

Supplementary

Table S1. Information on the *A. thaliana* accessions, flowering time and total number of leaves after flowering.

TAIR accessions	Abbreviated name	Flowering time (d)	Leaf number
CS28652	Pro-0	19.0±0.0	9.7±0.9
CS76537	Kz-9	21.0±1.0	10.6±0.8
CS28573	Nw-0	21.0±1.0	10.4±0.5
CS6845	Rd-0	21.0±1.0	10.7±0.8
CS6885	Wa-1	24.0±0.0	12.1±0.3
CS6905	Hs-0	24.0±1.0	12.4±0.6
CS6105	Kelsterbach-4	24.0±0.0	11.9±0.7
CS6673	Col-0	27.0±2.0	13.7±1.0
CS6675	Cvi-0	27.0±0.0	13.7±0.9
CS28128	Ca-0	28.0±2.0	14.3±0.7
CS28096	Bs-1	29.0±0.0	14.8±0.7
CS6797	Ms-0	29.4±1.8	14.3±1.1
CS6630	Bsch-0	30.0±0.9	14.7±1.1
CS6923	Ema-1	30.0±1.5	15.3±0.9
CS6732	Gy-0	31.0±0.8	15.7±0.6
CS6865	Stw-0	33.8±2.0	16.7±1.0
CS6600	Aa-0	35.0±1.0	17.7±0.8
CS6723	Gr-1	38.0±0.0	18.5±0.7
CS6862	Sp-0	39.0±0.8	19.7±0.7
CS6875	Tu-0	42.0±2.3	20.9±1.1
CS6626	Br-0	45.0±1.0	22.6±1.0
CS28344	Hey-1	45.0±0.8	22.5±1.0
CS28597	Per-1	45.0±2.0	22.5±1.3
CS28786	Ty-0	45.4±1.8	22.6±1.1
CS6867	Ta-0	46.5±1.1	23.9±1.0
CS22518	Tscha-1	54.0±2.3	26.7±0.9
CS6852	Se-0	55.4±1.2	27.3±0.9

TAIR, The Arabidopsis Information Resource. Data are shown as mean±standard errors.

Table S2. Number of methylated sites of autonomous pathway gene coding regions of different *A. thaliana* accessions.

Populatio n	Number of methylated sites													
	<i>FVE</i>	<i>FY</i>	<i>FLD</i>	<i>PEP</i>	<i>HDA5</i>	<i>PRP39-1</i>	<i>FCA</i>	<i>FLK</i>	<i>FPA</i>	<i>LD</i>	<i>PCFS4</i>	<i>DRM2</i>	<i>HDA6</i>	<i>PRMT5</i>
	AT2G19520	AT5G13480	AT3G10390	AT4G26000	AT5G61060	AT1G04080	AT4G16280	AT3G04610	AT2G43410	AT4G02560	AT4G04885	AT5G14620	AT5G63110	AT4G31120
Aa-0	29	49	56	31	48	88	79	35	43	45	70	50	8	59
Br-0	41	59	69	33	62	92	107	54	81	82	81	67	18	50
Bs-1	23	43	46	15	54	76	54	41	43	61	52	37	14	17
Bsch-0	37	52	60	25	30	77	84	45	66	80	71	50	6	70
Ca-0	33	58	42	19	49	86	83	43	71	57	64	38	10	53
Col-0	20	49	69	25	48	67	78	45	51	66	67	33	1	51
Cvi-0	19	31	33	9	18	40	47	19	36	51	33	56	0	13
Ema-1	36	66	59	34	41	76	78	57	62	74	85	29	10	69
Gr-1	13	44	46	16	51	70	73	18	41	81	46	32	15	39
Gy-0	25	52	54	35	42	85	78	35	56	55	67	30	7	54
Hey-1	22	62	64	36	44	74	83	44	66	52	64	58	0	56
Hs-0	28	44	56	32	40	83	88	37	66	81	79	61	14	54
Kelsterbach-4	23	42	51	21	32	79	64	48	74	61	63	62	7	36
Kz-9	22	40	50	16	25	62	91	39	47	63	55	86	7	62
Ms-0	46	27	69	34	53	61	93	56	74	66	78	48	23	46
Nw-0	37	59	67	21	61	100	85	54	78	81	93	77	12	45
Per-1	25	47	49	38	44	69	73	37	41	108	69	30	5	58
Pro-0	20	49	37	20	34	47	80	37	62	71	60	31	10	21
Rd-0	19	32	18	19	31	59	45	25	28	42	40	12	7	25
Se-0	31	53	58	45	44	82	84	53	60	73	84	64	20	49
Sp-0	32	47	57	36	38	84	2	40	79	5	2	25	8	65
Stw-0	25	50	39	26	38	79	88	37	38	67	48	37	10	57
Ta-0	42	67	73	44	54	79	106	56	78	92	85	72	14	58
Tscha-1	59	60	78	46	70	93	118	44	84	81	84	77	21	63
Tu-0	34	30	62	34	47	87	93	47	67	95	72	80	8	59
Ty-0	33	71	73	46	55	101	102	64	92	71	92	62	17	52
Wa-1	22	52	60	26	40	80	85	46	53	67	63	63	15	65

1 Table S2 (continued). Number of methylated sites of autonomous pathway gene coding regions of different *A. thaliana* accessions.

