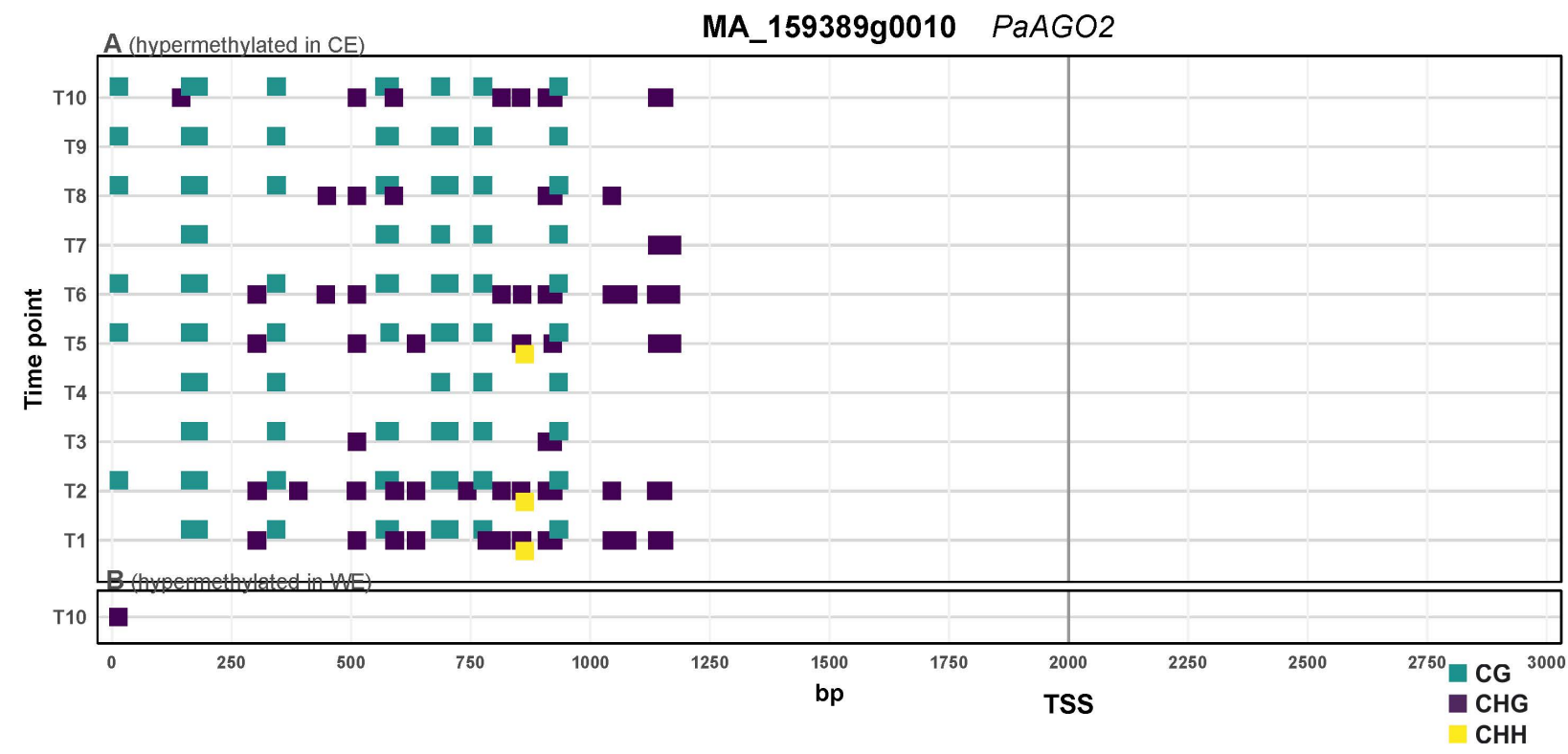
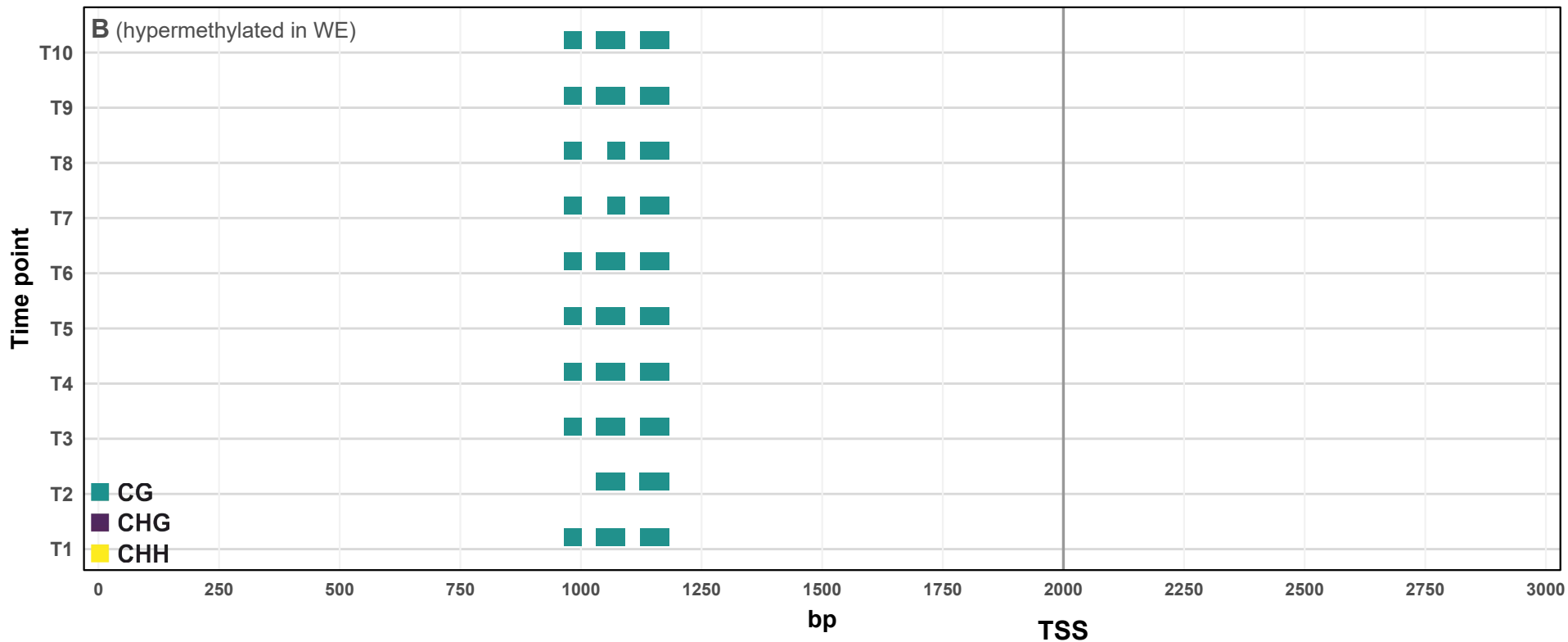


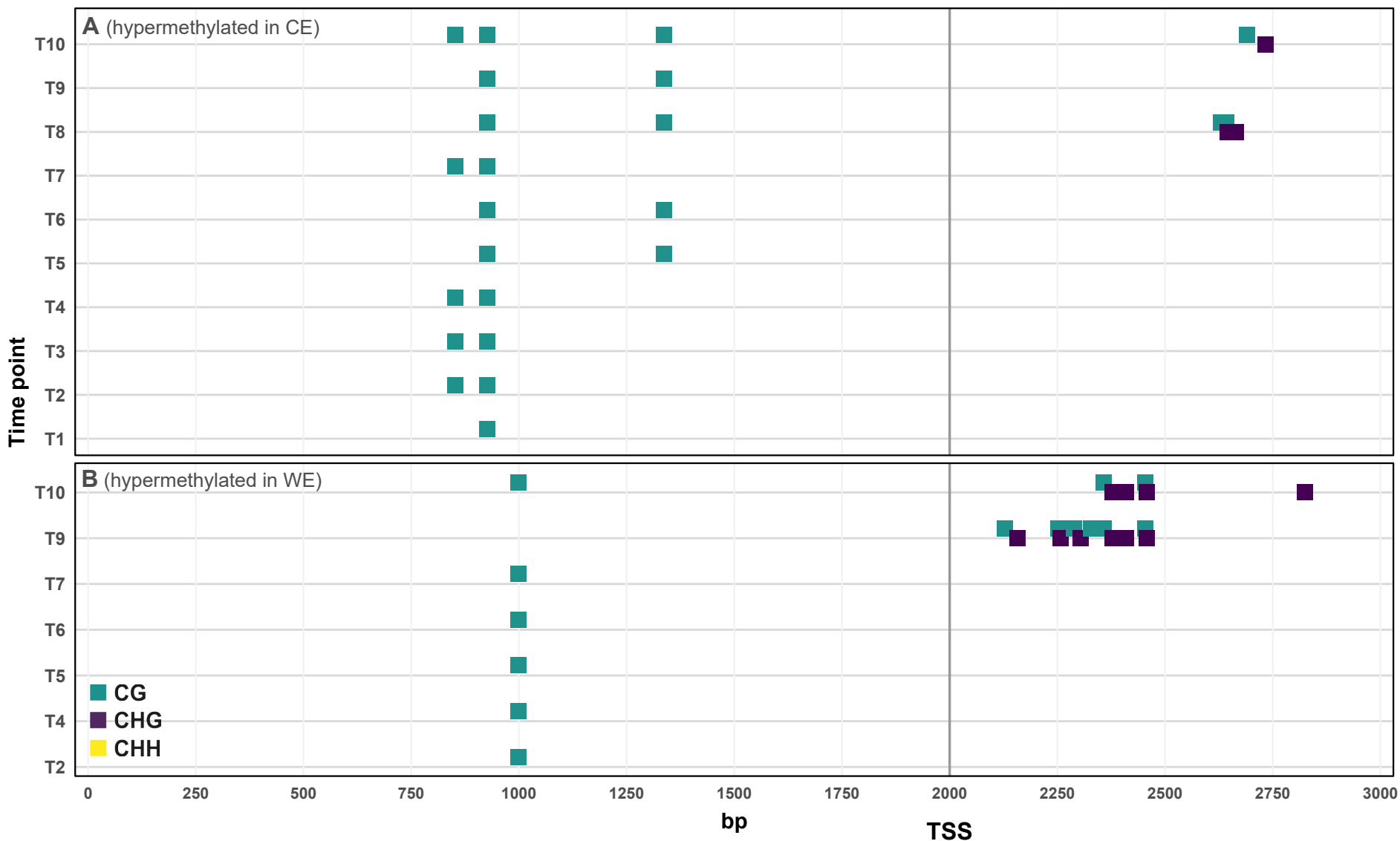
**Suppl. Fig. S4** Specific locations (positions) of the differentially methylated sites (DMS) where the addition (A) or removal (B) of a methyl group in CE significantly varies between epitypes for the selected genes. List and description of selected genes is presented in the table after the graphs



