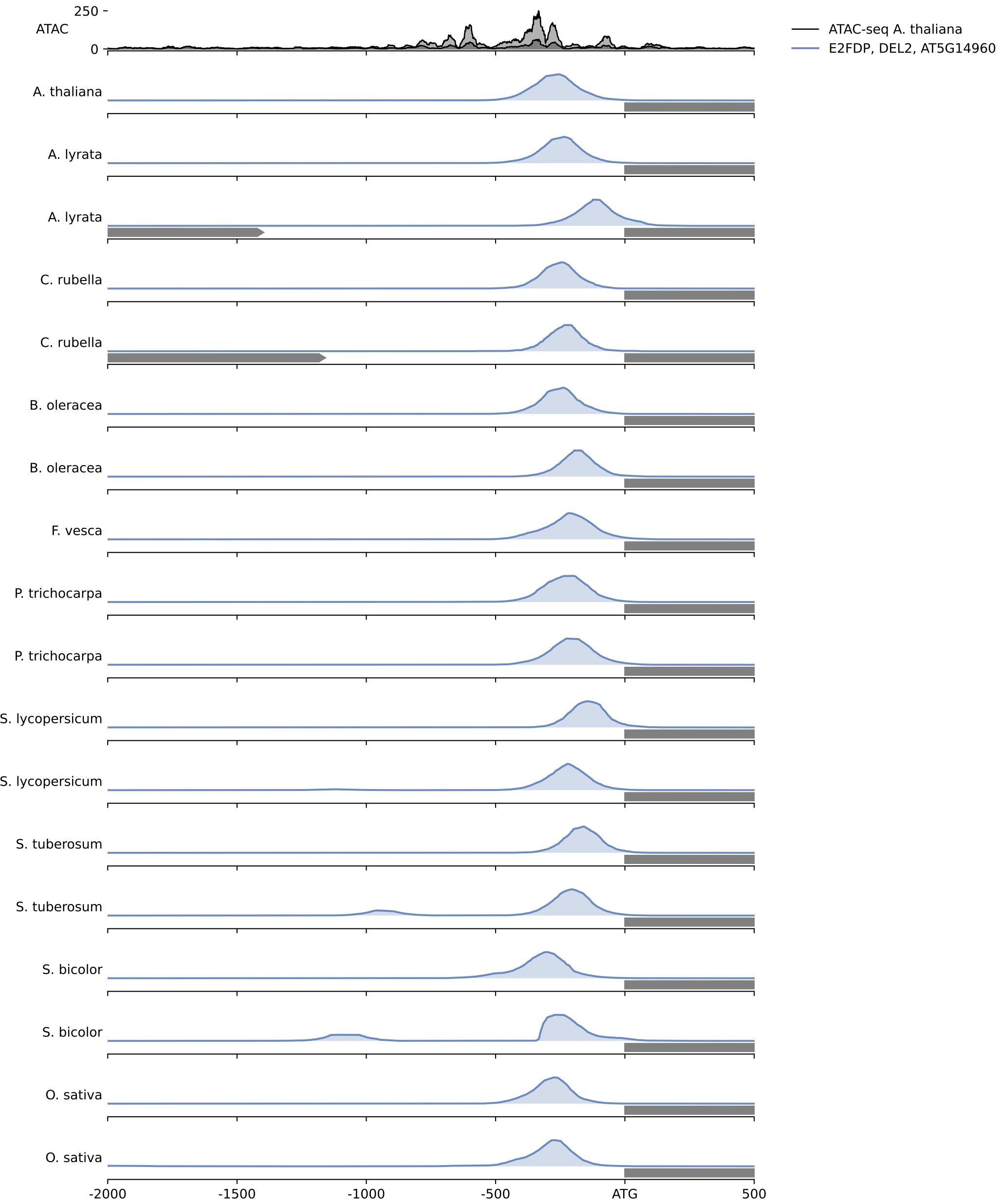
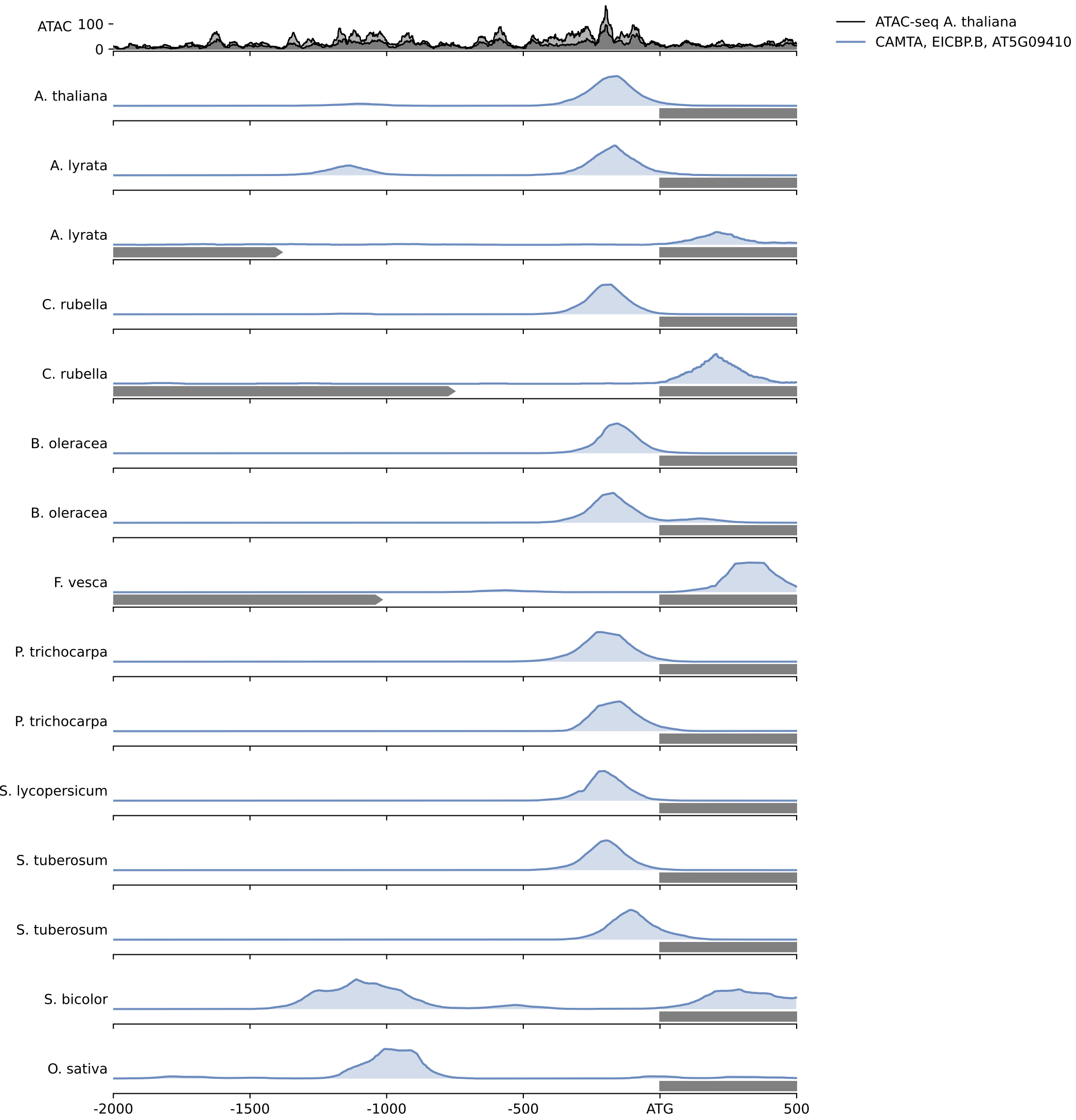
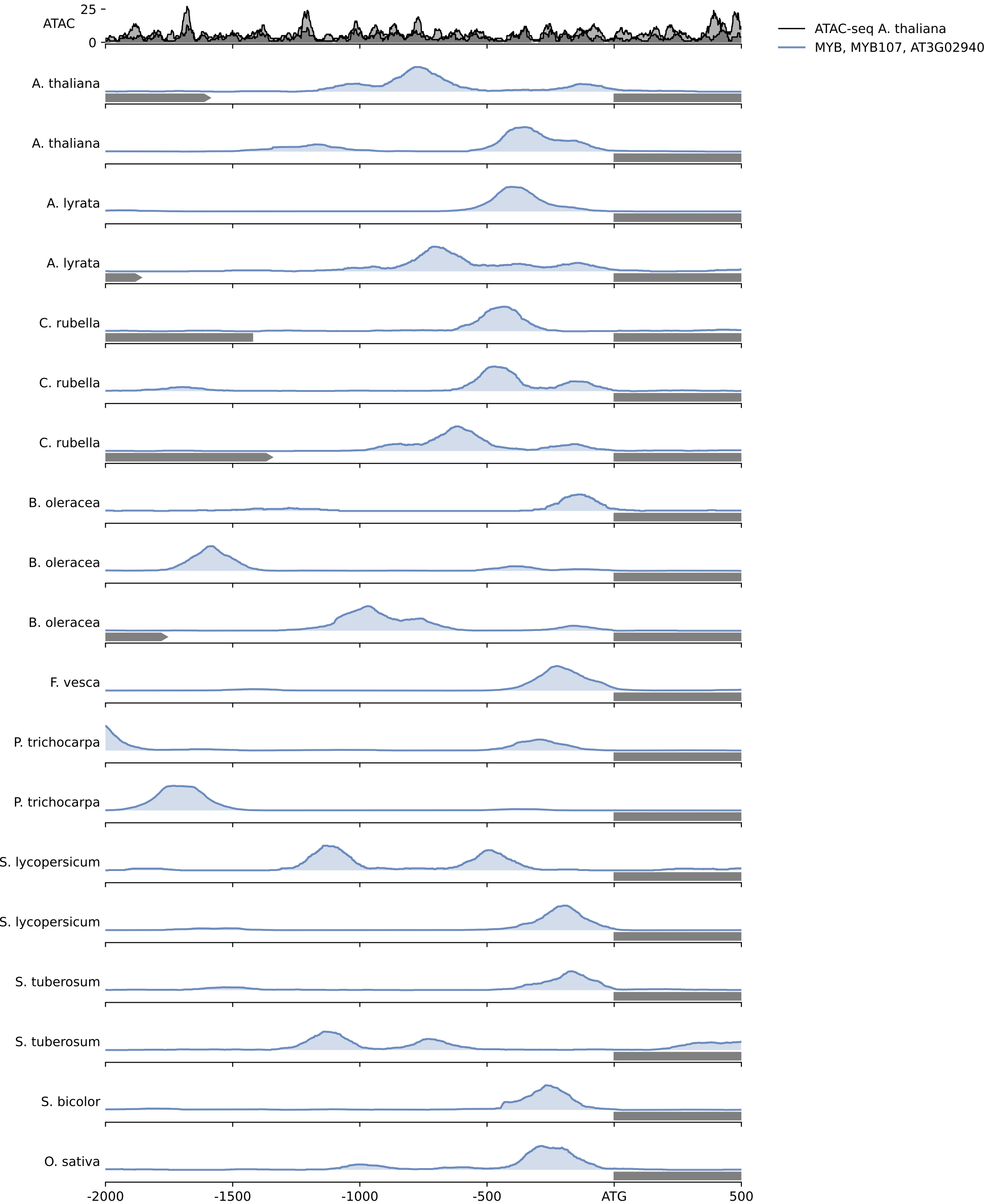




A. thaliana target: AT2G21790, RNR1, encodes large subunit of ribonucleotide reductase involved in the production of deoxyribonucleoside triphosphates (dNTPs) for DNA replication and repair

OG0003215

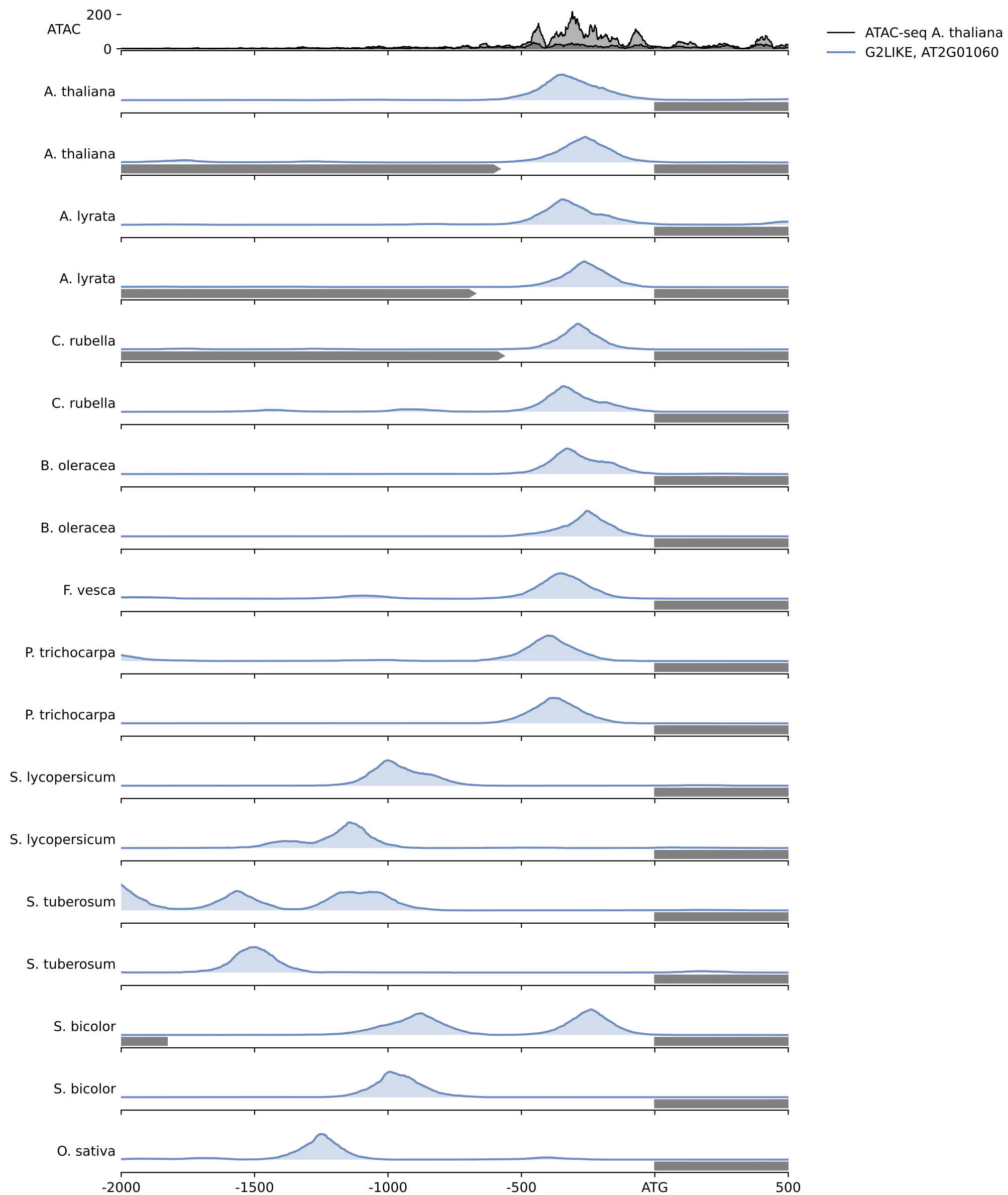




A. thaliana target: AT3G11430, GPAT5, sn-glycerol-3-phosphate 2-O-acyltransferas, involved in the biosynthesis of suberin polyester.

A. thaliana target: AT5G06090, GPAT7, putative sn-glycerol-3-phosphate 2-O-acyltransferase

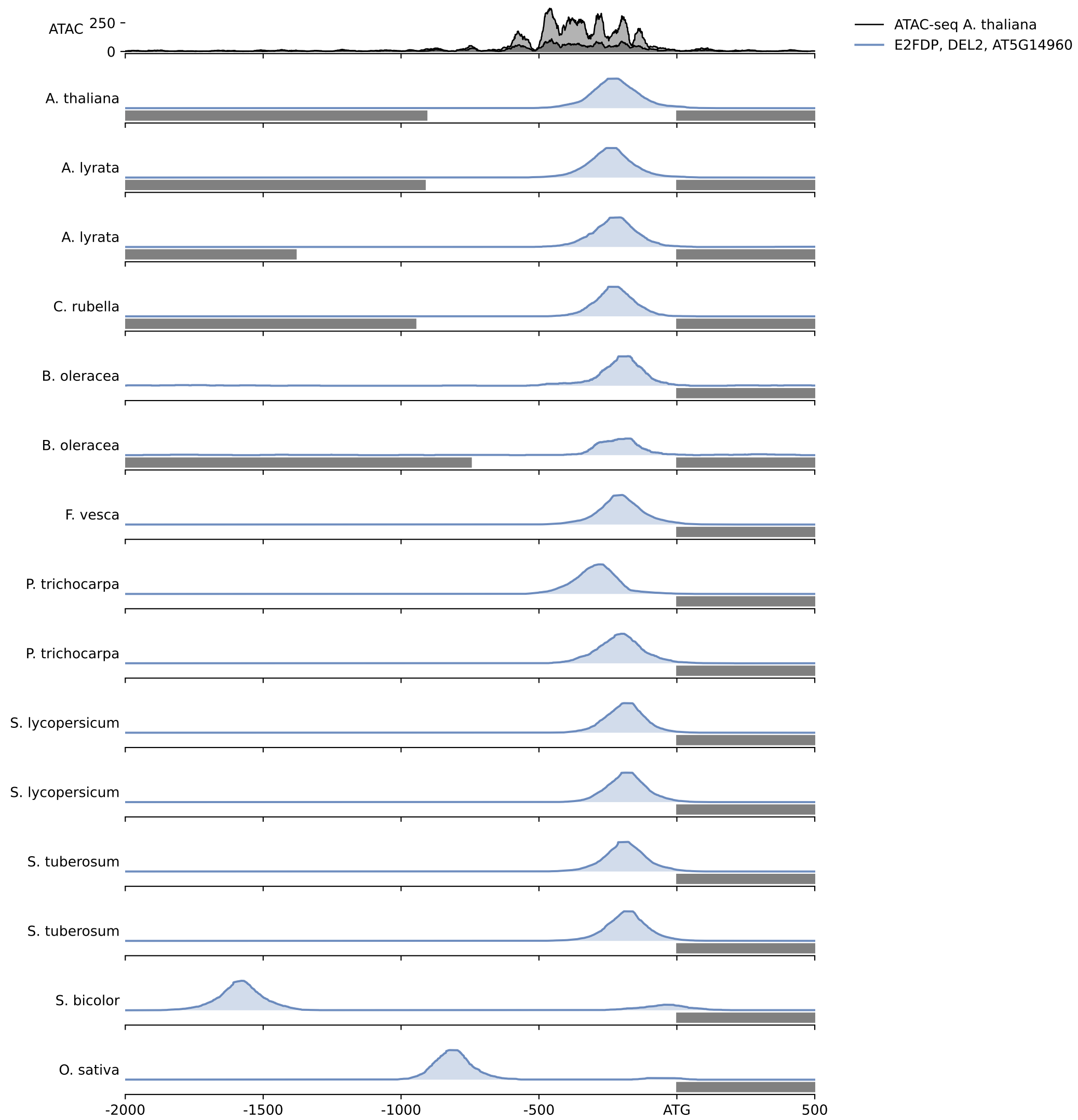
OG0003289



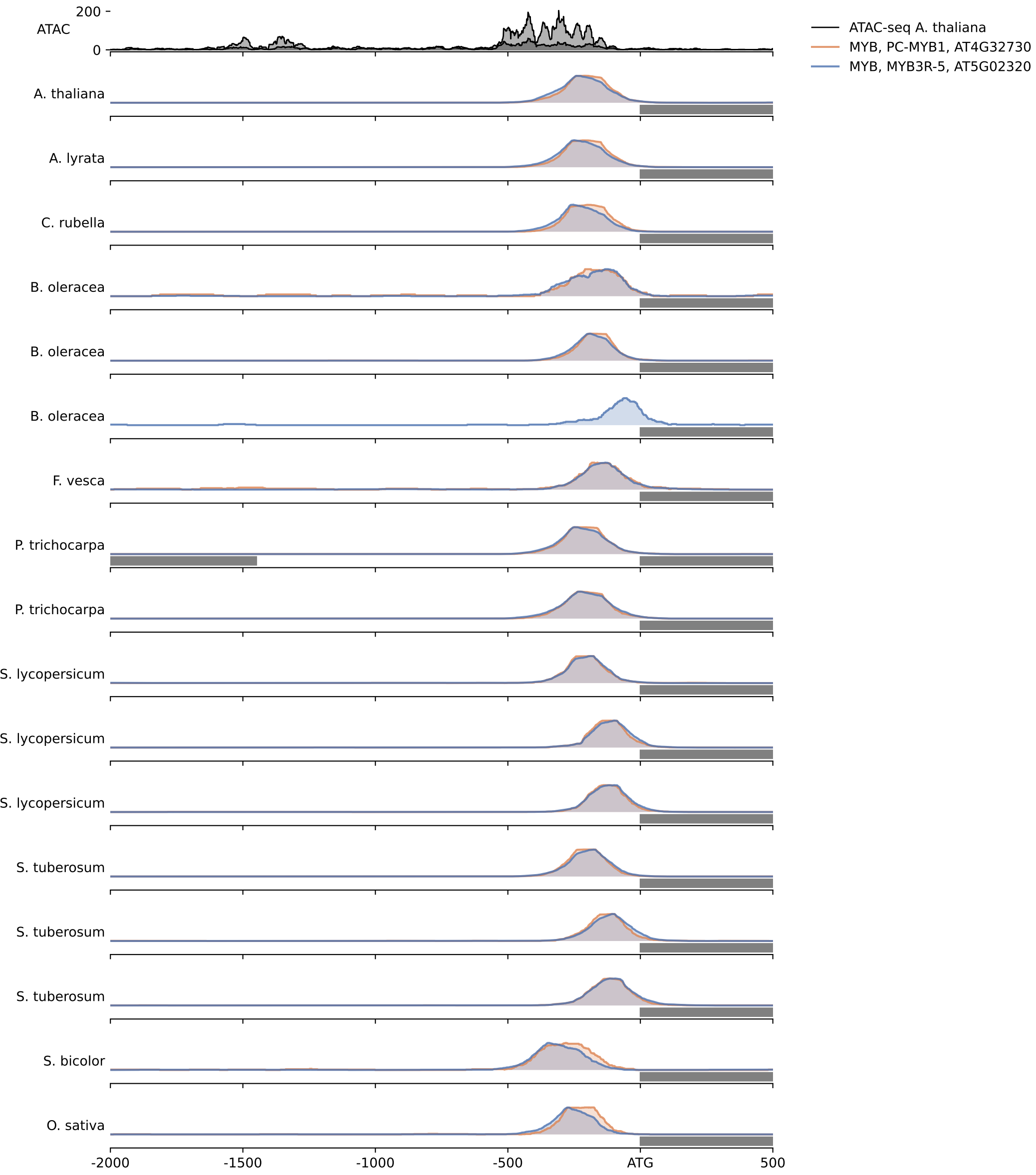
A. thaliana target: AT2G11810, MGDC, MGD3 is the major enzyme for galactolipid metabolism during phosphate starvation. Does not contribute to galactolipid synthesis under P1-sufficient conditions.

A. thaliana target: AT5G20410, MGD2, Encodes a type B monogalactosyldiacylglycerol (MGDG) synthase. Strongly induced by phosphate deprivation, and in non-photosynthetic tissues. Does not contribute to galactolipid synthesis under Pi-sufficient conditions but does under Pi starvation.