Population	Number of methylated sites												
	<i>PRMT10</i>	<i>REF6</i>	<i>AGL28</i>	<i>CK2</i>	<i>PP2A-B'γ</i>	<i>SYP22</i>	<i>ESD4</i>	<i>DBP1</i>	<i>DRM1</i>	<i>FLC</i>	<i>SOC1</i>	<i>LFY</i>	<i>API</i>
	AT1G04870	AT3G48430	AT1G01530	AT2G23080	AT4G15415	AT5G46860	AT4G15880	AT2G25620	AT5G15380	AT5G10140	AT2G45660	AT5G61850	AT1G69120
Aa-0	6	113	48	24	52	18	18	12	4	1	0	0	0
Br-0	14	116	40	30	67	18	15	22	0	2	0	0	0
Bs-1	23	109	41	39	44	0	18	13	0	5	0	2	0
Bsch-0	20	80	60	36	47	13	14	12	0	0	0	0	0
Ca-0	20	92	43	29	42	13	3	15	8	0	0	0	0
Col-0	8	74	39	23	37	1	8	18	0	0	0	0	0
Cvi-0	0	51	46	20	14	0	0	15	0	0	0	0	0
Ema-1	23	114	47	26	40	19	14	17	1	0	1	0	0
Gr-1	4	64	45	13	34	16	14	5	2	1	0	0	1
Gy-0	15	73	42	19	49	13	20	14	4	0	0	0	0
Hey-1	15	95	39	32	47	0	29	16	2	0	0	0	0
Hs-0	2	94	53	31	49	9	3	21	1	0	0	0	2
Kelsterbach-4	17	83	45	28	62	1	9	11	0	0	0	0	0
Kz-9	14	91	35	16	39	5	10	11	0	0	1	0	0
Ms-0	6	126	36	30	53	15	10	16	13	0	0	0	0
Nw-0	21	122	39	28	81	2	18	28	4	0	0	3	0
Per-1	6	109	28	10	41	9	4	13	4	0	0	0	0
Pro-0	0	68	36	21	34	13	20	8	2	2	0	0	0
Rd-0	8	45	18	14	32	2	5	15	0	0	0	0	0
Se-0	17	107	12	27	70	11	7	11	0	1	0	0	0
Sp-0	9	96	37	19	14	5	0	18	4	13	0	0	0
Stw-0	15	79	49	24	48	12	12	5	0	7	1	0	0
Ta-0	12	105	27	30	79	17	20	22	6	9	0	0	0
Tscha-1	6	84	37	24	66	2	14	14	0	0	0	0	0
Tu-0	6	97	43	27	75	2	17	15	10	1	0	0	0
Ty-0	20	120	32	24	56	27	24	21	1	0	0	0	0
Wa-1	11	90	52	27	55	10	17	12	0	0	0	0	0

Table S3. Number of methylated CG sites in the coding regions of autonomous pathway genes of different *A. thaliana* accessions.

