Supplementary Figures and Legends
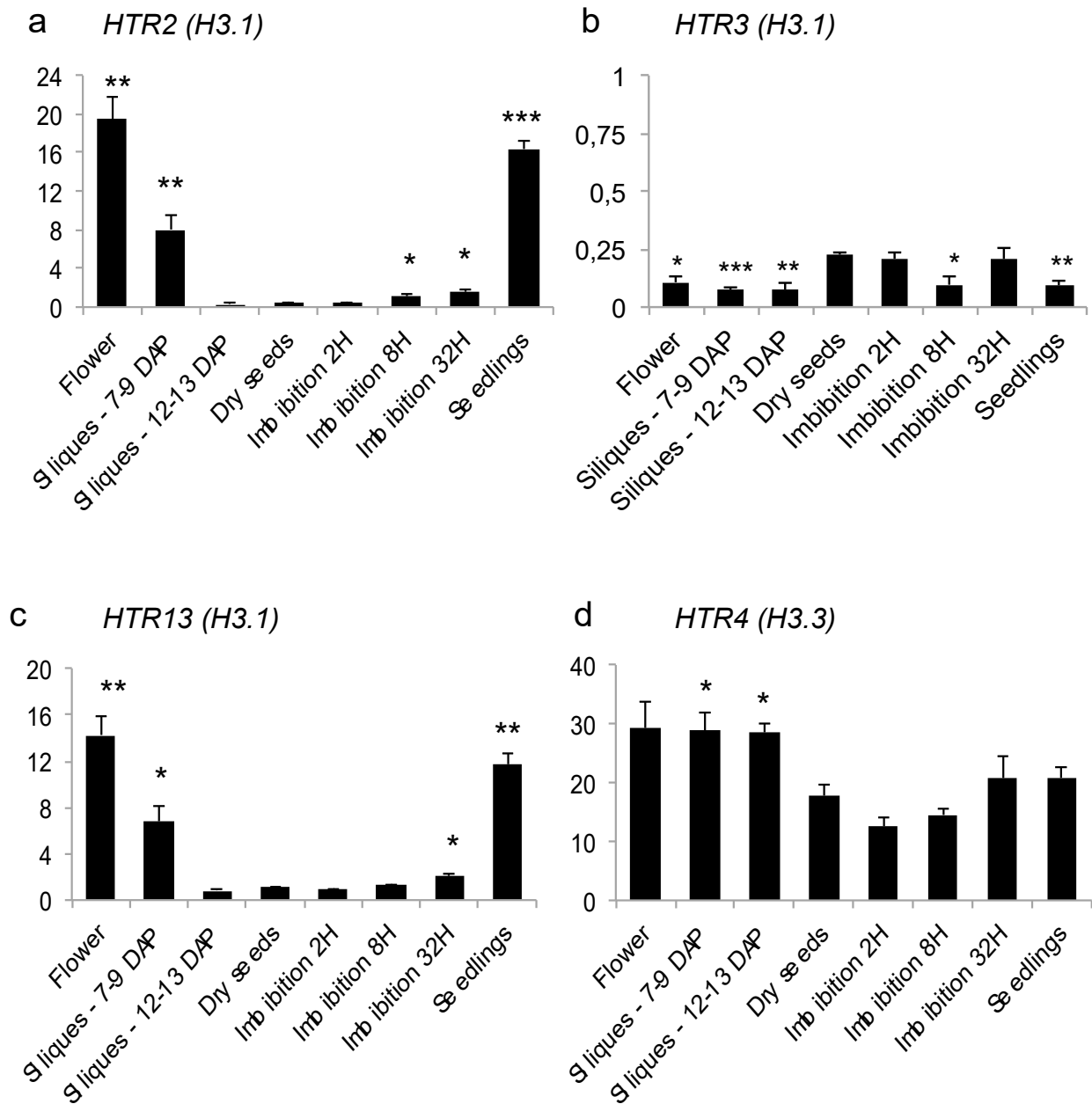

Figure S1. *HTR2, HTR3, HTR13* and *HTR4* expression at different developmental stages