# MA\_10425786g0020 *PaAGO7*



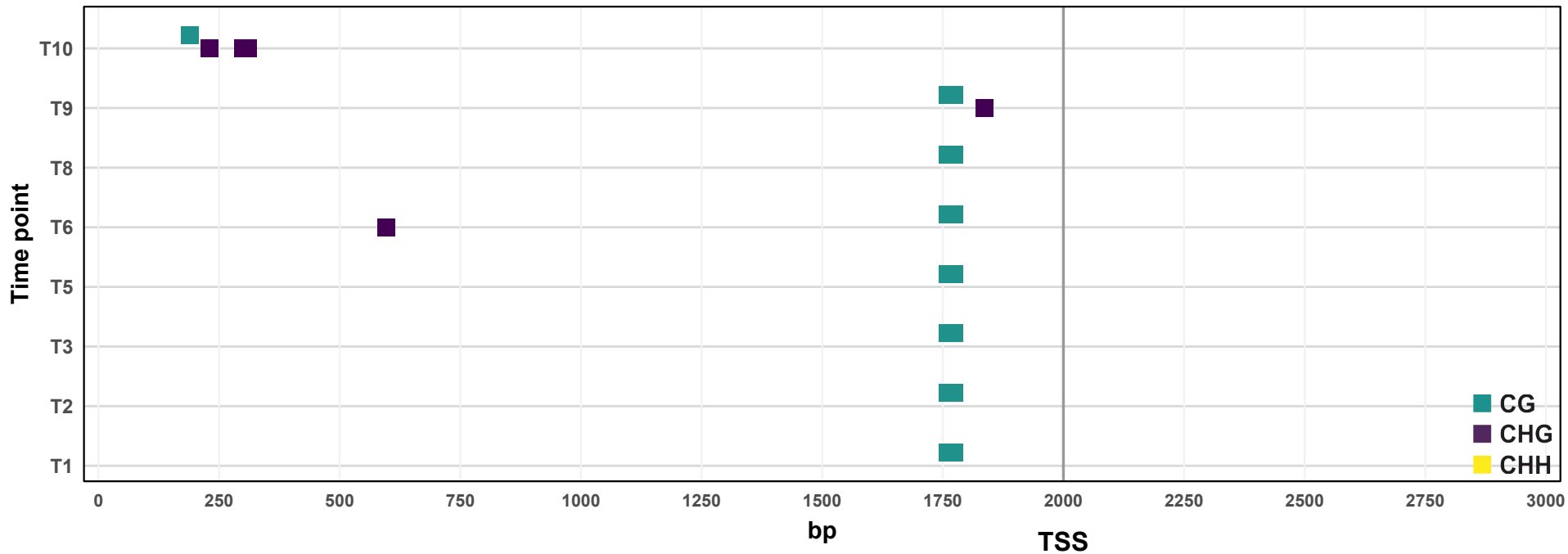
# MA\_99608g0010 PaGER5



**A** (hypermethylated in CE)

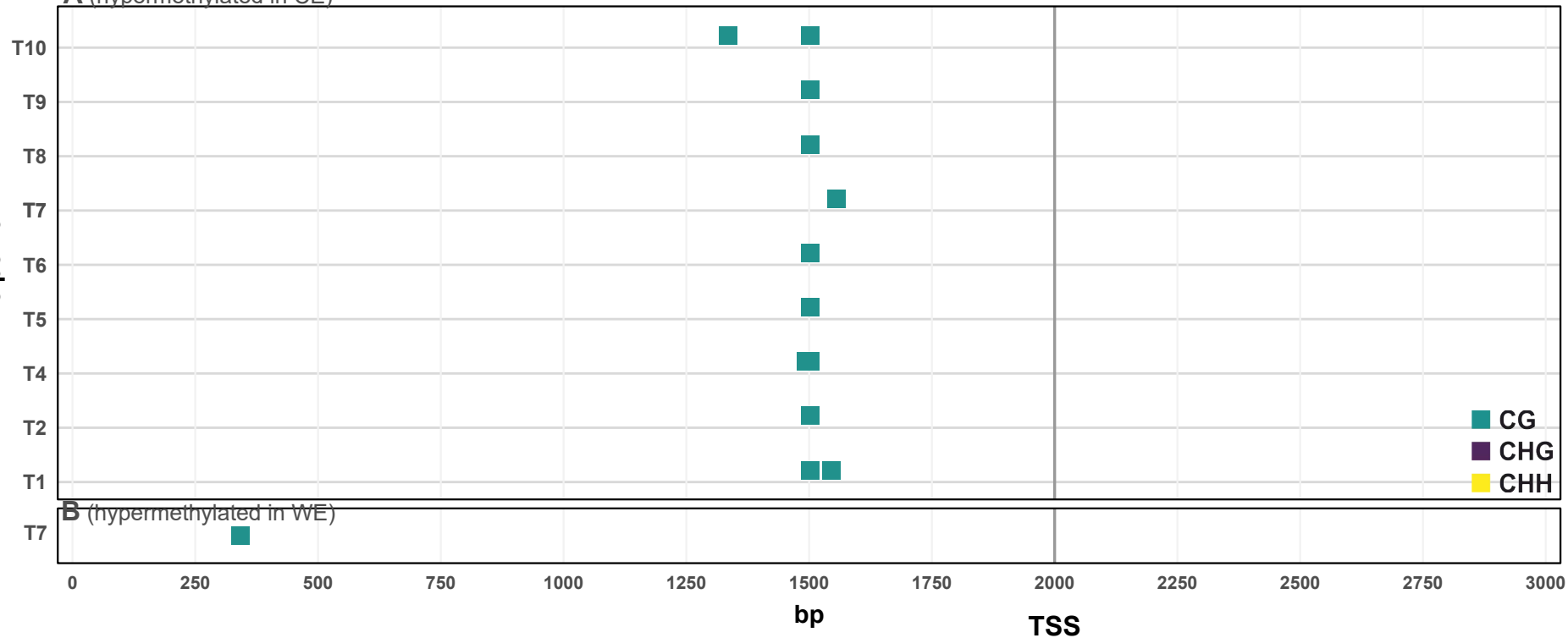
**MA\_10435200g0010**

*PaSPL2*

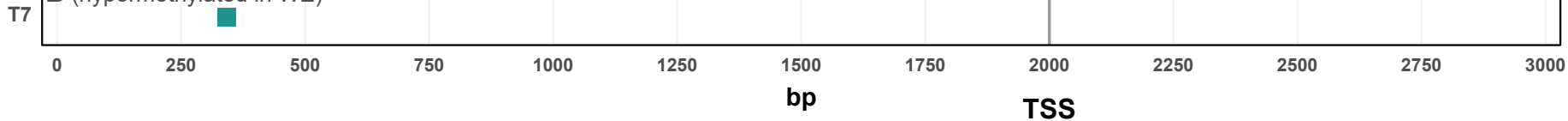


# MA\_9057g0030 PaGRF1

A (hypermethylated in CE)