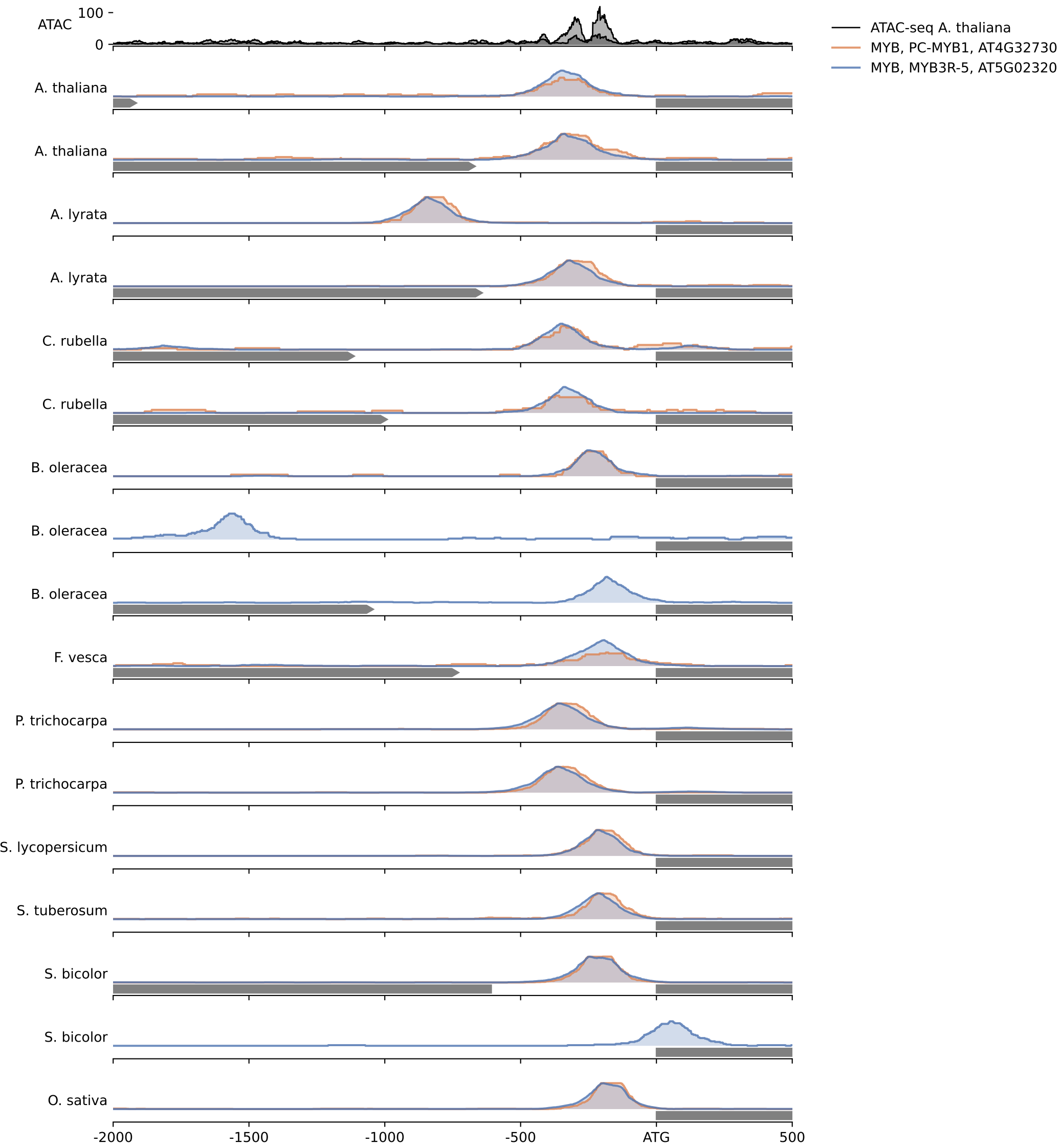
OG0003296



A. thaliana target: AT5G18620, CHR17, Encodes a member of the *A. thaliana* imitation switch (AtISWI) subfamily of chromatin remodeling factors. Double mutation in CHR17 and CHR11 results in the loss of the evenly spaced nucleosome pattern in gene bodies, but does not affect nucleosome density.

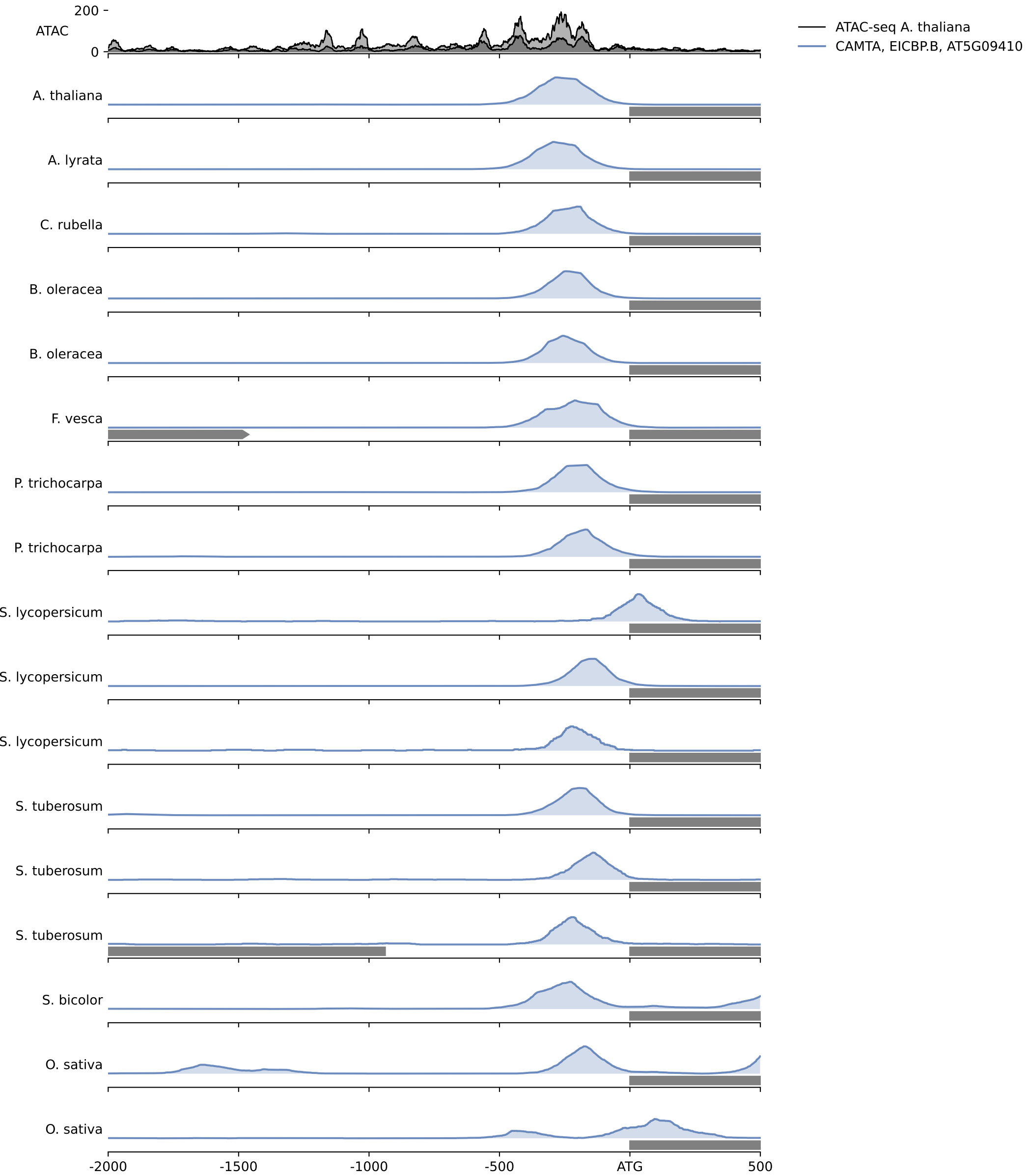


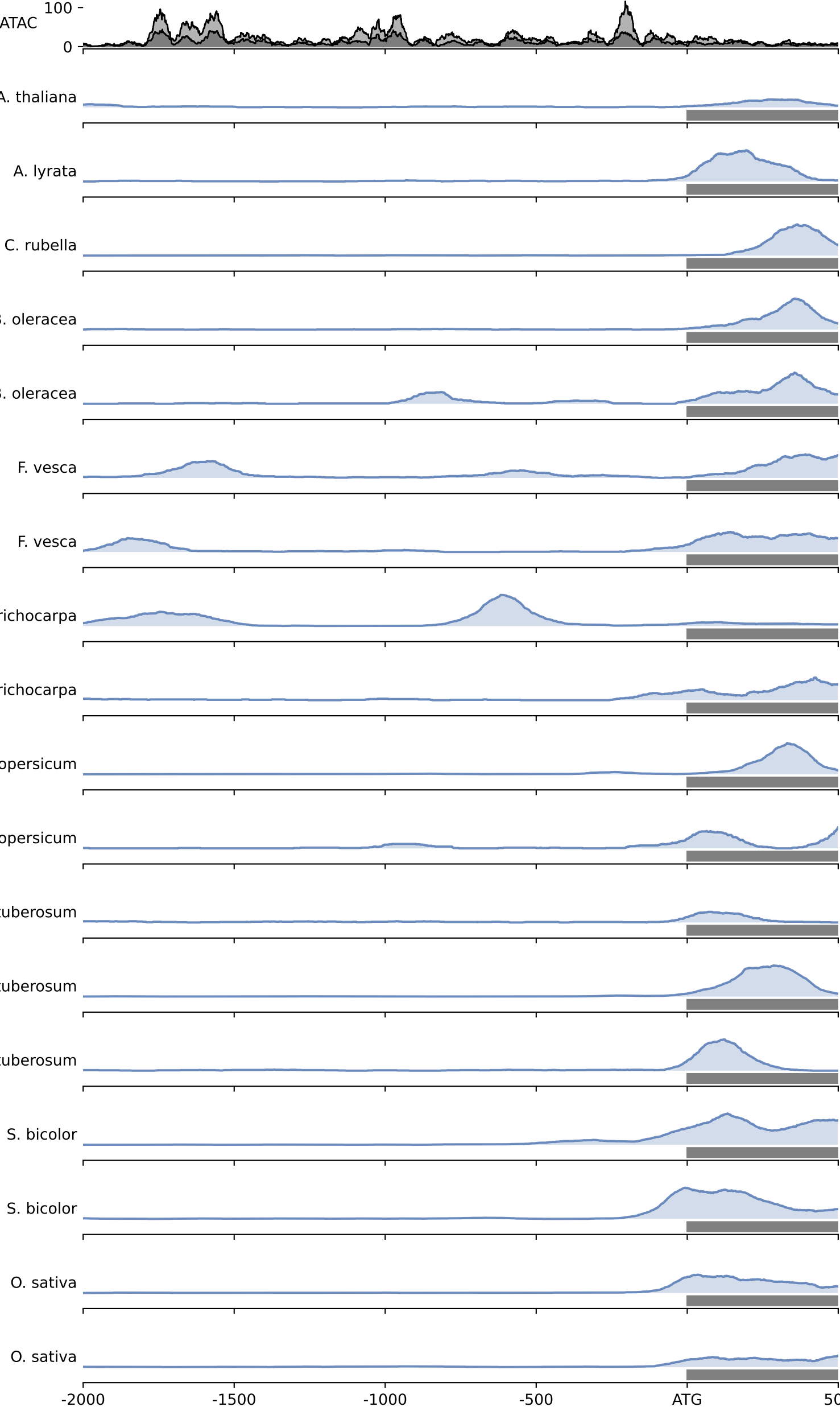
A. thaliana target: AT1G03780, TPX2, Homolog of vertebrate TPX2. Protein has three domains involved in nuclear targeting, one in nuclear export and two in microtubule binding. Involved in mitotic spindle assembly during late prophase and early prometaphase.



A. thaliana target: AT1G50490, UBC20, Encodes one of two ubiquitin-conjugating enzymes belonging to the E2-C gene family (the other being UBC19). Transcript is always found in dividing cells, but also in other non-dividing cells.

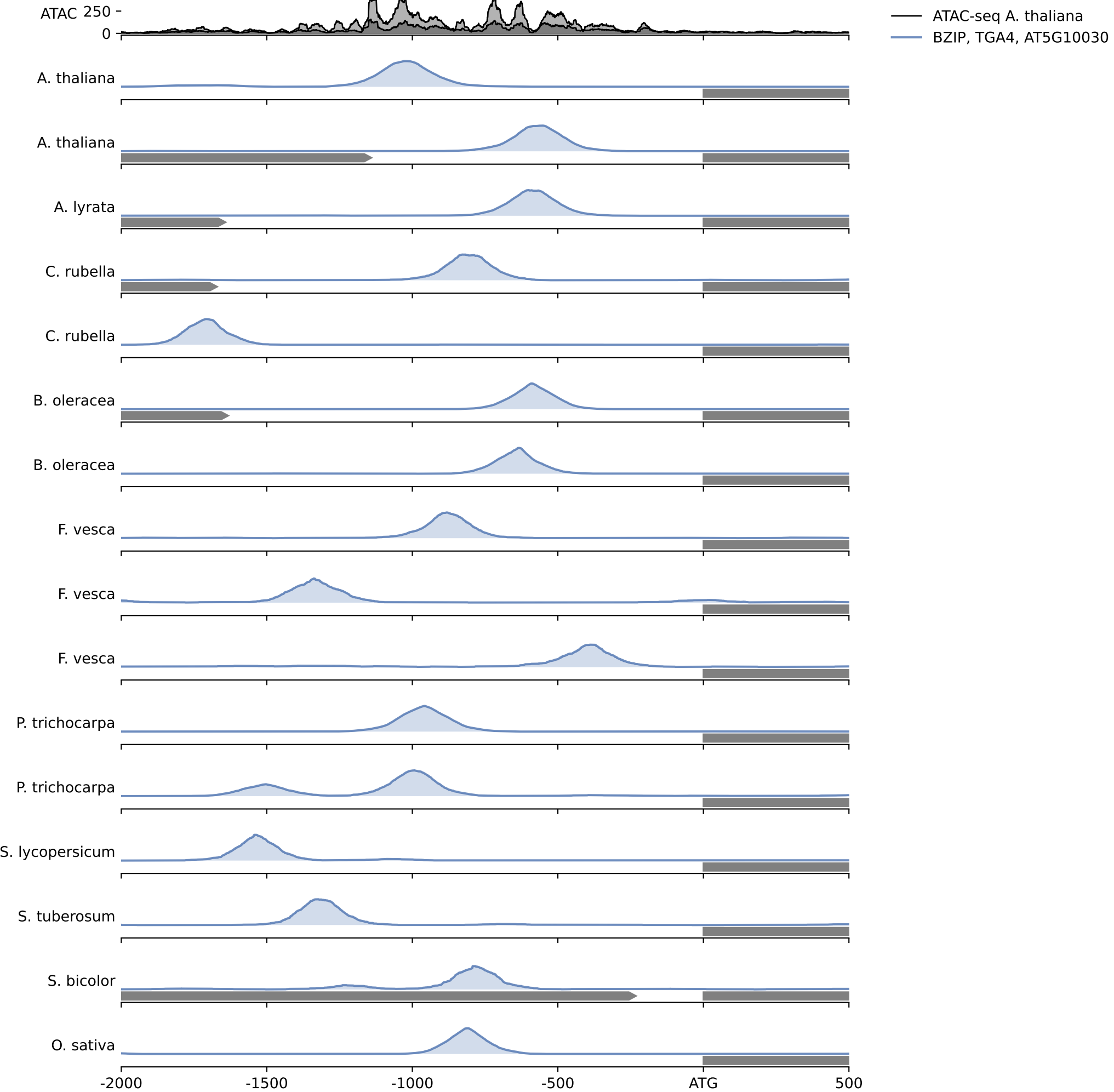
A. thaliana target: AT3G20060, UBC19, Encodes one of two ubiquitin-conjugating enzymes belonging to the E2-C gene family (the other being UBC19). Transcript is always found in dividing cells, but also in other non-dividing cells. Protein is localized to the cytoplasm as well as to the nucleus.





— ATAC-seq *A. thaliana*
— AP2EREBP, RAP2.1, AT1G46768

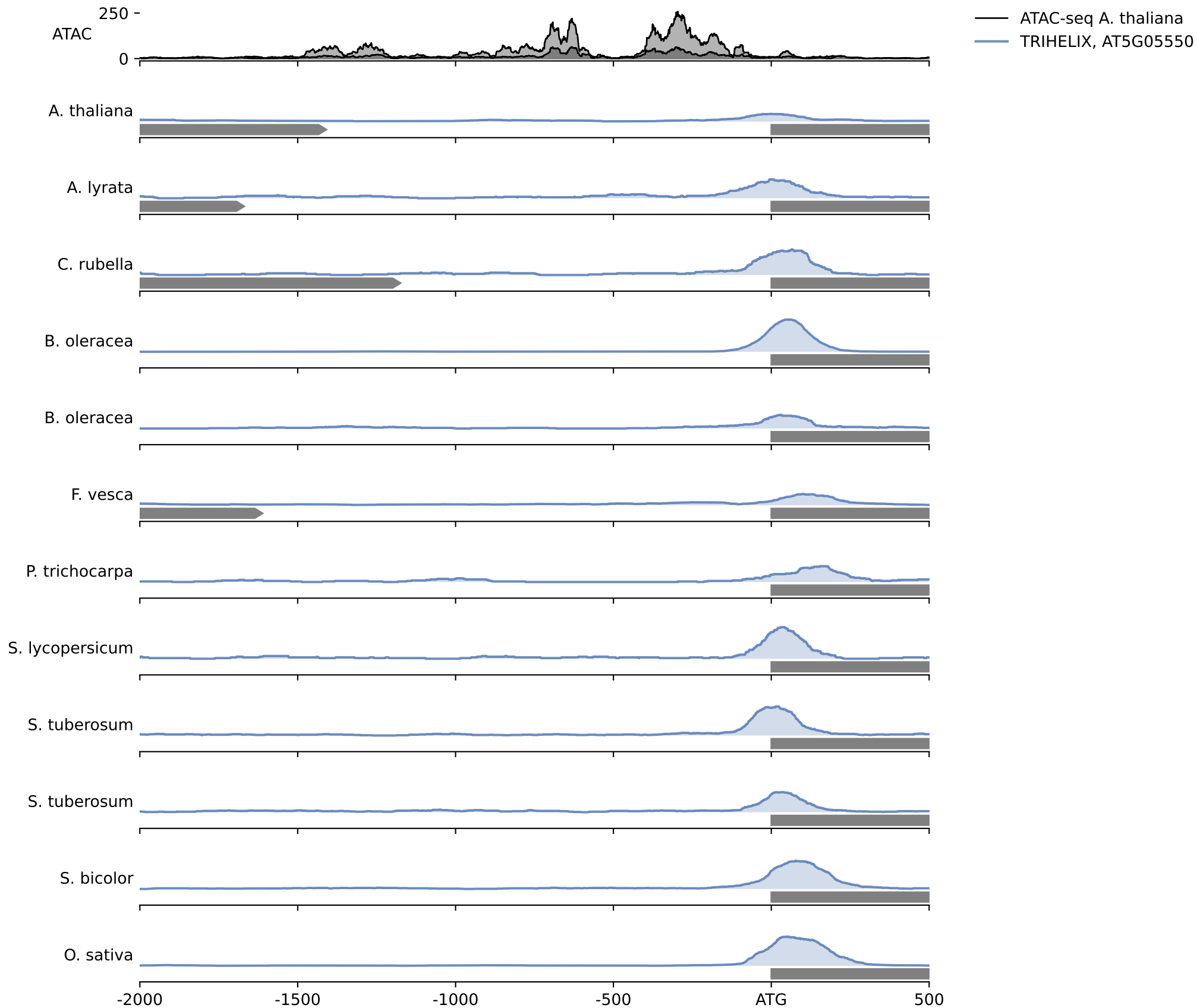
OG0003413



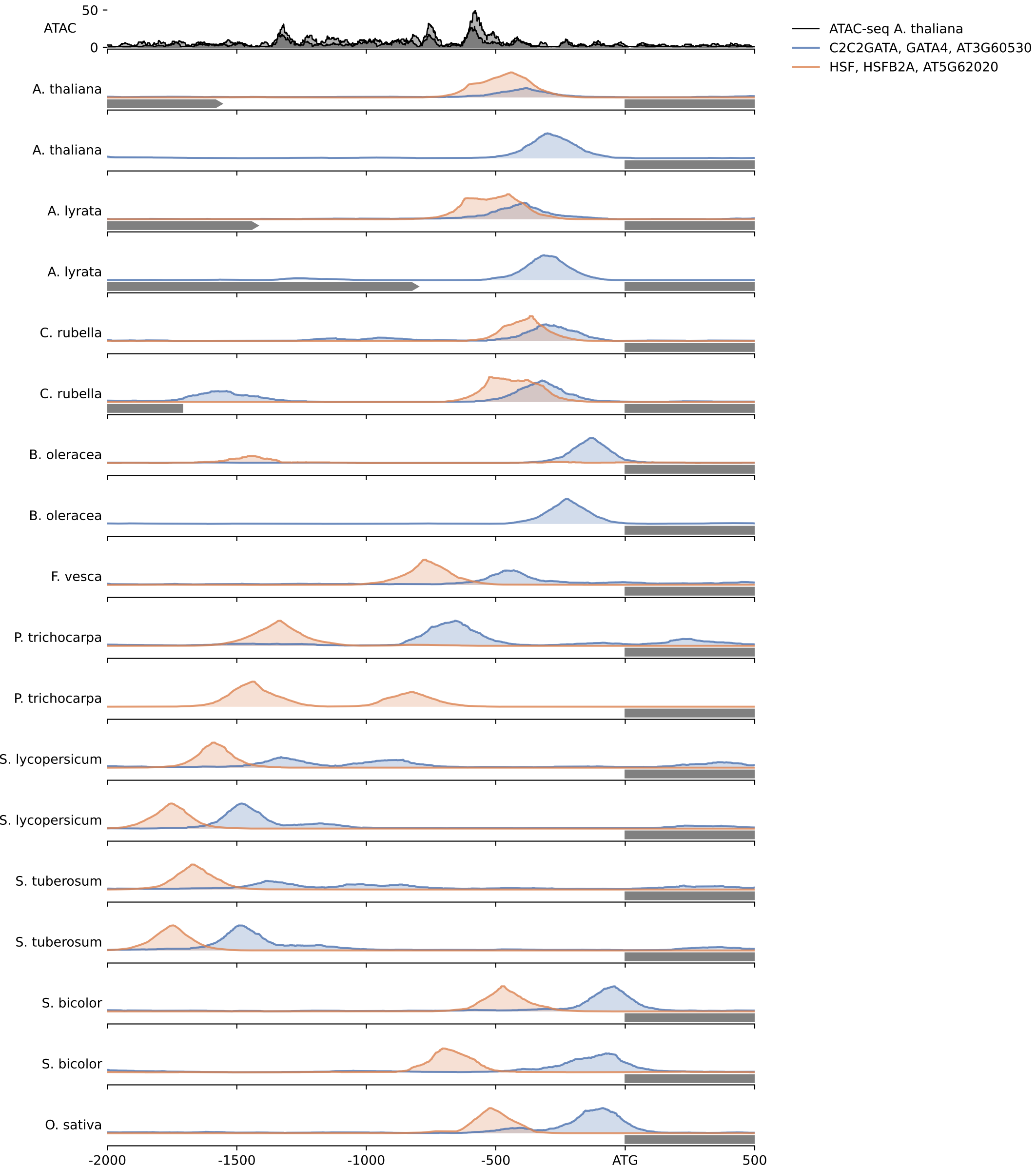
A. thaliana target: AT5G45110, NPR3, Encodes NPR3, a paralog of NPR1. Involved in negative regulation of defense responses against bacterial and oomycete pathogens. *npr3* mutants has elevated level of PR1 expression. Interacts with TGA2, TGA3, TGA5 and TGA6 in yeast two hybrid assays. NPR3 and NPR4 are receptors for the immune signal salicylic acid. The mRNA is cell-to-cell mobile.

A. thaliana target: AT4G19660, NPR4, Encodes NPR4, a ankyrin repeat BTB/POZ domain-containing protein with 36% sequence identity with NPR1. Mutants are more susceptible to the bacterial pathogen *Pseudomonas syringe* pv. tomato DC3000 and to the fungal pathogen *Erysiphe cichoracearum*, but do not differ markedly from wild type in interaction with virulent and avirulent strains of the oomycete *Peronospora parasitica*. NPR4 is required for basal defense against pathogens, and may be implicated in the cross-talk between the SA- and JA-dependent signaling pathways. NPR3 and NPR4 are receptors for the immune signal salicylic acid.

OG0003434

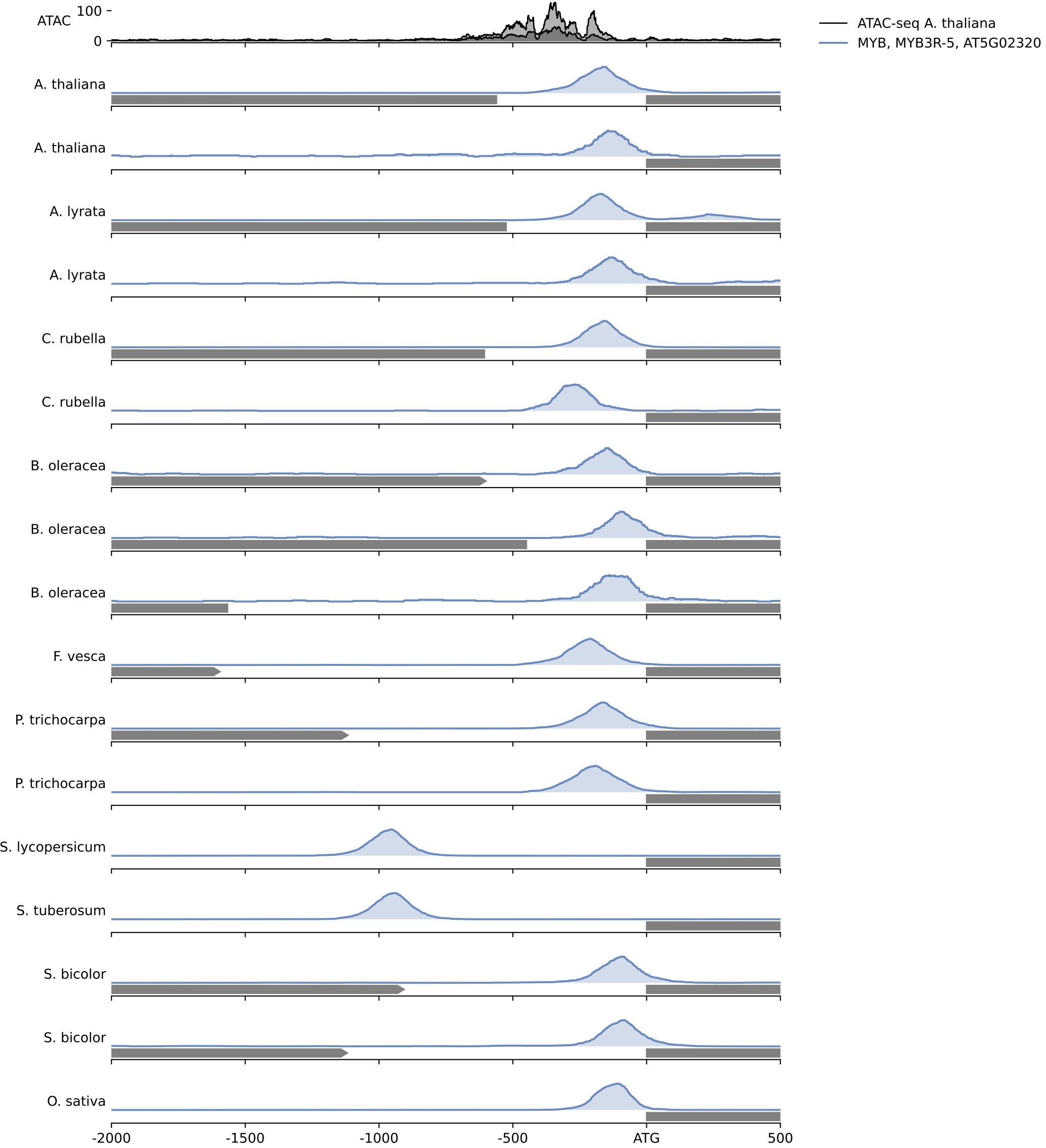


A. thaliana target: AT3G05630, PLDP2, Encodes a member of the PXPH-PLD subfamily of phospholipase D proteins. Regulates vesicle trafficking. Required for auxin transport and distribution and hence auxin responses. This subfamily is novel structurally different from the majority of plant PLDs by having phox homology (PX) and pleckstrin homology (PH) domains. Involved regulating root development in response to nutrient limitation. Plays a major role in phosphatidic acid production during phosphate deprivation. Induced upon Pi starvation in both shoots and roots. Involved in hydrolyzing phosphatidylcholine and phosphatidylethanolamine to produce diacylglycerol for digalactosyldiacylglycerol synthesis and free Pi to sustain other Pi-requiring processes. Does not appear to be involved in root hair patterning. Expression is upregulated in the shoot of cax1/cax3 mutant and is responsive to phosphate (Pi) and not phosphite (Phi) in roots and shoots.