Relative transcript levels of three genes encoding H3.1 (*HTR2* (**a**), *HTR3* (**b**) and *HTR13* (**c**)), as well as one gene encoding H3.3 (*HTR4 (d)*) in flowers, siliques (7-9 and 12-13 days after pollination (DAP)), dry seeds and seeds imbibed for 2 hours (H), 8H or 32H as well as 2 days old seedlings. Transcript levels are normalized to *MON1* (*At2g28390*). Error bars correspond to the SEM of three biological replicates and statistical significant differences relative to dry seeds were determined using a two-sided Student t-test (* p< 0,05; ** p < 0,01; *** p < 0,001).
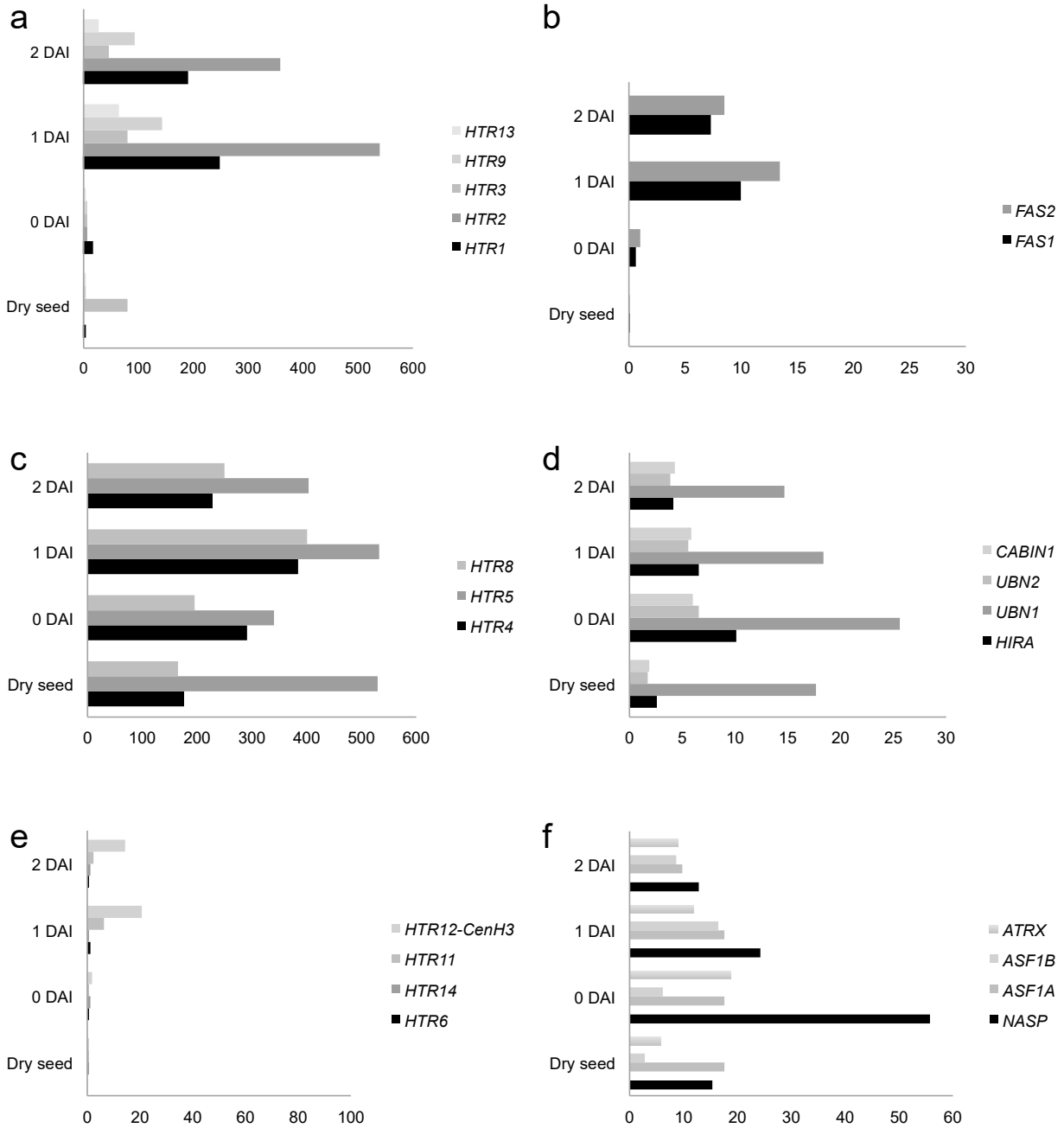
Figure S2: Dynamic expression of H3 histone chaperones during seed imbibition and germination

