

First off the mark: early seed germination

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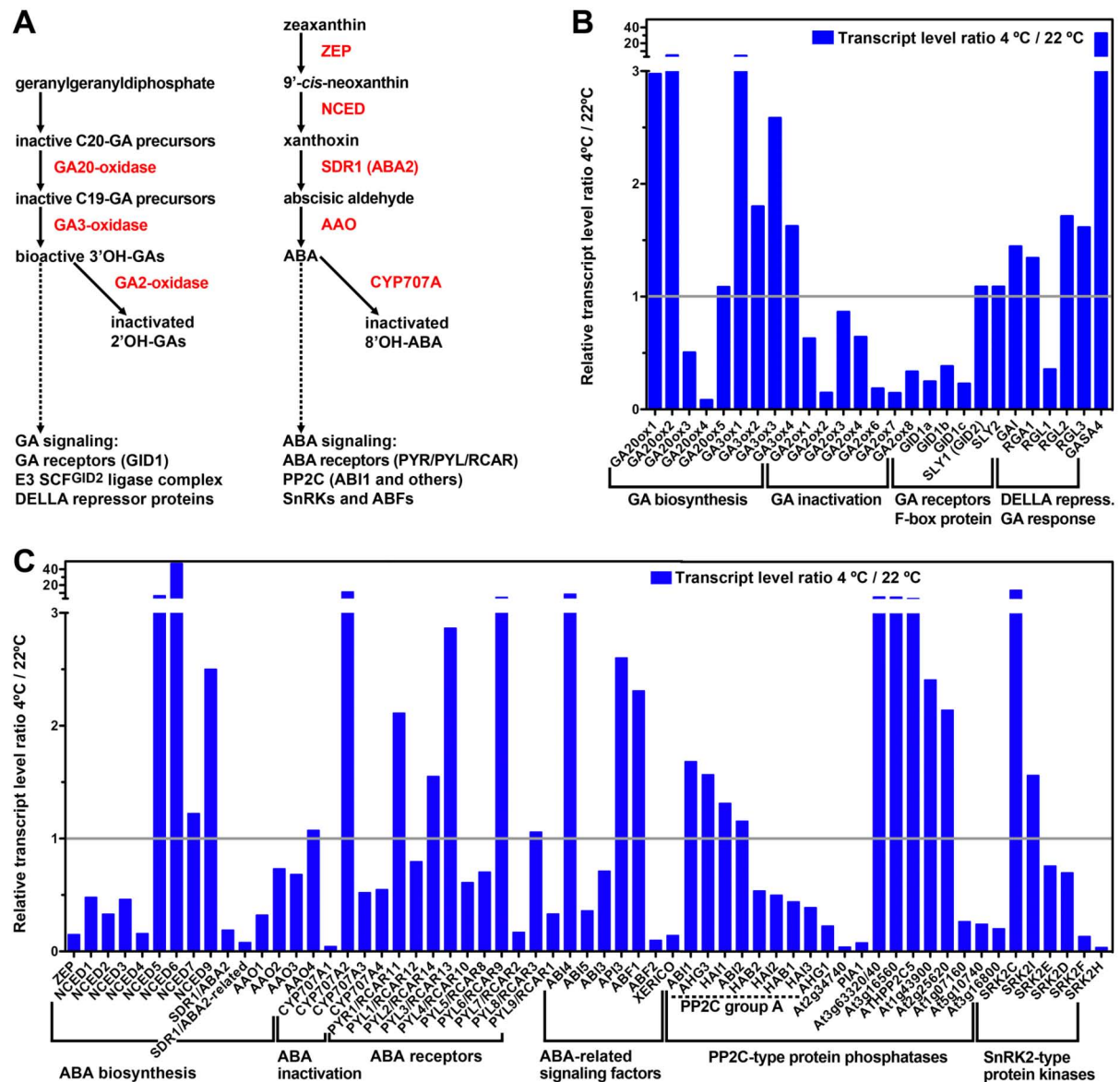
