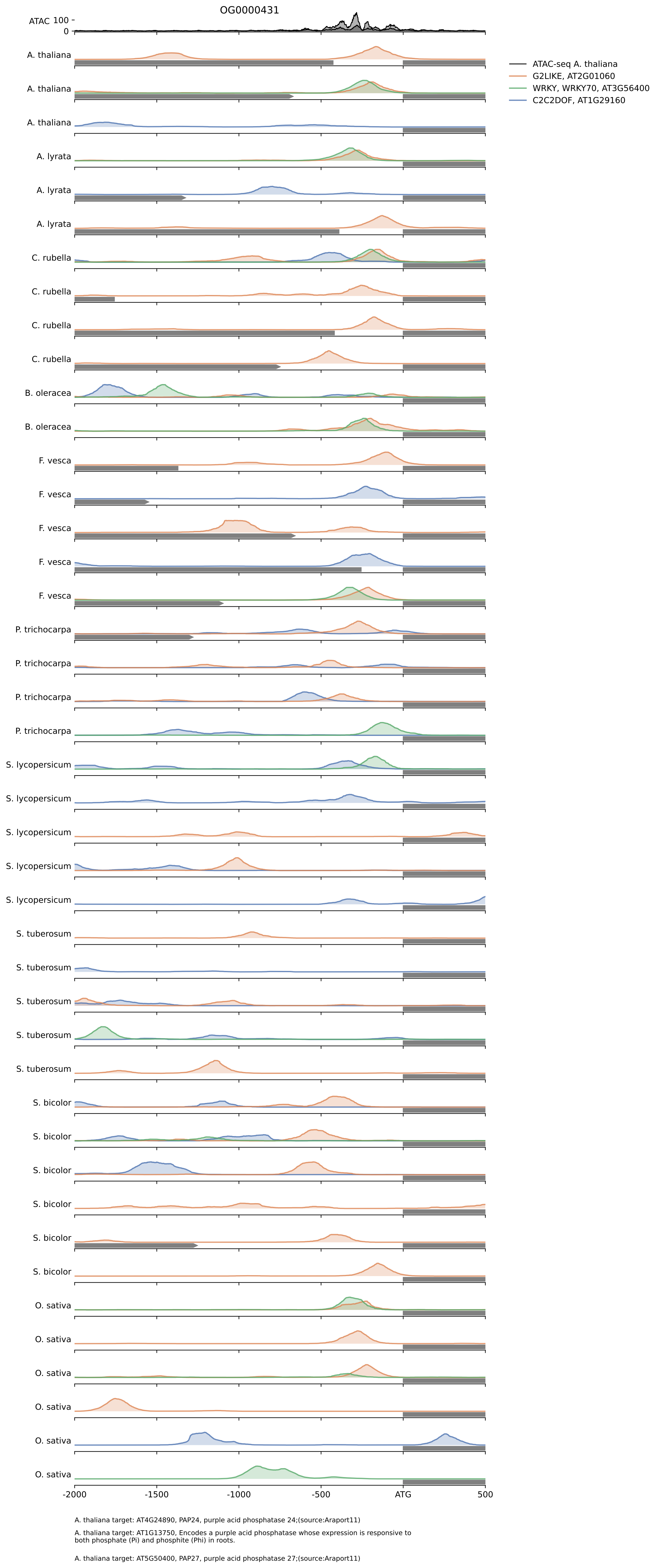
A. thaliana target: AT1G35580, CINV1, CINV1 / A/N-InvG is an alkaline/neutral invertase that breaks sucrose down into fructose and glucose (GH100). The exact localization of CINV1 remains under investigation but there is evidence that fluorescently-tagged CINV1 localizes to the cytoplasm. atinvg mutants have reduced root growth, reduced invertase activity, and increased expression of antioxidant genes under basal conditions. The levels of CINV1 / A/N-InvG transcripts rise in response to a hydrogen peroxide treatment. The protein has been shown to interact with PIP5K9.

A. thaliana target: AT1G72000, A/N-InvF, Plant neutral invertase family protein;(source:Araport11)

A. thaliana target: AT4G09510, CINV2, CINV2 appears to function as a neutral invertase based on the phenotype of a cinv1(AT1G35580)/cinv2 double mutant. It is predicted to be a cytosolic enzyme. CINV1, CINV2, and possibly other cytosolic invertases may play an important role in supplying carbon from sucrose to non-photosynthetic tissues.

A. thaliana target: AT4G34860, A/N-InvB, Plant neutral invertase family protein;(source:Araport11)

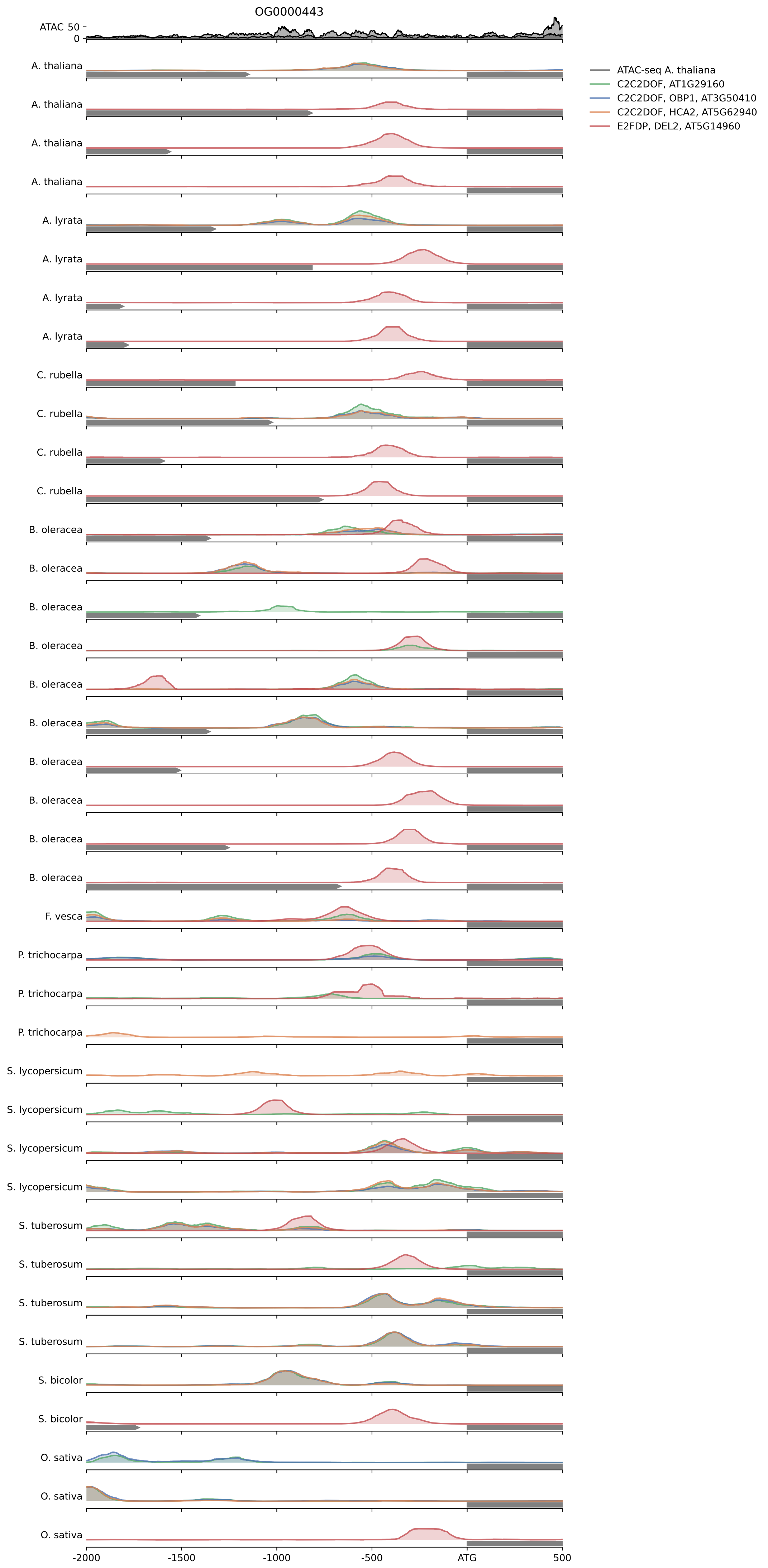
A. thaliana target: AT1G22650, A/N-InvD, Plant neutral invertase family protein;(source:Araport11)



A. thaliana target: AT4G24890, PAP24, purple acid phosphatase 24;(source:Araport11)

A. thaliana target: AT1G13750, Encodes a purple acid phosphatase whose expression is responsive to both phosphate (Pi) and phosphite (Phi) in roots.

A. thaliana target: AT5G50400, PAP27, purple acid phosphatase 27;(source:Araport11)

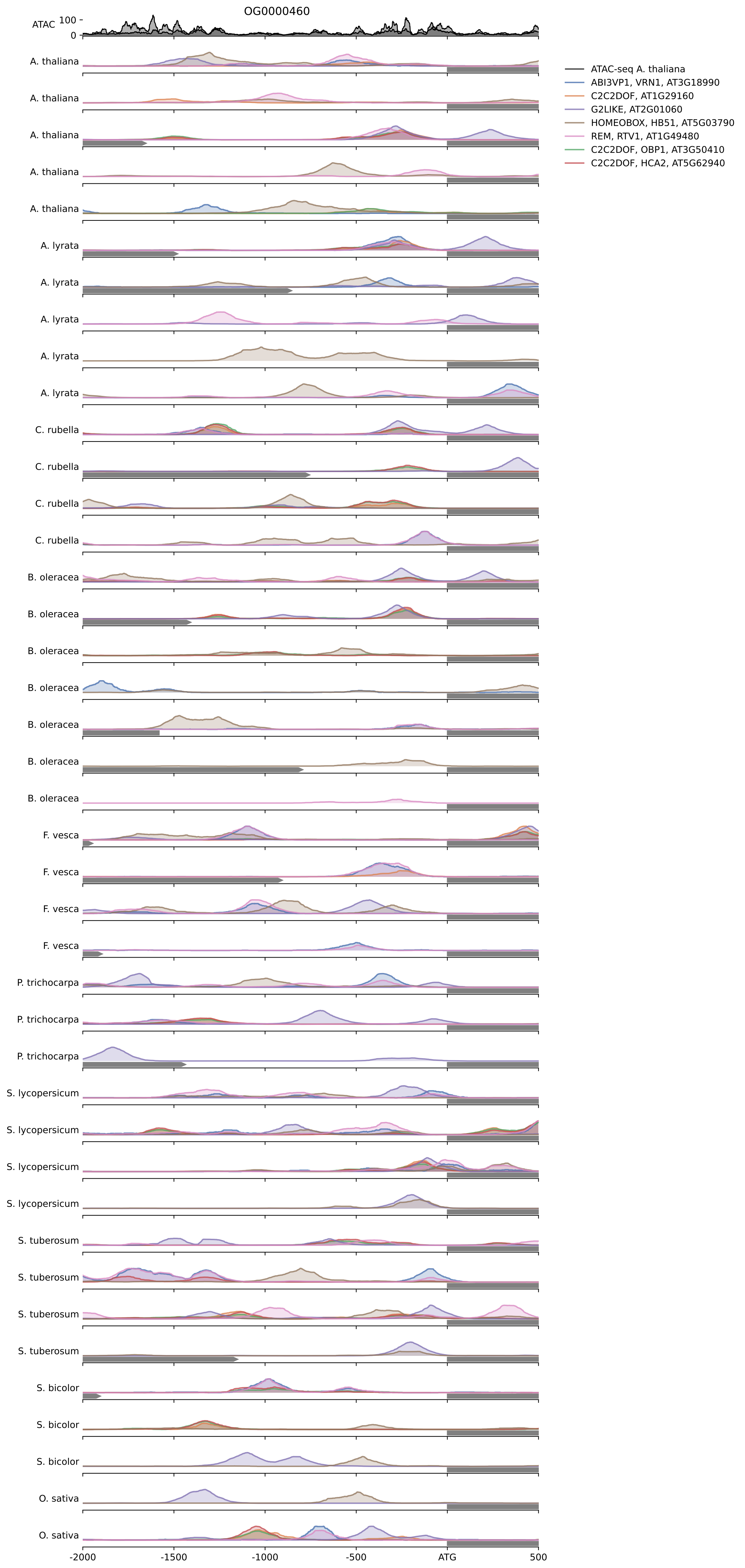


A. thaliana target: AT5G26930, GATA23, Encodes a member of the GATA factor family of zinc finger transcription factors. Controls lateral root founder cell specification.

