

SUPPLEMENTAL MATERIAL, FIGURE CAPTIONS

Figure S1.

A, The two independent *AtPP2CA* T-DNA insertion lines *pp2ca-1* and *pp2ca-2* exhibit very similar ABA hypersensitivity in germination assays. Comparison of germination rates of wild-type (Col-0; filled circles), *pp2ca-1* (open triangles) and *pp2ca-2* (open diamonds) seeds exposed to 0, 0.3, 0.5, 1 and 2.5 μ M ABA at 5 days. Data represent the mean \pm s.e.m. of $n = 3$ independent experiments with 36 seeds per genotype and experiment. Error bars are smaller than symbols, if not visible. B and C, Stomatal closing is ABA-hypersensitive in *pp2ca-1* (B) and *pp2ca-2* (C) and ABA-insensitive in *35S::AtPP2CA* plants. Ratios of measurements of stomatal apertures shown in Fig. 5B and Fig. 5C relative to stomatal heights of WT (open bars), *pp2ca-1* (B) and *pp2ca-2* (C) (shaded bars) and PP2CAox (black bars) in response to 1 μ M and 10 μ M ABA or no ABA. Data represent the mean of double-blind analyses of $n = 4$ independent experiments \pm s.e.m. with 4x 50 stomata per data point for Fig. S1B and the mean of $n = 2$ independent experiments \pm s.d. with 2x 50 stomata per data point for Fig. S1C. Stars indicate significant changes between the indicated background and WT (p-value < 0.001).

Figure S2. General down-regulation of *PP2Cs* from group A of the *Arabidopsis* *PP2C* family during wild-type seed imbibition. Pre-normalized data from wild-type microarray (ATH1 Genechip; Affymetrix, Santa Clara, CA, USA) experiments from Nakabayashi et al. (2005) during seed imbibition (24 hour-long water treatment) were downloaded (June 2005) from *GENEVESTIGATOR* (www.genevestigator.ethz.ch) (Zimmermann et al., 2004). Transcripts of the nine following *PP2C* genes *At5g51760* (247723_at), *At5g57050-ABI2* (247957_at), *At5g51760* (248428_at), *At4g26080-ABII* (253994_at), *At3g11410-AtPP2CA* (259231_at), *At1g72770-AtP2C-HAB1* (259922_at), *At1g17550-HAB2* (260712_at), *At1g07430* (261077_at), and *At2g29380* (266274_at) were analyzed and sorted from the highest to the weakest mRNA levels in dry seed using Microsoft Excel. *ACTIN7* (250458_s_at) values were included as controls. Error bars represent the standard deviation of two independent experiments (Nakabayashi et al., 2005). Note that

(i) *AtPP2CA* is the second most highly expressed *PP2C* gene from group A in dry seeds and that (ii) *ABII* is the only *PP2C* gene from group A whose mRNA level is not down-regulated during imbibition.

Figure S3. Transcription profile of *PP2Cs* from group A of the *Arabidopsis PP2C* family in guard cells in response to ABA treatment. Pre-normalized data from wild-type microarray (Arabidopsis Genome Array; Affymetrix, Santa Clara, CA, USA) experiments from Leonhardt et al. (2004) were downloaded (June 2005; <http://www-biology.ucsd.edu/labs/schroeder/index.html>). Transcript levels of five *PP2C* genes *At5g57050-ABI2* (probe# 17929_s_at), *At4g26080-ABII* (15586_s_at), *At3g11410-AtPP2CA* (19638_at), *At1g72770-AtP2C-HABI* (18936_at) and *At2g29380* (12470_at) are displayed. Error bars represent the standard deviation of three (guard cells, GC) or two (mesophyll cells, MC) independent experiments (Leonhardt et al., 2004).

LITERATURE CITED

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