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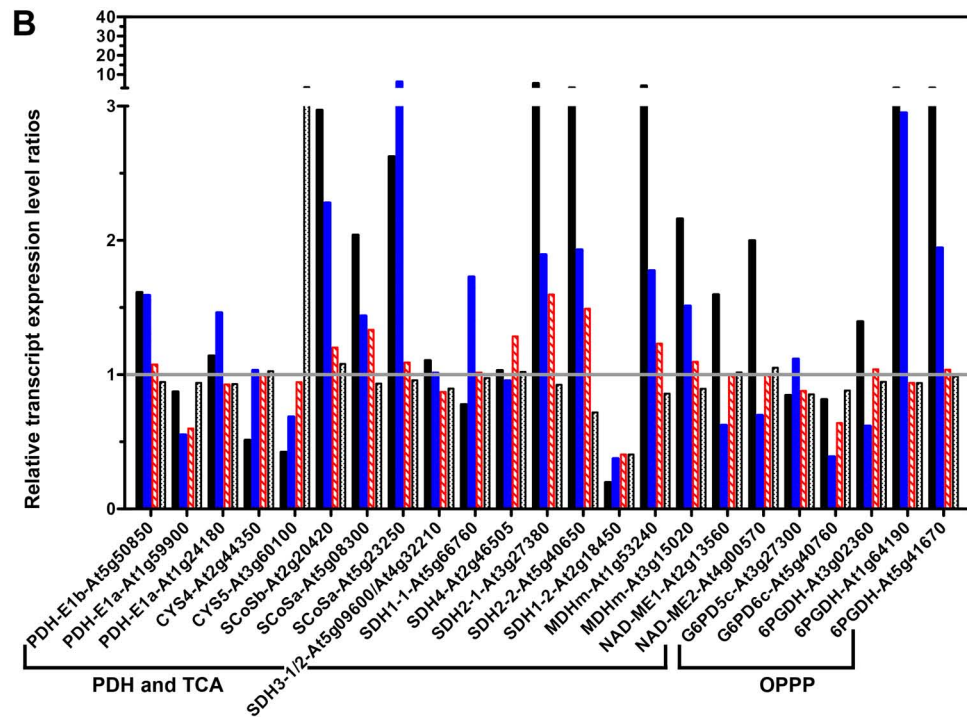
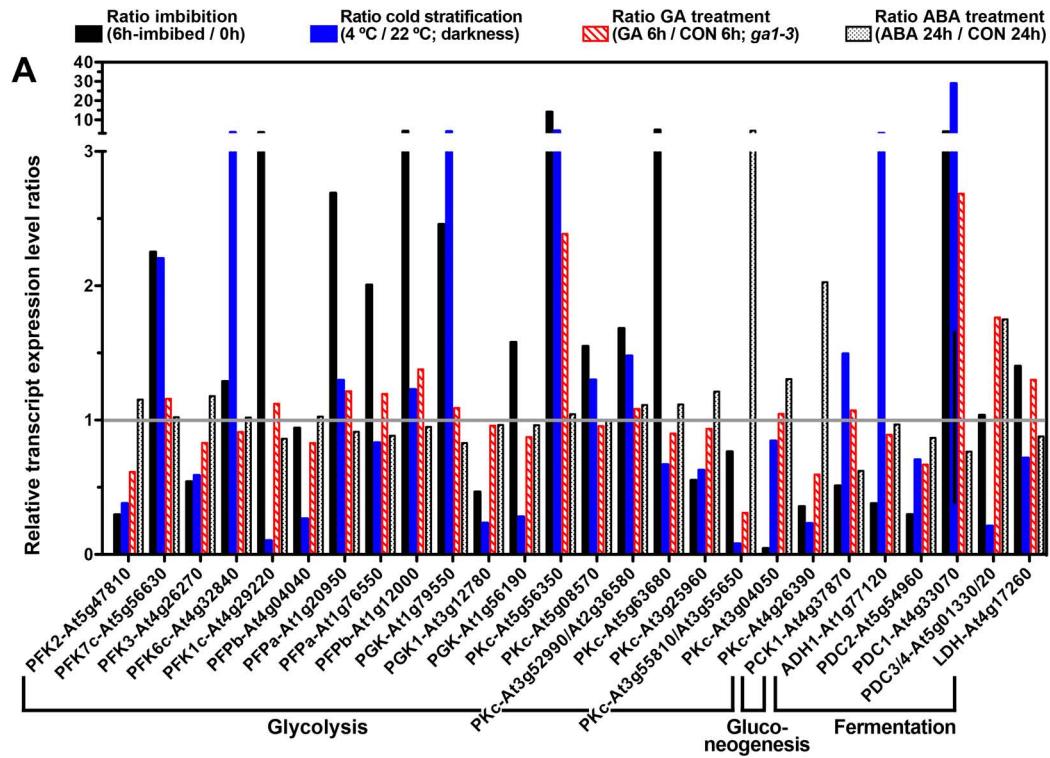
Supplementary Material

