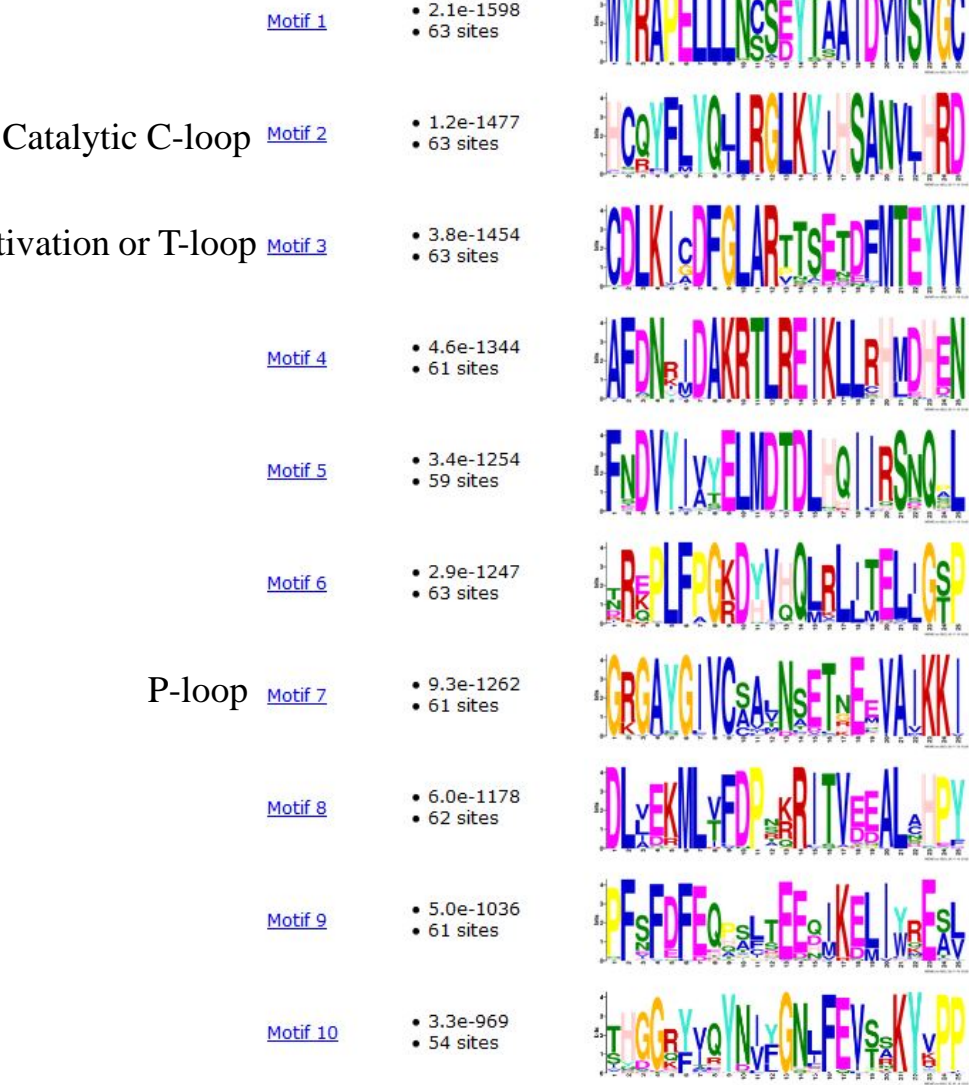
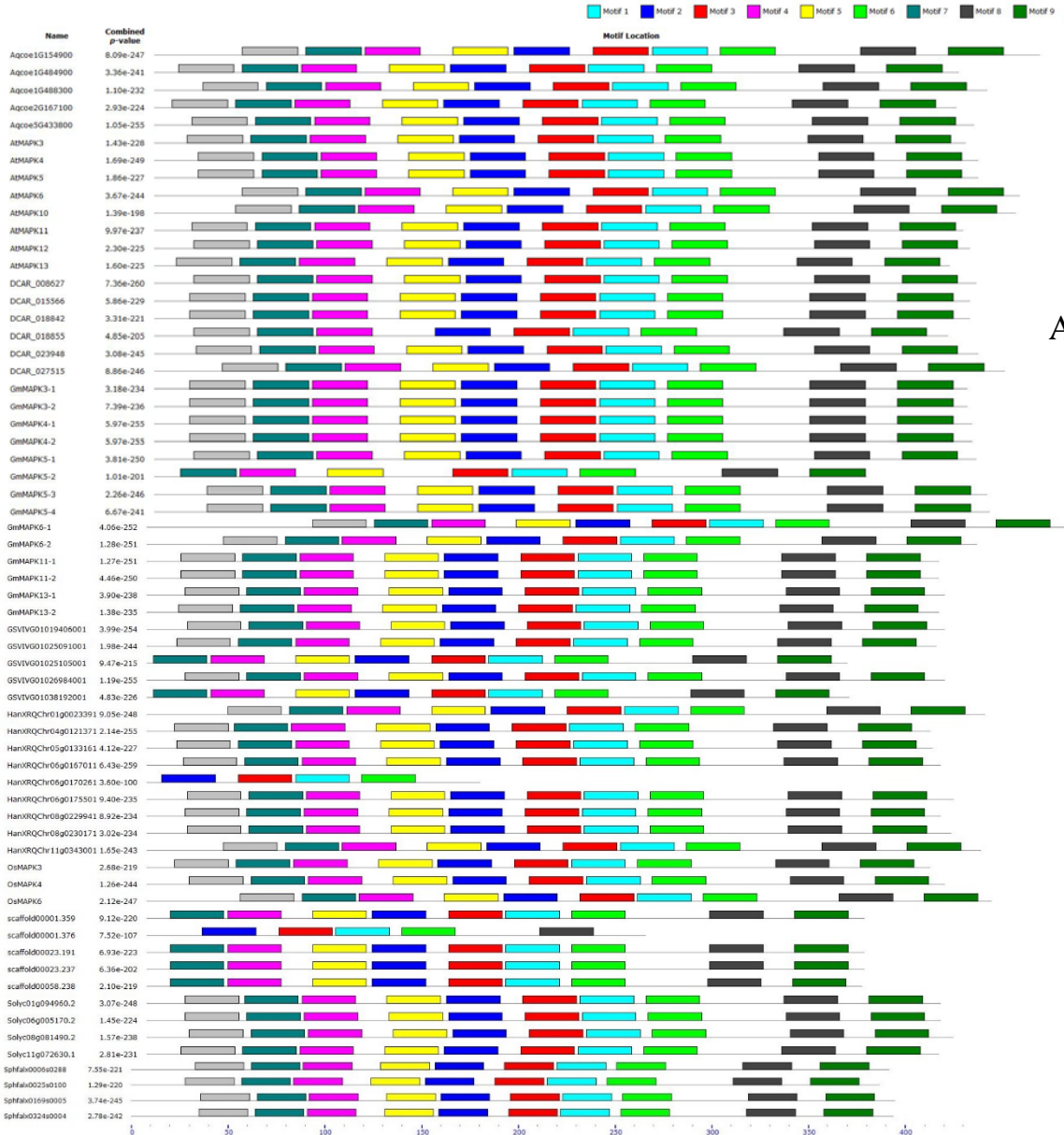