Population	Number of CG methylated sites													
	<i>FVE</i>	<i>FY</i>	<i>FLD</i>	<i>PEP</i>	<i>HDA5</i>	<i>PRP39-1</i>	<i>FCA</i>	<i>FLK</i>	<i>FPA</i>	<i>LD</i>	<i>PCFS4</i>	<i>DRM2</i>	<i>HDA6</i>	<i>PRMT5</i>
	AT2G19520	AT5G13480	AT3G10390	AT4G26000	AT5G61060	AT1G04080	AT4G16280	AT3G04610	AT2G43410	AT4G02560	AT4G04885	AT5G14620	AT5G63110	AT4G31120
Aa-0	29	49	56	31	48	88	79	35	43	45	70	22	8	59
Br-0	41	59	69	33	62	92	105	54	81	80	81	45	18	50
Bs-1	23	43	46	15	54	76	53	41	43	61	51	25	14	17
Bsch-0	37	51	58	25	30	77	82	44	66	80	71	30	5	70
Ca-0	33	58	42	19	49	86	83	43	71	57	63	25	10	53
Col-0	26	48	69	25	48	67	78	45	51	66	66	27	1	51
Cvi-0	19	31	33	9	18	40	44	19	36	51	33	22	0	13
Ema-1	36	66	59	34	41	76	78	57	61	74	85	29	10	69
Gr-1	13	44	46	16	50	70	73	18	41	79	46	16	15	39
Gy-0	25	52	54	35	42	85	78	35	56	55	67	21	7	54
Hey-1	22	62	64	36	44	74	83	44	66	52	64	40	0	56
Hs-0	28	44	55	32	40	83	88	37	66	81	79	39	14	53
Kelsterbach-4	23	42	51	21	32	75	63	48	74	61	63	30	7	36
Kz-9	22	39	49	16	25	62	90	38	47	63	54	31	7	62
Ms-0	46	27	69	34	53	61	92	56	74	66	77	31	23	46
Nw-0	37	57	65	21	61	99	83	54	77	78	93	33	12	45
Per-1	25	47	49	38	44	69	72	37	41	70	69	26	5	58
Pro-0	20	49	37	20	34	47	77	37	62	71	59	21	10	21
Rd-0	19	32	18	19	31	59	45	25	28	42	40	7	7	25
Se-0	31	53	58	45	44	82	82	53	60	73	84	27	20	49
Sp-0	32	47	57	36	38	83	1	40	79	5	2	24	8	64
Stw-0	25	50	39	26	38	79	85	37	38	66	48	20	10	57
Ta-0	42	67	73	44	54	79	106	56	78	92	85	42	14	58
Tscha-1	55	60	76	46	68	93	114	44	82	81	83	36	21	62
Tu-0	34	29	62	34	46	86	93	46	67	93	72	37	8	59
Ty-0	33	70	73	46	55	100	96	64	91	70	91	29	17	52
Wa-1	22	52	60	26	39	80	85	46	53	67	63	29	15	65

Table S3 (continued). Number of methylated CG sites in the coding regions of autonomous pathway genes of different *A. thaliana* accessions.

Population	Number of CG methylated sites												
	<i>PRMT10</i>	<i>REF6</i>	<i>AGL28</i>	<i>CK2</i>	<i>PP2A-B'γ</i>	<i>SYP22</i>	<i>ESD4</i>	<i>DBP1</i>	<i>DRM1</i>	<i>FLC</i>	<i>SOC1</i>	<i>LFY</i>	<i>API</i>
	AT1G04870	AT3G48430	AT1G01530	AT2G23080	AT4G15415	AT5G46860	AT4G15880	AT2G25620	AT5G15380	AT5G10140	AT2G45660	AT5G61850	AT1G69120
Aa-0	6	113	26	24	52	18	18	12	4	1	0	0	0
Br-0	14	116	26	30	67	18	15	22	0	2	0	0	0
Bs-1	23	109	25	39	44	0	16	13	0	5	0	2	0
Bsch-0	20	80	26	36	47	13	14	12	0	0	0	0	0
Ca-0	20	92	24	29	42	13	3	15	8	0	0	0	0
Col-0	8	74	25	23	37	1	8	18	0	0	0	0	0
Cvi-0	0	51	22	20	14	0	0	15	0	0	0	0	0
Ema-1	23	114	26	26	40	19	14	17	0	0	0	0	0
Gr-1	4	64	25	13	34	16	14	5	2	0	0	0	0
Gy-0	15	73	24	19	49	13	20	14	4	0	0	0	0
Hey-1	15	95	23	32	47	0	29	16	2	0	0	0	0
Hs-0	2	94	27	31	49	9	3	20	1	0	0	0	2
Kelsterbach-4	17	83	26	28	62	1	9	11	0	0	0	0	0
Kz-9	14	91	26	16	39	5	10	10	0	0	1	0	0
Ms-0	6	125	26	30	53	15	10	15	13	0	0	0	0
Nw-0	21	122	26	28	81	2	18	26	4	0	0	3	0
Per-1	6	109	23	10	41	9	4	13	4	0	0	0	0
Pro-0	0	68	23	21	33	13	20	8	2	2	0	0	0
Rd-0	8	45	13	14	32	2	5	15	0	0	0	0	0
Se-0	17	107	0	27	70	11	7	11	0	1	0	0	0
Sp-0	9	96	26	19	14	5	0	18	4	4	0	0	0
Stw-0	15	77	26	24	48	12	12	5	0	3	1	0	0
Ta-0	12	105	23	30	79	17	20	22	6	8	0	0	0
Tscha-1	6	84	25	24	66	2	14	14	0	0	0	0	0
Tu-0	6	93	26	26	75	2	17	15	10	0	0	0	0
Ty-0	20	119	26	24	56	27	23	20	0	0	0	0	0
Wa-1	11	90	26	27	55	10	15	12	0	0	0	0	0

Table S4 (continued). Number of methylated CHG sites in the coding regions of autonomous pathway genes of different *A. thaliana* accessions.