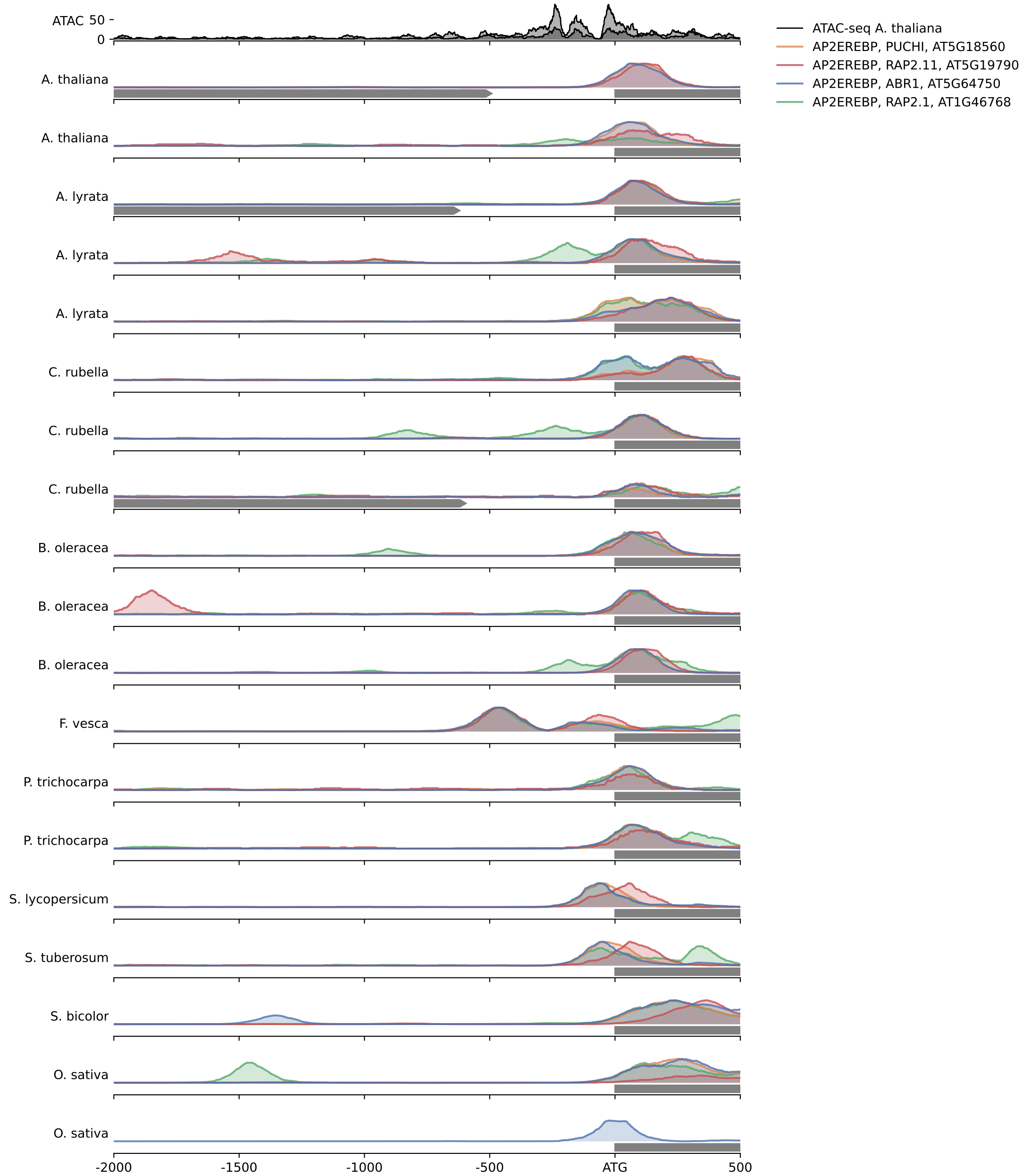
A. thaliana target: AT1G79920, Hsp70-15, Heat shock protein 70 (Hsp 70) family protein;(source:Araport11)

A. thaliana target: AT1G79930, HSP91, encodes high molecular weight heat shock protein 70 not a HSP90 homolog, mRNA is constitutively expressed but transiently induced after heat shock



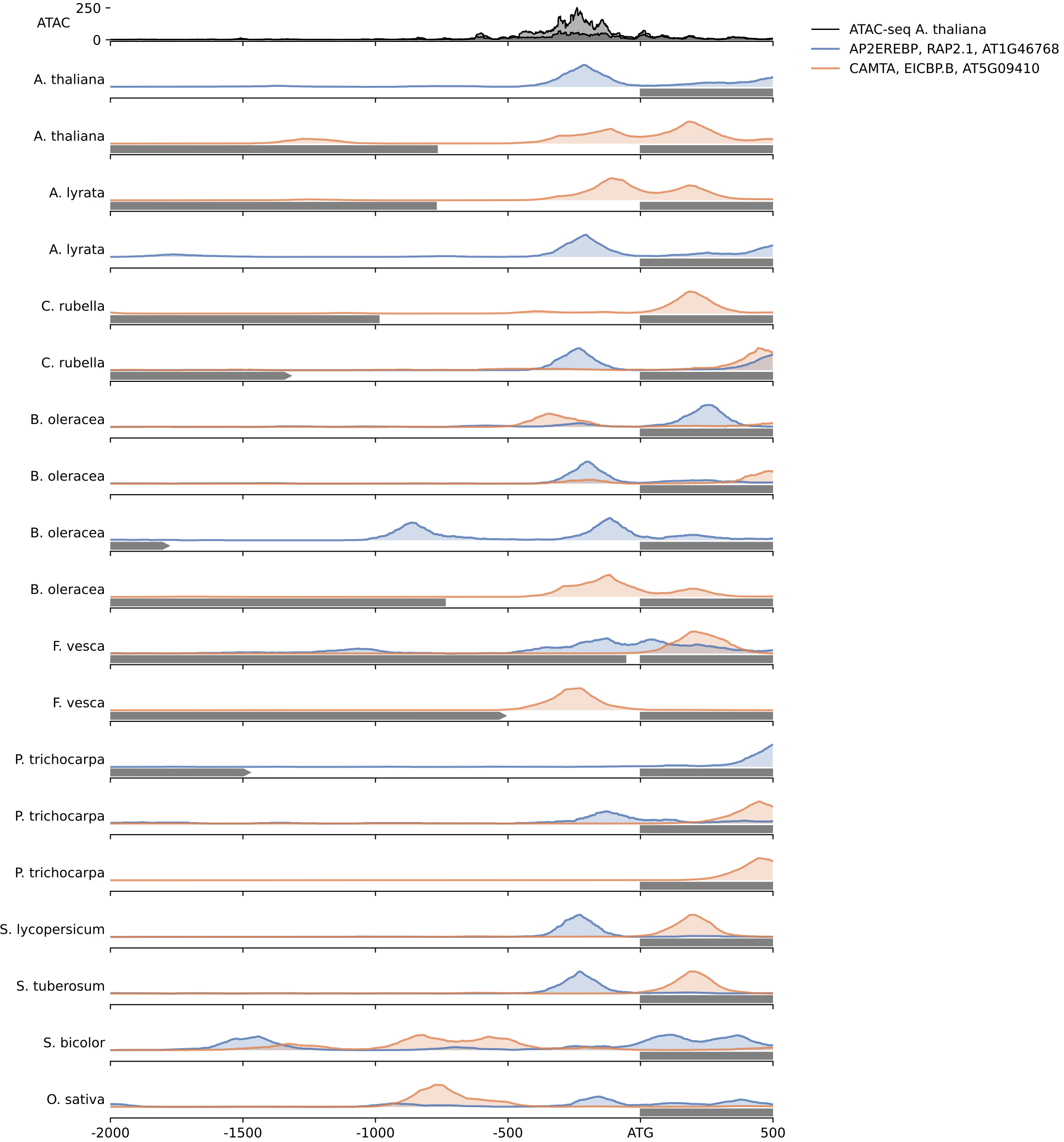
A. thaliana target: AT2G44190, EDE1, Encodes a novel microtubule binding protein that preferentially associates with nuclear microtubules during mitosis and is essential during the mitotic and cytokinetic stages that generate the endosperm and embryo.

A. thaliana target: AT3G60000, QWRF6, QWRF motif protein (DUF566);(source:Araport11)



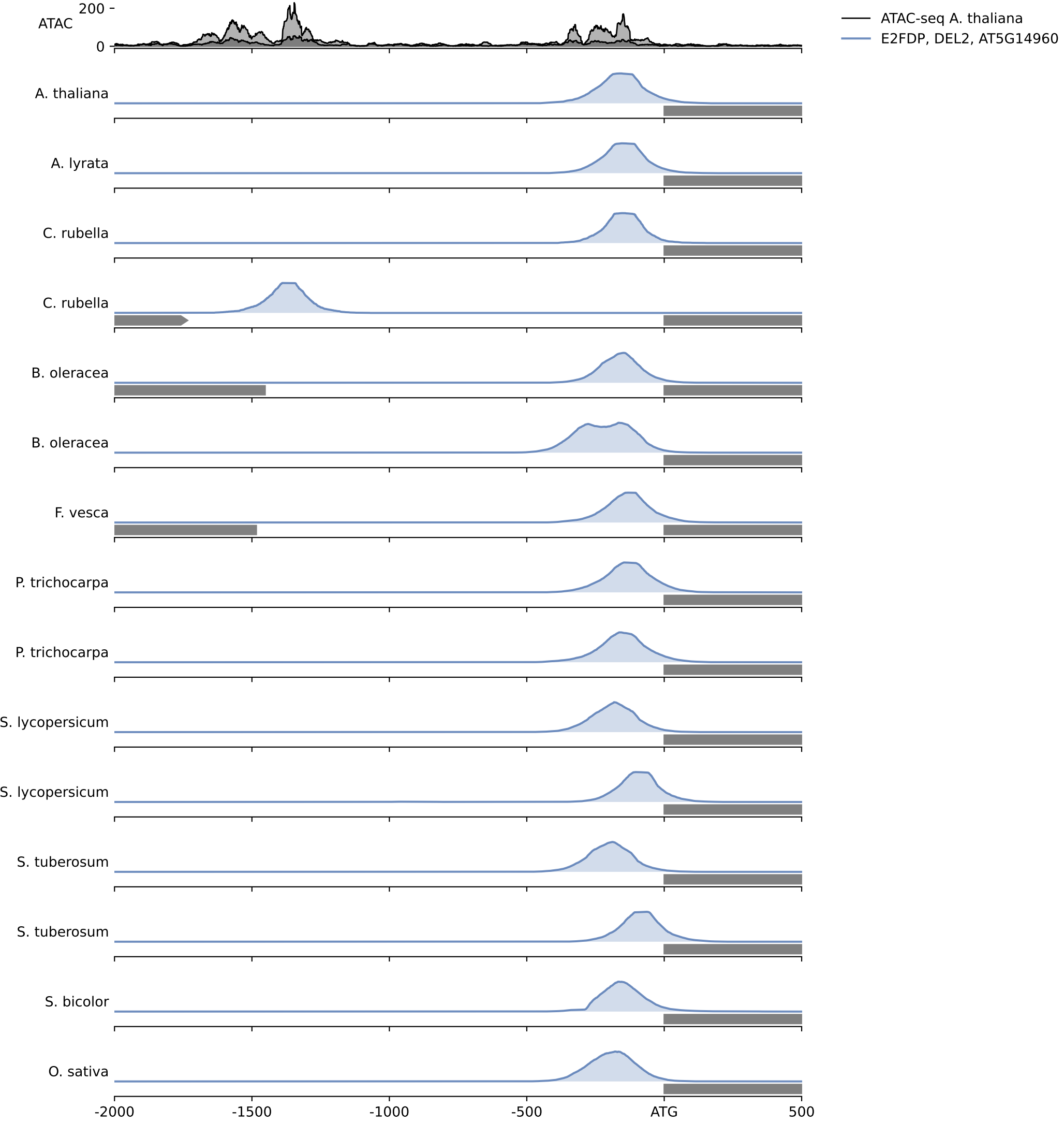
A. thaliana target: AT1G02110, bZIP domain class transcription factor (DUF630 and DUF632);(source:Araport11)

A. thaliana target: AT3G60320, bZIP domain class transcription factor (DUF630 and DUF632);(source:Araport11)



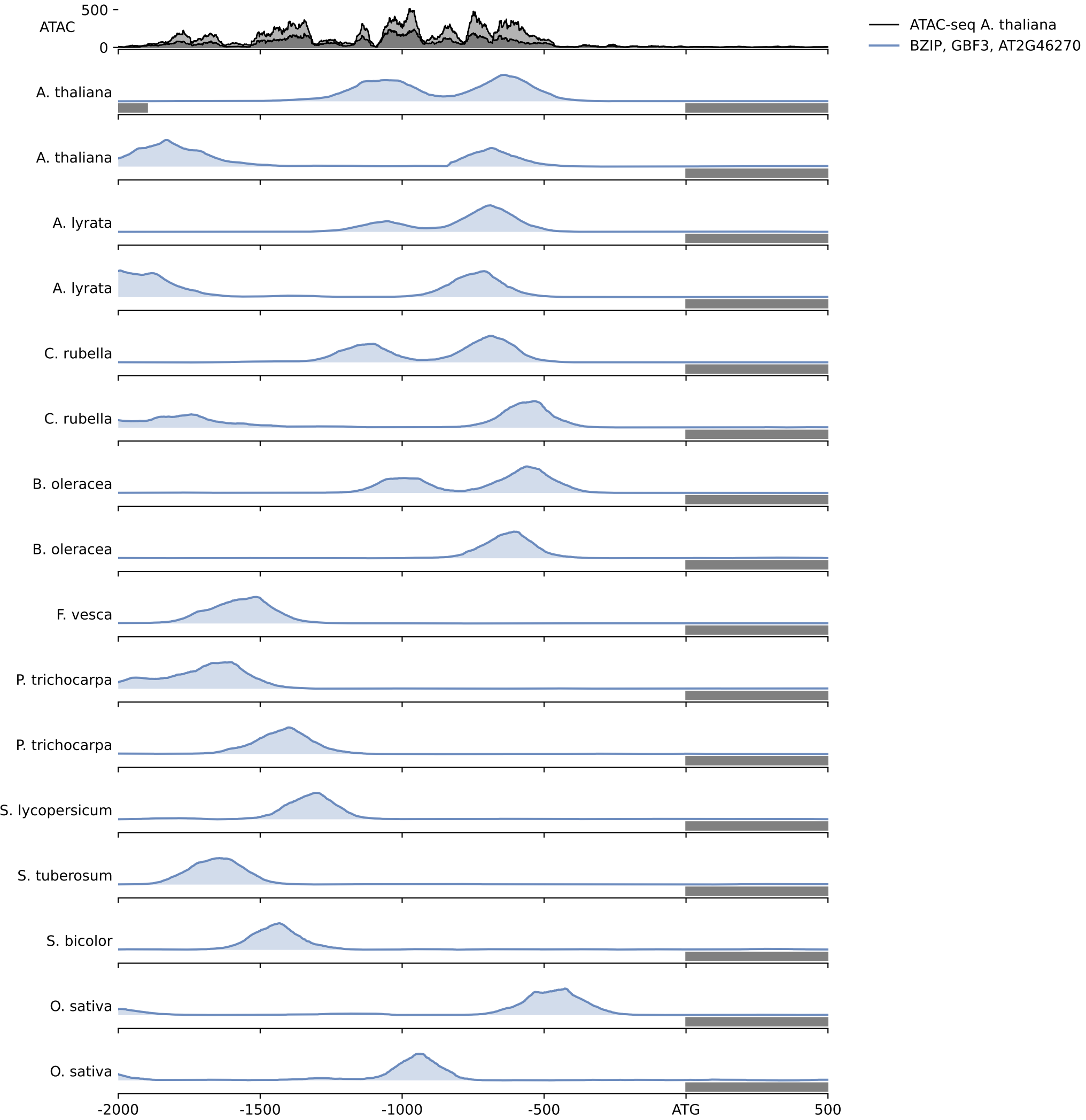
A. thaliana target: AT4G02500, XT2, Encodes a protein with xylosyltransferase activity, which is specific for UDP-xylose as donor substrate and for oligosaccharides with a degree of polymerization >4. Although the enzyme utilizes either cellopentaose or cellohexaose, its activity is four-fold higher with cellohexaose as an acceptor compared to cellopentaose. The enzyme is able to add several xylosyl residues to the acceptor forming mono-, di- and trixylosylated polysaccharides. The mRNA is cell-to-cell mobile.

A. thaliana target: AT3G62720, XT1, Encodes a protein with xylosyltransferase activity, which is specific for UDP-xylose as donor substrate and for oligosaccharides with a degree of polymerization >4. Although the enzyme utilizes either cellopentaose or cellohexaose, its activity is four-fold higher with cellohexaose as an acceptor compared to cellopentaose. The enzyme is able to add several xylosyl residues to the acceptor forming mono-, di- and trixylosylated polysaccharides.



A. thaliana target: AT2G31270, CDT1A, Encodes a cyclin-dependent protein kinase. Involved in nuclear DNA replication and plastid division. Located in nucleus and chloroplast.

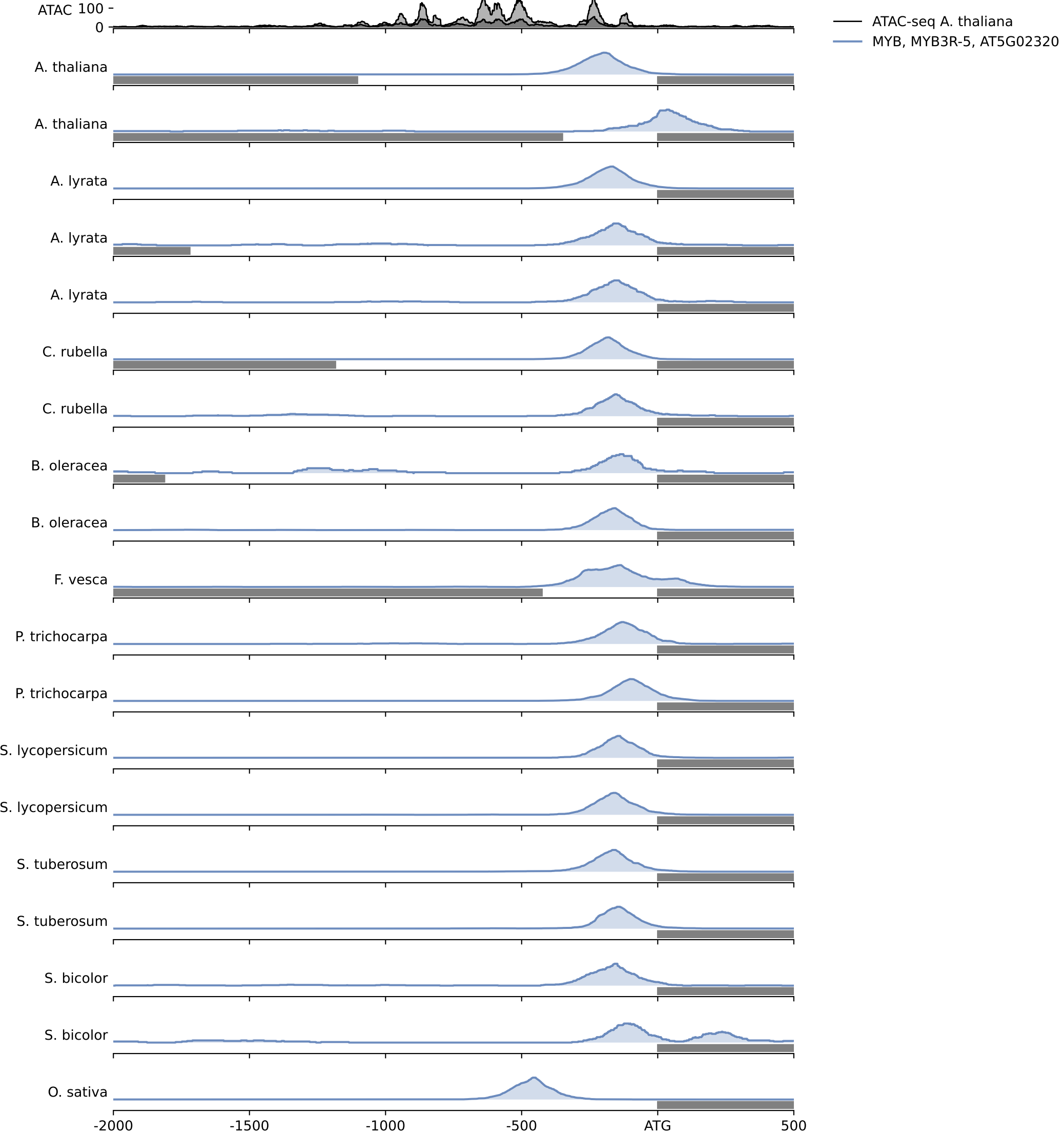
OG0003568



A. thaliana target: AT4G01120, GBF2, bZIP (basic leucine zipper) transcription factor that binds to the G-box regulatory element found in many plant promoters. GBF2 nuclear localization is increased by blue light

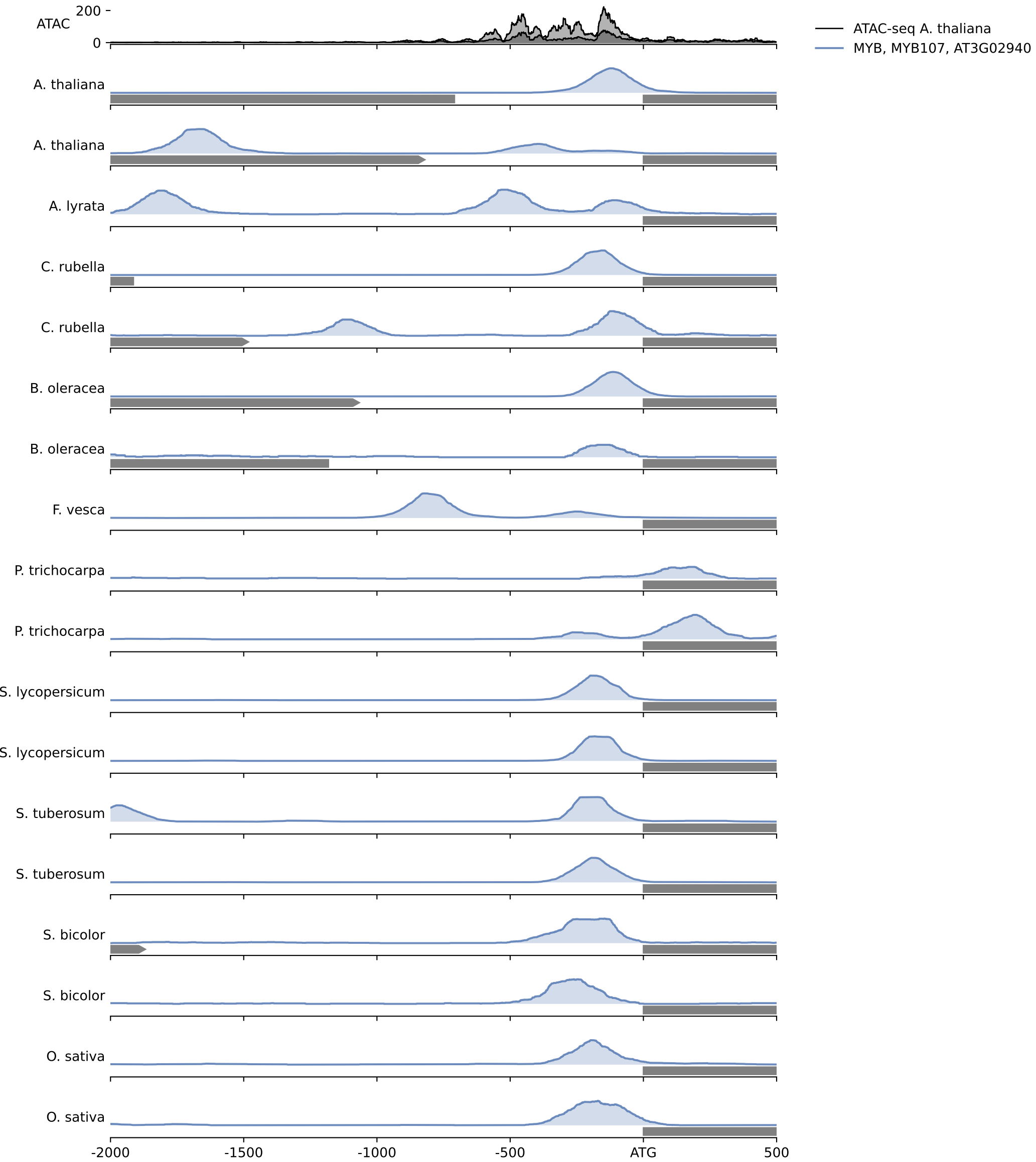
A. thaliana target: AT2G46270, GBF3, encodes a bZIP G-box binding protein whose expression is induced by ABA. It has been shown to bind to Adh that contains the G-box and is induced by cold and water deprivation. GBF3 has been shown to be expressed mostly in the root and dark-grown leaves. GBF3 can act as homodimers and as heterodimers with GFB1, GBF2 and GBF4. In addition, GBF3!?'s DNA binding activity is enhanced by GIP1, GPRI1 and GPRI2.