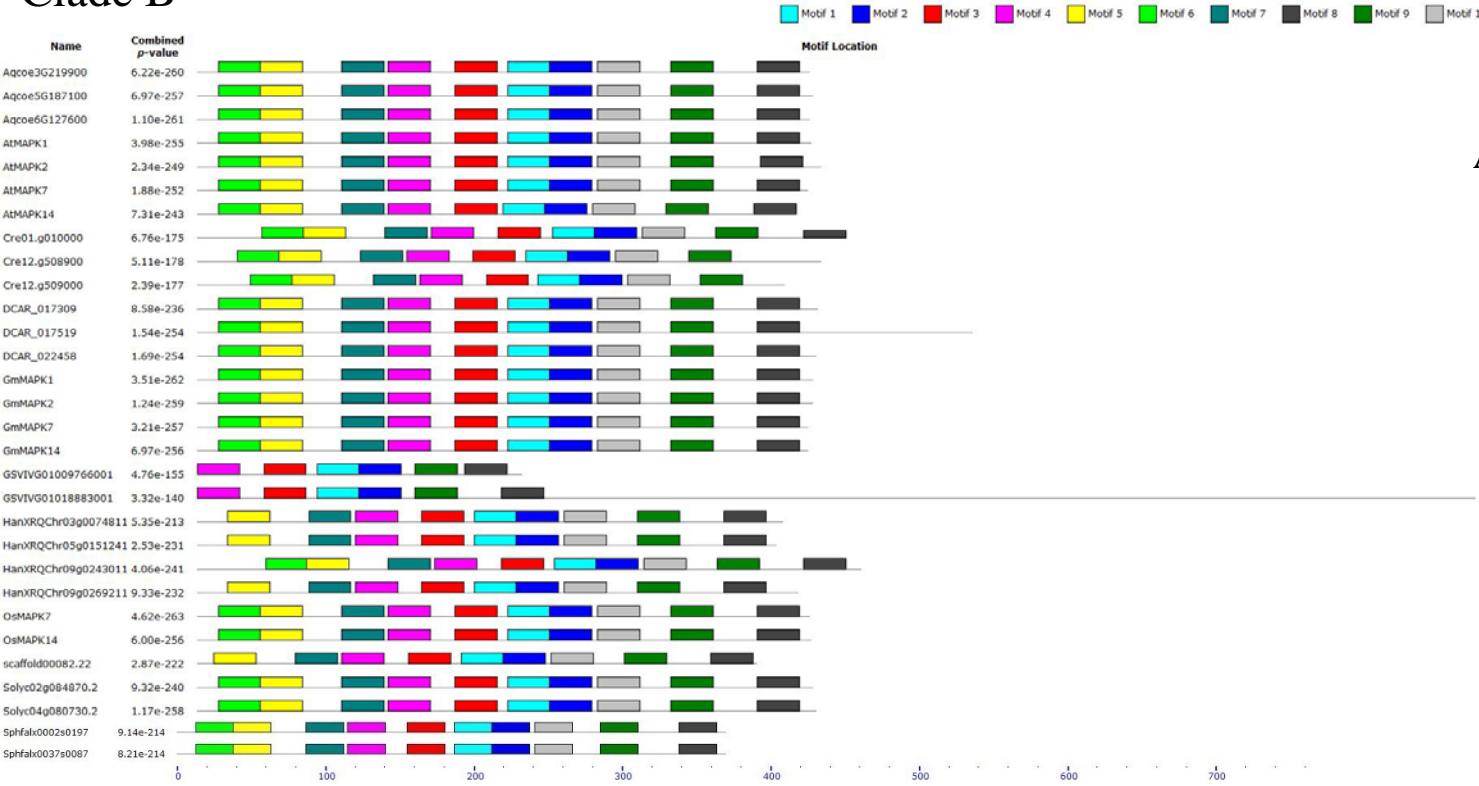