A. thaliana target: AT3G06740, GATA15, Encodes a member of the GATA factor family of zinc finger transcription factors.

A. thaliana target: AT4G16141, GATA type zinc finger transcription factor family protein;(source:Araport11)

A. thaliana target: AT5G49300, GATA16, Encodes a member of the GATA factor family of zinc finger transcription factors.



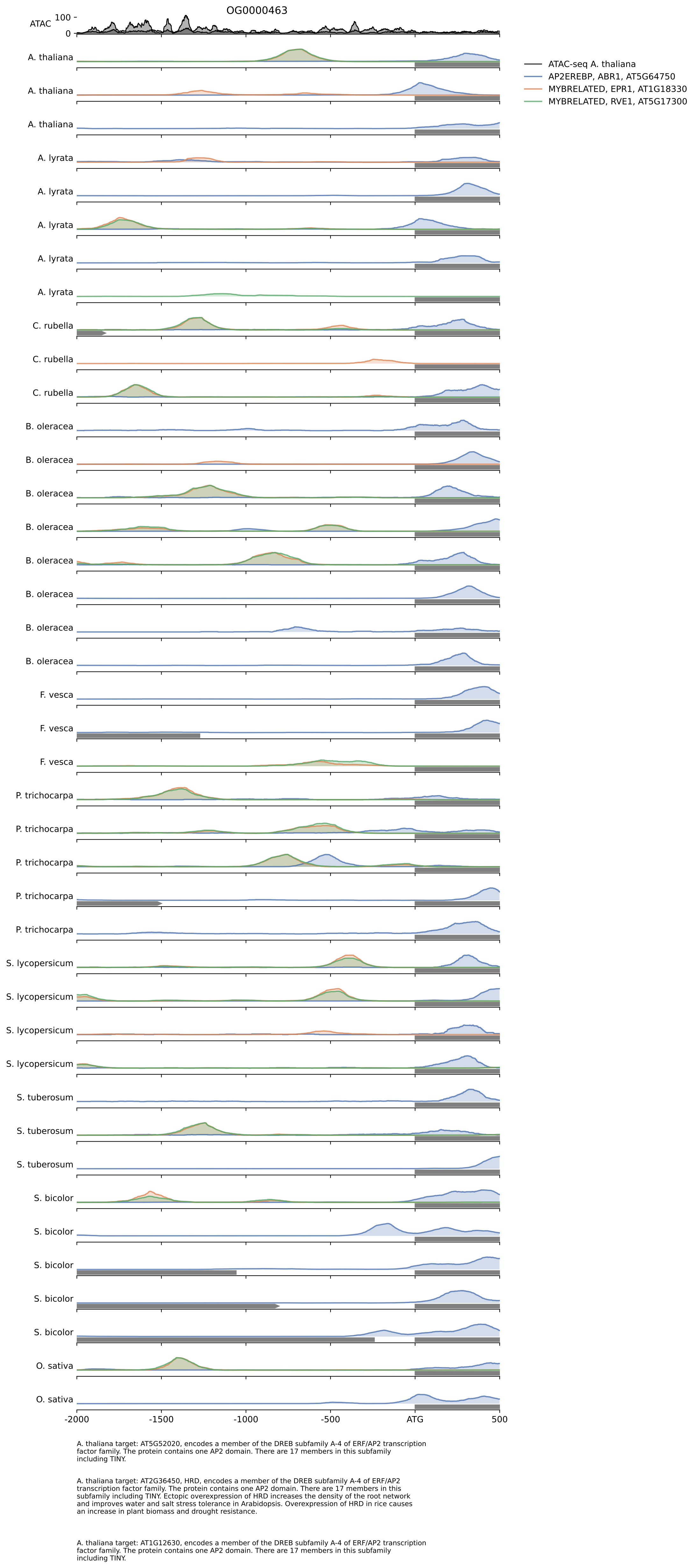
A. thaliana target: AT2G01890, PAP8, Encodes a purple acid phosphatase (PAP) belonging to the low molecular weight plant PAP group.

A. thaliana target: AT2G01880, PAP7, PEP complex component.

A. thaliana target: AT3G17790, PAP17, Expression is upregulated in the shoot of cax1/cax3 mutant and is responsive to phosphate (Pi) and not phosphite (Phi) in roots and shoots.

A. thaliana target: AT1G14700, PAP3, purple acid phosphatase 3;(source:Araport11)

A. thaliana target: AT1G25230, Calcineurin-like metallo-phosphoesterase superfamily protein;(source:Araport11)



A. thaliana target: AT5G52020, encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.

A. thaliana target: AT2G36450, HRD, encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY. Ectopic overexpression of HRD increases the density of the root network and improves water and salt stress tolerance in Arabidopsis. Overexpression of HRD in rice causes an increase in plant biomass and drought resistance.

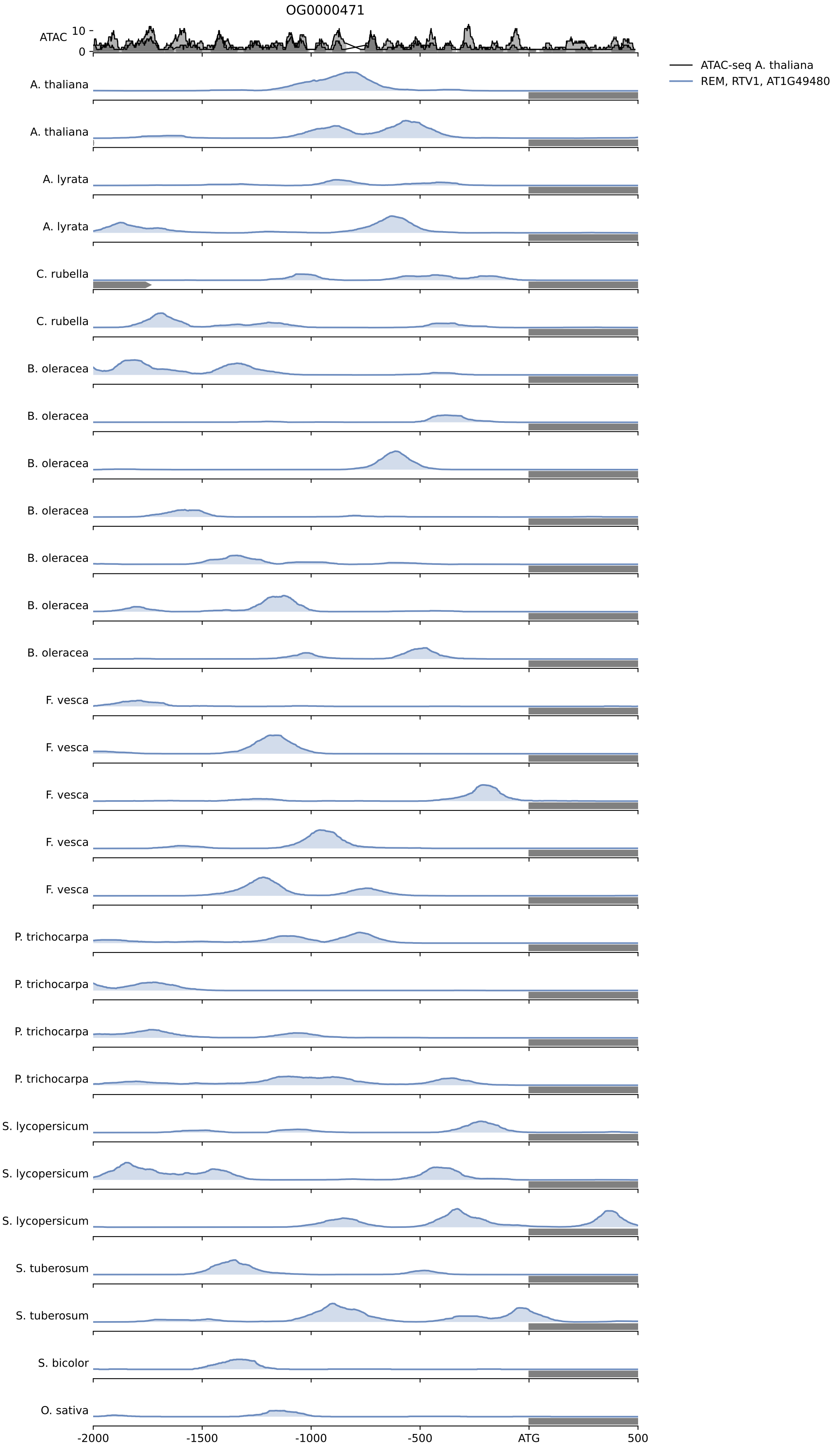
A. thaliana target: AT1G12630, encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.

A. thaliana target: AT1G02500, SAM1, encodes a S-adenosylmethionine synthetase. SAM1 is regulated by protein S-nitrosylation. The covalent binding of nitric oxide (NO) to the Cys114 residue inhibits the enzyme activity.

A. thaliana target: AT2G36880, MAT3, Topoisomerase VI physically interacts with S-adenosylmethionine synthase methionine adenosyl transferase 3 (MAT3), which is required for H3K9me2. A Topoisomerase VI defect affects MAT3 occupancy on heterochromatic elements and its exclusion from euchromatic islands, thereby providing a possible mechanistic explanation to the essential role of Topoisomerase VI in the delimitation of chromatin domains.

