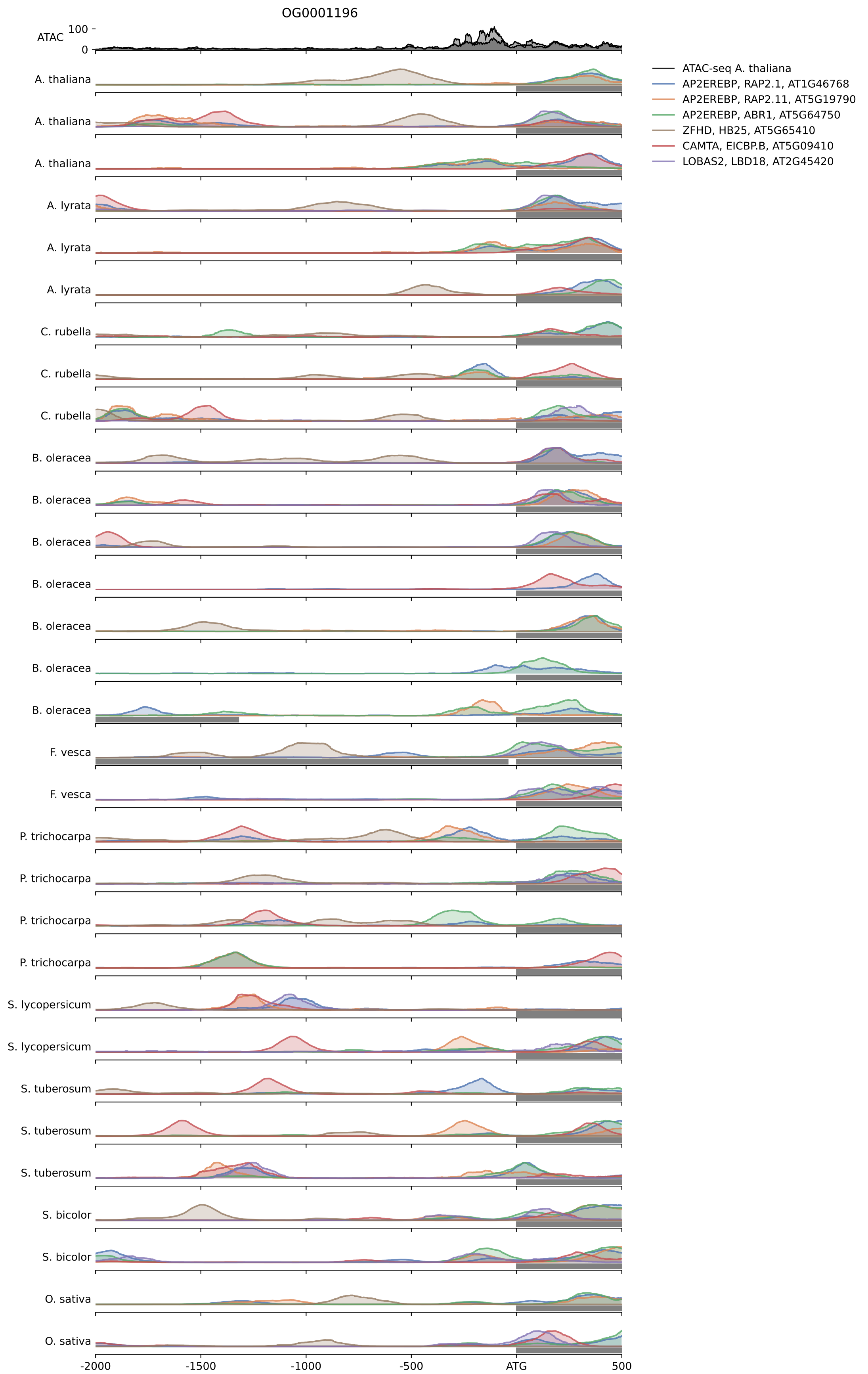
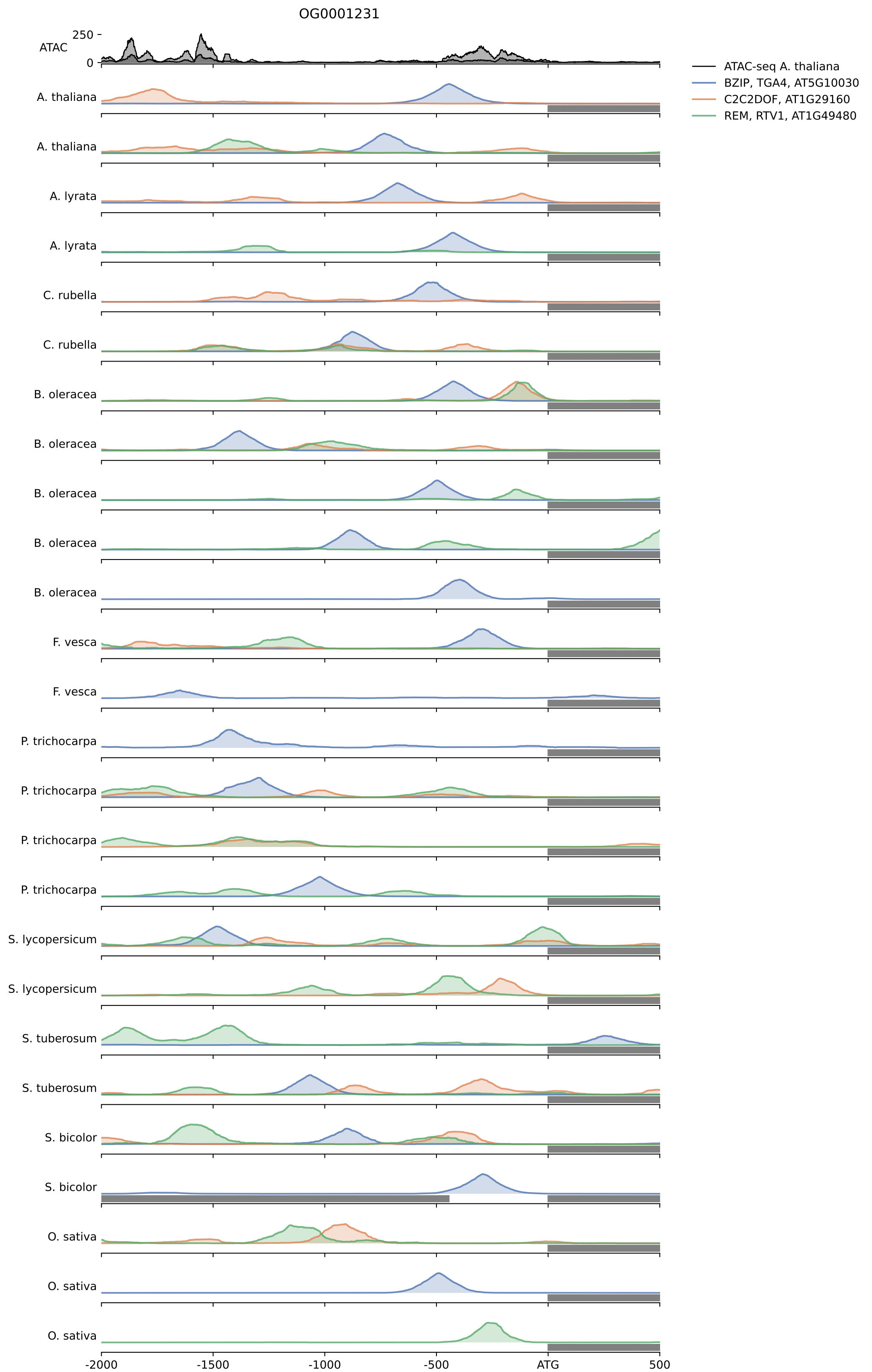


A. thaliana target: AT1G53170, ERF8, encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-8). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.

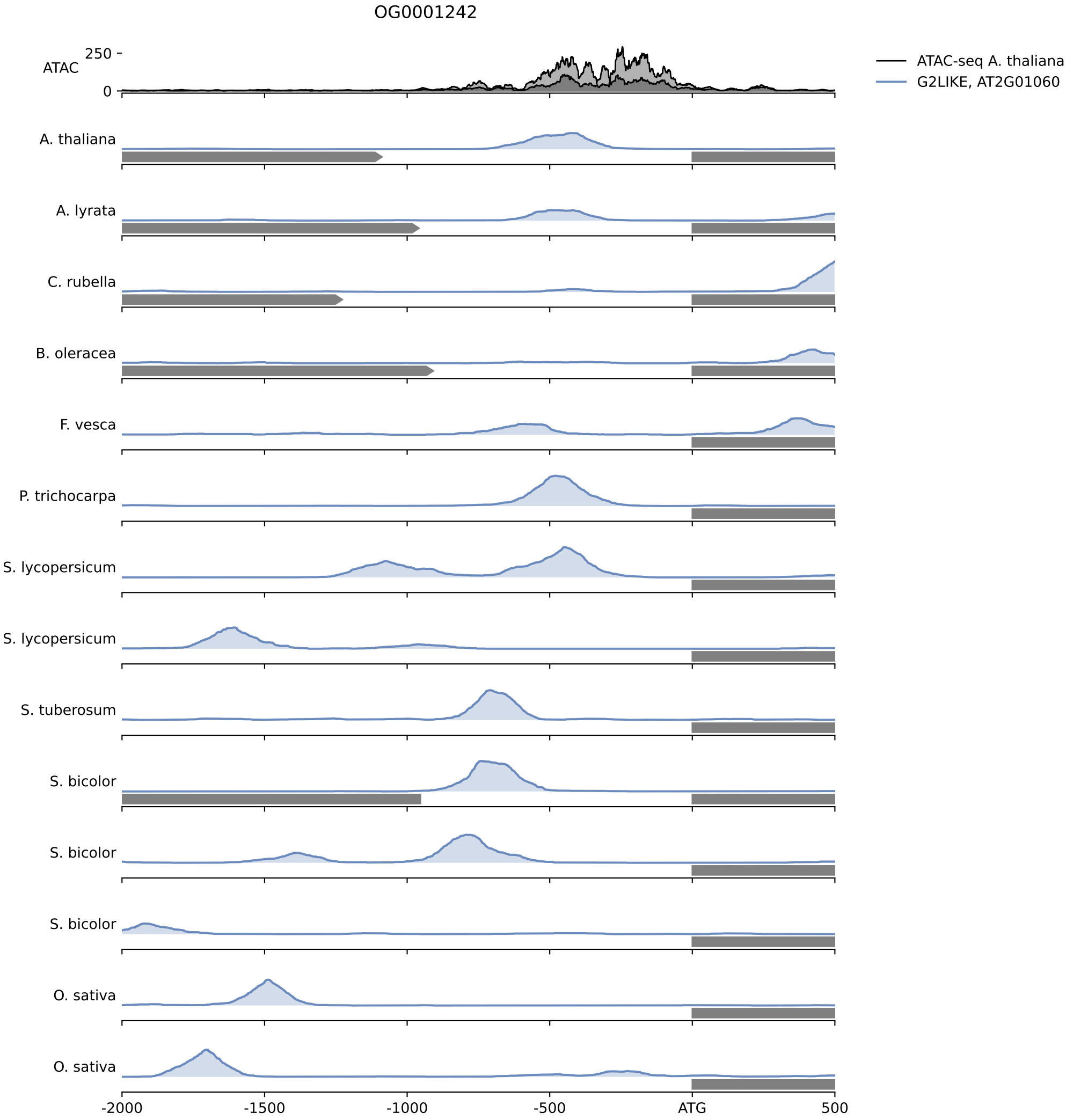
A. thaliana target: AT3G15210, ERF4, Encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-4). The protein contains one AP2 domain. Acts as a negative regulator of JA-responsive defense gene expression and resistance to the necrotrophic fungal pathogen Fusarium oxysporum and antagonizes JA inhibition of root elongation. The mRNA is cell-to-cell mobile.

A. thaliana target: AT5G44210, ERF9, encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-9). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.

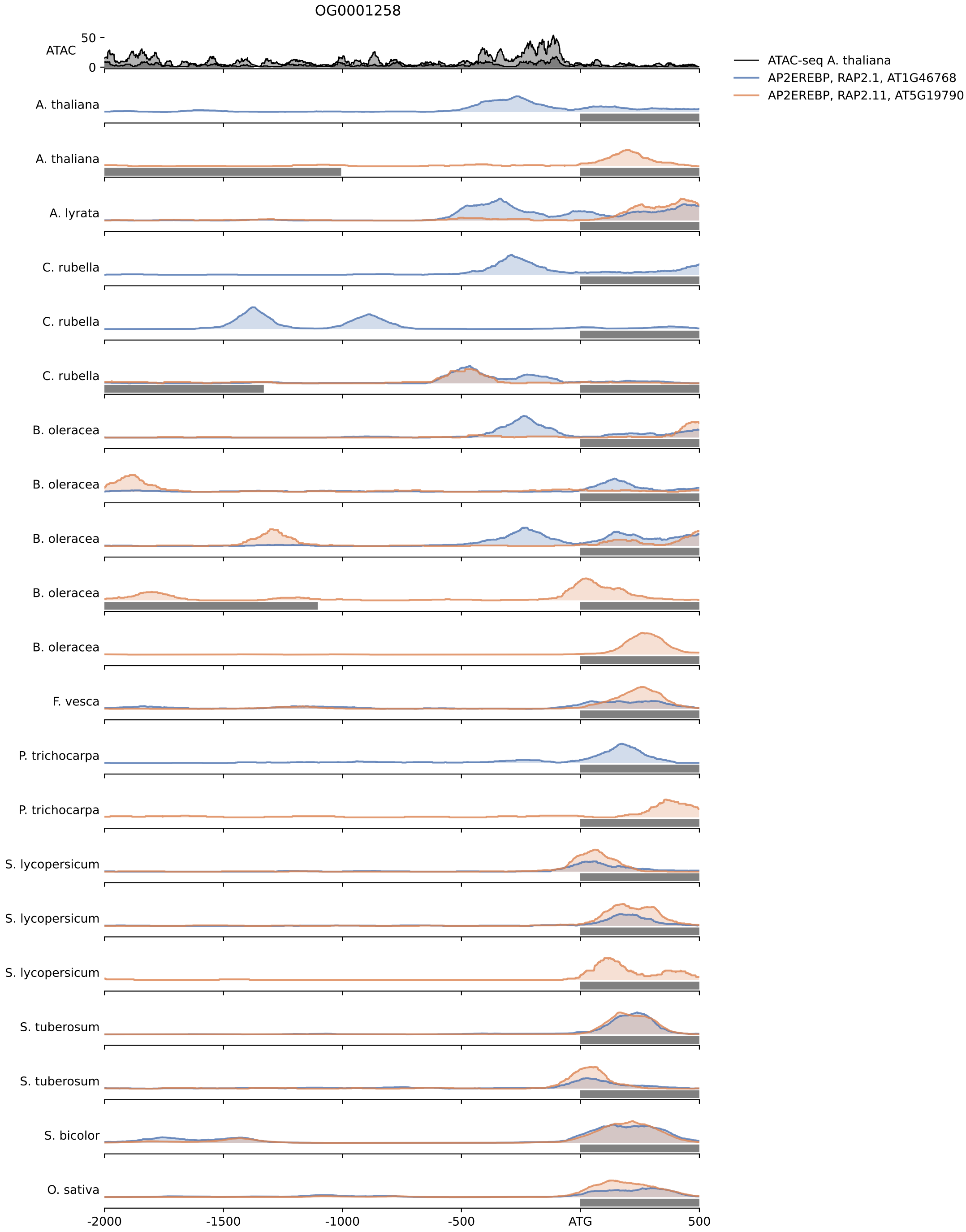


A. thaliana target: AT3G56710, SIB1, Sig1 binding protein; interacts with Sig1R4. As well as Sig1, SibI is imported into chloroplasts and its expression is light-dependent in mature chloroplasts.

A. thaliana target: AT2G41180, SIB2, VQ motif-containing protein;(source:Araport11)

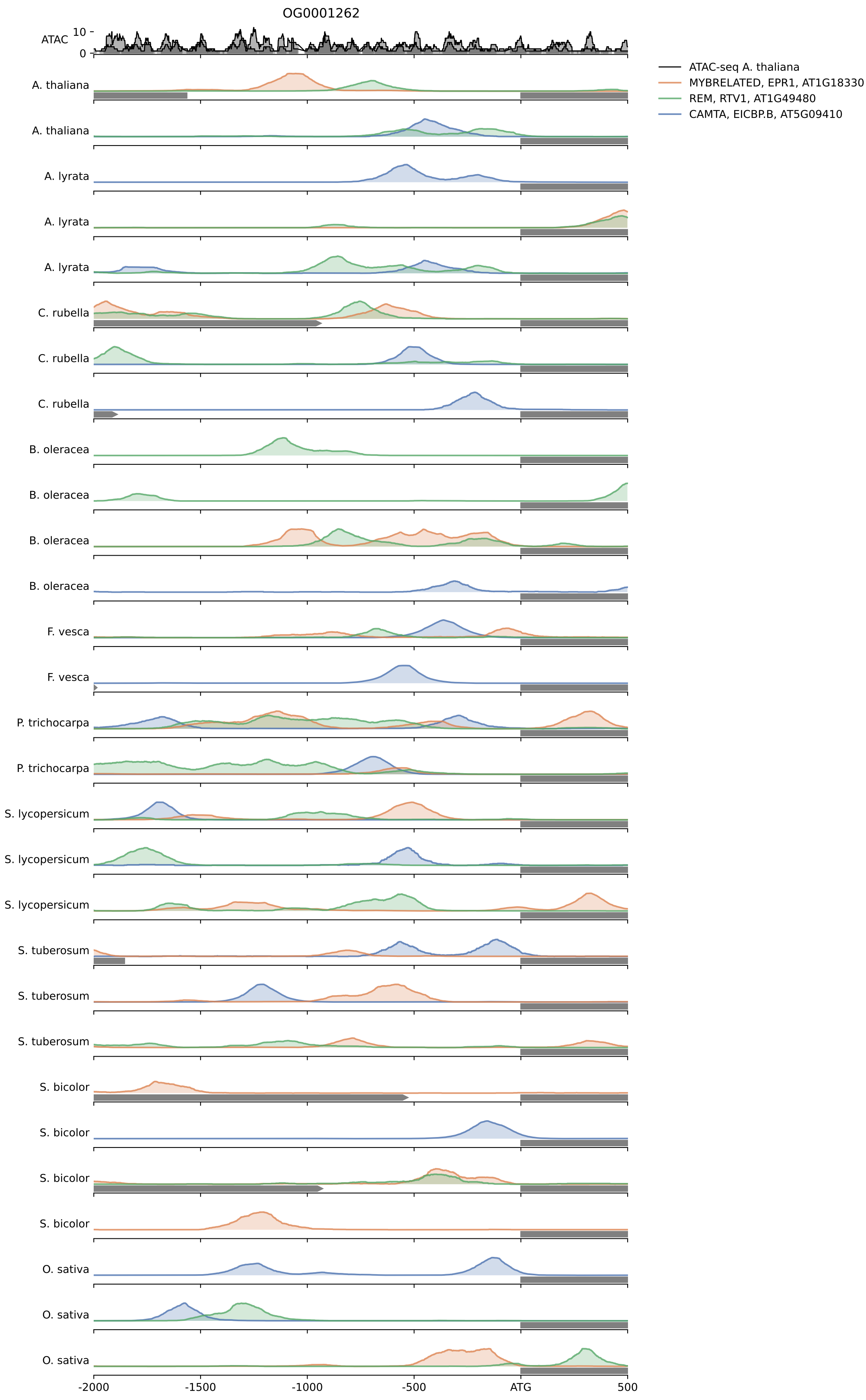


A. thaliana target: AT3G57870, SCE1, Encodes a SUMO ligase that directs the attachment of the small protein SUMO to target proteins via an isopeptide bond. This enzyme is localized to the nucleus and plants with reduced levels of this protein show higher sensitivity to ABA in root growth inhibition assays. It has high similarity to the yeast UBC9 SUMO ligase and is sometimes referred to by that name.



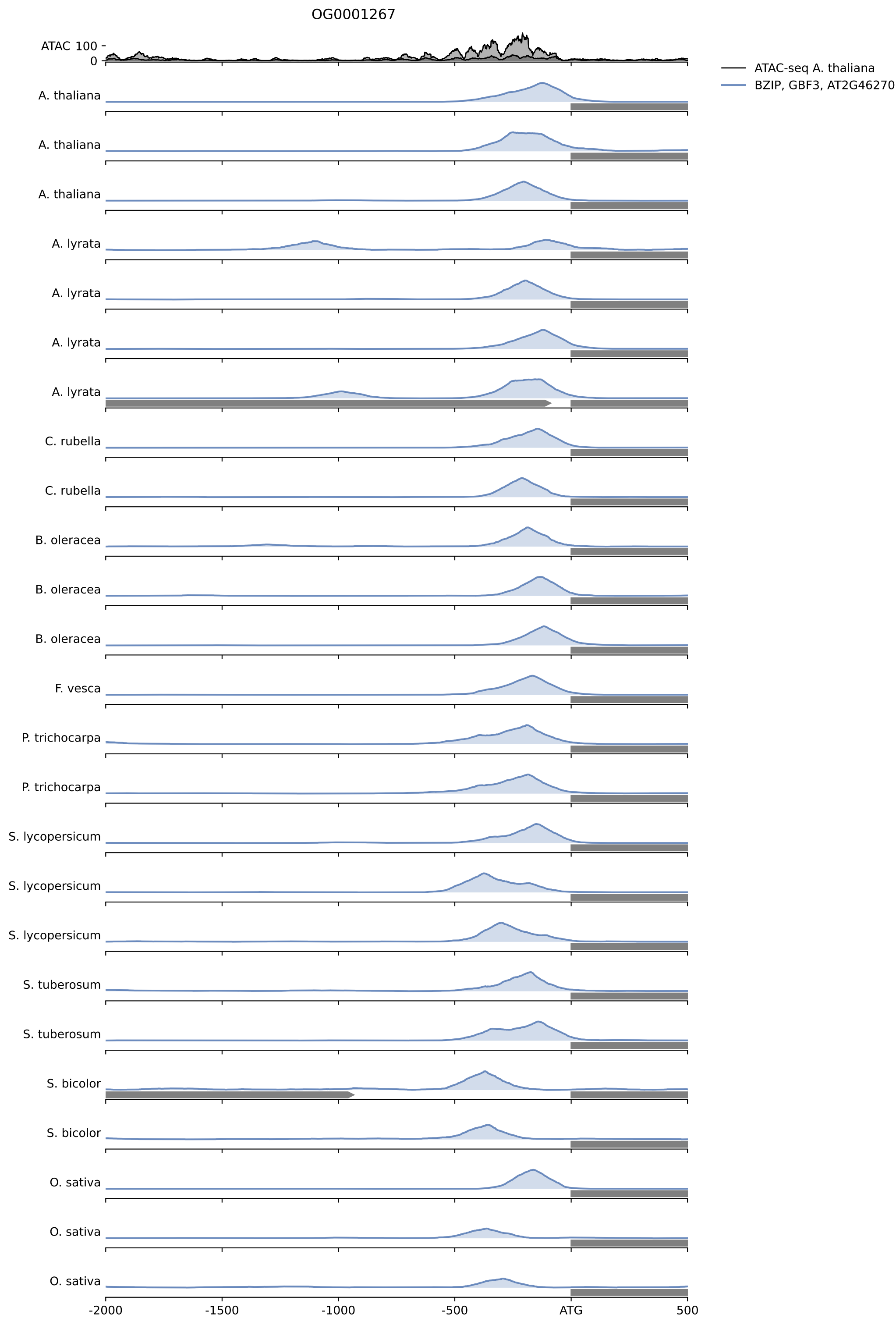
A. thaliana target: AT2G40180, PP2C5, Encodes PP2C5, a member of the PP2C family phosphatases. PP2C5 acts as a MAPK phosphatase that positively regulates seed germination, stomatal closure and ABA-inducible gene expression.

A. thaliana target: AT1G07160, Protein phosphatase 2C family protein;(source:Araport11)



A. thaliana target: AT2G22950, ACA7, Encodes a putative auto-regulated Ca2+-ATPase located in the plasma membrane involved in transporting Ca2+ outside developing pollen grains. This activity is important to support normal pollen development, particularly the progression to uninucleated microspores to bicellular pollen grains.