OG0003580



A. thaliana target: AT4G32830, AUR1, Encodes a member of a family of Ser/Thr kinases whose activities peak during cell division. Transcripts are abundant in tissues rich in dividing cells like roots and flowers but are low or absent in fully expanded leaves and stems. In interphase cells, the protein is predominantly nuclear. During mitosis, the protein associates with plant-specific cytoskeletal structures (preprophase band, phragmoplast, nascent cell plate) that are necessary for cytokinesis as well as with the microtubule spindle. It specifically phosphorylates Ser10 of histone H3 and colocalizes with phosphorylated histone H3 during mitosis.

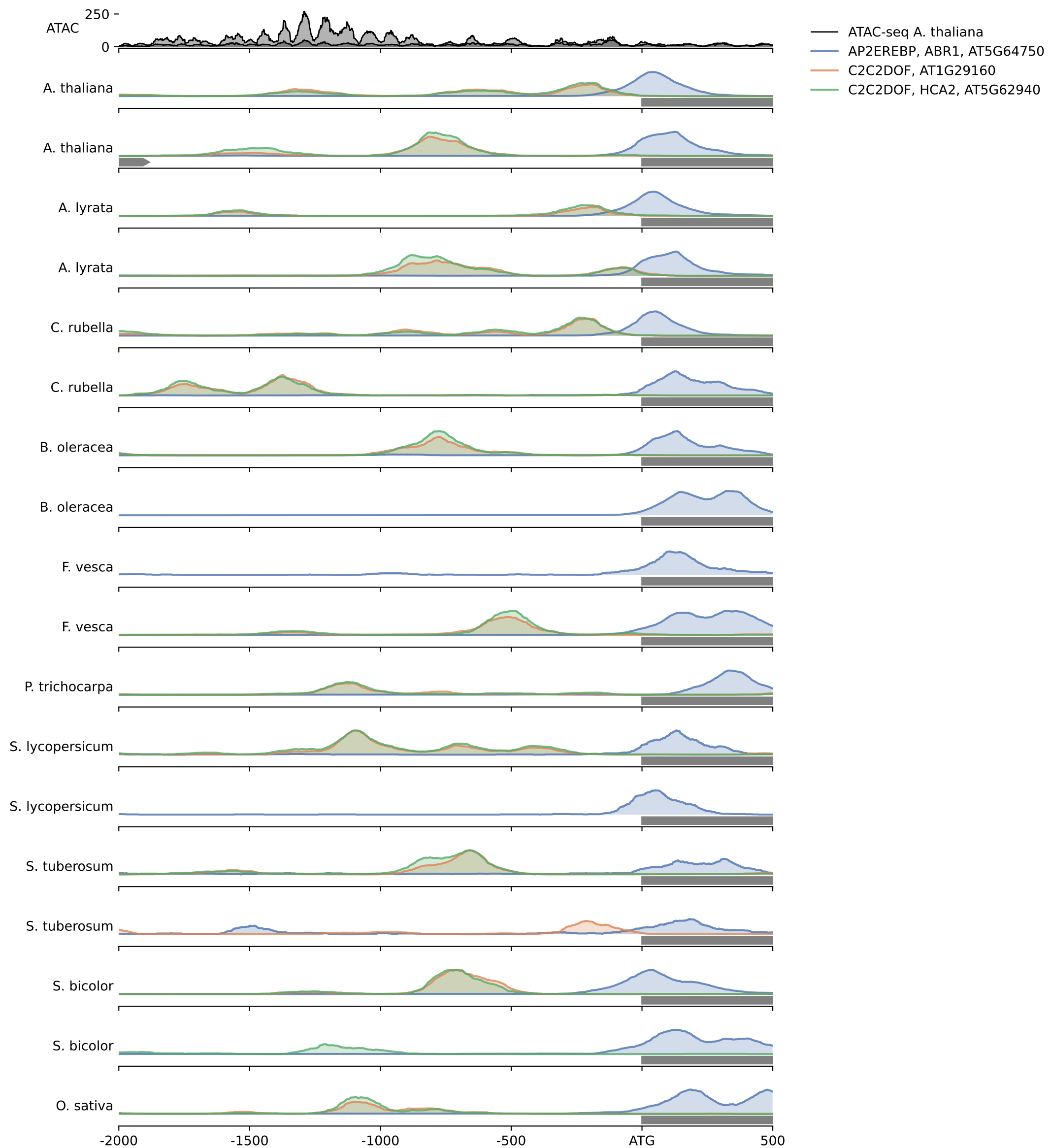
A. thaliana target: AT2G25880, AUR2, Encodes a member of a family of Ser/Thr kinases whose activities peak during cell division. Transcripts are abundant in tissues rich in dividing cells like roots and flowers but are low or absent in fully expanded leaves and stems. In interphase cells, the protein is predominantly nuclear. During mitosis, the protein associates with plant-specific cytoskeletal structures (preprophase band, phragmoplast, nascent cell plate) that are necessary for cytokinesis as well as with the microtubule spindle.



A. thaliana target: AT1G08250, ADT6, Encodes a plastid-localized arogenate dehydratase involved in phenylalanine biosynthesis. Although this enzyme has sequence similarity to prephenate dehydratases, it is 98 times more active with arogenate than prephenate in enzymatic assays.

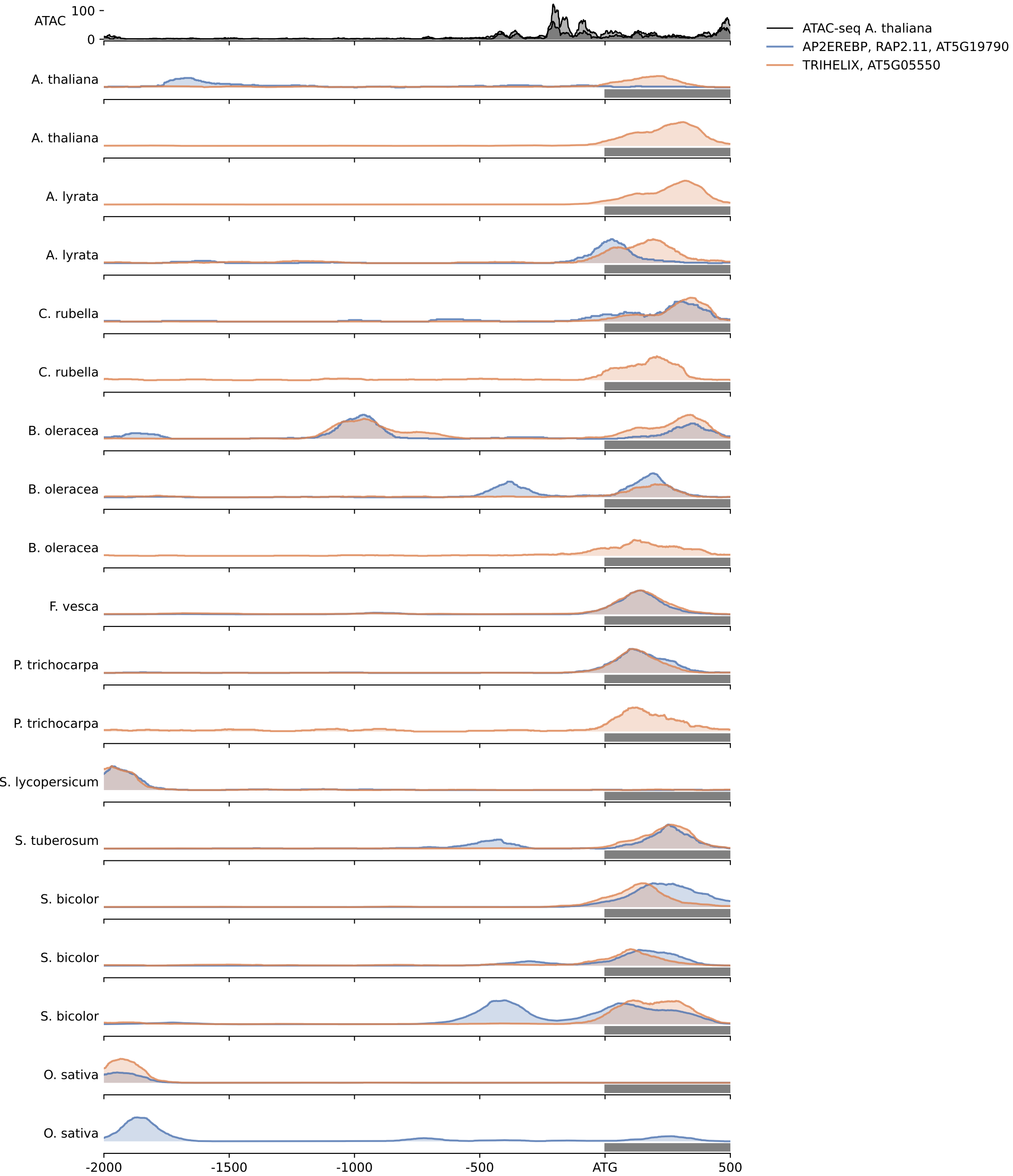
A. thaliana target: AT2G27820, PD1, Encodes a plastid-localized arogenate dehydratase involved in phenylalanine biosynthesis. Not less than six genes encoding ADT were identified in the Arabidopsis genome: ADT1 [At1g11790]; ADT2 [At3g07630]; ADT3 [At2g27820]; ADT4 [At3g44720]; ADT5 [At5g22630]; and ADT6 [At1g08250].

OG0003630



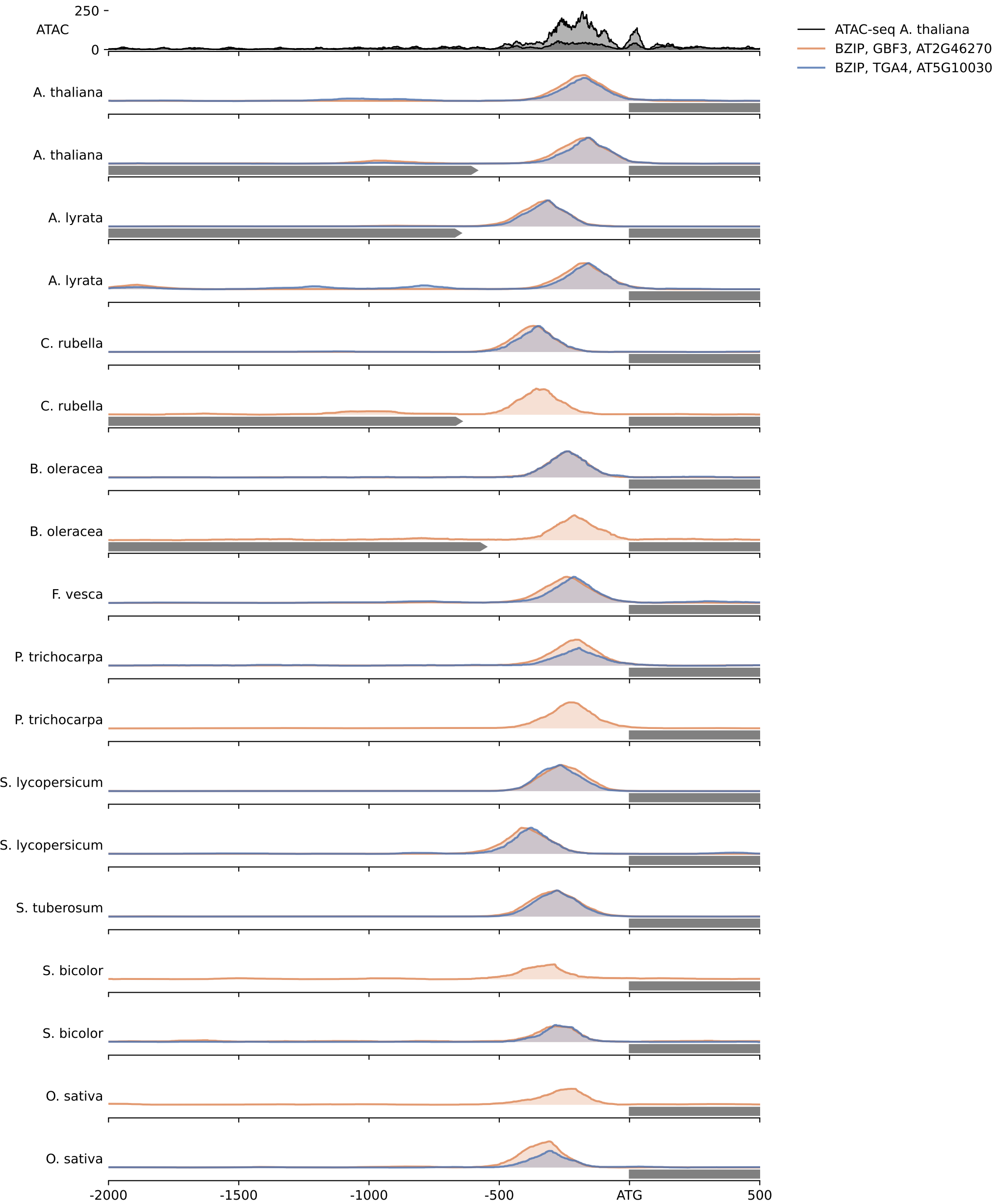
A. thaliana target: AT4G03550, GSL05, Encodes a callose synthase that is required for wound and papillary callose formation in response to fungal pathogens Erysiphe and Blumeria. Mutants are resistant to *P. parasitica* and exhibit an exaggerated PR1 response. Contributes to PAMP-induced basal defense. The mRNA is cell-to-cell mobile.

A. thaliana target: AT4G04970, GSL1, encodes a gene similar to callose synthase The mRNA is cell-to-cell mobile.



A. thaliana target: AT4G12460, ORP2B, OSBP(oxysterol binding protein)-related protein 2B;(source:Araport11)

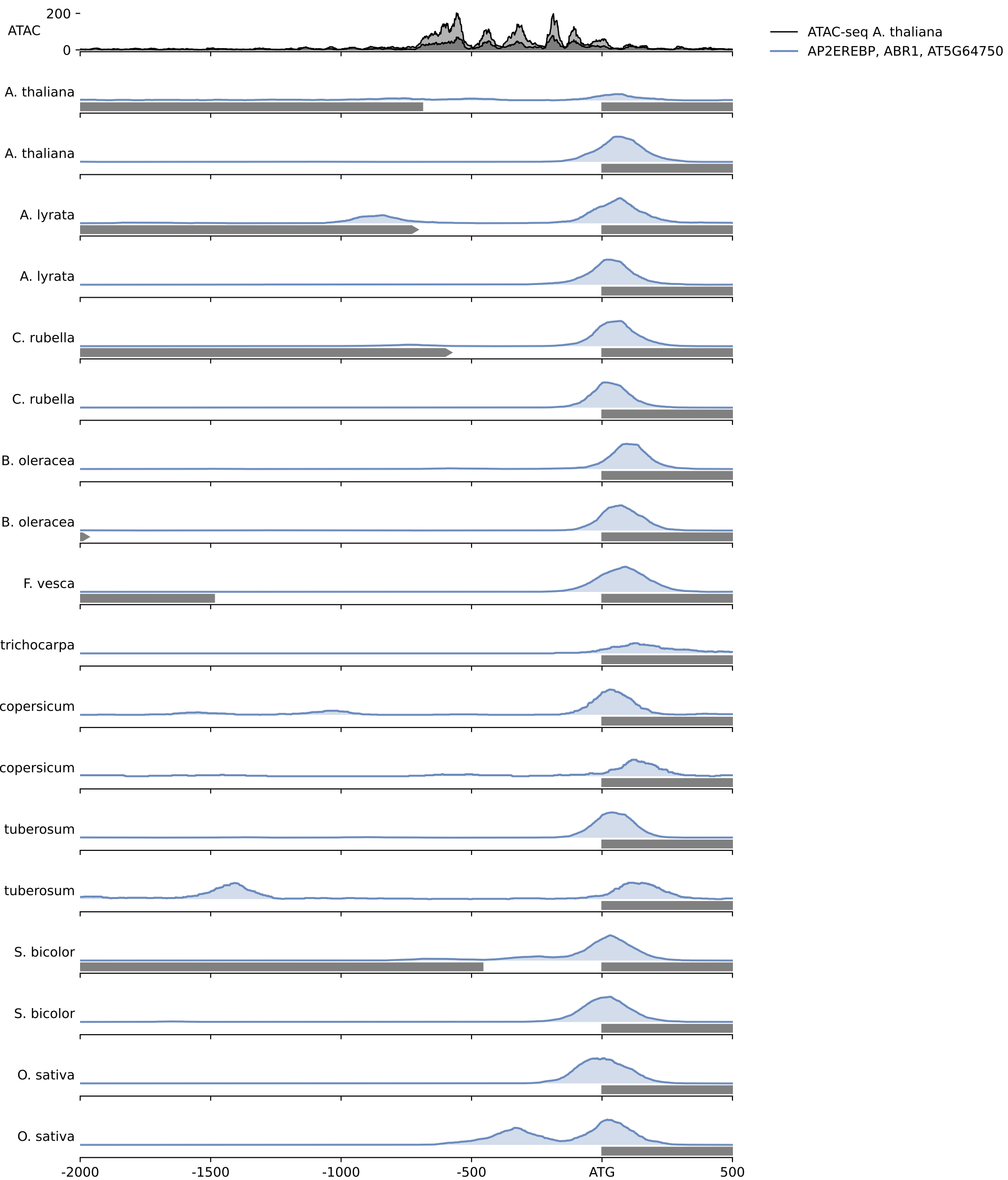
A. thaliana target: AT4G22540, ORP2A, OSBP(oxysterol binding protein)-related protein 2A;(source:Araport11)



A. thaliana target: AT4G10730, Protein kinase superfamily protein

A. thaliana target: AT4G24100, Protein kinase superfamily protein

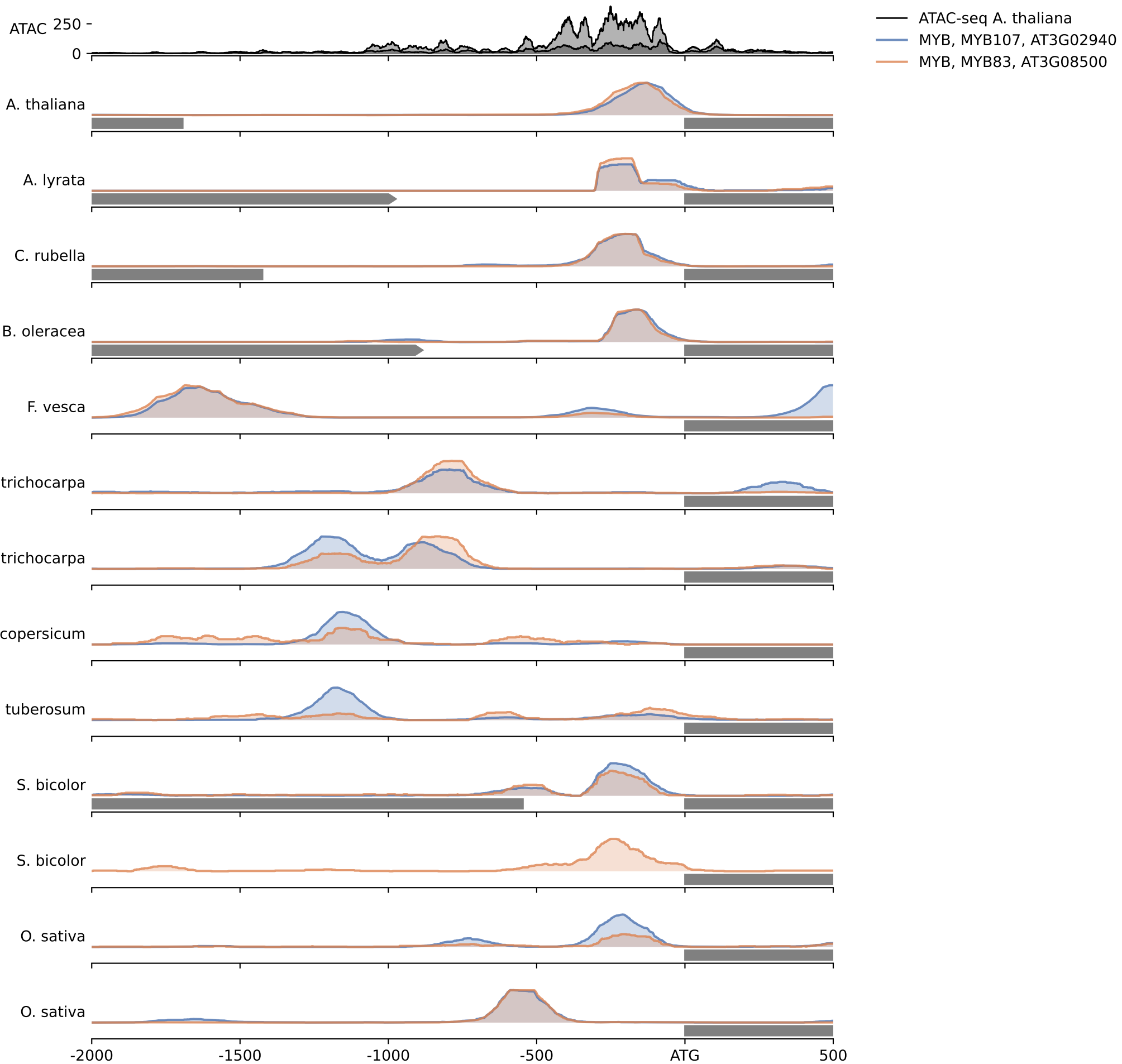
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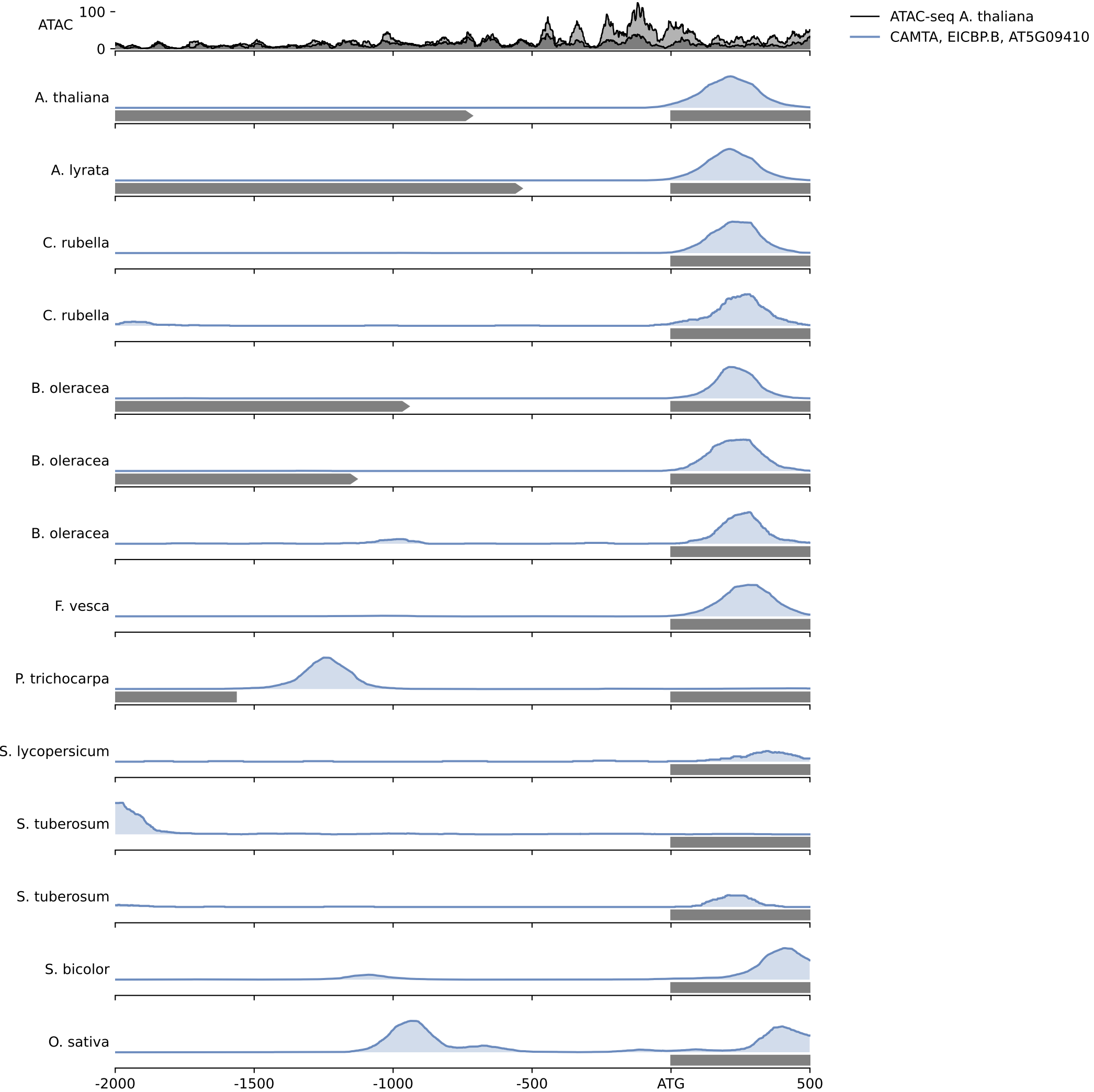
A. thaliana target: AT4G26860, Putative pyridoxal phosphate-dependent enzyme, YBL036C type;(source:Araport11)

