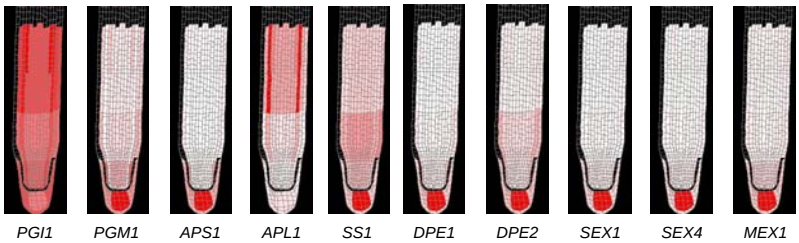

Normalized microarray data of 51 starch metabolism genes (defined by Smith et al., 2004) were extracted from AREX (www.arexdb.org; Birnbaum et al., 2003)

Condition 1:
exclude genes expressing high in tissues other than columella and lateral root cap cells
a. [Columella]/[others, except LRCs]>1.51
b. [Columella] & [LRCs]>100
c. [others except Columella and LRCs]<500

Condition 2:
exclude genes expressing low in tissues aboveground (nascarrays-60; Smith et al., 2004)

Group I (24 genes)

Genes expressed mainly in leaves and root tips

Group II (27 genes)

Signal>500 (except columella and lateral root cap) in roots

Signal < 50 (at least in 6 time points) in leaves

1. Gene expression map of development (Schmid et al., 2005)

2. Regulatory elements of promoters analysis

Figure S1. A flow-chart diagram for steps and parameters used in the expression profile analysis of starch metabolism genes.

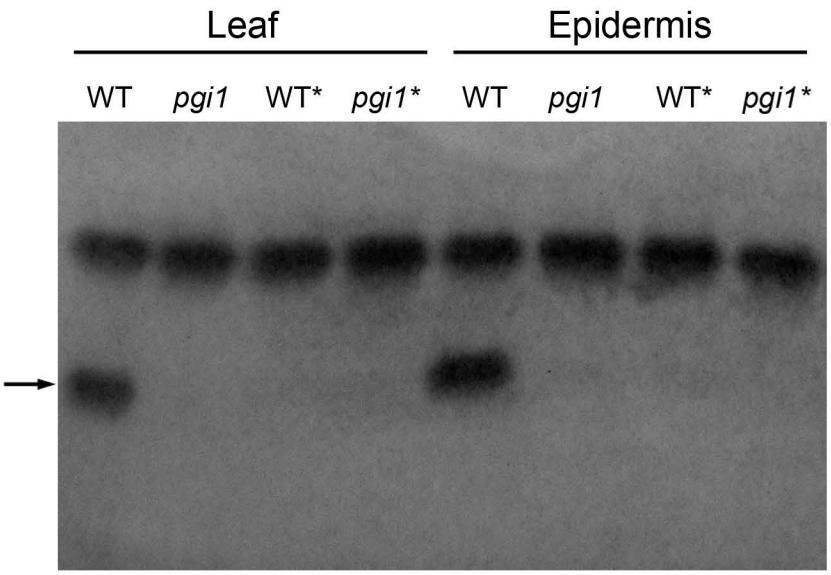

Figure S2. Heat inactivation of PGI isozymes in epidermis and leaf extracts of wild type and *pgi1* mutant

Epidermis and Leaf extracts of the wild type (WT) and *pgi1* were separated by a 7.5% native gel and stained for PGI activity. From each extract 20 µg of total protein was loaded. Two PGI activity bands were detected in the wild type extract. The plastidial PGI activity (arrow) was not present in the *pgi1* extract. For heat inactivation, the extracts were treated at 50°C for 10 min (asterisk). Upon heat inactivation, the plastidial PGI activity in the wild type was inactivated, while the cytosolic PGI activity was not affected.