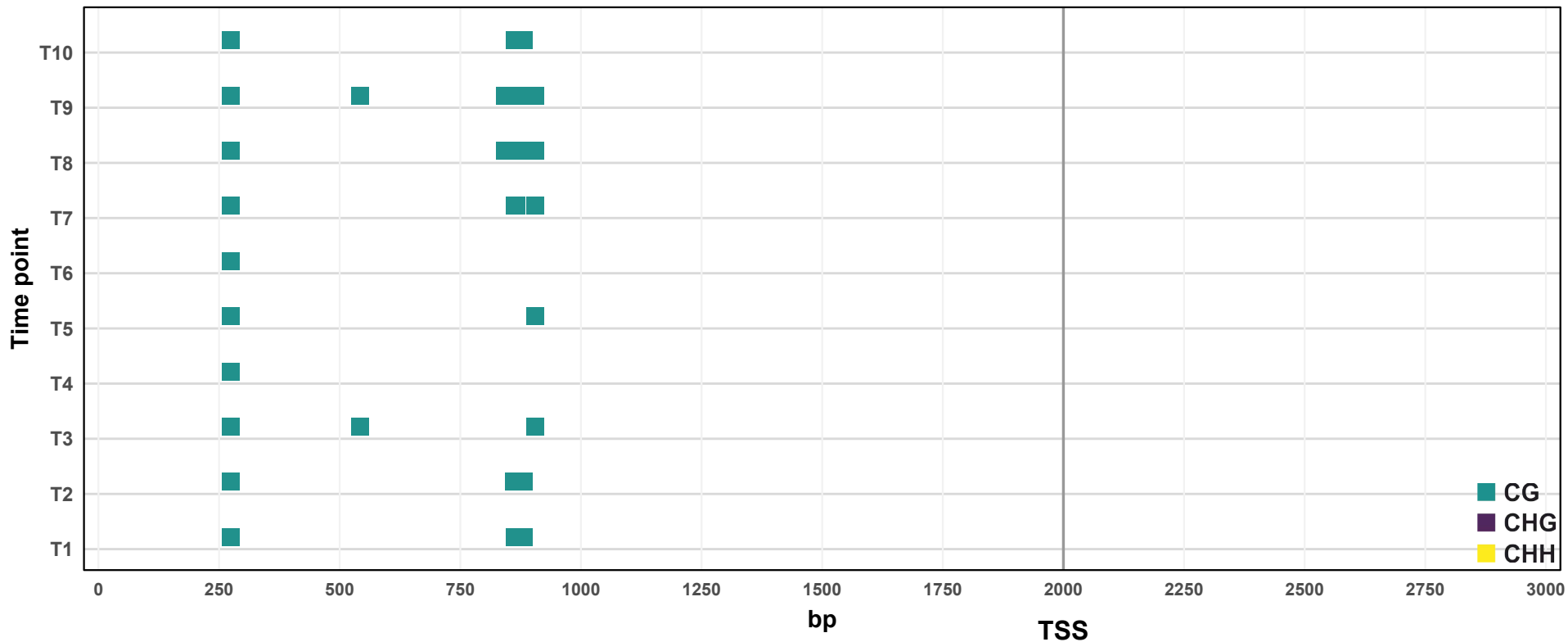


B (hypermethylated in WE)



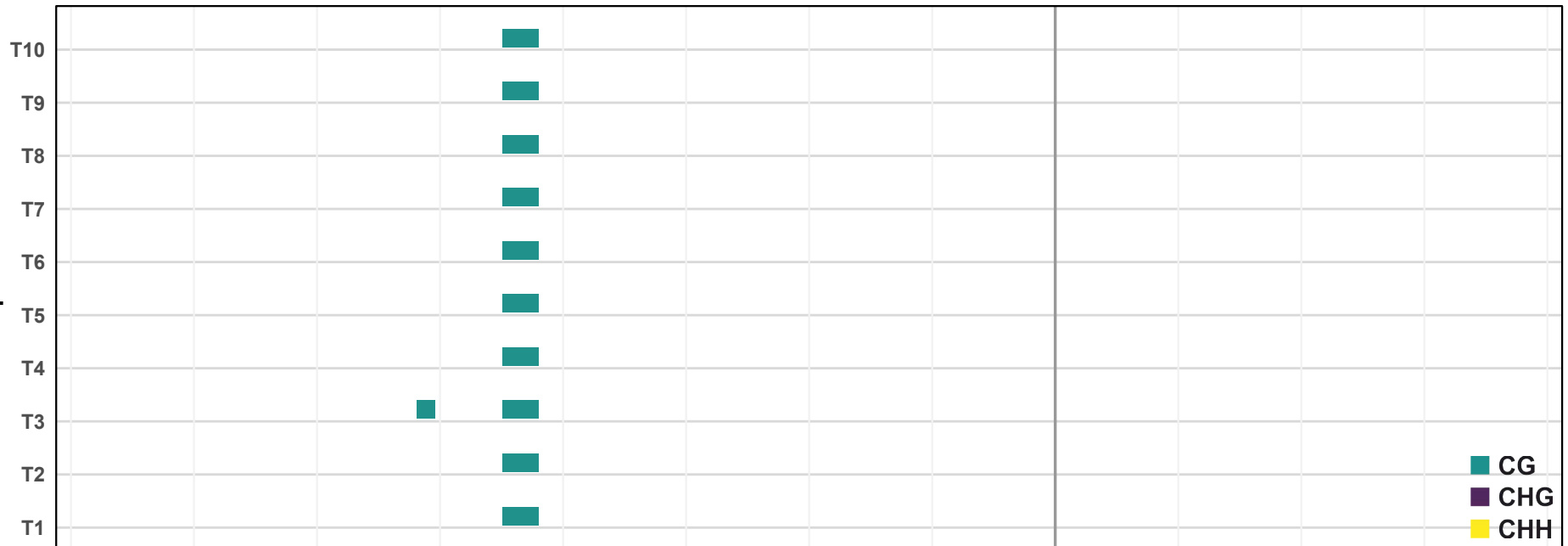
**A** (hypermethylated in CE)