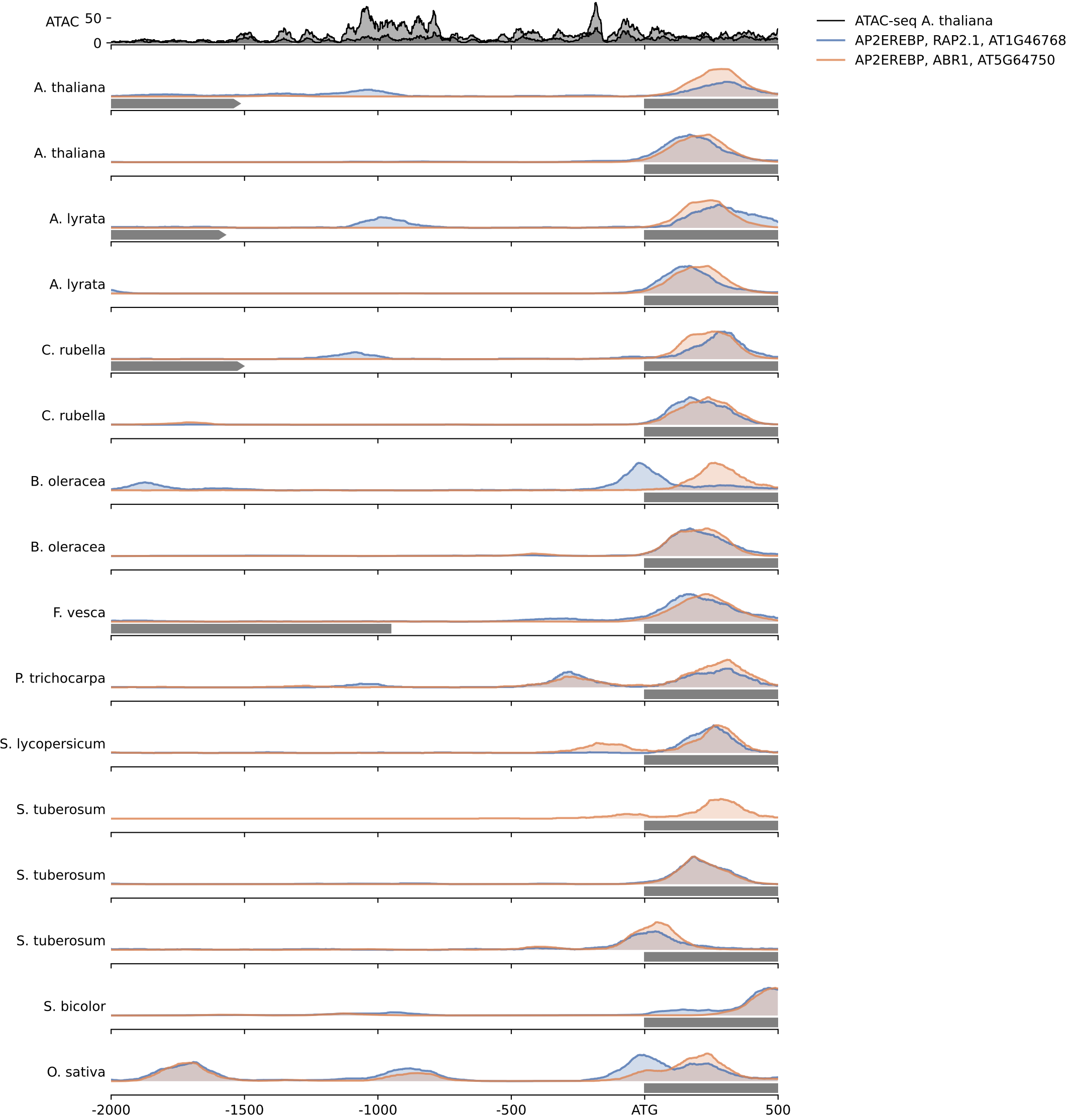
A. thaliana target: AT1G11930, Putative pyridoxal phosphate-dependent enzyme, YBL036C type;(source:Araport11)

OG0003723



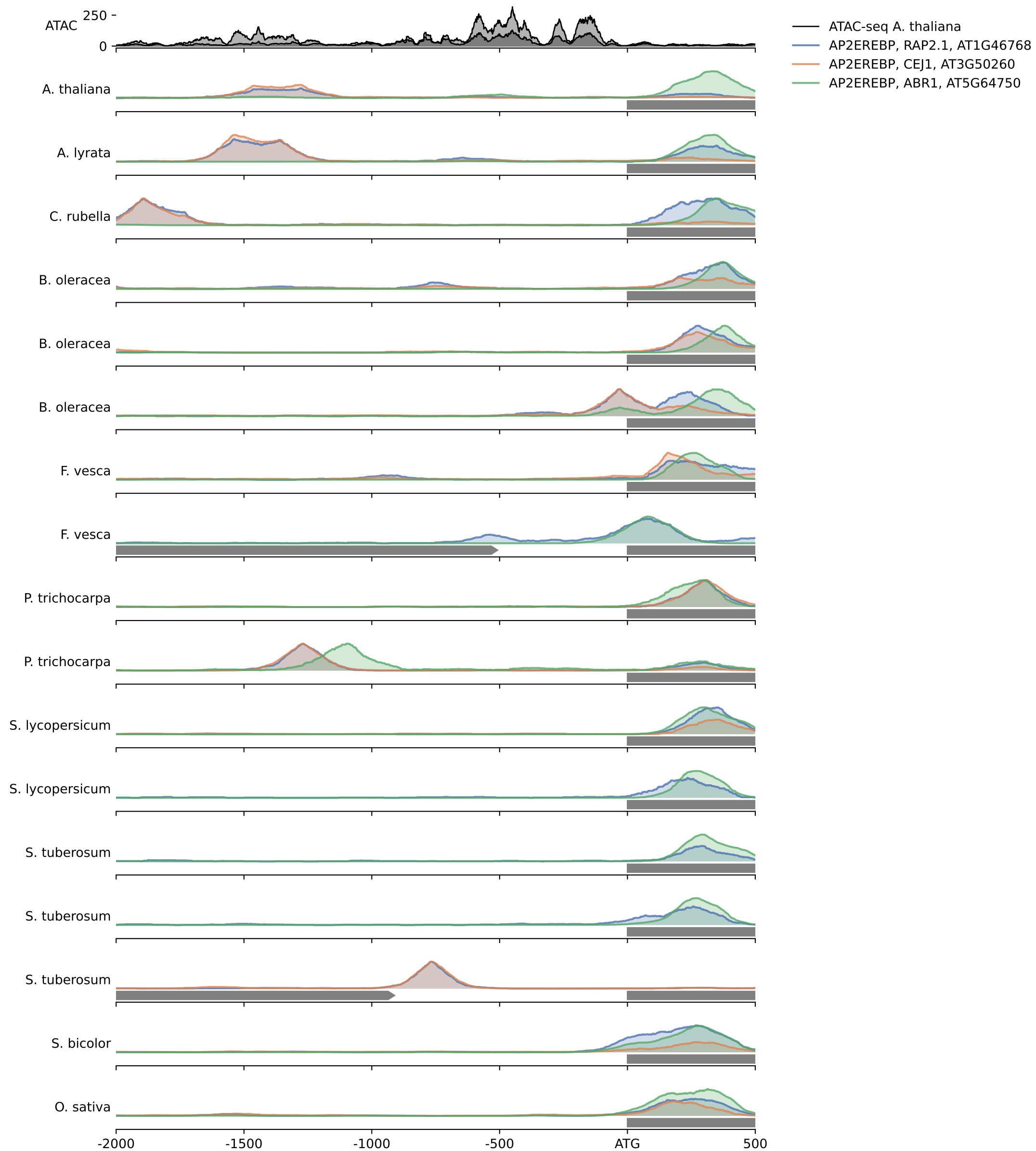
A. thaliana target: AT5G48930, HCT, At5g48930 has been shown to encode for the hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase (HCT) both synthesizing and catabolizing the hydroxycinnamoyl esters (coumaroyl/caffeoyl shikimate and quinate) involved in the phenylpropanoid pathway. Influence on the accumulation of flavonoids which in turn inhibit auxin transport and reduce plant growth. The mRNA is cell-to-cell mobile.

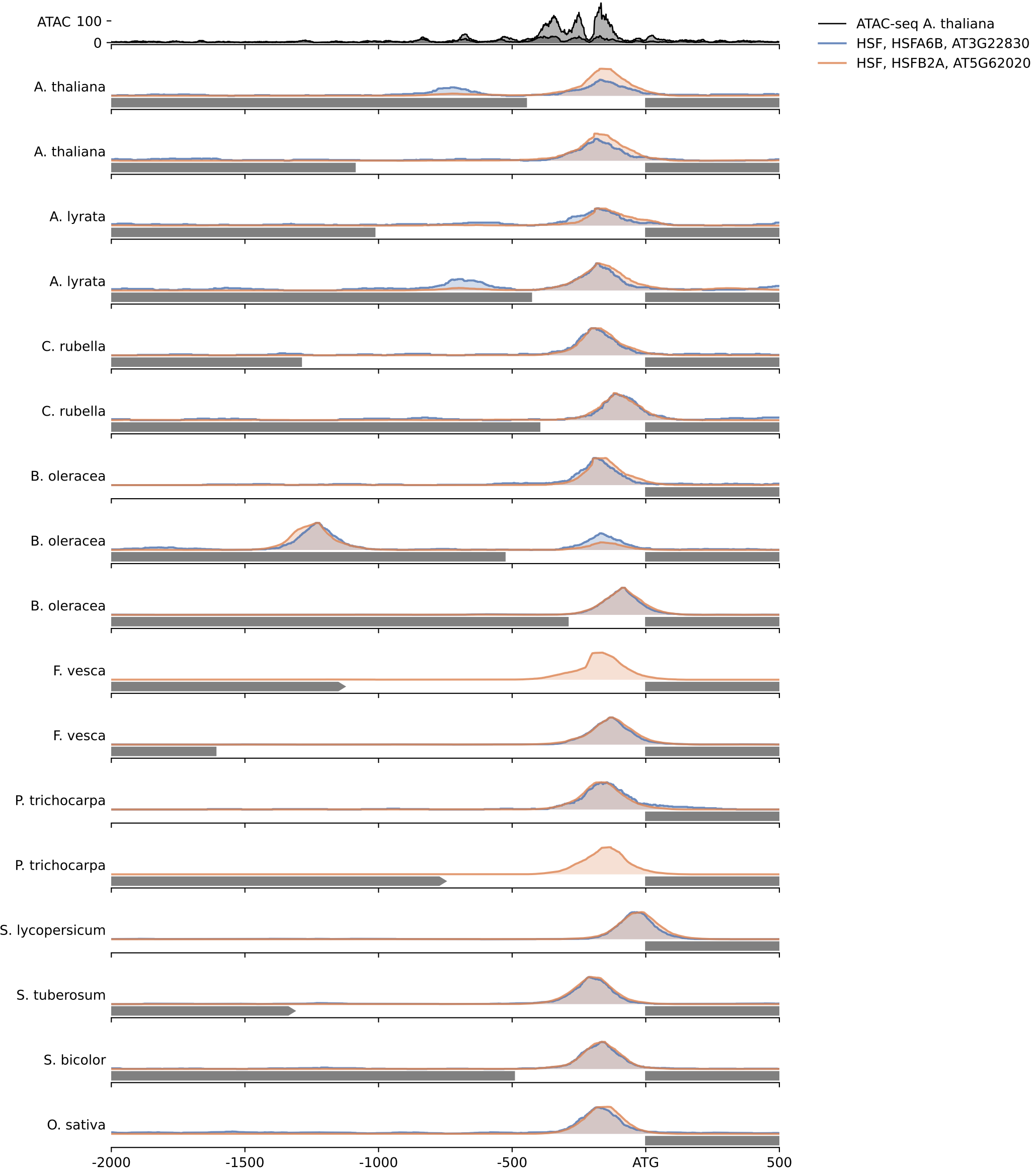




A. thaliana target: AT4G36830, HOS3-1, ELO family protein.

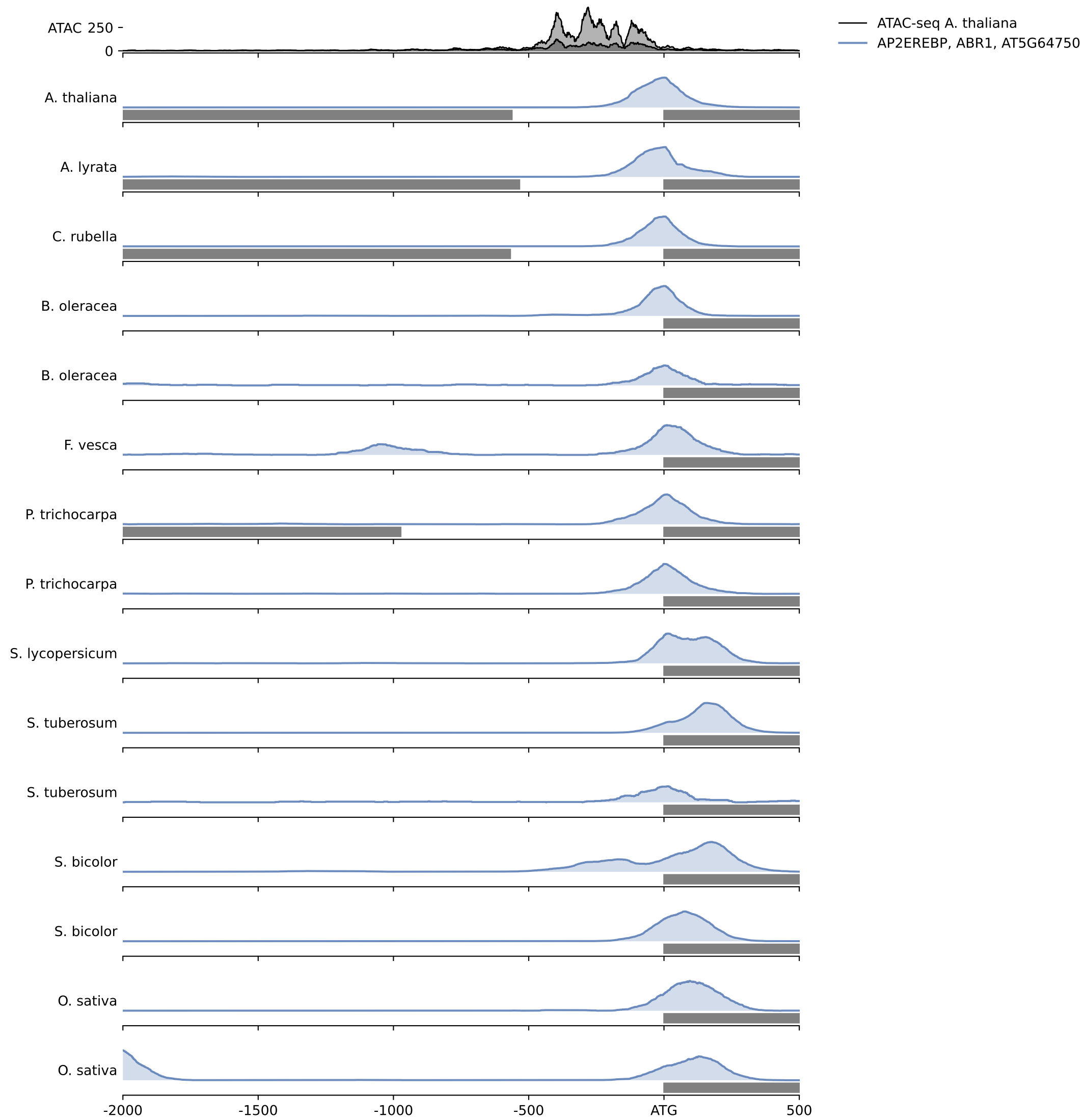
A. thaliana target: AT1G75000, ELO family protein; fatty acid elongase which takes part in the elongation of LCFAs to VLCFAs; putative mediator of NOS.



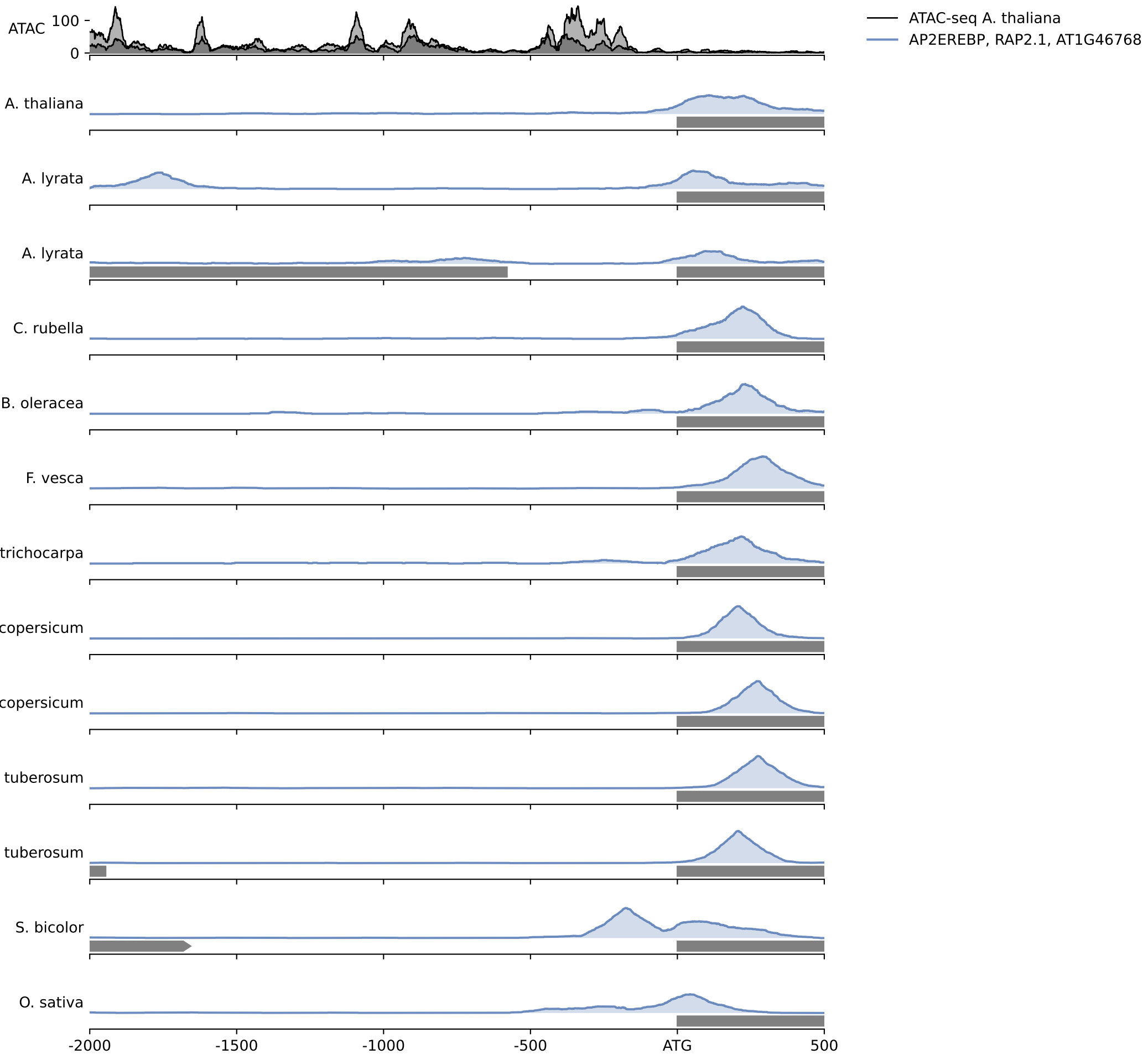


A. thaliana target: AT5G51440, HSP20-like chaperones superfamily protein;(source:Araport11)

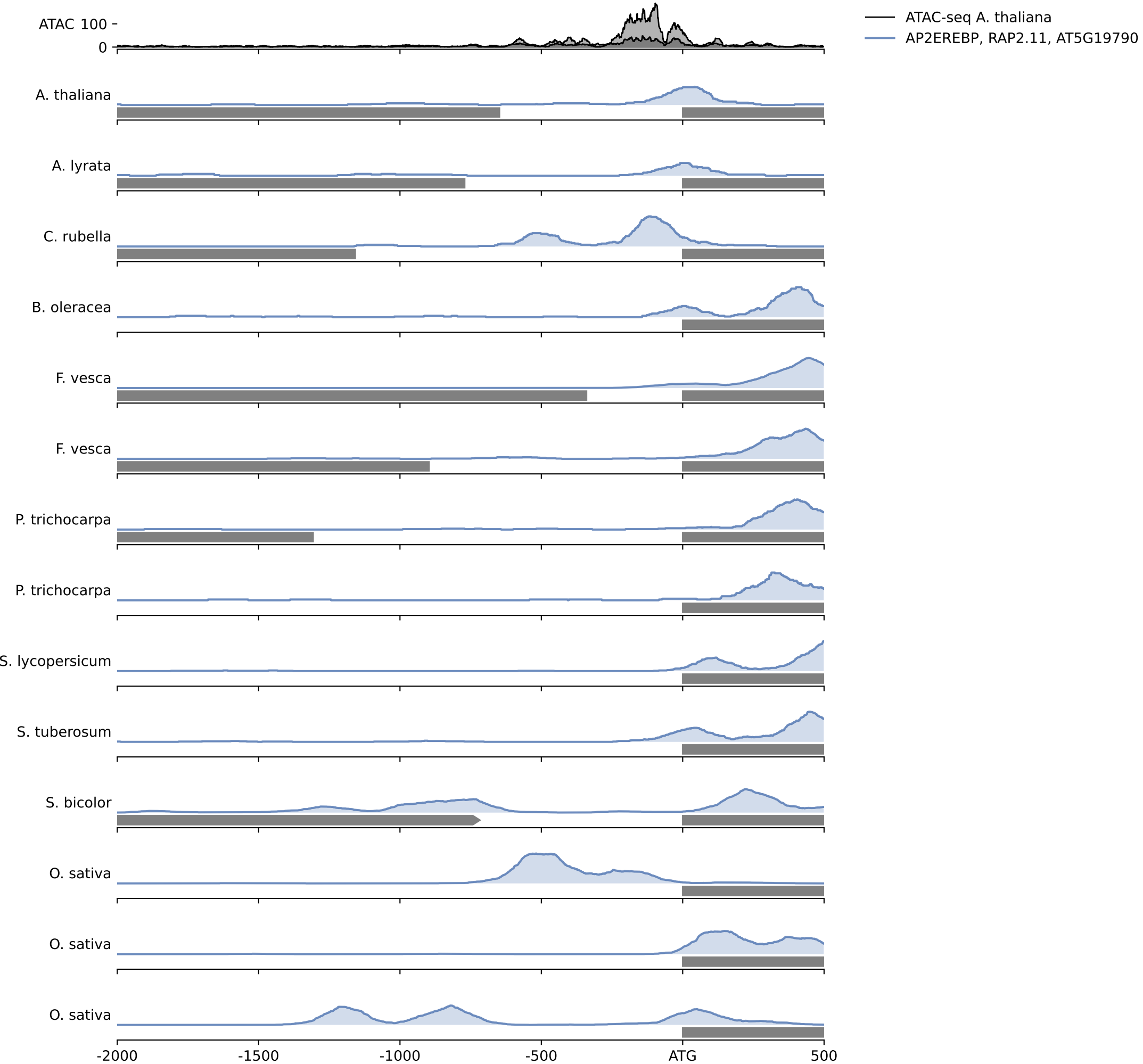
A. thaliana target: AT4G25200, HSP23.6-MITO, AtHSP23.6-mito mRNA, nuclear gene encoding mitochondrial