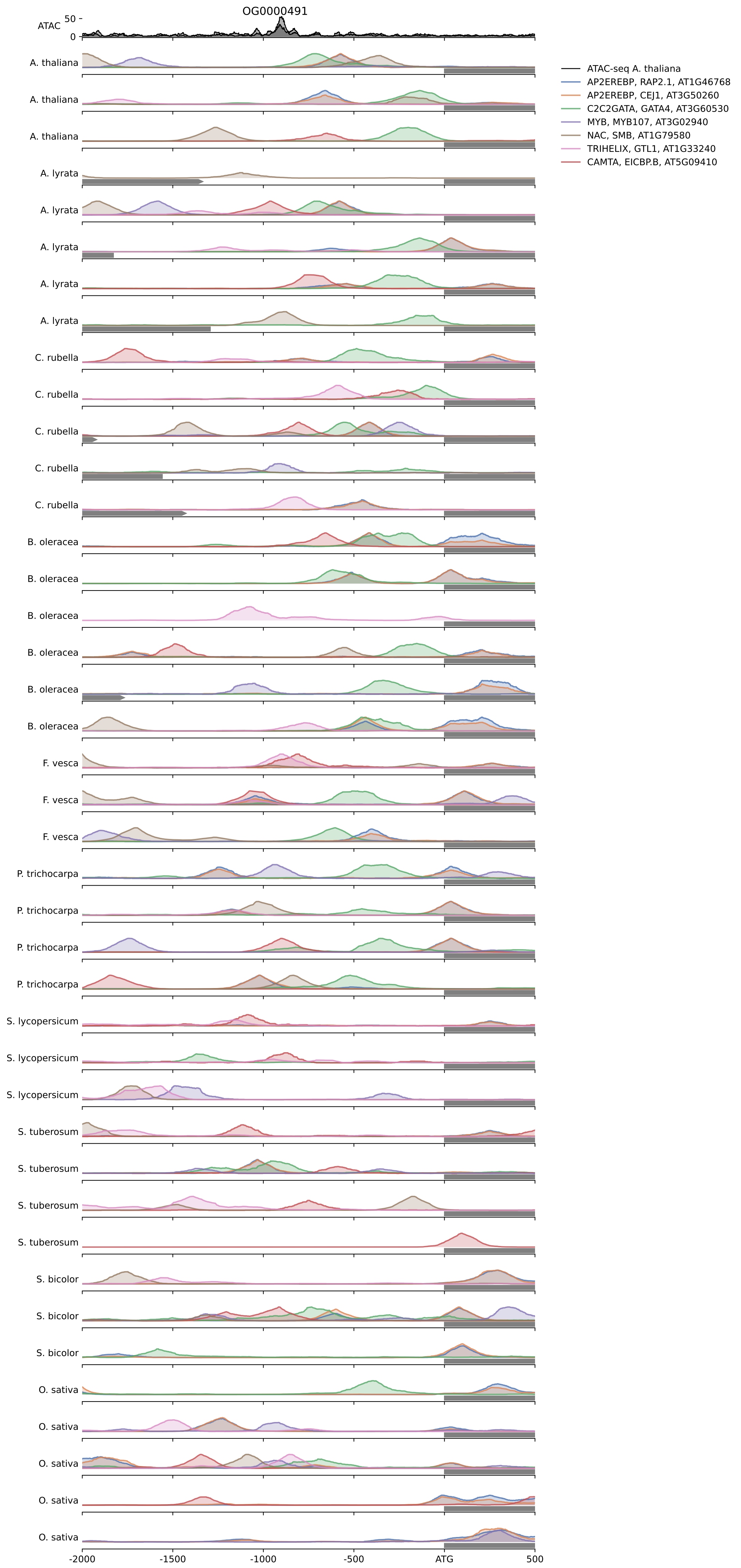
A. thaliana target: AT4G01850, SAM-2, Encodes an S-adenosylmethionine synthase that catalyzes the formation of S-adenosylmethionine from methionine and ATP. Functions in ethylene biosynthetic pathway.

A. thaliana target: AT3G17390, MTO3, S-adenosylmethionine synthetase



A. thaliana target: AT3G11680, aluminum activated malate transporter family protein;(source:Araport11)

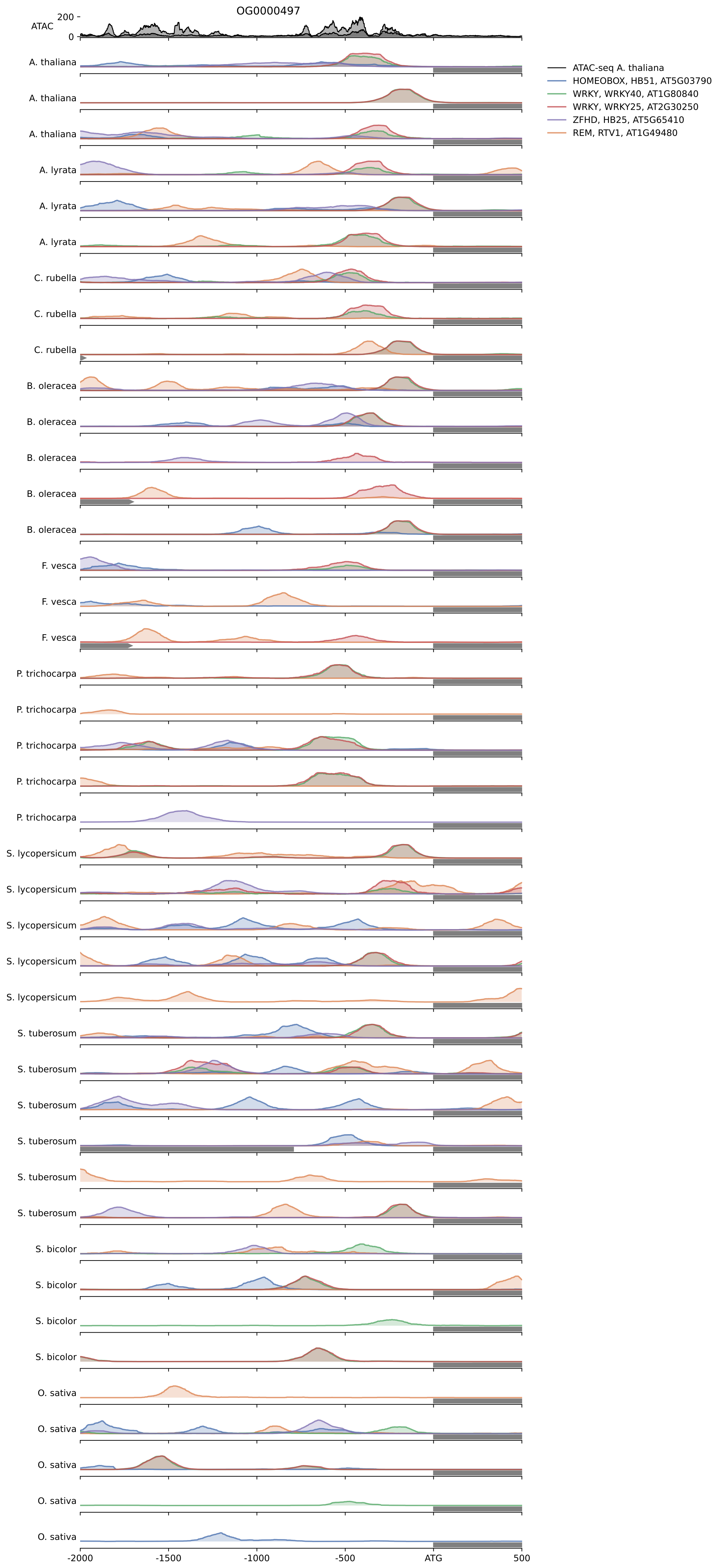
A. thaliana target: AT1G08440, aluminum activated malate transporter family protein;(source:Araport11)



A. thaliana target: AT5G15490, UGD3, Encodes one of four UDP-glucose dehydrogenase UGD) genes. Mutation of this gene in combination with UGD2 leads to swollen plant cell walls and severe developmental defects associated with changes in pectic polysaccharides.

A. thaliana target: AT5G39320, UDG4, UDP-glucose 6-dehydrogenase family protein;(source:Araport11)

A. thaliana target: AT3G29360, UGD2, Encodes one of four UDP-glucose dehydrogenase UGD) genes. Mutation of this gene in combination with UGD3 leads to swollen plant cell walls and severe developmental defects associated with changes in pectic polysaccharides.



A. thaliana target: AT4G23810, WRKY53, member of WRKY Transcription Factor; Group III; t WRKY53 and CRK5 are antagonistic regulators of chlorophyll synthesis/degradation, senescence, and stomatal conductance.

A. thaliana target: AT5G24110, WRKY30, member of WRKY Transcription Factor; Group III

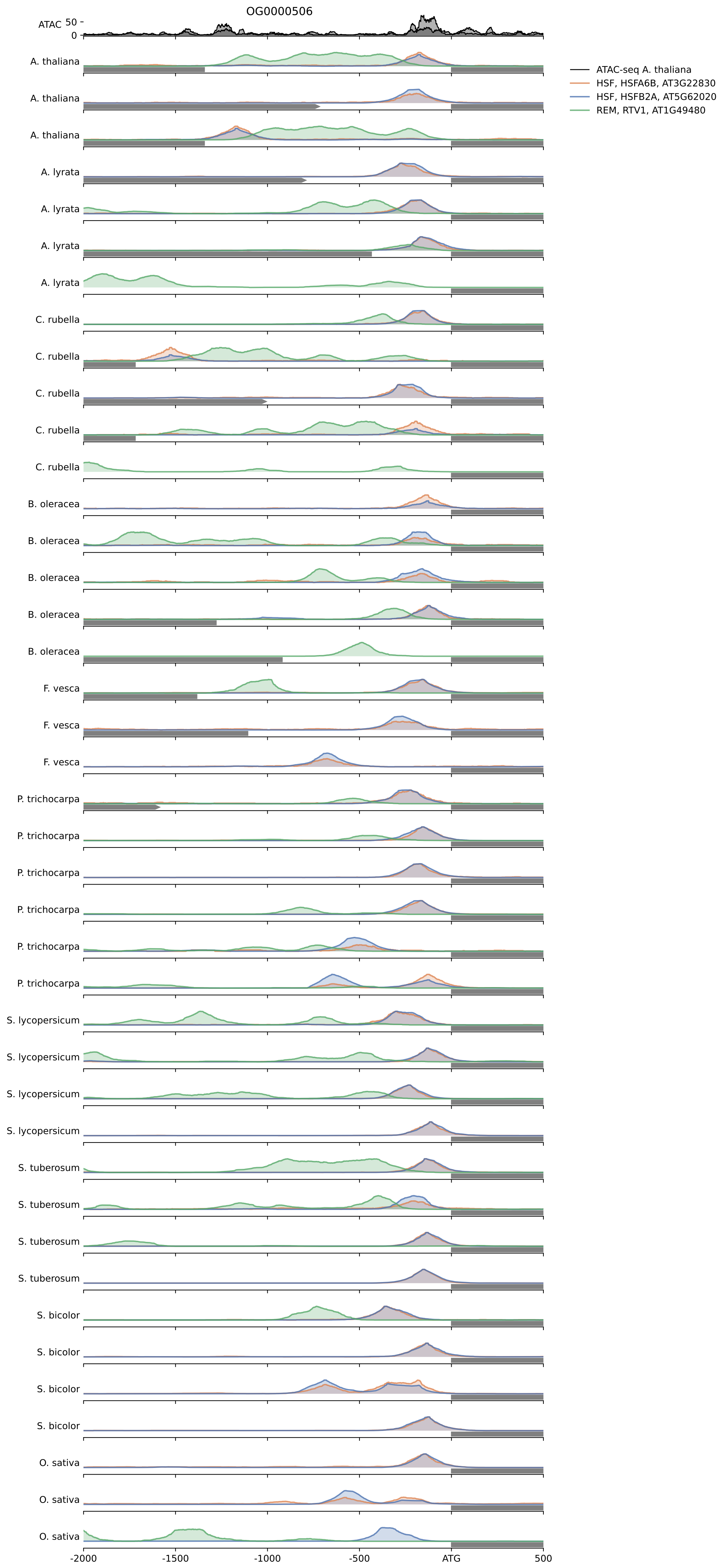
A. thaliana target: AT4G11070, WRKY41, member of WRKY Transcription Factor; Group III; AvrRps4C can associate with the DNA-binding domain.