Supplementary File S3. MEME predicted conserved motifs in MPK proteins belonging to different phylogenetic clades. A set of parameters used in MEME analysis included maxsize: 100,000, mod: zoops, nmotifs: 10, minw: 6, and maxw: 25.

Clade A



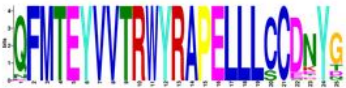
Clade B



Activation or T-loop

[Motif 1](#)

- 3.6e-723
- 30 sites



[Motif 2](#)

- 2.4e-683
- 30 sites



Catalytic C-loop

[Motif 3](#)

- 1.8e-663
- 30 sites



[Motif 4](#)

- 6.0e-639
- 30 sites



P-loop

[Motif 5](#)

- 1.9e-573
- 28 sites



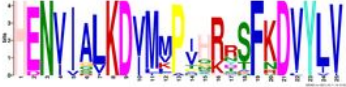
[Motif 6](#)

- 1.2e-443
- 24 sites



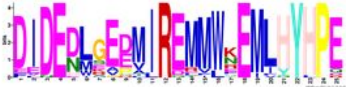
[Motif 7](#)

- 8.8e-487
- 28 sites



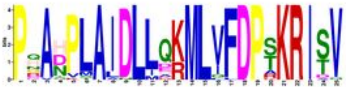
[Motif 8](#)

- 6.3e-484
- 27 sites



[Motif 9](#)