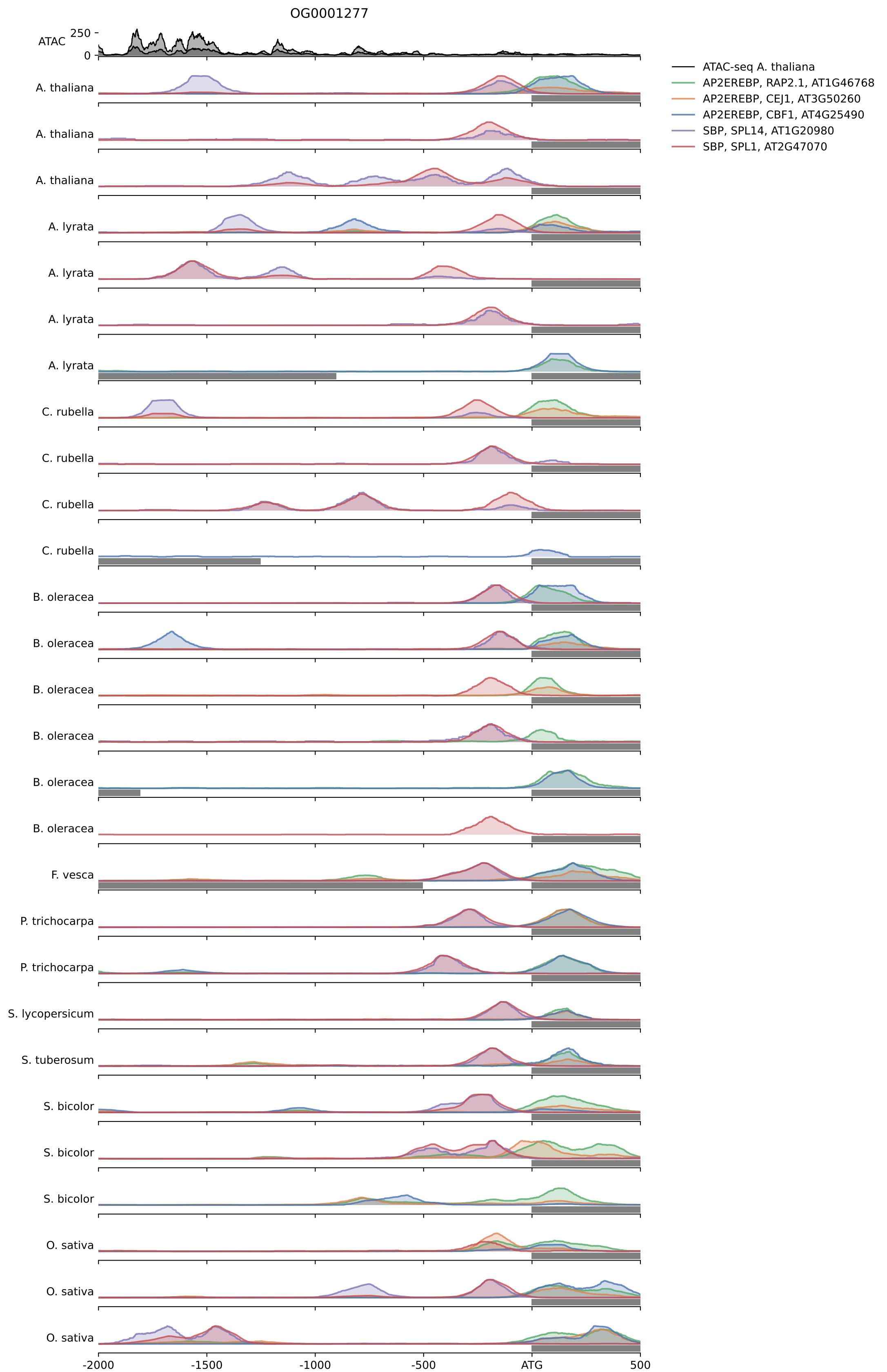
A. thaliana target: AT4G37640, ACA2, Encodes a calmodulin-regulated Ca(2+)-pump located in the endoplasmic reticulum. Belongs to plant 2B ATPase's with an N-terminal autoinhibitor.



A. thaliana target: AT4G37390, BRU6, Encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro. Lines carrying insertions in this gene are hypersensitive to auxin. May function as a negative component in auxin signaling by regulating auxin activity.

A. thaliana target: AT2G23170, GH3.3, encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro.

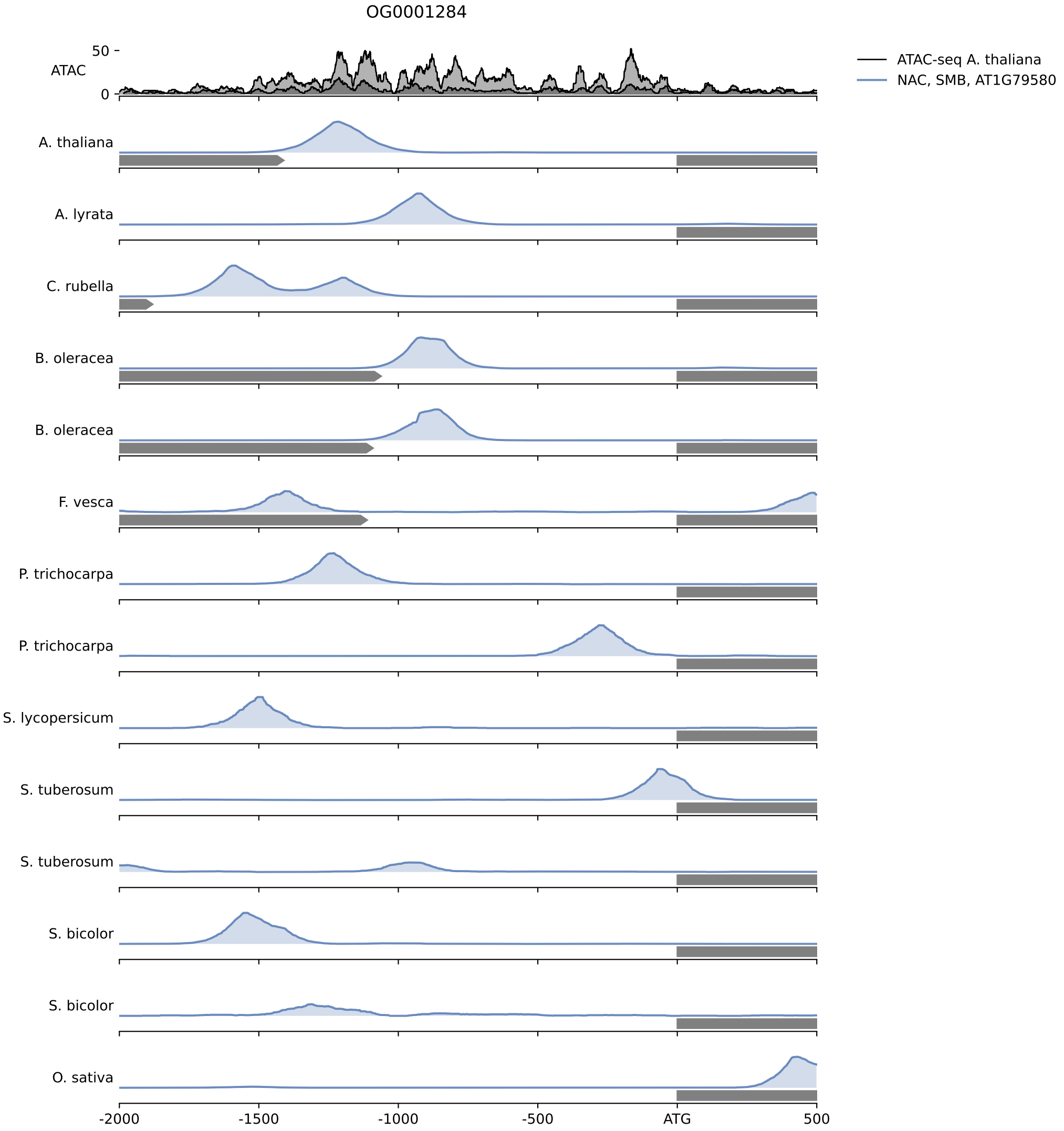
A. thaliana target: AT2G14960, GH3.1, encodes a protein similar to IAA-amido synthases. Lines carrying an insertion in this gene are hypersensitive to auxin. Group II member of the GRETCHEN HAGEN 3 (GH3) gene family which code for acyl acid amido synthetases catalysing the conjugation of IAA to amino acids.



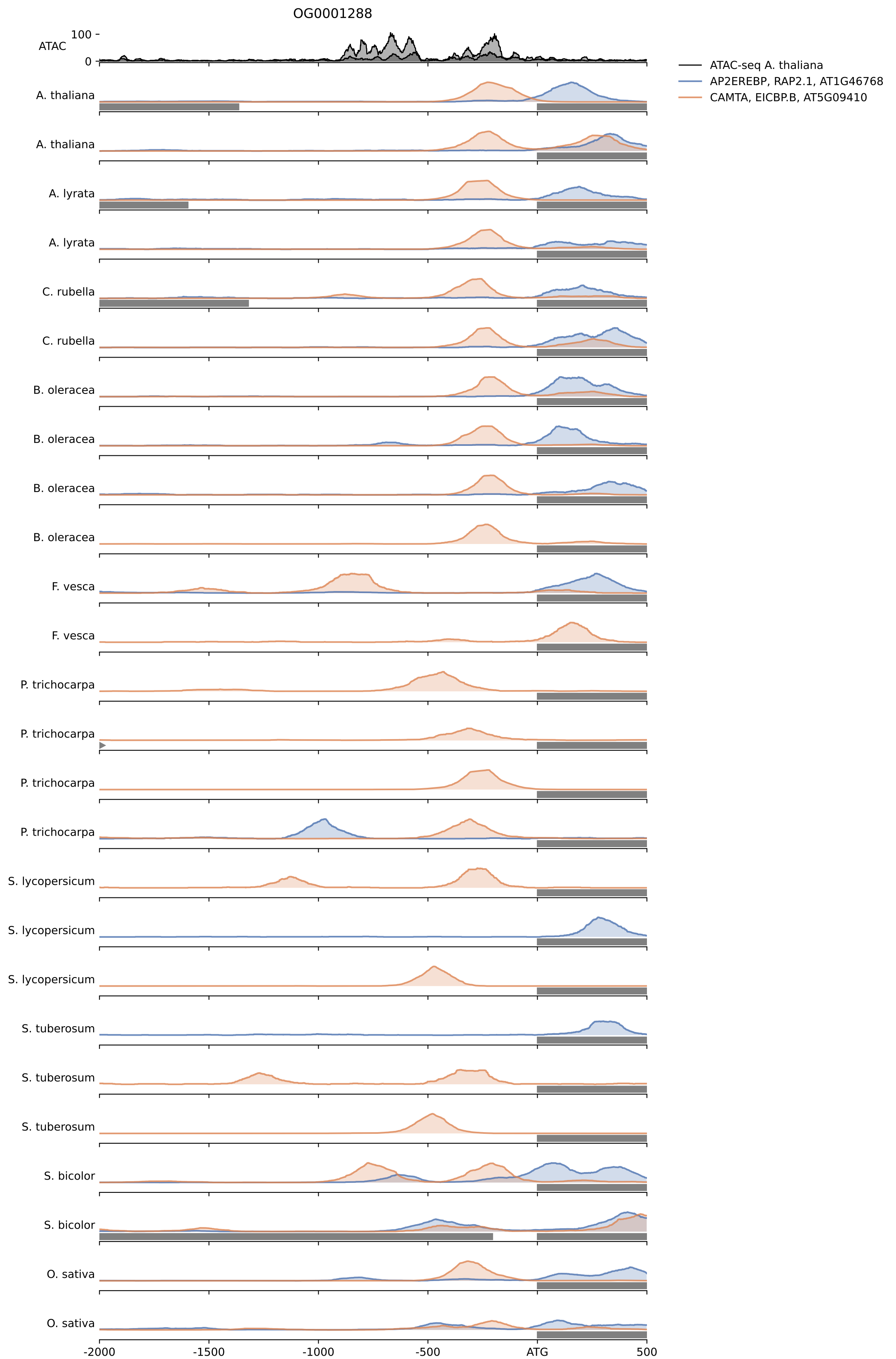
A. thaliana target: AT1G16510, Encodes a clade III SAUR gene with a distinctive expression pattern in root meristems. It is normally expressed in the quiescent center and cortex/endodermis initials and upon auxin stimulation, the expression is found in the endodermal layer. Overexpression studies suggest roles in cell expansion and auxin transport.

A. thaliana target: AT3G12830, SAUR-like auxin-responsive protein family;(source:Araport11)

A. thaliana target: AT1G56150, SAUR-like auxin-responsive protein family;(source:Araport11)

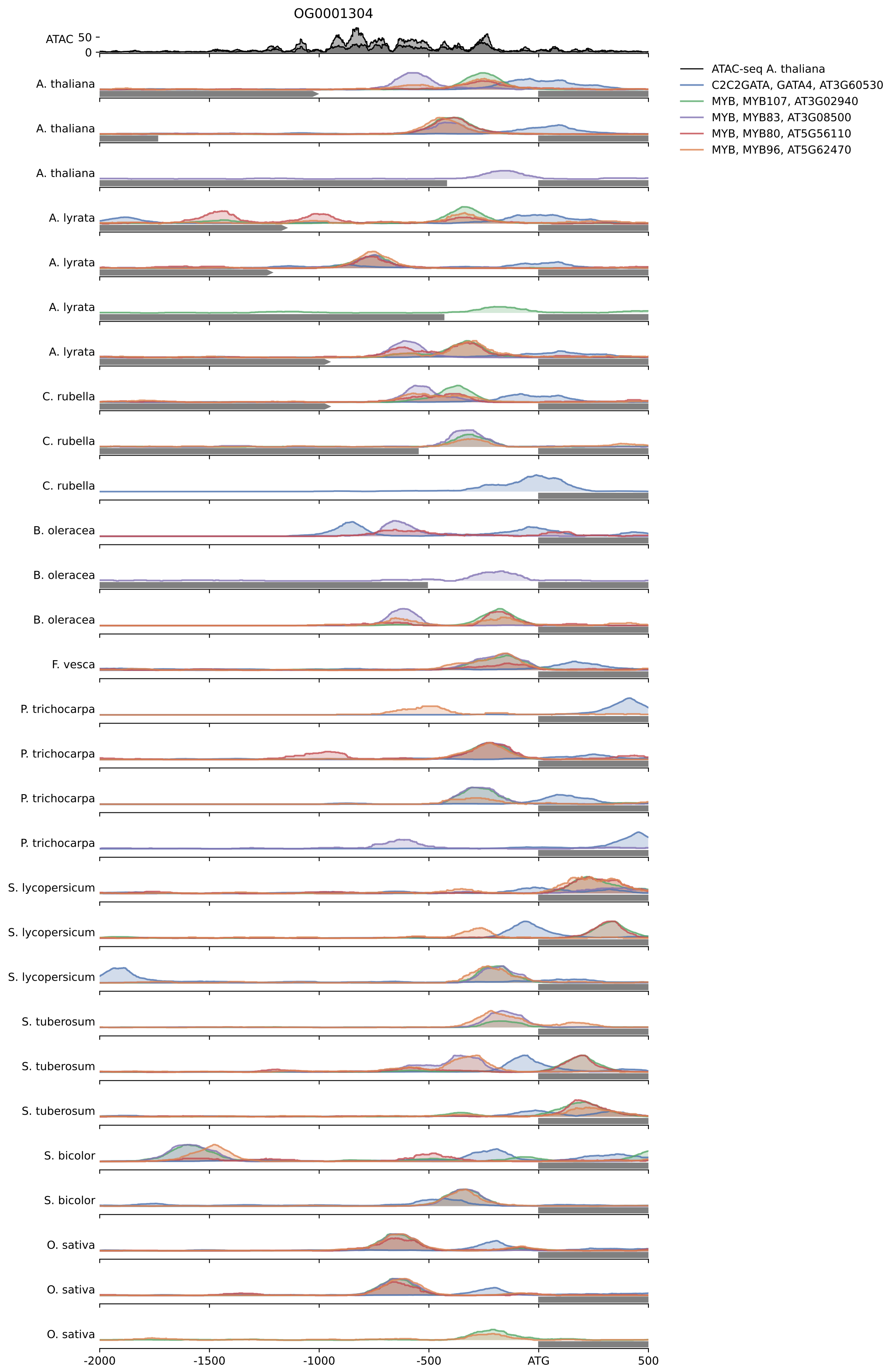


A. thaliana target: AT5G08370, AGAL2, Member of Glycoside Hydrolase Family 27 (GH27)that functions as an α-galactosidase.



A. thaliana target: AT3G03280, PADRE protein up-regulated after infection by S. sclerotiorum.

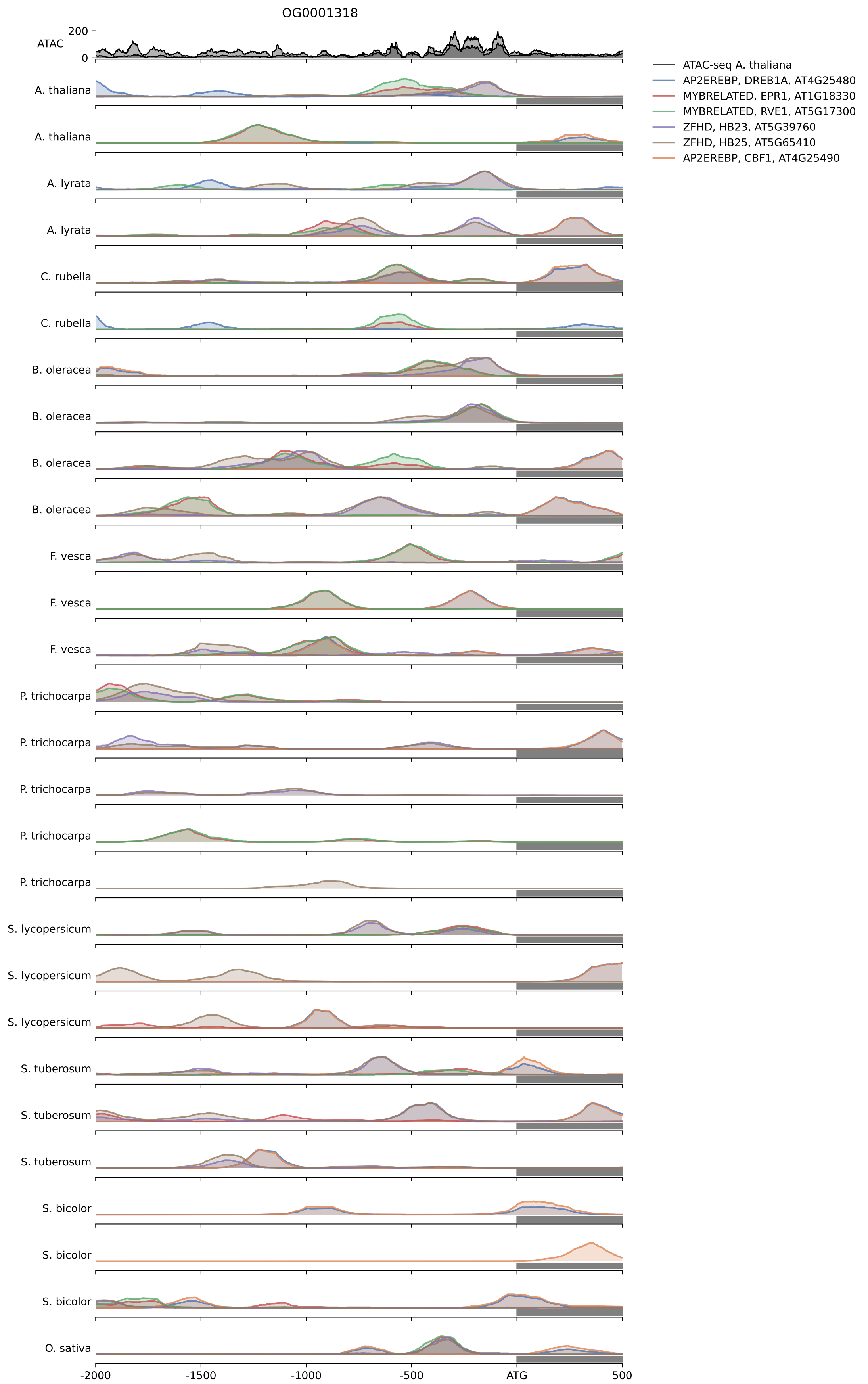
A. thaliana target: AT5G17350, PADRE protein up-regulated after infection by S. sclerotiorum.



A. thaliana target: AT1G10670, ACLA-1, One of the three genes encoding subunit A of the trimeric protein ATP Citrate Lyase. Antisense ACLA-1 plants cause a reduction in cytosolic acetyl-CoA metabolism and have upregulation of stress-related genes and down-regulation of primary metabolism and growth genes, suggesting the mutation restricts normal growth and developmental processes and puts the plant into a state of stress.

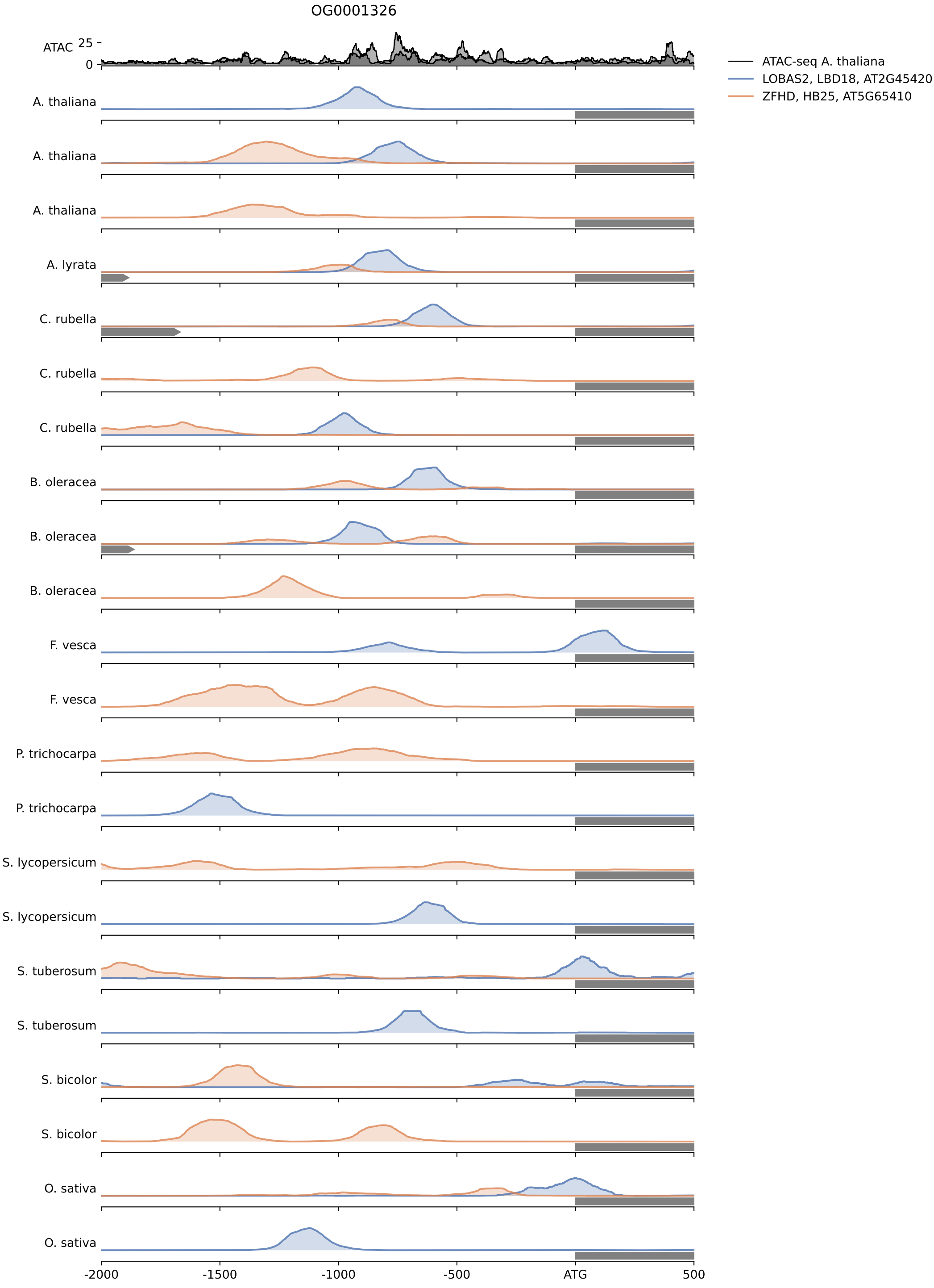
A. thaliana target: AT1G60810, ACLA-2, One of the three genes encoding subunit A of the trimeric enzyme ATP Citrate lyase

A. thaliana target: AT1G09430, ACLA-3, Encodes subunit A of the heteromeric enzyme ATP citrate lyase (ACL). In animals, ACL is encoded by a single gene; ACL in Arabidopsis is composed of two polypeptides, ACLA (encoded by 3 genes) and ACLB (encoded by 2 genes). The holoenzyme has an A(4)B(4)stoichiometry. Expression of both ACLA and ACLB but not of either of the subunits alone results in ACL activity.