OG0003973

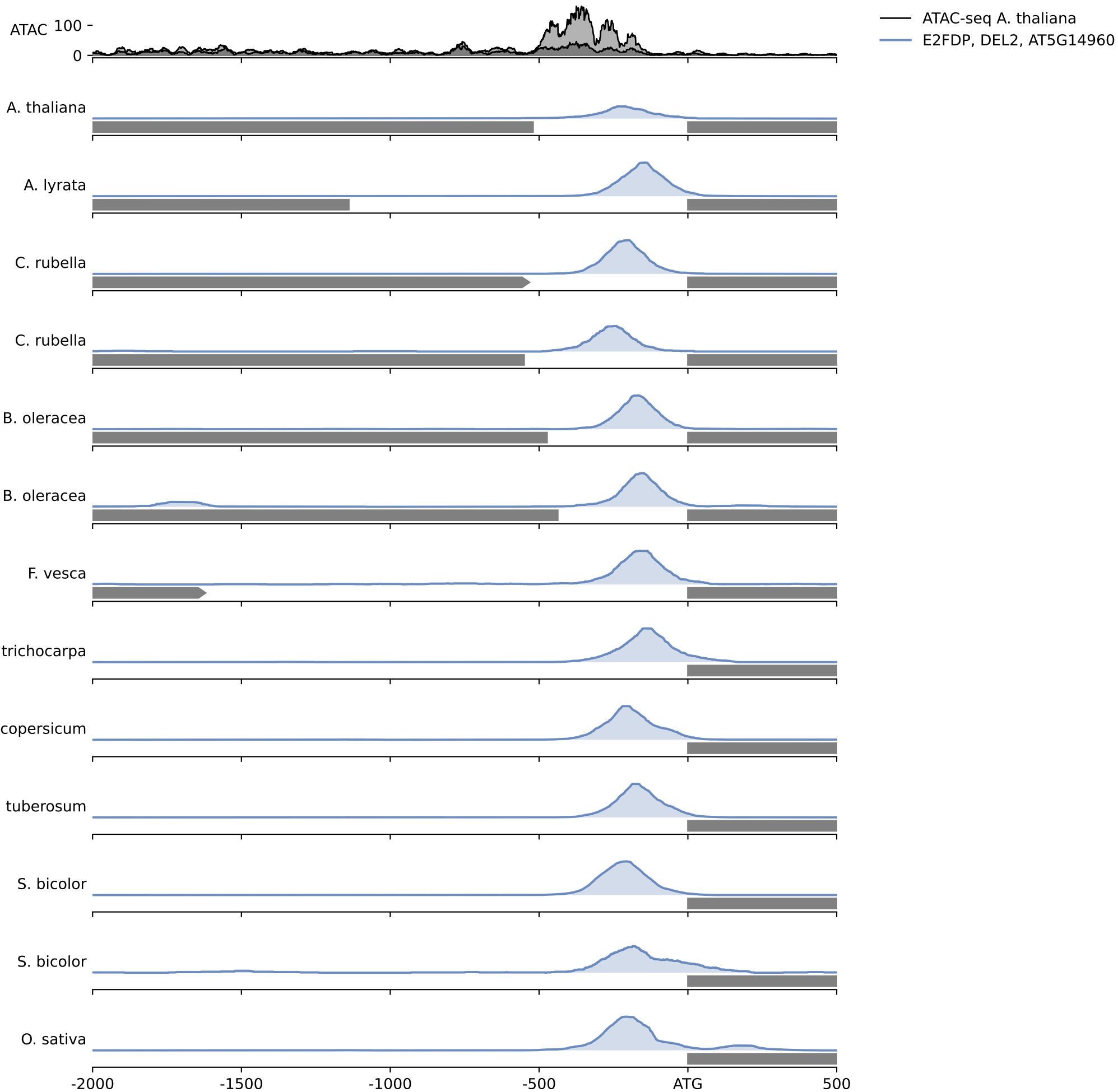


A. thaliana target: AT5G14870, CNGC18, Encodes a member of the cyclic nucleotide gated channel family that is asymmetrically localized to the plasma membrane at the growing tip of the pollen tube and is involved in pollen tube growth and pollen tube guidance to ovules. It likely directly transduces a cNMP signal into an ion flux that can produce a localized signal capable of regulating the pollen tip-growth machinery. Also functions as a Ca²⁺ permeable channel.



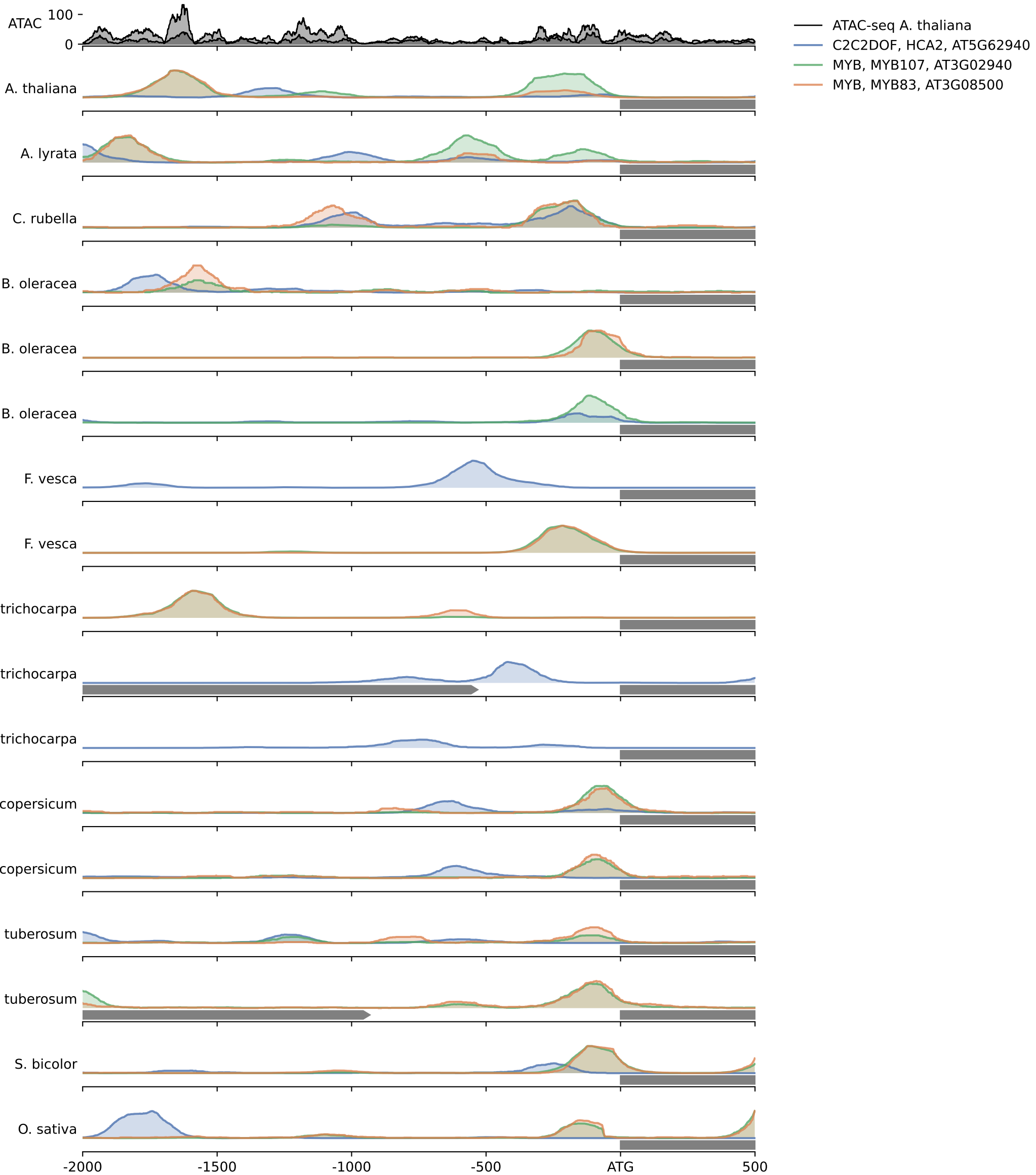
A. thaliana target: AT3G46740, TOC75-III, Component of the translocon outer membrane (TOC) complex. Forms the outer envelope translocation channel (beta-barrel). Plays a role in preprotein conductance. Imported into chloroplast. Expressed in young dividing photosynthetic tissues. Knockout mutants are embryo lethal with arrested development at the two-cell stage. Knockout mutants have abnormal etioplasts.

OG0003985

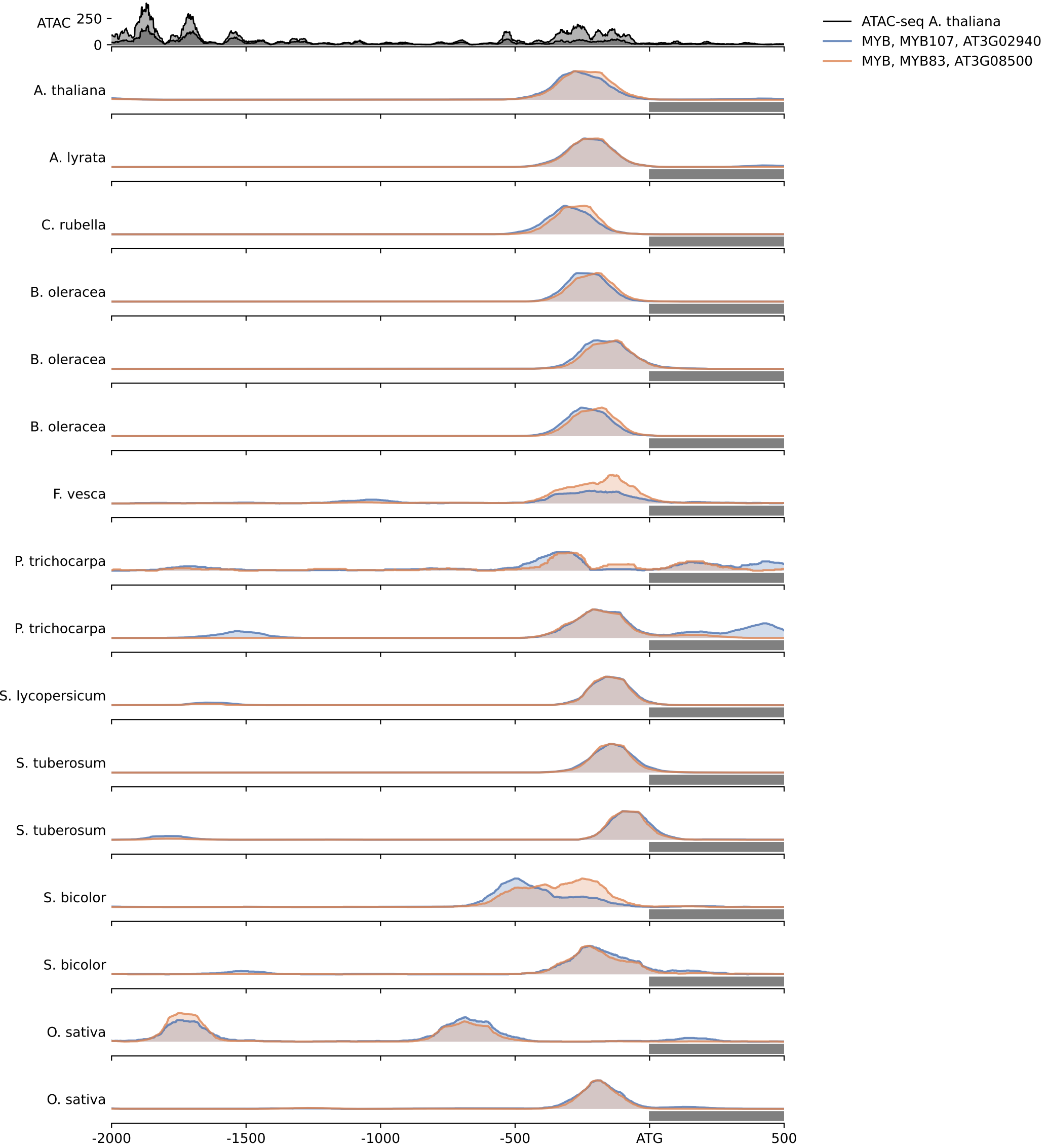


A. thaliana target: AT3G59550, SYN3, Encodes an alpha-kleisin protein that is localized primarily in the nucleolus and is essential for megagametogenesis and plays an important role in pollen development. alpha-kleisins are core components of meiotic and mitotic cohesin complexes.

OG0004035

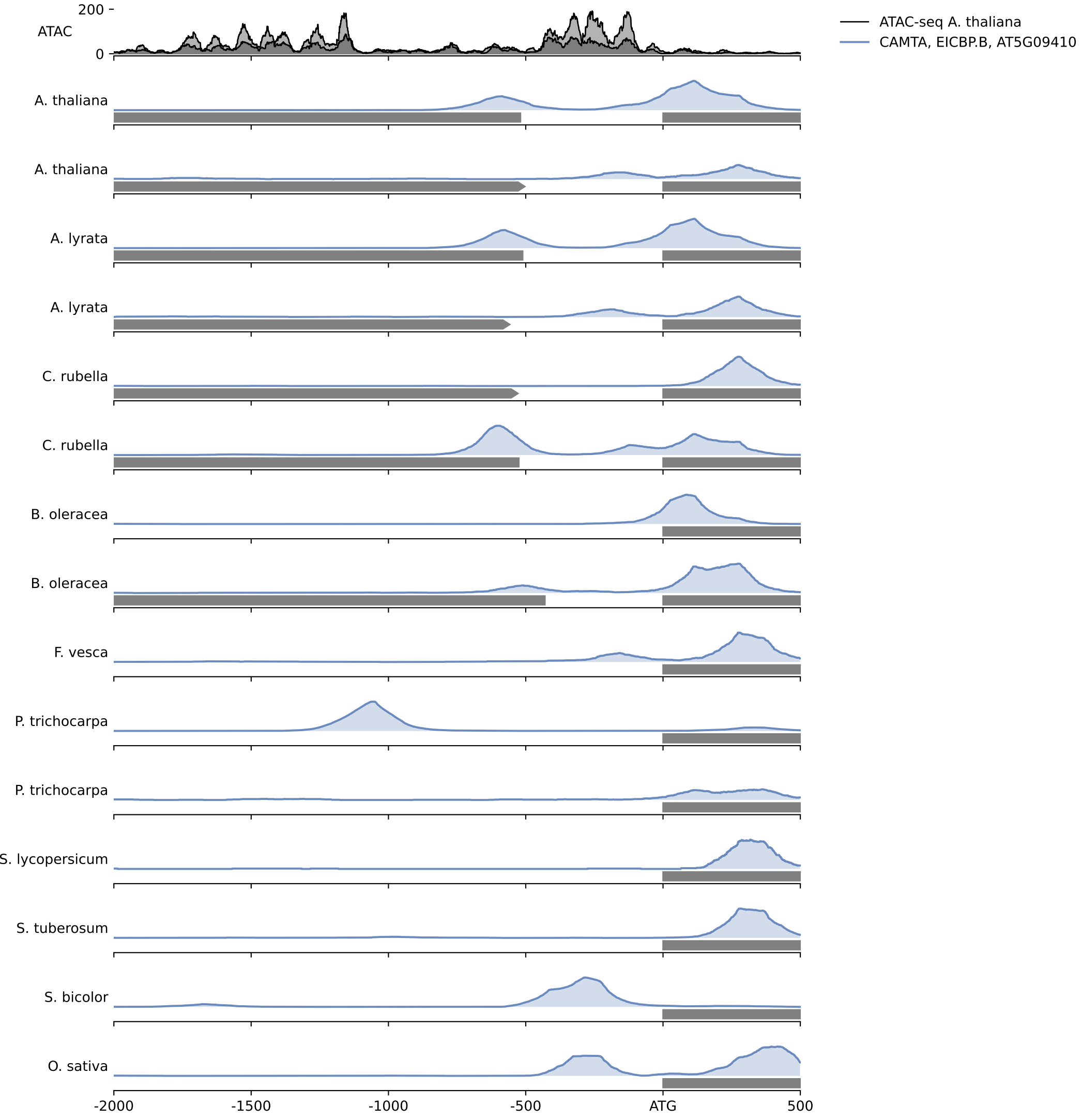


A. thaliana target: AT2G40890, CYP98A3, encodes coumarate 3-hydroxylase (C3H), a P450-dependent monooxygenase. Involved in lignin biosynthesis and flavonoid biosynthesis. Also affects the biosynthesis of coumarins such as scopoletin and scopolin as a branching-out-pathway from the phenylpropanoid acid level.



A. thaliana target: AT2G30490, C4H, Encodes a cinnamate-4-hydroxylase. Mutations in this gene impact phenylpropanoid metabolism, growth and development.

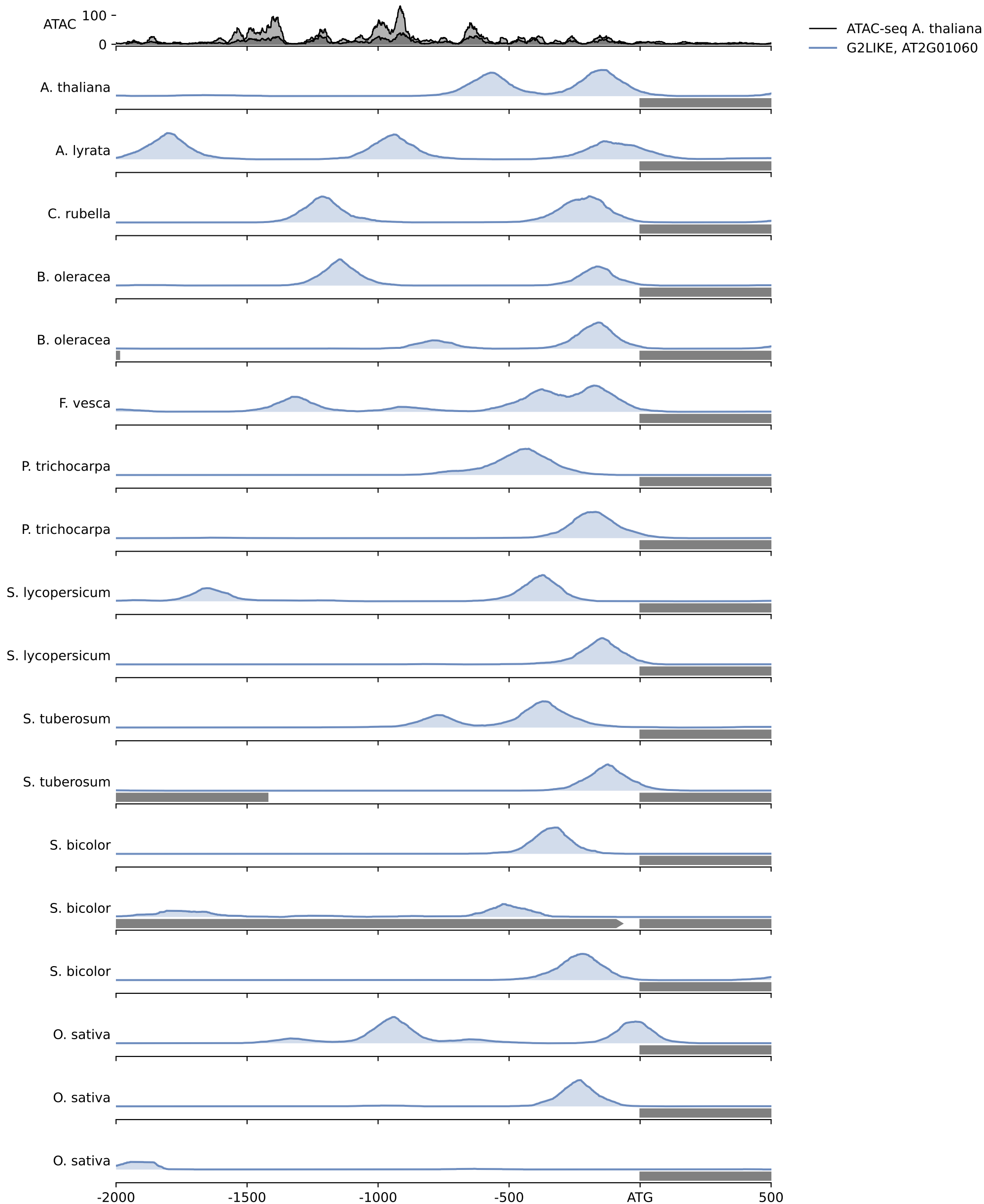
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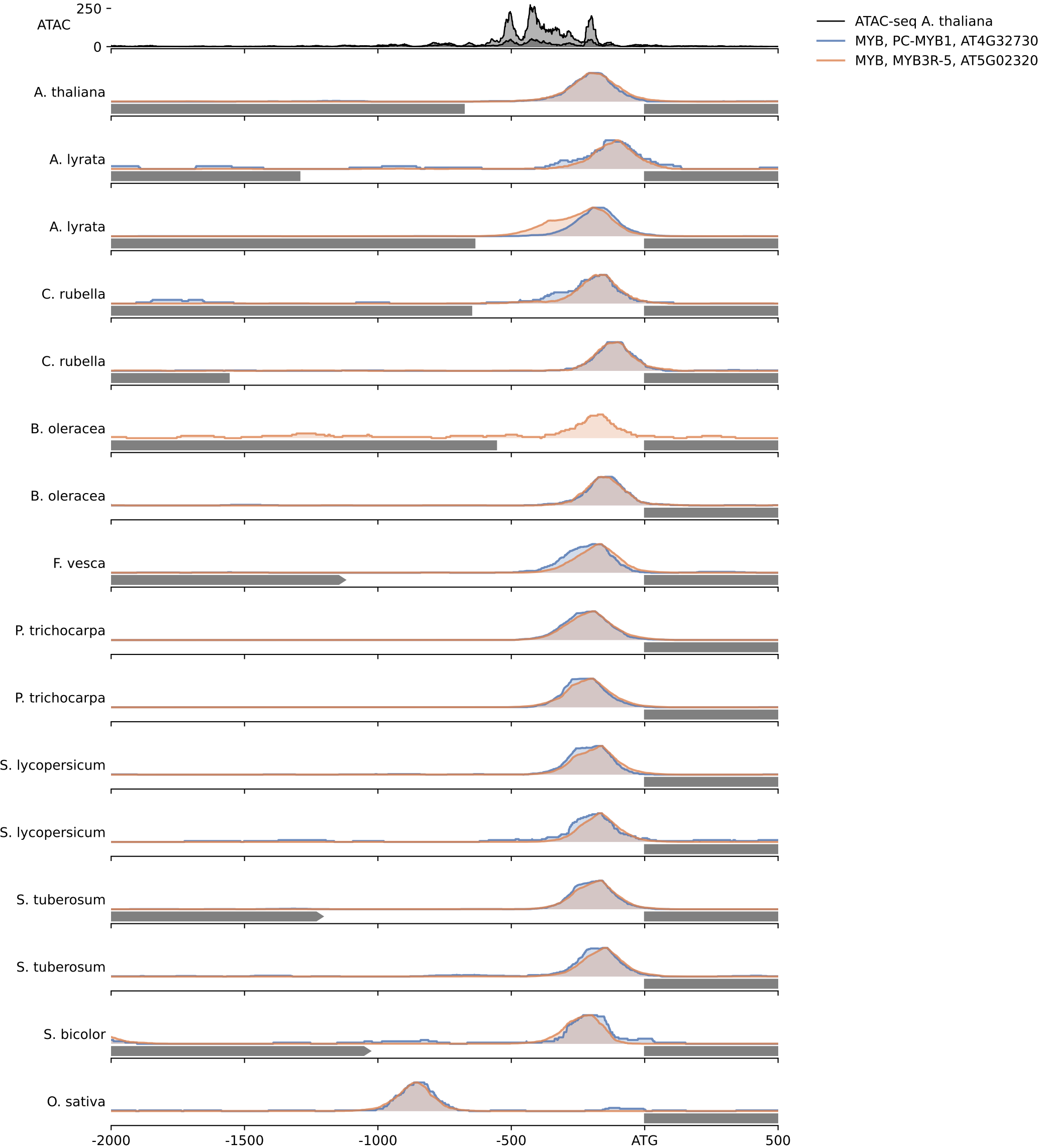
A. thaliana target: AT3G03160, B-cell receptor-associated-like protein;(source:Araport11)

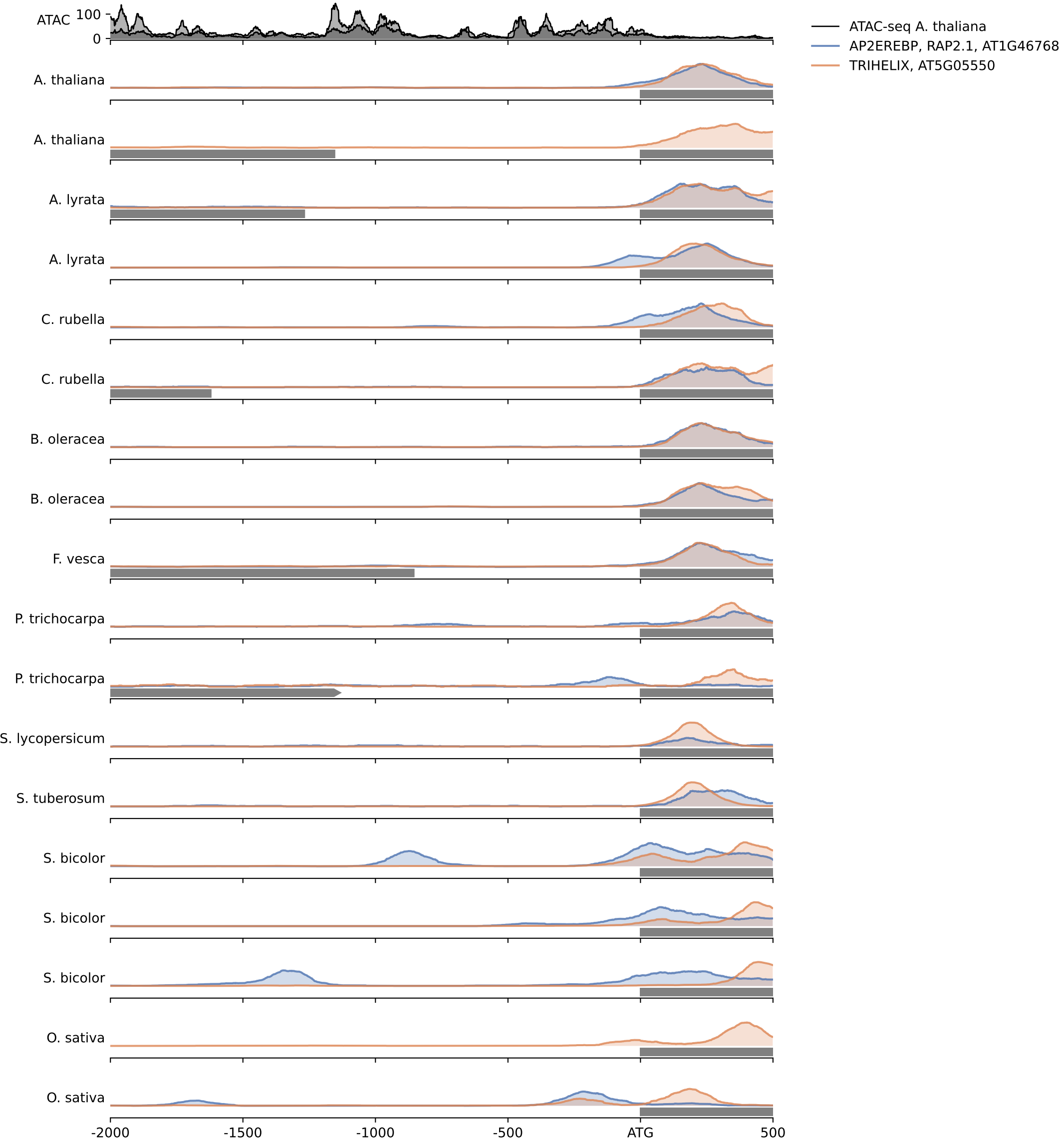
A. thaliana target: AT5G17190, B-cell receptor-associated-like protein;(source:Araport11)

OG0004069



A. thaliana target: AT5G01220, SQD2, Encodes a UDP-sulfoquinovose:DAG sulfoquinovosyltransferase that is involved in sulfolipid biosynthesis and whose expression is responsive to both phosphate (Pi) and phosphite (Phi) in both roots and shoots.