Population	Number of CHG methylated sites												
	<i>PRMT10</i>	<i>REF6</i>	<i>AGL28</i>	<i>CK2</i>	<i>PP2A-B'γ</i>	<i>SYP22</i>	<i>ESD4</i>	<i>DBP1</i>	<i>DRM1</i>	<i>FLC</i>	<i>SOC1</i>	<i>LFY</i>	<i>API</i>
	AT1G04870	AT3G48430	AT1G01530	AT2G23080	AT4G15415	AT5G46860	AT4G15880	AT2G25620	AT5G15380	AT5G10140	AT2G45660	AT5G61850	AT1G69120
Aa-0	0	0	11	0	0	0	0	0	0	0	0	0	0
Br-0	0	0	10	0	0	0	0	0	0	0	0	0	0
Bs-1	0	0	9	0	0	0	2	0	0	0	0	0	0
Bsch-0	0	0	12	0	0	0	0	0	0	0	0	0	0
Ca-0	0	0	8	0	0	0	0	0	0	0	0	0	0
Col-0	0	0	8	0	0	0	0	0	0	0	0	0	0
Cvi-0	0	0	13	0	0	0	0	0	0	0	0	0	0
Ema-1	0	0	9	0	0	0	0	0	0	0	0	0	0
Gr-1	0	0	8	0	0	0	0	0	0	0	0	0	0
Gy-0	0	0	7	0	0	0	0	0	0	0	0	0	0
Hey-1	0	0	7	0	0	0	0	0	0	0	0	0	0
Hs-0	0	0	10	0	0	0	0	1	0	0	0	0	0
Kelsterbach-4	0	0	10	0	0	0	0	0	0	0	0	0	0
Kz-9	0	0	9	0	0	0	0	1	0	0	0	0	0
Ms-0	0	1	9	0	0	0	0	0	0	0	0	0	0
Nw-0	0	0	10	0	0	0	0	2	0	0	0	0	0
Per-1	0	0	5	0	0	0	0	0	0	0	0	0	0
Pro-0	0	0	8	0	0	0	0	0	0	0	0	0	0
Rd-0	0	0	5	0	0	0	0	0	0	0	0	0	0
Se-0	0	0	11	0	0	0	0	0	0	0	0	0	0
Sp-0	0	0	10	0	0	0	0	0	0	5	0	0	0
Stw-0	0	2	9	0	0	0	0	0	0	1	0	0	0
Ta-0	0	0	4	0	0	0	0	0	0	0	0	0	0
Tscha-1	0	0	7	0	0	0	0	0	0	0	0	0	0
Tu-0	0	4	9	1	0	0	0	0	0	0	0	0	0
Ty-0	0	1	6	0	0	0	1	1	1	0	0	0	0
Wa-1	0	0	9	0	0	0	2	0	0	0	0	0	0

Table S5. Number of methylated CHH sites in the coding regions of autonomous pathway genes of different *A. thaliana* accessions.

[illegible]

Table S5 (continued). Number of methylated CHH sites in the coding regions of autonomous pathway genes of different *A. thaliana* accessions.

[illegible]

Table S6. Correlation analysis between flowering time, leaf number and DNA methylation level of gene coding region of different *A. thaliana* accessions.

