**FileS9.** ABRE motifs, siRNA abundance, and DNA methylation for predicted primary ABA and MOP1 targets.

1. Sequence logo of putative 9-bp ABRE motif. Motif discovery was performed using MEME Suite (Bailey et al., 2015)



|  |  |  |
| --- | --- | --- |
| **v4 gene id** | **Locus** | **24-nt siRNA reads** |
| ***Mop1* WT bio rep 1** | ***Mop1* WT bio rep 2** | ***Mop1* WT bio rep 3** | ***mop1-1* mut bio rep 1** | ***mop1-1* mut bio rep 2** |
| Zm00001d050728 | 4:118954002-118954010 | 0 | 0 | 2 | 0 | 0 |
| Zm00001d050728 | 4:118954005-118954013 | 0 | 0 | 1 | 0 | 0 |
| Zm00001d051526 | 4:161419373-161419381 | 2 | 0 | 0 | 0 | 1 |
| Zm00001d051526 | 4:161419605-161419613 | 1 | 0 | 0 | 0 | 0 |
| Zm00001d051526 | 4:161419618-161419626 | 1 | 0 | 1 | 0 | 0 |
| Zm00001d051526 | 4:161419623-161419631 | 1 | 0 | 1 | 0 | 0 |
| Zm00001d051526 | 4:161420659-161420667 | 0 | 1 | 0 | 0 | 0 |
| Zm00001d016299 | 5:156147175-156147183 | 0 | 2 | 1 | 0 | 0 |
| Zm00001d016299 | 5:156147347-156147355 | 0 | 0 | 1 | 0 | 0 |
| Zm00001d016299 | 5:156147642-156147650 | 1 | 0 | 1 | 0 | 0 |
| Zm00001d016299 | 5:156148105-156148113 | 1 | 0 | 0 | 0 | 0 |
| Zm00001d016299 | 5:156148148-156148156 | 0 | 0 | 1 | 0 | 0 |
| Zm00001d016299 | 5:156148553-156148561 | 2 | 3 | 3 | 0 | 0 |
| Zm00001d012387 | 8:173337368-173337376 | 1 | 0 | 2 | 0 | 0 |
| Zm00001d048055 | 9:149064674-149064682 | 2 | 1 | 4 | 0 | 0 |
| Zm00001d048055 | 9:149064830-149064838 | 8 | 7 | 6 | 0 | 1 |

1. 24-nt siRNA read count overlapping ABRE sites in the promoter region of MOP1-dependent ABA-responsive genes. ShortStack v3 (Johnson et al., 2016) was used to align siRNAs from Wang et al., 2017.

1. *Mitochondrial carrier family protein1 (Mcf1*) loss of CHH methylation at one ABRE site in *Mcf1* promoter region when comparing *mop1-1* mutant with *Mop1* wildtype.

|  |
| --- |
| **v4 gene id:** Zm00001d016299; mitochondrial carrier family protein1 (*Mcf1*) |
| **Locus:** 5:156147175-156147183 |
| **DNA Methylation context** | **DNA Methylation ratio *mop1-1* MS** | **Coverage *mop1-1* MS** | **Methylation sites *mop1-1* MS** | **DNA Methylation ratio *Mop1* MS** | **Coverage *Mop1* MS** | **Methylation sites *Mop1* MS** | **DNA Methylation % difference (mop1-1 MS – *Mop1* MS)\*100** |
| CHH | 0.143 | 7 | 3 | 0.231 | 4.33 | 3 | -8.79 |