A. thaliana target: AT4G36040, J11, DNA J protein.

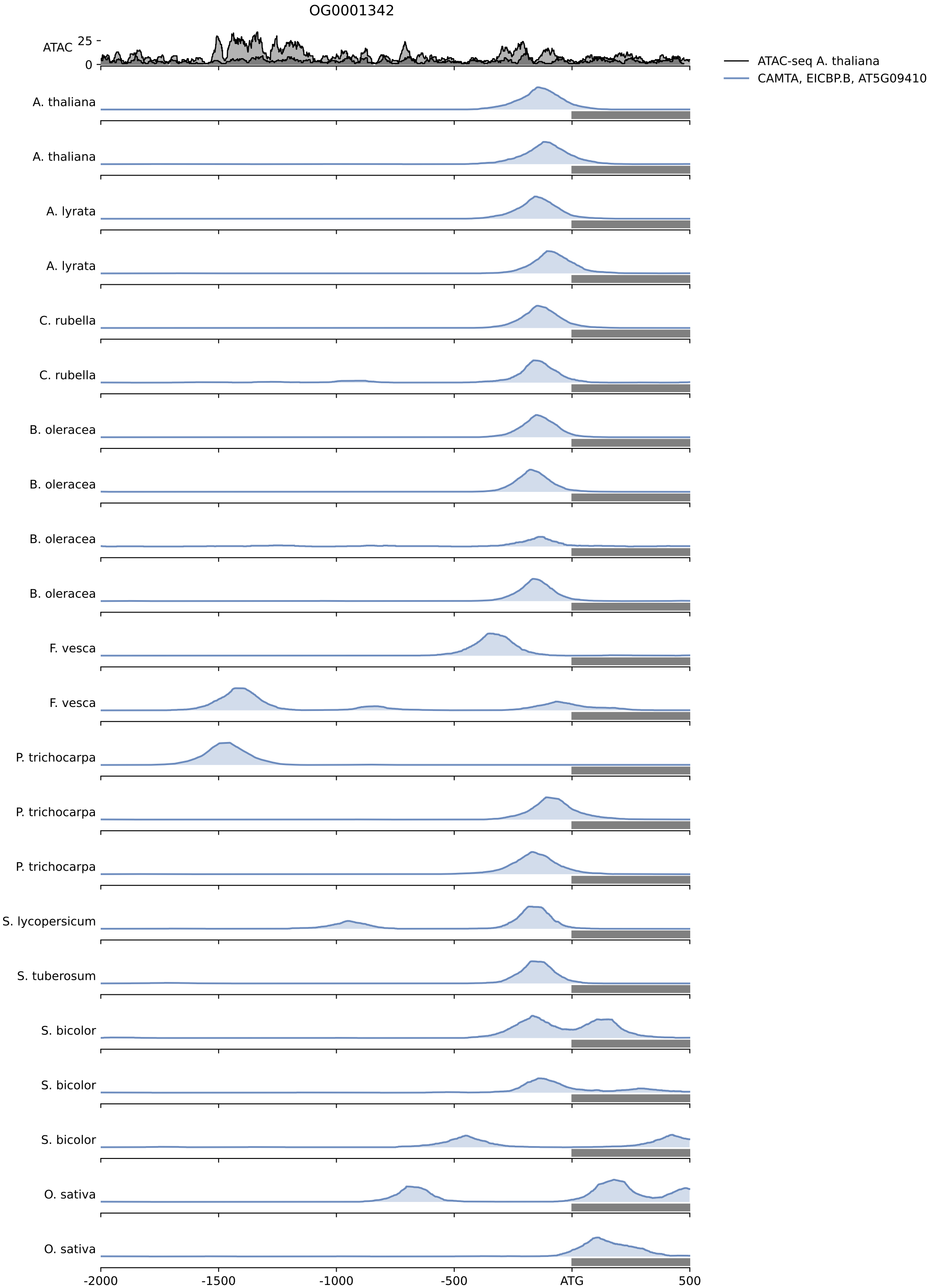
A. thaliana target: AT2G17880, Chaperone DnaJ-domain superfamily protein;(source:Araport11)



A. thaliana target: AT1G68510, LBD42, LOB domain protein.

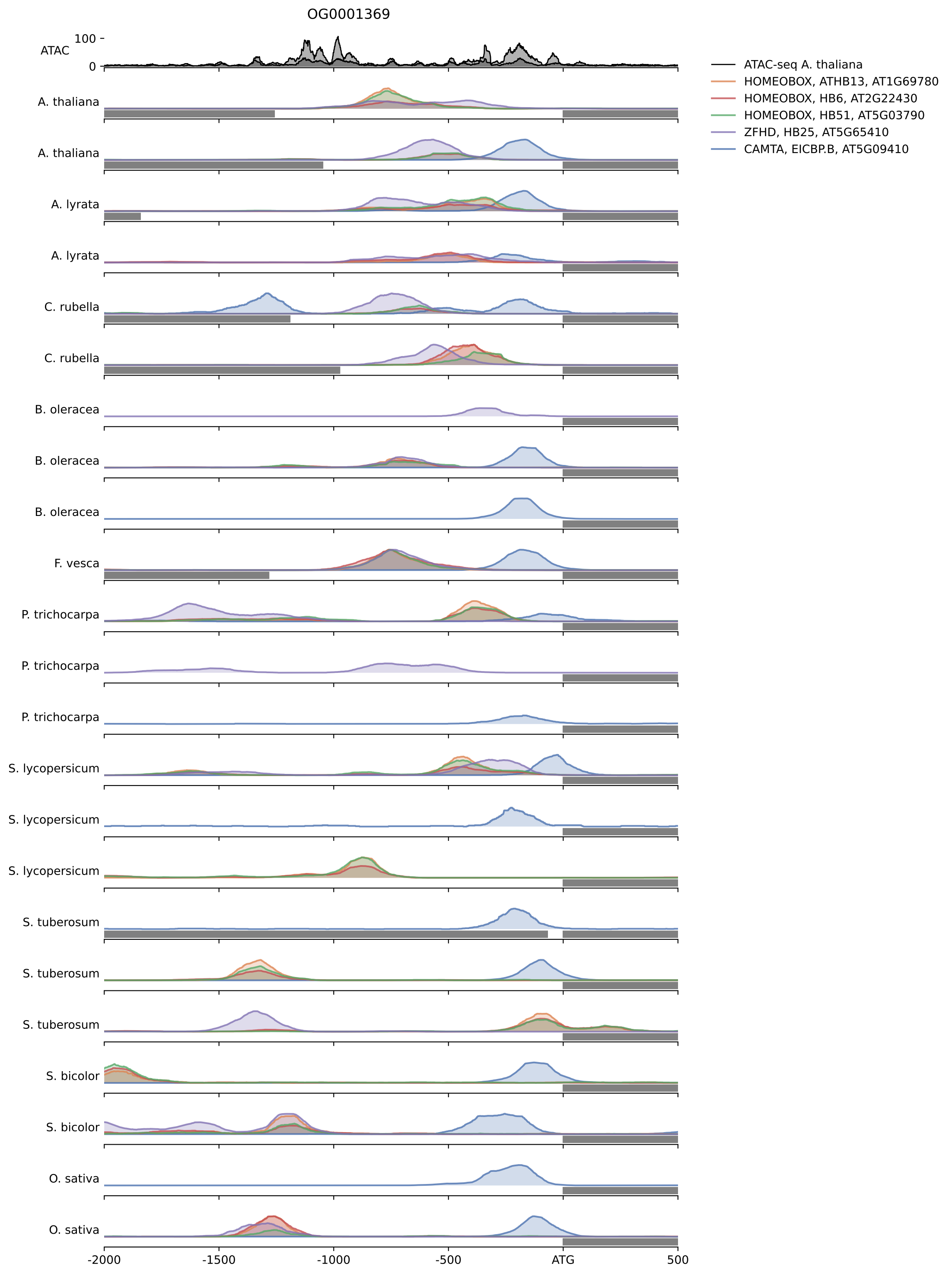
A. thaliana target: AT3G02550, LBD41, LOB domain-containing protein 41;(source:Araport11)

A. thaliana target: AT1G67100, LBD40, LOB domain-containing protein 40;(source:Araport11)



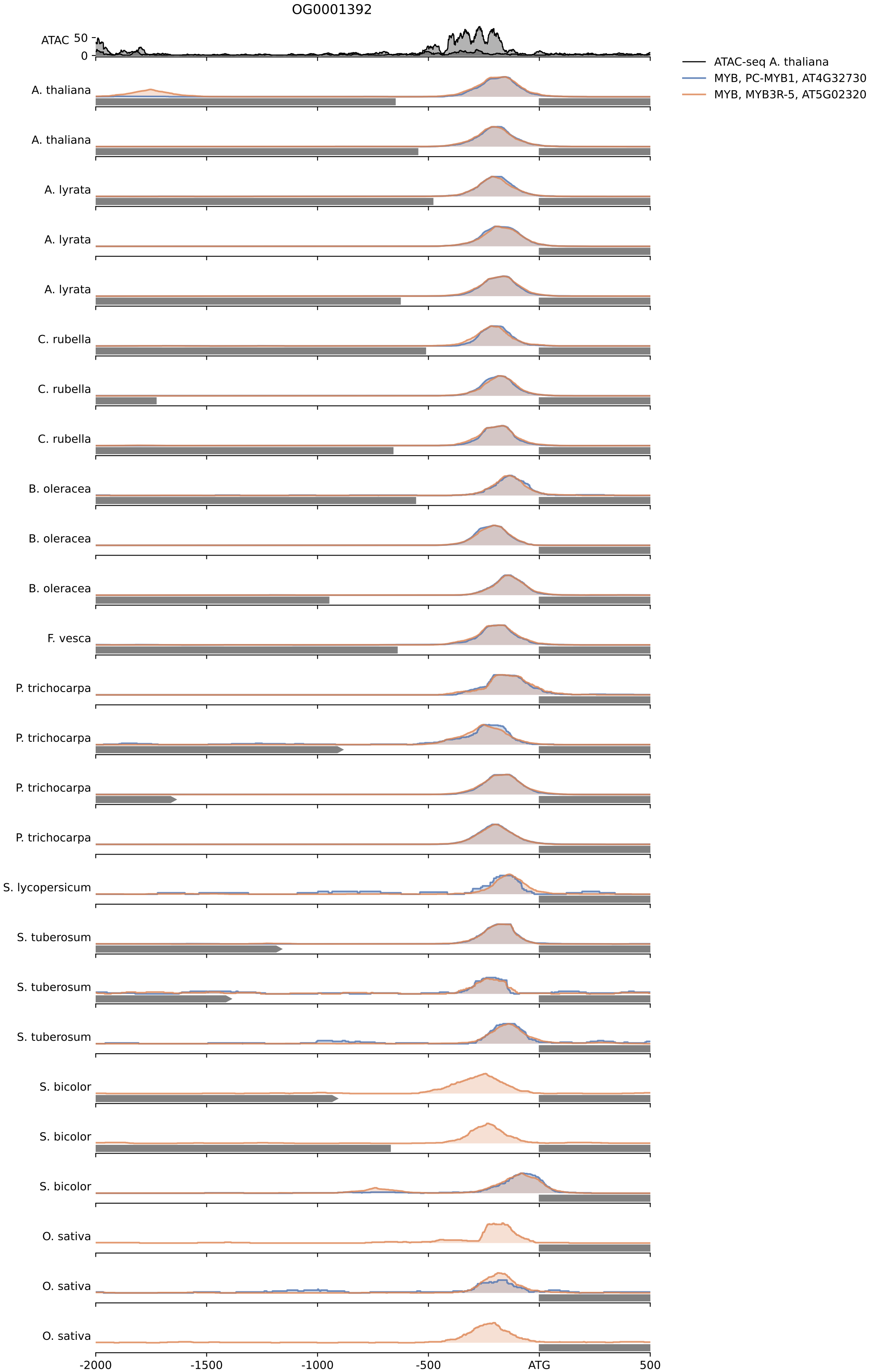
A. thaliana target: AT5G22380, NAC090, NAC domain containing protein 90;(source:Araport11)

A. thaliana target: AT3G44350, NAC061, NAC domain containing protein 61;(source:Araport11)



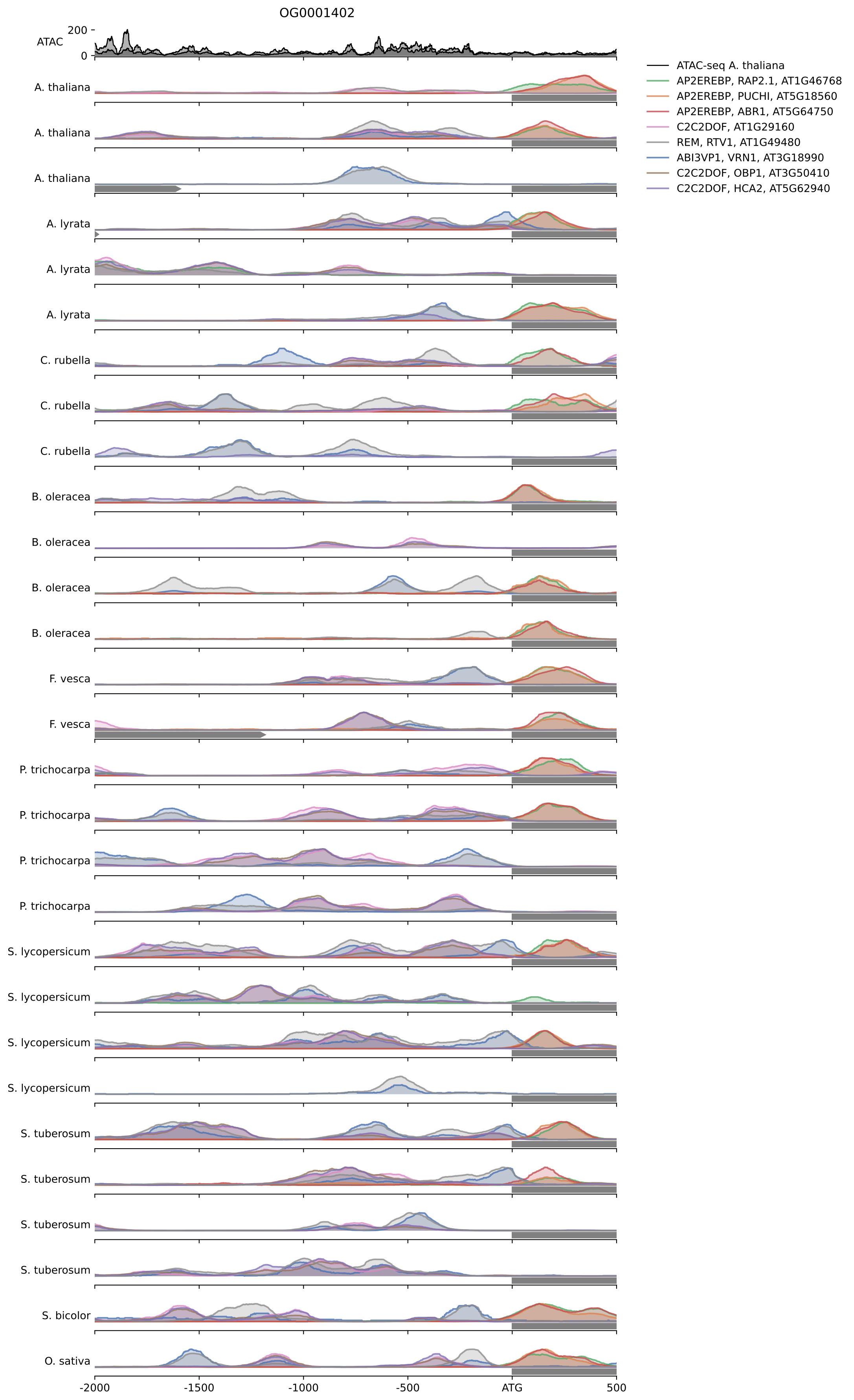
A. thaliana target: AT4G35985, Senescence/dehydration-associated protein-like protein;(source:Araport11)

A. thaliana target: AT2G17840, ERD7, Identified as drought-inducible gene by differential hybridization. Upregulated by high light, drought, cold and salt stress determined by microarray analysis.



A. thaliana target: AT3G02640, transmembrane protein;(source:Araport11)

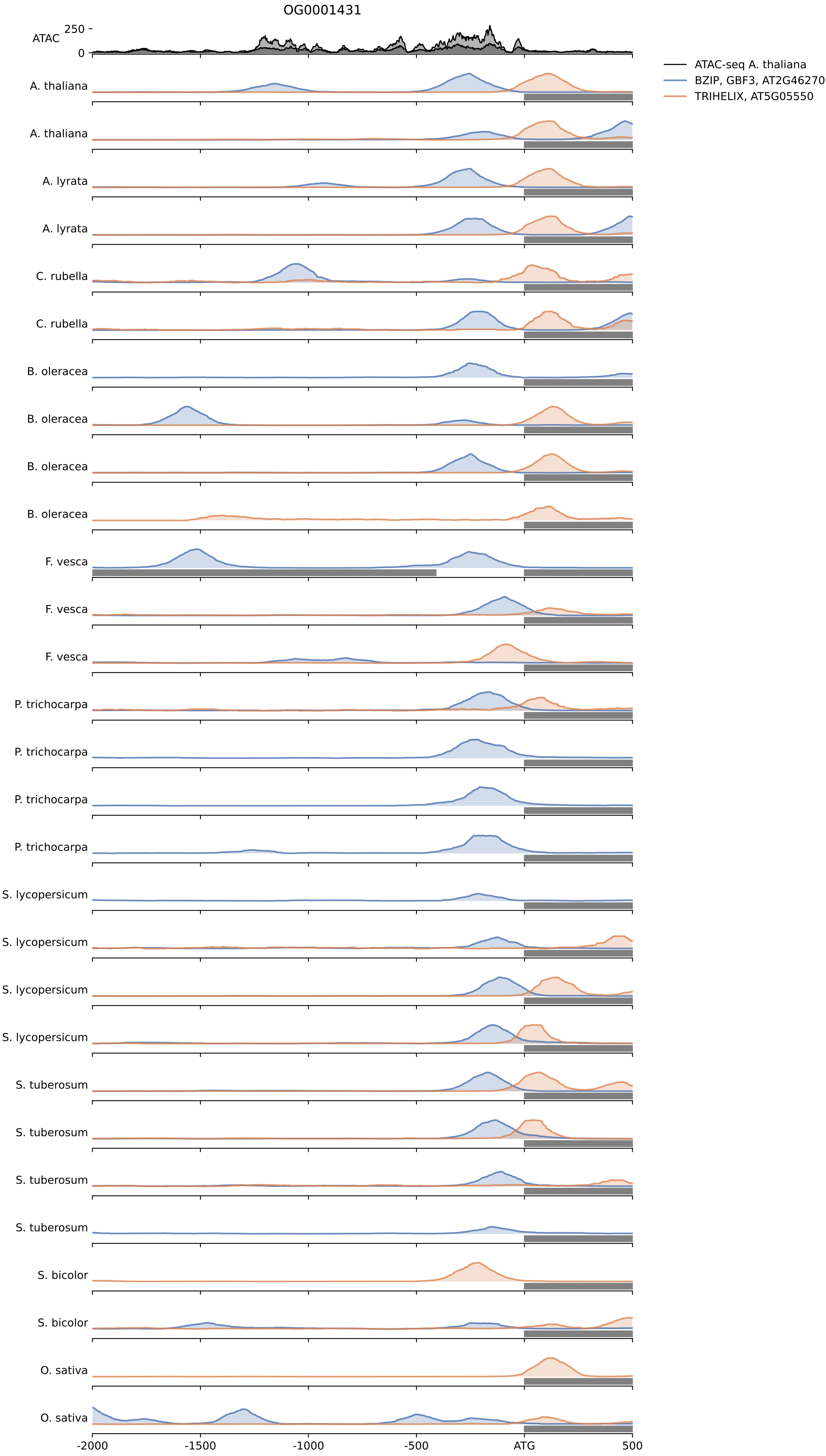
A. thaliana target: AT5G16250, transmembrane protein;(source:Araport11)



A. thaliana target: AT4G12080, AHL1, AT-hook motif nuclear-localized protein 1;(source:Araport11)

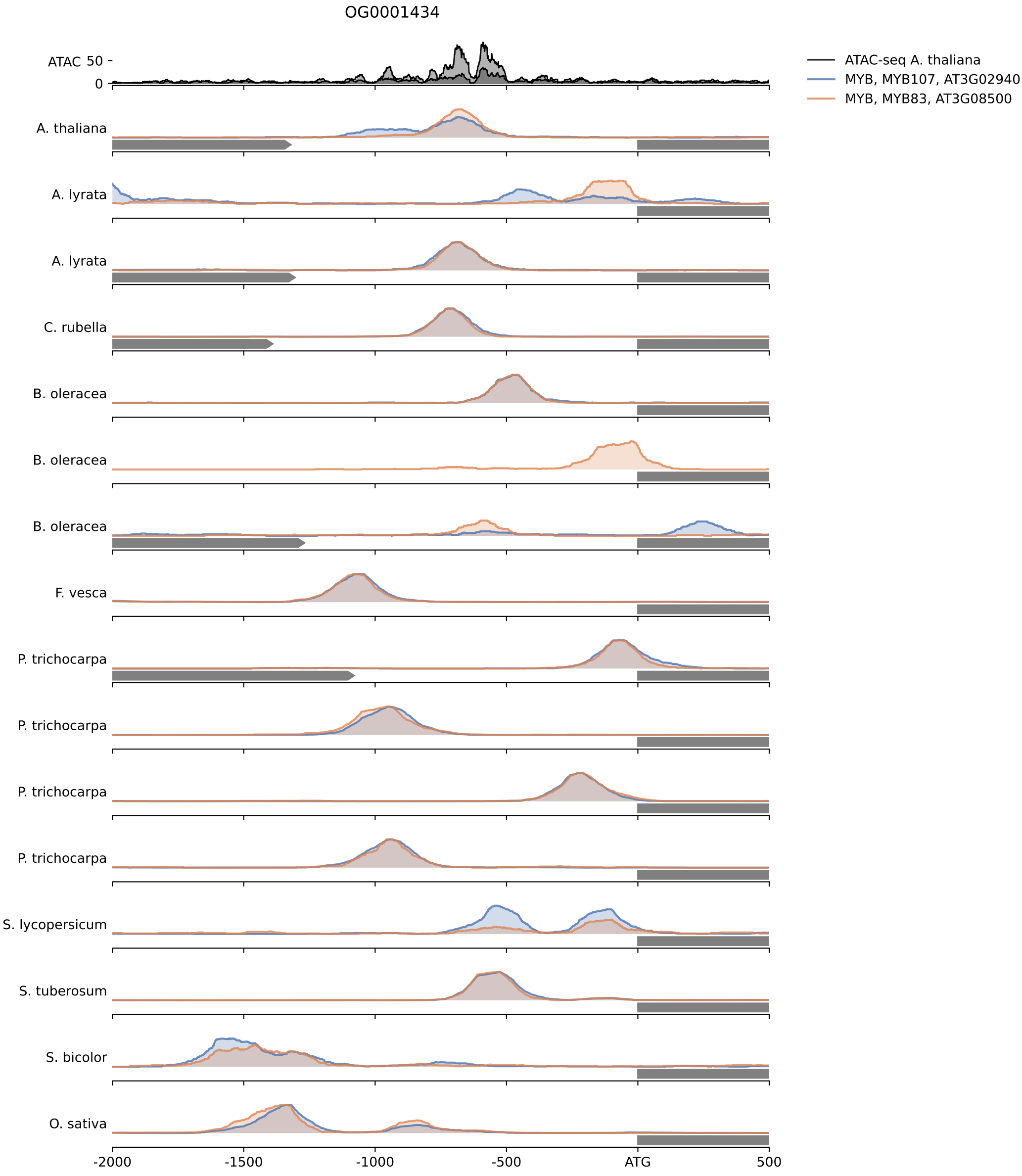
A. thaliana target: AT4G22770, AT hook motif DNA-binding family protein;(source:Araport11)

A. thaliana target: AT4G00200, AT hook motif DNA-binding family protein;(source:Araport11)

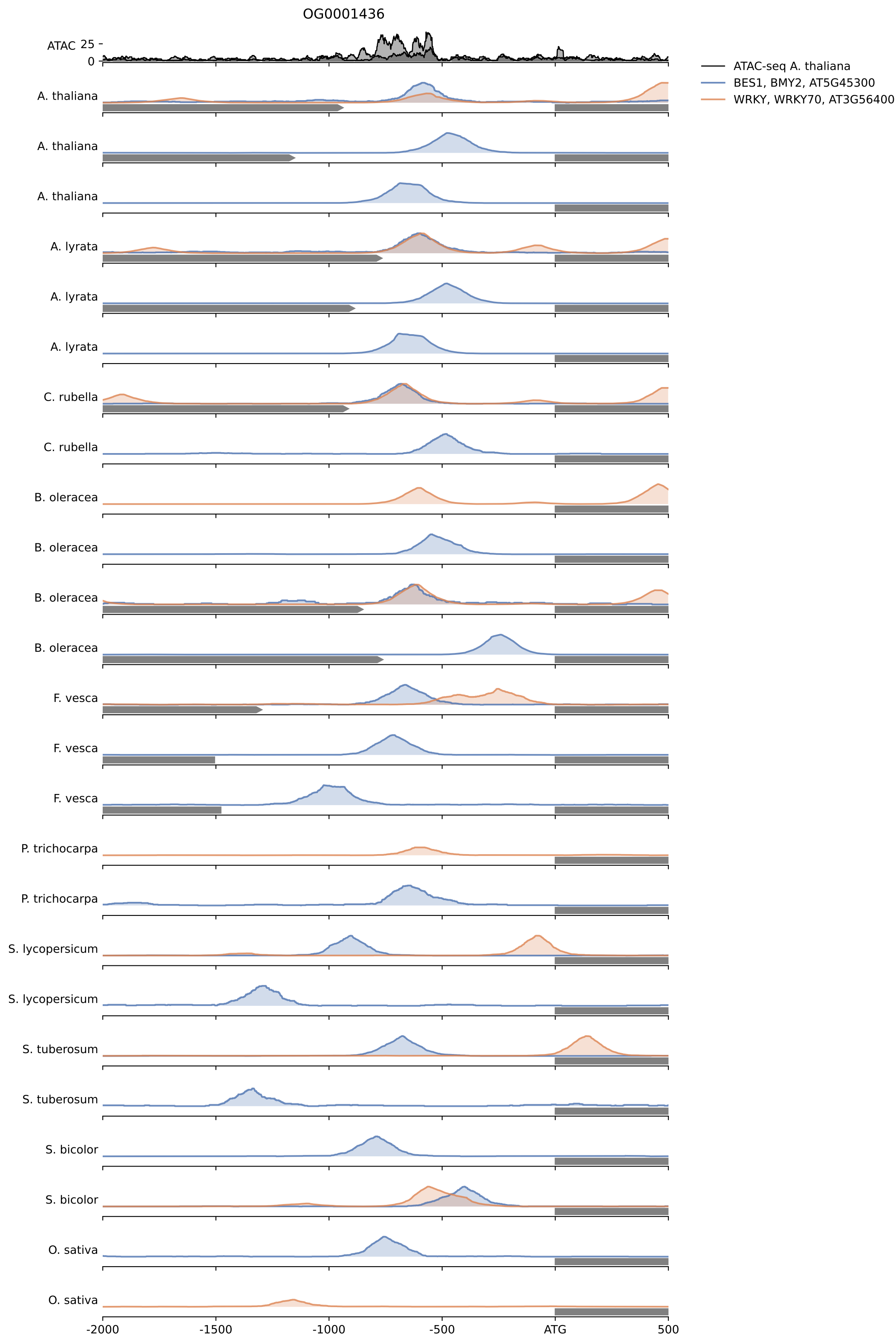


A. thaliana target: AT4G32480, Phosphorus (P) stress-inducible DUF506 gene family member

A. thaliana target: AT2G20670, Phosphorus (P) stress-inducible DUF506 gene family member



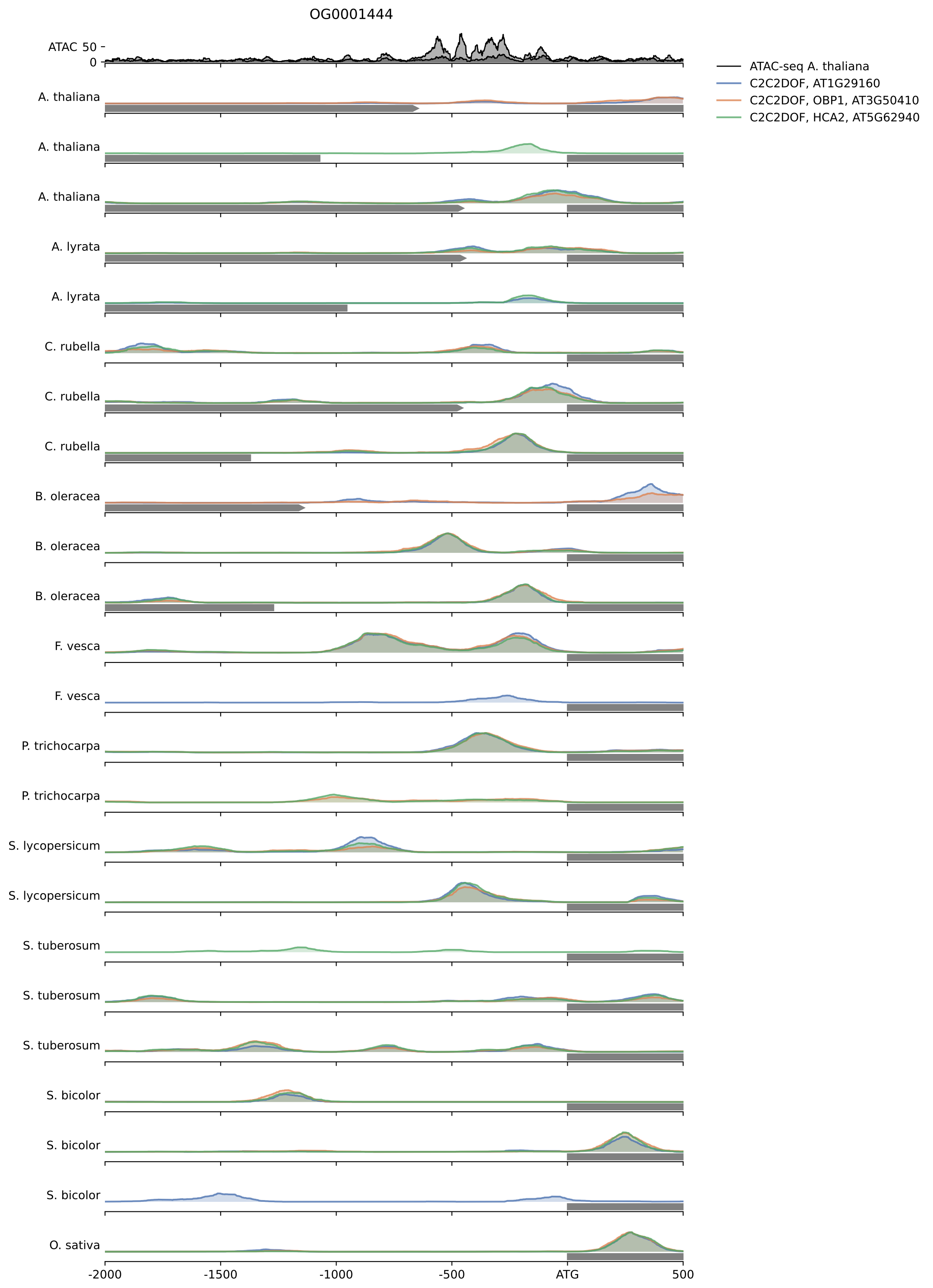
A. thaliana target: AT3G02360, 6-phosphogluconate dehydrogenase family protein;(source:Araport11)