	F T	L N	FV E	FY	FLD	PEP	HD A5	PRP3 9-1	FC A	FLK	FPA	LD	PCF S4	DR M2	HD A6	PRM T5	PRM T10	RE F6	AGL 28	CK2	PP2A- B γ	SYP 22	ESD 4	DBP 1	DR M1	FL C	SO C1	LF Y	A PI
FT			.01 6*	.03 9*	.007 **	.000 **	.006 **	.027*	.116	.138	.080	.192	.193	.215	.089	.070	.868	.082	.053	.895	.061	.251	.326	.784	.712	.2 78	.35 3	.19 9	.5 17
LN			.01 6*	.03 2*	.007 **	.000 **	.006 **	.027*	.123	.134	.078	.205	.197	.223	.103	.070	.867	.079	.050	.876	.065	.246	.326	.705	.714	.2 38	.35 0	.19 4	.5 21
FVE				.08 3	.000 **	.001 **	.001 **	.007* *	.008 **	.001 **	.000 **	.191	.005 **	.028 *	.002 **	.019 *	.397	.004 **	.778	.045 *	.003* *	.260	.609	.020 *	.079	.6 60	.74 7	.79 0	.3 81
FY					.007 **	.008 **	.015 *	.002* *	.034 *	.004 **	.006 **	.370	.010 **	.465	.378	.022 *	.005* *	.049 *	.903	.227	.076	.016 *	.010 **	.083	.235	.6 25	.68 9	.69 9	.5 18
FLD						.000 **	.000 **	.001* *	.002 **	.000 **	.000 **	.099	.001 **	.002 **	.038 *	.001 **	.307	.000 **	.790	.033 *	.001* *	.246	.031 *	.006 **	.306	.9 68	.43 3	.74 4	.7 92
PEP							.008 **	.004* *	.037 *	.001 **	.002 **	.240	.010 **	.258	.034 *	.001 **	.718	.006 **	.078	.625	.011* *	.049 *	.182	.121	.308	.4 32	.52 9	.15 2	.7 64
HDA5								.000* *	.007 **	.011 *	.006 **	.071	.003 **	.228	.001 **	.309	.370	.002 **	.438	.157	.001* *	.246	.042 *	.036 *	.167	.8 31	.13 8	.08 5	.9 52
PRP3 9-1									.073	.003 **	.001 **	.473	.013 **	.064	.040 *	.004 **	.008* *	.002 **	.650	.082	.000* *	.173	.101	.029 *	.708	.6 46	.57 1	.18 2	.8 68
FCA										.011 *	.054	.000 **	.000 **	.001 **	.017 *	.078	.614	.077	.853	.149	.000* *	.047 *	.009 **	.532	.599	.0 39	.61 6	.68 0	.8 26
FLK											.000 **	.157	.000 **	.027 *	.022 *	.026 *	.002* *	.000 **	.460	.004 **	.000* *	.083	.059	.005 *	.280	.8 95	.80 7	.44 9	.1 31
FPA												.529	.013 *	.015 *	.021 *	.067	.170	.004 **	.965	.022 *	.007* *	.191	.176	.002 **	.165	.5 74	.21 2	.78 0	.8 13
LD													.000 **	.046 *	.154	.439	.956	.196	.983	.634	.002* *	.294	.254	.729	.656	.0 75	.97 9	.70 8	.3 60
PCFS 4														.008 **	.022 *	.138	.129	.002 **	.735	.043 *	.000* *	.047 *	.017 *	.039 *	.506	.01 1	.80 4	.43 2	.8 63
DRM 2															.162	.208	.682	.058	.827	.074	.000* *	.648	.175	.117	.864	.3 85	.99 7	.45 9	.9 62
HDA6																.675	.671	.013 *	.289	.204	.009* *	.020 *	.549	.627	.393	.7 67	.63 2	.61 8	.4 09

<i>PRM</i> <i>T5</i>	.235	.039 *	.269	.723	.149	.112	.547	.519	.467	.6 88	.13 1	.13 8	.9 41
<i>PRM</i> <i>T10</i>		.028 *	.906	.012 *	.110	.454	.129	.308	.439	.9 24	.14 8	.03 6*	.0 69
<i>REF6</i>			.671	.025 *	.004* *	.052	.151	.012	.055	.6 65	.85 5	.10 1	.5 90
<i>AGL2</i> <i>8</i>				.083	.501	.834	.663	.526	.739	.6 00	.47 6	.97 7	.1 49
<i>CK2</i>					.017*	.986	.091	.129	.714	.8 01	.45 4	.11 4	.9 77
<i>PP2A-</i> <i>B'γ</i>						.469	.013 *	.077	.278	.5 28	.47 5	.15 5	.6 84
<i>SYP2</i> <i>2</i>							.177	.961	.429	.8 89	.52 2	.11 2	.7 19
<i>ESD4</i>								.740	.924	.6 68	.86 5	.31 1	.2 64
<i>DBP1</i>									.331	.8 84	.18 1	.04 3*	.8 24
<i>DRM</i> <i>1</i>										.6 86	.26 4	.98 5	.6 60
<i>FLC</i>											.66 7	.84 7	.6 09
<i>SOC1</i>												.62 7	.6 39
<i>LFY</i>													.7 14
<i>API</i>													

FT: Flowering time; LN: Leaf number; * Correlation is significant at the 0.05 level (2-tailed); ** Correlation is also significant at the 0.01 level (2-tailed).

Table S7. Correlation analysis between flowering time, leaf number and CG methylation level of gene coding region of different *A. thaliana* accessions.