A. thaliana target: AT4G35480, RHA3B, Encodes a putative RING-H2 finger protein RHA3b.

A. thaliana target: AT2G17450, RHA3A, Encodes a putative RING-H2 finger protein RHA3a.

A. thaliana target: AT1G20823, Encodes a RING E3 ubiquitin ligase ATL80. Involved in phosphate mobilization and cold stress response in sufficient phosphate growth conditions. The mRNA is cell-to-cell mobile.

A. thaliana target: AT1G76410, ATL8, RING/U-box superfamily protein;(source:Araport11)



A. thaliana target: AT5G56010, HSP81-3, A member of heat shock protein 90 (HSP90) gene family. Expressed in all tissues and abundant in root apical meristem, pollen and tapetum. Expression is NOT heat-induced but induced by IAA and NaCl. Overexpression reduced tolerance to heat and conferred higher tolerance to calcium. The mRNA is cell-to-cell mobile.

A. thaliana target: AT5G56030, HSP81-2, A member of heat shock protein 90 (HSP90) gene family. Expressed in all tissues and abundant in root apical meristem, pollen and tapetum. Expression is NOT heat-induced but induced by IAA and NaCl. Interacts with HsfA1d in the cytosol and the nucleus and negatively regulates HsfA1d. Did not bind to AtHsfA4c. The mRNA is cell-to-cell mobile.

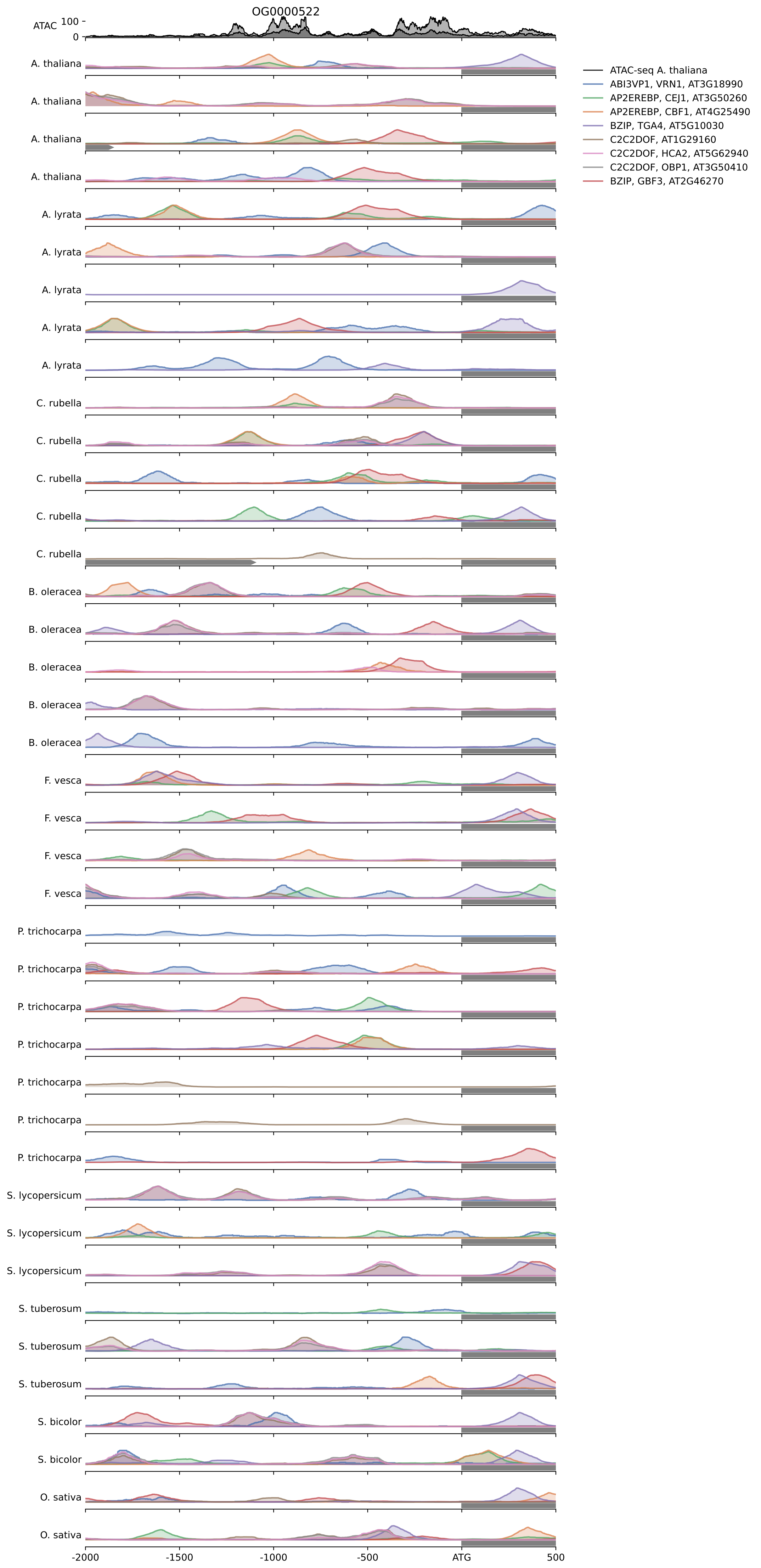
A. thaliana target: AT5G56000, Hsp81.4, HEAT SHOCK PROTEIN 81.4;(source:Araport11)

A. thaliana target: AT5G14390, alpha/beta-Hydrolases superfamily protein;(source:Araport11)

A. thaliana target: AT3G30380, alpha/beta-Hydrolases superfamily protein;(source:Araport11)

A. thaliana target: AT3G01690, alpha/beta-Hydrolases superfamily protein;(source:Araport11)

A. thaliana target: AT4G24760, alpha/beta-Hydrolases superfamily protein;(source:Araport11)

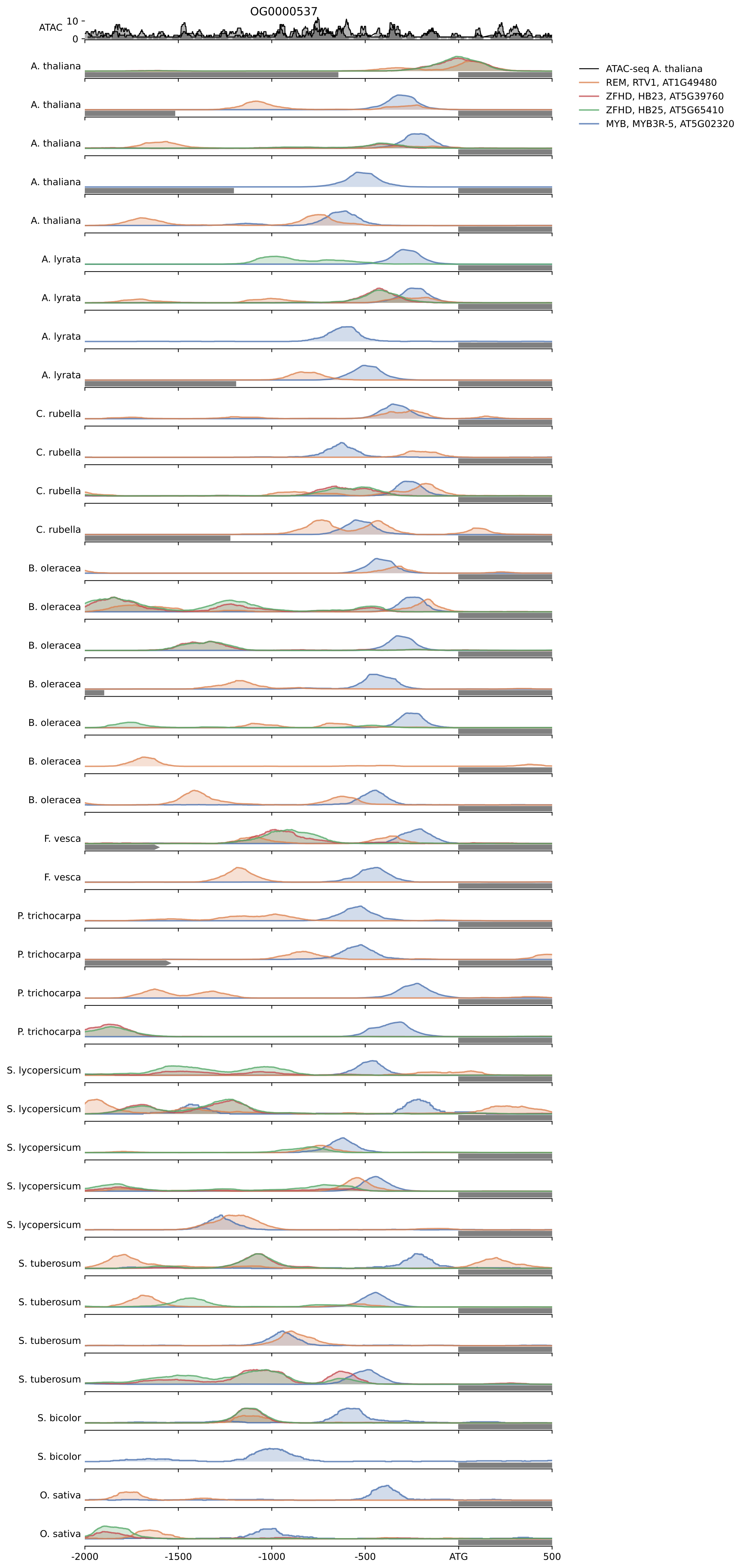


A. thaliana target: AT2G47180, GolS1, GolS1 is a galactinol synthase that catalyzes the formation of galactinol from UDP-galactose and myo-inositol. GolS1 transcript levels rise in response to methyl viologen, an oxidative damage-inducing agent. Plants over-expressing GolS1 have increased tolerance to salt, chilling, and high-light stress.

A. thaliana target: AT1G60470, GolS4, Predicted to encode a galactinol synthase.

A. thaliana target: AT1G09350, GolS3, Predicted to encode a galactinol synthase

A. thaliana target: AT1G56600, GolS2, GolS2 is a galactinol synthase that catalyzes the formation of galactinol from UDP-galactose and myo-inositol. GolS2 transcript levels rise in response to methyl viologen, an oxidative damage-inducing agent. Plants over-expressing GolS2 have increased tolerance to salt, chilling, and high-light stress.