Expression in FPKM (Fragments Per Kilobase Million) of genes encoding H3 histones: replicative variants (**a**) *HTR1, HTR2, HTR3, HTR9* and *HTR13*; replacement variants (**c**) *HTR4, HTR5* and *HTR8*, the atypical variants H3.6 (*HTR6*), H3.14 (*HTR14*), H3.11 (*HTR11*) and the centromeric variant CenH3 (*HTR12*) (**e**) as well as genes encoding known H3 histone chaperones; including the CAF-1 complex (**b**), the HIRA complex (**d**) and genes encoding ATRX, NASP and ASF1a and b (**f**) in dry seeds, seeds after 4 days of stratification (0 Days after imbibition (DAI)) and after 1 or 2 days under long day conditions at 22°C (1 DAI, 2 DAI). Expression data are from [1]. *HTR10* (*H3.10*) and *H3.15 (HTR15)* are not expressed in these tissues.
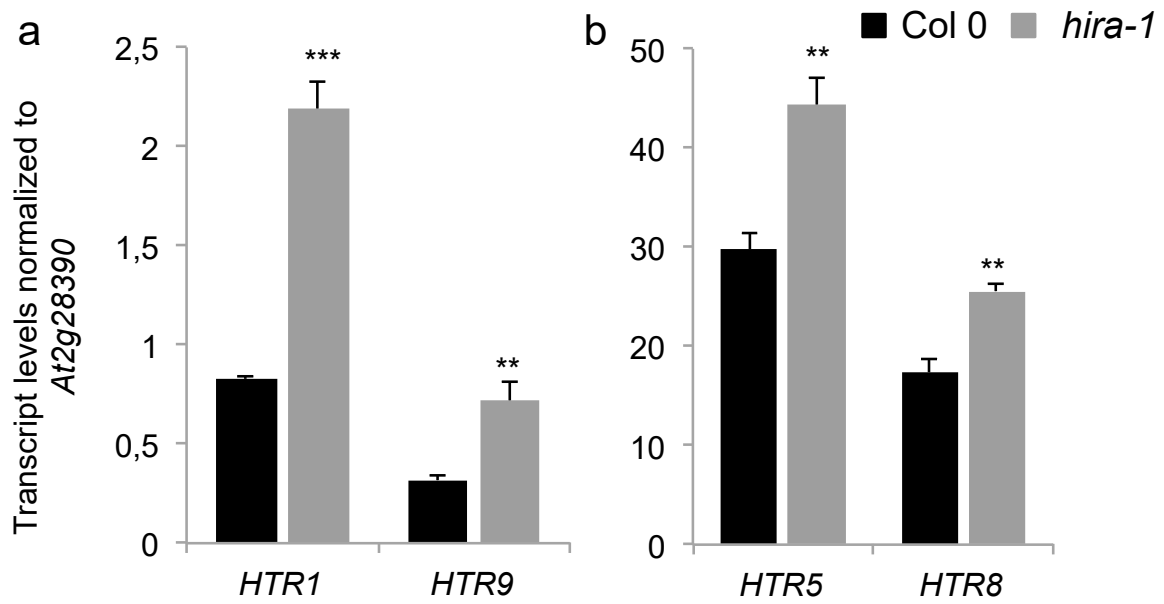
Figure S3: H3.1 and H3.3 expression in *hira-1* mutant seeds