	F T	L N	FV E	FY	FLD	PEP	HDA 5	PRP3 9-1	FCA	FLK	FPA	LD	PCF S4	DRM 2	HDA 6	PRM T5	PRM T10	REF 6	AGL 28	CK2	PP2A- B γ	SYP 22	ESD 4	DBP 1	DR M1	FL C	SO C1	LF Y	AP 1
FT			.02 1*	.03 3*	.006 **	.000 **	.007 **	.023 *	.133	.134	.083	.328	.186	.059	.089	.072	.868	.088	.13 1	.912	.060	.25 1	.295	.662	.74 7	.2 71	.38 9	.1 99	.3 57
LN			.02 1*	.02 7*	.006 **	.000 **	.007 **	.022 *	.140	.130	.082	.348	.190	.052	.102	.072	.867	.084	.13 8	.893	.063	.24 6	.296	.580	.75 0	.2 15	.36 8	.1 94	.3 87
FVE				.08 4	.000 **	.001 **	.001 **	.006 **	.010 **	.000 **	.000 **	.095	.003 **	.001 **	.004 **	.016 *	.367	.003 **	.52 4	.036 *	.003 **	.25 5	.596	.009 **	.07 9	.4 84	.35 7	.7 85	.8 71
FY					.009 **	.007 **	.014 *	.002 **	.044 *	.004 **	.008 **	.312	.012 *	.061	.365	.024 *	.006 **	.046 *	.79 2	.213	.090	.01 4*	.010 **	.084	.16 9	.2 66	.55 6	.7 86	.6 52
FLD						.000 **	.000 **	.001 **	.003 **	.000 **	.000 **	.050 *	.001 **	.000 **	.041 *	.002 **	.315	.000 **	.19 3	.037 *	.001 **	.21 9	.027 *	.007 **	.32 8	.7 03	.23 9	.8 11	.9 96
PEP							.008 **	.003 **	.041 *	.001 **	.002 **	.337	.009 **	.015 *	.034 *	.002 **	.718	.006 **	.39 4	.634	.011*	.04 9*	.159	.099	.37 6	.4 59	.26 5	.1 52	.7 71
HDA5								.000 **	.008 **	.007 **	.006 **	.060	.003 **	.028 *	.001 **	.327	.330	.001 **	.50 4	.145	.001 **	.22 5	.043 *	.029 *	.17 8	.3 57	.11 3	.0 76	.7 31
PRP3 9-1									.063	.003 **	.002 **	.332	.011 *	.029 *	.036 *	.003 **	.008 **	.002 **	.43 1	.086	.000 **	.14 8	.099	.030 *	.77 4	.7 96	.53 9	.1 86	.6 55
FCA										.013 *	.071	.000 **	.000 **	.001 **	.023 *	.061	.625	.084	.55 0	.148	.000 **	.05 2	.007 **	.585	.56 2	.5 62	.54 7	.6 59	.6 61
FLK											.000 **	.080	.000 **	.000 **	.021 *	.028 *	.003 **	.000 **	.80 1	.004 **	.000 **	.07 9	.063	.005 **	.38 4	.4 59	.50 1	.4 40	.6 10
FPA												.263	.015 *	.000 **	.024 *	.072	.174	.004 **	.25 6	.021 *	.007 **	.18 8	.162	.002 **	.19 2	.6 12	.11 5	.8 04	.7 41
LD													.000 **	.008 **	.055	.499	.802	.314	.76 3	.159	.000 **	.24 1	.077	.689	.81 3	.8 51	.91 1	.6 75	.3 95
PCFS 4														.002 **	.025 *	.124	.129	.002 **	.92 3	.045 *	.000 **	.04 7*	.014 *	.049 *	.60 5	.3 93	.30 5	.4 35	.4 89
DRM2															.228	.029 *	.450	.002 **	.15 8	.002 **	.001 **	.88 4	.111	.003 **	.46 0	.4 63	.63 1	.8 01	.1 96
HDA6																.722	.700	.012 *	.51 9	.220	.009 **	.02 1*	.612	.697	.42 0	.3 98	.62 5	.6 14	.5 81

<i>PRMT</i> <i>5</i>	.219	.040 *	.22 6	.734	.138	.10 6	.478	.517	.51 4	.6 69	.36 2	.1 39	.8 34
<i>PRMT</i> <i>10</i>		.026 *	.90 5	.011 *	.106	.45 4	.152	.319	.35 8	.6 07	.57 8	.0 36	.1 58
<i>REF6</i>			.45 8	.026 *	.005 **	.05 1	.173	.015 *	.09 7	.3 75	.58 0	.0 95	.9 32
<i>AGL2</i> <i>8</i>				.498	.741	.66 8	.292	.480	.41 4	.9 81	.54 5	.6 25	.5 47
<i>CK2</i>					.020 *	.99 1	.115	.121	.76 6	.1 86	.30 9	.11 1	.3 66
<i>PP2A-</i> <i>B'γ</i>						.47 4	.012 *	.086	.28 1	.5 79	.63 9	.1 55	.9 95
<i>SYP22</i>							.169	.975	.56 6	.6 01	.86 6	.1 12	.9 60
<i>ESD4</i>								.737	.92 8	.5 38	.76 5	.3 62	.1 85
<i>DBP1</i>									.41 0	.5 30	.03 1*	.0 69	.2 71
<i>DRM1</i>										.7 69	.32 3	.9 90	.6 94
<i>FLC</i>											.69 4	.4 55	.6 24
<i>SOC1</i>												.6 98	.7 83
<i>LFY</i>													.7 88
<i>API</i>													

FT: Flowering time; LN: Leaf number; * Correlation is significant at the 0.05 level (2-tailed); ** Correlation is also significant at the 0.01 level (2-tailed).