Supplemental Table S1. Starch metabolism genes defined by Smith et al., 2004 (Smith et al., 2004)

	Genome locus	Gene name
Group I.		
	At1g03310	*ISA2*
	At1g10760	*GWD1*
	At1g11720	*SS3*
	At1g32900	*GBS1*
	At1g69830	*AMY3*
	At1g76130	*AMY2*
	At2g36390	*SBE3*
	At2g39930	*ISA1*
	At2g40840	*DPE2*
	At3g01180	*SS2*
	At3g10940	*SEX4-Like2*[a]
	At3g29320	*PHS1*
	At3g46970	*PHS2*
	At3g52180	*SEX4*[a]
	At4g00490	*BAM2*
	At4g09020	*ISA3*
	At4g18240	*SS4*
	At5g03650	*SBE2*
	At5g17520	*MEX1*
	At5g24300	*SS1*
	At5g26570	*GWD3*
	At5g48300	*APS1*
	At5g51820	*PGM1*
	At5g64860	*DPE1*
Group II.		
	At1g05610	*APS2*
	At1g27680	*APL2*
	At1g68560	*AGL5*
	At2g21590	*APL4*
	At2g32290	*BAM6*
	At2g45880	*BAM7*
	At3g01510	*SEX4-Like1*[a]
	At3g20440	*SBE1*

At3g23640	*AGL1*
At3g23920	*BAM1*
At3g45940	*AGL3*
At4g15210	*BAM5*
At4g17090	*BAM3*
At4g24450	*GWD2*
At4g24620	*PGI1*
At4g25000	*AMY1*
At4g39210	*APL3*
At5g04360	*LDA1*
At5g11720	*AGL4*
At5g16150	*GLT1*
At5g18670	*BAM9*
At5g19220	*APL1*
At5g45300	*BAM8*
At5g46110	*TPT1*
At5g55700	*BAM4*
At5g63840	*AGL2*
At5g65685	*GLS1*

[a]*SEX4* was proved involved in starch degradation (Niittyla et al., 2006; Kotting et al., 2009)

Supplemental Table S2. Samples extracted from microarray data of AT-40[a]

Tissue No. [b]	Organism part name
1	Col-0_cotyl
2	Col-0_hyp
3	Col-0_root7
4	Col-0_veg_leaf
5	Col-0_leaf_1-2
6	Col-0_shoot_veg
7	Col-0_seedl_green
8	Col-0_shoot_trans
9	Col-0_root17
10	Col-0_roset4_11
11	Col-0_roset2
12	Col-0_roset4
13	Col-0_roset6
14	Col-0_roset8
15	Col-0_roset10
16	Col-0_roset12
17	Col-0_lf7_petio
18	Col-0_lf7_prox
19	Col-0_lf7_distal
20	Col-0_whole21d
21	Col-0_whole22d
22	Col-0_whole23d
23	Col-0_senescent
24	Col-0_cauline
25	Col-0_stem_2nd
26	Col-0_stem_1st
27	Col-0_inflo
28	Col-0_flow9
29	Col-0_flow10/11
30	Col-0_flow12
31	Col-0_flow12_sepal
32	Col-0_flow12_petal
33	Col-0_flow12_stam
34	Col-0_flow12_carp
35	Col-0_flow15

36	Col-0_flow15_pedi
37	Col-0_flow15_sepal
38	Col-0_flow15_petal
39	Col-0_flow15_stam
40	Col-0_flow15_carp
41	Col-0_pollen
42	Col-0_sil3
43	Col-0_sil4
44	Col-0_sil5
45	Col-0_seed6
46	Col-0_seed7
47	Col-0_seed8
48	Col-0_seed9
49	Col-0_seed10
50	Col-0_roset7
51	Col-0_roset14
52	Col-0_roset21
53	Col-0_leaf
54	Col-0_flower
55	Col-0_root_MS1
56	Col-0_root_GM-8
57	Col-0_root_GM5-8
58	Col-0_seedl_GM
59	Col-0_seedl_GM5
60	Col-0_root_GM-21
61	Col-0_root_GM5-21
62	Col-0_sedlGM-21
63	Col-0_sedlGM5-21

[a]Submission Number is ME00319 at PLEXdb; TAIR Accession is ExpressionSet: 1006710873

[b]Tissue descriptions can be found in the public data (Schmid et al., 2005).