Relative transcript levels of two genes encoding H3.1 (**a**, *HTR1, HTR9*) or H3.3 (**b**, *HTR5, HTR8*) in WT and *hira-1* mutant dry seeds. Error bars correspond to the SEM of four biological replicates and statistical significant differences relative to WT were determined using a two-sided Student t-test (** p< 0,01; *** p < 0,001).
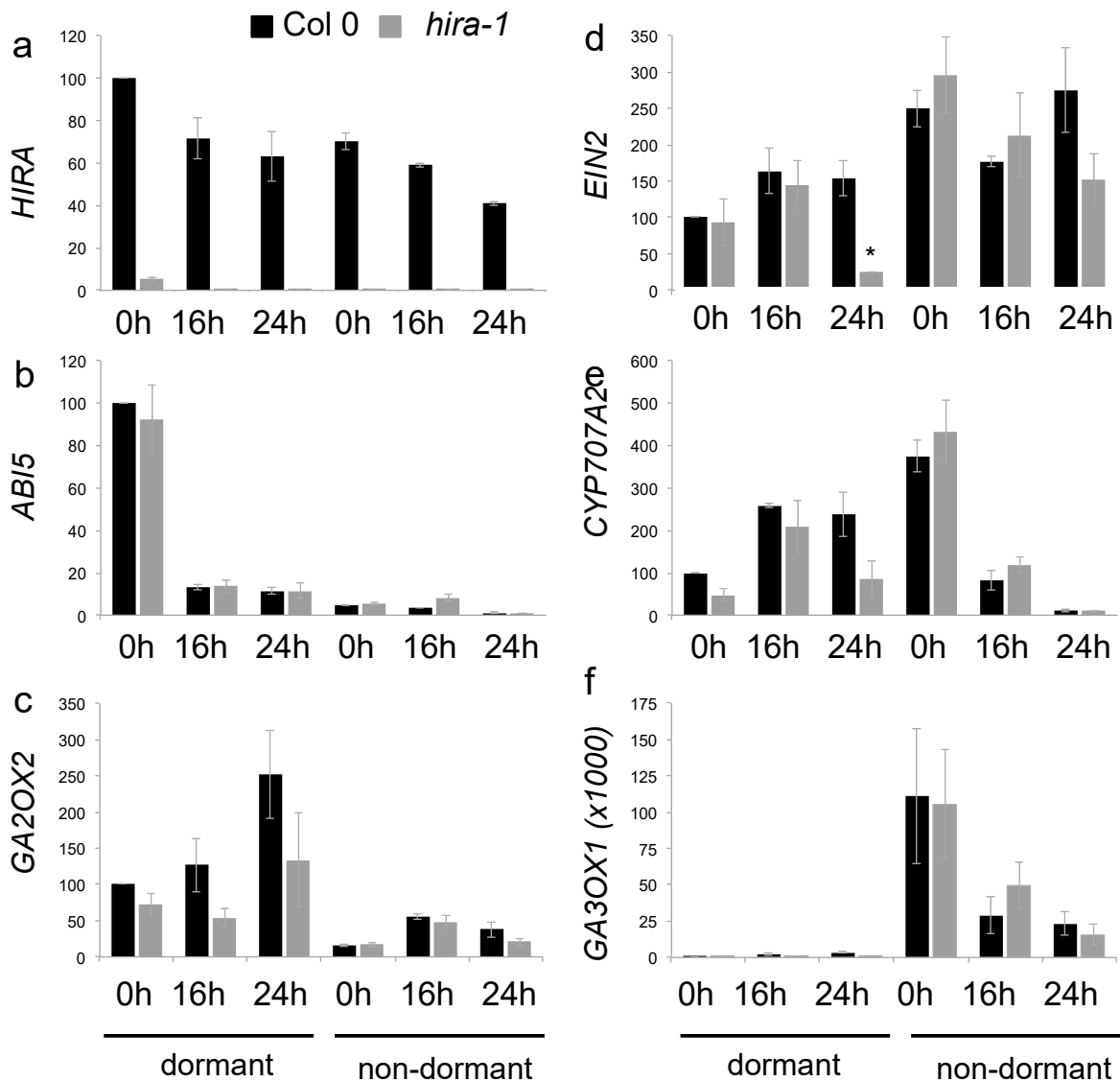
Figure S4: Gene expression in *hira-1* mutant seeds

