**Supporting Information**

**Supplementary data**

**Table S1** Primer pairs used for qRT-PCR in this study.

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| **Gene** | **Gene information** | **Primers sequence** |
| *AsActin* | KP257585 | Forward : 5’- GCTGTGCTTTCCCTCTATGC -3’  Reverse : 5’- GGACATCAAGGAGAAGCTCG -3’ |
| *AsPAL* | MH507022 | Forward : 5’- GACAACCCGCTCATTGACGT -3’  Reverse : 5’- ATCTCAGCACCCTTGAAGCC -3’ |
| *As4CL* | MH397063 | Forward : 5’- CAGAGGCCACAAAGAACACG -3’  Reverse : 5’- GCCGGAGGAACTTGGAATCC-3’ |
| *AsCCoAOMT* | MK577959 | Forward : 5’- CATGGAGATCGGCGTGTACA -3’  Reverse : 5’- TAGTTGTCGCGGTTGATGTC -3’ |
| *AsHHT1* | AB076980 | Forward : 5’- AATGAACAAACAGCACGCCC -3’  Reverse : 5’- TTGCAGTAGTAGCTACGTCTGG -3’ |
| *AsHHT2* | AB076981 | Forward : 5’- TCGCCTTCGTGCTCCCCAG -3’  Reverse : 5’- GCGCGTGCTGTTTGTTCGTT -3’ |
| *AsHHT3* | AB076982 | Forward : 5’- CGGCGACGCGTGCTGCTA -3’  Reverse : 5’- CACCCCCTCAGCGTTGCAG -3’ |
| *AsHHT4* | MH397064 | Forward : 5’- CTGGAGCCGGAGCGGGA -3’  Reverse : 5’- CGACGAAGAGCACCCCCTC -3’ |
| *AsHHT5* | MH397065 | Forward : 5’- GGGCGCTGTGGCAGATGGAG -3’  Reverse : 5’- TCCCCAACCGAAATCCGCGTT -3’ |
| *AsHHT6* | MH397066 | Forward : 5’- GAGCCGGAGCAGGGGAGG -3’  Reverse : 5’- CGACGAAGAGCACCCCCTC -3’ |

PAL, phenylalanine ammonia lyase; 4CL, 4-coumarate-CoA ligase; CCoAOMT, caffeoyl-CoA O-methyltransferase; HHT, hydroxycinnamoyl-CoA:hydroxyanthranilate N-hydroxycinnamoyl transferase.

Primers were designed using the Beacon designer™ software (Premier Biosoft).

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**Figure S1.** The relative expression of avenanthramide-biosynthetic genes following co-treatment with MeJA and ABA of germinating oats. Transcript levels of *PAL, 4CL, CCoAOMT, HHT1, HHT2, HHT3, HHT4, HHT5*, and *HHT6* were analyzed by qRT-PCR in germinating oats treated with 75 μM MeJA and 25 μM ABA for 3 days. Relative expression levels were normalized against *AsActin* (KP257585) and are presented as fold induction relative to *AsActin*. Data represent the mean of three independent replicates ± SD.



**Figure S2.** The relative expression levels of avenanthramide-biosynthetic genes in three types of oat tissues: (A) leaves, (B) grains, and (C) roots. Combined treatment (MeJA + ABA) comprised 75 μM MeJA and 25 μM ABA. Two-day-old germinating oats were treated for 3 days, and transcript levels of *PAL, 4CL, CCoAOMT, HHT1, HHT2, HHT3, HHT4, HHT5*, and *HHT6* were analyzed by qRT-PCR. Relative expression levels were normalized against *AsActin* (KP257585) and are presented as fold induction relative to the control. Data represent the mean of three independent replicates ± SD.