Supplemental Table S3. Motif matching positions in upstream regions of Group I genes

Gene Name	Sequence ID[a]	Start[b]	End[b]	Matching sequence[c]	Strand
ISA2	AT1G03310	-339	-328	AACAAAAGTAGT	Forward
GWD1	AT1G10760	-276	-265	TATAAAAGACGA	Forward
GWD1	AT1G10760	-49	-38	AAGTAAAGTAGA	Reverse
SS3	AT1G11720	-680	-669	TCGAAAAGGCGA	Reverse
GBS1	AT1G32900	-523	-512	ACTTAAAGTAAT	Forward
AMY3	AT1G69830	-871	-860	TCTCAAAGTACA	Forward
AMY3	AT1G69830	-514	-503	AATAAAAGGAAA	Forward
AMY2	AT1G76130	-834	-823	CACAAAAGTCGA	Forward
AMY2	AT1G76130	-17	-6	CCTTAAAGAAAC	Reverse
SBE3	AT2G36390	-656	-645	AAGCAAAGGCAA	Reverse
ISA1	AT2G39930	-106	-95	CCCTAAAGCCCA	Forward
SS2	AT3G01180	-661	-650	AACAAAAGCCAT	Forward
SS2	AT3G01180	-69	-58	AACAAAAGAAGA	Reverse
PHS2	AT3G46970	-812	-801	TAGTAAAGAAGT	Forward
SEX4	AT3G52180	-827	-816	TACCAAAGGAGT	Forward
BAM2	AT4G00490	-628	-617	TCCCAAAGTAAA	Forward
BAM2	AT4G00490	-166	-155	CACAAAAGCCCC	Forward
BAM2	AT4G00490	-609	-598	ACCAAAAGAAAC	Reverse
ISA3	AT4G09020	-951	-940	AACAAAAGTAGT	Forward
ISA3	AT4G09020	-402	-391	ACCCAAAGGACC	Forward
ISA3	AT4G09020	-82	-71	TCCCAAAGTCCC	Forward
SS4	AT4G18240	-540	-529	TCCAAAAGGAGC	Reverse
SBE2	AT5G03650	-140	-129	CACAAAAGTAGC	Forward
MEX1	AT5G17520	-969	-958	TACTAAAGAAGC	Forward
MEX1	AT5G17520	-837	-826	AAGTAAAGTAGA	Forward
MEX1	AT5G17520	-933	-922	AAGCAAAGAACT	Reverse
SS1	AT5G24300	-454	-443	ACCAAAAGCCCA	Forward
SS1	AT5G24300	-250	-239	AACCAAAGGCAA	Forward
SS1	AT5G24300	-945	-934	TCCAAAAGTAAT	Reverse
APS1	AT5G48300	-513	-502	AACTAAAGAAGC	Forward
PGM1	AT5G51820	-808	-797	TCTAAAAGTCAT	Forward
PGM1	AT5G51820	-707	-696	TATTAAAGACAT	Reverse
DPE1	AT5G64860	-914	-903	AATTAAAGAAGC	Reverse

[a]Promoter regions were included the 1000 bp from upstream of transcription start site

(+1)

[b]Number assignment is corresponding to the transcription start site (+1)

[c]Sequences matching to the pattern of [ATC] [AC] [CGT] [ATC] AAAGN [AC] [GCA] [ATC]

Supplemental Table S4. Heat inactivation of PGI activity in extracts of leaf and epidermis from the wild type and *pgi1* mutant

	Total activity	Activity after heat treatment	Heat Inactivation (%)
	Units /μg protein	Units /μg protein	
WT leaves	16.3 ± 1.8	10.2 ± 1.2	37.4
pgi1 leaves	9.5 ± 0.5	9.3 ± 0.1	2.2
WT epidermis	13.4 ± 1.1	8.2 ± 0.3	38.8
pgi1 epidermis	7.4 ± 0.1	7.2 ± 0.3	2.7

Values are the mean ± S.E. from three replicate extracts, each extract made from three plants. The amount of proteins in the extract was quantified with Lowry reagent. For heat inactivation, the extracts were treated at 50°C for 10 min in a thermocycler.

SUPPLEMENTAL LITERATURE CITED

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