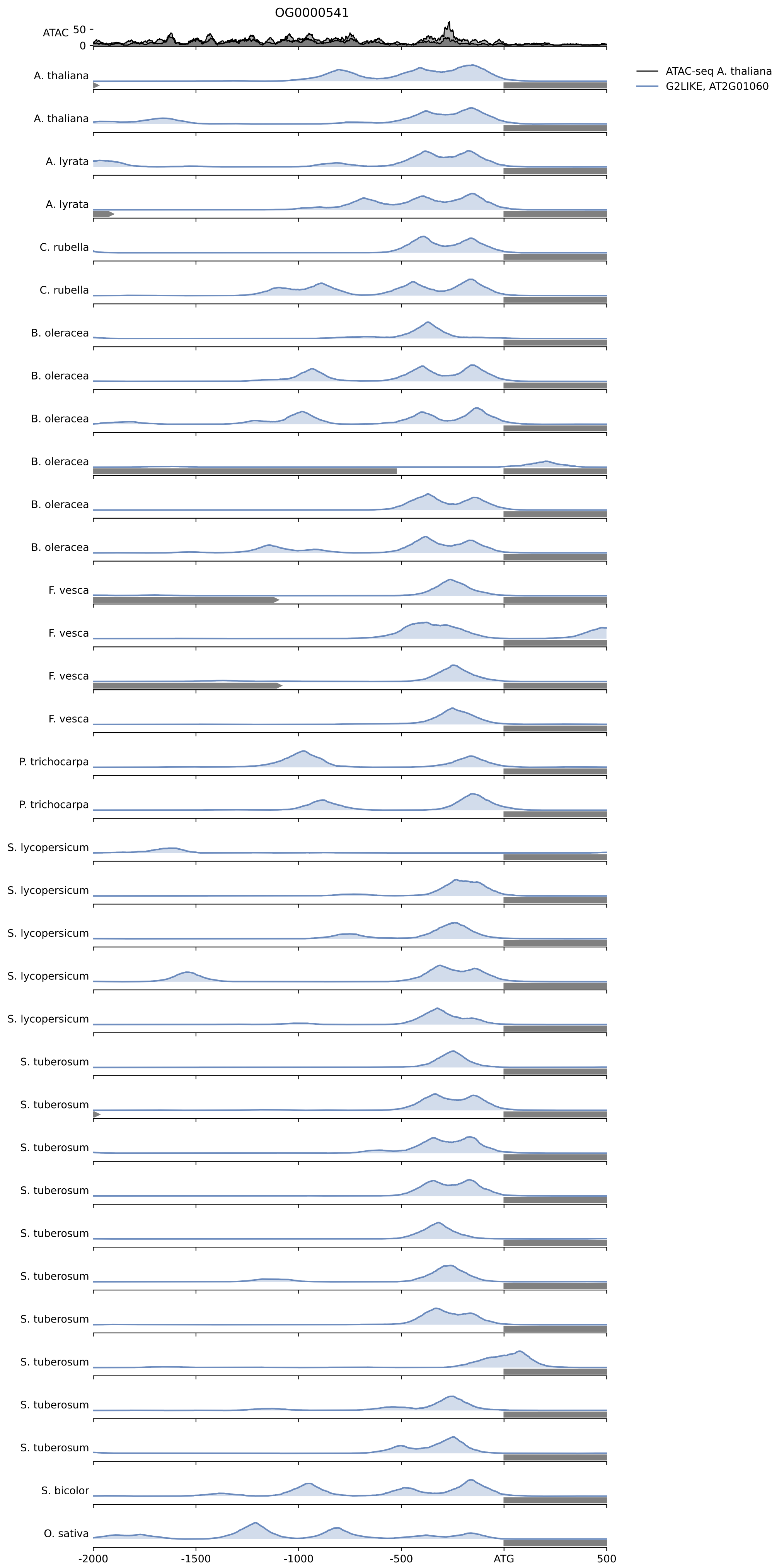
A. thaliana target: AT1G20590, cyclin;(source:Araport11)

A. thaliana target: AT4G35620, CYCB2;2, Cyclin B2;(source:Araport11)

A. thaliana target: AT2G17620, CYCB2;1, Cyclin B2;(source:Araport11)

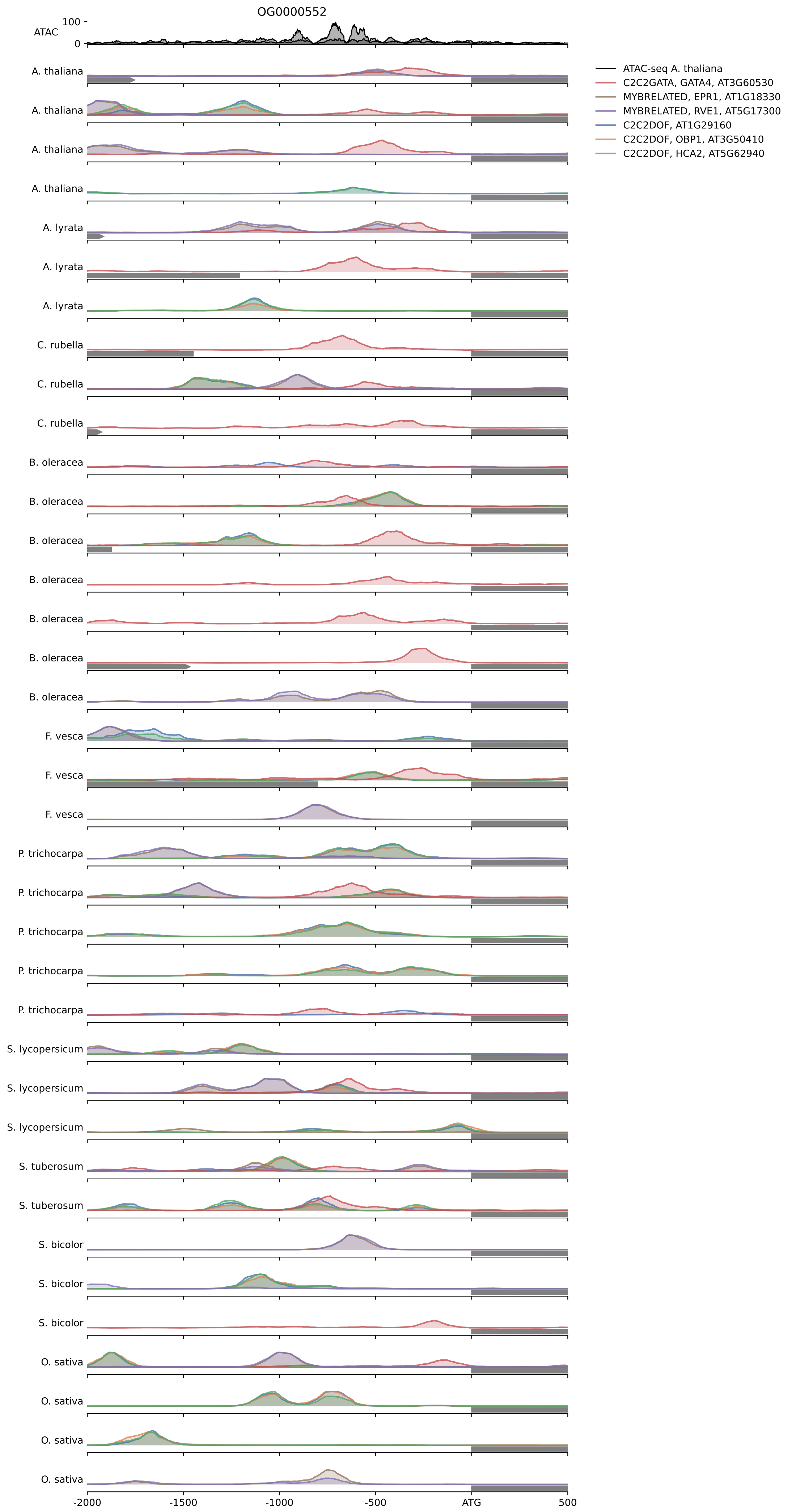
A. thaliana target: AT1G76310, CYCB2;4, core cell cycle genes

A. thaliana target: AT1G20610, CYCB2;3, Cyclin B2;(source:Araport11)



A. thaliana target: AT1G17710, PEPC1, Encodes a phosphoethanolamine/phosphocholine phosphatase. It is likely to be involved in the liberation of inorganic phosphate from intracellular sources. Expression is upregulated in the shoot of cax1/cax3 mutant.

A. thaliana target: AT1G73010, PS2, Encodes PPsPase1, a pyrophosphate-specific phosphatase catalyzing the specific cleavage of pyrophosphate (Km 38.8 uM) with an alkaline catalytic pH optimum. Expression is upregulated in the shoot of cax1/cax3 mutant.