A. thaliana target: AT5G67410, transcriptional regulator of RNA polII, SAGA, subunit;(source:Araport11)

A. thaliana target: AT4G33890, Component of SAGA complex, SPT module subunit, interacts with HAG1.

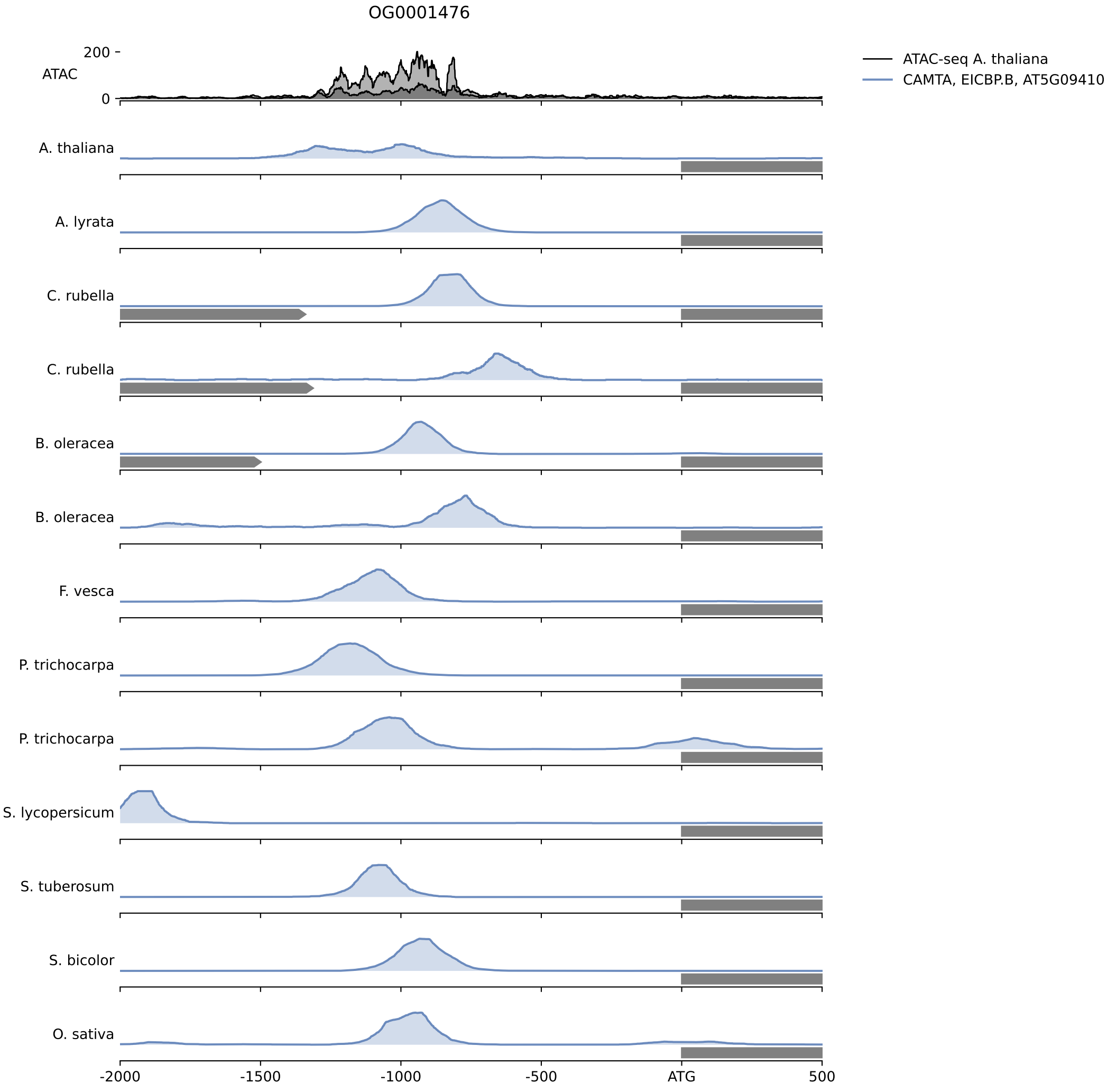
A. thaliana target: AT2G14850, SPT module subunit, interacts with HAG1.



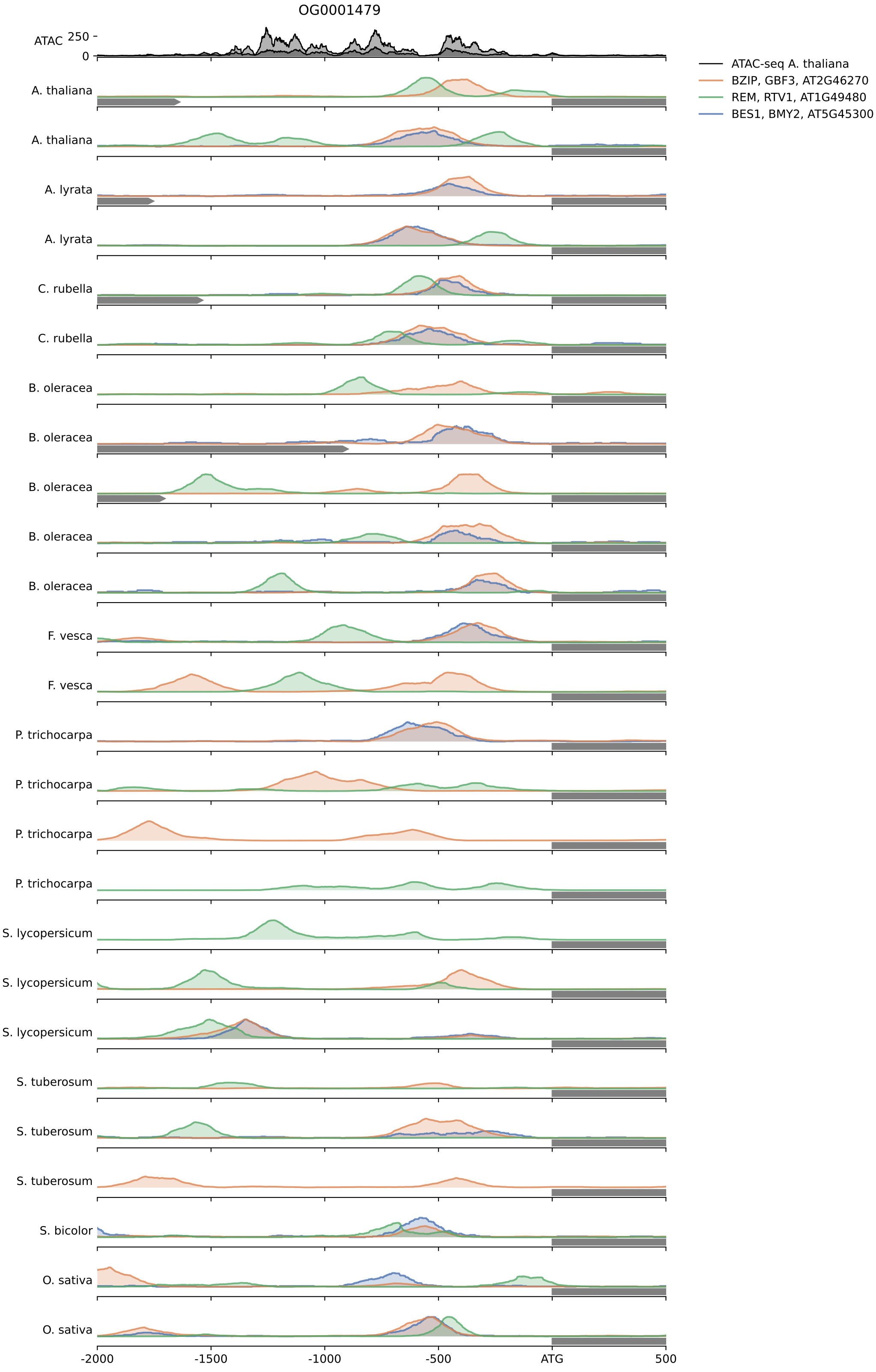
A. thaliana target: AT5G45160, RL2, Root hair defective 3 GTP-binding protein (RHD3);(source:Araport11)

A. thaliana target: AT3G13870, RHD3, required for regulated cell expansion and normal root hair development. Encodes an evolutionarily conserved protein with putative GTP-binding motifs that is implicated in the control of vesicle trafficking between the endoplasmic reticulum and the Golgi compartments. Degraded by LNP1 and 2 to maintain a tubular ER network.

A. thaliana target: AT1G72960, Root hair defective 3 GTP-binding protein (RHD3);(source:Araport11)

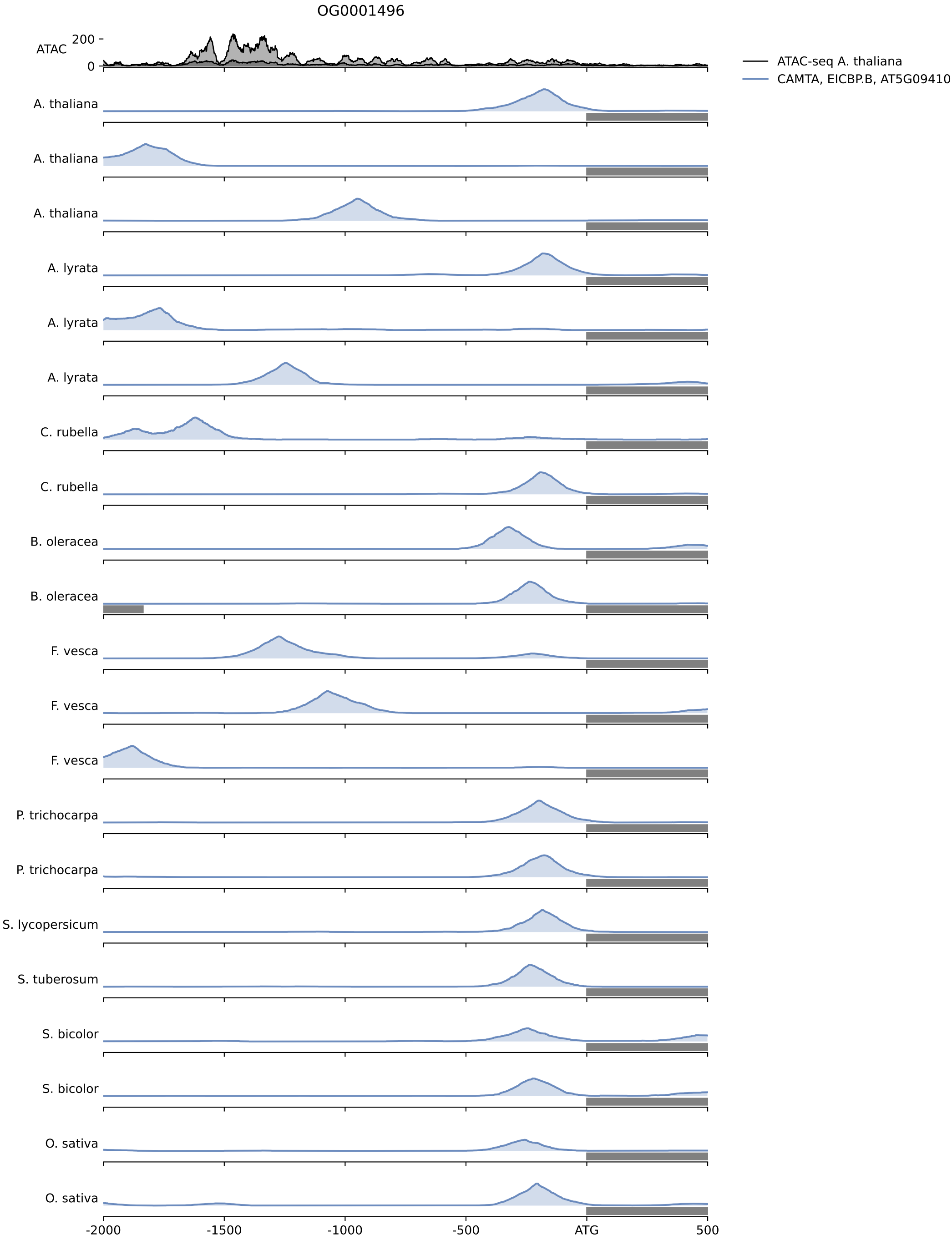


A. thaliana target: AT3G27260, GTE8, Kinase like protein with similarity to yeast BDF1 and human RING3 protein, which have two bromodomains GTE8 has a single bromodomain



A. thaliana target: AT1G13740, AFP2, Encodes a member of a small plant-specific gene family whose members interact with ABI5 and appear to be involved in mediating stress responses. AFP2 mutants affect a number of ABA mediated processes such as germination and response to osmotic and sugar stress. AFP2 nuclear localization is stress dependent.

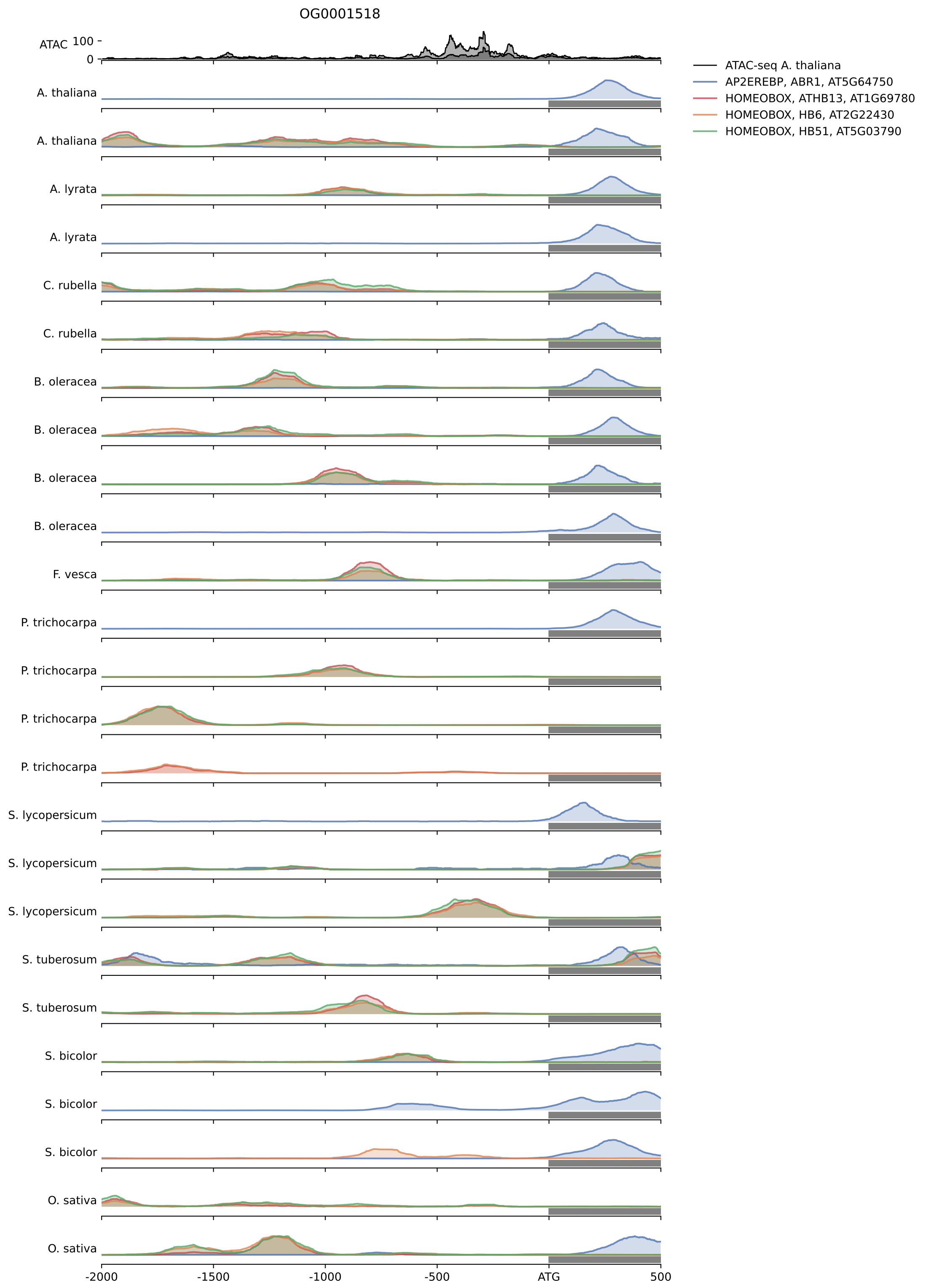
A. thaliana target: AT3G29575, AFP3, ABI five binding protein 3;(source:Araport11)



A. thaliana target: AT1G02810, probable pseudogene

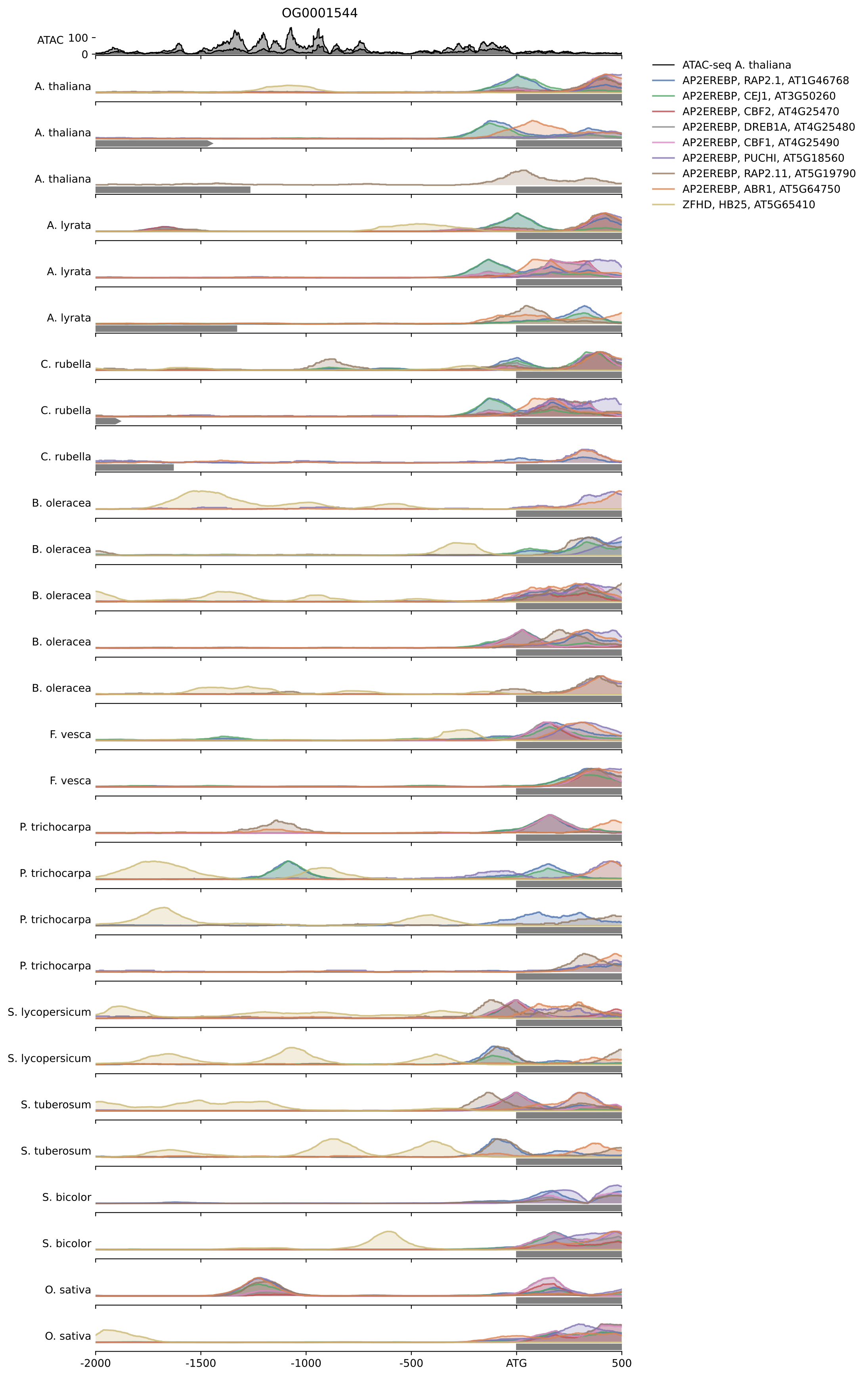
A. thaliana target: AT2G47550, Pectin methylesterase inhibitor; INVI-PMEI protein isoform which clusters with a PME.

A. thaliana target: AT4G02330, ATPMEPCRB, Encodes a pectin methylesterase that is sensitive to chilling stress and brassinosteroid regulation, response to Botrytis cinerea.