A. thaliana target: AT5G04770, CAT6, Encodes a member of the cationic amino acid transporter (CAT) subfamily of amino acid polyamine choline transporters. Does not mediate efficient uptake of basic amino acids in yeast or Xenopus systems but can transport neutral and acidic amino acid analogs. Expressed in sink tissues. Induced during infestation of roots by the plant parasitic root-knot nematode, Meloidogyne incognita. Localized in the plasma membrane.

A. thaliana target: AT3G10600, CAT7, Encodes a member of the cationic amino acid transporter (CAT) subfamily of amino acid polyamine choline transporters.

OG0004160

ATAC 250 -
0

— ATAC-seq A. thaliana
— MYB, MYB107, AT3G02940

A. thaliana

A. lyrata

C. rubella

B. oleracea

F. vesca

P. trichocarpa

S. lycopersicum

S. lycopersicum

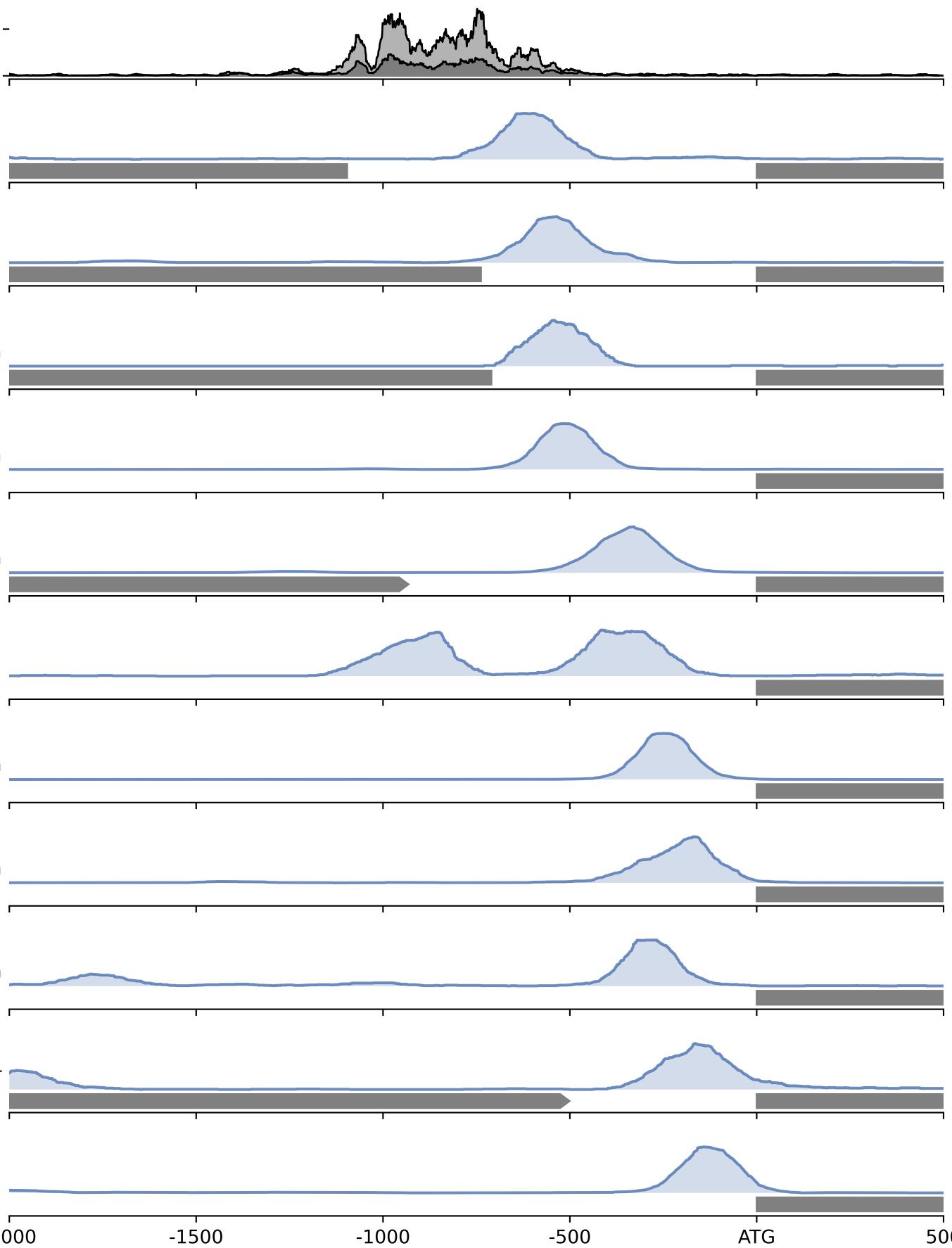
S. tuberosum

S. bicolor

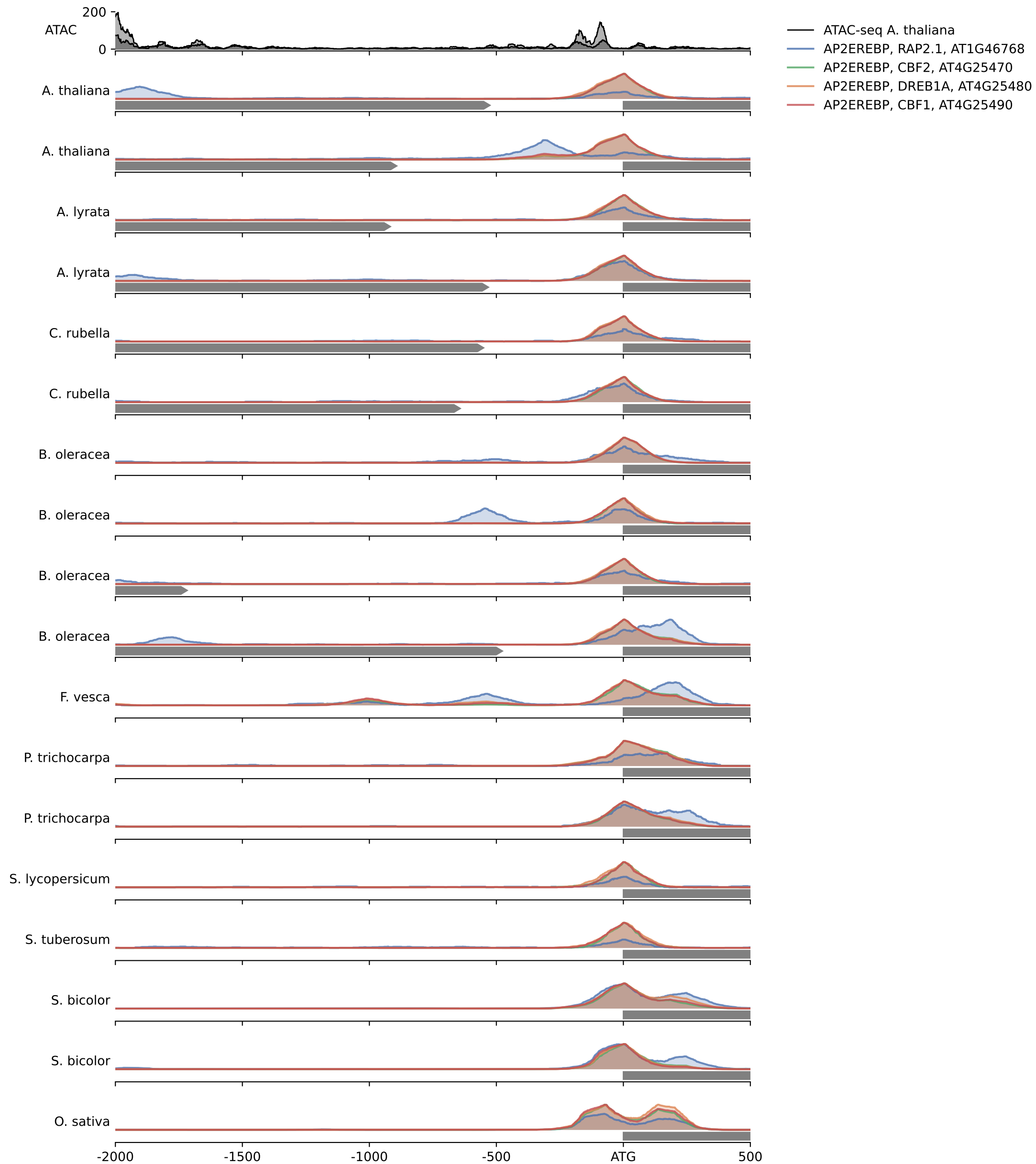
O. sativa

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A. thaliana target: AT1G06550, ATP-dependent caseinolytic (Clp) protease/crotonase family protein;(source:Araport11)

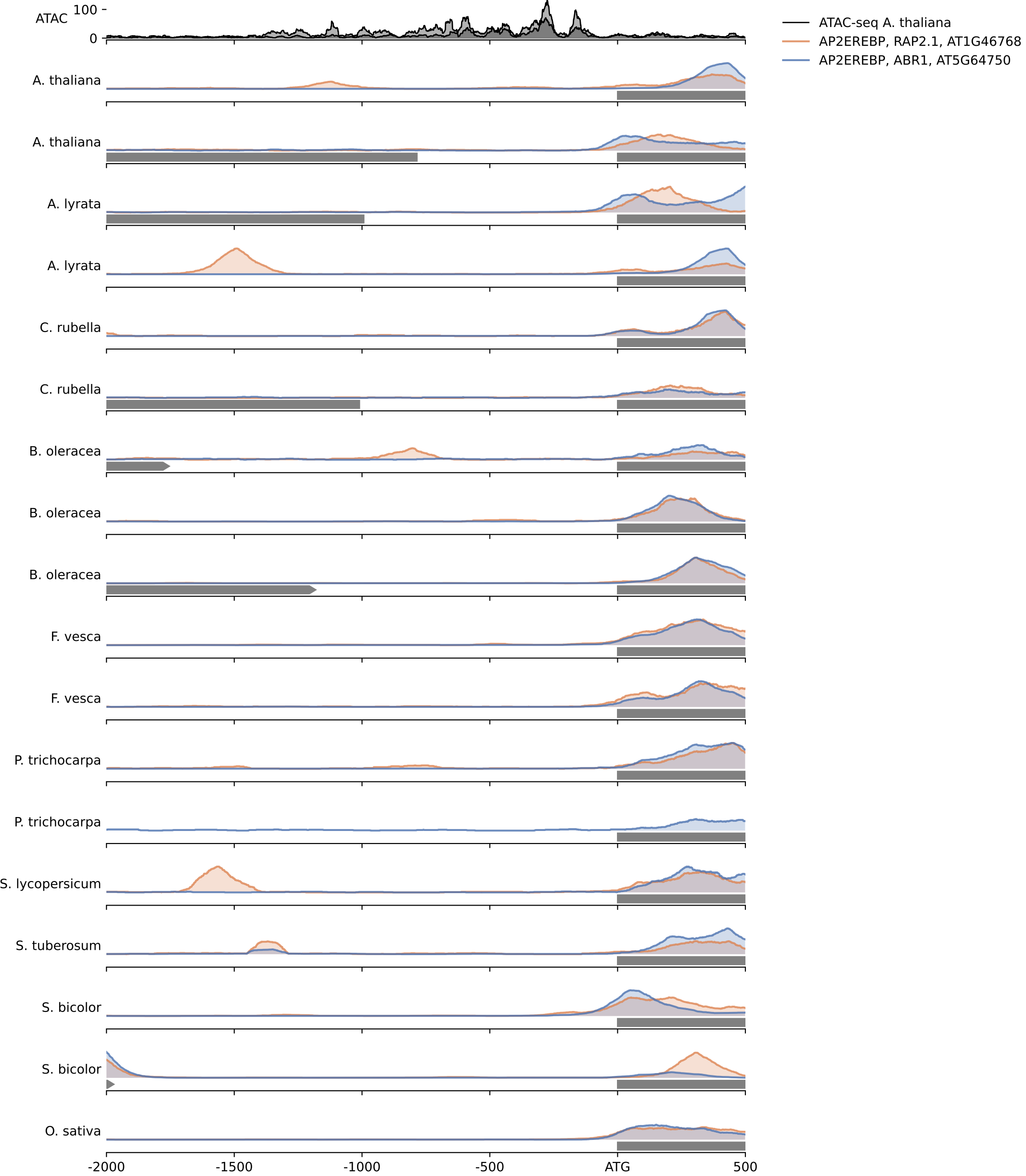


OG0004167



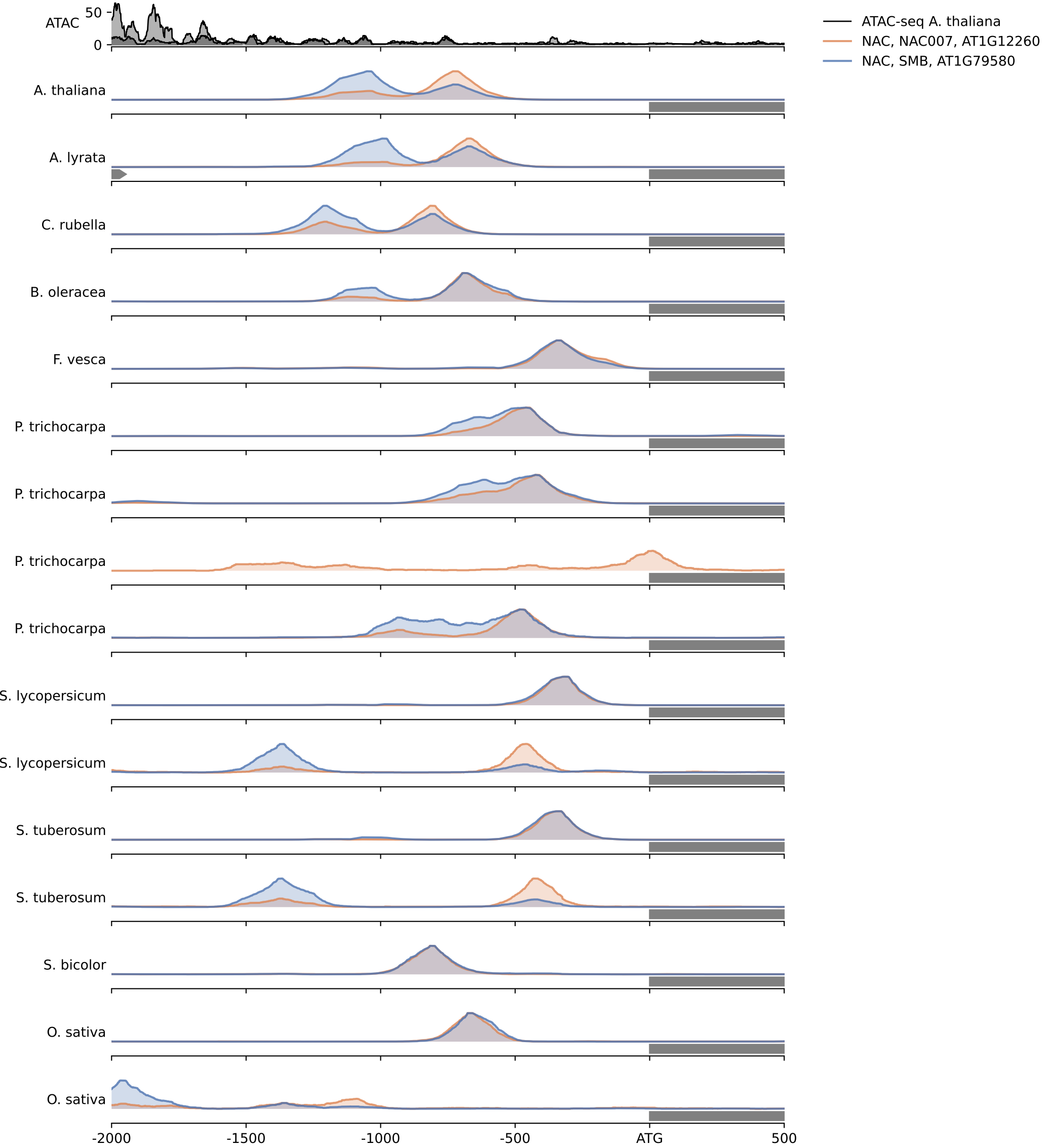
A. thaliana target: AT1G21720, PBC1, 20S proteasome beta subunit PBC1 truncated protein (PBC1)

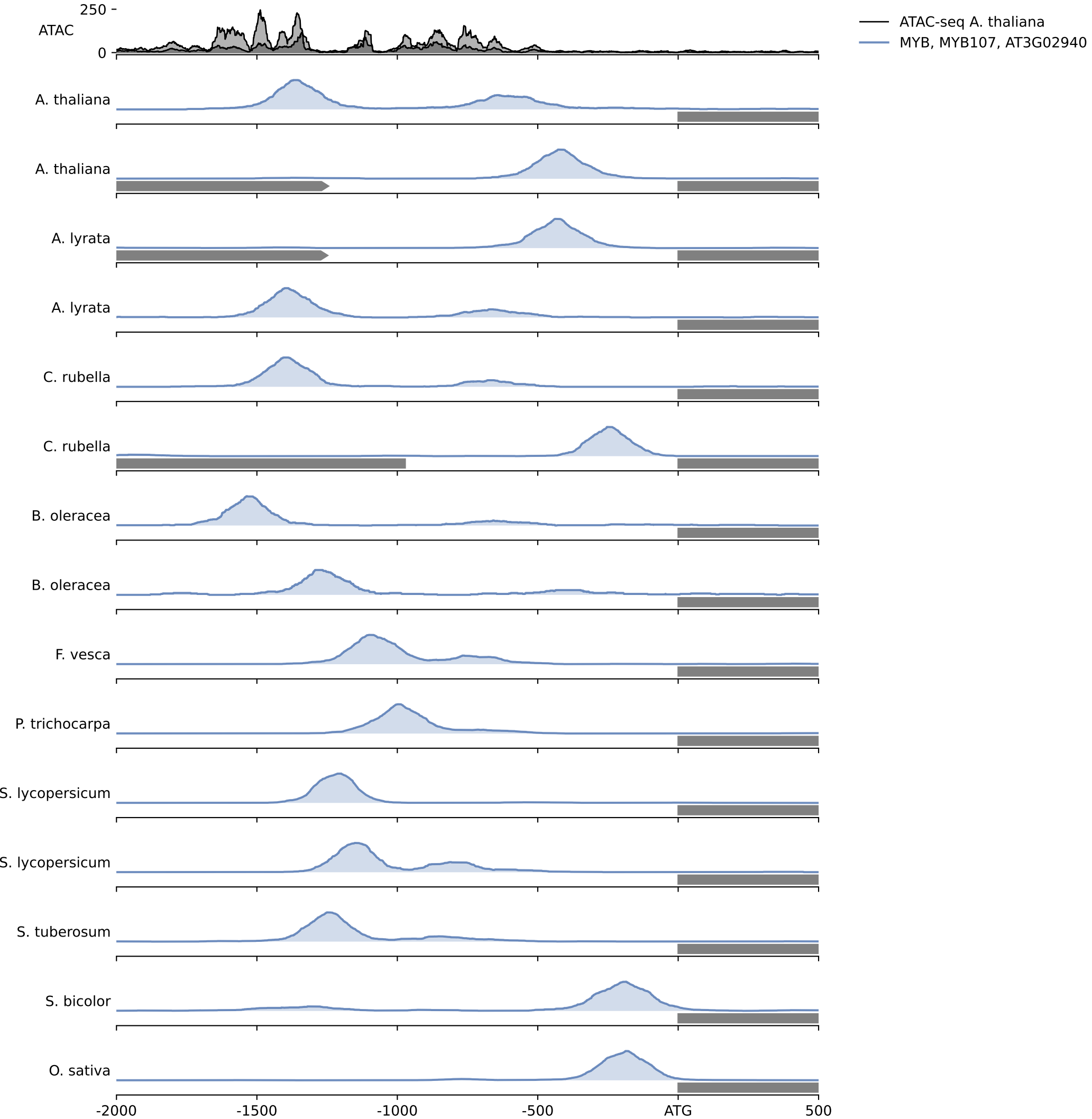
A. thaliana target: AT1G77440, PBC2, Encodes beta subunit of 20s proteasome complex which is involved in protein degradation.



