First off the mark: early seed germination

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Supplementary Material

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Supplementary Figure S1. Regulation of GA- and ABA-related transcripts by cold stratification of Arabidopsis thaliana seeds. (A) Important steps in gibberellin (GA) and abscisic acid (ABA) biosynthesis, degradation and signaling. ZEP = zeaxanthin epoxidase, NCED = nine-cis-epoxycarotenoid dioxygenase, SDR1/ABA2 = short-chain dehydrogenase reductase, AAO = abscisic aldehyde oxidase, CYP707A = ABA 8'-hydroxylase. (B) and (C) The transcript level ratios 4 °C / 22 °C for GA- and ABA-related genes calculated from seeds incubated for 96 h in darkness (Yamauchi et al., 2004), data are available via the seed-specific eFP-browser at www.bar.utoronto.ca (Winter et al., 2007; Bassel et al., 2008).
Supplementary Figure S2. Regulation of transcripts for the energy metabolism of *Arabidopsis thaliana* seeds by imbibition (ratio 6h/dry of Col seeds incubated in the light at 22 °C), cold stratification (ratio 4 °C / 22 °C after 96h of dark incubation of Col seeds), GA (ratio +GA/-GA of GA-deficient *ga1-3* seeds at 6h) and ABA (ratio +ABA/-ABA of Ler seeds at 24h), data are available via the seed-specific eFP-browser at www.bar.utoronto.ca (Winter *et al.*, 2007; Bassel *et al.*, 2008).
Supplementary Table 1. Transcriptome analysis for energy metabolism genes during Arabidopsis thaliana germination sensu strictu and its regulation by hormones and cold stratification. The seed-specific eFP-browser and the eNorthern tool at www.bar.utoronto.ca were used to analyse transcript expression patterns based on global transcriptome analyses during Arabidopsis seed germination (Winter et al., 2007; Bassel et al., 2008). The time course of transcriptional changes of key metabolic enzyme genes during the early phase of germination (dry seed (0h) to 24h) of non-dormant, non-stratified Arabidopsis Col seeds are listed as relative values (Nakabayashi et al., 2005; Preston et al., 2009); in addition the absolute values in dry seeds and at 6h are listed (in red). The imbibition-mediated transcript expression patterns the ratios 6h/dry were calculated and classified as follows: up-regulation if ratio ≥2, equal if ratio 0.5 to 2, down-regulation if ratio ≤0.5, up24 if up-regulation is only evident at 24h. The transcript regulation patterns by moist cold-stratification were determined from the ratios 4°C / 22°C of seeds imbibed in darkness for 96h (Yamauchi et al., 2004). The regulation by gibberellins (GA) was analysed by calculating the ratios obtained with 6h-imbibed GA-deficient ga1-3 seeds ±GA (RIKEN transcriptome sets at www.bar.utoronto.ca). The regulation by abscisic acid (ABA) was analysed by calculating the ratios obtained with 24h-imbibed Ler seeds ±ABA (RIKEN transcriptome sets at www.bar.utoronto.ca). The column "proteome analysis" contains the corresponding protein expression patterns for germination sensu strictu compiled from the following publications: (1) Arabidopsis whole seed, germination sensu strictu after cold-stratification (Fu et al. 2005). (2) Arabidopsis whole seed, germination sensu strictu, www.seedproteome.com. (3) Lepidium sativum endosperm cap, germination sensu strictu, no cold-stratification (Müller et al. 2010). (4) Arabidopsis whole seed ratio, germination sensu strictu, α-amanitin/control (Rajjou et al. 2004). (5) Arabidopsis whole seed, germination sensu strictu (Gallardo et al. 2001).

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