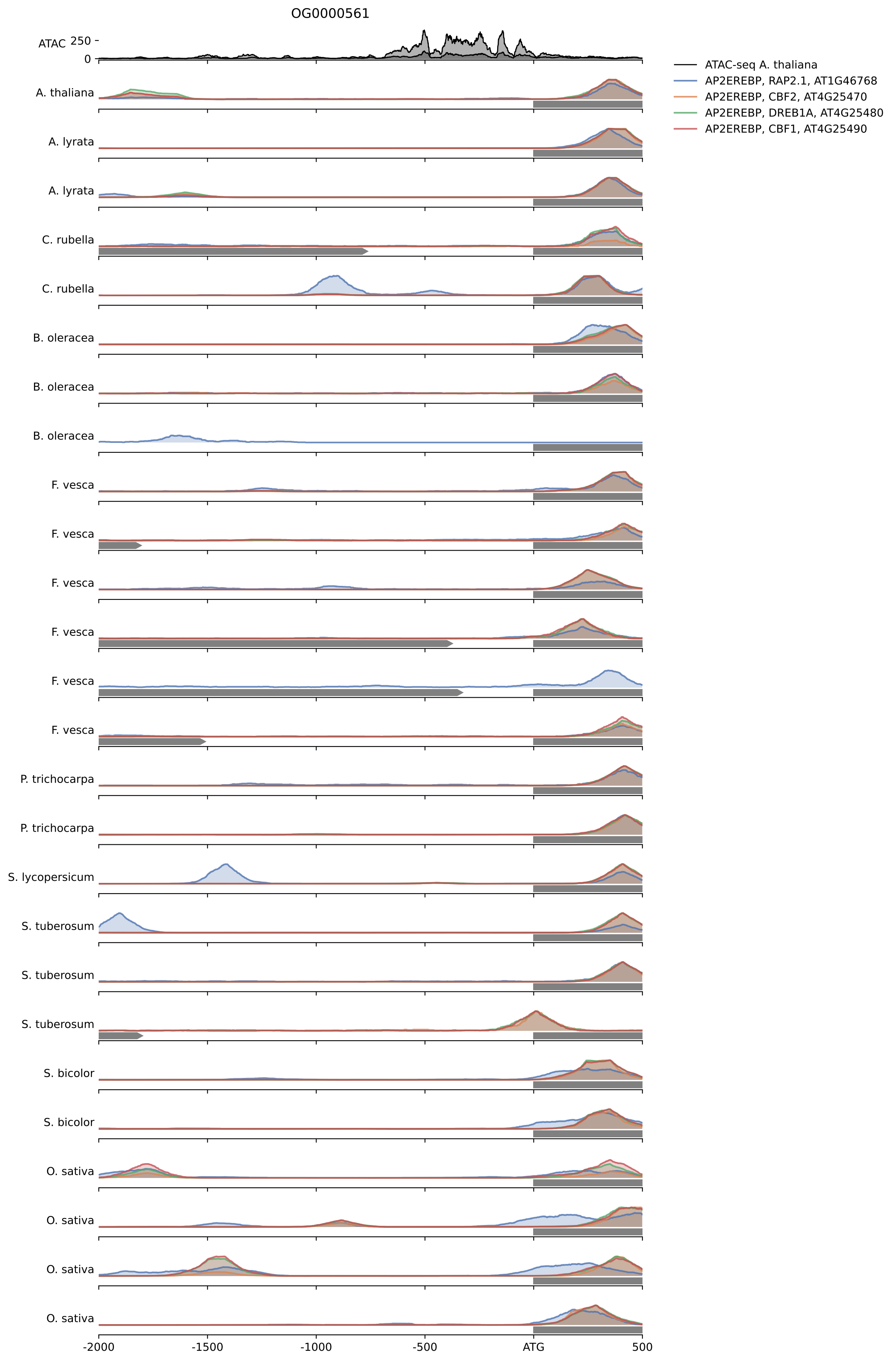


A. thaliana target: AT2G34300, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)

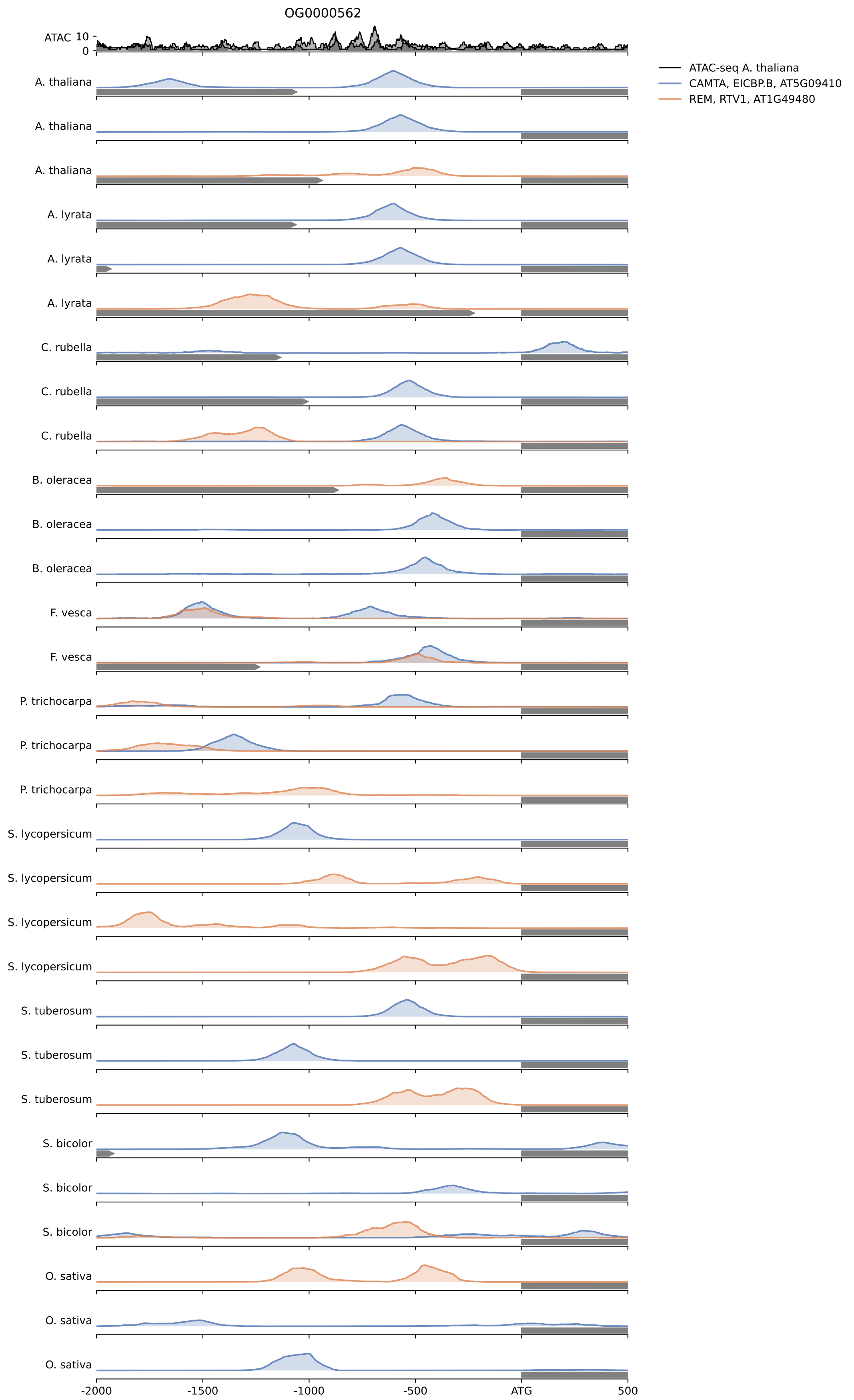
A. thaliana target: AT5G64030, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)

A. thaliana target: AT1G29470, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)

A. thaliana target: AT3G51070, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)



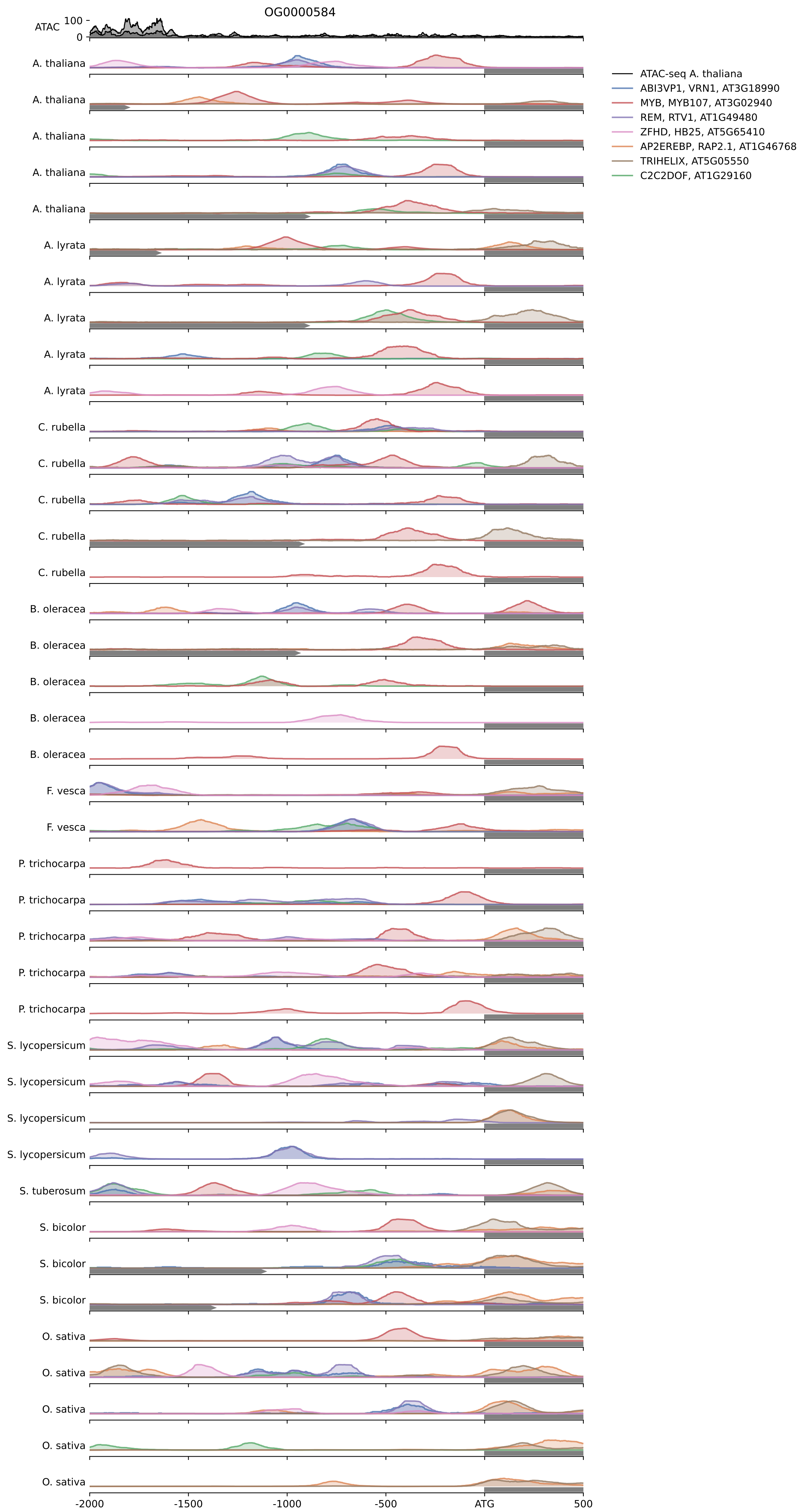
A. thaliana target: AT2G30140, UGT87A2, Encodes a putative glycosyltransferase. Regulates flowering time via FLOWERING LOCUS C.



A. thaliana target: AT3G10660, CPK2, predicted to encode calcium-dependent protein kinase and is localized to the ER. Protein is myristoylated in a cell-free extract. Changing the proposed myristoylated site, G residue in the amino terminal, to A prevented the meristoylation . The G to A mutation decreased AtCPK2 membrane association by approximately 50%.

A. thaliana target: AT5G04870, CPK1, A calcium-dependent protein kinase that can phosphorylate phenylalanine ammonia lyase (PAL), a key enzyme in pathogen defense.Phosphorylates, in vivo, the transcription factor ORE1, a master regulator of senescence.

A. thaliana target: AT2G38910, CPK20, member of Calcium Dependent Protein Kinase



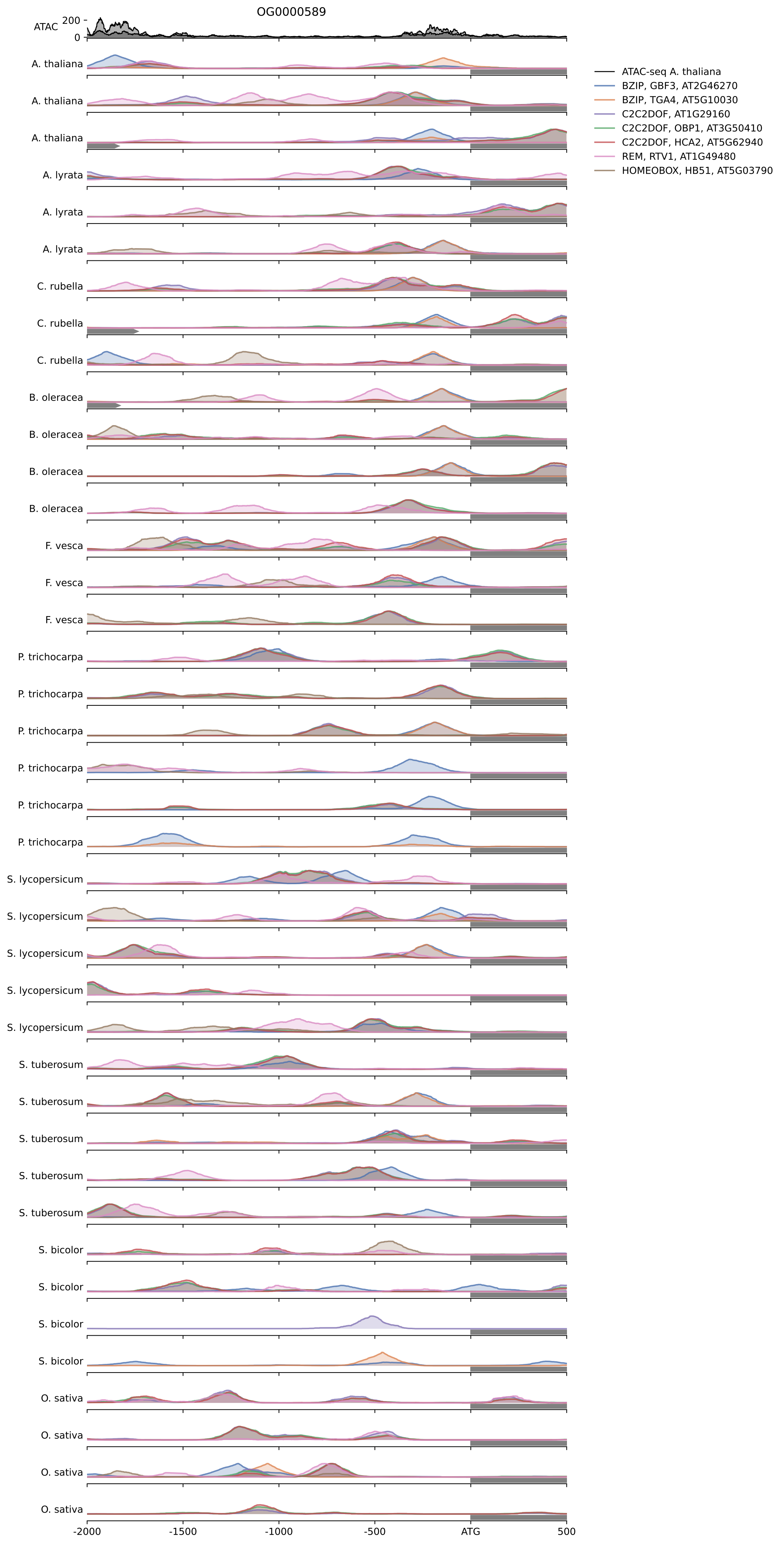
A. thaliana target: AT3G53510, ABCG20, Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters that are required for synthesis of an effective suberin barrier in roots and seed coats (ABCG2, ABCG6, and ABCG20) and for synthesis of an intact pollen wall (ABCG1 and ABCG16). Phloem-expressed and plasma membrane-localized jasmonate transporter which together with JAT3 and GLR3.3 involved in regulating long-distance translocation of JA, which is important for driving the loading, translocation of JA in the phloem pathway by a self-propagation mode, contributing to wound-induced systemic response/resistance.