A. thaliana target: AT5G11590, TINY2, 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.

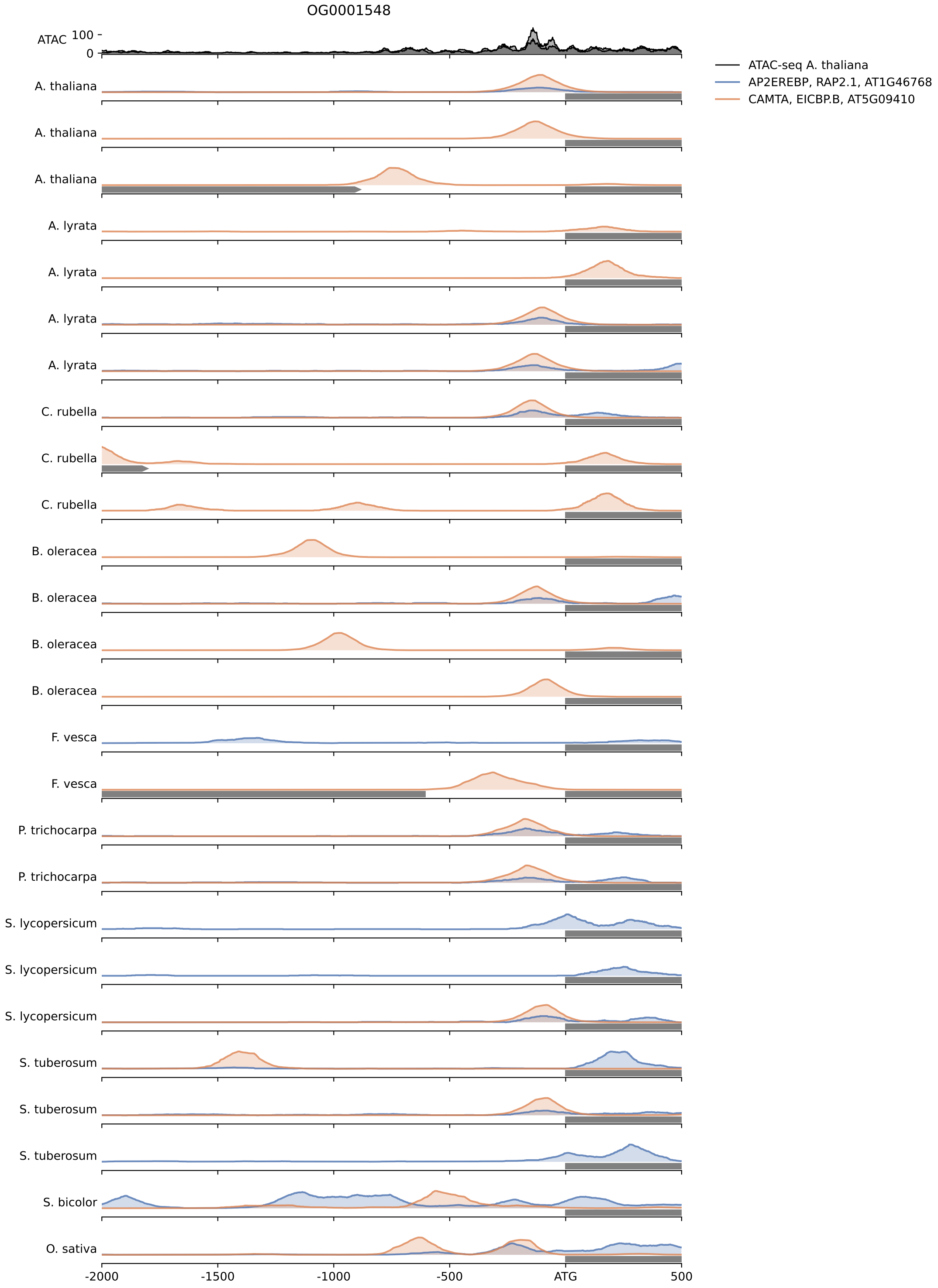
A. thaliana target: AT5G25810, tny, encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family (TINY). The protein contains one AP2 domain. There are 17 members in this subfamily including TINY. Ectopic or overexpression of this gene in a Ds tagged line has reduced cell expansion. The expression of this gene is induced by ethylene and light and appears to stimulate cytokinin biosynthesis.



A. thaliana target: AT1G27210, ARM repeat superfamily protein;(source:Araport11)

A. thaliana target: AT5G62580, ARM repeat superfamily protein;(source:Araport11)

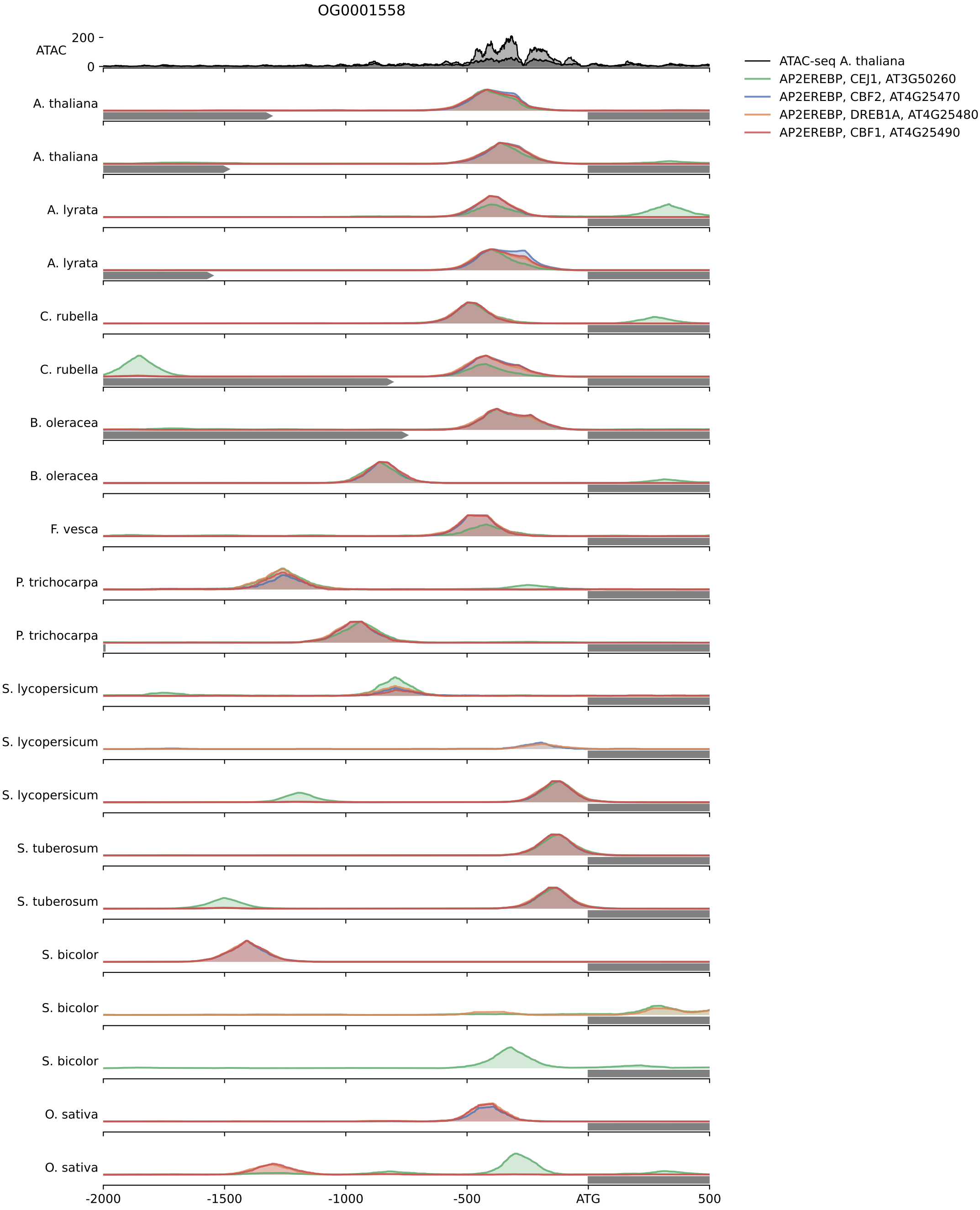
A. thaliana target: AT1G59850, ARM repeat superfamily protein;(source:Araport11)



A. thaliana target: AT1G66400, CML23, Encodes a calmodulin-like protein. Regulates nitric oxide levels and transition to flowering.

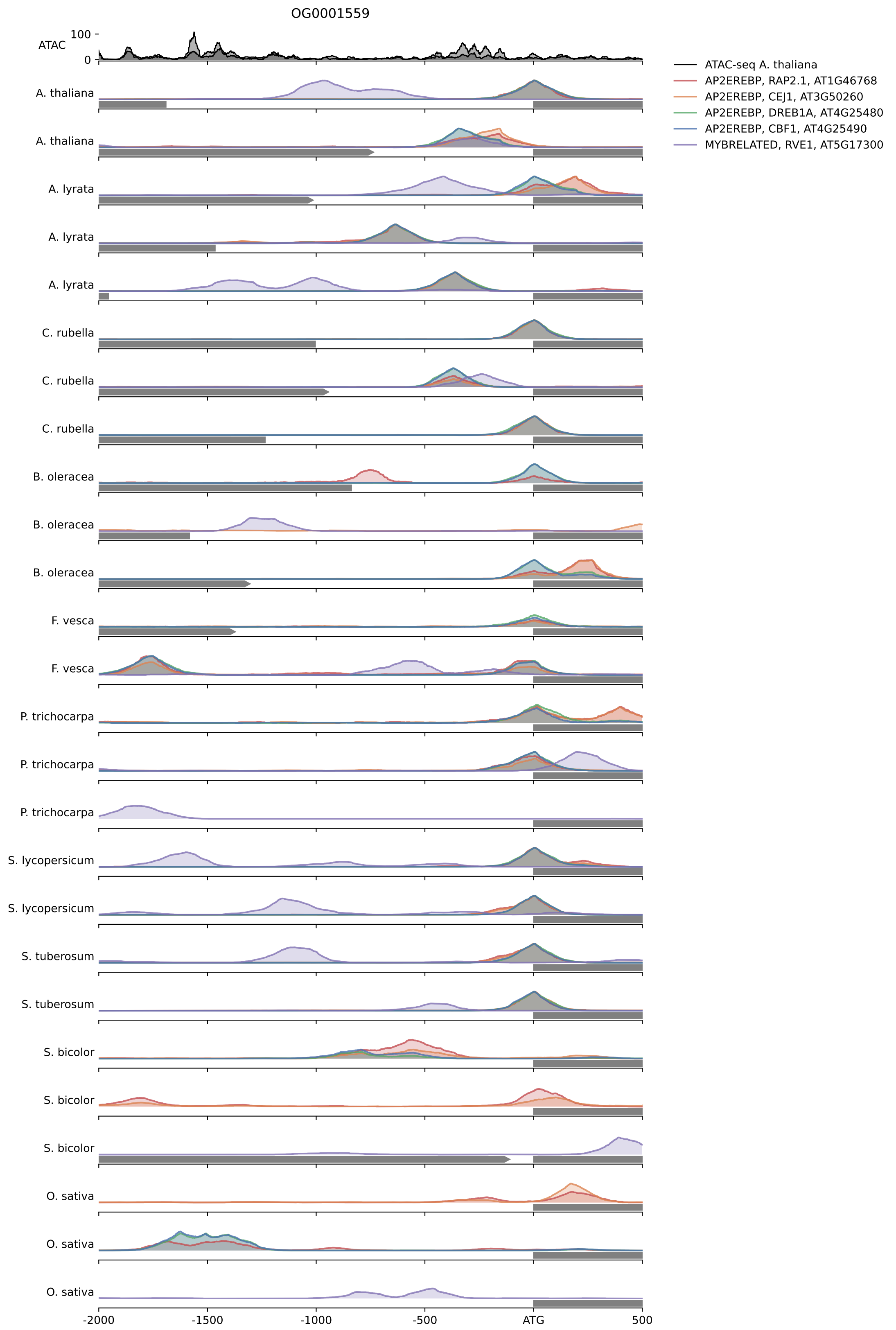
A. thaliana target: AT5G37770, TCH2, Encodes a protein with 40% similarity to calmodulin. Binds Ca(2+) and, as a consequence, undergoes conformational changes. CML24 expression occurs in all major organs, and transcript levels are increased from 2- to 15-fold in plants subjected to touch, darkness, heat, cold, hydrogen peroxide, abscisic acid (ABA), and indole-3-acetic acid. However, CML24 protein accumulation changes were not detectable. The putative CML24 regulatory region confers reporter expression at sites of predicted mechanical stress; in regions undergoing growth; in vascular tissues and various floral organs; and in stomata, trichomes, and hydathodes. CML24-underexpressing transgenics are resistant to ABA inhibition of germination and seedling growth, are defective in long-day induction of flowering, and have enhanced tolerance to CoCl(2), molybdic acid, ZnSO(4), and MgCl(2). Also regulates nitric oxide levels.

A. thaliana target: AT1G18210, Calcium-binding EF-hand family protein;(source:Araport11)



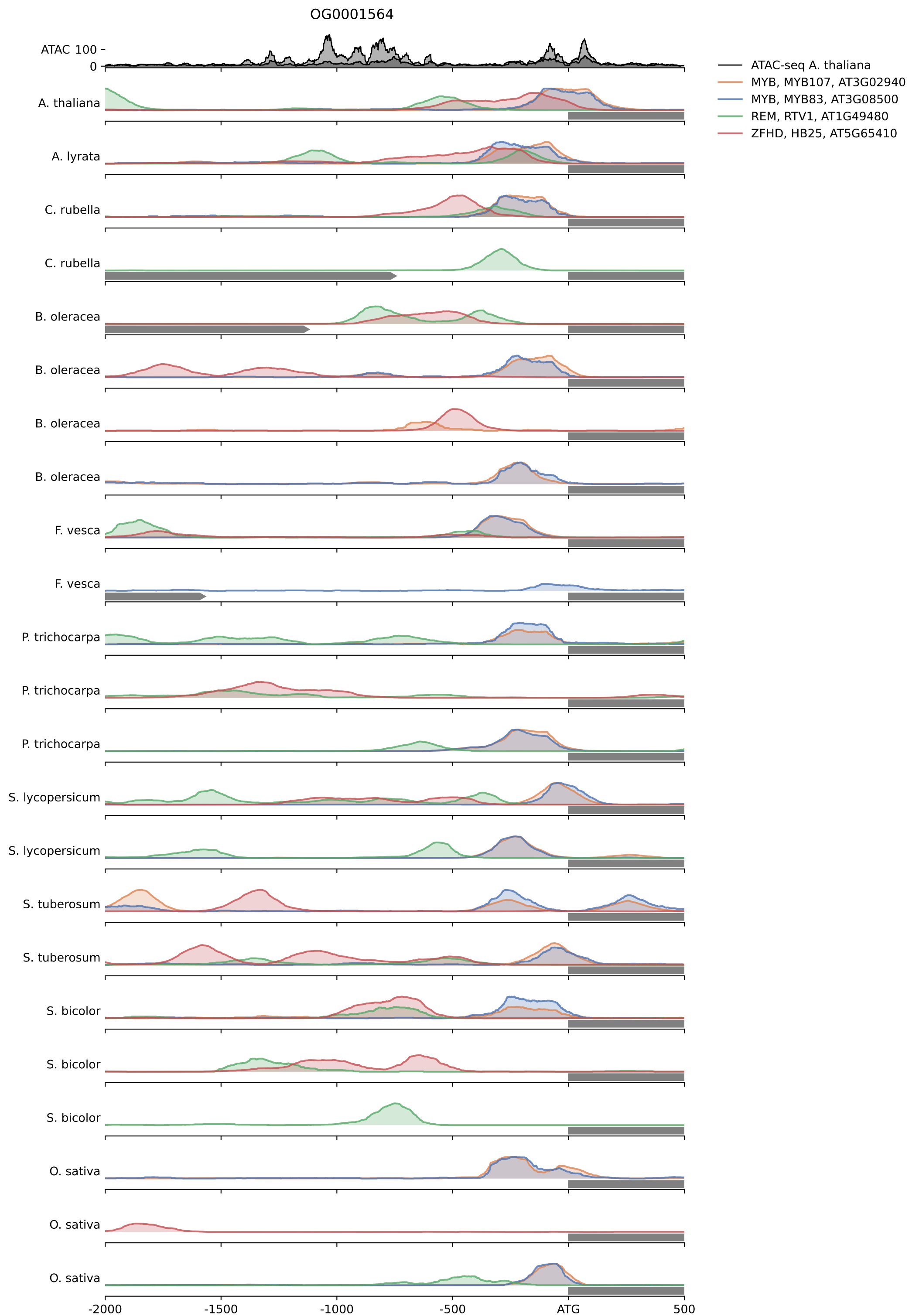
A. thaliana target: AT4G24960, HVA22D, Homologous to a eukaryote specific ABA- and stress-inducible gene first isolated from barley. Groups in one subfamily with ATHVA22E. Along with other members of the ATHVA22 family, it may be involved in regulation of autophagy during development. The mRNA is cell-to-cell mobile.

A. thaliana target: AT5G50720, HVA22E, Encodes one of five HVA22 homologs in Arabidopsis. HVA22 is an ABA- and stress-inducible gene first isolated from barley. Members of this gene family have only been found in eukaryotes. AtHVA22e mRNA is upregulated to varying degrees in response to cold stress, salt stress, ABA treatment or dehydration.

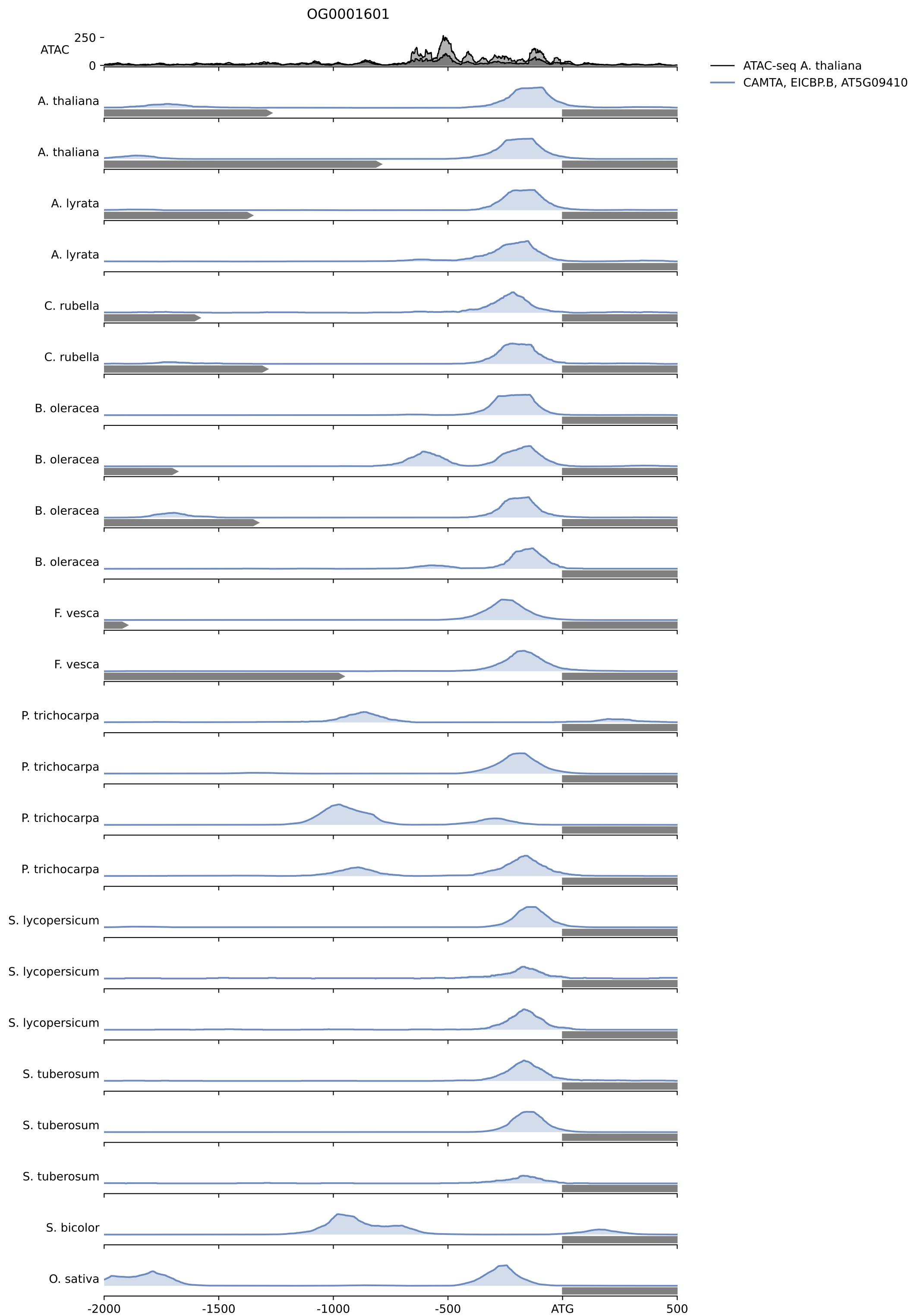


A. thaliana target: AT5G46870, ACD11 binding partner, negatively regulates ROS-mediated defense response.

A. thaliana target: AT1G67950, ACD11 binding partner, negatively regulates ROS-mediated defense response.

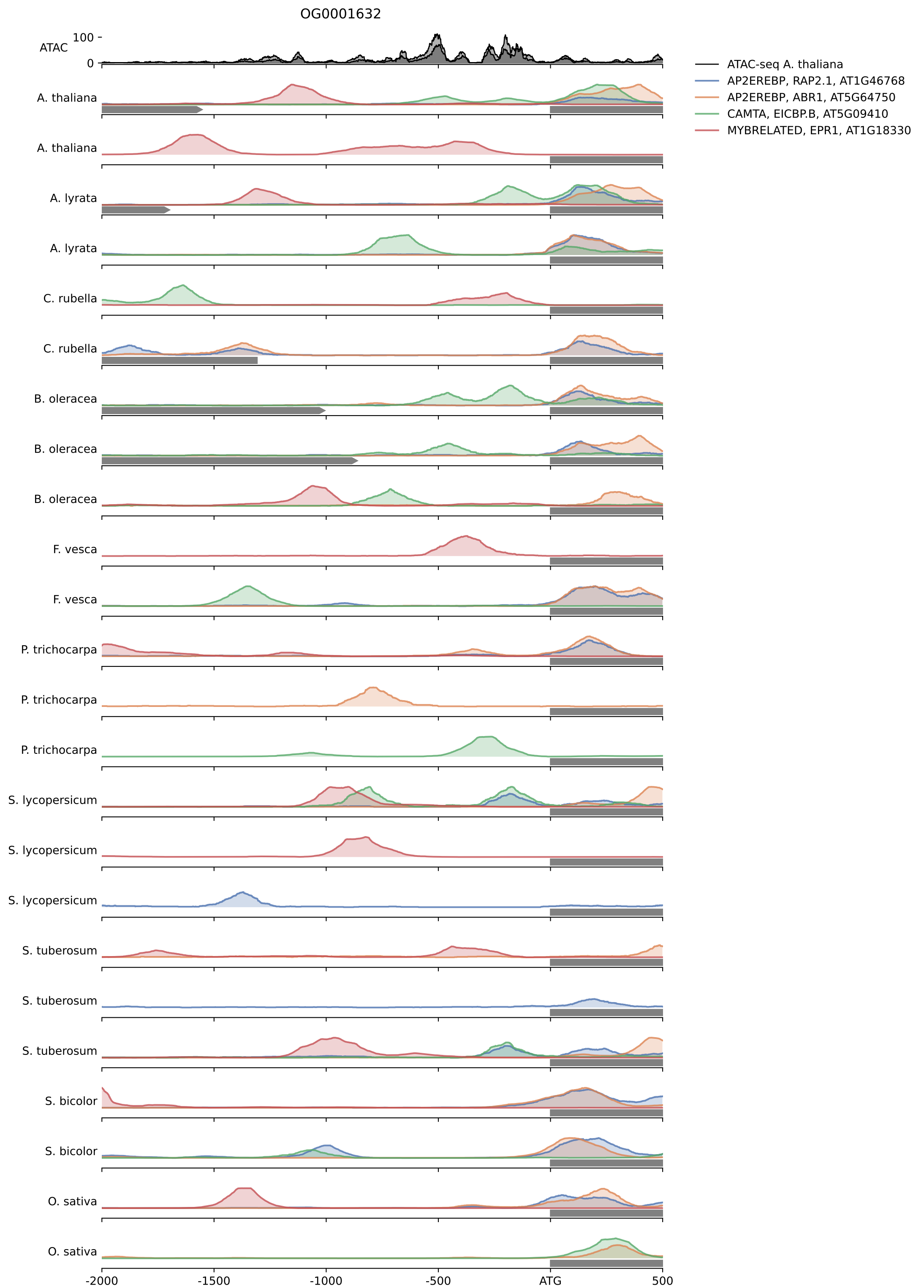


A. thaliana target: AT4G30210, ATR2, Encodes NADPH-cytochrome P450 reductase that catalyzes the first oxidative step of the phenylpropanoid general pathway.The mRNA is cell-to-cell mobile.