- 1.5e-530
- 30 sites

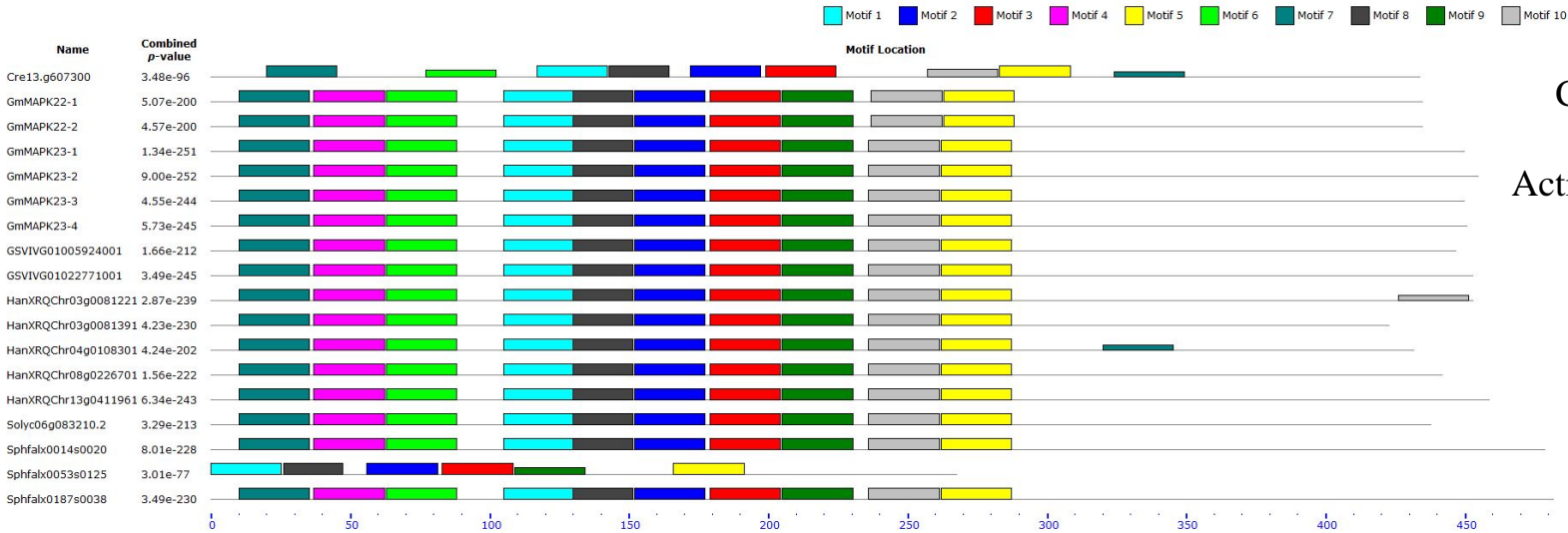


[Motif 10](#)

- 2.9e-443
- 28 sites



Clade C



Catalytic C-loop

[Motif 1](#)

- 1.0e-327
- 18 sites



Activation or T-loop

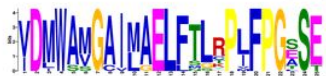
[Motif 2](#)

- 4.3e-322
- 18 sites



[Motif 3](#)

- 3.4e-310
- 18 sites



[Motif 4](#)

- 1.2e-305
- 16 sites



[Motif 5](#)

- 6.8e-285
- 18 sites



[Motif 6](#)

- 2.6e-281
- 16 sites



P-loop

[Motif 7](#)

- 9.9e-250
- 17 sites



[Motif 8](#)

- 1.9e-226
- 18 sites



[Motif 9](#)

- 5.7e-196
- 16 sites

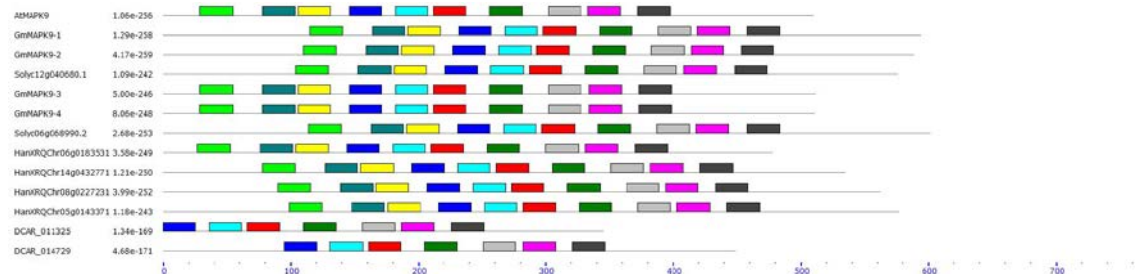


[Motif 10](#)

- 1.5e-153
- 16 sites



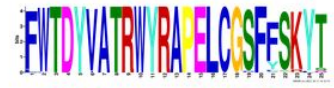
Clade D



Activation or T-loop

Motif 1

- 3.0e-1920
- 71 sites



Catalytic C-loop

Motif 2

- 1.9e-1756
- 71 sites



Motif 3

- 5.2e-1690
- 69 sites



Motif 4

- 9.4e-1503
- 72 sites



Motif 5

- 1.1e-1479
- 63 sites



P-loop

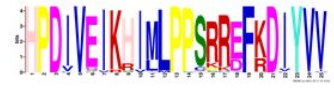
Motif 6

- 8.3e-1355
- 61 sites



Motif 7

- 9.3e-1351
- 61 sites



Motif 8

- 8.9e-1217
- 69 sites



Motif 9

- 1.7e-1320
- 70 sites



Motif 10

- 1.0e-1289
- 72 sites