Table S8. Correlation analysis between flowering time, leaf number and CHG methylation level of gene coding region of different *A. thaliana* accessions.

	F T	L N	FV E	FY	FLD	PE P	HD A5	PRP3 9-1	FC A	FLK	FPA	LD	PCF S4	DR M2	HDA 6	PRM T5	PRMT 10	REF 6	AGL 28	CK2	PP2A- B'γ	SYP 22	ES D4	DBP1	DRM 1	FL C	SO CI	LF Y	AP I
FT			.76 6	.32 2	.694	N A	.09 2	.564	.23 7	.647	.169	.25 4	.514	.54 0	.728	.072	NA	.38 9	.236	.430	NA	NA	.57 8	.168	.263	.61 8	NA	N A	N A
LN			.76 5	.29 1	.640	N A	.11 0	.533	.26 6	.608	.180	.25 5	.505	.57 9	.675	.072	NA	.42 2	.207	.440	NA	NA	.59 5	.161	.268	.59 9	NA	N A	N A
FVE				.29 1	.453	N A	.17 1	.627	.87 1	.639	.171	.73 7	.033 *	.67 5	.795	.182	NA	.64 5	.538	.795	NA	NA	.65 3	.604	.795	.75 8	NA	N A	N A
FY					.004 **	N A	.82 4	.393	.34 6	.007 **	.194	.85 4	.469	.02 0*	.155	.479	NA	.21 5	.537	.155	NA	NA	.84 7	.000 **	.155	.56 2	NA	N A	N A
FLD							.12 9	.898	.27 6	.051	.004 **	.73 9	.700	.02 6*	.007 *8	.124	NA	.43 5	.278	.661	NA	NA	.44 6	.004 **	.661	.60 2	NA	N A	N A
PEP							NA	NA	N A	NA	NA	N A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	N A	NA	N A	N A
HDA5								.818	.56 1	.583	.007 **	.78 4	.660	.08 1	.704	.010 **	NA	.24 7	.556	.086	NA	NA	.44 5	.448	.704	.65 3	NA	N A	N A
PRP39 -1									.56 5	.936	.804	.78 7	.494	.28 3	.722	.724	NA	.48 2	.513	.394	NA	NA	.84 2	.465	.394	.44 2	NA	N A	N A
FCA										.575	.004 **	.52 4	.060	.08 4	.924	.202	NA	.58 5	.661	.457	NA	NA	.61 5	.169	.000 **	.88 8	NA	N A	N A
FLK											.492	.77 8	.887	.02 9*	.003 **	.620	NA	.02 5*	.241	.003 **	NA	NA	.55 2	.583	.731	.68 4	NA	N A	N A
FPA												.78 4	.191	.19 0	.704	.010 **	NA	.82 7	.437	.704	NA	NA	.95 8	.081	.086	.65 3	NA	N A	N A
LD													.445	.28 3	.805	.722	NA	.91 6	.088	.980	NA	NA	.70 4	.911	.912	.79 0	NA	N A	N A
PCFS4														.79 7	.527	.531	NA	.86 2	.325	.527	NA	NA	.25 9	.660	.125	.45 3	NA	N A	N A
DRM2															.881	.905	NA	.23 5	.209	.152	NA	NA	.74 6	.013 *	.464	.12 8	NA	N A	N A
HDA6																.783	NA	.73 6	.105	.849	NA	NA	.74 2	.704	.849	.82 1	NA	N A	N A

<i>PRMT5</i>	NA	.626	.930	.783	NA	NA	.635	.583	.783	.000	NA	NA	NA
<i>PRMT10</i>			NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>REF6</i>			.997	.000**	NA	NA	.850	.827	.420	.960	NA	NA	NA
<i>AGL28</i>				.862	NA	NA	.853	.730	.211	.502	NA	NA	NA
<i>CK2</i>					NA	NA	.742	.704	.849	.821	NA	NA	NA
<i>PP2A-B'γ</i>						NA	NA	NA	NA	NA	NA	NA	NA
<i>SYP22</i>							NA	NA	NA	NA	NA	NA	NA
<i>ESD4</i>								.958	.139	.696	NA	NA	NA
<i>DBP1</i>									.086	.653	NA	NA	NA
<i>DRM1</i>										.821	NA	NA	NA
<i>FLC</i>											NA	NA	NA
<i>SOC1</i>												NA	NA
<i>LFY</i>													NA
<i>API</i>													NA

FT: Flowering time; LN: Leaf number; * Correlation is significant at the 0.05 level (2-tailed); ** Correlation is also significant at the 0.01 level (2-tailed); NA, not applicable.

Table S9. Correlation analysis between flowering time, leaf number and CHH methylation level of gene coding region of different *A. thaliana* accessions.