A. thaliana target: AT3G55090, ABCG16, Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters that are required for synthesis of an effective suberin barrier in roots and seed coats (ABCG2, ABCG6, and ABCG20) and for synthesis of an intact pollen wall (ABCG1 and ABCG16).

A. thaliana target: AT2G39350, ABCG1, Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters that are required for synthesis of an effective suberin barrier in roots and seed coats (ABCG2, ABCG6, and ABCG20) and for synthesis of an intact pollen wall (ABCG1 and ABCG16).

A. thaliana target: AT2G37360, ABCG2, Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters that are required for synthesis of an effective suberin barrier in roots and seed coats (ABCG2, ABCG6, and ABCG20) and for synthesis of an intact pollen wall (ABCG1 and ABCG16).

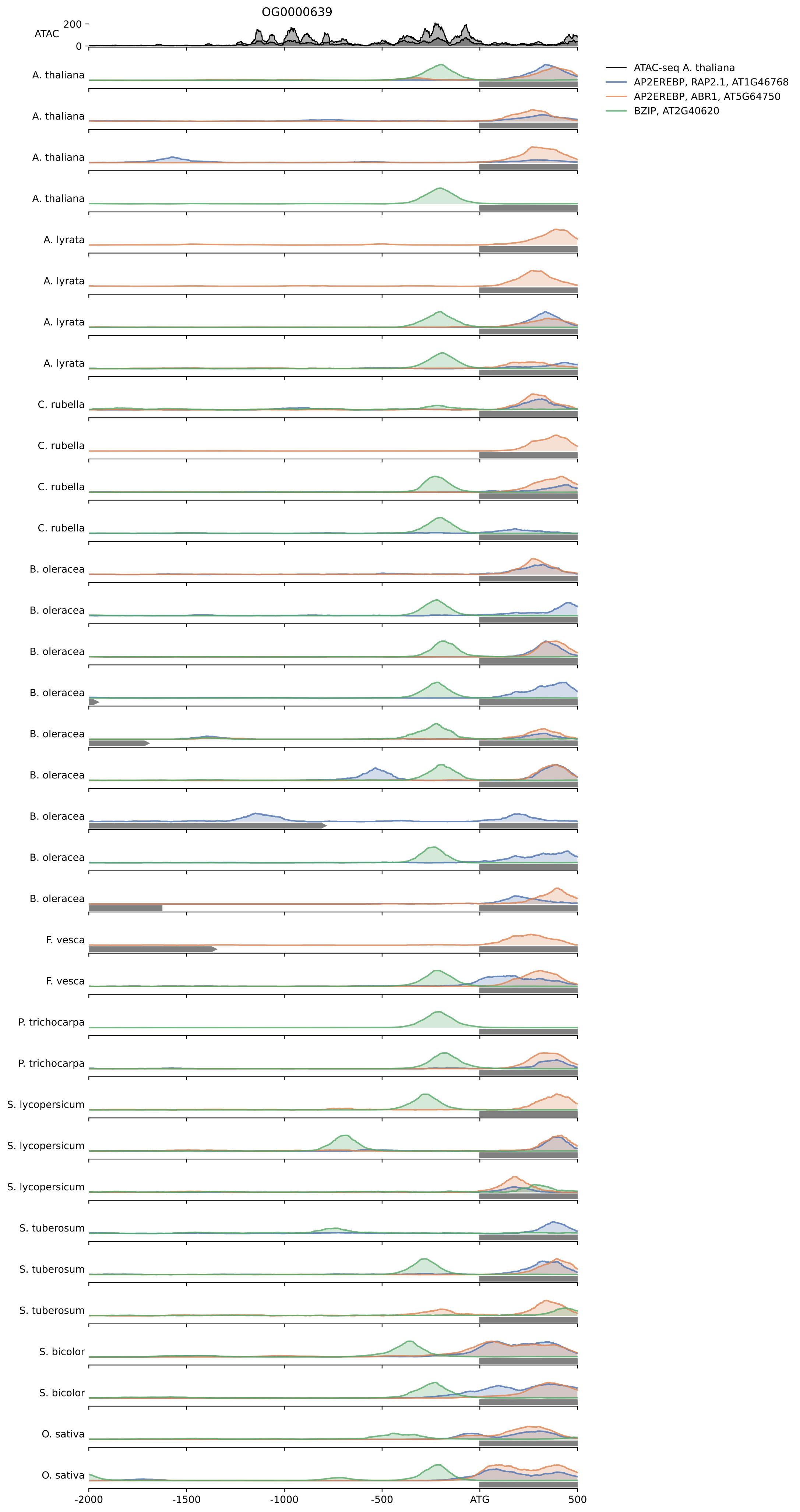
A. thaliana target: AT5G13580, ABCG6, Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters that are required for synthesis of an effective suberin barrier in roots and seed coats (ABCG2, ABCG6, and ABCG20) and for synthesis of an intact pollen wall (ABCG1 and ABCG16). Phloem-expressed and plasma membrane-localized jasmonate transporter which together with JAT4 and GLR3.3 involved in regulating long-distance translocation of JA, which is important for driving the loading, translocation of JA in the phloem pathway by a self-propagation mode, contributing to wound-induced systemic response/resistance.



A. thaliana target: AT3G47500, CDF3, Dof-type zinc finger domain-containing protein, identical to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana). Interacts with LKP2 and FKF1, but its overexpression does not change flowering time under short or long day conditions.

A. thaliana target: AT5G39660, CDF2, Dof-type zinc finger domain-containing protein, identical to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana). Interacts with LKP2 and FKF1, but its overexpression does not change flowering time under short or long day conditions.

A. thaliana target: AT5G62430, CDF1, Dof-type zinc finger domain-containing protein, similar to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana). Represses expression of Constans (CO), a circadian regulator of flowering time. Interacts with LKP2 and FKF1. Expression oscillates under constant light conditions. Mainly expressed in the vasculature of cotyledons, leaves and hypocotyls, but also in stomata. Localized to the nucleus and acts as a repressor of CONSTANS through binding to the Dof binding sites in the CO promoter. Protein gets degraded by FKF1 in the afternoon. CDF1 binds to the TOPLESS co-repressor protein through an N-terminal motif which is conserved across CDF-like proteins throughout land-plants. This interaction is important for the repression of CO and FT genes during the morning. Loss of CDF1 dependent repression through omission of TPL coordinating residues or through the loss of TPL function in phloem companion cells results in early flowering due to an up regulation of FT.

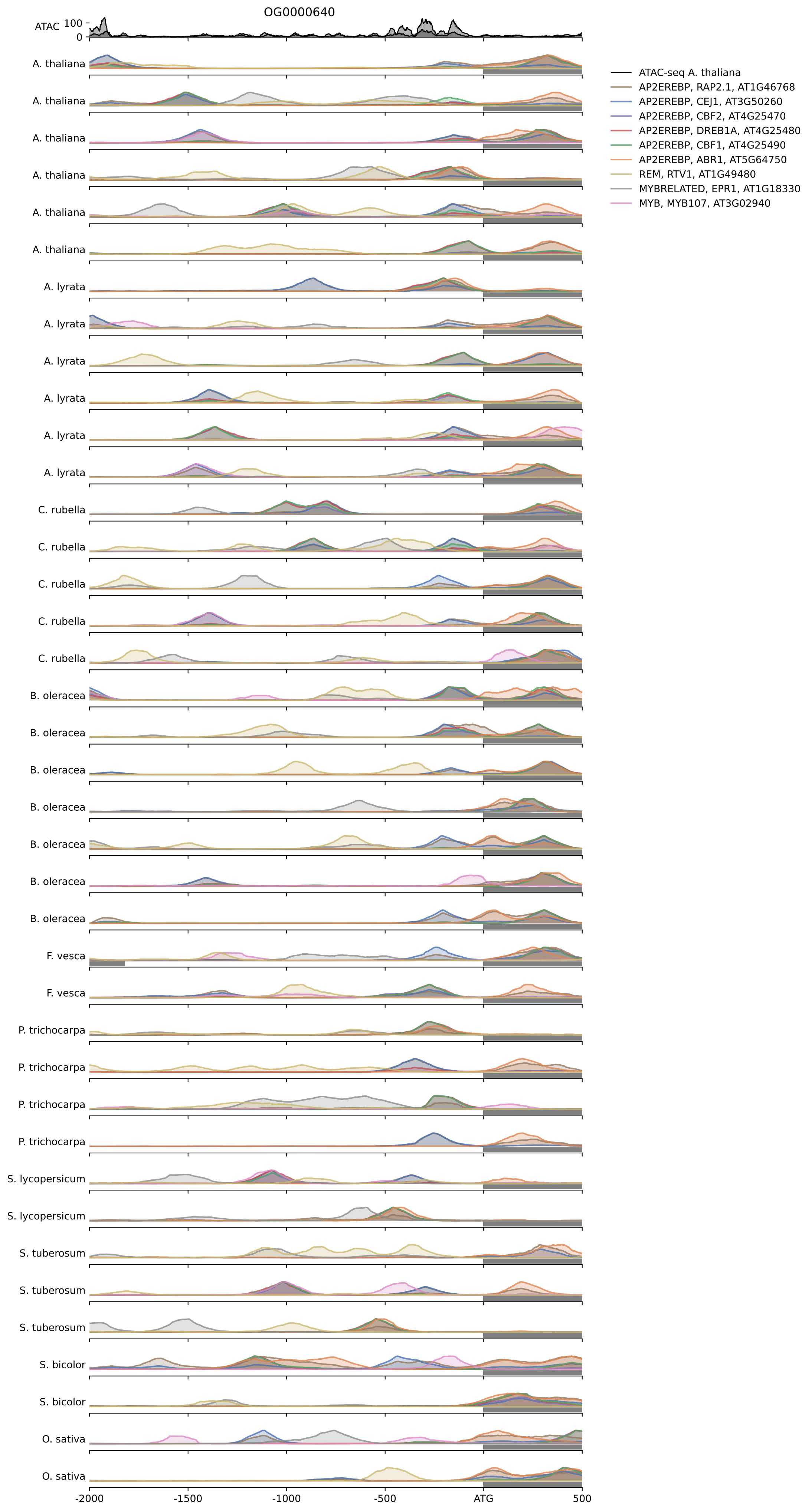


A. thaliana target: AT2G23690, PADRE protein.

A. thaliana target: AT5G66580, PADRE protein.

A. thaliana target: AT3G50800, PADRE protein.

A. thaliana target: AT4G37240, PADRE protein down-regulated after infection by S. sclerotiorun.



A. thaliana target: AT4G36900, RAP2.10, Encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family (RAP2.10). The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.9 and RAP2.1.