A. thaliana target: AT1G62050, Ankyrin repeat family protein;(source:Araport11)

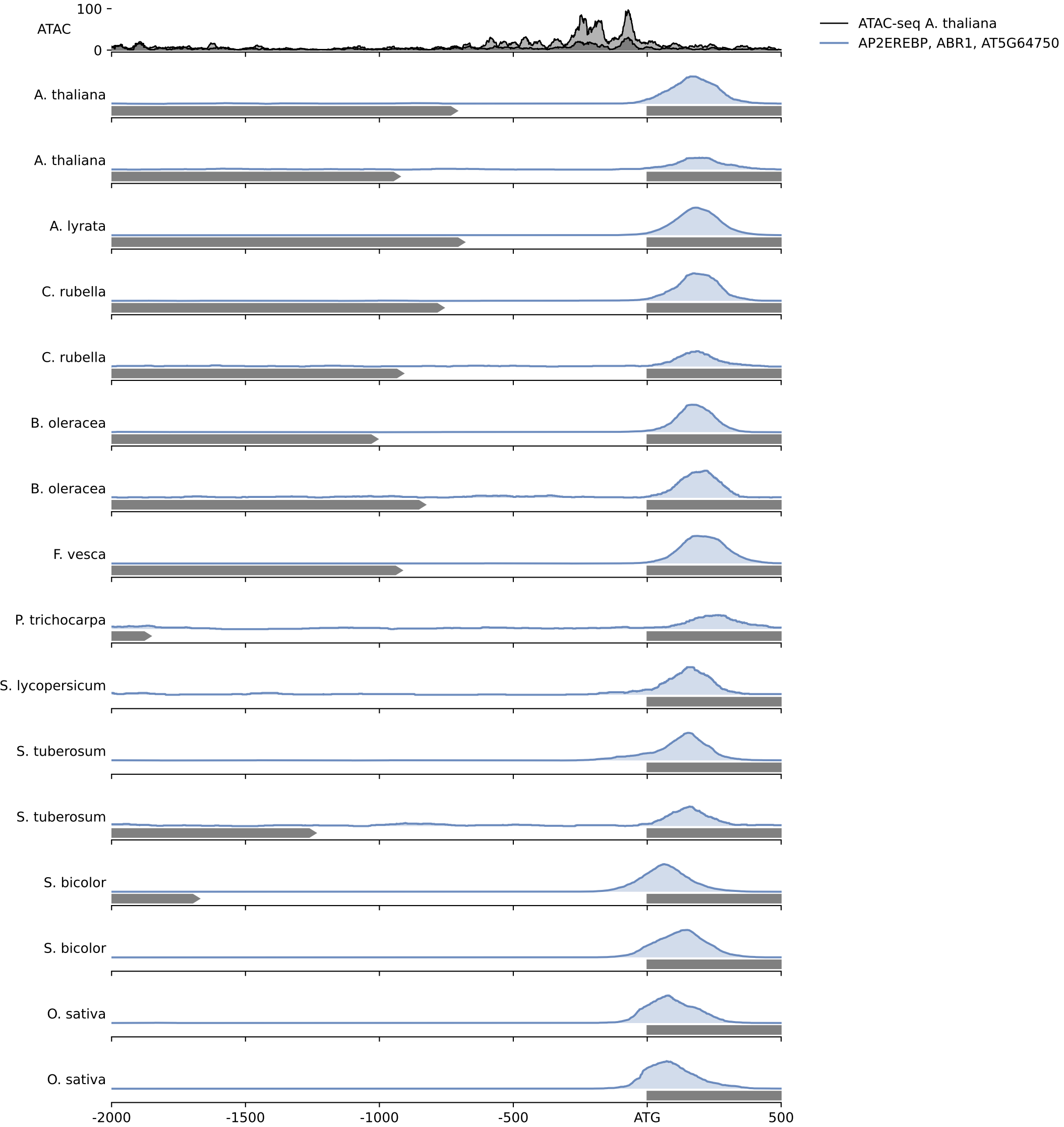
A. thaliana target: AT1G11740, ankyrin repeat family protein;(source:Araport11)





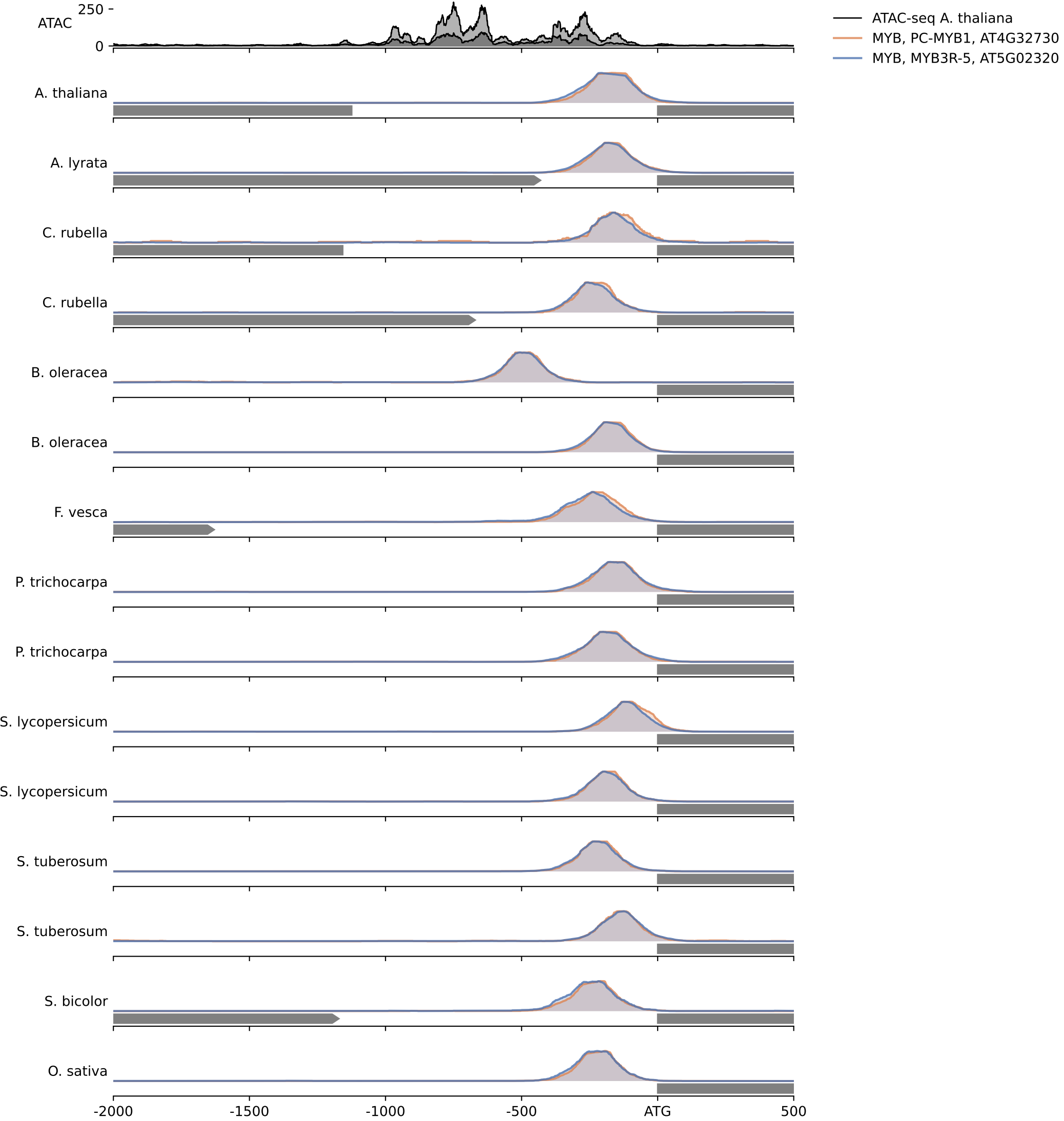
A. thaliana target: AT5G55970, Drought-induced gene encoding an ER-localized RING-type E3 Ub ligase.

A. thaliana target: AT4G26580, RING/U-box superfamily protein;(source:Araport11)

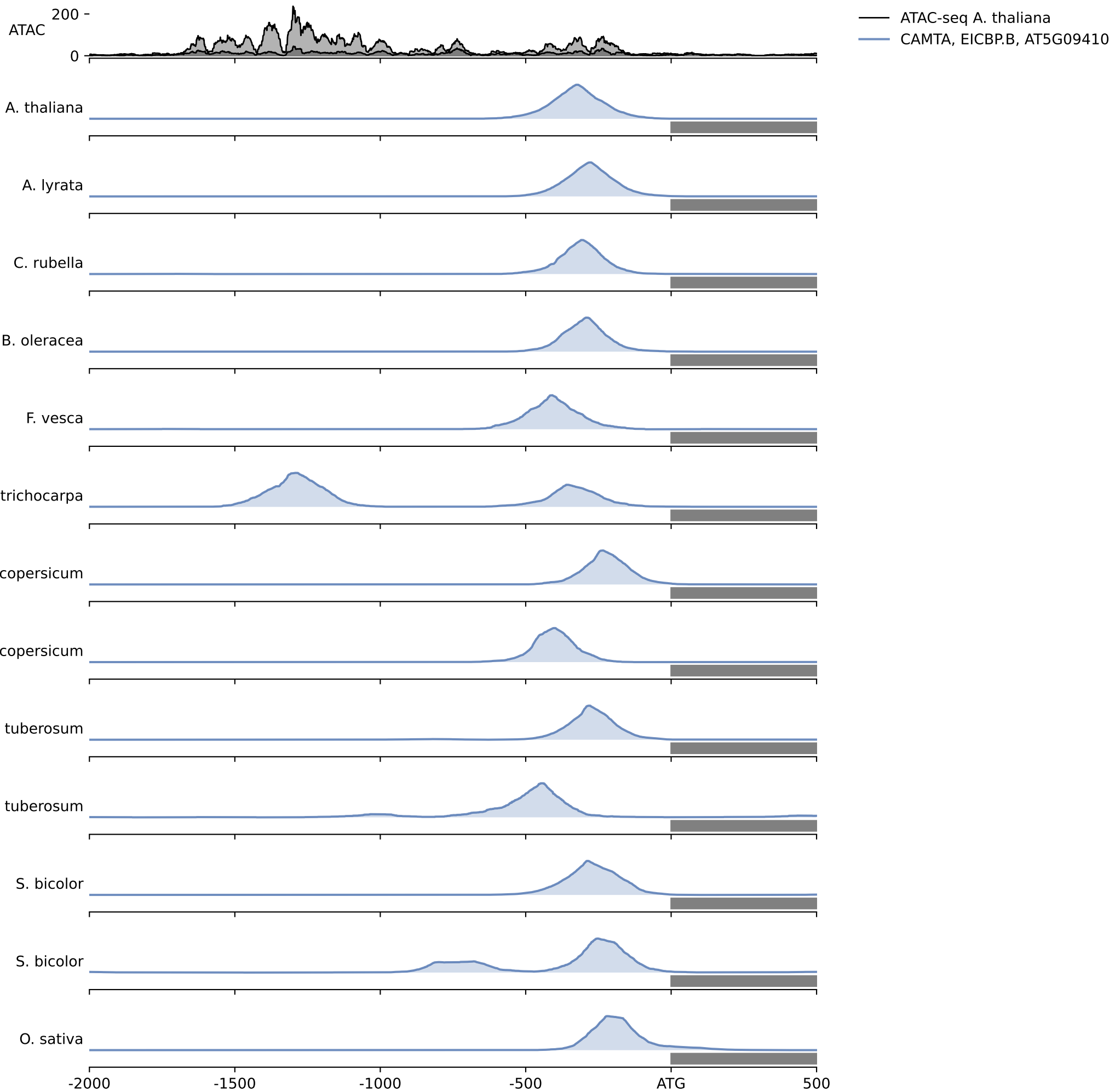


A. thaliana target: AT3G17240, mtLPD2, lipoamide dehydrogenase precursor

A. thaliana target: AT1G48030, mtLPD1, Encodes a mitochondrial lipoamide dehydrogenase whose expression is induced by light.

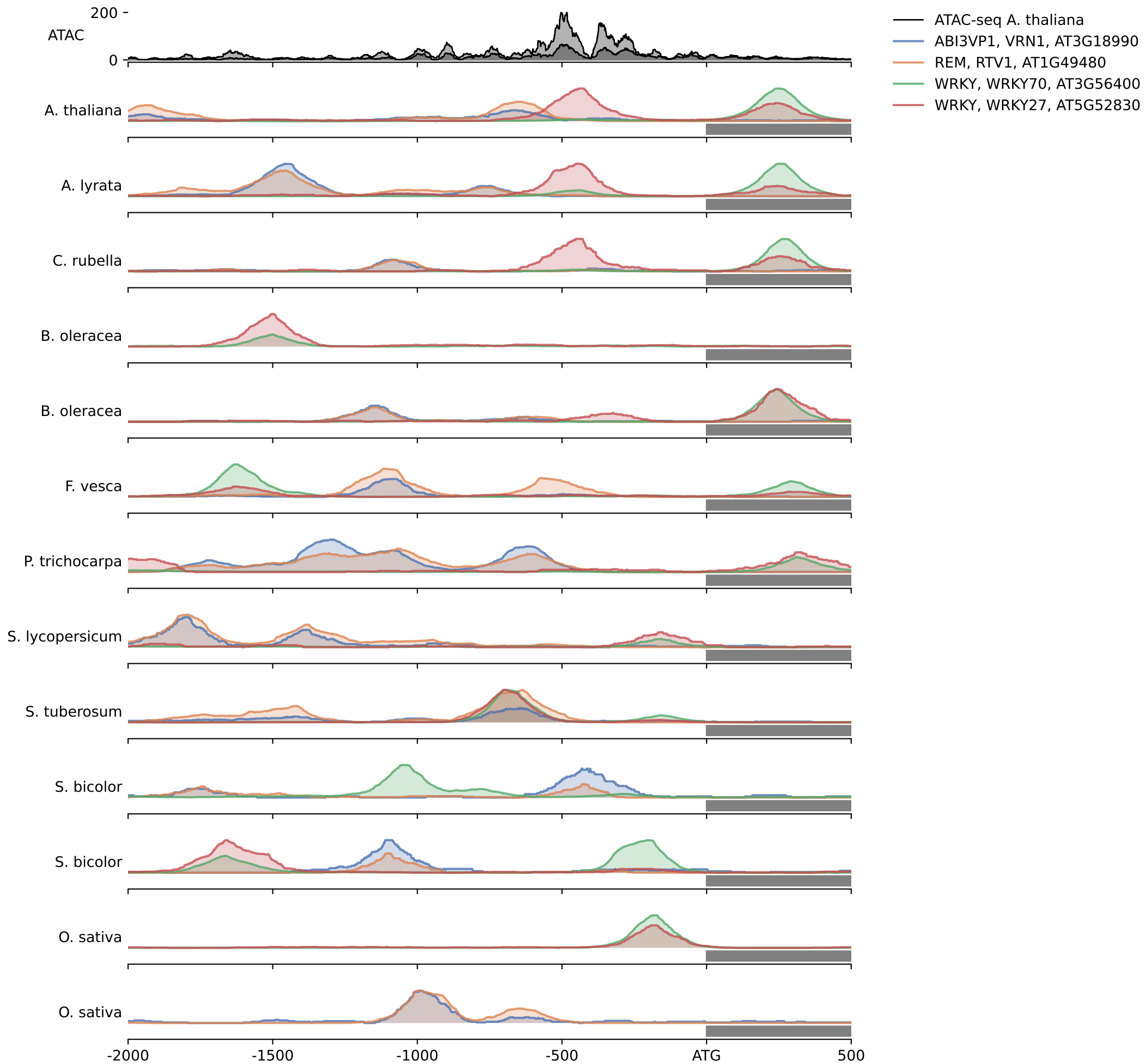


OG0004433

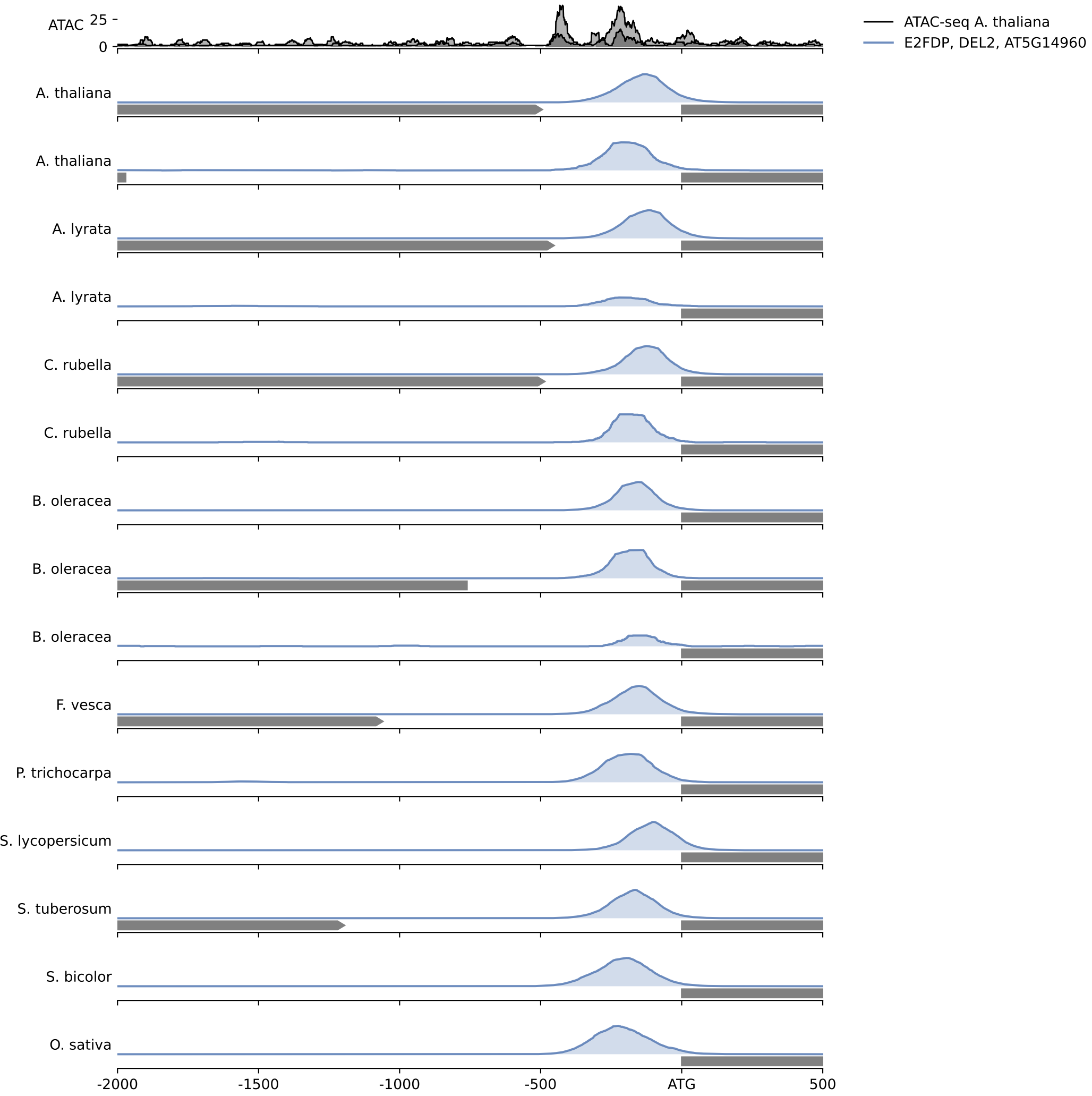


A. thaliana target: AT3G59080, Eukaryotic aspartyl protease family protein;(source:Araport11)

OG0004507

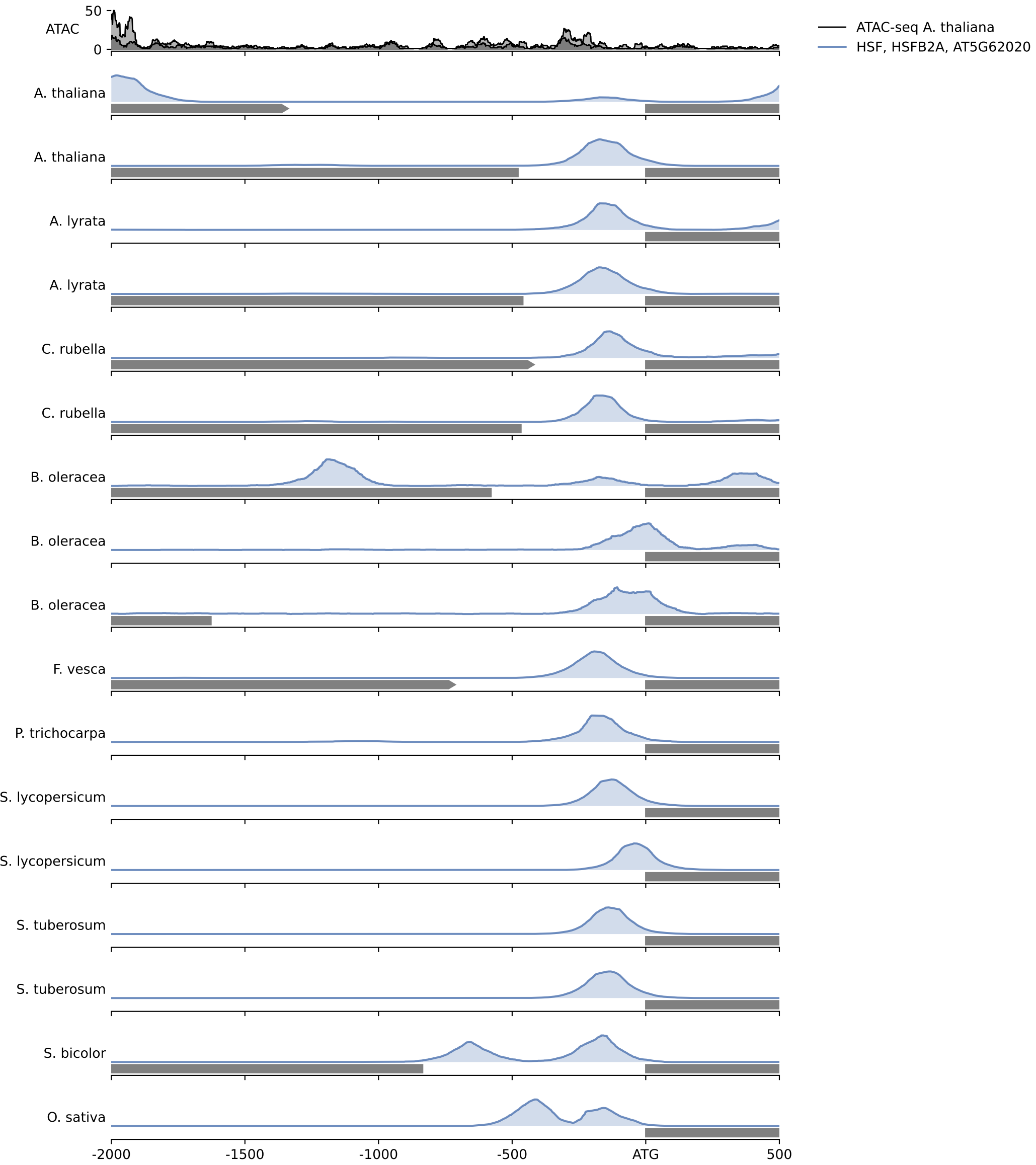


A. thaliana target: AT2G30440, TPP, Encodes a thylakoidal processing peptidase that removes signal sequences from proteins synthesized in the cytoplasm and transported into the thylakoid lumen. The mRNA is cell-to-cell mobile.



A. thaliana target: AT5G08020, RPA70B, Encodes a homolog of Replication Protein A. rpa70b mutants are hypersensitive to UV-B radiation and MMS treatments suggesting a role for this protein in DNA damage repair. The mRNA is cell-to-cell mobile.

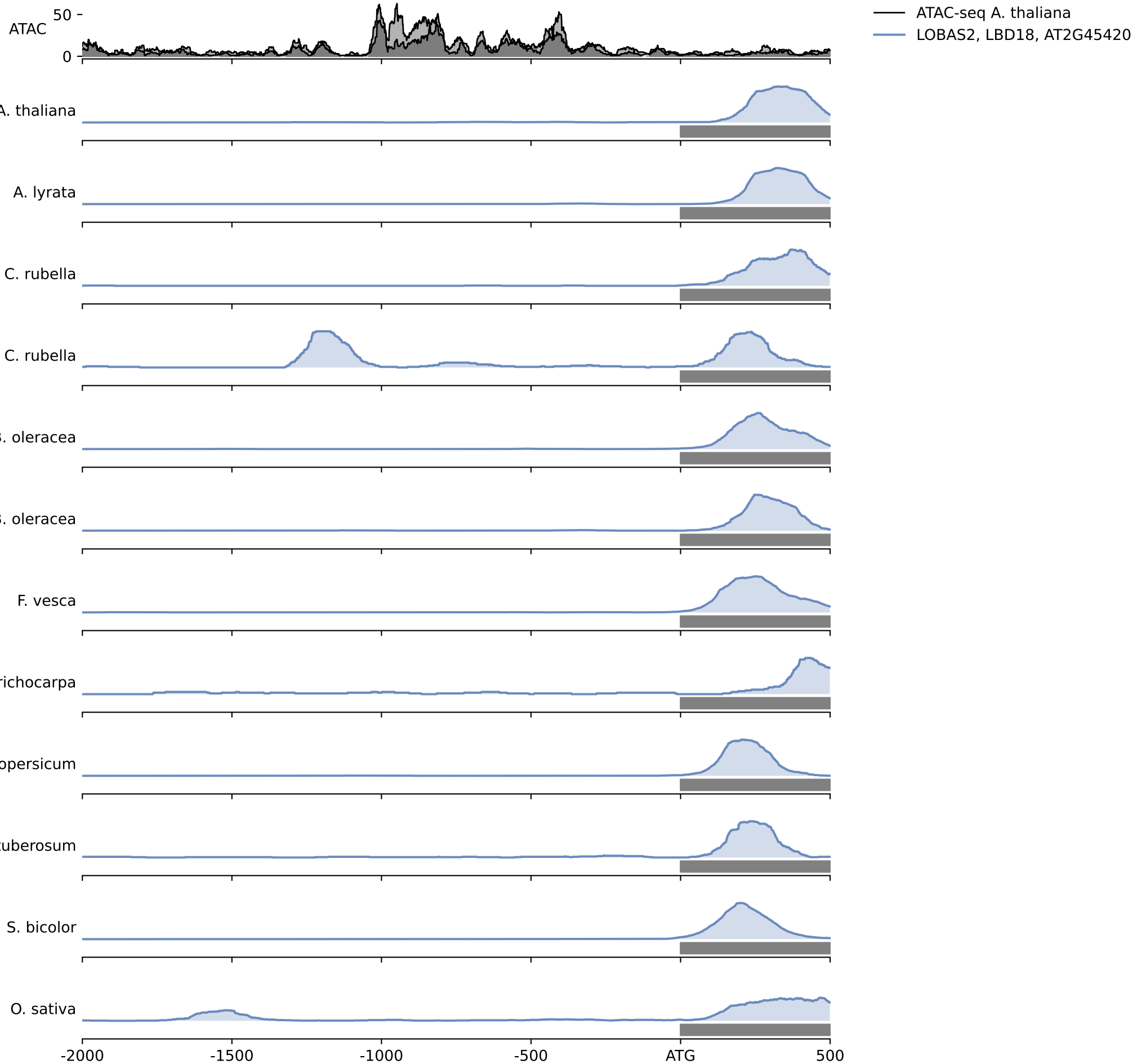
A. thaliana target: AT5G61000, RPA70D, Replication factor-A protein 1-like protein;(source:Araport11)



A. thaliana target: AT5G12020, HSP17.6II, 17.6 kDa class II heat shock protein;(source:Araport11)

A. thaliana target: AT5G12030, HSP17.6A, Encodes a cytosolic small heat shock protein with chaperone activity that is induced by heat and osmotic stress and is also expressed late in seed development.

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A. thaliana target: AT1G03440, Leucine-rich repeat (LRR) family protein;(source:Araport11)