**MA\_94930g0010** *PaPB1*

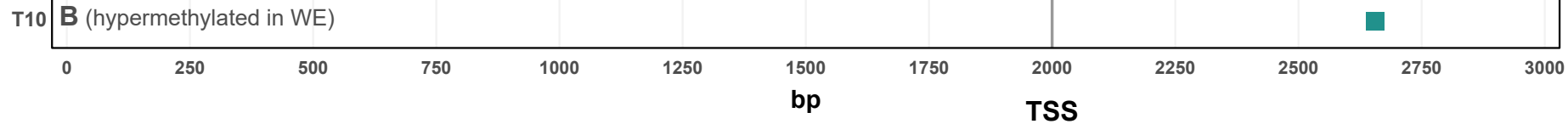


**A** (hypermethylated in CE)

**MA\_117712g0010** *PaAP1*

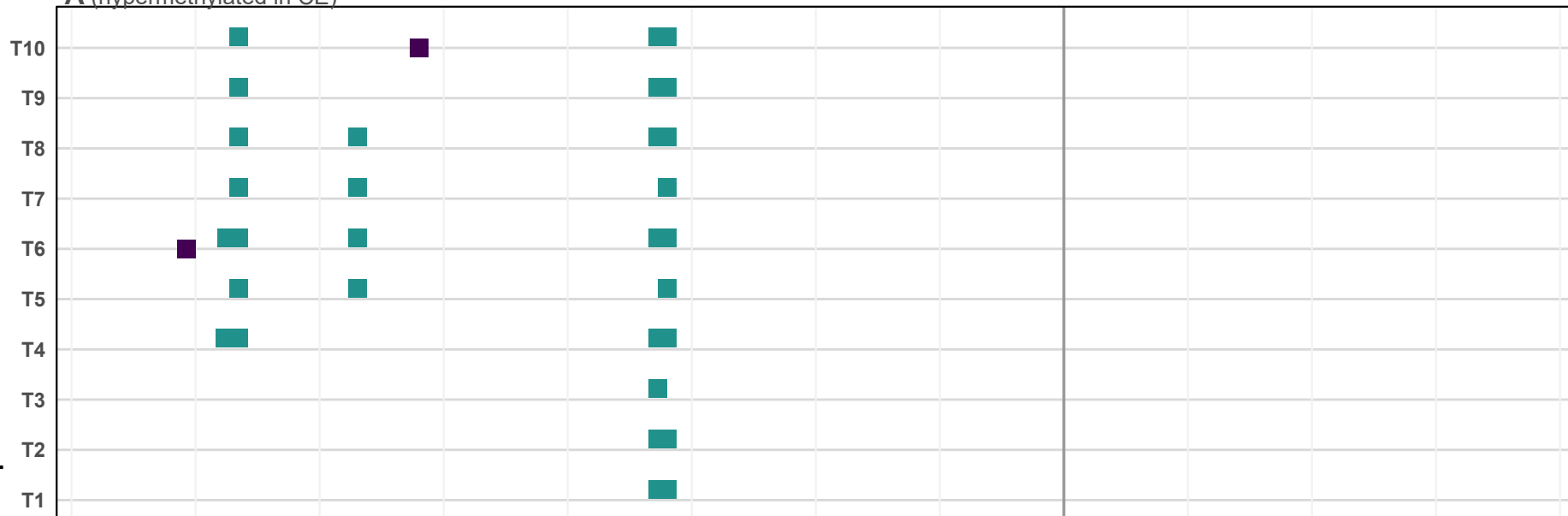


**B** (hypermethylated in WE)

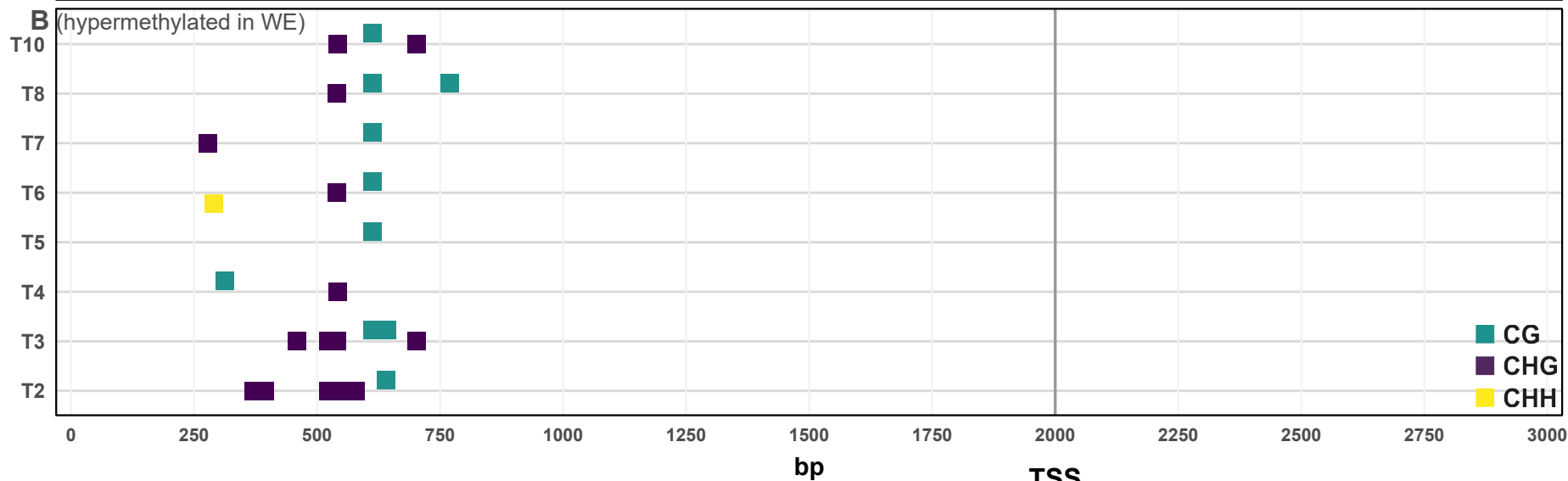


# MA\_126789g0010 PaBEBT1

**A** (hypermethylated in CE)



**B** (hypermethylated in WE)



# MA\_1408g0010 *PaUPL1*

**A** (hypermethylated in CE)

T7