Relative transcript levels of *HIRA* (**a**), *ABA INSENSITIVE 5 (ABI5)* (**b**), *GIBBERELLIN 2-OXIDASE 2 (GA2OX2)* (**c**), *ETHYLENE-INSENSITIVE PROTEIN2 (EIN2)* (**d**), *CYTOCHROME P450, FAMILY 707, SUBFAMILY A (CYP707A)* (**e**) and *GIBBERELLIN 3-OXIDASE 1 (GA3OX1)* (**f**) in dormant or non-dormant seeds (after 48 hours of imbibition) with or without incubation for 16 or 24 hours at 25°C in darkness. Error bars indicate SD for three biological replicates.
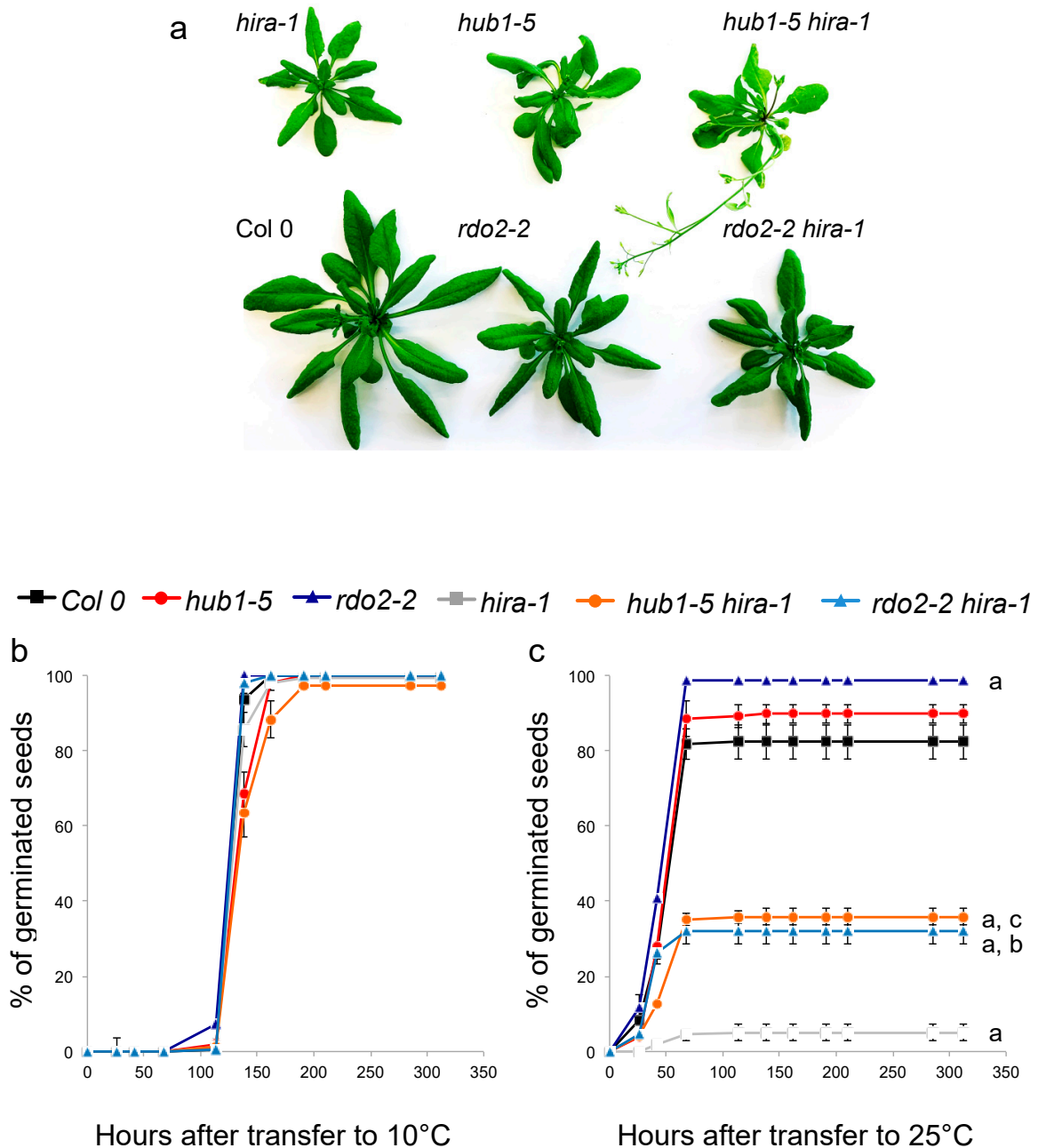
Figure S5: Growth and dormancy phenotypes of single and multiple *hira-1, hub1-5* and *rdo2-2* mutants