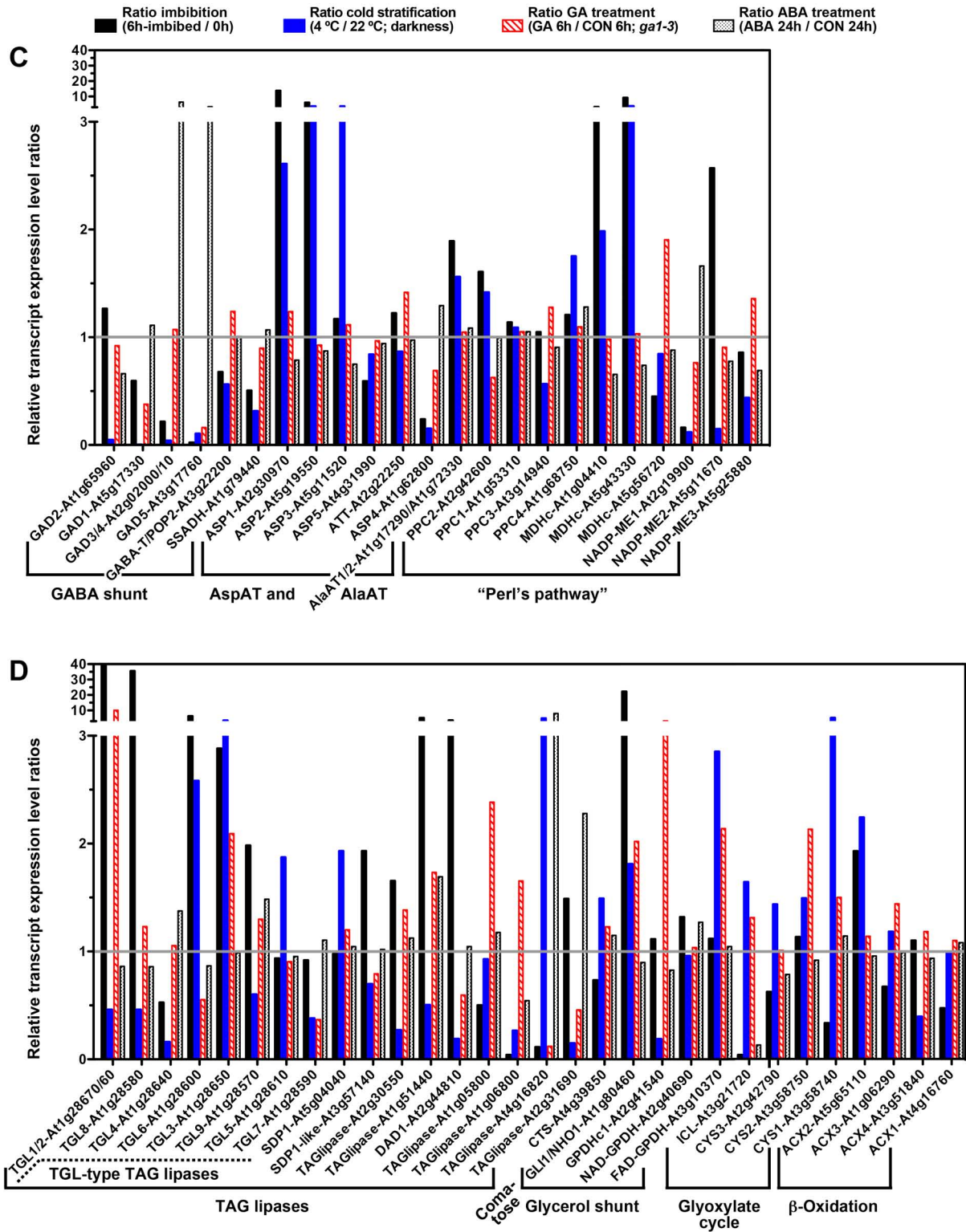
Darwin Review

Journal of Experimental Botany (2011)



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 \pm 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 \pm 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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