**B** (hypermethylated in WE)

T10

T9

T8

T7

T6

T4

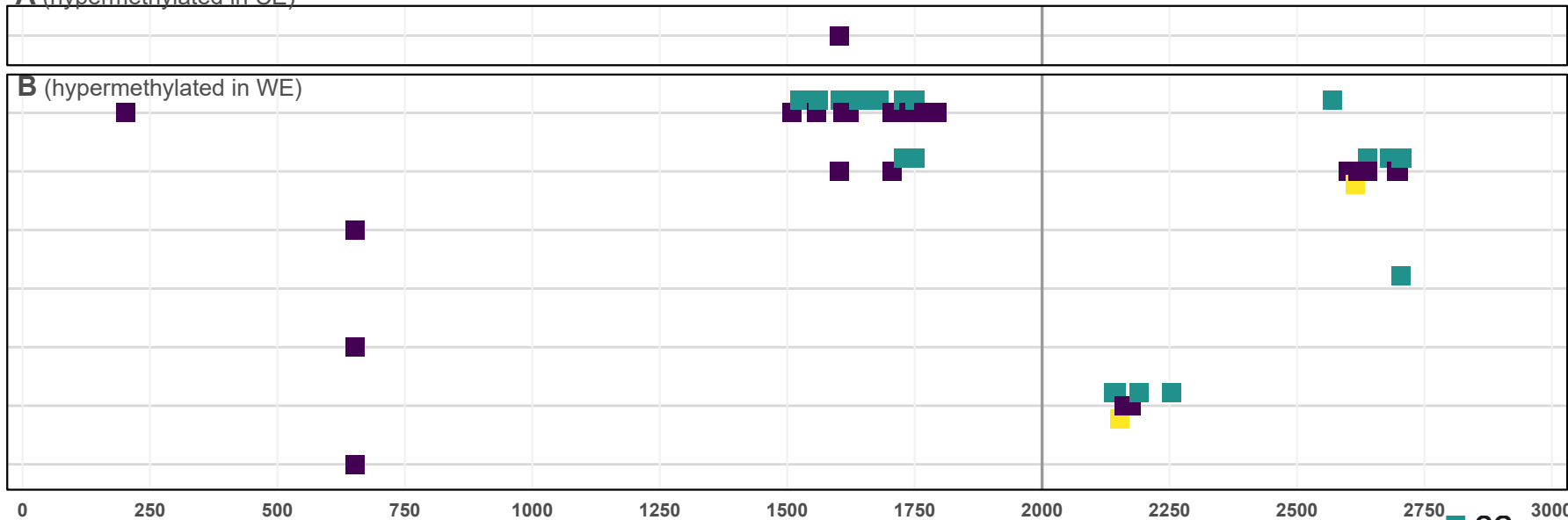
T3

bp

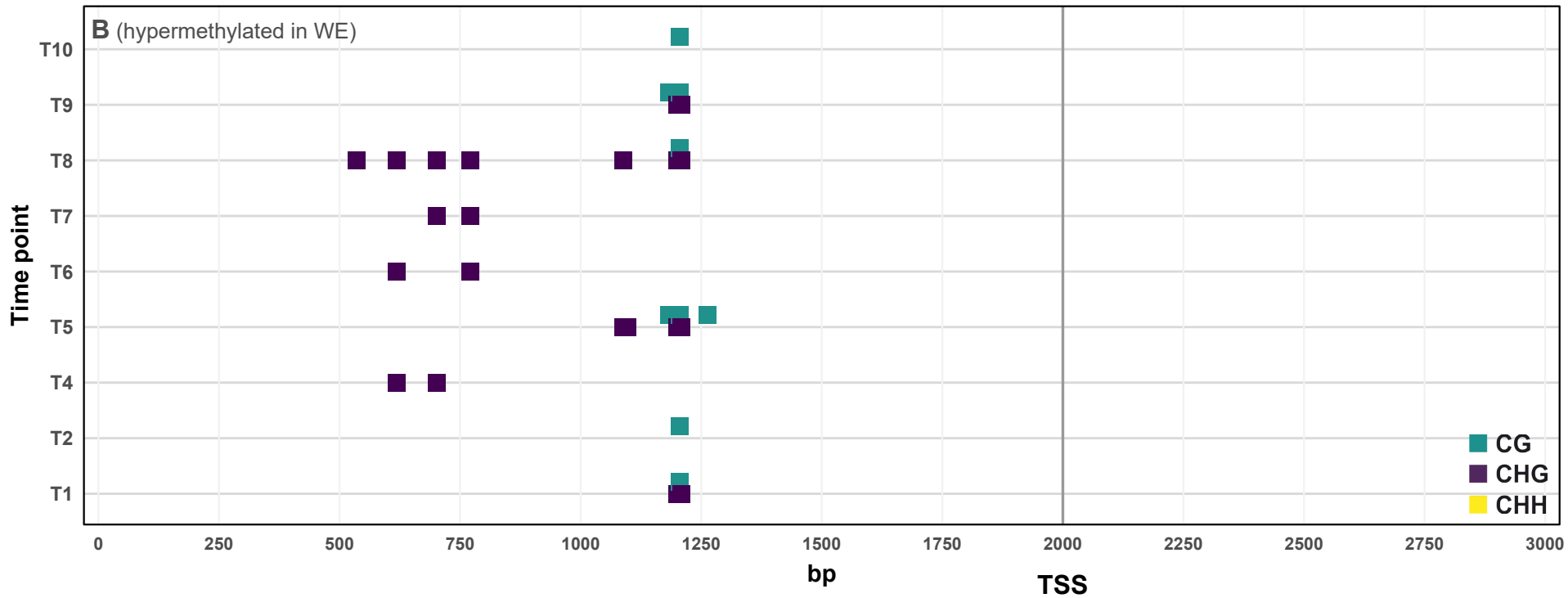
TSS

CG  
CHG  
CHH

Time point



# MA\_11144g0010 *PaCER1*

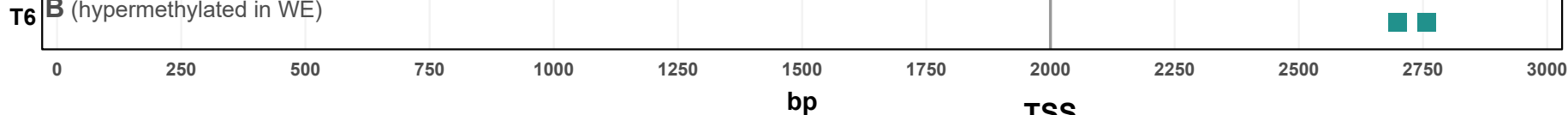


# MA\_27101g0010 PaCRK42

**A** (hypermethylated in CE)

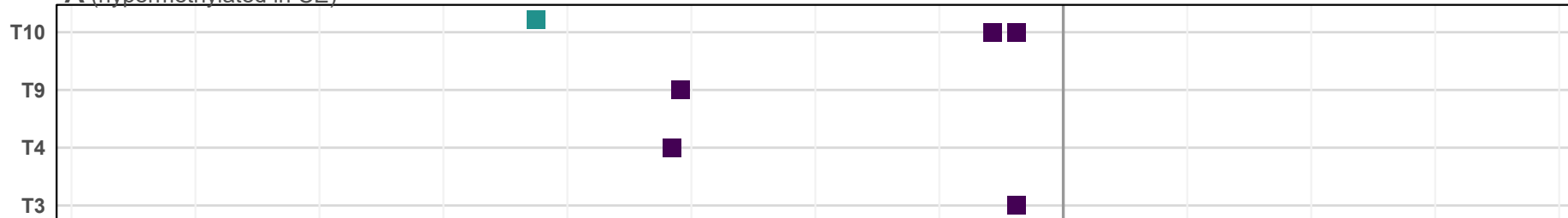


**B** (hypermethylated in WE)

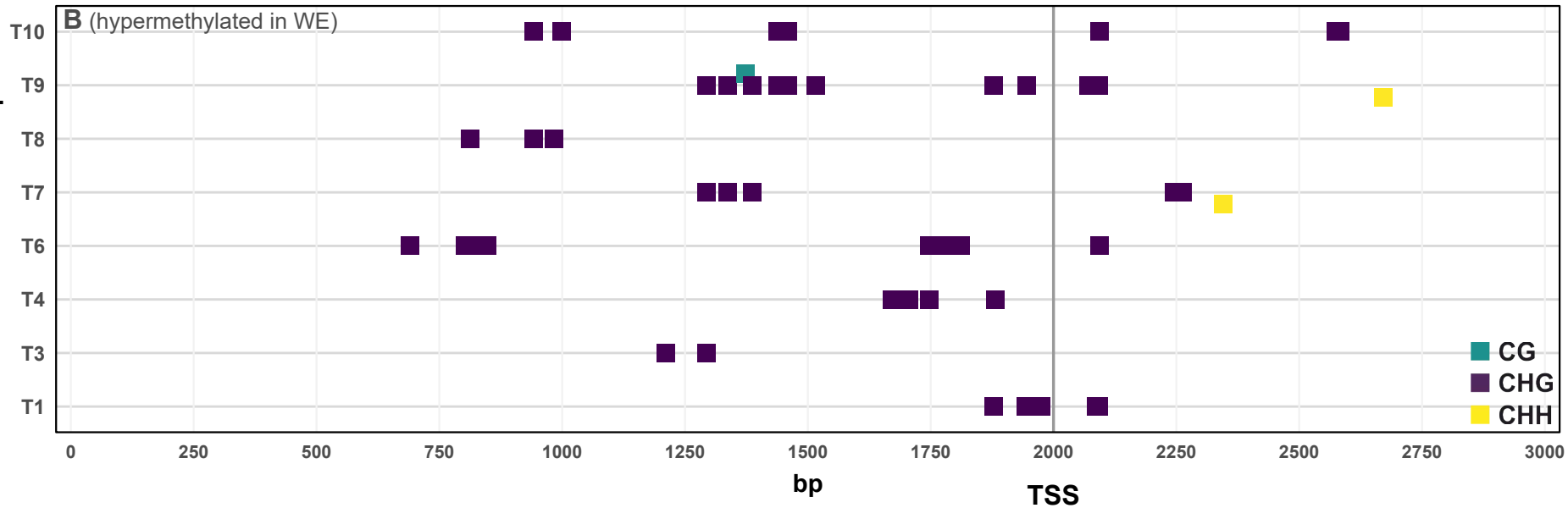