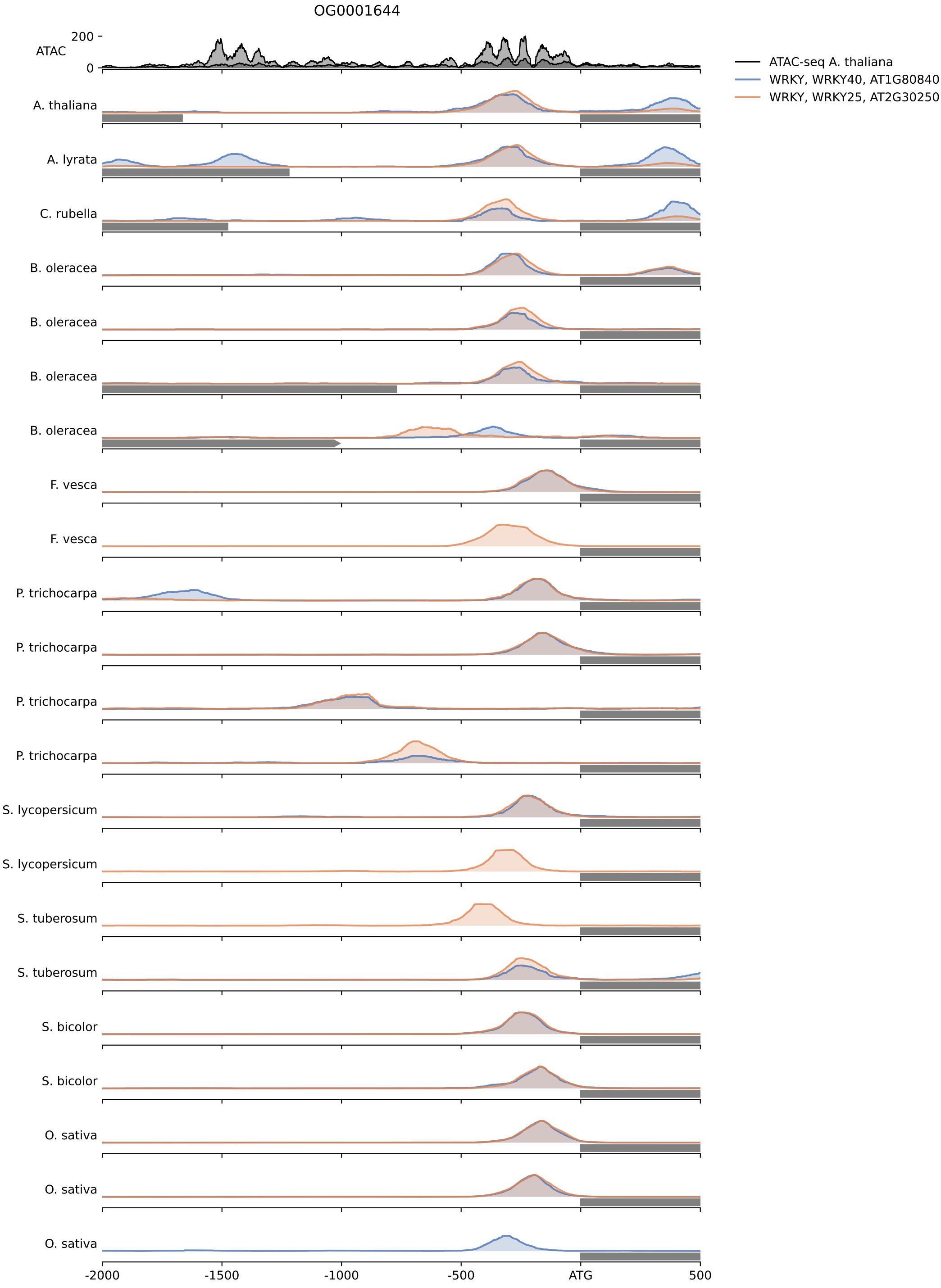
A. thaliana target: AT1G15010, mediator of RNA polymerase II transcription subunit;(source:Araport11)

A. thaliana target: AT2G01300, mediator of RNA polymerase II transcription subunit;(source:Araport11)

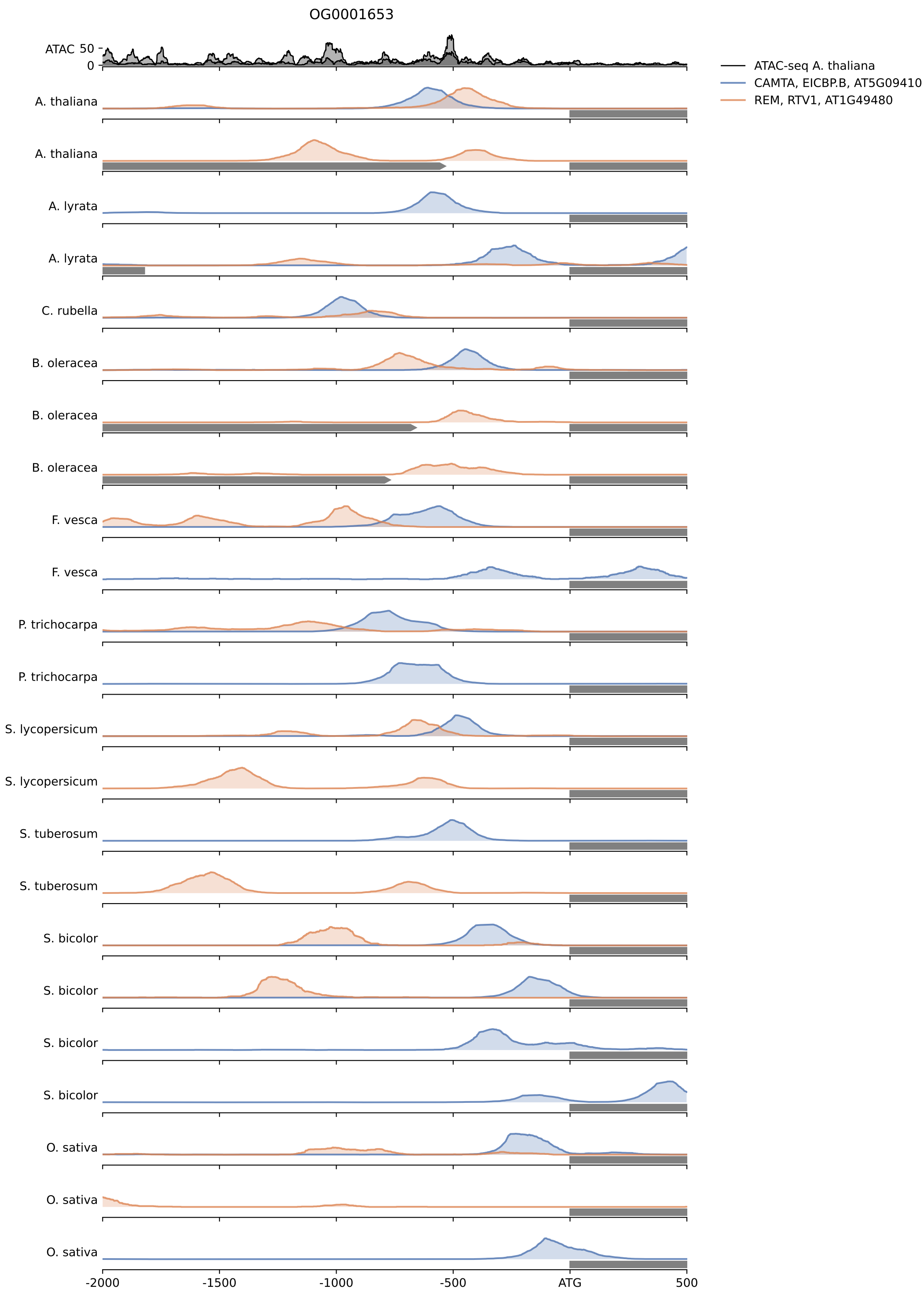


A. thaliana target: AT2G45750, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)

A. thaliana target: AT4G00750, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;(source:Araport11)

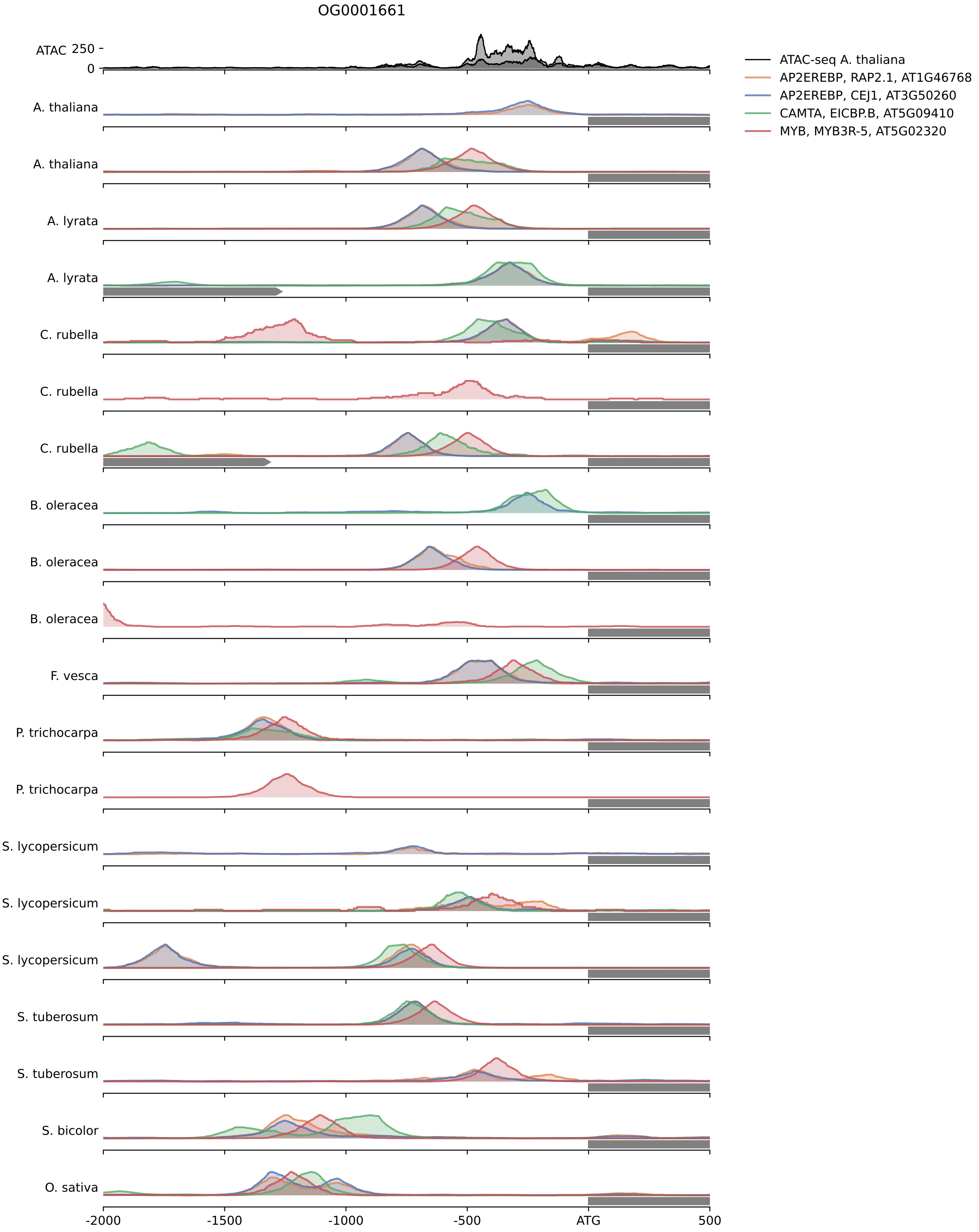


A. thaliana target: AT2G38470, WRKY33, Member of the plant WRKY transcription factor family. Regulates the antagonistic relationship between defense pathways mediating responses to P. syringae and necrotrophic fungal pathogens. Located in nucleus. Involved in response to various abiotic stresses - especially salt stress. Regulates cytochrome P450 gene CYP94B1 to control apoplastic barrier formation in roots to confer salt tolerance.



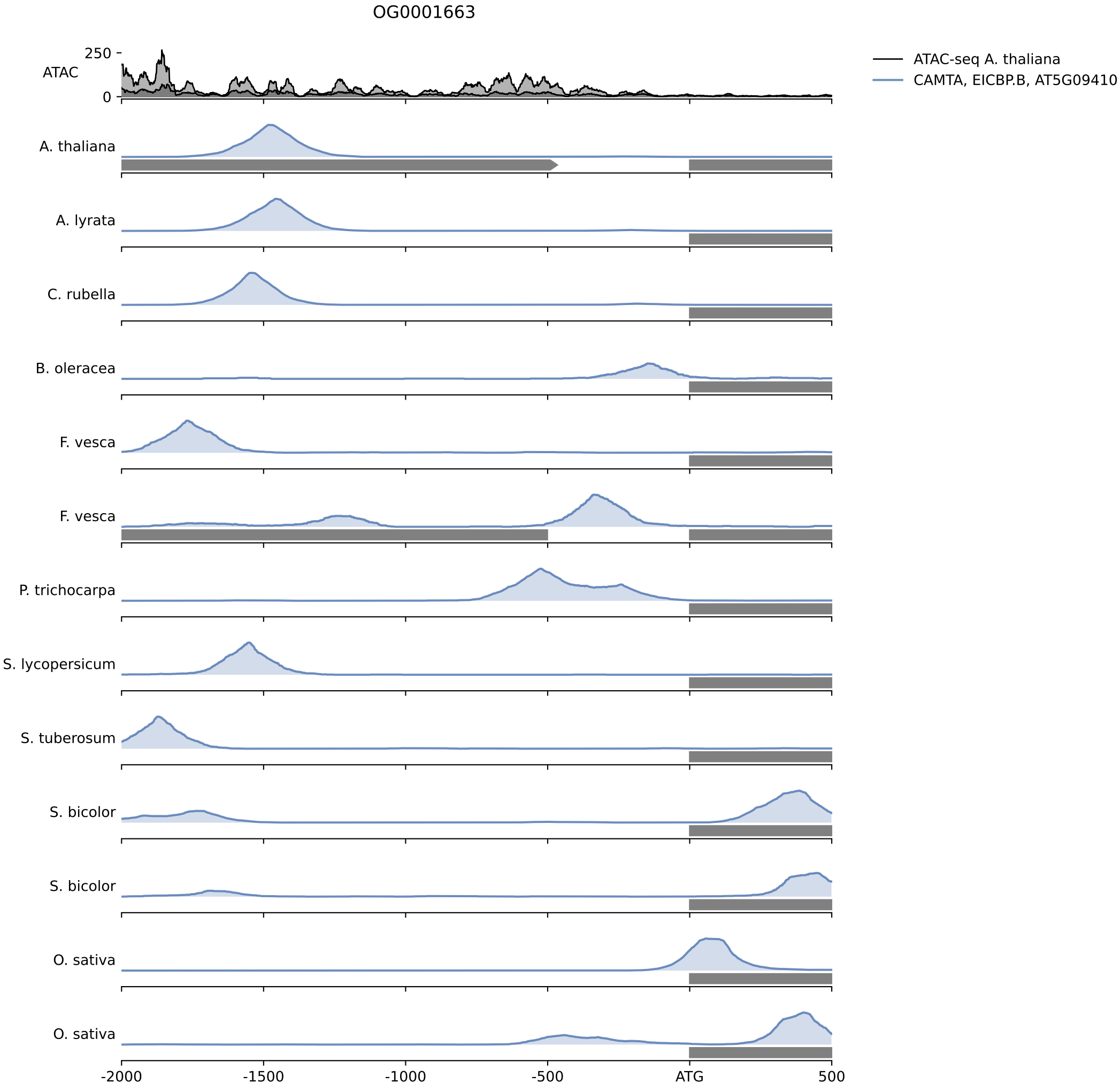
A. thaliana target: AT4G38900, Basic-leucine zipper (bZIP) transcription factor family protein;(source:Araport11)

A. thaliana target: AT2G21230, bZIP30 is a transcriptional activator that is involved in regulation of growth and development of reproductive organs. It interacts with a number of developmental regulators including WUS, HEC1, KNAT1/BP, KNAT2, JAB, BEL1, and NGA1.

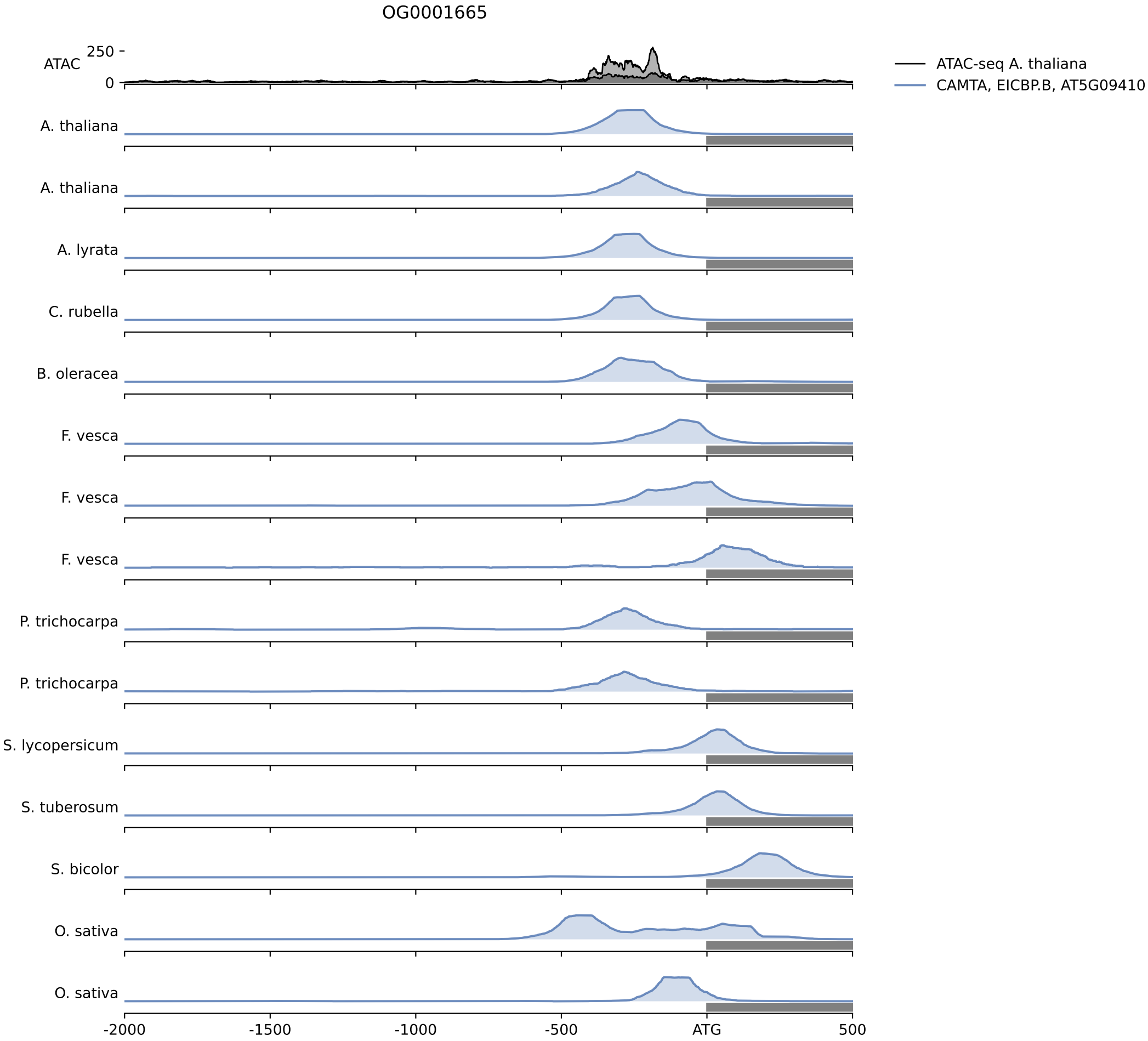


A. thaliana target: AT4G05010, FBS3, F-box family protein; mutant is hypersensitive to salt stress.

A. thaliana target: AT1G61340, FBS1, Encodes a F-box protein induced by various biotic or abiotic stress.

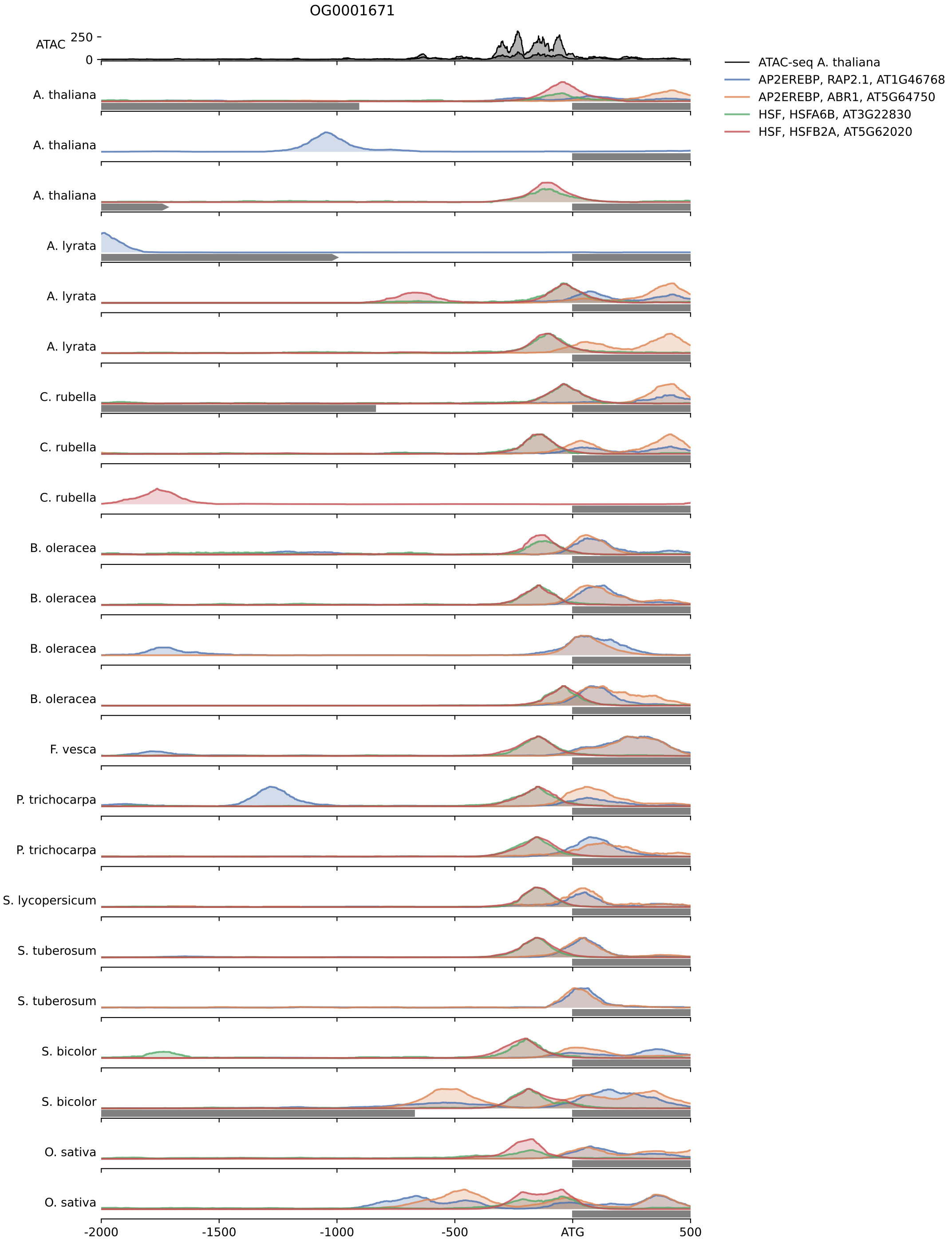


A. thaliana target: AT5G17850, CCX2 is a putative cation/Ca2+ exchange protein. It is located in the endoplasmic reticulum. It plays a role in salt induced calcium signaling. Loss of function results in decreased cytosolic and increased ER Ca2+ concentrations.



A. thaliana target: AT4G08500, MEKK1, Encodes a member of the A1 subgroup of the MEKK (MAPK/ERK kinase kinase) family. MEKK is another name for Mitogen-Activated Protein Kinase Kinase Kinase (MAPKKK or MAP3K). This subgroup has four members: At4g08500 (MEKK1, also known as ARAKIN, MAP3Kb1, MAPKKK8), At4g08480 (MEKK2, also known as MAP3Kb4, MAPKKK9), At4g08470 (MEKK3, also known as MAP3Kb3, MAPKKK10) and At4g12020 (MEKK4, also known as MAP3Kb5, MAPKKK11, WRKY19). Nomenclatures for mitogen-activated protein kinases are described in Trends in Plant Science 2002, 7(7):301.
Mediates cold, salt, cadmium and wounding stress signalling. Phosphorylates MEK1.

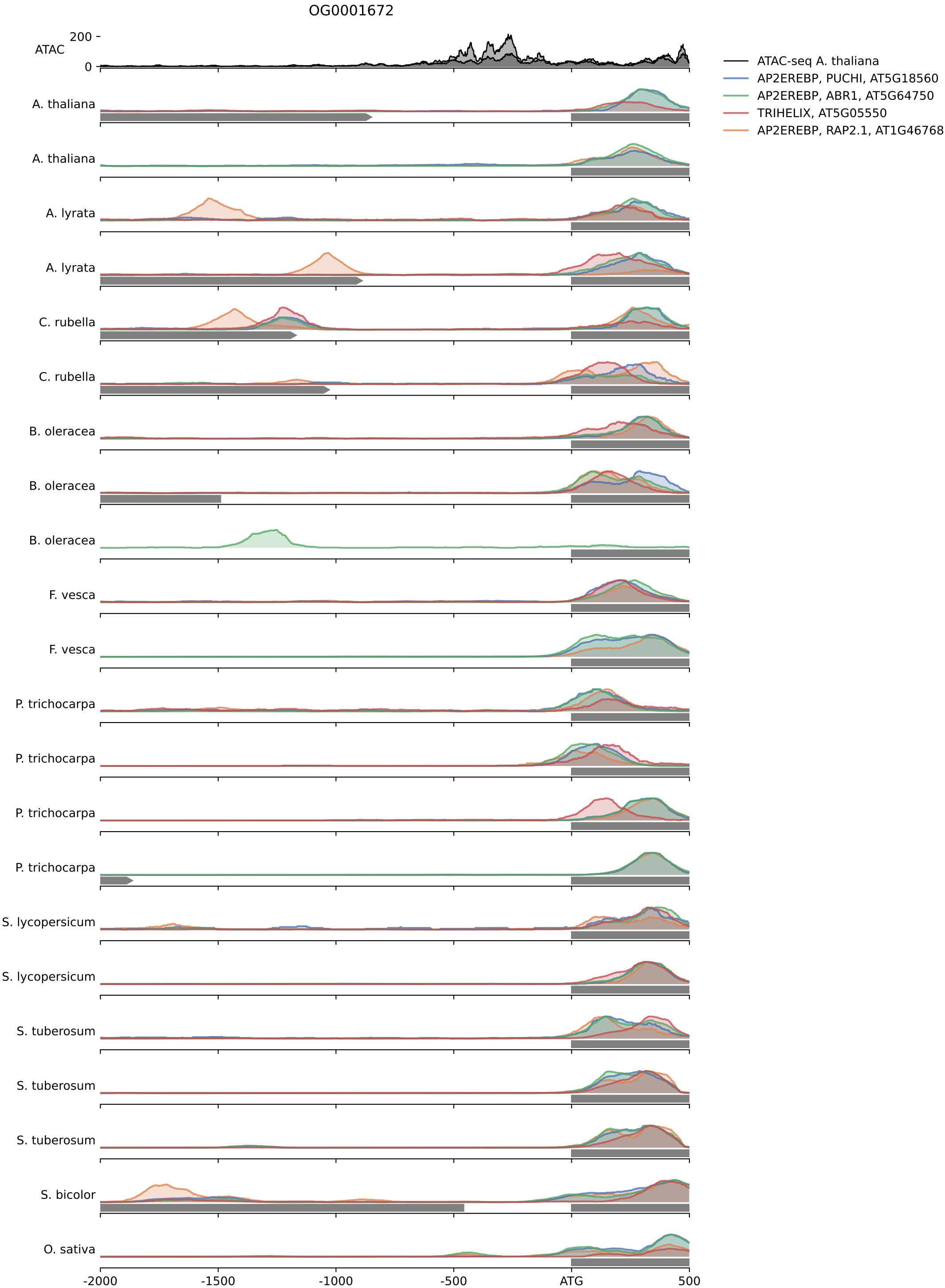
A. thaliana target: AT4G08480, MAPKKK9, Encodes a member of the A1 subgroup of the MEKK (MAPK/ERK kinase kinase) family. MEKK is another name for Mitogen-Activated Protein Kinase Kinase Kinase (MAPKKK or MAP3K). This subgroup has four members: At4g08500 (MEKK1, also known as ARAKIN, MAP3Kb1, MAPKKK8), At4g08480 (MEKK2, also known as MAP3Kb4, MAPKKK9), At4g08470 (MEKK3, also known as MAP3Kb3, MAPKKK10) and At4g12020 (MEKK4, also known as MAP3Kb5, MAPKKK11, WRKY19). Nomenclatures for mitogen-activated protein kinases are described in Trends in Plant Science 2002, 7(7):301.



