SUPPLEMENTARY DATA

TABLE S3. Information on the individual microarray slides used in the analysis to produce Fig. 5A in the main text

Experiment name[1]	**Slides**[2]
Roots[A,B]	
A gene expression map of the Arabidopsis root (NASCARRAYS-367)	Birnbaum_1-1_src5-1_Rep1_ATH1, Birnbaum_1-2_src5-2_Rep2_ATH1, Birnbaum_1-3_src5-3_Rep3_ATH1, Birnbaum_1-16_wol-1_Rep1_ATH1, Birnbaum_1-17_wol-2_Rep2_ATH1, Birnbaum_1-18_wol-3_Rep3_ATH1, Birnbaum_1-19_LRC-1_Rep1_ATH1, Birnbaum_1-20_LRC-2_Rep2_ATH1, Birnbaum_1-21_LRC-3_Rep3_ATH1, Birnbaum_1-22_gl2-1_Rep1_ATH1, Birnbaum_1-23_gl2-2_Rep2_ATH1, Birnbaum_1-24_gl2-3_Rep3_ATH1, Birnbaum_1-25_J0571-1_Rep1_ATH1, Birnbaum_1-26_J0571-2_Rep2_ATH1, Birnbaum_1-27_J0571-3_Rep3_ATH1, Birnbaum_1-4_StageI-1_Rep1_ATH1, Birnbaum_1-5_StageI-2_Rep2_ATH1, Birnbaum_1-6_StageI-3_Rep3_ATH1, Birnbaum_1-7_StageI-4_Rep4_ATH1, Birnbaum_1-8_StageII-1_Rep1_ATH1, Birnbaum_1-9_StageII-2_Rep2_ATH1, Birnbaum_1-10_StageII-3_Rep3_ATH1, Birnbaum_1-11_StageII-4_Rep4_ATH1, Birnbaum_1-12_StageIII-1_Rep1_ATH1, Birnbaum_1-13_StageIII-2_Rep2_ATH1, Birnbaum_1-14_StageIII-3_Rep3_ATH1, and Birnbaum_1-15_StageIII-4_Rep4_ATH1
AtGenExpress: Developmental series (roots)(NASCARRAYS-151)	ATGE_3 A-C, ATGE_9 A-C, ATGE_93 A-C, ATGE_94 A-C, ATGE_95 A-C, ATGE_98 A-C and ATGE_99 A-C
Seedlings[A]	
AtGenExpress: Developmental series (seedlings and whole plants)(NASCARRAYS-149)	ATGE_1 A-C, ATGE_2 A-C, ATGE_7 A-C, ATGE_96 A-C, ATGE_97 A-C, ATGE_100 A-C, and ATGE_101 A-C
Leaves[A]	
AtGenExpress: Developmental series (leaves)(NASCARRAYS-150)	ATGE_5 A-C, ATGE_10 A-C, ATGE_12 A-C, ATGE_13 A-C, ATGE_14 A-C, ATGE_15 A-C, ATGE_16 A-C, ATGE_17 A-C, ATGE_19 A-C, ATGE_20 A-C, ATGE_21 A-C, ATGE_22 A-C, ATGE_23 A-C, ATGE_24 A-C, ATGE_26 A-C, ATGE_87 A-C, ATGE_89 A-C, ATGE_90 A-C and ATGE_91 A-C
Senescing leaves[A]	
AtGenExpress: Developmental series (leaves)(NASCARRAYS-150)	ATGE_25 A-C
Shoot apex[A]	
AtGenExpress: Developmental series (shoots and stems)(NASCARRAYS-153)	ATGE_4 A-C, ATGE_6 A-C, ATGE_8 A-C and ATGE_29 A-C
Stems[A]	
AtGenExpress: Developmental series (shoots and stems)(NASCARRAYS-153)	ATGE_27 A-C and ATGE_28 A-C
Flowering induction[C]	
AtGenExpress: Developmental series (mutants and other ecotypes)(NASCARRAYS-155)	Col-0_0_1, Col-0_0_2, Col-0_3_1, Col-0_3_2, Col-0_5_1, Col-0_5_2, Col-0_7_1, Col-0_7_2
Flowers[A]	
AtGenExpress: Developmental series (flowers and pollen) (NASCARRAYS-152)	Whole flower ATGE_31 A-C, ATGE_32 A-C, ATGE_33 A-C, and ATGE_39 A-C), Sepals (ATGE_34 A-C and ATGE_41 A-C), Petals (ATGE_35 A-C and ATGE_42 A-C), Stamens (ATGE_36 A-C and ATGE_43 A-C) and Carpels (ATGE_37 A-C and ATGE_45 A-C)
Pollen development[A,D]	
Transcriptome analysis of Arabidopsis microgametogenesis (NASCARRAYS-48)	Honys_UNM1_SLD, Honys_UNM2_SLD, Honys_BCP1_SLD, Honys_BCP2_SLD, Honys_TCP1_SLD, Honys_TCP2_SLD and Honys_MPG1_SLD
AtGenExpress: Developmental series (flowers and pollen) (NASCARRAYS-152)	ATGE_73 A-C
Siliques[A]	
Developmental series (siliques and seeds) (NASCARRAYS-154)	ATGE_76 A-C, ATGE_77 A-C and ATGE_78 A-C
Seeds development[A]	
Developmental series (siliques and seeds) (NASCARRAYS-154)	ATGE_79 A-C, ATGE_81 A-C, ATGE_82 A-C, ATGE_83 A-C and ATGE_84 A-C
Seed germination[E]	
AtGenExpress: Expression profiling of early germinating seeds (NASCARRAYS-195)	RIKEN-PRESTON0A, RIKEN-PRESTON0B, RIKEN-PRESTON1A, RIKEN-PRESTON1B, RIKEN-PRESTON2A and RIKEN-PRESTON2B

[1] The names are the same as they appear in the NASC's International Affymetrix Service (http://affymetrix.arabidopsis.info/).

[2] Sources of the microarrays are noted as the following:

[A] AtgenExpress developmental series (http://www.weigelworld.org/resources/microarray/AtGenExpress/) (183 slides) (Schmid *et al*., 2005);

[B] Src - endodermis, wol - stele, LRC - lateral root cap, gl2 – atrichoblasts, and J0571 - endodermis and cortex (15 slides) are from “Transcriptional profile of the Arabidopsis root quiescent center” (annotations according to Nawy et al., 2005) and StageI - stage 1, StageII - stage 2, and StageIII - stage 3 (12 slides) are from “*in situ* digital hybridization in root” (annotations according to Birnbaum et al., 2003).

[C] Data for 0D, 3D, 5D and 7D (Days) treatments after plants were transferred from short-day (9 hours light, 15 hours dark) to long-day (16 hours light, 8 hours dark) conditions (8 slides) are from “Global expression analysis of floral induction” (Schmid et al., 2003);

[D] UNM; uninuclear microspores, BCP; bicellular pollen, TCP; tricellular pollen and MPG; mature pollen (7 slides) are from “Transcriptome analysis of Arabidopsis microgametogenesis” (Honys and Twell, 2004); and

[E] 0hr, 1hr and 3hr (hour) after seed stratification (6 slides) are from “Expression profiling of early germinating seeds” (http://affymetrix.arabidopsis.info/narrays/experimentpage.pl?experimentid=195).