# MA\_94046g0010 PaSKIP4

**A** (hypermethylated in CE)

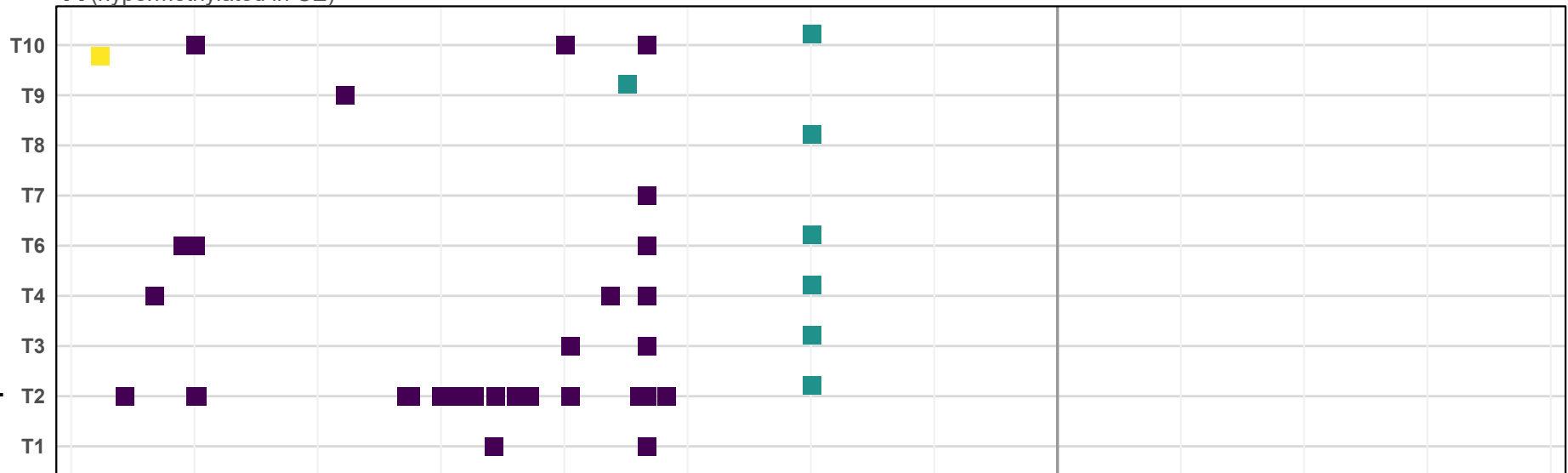


**B** (hypermethylated in WE)

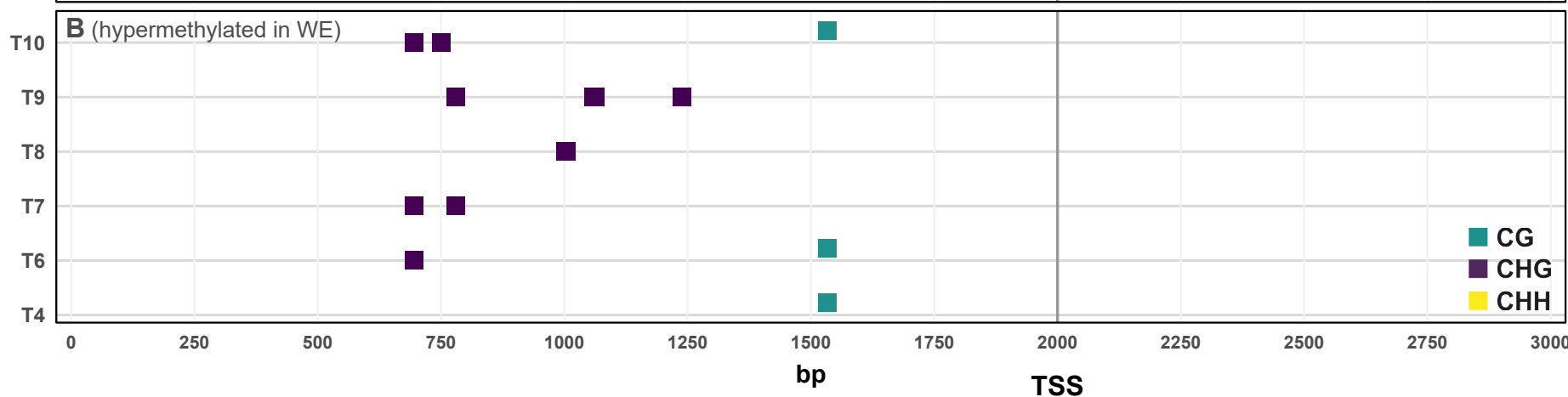


# MA\_168616g0030 PaELP1

**A** (hypermethylated in CE)

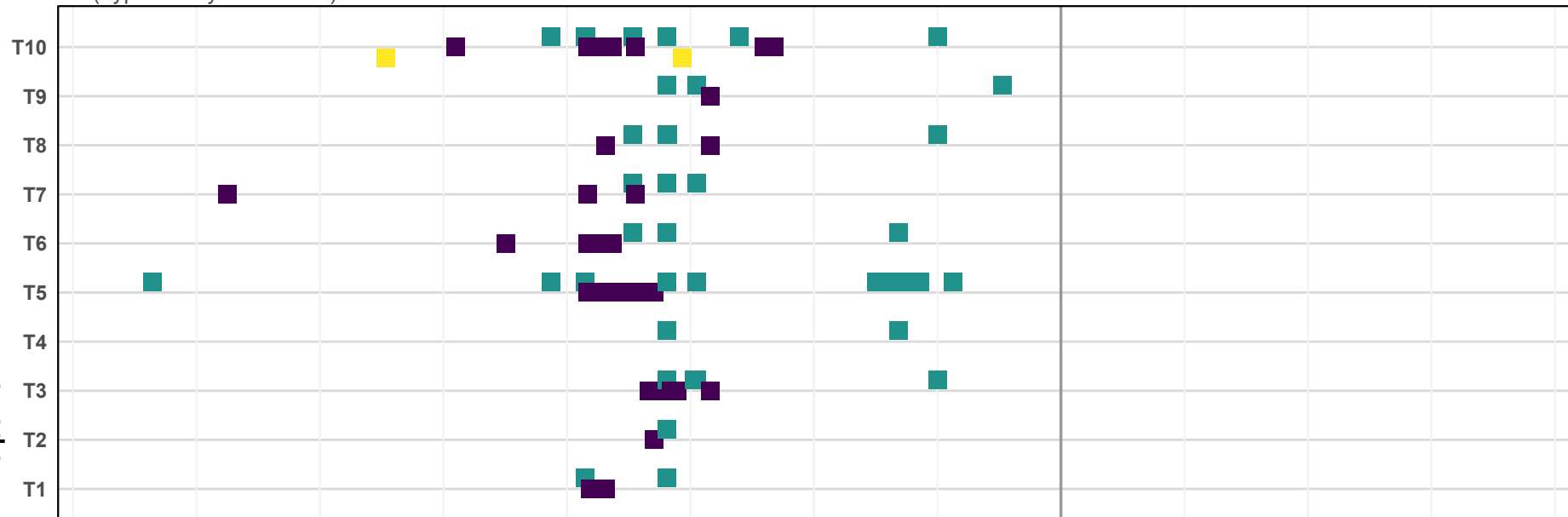


**B** (hypermethylated in WE)

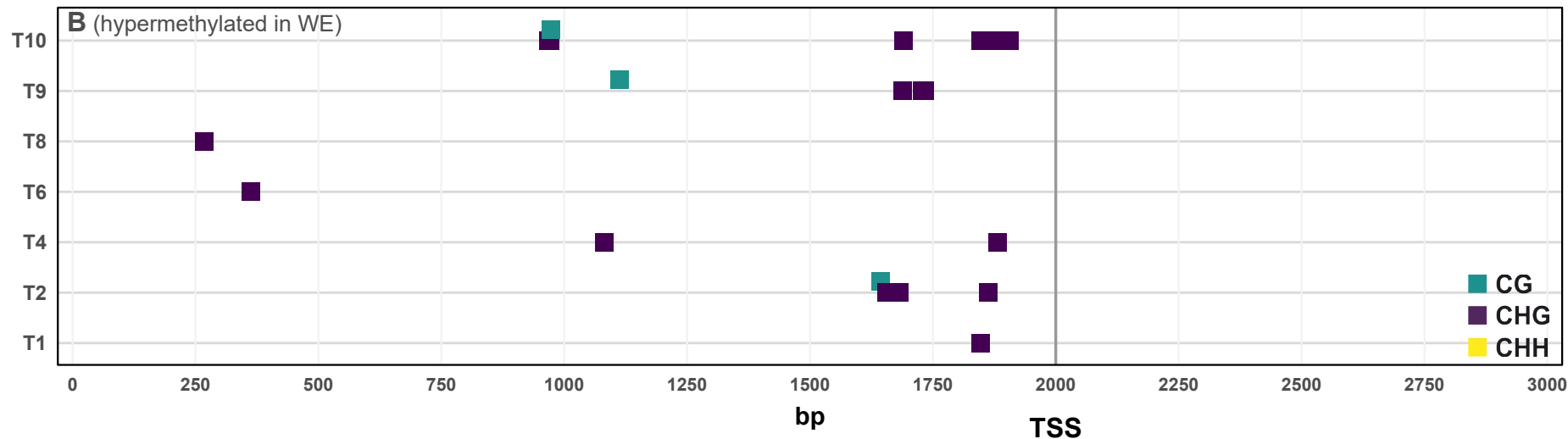