(**a**) Representative images of WT, *hira-1, hub1-5, rdo2-2, rdo2-2 hira-1* and *hub1-5 hira-1* mutant plants. (**b-c**) Same as Figure 5; data obtained with an independent seed batch. Germination of freshly harvested seeds of Col 0 (black), *hub1-5* (red), *rdo2-2* (dark blue), *hira-1* (grey), *hub1-5 hira-1* (orange) and *rdo2-2 hira-1* (light blue) at 10°C (seed viability test; a) or at 25°C (dormancy test; b) in darkness. Means of biological triplicates with SEM are shown. Statistical significant differences were determined using a two-sided Student t-test (a = p < 0,01 relative to Col 0; b = p < 0,01 relative to *hub1-5*; c = p < 0,01 relative to *rdo2-2*).
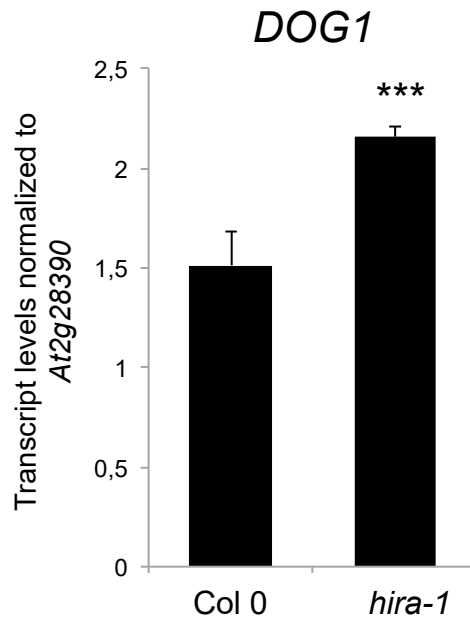
Figure S6: *DOG1* expression in *hira-1* mutant seeds

Relative *DOG1* transcript levels in WT and *hira-1* mutant dormant dry seeds. Error bars correspond to the SEM of four biological replicates and statistical significant differences relative to WT were determined using a two-sided Student t-test (*** $p < 0,001$).

Table S1. Primers used in this study.

Gene	Forward and Reverse primers (5' to 3')
MON1 (At2g28390)	AACTCTATGCAGCATTTGATCCACT TGATTGCATATCTTTATCGCCATC
HTR1 (At5g65360)	AGCGATCTCACGAACCAAAC GAAATCCACCGGAGGAAAAG
HTR2 (At1g09200)	GCAGACGGCTAGGAAATCAA TTCCGGGTCTGAATCTGTGT
HTR3 (At3g27360)	CTGAAGTGTCTTCCAGATGT ACAAGTCACTAAGACCTGAA
HTR4 (At4g40030)	AATAAAGATGGCTCGTACCA CTTACGGATTTCACGGAGAG
HTR5 (At4g40040)	TTGCACTACGTGAAATTCGT CACAAGGTATGCTTCAGCAG
HTR8 (At5g10980)	AAGAGCTAACACCGCGTGAC AGGAAATCAGCACCAACCAC
HTR9 (At5g10400)	TAATCTCTGTGCGATTCATGCT CGAAAACGAAAAGAGACAGCTT
HTR13 (At5g10390)	AAGCACCAAGAAAGCAACTC CTTACGGATCAGAAGCTCAG
CB5-E (At5g53560)	TGAAGAAGTTTCAAAGCACAACA TCATCCATGAATGGAGTCACA
TIP41 (At4g34270)	GTGAAAACTGTTGGAGAGAAGCAA TCAACTGGATACCCTTTCGCA
RHIP1 (At4g26410)	GAGCTGAAGTGGCTTCCATGAC GGTCCGACATACCCATGATCC
HIRA (At3g44530)	AACAAGACCAGAACTCAAGA CTTTAACAACGCCTAACTGAG
DOG1 (At5G45830)	TCTCGTCTCGACAAGTCAGC ACCAAATCTGCCAAGTCCAT
ABI5 (At2g36270)	AACATGCATTGGCGGAGTTG GCAATTTCGGTTGTGCCCTT
GA2OX2 (At1g30040)	ATGGTGAAGGTGGGGTTTGG CTCCCGTTAGTCATAACCTGAAG
GA3OX1 (At1g15550)	CATCACCTCAACTACTGCGATA TTAGCTGGAGAGCAGCTTGG
CYP707A2 (At2g29090)	CTCGCCAAAACAAGTACGGG AGCCGCCTCTGGACTACTTTA
EIN2 (At5g03280)	CACCACTCTGCTTGTATCGTC TCGTCTTCGTTCCTCCTTGT

References

1. Kawakatsu, T.; Nery, J.R.; Castanon, R.; Ecker, J.R. Dynamic DNA methylation reconfiguration during seed development and germination. *Genome Biol.* **2017**, *18*, 171, doi:10.1186/s13059-017-1251-x.