A. thaliana target: AT1G62740, Hop2, Encodes one of the 36 carboxylate clamp (CC)-tetratricopeptide repeat (TPR) proteins (Prasad 2010, Pubmed ID: 20856808) with potential to interact with Hsp90/Hsp70 as co-chaperones. The mRNA is cell-to-cell mobile.

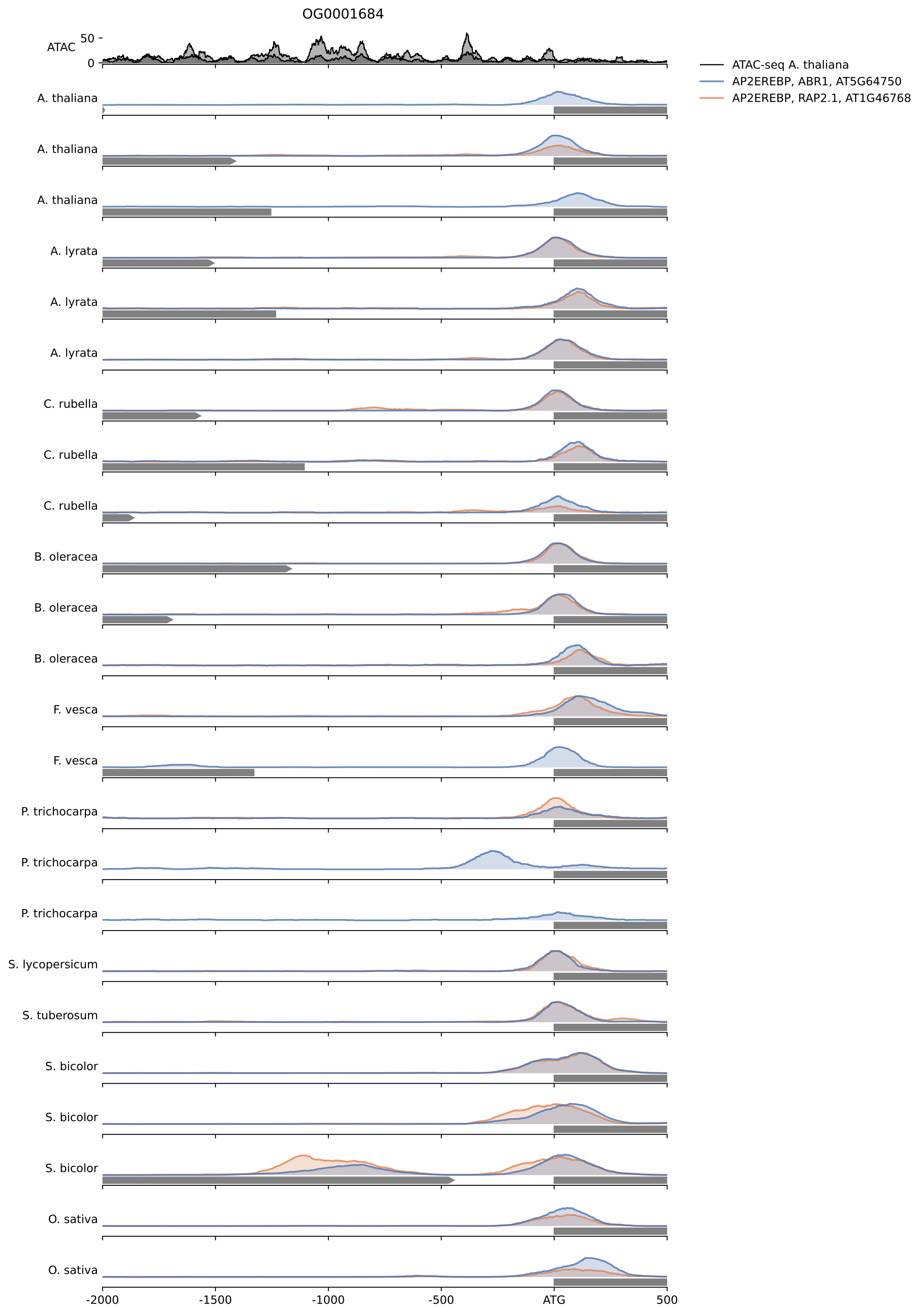
A. thaliana target: AT1G12270, Hop1, Encodes one of the 36 carboxylate clamp (CC)-tetratricopeptide repeat (TPR) proteins (Prasad 2010, Pubmed ID: 20856808) with potential to interact with Hsp90/Hsp70 as co-chaperones.

A. thaliana target: AT4G12400, Hop3, Encodes one of the 36 carboxylate clamp (CC)-tetratricopeptide repeat (TPR) proteins (Prasad 2010, Pubmed ID: 20856808) with potential to interact with Hsp90/Hsp70 as co-chaperones.



A. thaliana target: AT5G16200, 50S ribosomal protein-like protein;(source:Araport11)

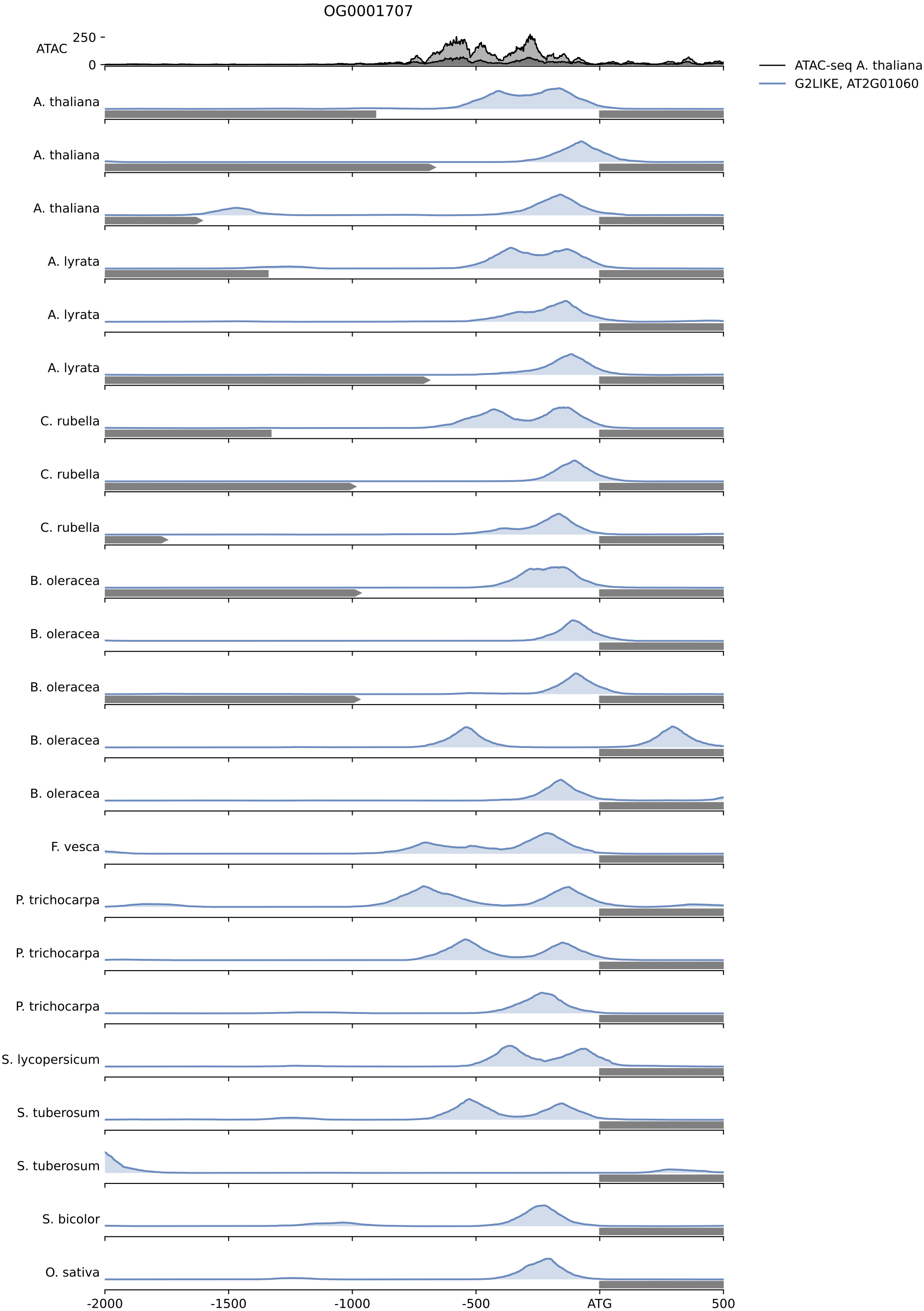
A. thaliana target: AT1G66890, 50S ribosomal-like protein;(source:Araport11)



A. thaliana target: AT1G20550, O-fucosyltransferase family protein;(source:Araport11)

A. thaliana target: AT1G76270, O-fucosyltransferase family protein;(source:Araport11)

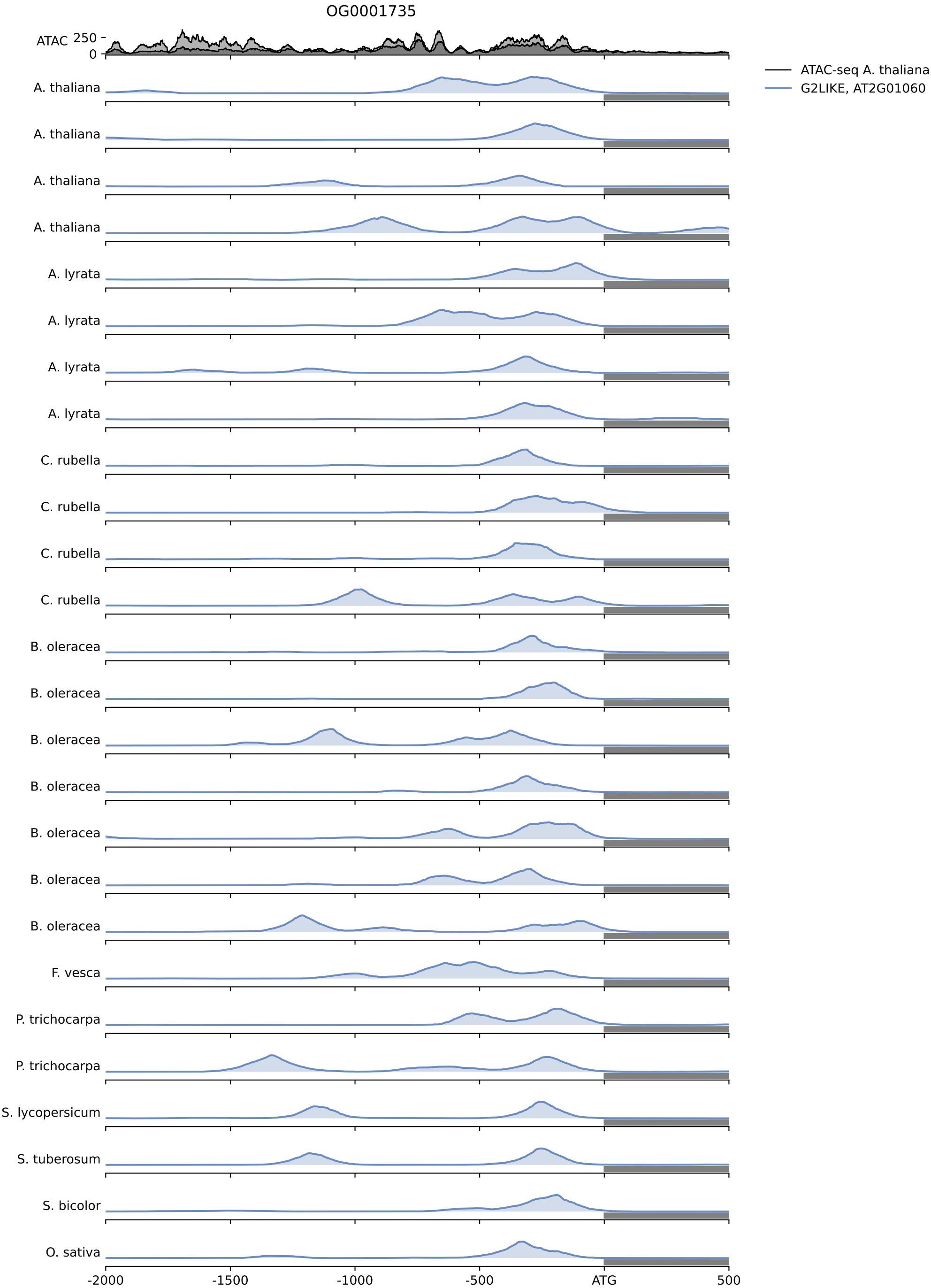
A. thaliana target: AT4G38390, RHS17, root hair specific 17;(source:Araport11)



A. thaliana target: AT3G02040, SRG3, Encodes a member of the glycerophosphodiester phosphodiesterase (GDPD) family. Has glycerophosphodiester phosphodiesterase activity. Functions in maintaining cellular phosphate homeostasis under phosphate starvation. The mRNA is cell-to-cell mobile.

A. thaliana target: AT5G43300, GDPD3, Encodes a member of the glycerophosphodiester phosphodiesterase (GDPD) family.

A. thaliana target: AT5G41080, GDPD2, Encodes a member of the glycerophosphodiester phosphodiesterase (GDPD) family.

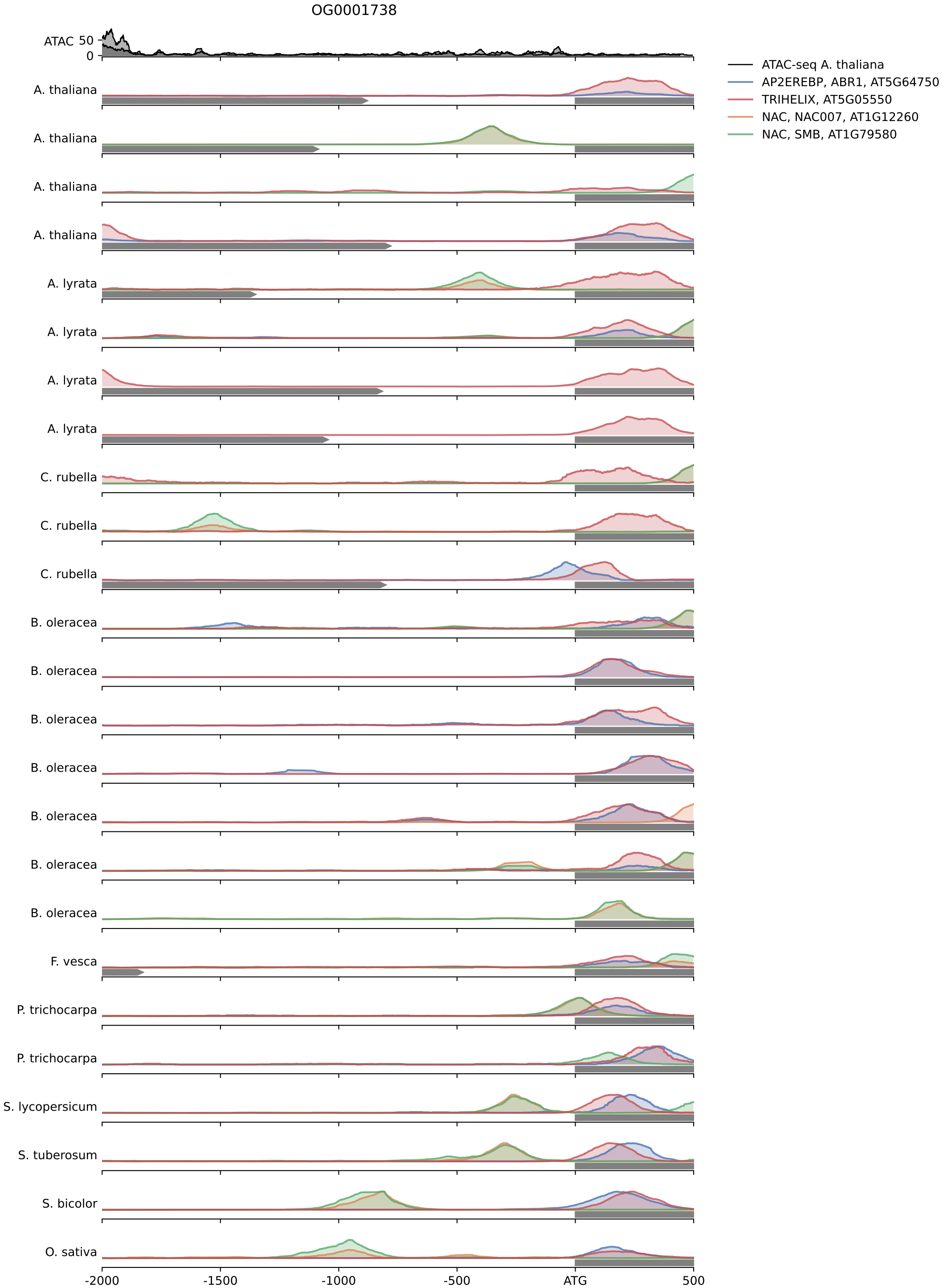


A. thaliana target: AT1G25550, Member of HHO/HRS GARP type transcriptional repressor family. Involved in Pi uptake and Pi starvation signaling. Transcriptional repressors that functions with other NIGT genes as an important hub in the nutrient signaling network associated with the acquisition and use of nitrogen and phosphorus.

A. thaliana target: AT3G25790, Encodes a nuclear localized member of the GARP family of transcription factors. Along with AtNIGT1/HRS1 it is involved in nitrate and phosphate signaling in the root. Transcriptional repressors that functions with other NIGT genes as an important hub in the nutrient signaling network associated with the acquisition and use of nitrogen and phosphorus.

A. thaliana target: AT1G13300, HRS1, Encodes a nuclear localized member of the GARP family of transcription factors. Involved in nitrate/phosphate signaling in roots. It is transcriptionally regulated by nitrate and post transcriptionally by phosphate and functions to integrate these two nutrient signaling pathways in the root. HRS1 and HHO2 are involved in Ni cross regulation of Pi signaling. They function as transcriptional repressors of SPX1, SPX2, and SPX4 as part of a cascade to regulate nitrogen and phosphorus balance.

A. thaliana target: AT1G68670, HHO2 is a HRS1 homolog. Nitrate-inducible expression. Also induced in roots by low Pi and is likely involved in maintaining phosphate homeostasis. It is target of PHR1.Both HHO2 and HRS1 are involved in Ni cross regulation of Pi signaling. They function as transcriptional repressors of SPX1, SPX2, and SPX4 as part of a cascade to regulate nitrogen and phosphorus balance. Transcriptional repressors that functions with other NIGT genes as an important hub in the nutrient signaling network associated with the acquisition and use of nitrogen and phosphorus.

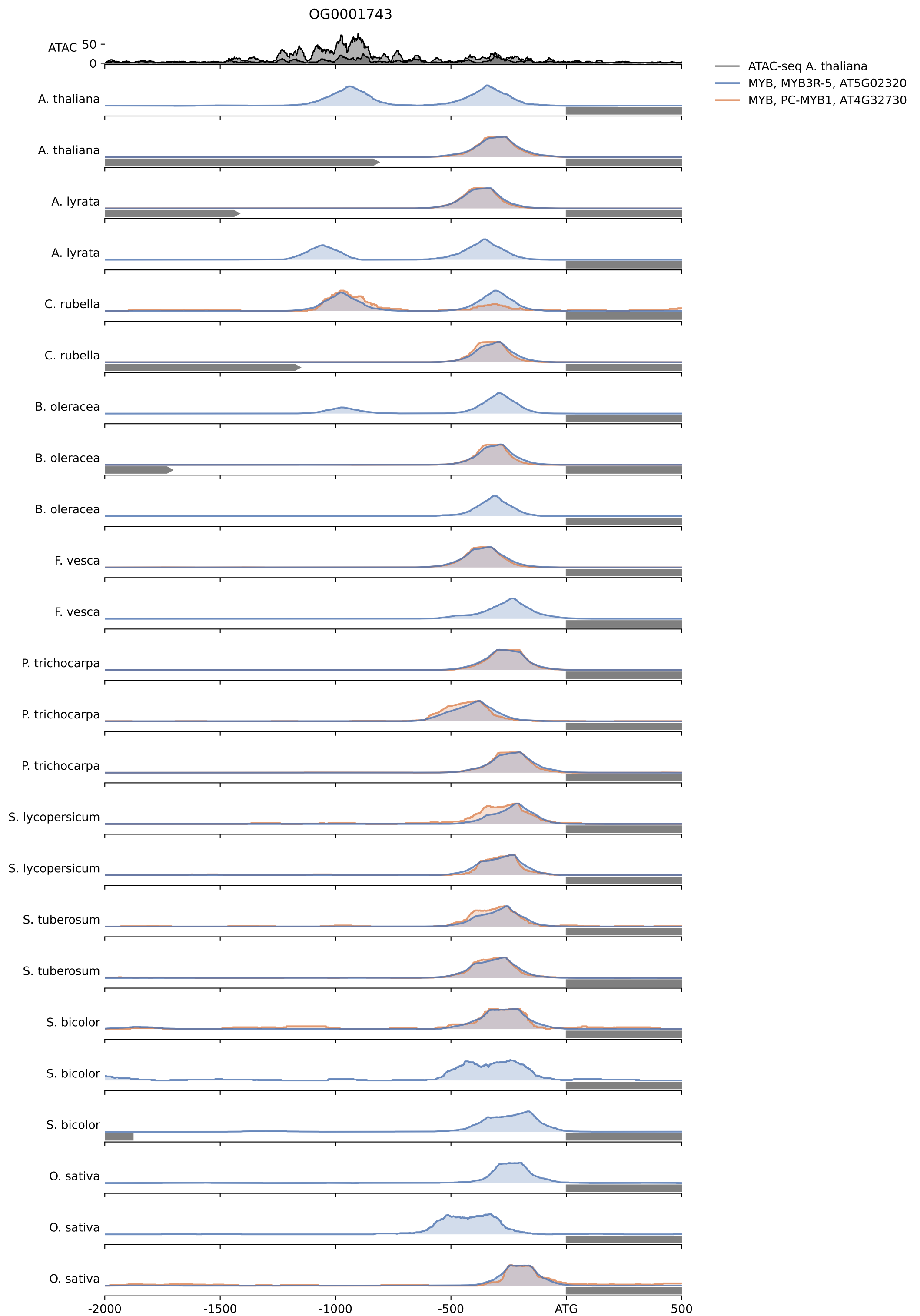


A. thaliana target: AT1G06020, Encodes a member of the fructokinase gene family. Nomenclature according to Riggs 2017 has been adopted for the family by the community (personal communication, Boernke, Callis, Granot, Boernke, and Smeekens).

A. thaliana target: AT2G31390, Encodes a member of the fructokinase gene family. Nomenclature according to Riggs 2017 has been adopted for the family by the community (personal communication, Boernke, Callis, Granot, Boernke, and Smeekens).

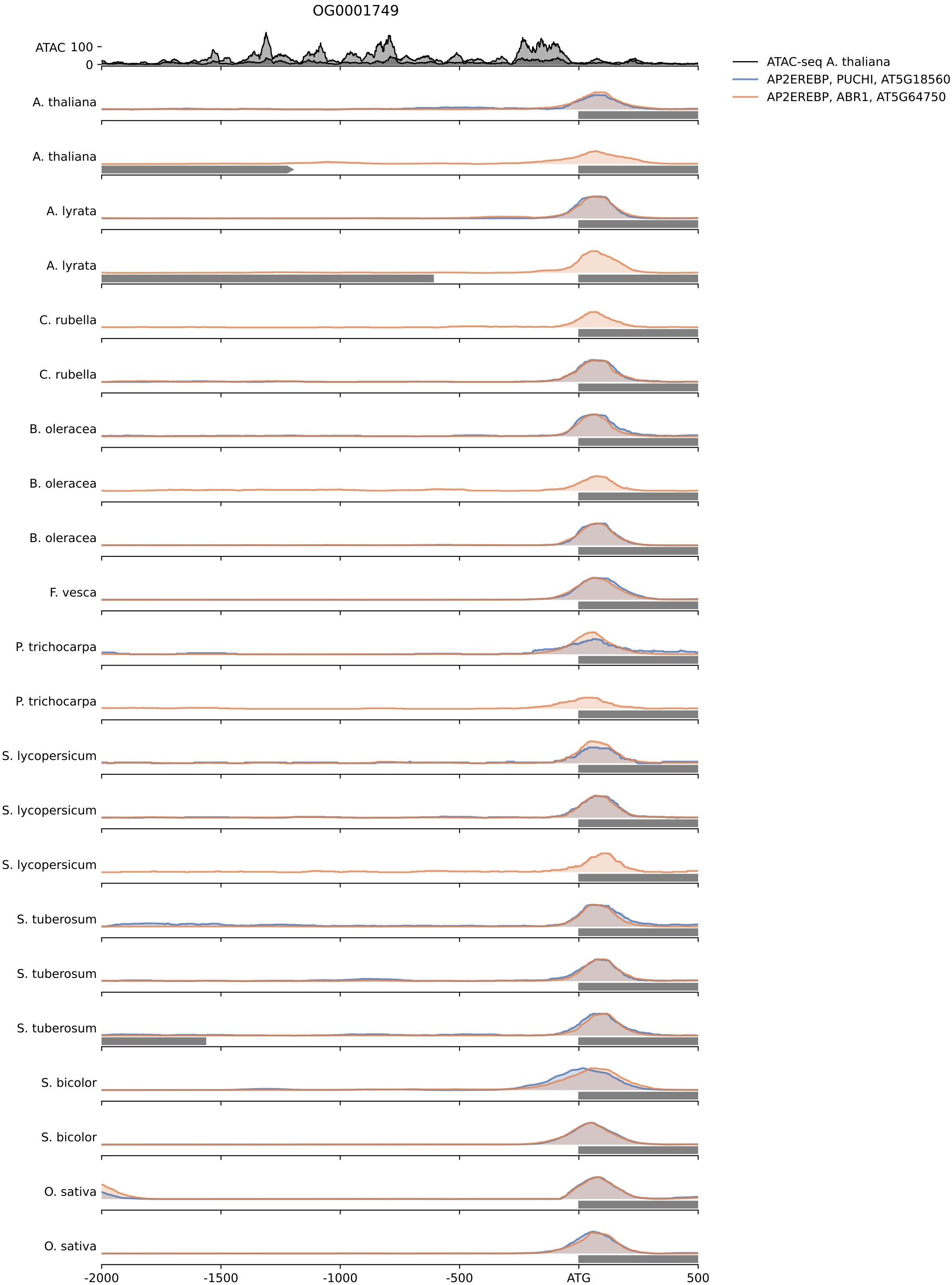
A. thaliana target: AT3G59480, Encodes a member of the fructokinase gene family. Nomenclature according to Riggs 2017 has been adopted for the family by the community (personal communication, Boernke, Callis, Granot, Boernke, and Smeekens).