# MA\_10013703g0010 PaADR1

**A** (hypermethylated in CE)

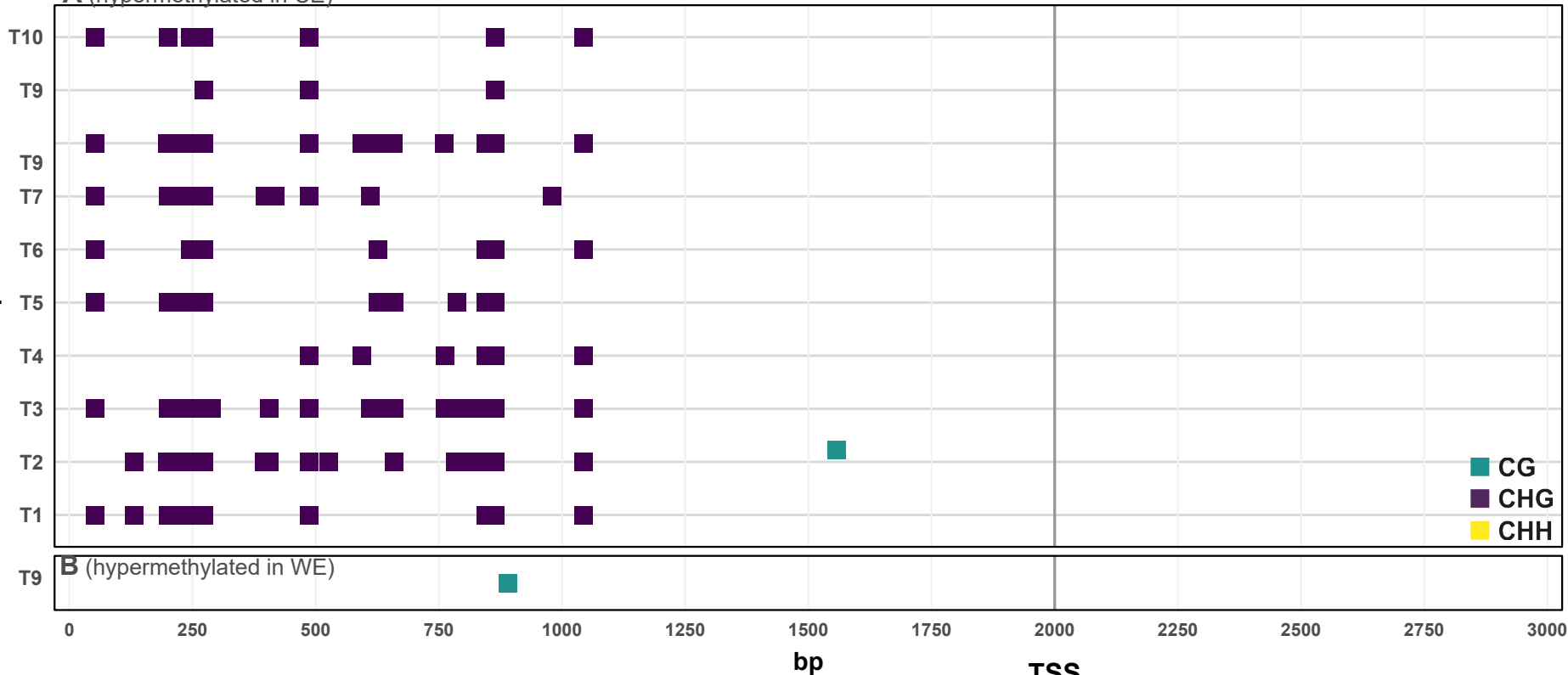


**B** (hypermethylated in WE)



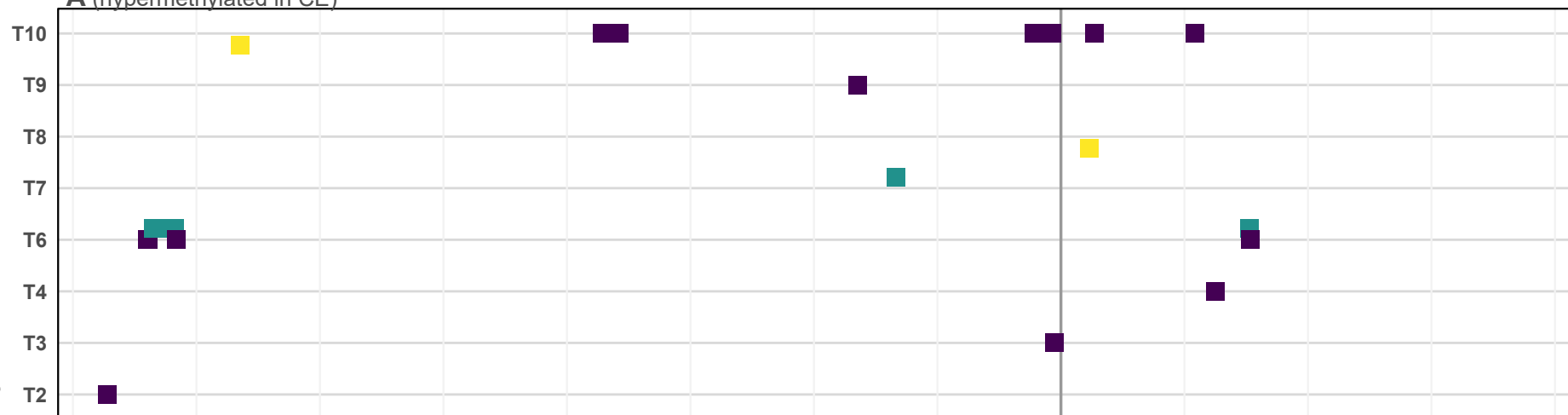
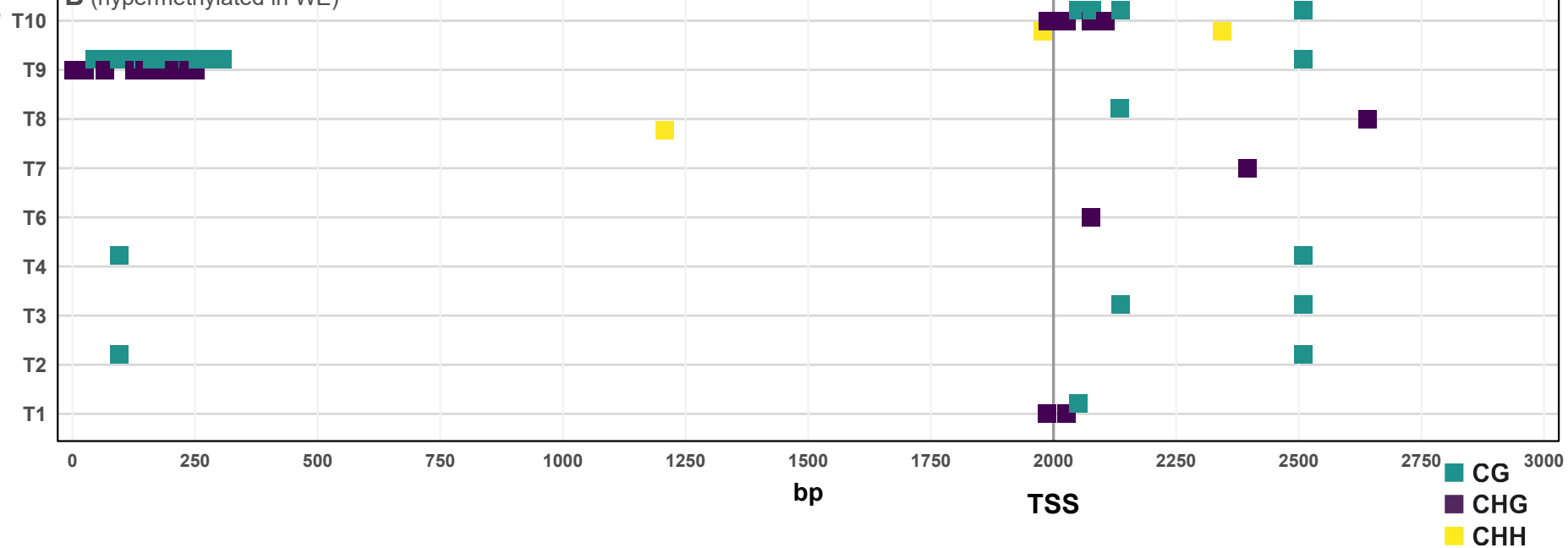
# MA\_10431106g0020 PaTGH1a

**A** (hypermethylated in CE)



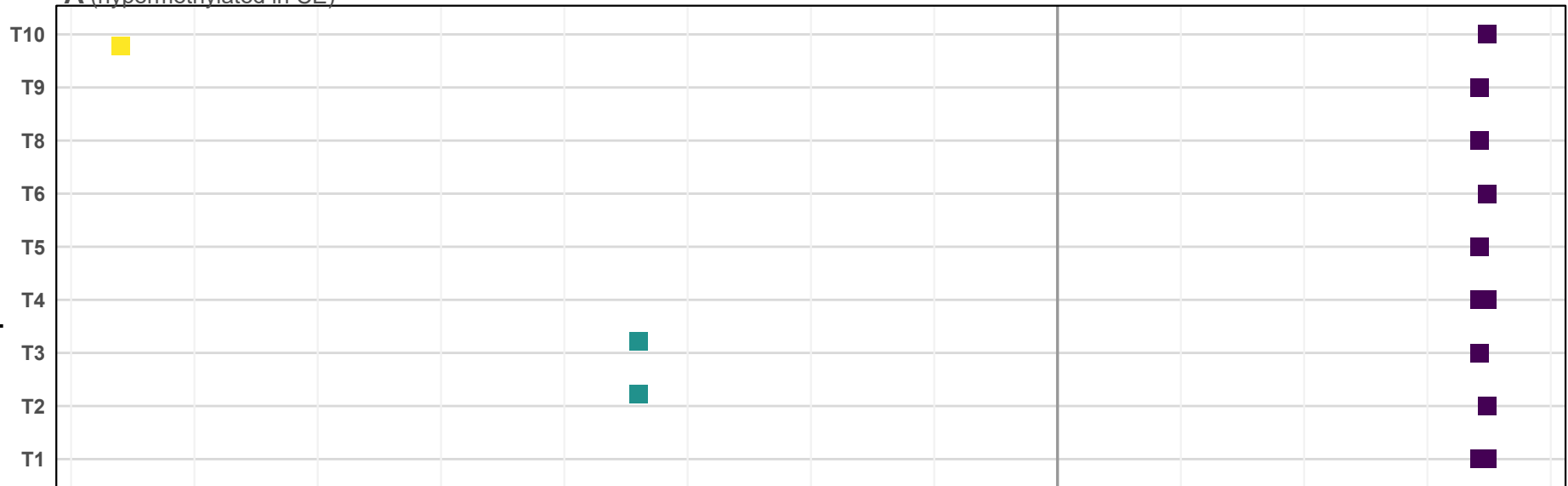
MA\_10431337g0020

PaAMPD1/PaFAC

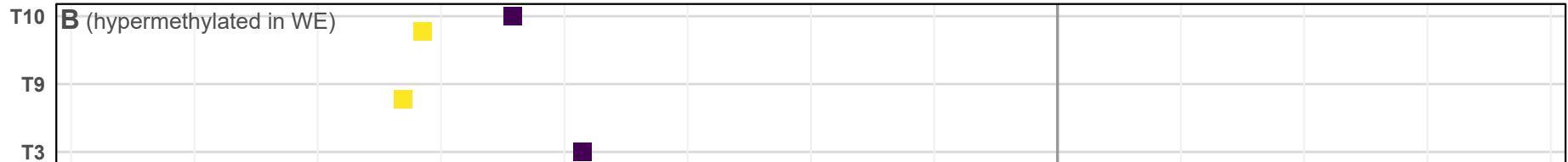
**A** (hypermethylated in CE)**B** (hypermethylated in WE)