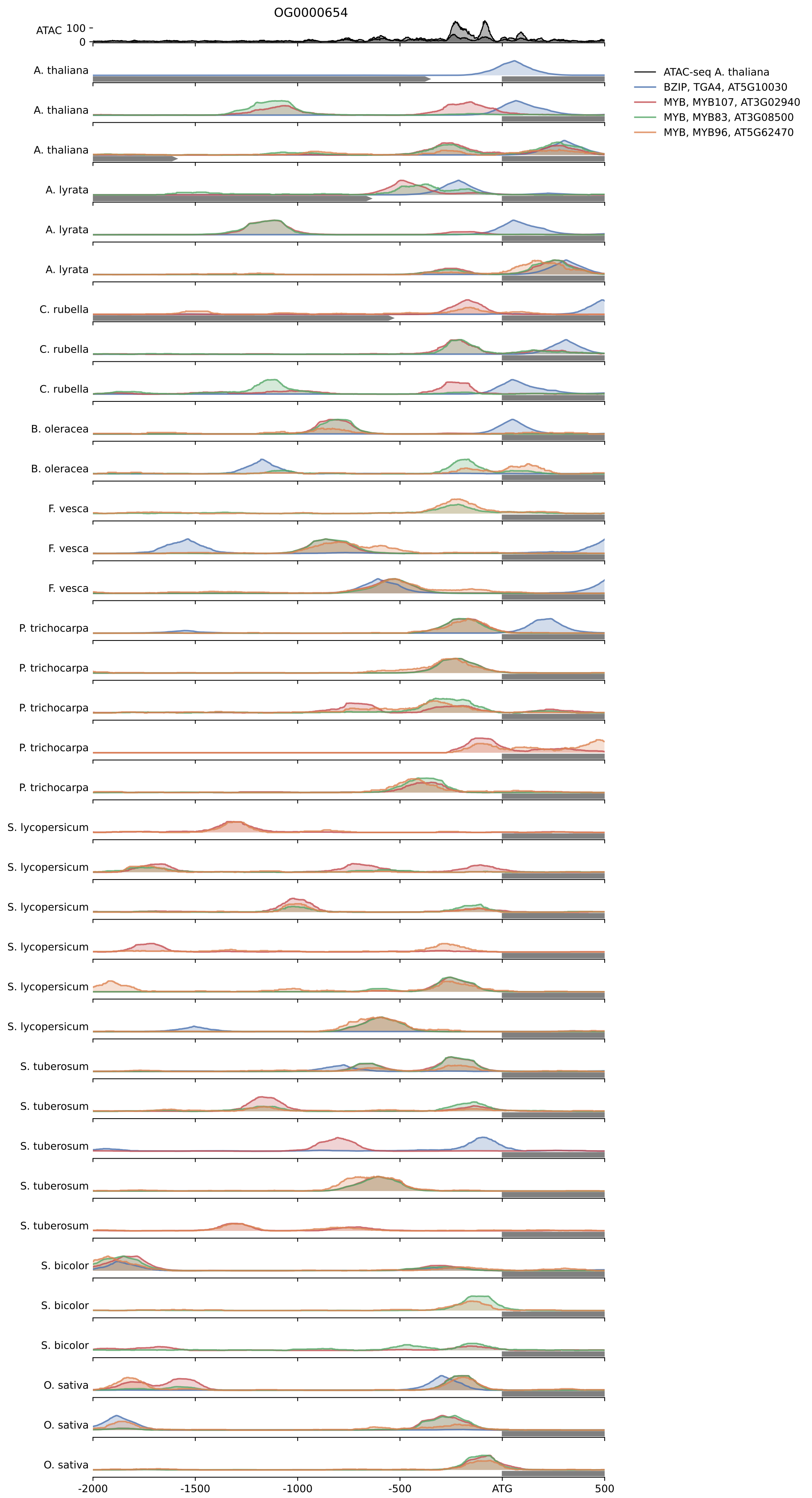
A. thaliana target: AT3G50260, CEJ1, Encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. Involved in defense and freezing stress responses. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10. The mRNA is cell-to-cell mobile.

A. thaliana target: AT5G67190, DEAR2, encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.

A. thaliana target: AT4G06746, RAP2.9, encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family (RAP2.9). The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1 and RAP2.10.

A. thaliana target: AT2G23340, DEAR3, encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.

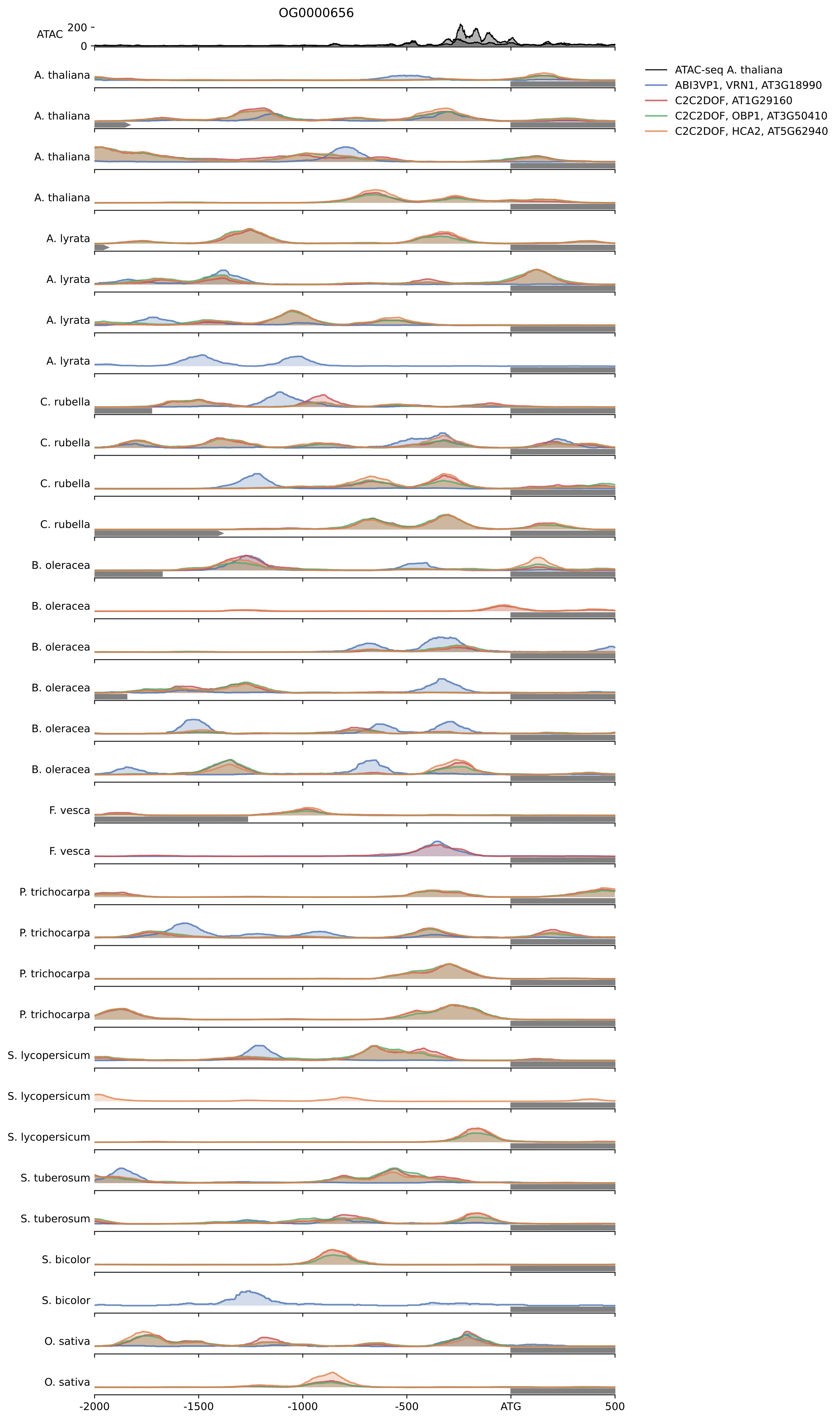
A. thaliana target: AT1G46768, RAP2.1, encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family (RAP2.1). The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.9 and RAP2.10.



A. thaliana target: AT3G21240, 4CL2, encodes an isoform of 4-coumarate:CoA ligase (4CL), which is involved in the last step of the general phenylpropanoid pathway. The catalytic efficiency was in the following (descending) order: p-coumaric acid, caffeic acid, ferulic acid, 5-OH-ferulic acid and cinnamic acid. At4CL2 was unable to use sinapic acid as substrate.

A. thaliana target: AT1G51680, 4CL1, encodes an isoform of 4-coumarate:CoA ligase (4CL), which is involved in the last step of the general phenylpropanoid pathway. In addition to 4-coumarate, it also converts ferulate. The catalytic efficiency was in the following (descending) order: p-coumaric acid, ferulic acid, caffeic acid and 5-OH-ferulic acid. At4CL1 was unable to use sinapic acid as substrate.

A. thaliana target: AT1G65060, 4CL3, encodes an isoform of 4-coumarate:CoA ligase (4CL), which is involved in the last step of the general phenylpropanoid pathway. mRNA levels are not induced in response to wounding or to fungal infection by P. parasitica. mRNA is expressed in flowers, to a lesser degree in mature leaves and siliques and marginally in seedling roots and bolting stems of mature plants. The catalytic efficiency was in the following (descending) order: p-coumaric acid, caffeic acid, ferulic acid, cinnamic acid and 5-OH-ferulic acid. At4CL3 was unable to use sinapic acid as substrate.



A. thaliana target: AT2G13800, SERK5, somatic embryogenesis receptor-like kinase 5;(source:Araport11)

A. thaliana target: AT1G71830, SERK1, Plasma membrane LRR receptor-like serine threonine kinase expressed during embryogenesis in locules until stage 6 anthers, with higher expression in the tapetal cell layer. SERK1 and SERK2 receptor kinases function redundantly as an important control point for sporophytic development controlling male gametophyte production. SERK1 interacts with and transphosphorylates EMS1

A. thaliana target: AT2G13790, SERK4, Receptor-like protein kinase that plays a role in myriad processes such as plant-type hypersensitive response, defense response, stomatal movement,and brassinosteroid signalling.

A. thaliana target: AT1G34210, SERK2, Plasma membrane LRR receptor-like serine threonine kinase expressed during embryogenesis in locules until stage 6 anthers, with higher expression in the tapetal cell layer. SERK1 and SERK2 receptor kinases function redundantly as an important control point for sporophytic development controlling male gametophyte production. The mRNA is cell-to-cell mobile.