A. thaliana target: AT1G06030, Encodes a member of the fructokinase gene family. Nomenclature according to Riggs 2017 has been adopted for the family by the community (personal communication, Boernke, Callis, Granot, Boernke, and Smeekens).



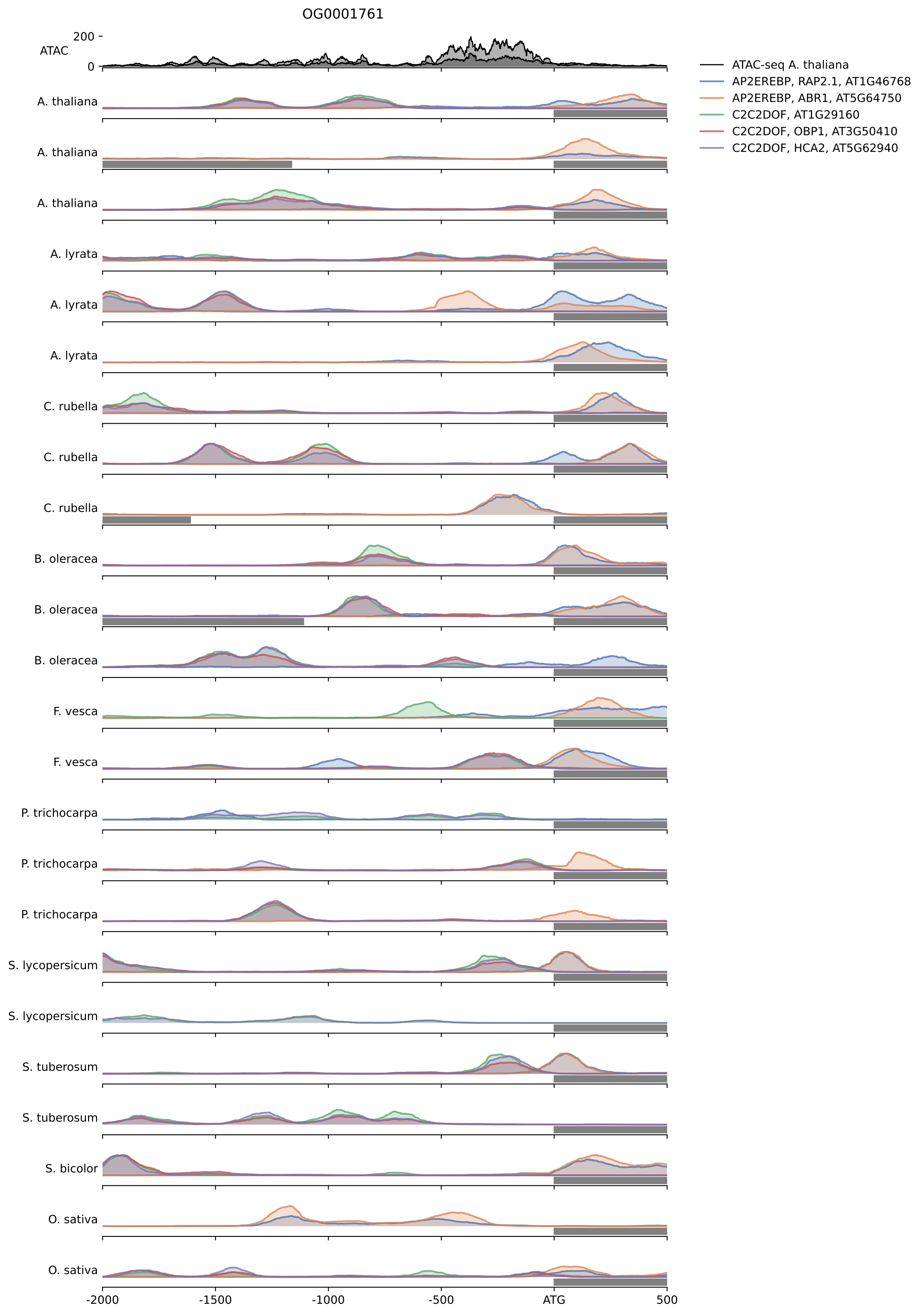
A. thaliana target: AT3G56100, MRLK, Protein kinase expressed in meristematic cells. Phosphorylates AGL24.

A. thaliana target: AT3G51740, IMK2, encodes a leucine-repeat receptor kinase expressed in inflorescence meristem. Locus association was made from performing sequence analysis with IMK3 (MRLK) whose locus association was provided by the authors. The mRNA is cell-to-cell mobile.



A. thaliana target: AT5G40770, PHB3, prohibitin 3

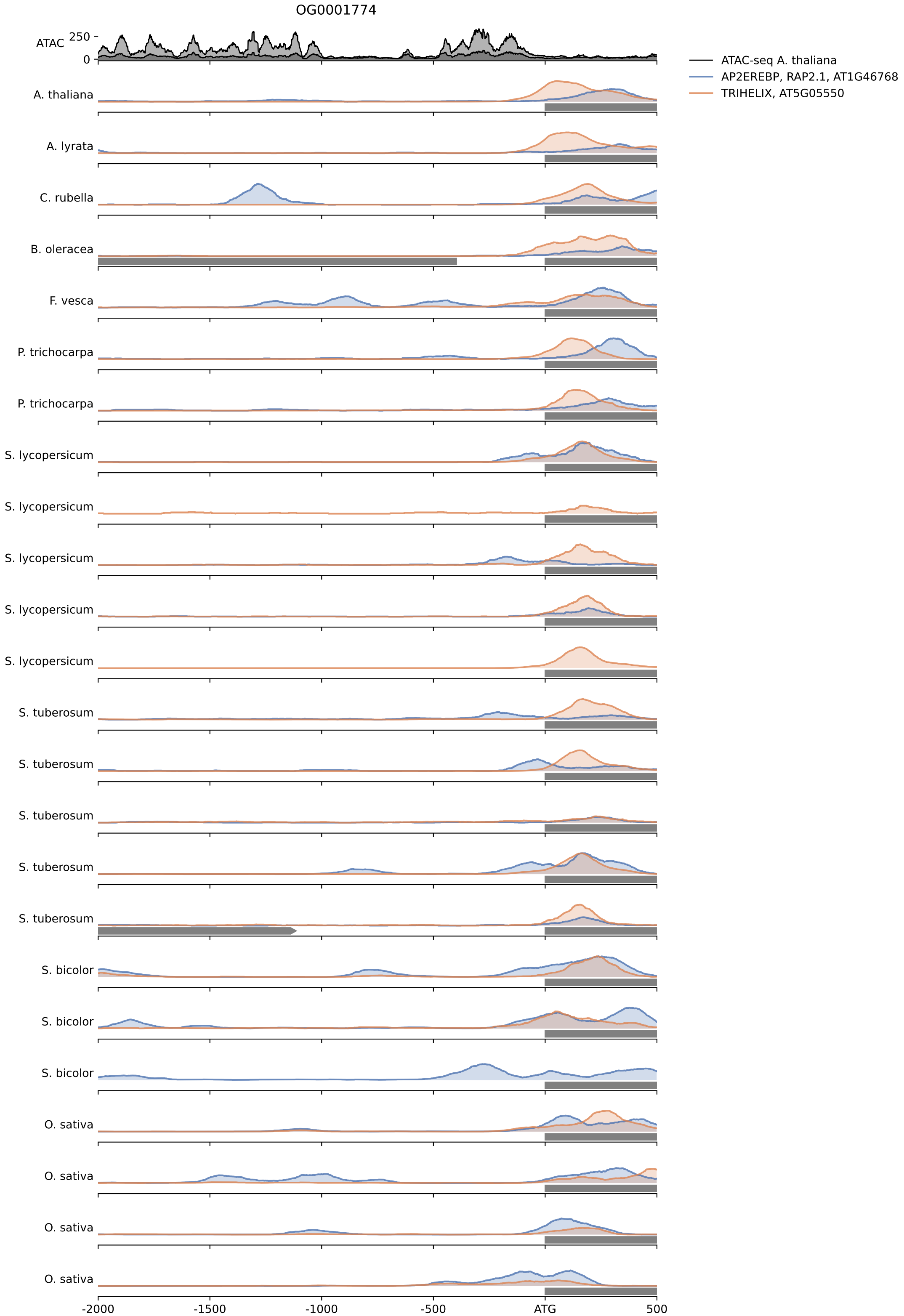
A. thaliana target: AT3G27280, PHB4, Part of protein complexes that are necessary for proficient mitochondrial function or biogenesis, thereby supporting cell division and differentiation in apical tissues



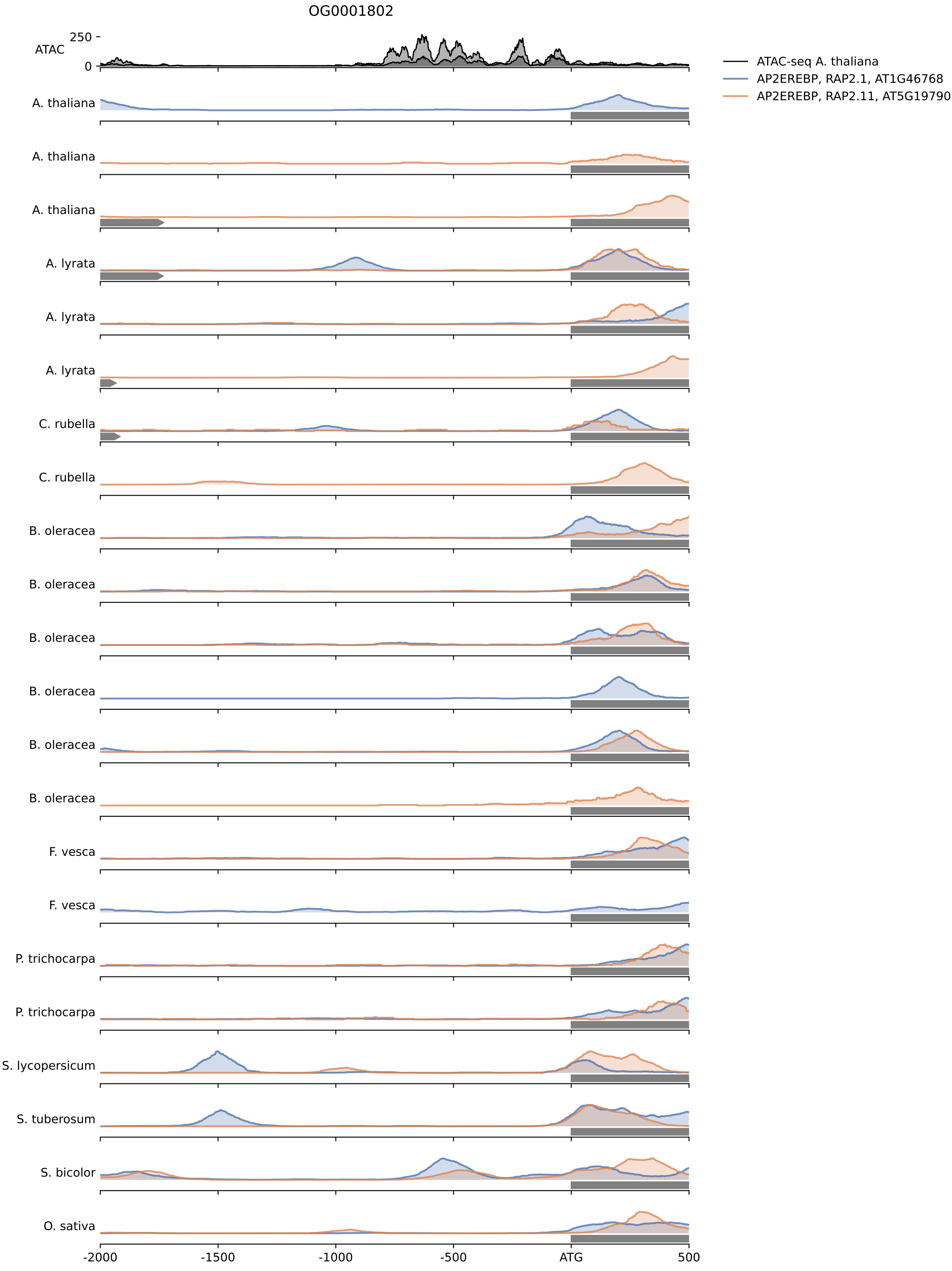
A. thaliana target: AT2G45590, Protein kinase superfamily protein;(source:Araport11)

A. thaliana target: AT4G25390, Protein kinase superfamily protein;(source:Araport11)

A. thaliana target: AT5G51770, Protein kinase superfamily protein;(source:Araport11)



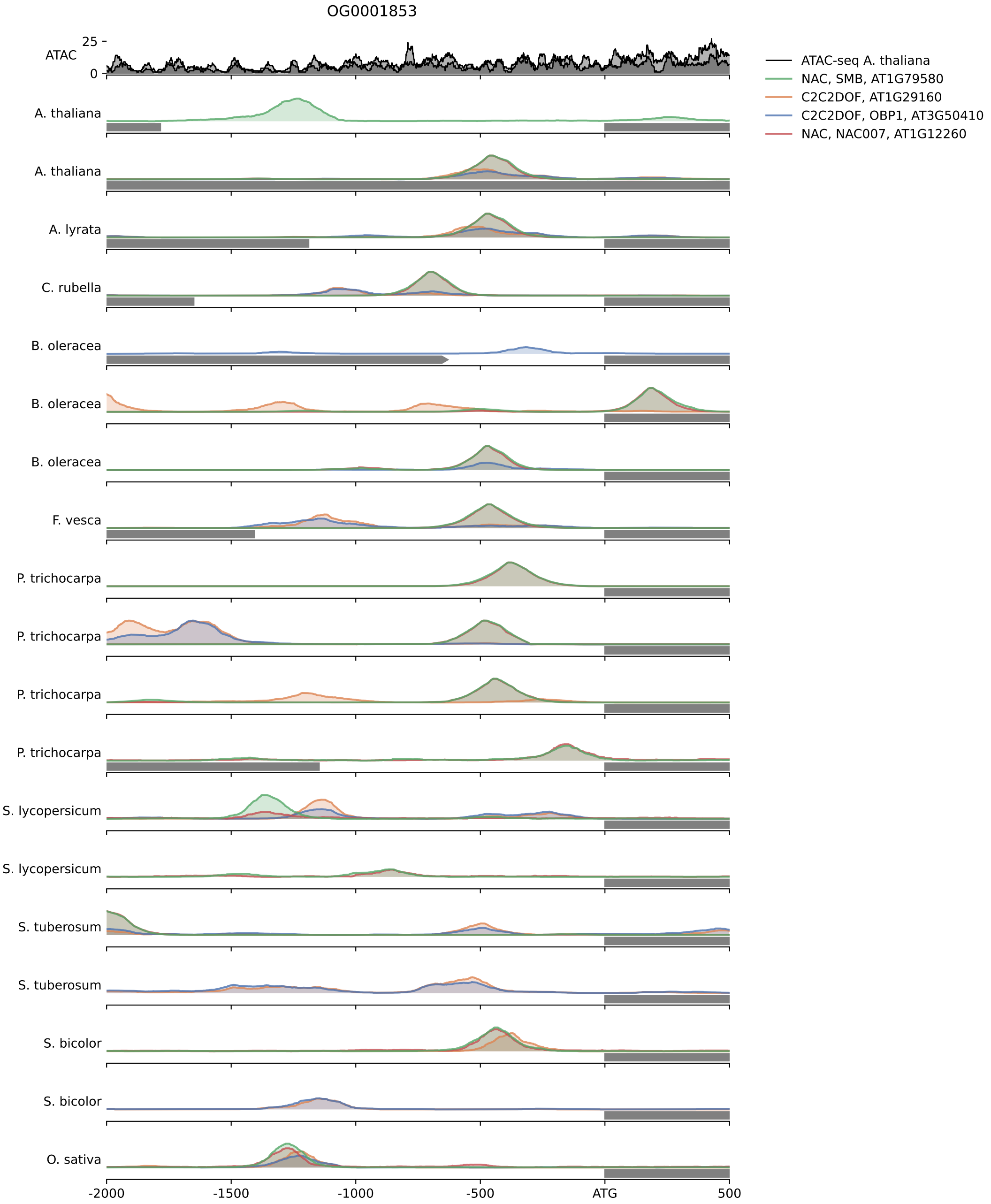
A. thaliana target: AT2G27830, hypothetical protein;(source:Araport11)



A. thaliana target: AT3G20820, Leucine-rich repeat (LRR) family protein;(source:Araport11)

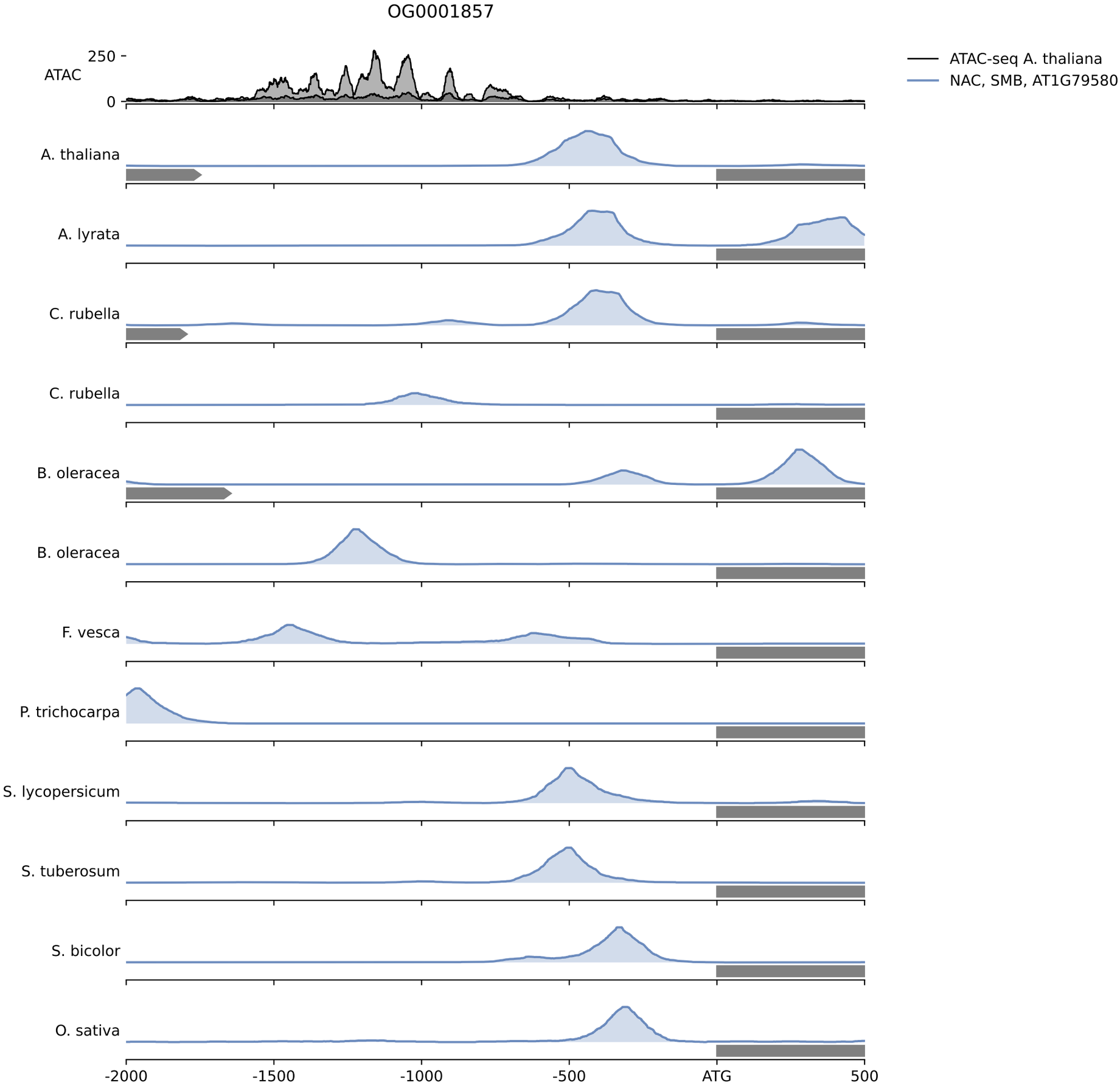
A. thaliana target: AT5G12940, Leucine-rich repeat (LRR) family protein;(source:Araport11)

A. thaliana target: AT3G12610, DRT100, Plays role in DNA-damage repair/toleration. Partially complements RecA- phenotypes.

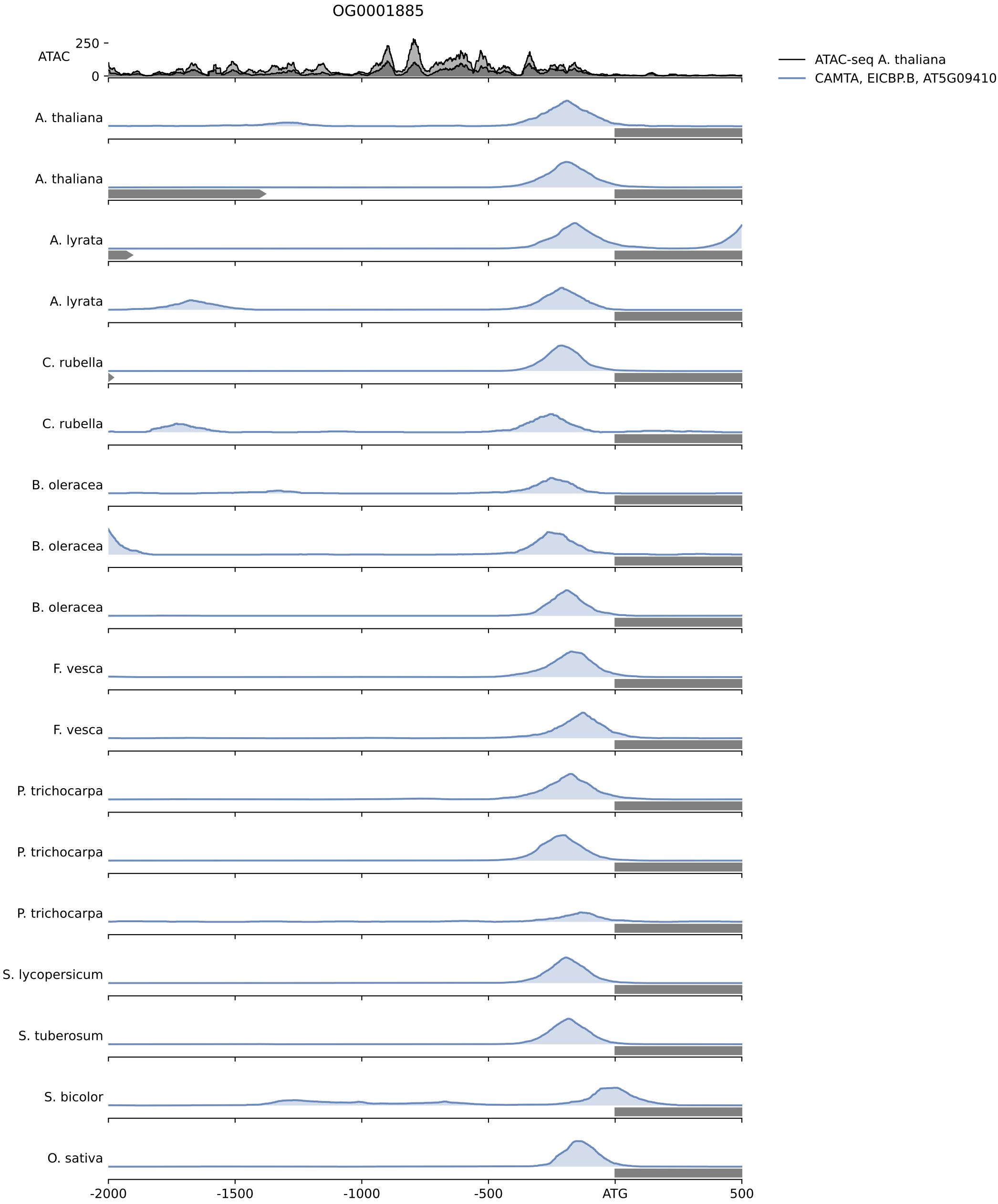


A. thaliana target: AT2G04910, Carbohydrate-binding X8 domain superfamily protein;(source:Araport11)

A. thaliana target: AT1G79480, Carbohydrate-binding X8 domain superfamily protein;(source:Araport11)



A. thaliana target: AT4G18640, MRH1, Required for root hair elongation during tip growth. The mRNA is cell-to-cell mobile.



A. thaliana target: AT3G56050, Protein kinase family protein;(source:Araport11)

A. thaliana target: AT2G40270, Protein kinase family protein;(source:Araport11)