# MA\_10436404g0010 PaRDL1

**A** (hypermethylated in CE)

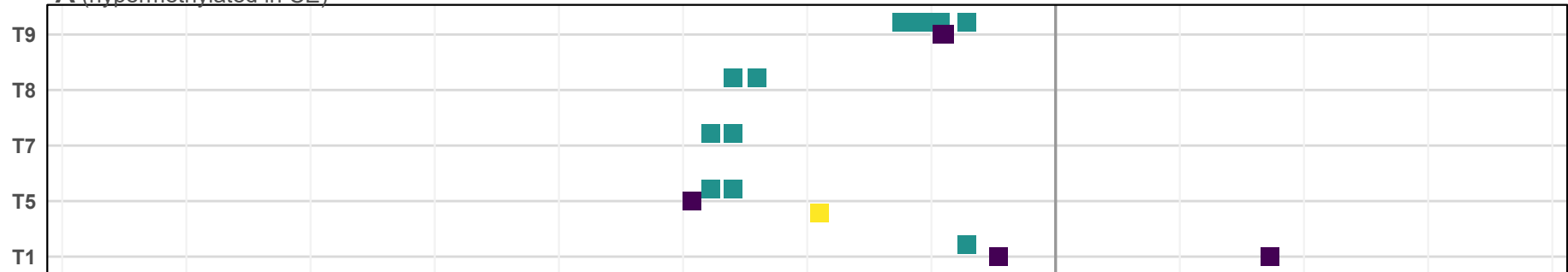


**B** (hypermethylated in WE)

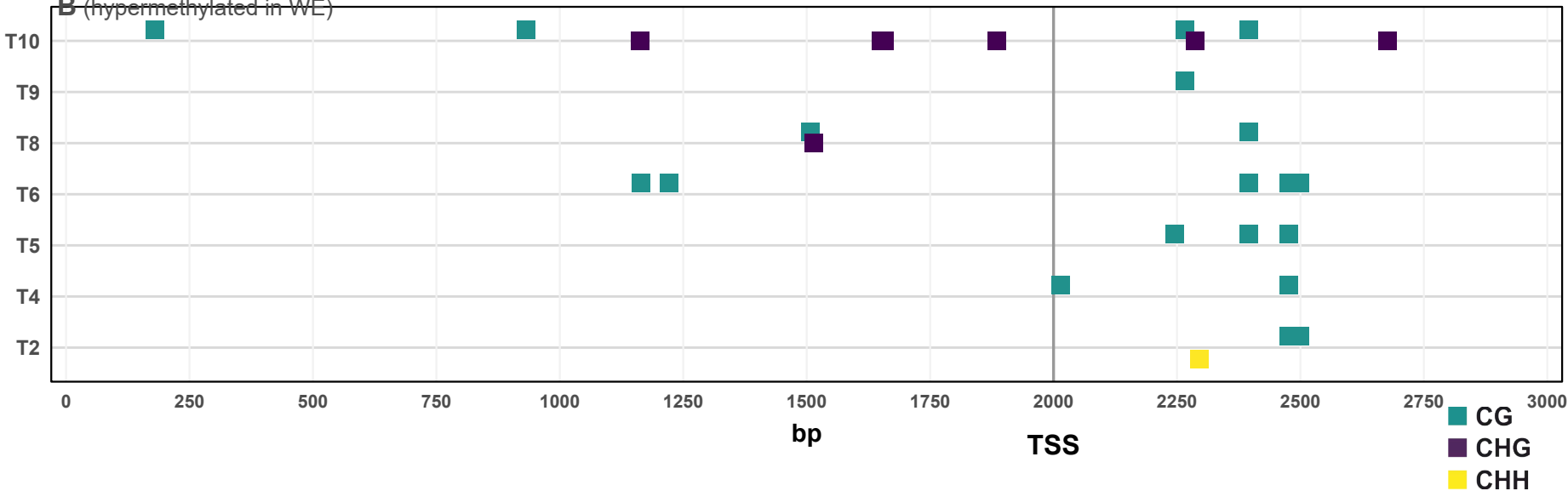


# MA\_91728g0010 PaMAPK1

**A** (hypermethylated in CE)



**B** (hypermethylated in WE)



CG  
CHG  
CHH

| Gene model ID    | Gene name               | Pfam annotation                                                                                                                                | Arabidopsos ortholog | Annotation                                                                             | Putative functions                                                                                                                                                                                                                                                                                                                                                                                                                         |
|------------------|-------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|----------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| MA_10435200g0010 | <i>PaSPL2</i>           | E3 ubiquitin-protein ligase SPL2                                                                                                               | AT1G54150.1          | RING-type E3 Ubiquitin ligase family protein                                           | SPL2 is a critical regulator of plastid operation and development, controlling how proteins enter the chloroplast                                                                                                                                                                                                                                                                                                                          |
| MA_10436404g0010 | <i>PaRDL1</i>           | PF00581-Rhodanese-like domain                                                                                                                  | AT2G42220.1          | Rhodanese/Cell cycle control phosphatase superfamily protein                           | encode a versatile group of <b>sulfurtransferase enzymes</b> essential for sulfur trafficking, cellular redox homeostasis                                                                                                                                                                                                                                                                                                                  |
| MA_11144g0010    | <i>PaCER1</i>           | PF04116-Fatty acid hydroxylase superfamily;PF12076-WAX2 C-terminal domain;PF13460-NADH(P)-binding                                              | AT1G02205.3          | ECERIFERUM 1-like; CER1, Fatty acid hydroxylase superfamily                            | The CER1 protein is an integral membrane enzyme located in the endoplasmic reticulum (ER) of epidermal cells. Involved in build the plant's cuticular wax layer                                                                                                                                                                                                                                                                            |
| MA_117712g0010   | <i>PaAP1</i>            | PF14541, PF14543-Xylanase inhibitor N-and C-terminals; PF00026-Eukaryotic aspartyl protease                                                    | AT1G01300.1          | Eukaryotic aspartyl protease family protein                                            | Functions as an anti-cell-death component in reproduction and embryogenesis                                                                                                                                                                                                                                                                                                                                                                |
| MA_126789g0010   | <i>PaBEBT1</i>          | PF02458-Transferase family; aliphatic suberin feruloyl-transferase; ASFT;                                                                      | AT5G17540.1          | Benzyl alcohol O-benzoyltransferase (BEBT); HXXXD-type acyl-transferase family protein | BEBT catalyzes the transfer of a benzoyl group from benzoyl-CoA to an alcohol to form defensive and fragrant volatile esters, such as benzyl benzoate. BEBT uses Coenzyme A (CoA) thioesters as the acyl donor. It facilitates the synthesis of biologically active compounds ranging from floral scents to active metabolites in traditional herbal medicines                                                                             |
| MA_27101g0010    | <i>PaCRK4 2</i>         | PF00069-Protein kinase domain;PF01636-Phosphotransferase enzyme family;PF01657-Salt stress response/antifungal;PF07714-Protein tyrosine kinase | AT5G40380.1          | CRK42, CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 42                             | CRK42 acts as a cellular sensor crucial for plant immunity, reactive oxygen species (ROS) signaling, and abiotic stress responses                                                                                                                                                                                                                                                                                                          |
| MA_9057g0030     | <i>PaGRF1</i>           | PF00098-Zinc knuckle; PF06839-GRF zinc finger                                                                                                  | AT5G13920.1          | GRF (GROWTH-REGULATING FACTOR ) zinc finger / Zinc knuckle protein                     | The growth-regulating factor (GRF) family of transcriptional factors are involved in the control of leaf size and senescence, inflorescence and root growth, grain size, and plant regeneration.                                                                                                                                                                                                                                           |
| MA_94930g0010    | <i>PaPB1</i>            | PF00564-PB1 domain                                                                                                                             | AT3G26510.4          | Octicosapeptide/Phox/Bem1p family protein;                                             | Protein binding. Protein interaction data indicates it may participate in signaling pathways alongside other proteins such as the calcium-dependent protein kinase CPK11                                                                                                                                                                                                                                                                   |
| MA_99608g0010    | <i>PaGER5</i>           | GRAM domain family protein                                                                                                                     | AT5G13200.1          | GEM-RELATED 5;GER5                                                                     | Encodes a protein with unknown function that is involved in hormone mediated regulation of seed germination/dormancy, Absciscic acid responsive.                                                                                                                                                                                                                                                                                           |
| MA_159389g0010   | <i>PaAGO2</i>           | PF02171-Piwi domain                                                                                                                            | AT1G69440.1          | AGO2, ARGONAUTE2, PIWI                                                                 | Acts as the catalytic engine of the RNA-induced silencing complex (RISC)                                                                                                                                                                                                                                                                                                                                                                   |
| MA_10425786g0020 | <i>PaAGO7</i>           | PF02170-PAZ domain;PF08699-Domain of unknown function (DUF1785)                                                                                | AT1G69440.1          | AGO7, ARGONAUTE7, ZIP, ZIPPY                                                           | Acts as the catalytic engine of the RNA-induced silencing complex (RISC)                                                                                                                                                                                                                                                                                                                                                                   |
| MA_10431106g0020 | <i>PaTGH1 a</i>         | PF01805-Surp module; SWAP/Surp superfamily                                                                                                     | AT5G23080.2          | TGH, TOUGH - RNA binding and processing proteins                                       | It is an important component of miRNA and siRNA biogenesis.                                                                                                                                                                                                                                                                                                                                                                                |
| MA_94046g0010    | <i>PaSKIP4</i>          | F-box Kelch-repeat protein                                                                                                                     |                      | F-box, Kelch_1                                                                         | F-box Kelch-repeat proteins (KFBs) are large, largely plant-specific gene families involved in targeted protein degradation. By linking specific target proteins to the SCF (SKP-CULLIN-F-BOX) ubiquitin-ligase complex, they act as molecular matchmakers that regulate plant growth, stress responses, flowering time, and the circadian clock                                                                                           |
| MA_168616g0030   | <i>PaELP1</i>           | elongator complex protein                                                                                                                      |                      | WD domain, G-beta repeat                                                               | The <b>Elongator complex</b> in plants (frequently referred to as <b>ELO/ELP</b> ) is a highly conserved, 6-subunit eukaryotic complex associated with RNA polymerase II. These WD domains act as a scaffold for protein-protein interactions, holding the catalytic subcomplexes together and recognizing target tRNAs. In plants, this specific gene family is deeply involved in morphological development and environmental adaptation |
| MA_10431337g0020 | <i>PaAMPD 1/PaFAC 1</i> | AMP deaminase/Embryonic Factor 1                                                                                                               |                      | Adenosine/AMP deaminase                                                                | FAC1 is one of the earliest expressed genes in plant embryogenesis. While it is expressed at low levels in mature plant organs, its transcription surges during early zygotic development, endosperm formation, and somatic embryogenesis. Arabidopsis thaliana—encodes an AMP deaminase (AMPD)                                                                                                                                            |
| MA_10013703g0010 | <i>PaADR1</i>           | disease resistance NB-LRR family                                                                                                               |                      | NB-ARC, RPW8                                                                           | The <b>ADR1</b> (Activated Disease Resistance 1) gene family in plants encodes a critical group of <b>helper NLR</b> (Nucleotide-Binding Leucine-Rich Repeat) immune receptors.                                                                                                                                                                                                                                                            |
| MA_91728g0010    | <i>PaMAPK 1</i>         | mitogen-activated protein kinase                                                                                                               |                      | Pkinase                                                                                | Mitogen-activated protein kinase (MAPK) genes in plants encode highly conserved signaling proteins that regulate vital growth, developmental, and defense processes. Acting via sequential phosphorylation cascades (MAPKKK → MAPKK → MAPK), they transduce extracellular environmental cues into intracellular responses                                                                                                                  |
| MA_1408g0010     | <i>PaUPL1</i>           | E3 ubiquitin-protein ligase RF298                                                                                                              |                      | Zinc finger, C3HC4 type (RING finger)                                                  | The <b>RF298 gene</b> in plants (best studied in <i>Arabidopsis thaliana</i> ) encodes a <b>RING-finger E3 ubiquitin-protein ligase</b> . It is a vital post-translational regulator of cellular proteins, playing significant roles in stress responses and hormone signaling (such as ABA signaling), and acts via the ubiquitin-proteasome system (UPS) to target specific proteins for degradation                                     |