[illegible]

<i>PRMT5</i>	NA	NA	.147	NA	.849	NA	NA	.849	.849	.704	.849	NA	.849
<i>PRMT10</i>		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>REF6</i>			NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>AGL28</i>				NA	.713	NA	NA	.304	.438	.831	.438	NA	.438
<i>CK2</i>					NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>PP2A-B7</i>						NA	NA	.849	.849	.704	.849	NA	.849
<i>SYP22</i>							NA	NA	NA	NA	NA	NA	NA
<i>ESD4</i>								NA	NA	NA	NA	NA	NA
<i>DBP1</i>									.849	.704	.849	NA	.849
<i>DRM1</i>										.704	NA	NA	.849
<i>FLC</i>											.704	NA	.518
<i>SOC1</i>												NA	.849
<i>LFY</i>													NA
<i>API</i>													

FT: Flowering time; LN: Leaf number; NA, not applicable.

Table S10. Number of methylated sites of autonomous pathway gene promoter regions of different *A. thaliana* accessions.

Population	Flowering time*	Leaf number*	Number of methylated sites													
			<i>FVE</i>	<i>FY</i>	<i>FLD</i>	<i>PEP</i>	<i>HDA5</i>	<i>PRP39-1</i>	<i>FCA</i>	<i>FLK</i>	<i>FPA</i>	<i>LD</i>	<i>PCFS4</i>	<i>DRM2</i>	<i>HDA6</i>	<i>PRMT5</i>
			AT2G19520	AT5G13480	AT3G10390	AT4G26000	AT5G61060	AT1G04080	AT4G16280	AT3G04610	AT2G43410	AT4G02560	AT4G04885	AT5G14620	AT5G63110	AT4G31120
Aa-0	35±1.0	17.7±0.8	16	0	3	0	32	0	18	0	2	0	89	0	7	8
Br-0	45±0.0	22.6±1.0	19	0	1	0	26	0	62	0	3	3	46	0	6	6
Bs-1	29±0.0	14.8±0.7	18	6	3	0	23	0	16	0	2	0	64	1	2	3
Bsch-0	30±0.9	14.7±1.1	33	0	1	0	31	0	72	1	12	2	167	0	12	9
Ca-0	28±0.0	14.3±0.7	34	0	1	0	34	0	27	0	9	3	133	0	1	4
Col-0	27±2.0	13.7±1.0	100	0	2	0	33	0	43	0	8	5	98	0	3	11
Cvi-0	27±0.0	13.7±0.9	8	0	2	0	17	0	66	0	1	0	141	0	10	0
Ema-1	30±1.5	15.3±0.9	29	0	2	0	35	0	69	0	12	8	127	0	5	6
Gr-1	38±0.0	18.5±0.7	19	0	1	0	26	0	62	0	3	3	66	0	6	6
Gy-0	31±0.8	15.7±0.6	9	0	2	0	41	0	0	0	8	3	88	0	3	3
Hey-1	45±0.8	22.5±1.0	42	0	3	0	28	0	26	0	5	4	104	0	1	11
Hs-0	24±0.0	12.4±0.6	19	0	6	0	17	0	73	0	12	5	119	1	2	8
Kelsterbach-4	24±0.0	11.9±0.7	17	15	1	0	31	0	0	0	12	1	112	0	15	8
Kz-9	21±0.6	10.6±0.8	13	0	2	0	2	0	0	0	0	1	84	0	3	4
Ms-0	29.4±1.8	14.3±1.1	46	0	8	0	32	0	63	0	1	6	75	0	11	4
Nw-0	21±0.4	10.4±0.5	19	0	3	0	38	0	33	0	12	6	72	0	10	10
Per-1	45±2.2	22.5±1.3	16	0	3	0	20	0	24	0	7	2	66	0	3	1
Pro-0	19±0.7	9.7±0.9	19	0	3	0	42	0	23	0	29	4	127	0	5	0
Rd-0	21±0.0	10.7±0.8	0	0	2	0	25	0	29	0	1	1	22	0	1	2
Se-0	55.4±1.2	27.3±0.9	20	0	1	0	44	0	0	0	15	2	78	0	13	12
Sp-0	39±0.8	19.7±0.7	68	0	2	0	36	0	33	0	0	0	80	0	4	1
Stw-0	33.8±2.0	16.7±1.0	44	0	3	0	32	0	30	0	7	4	98	0	9	2
Ta-0	46.5±1.1	23.9±1.0	19	0	3	0	42	0	23	0	29	4	58	0	5	0
Tscha-1	54±2.3	26.7±0.9	50	0	2	0	44	0	54	0	0	3	85	0	6	10
Tu-0	42±2.3	20.9±1.1	81	4	1	0	33	0	31	0	19	4	95	0	1	5
Ty-0	45.4±1.8	22.6±1.1	61	2	0	0	37	0	0	0	6	4	73	0	12	18
Wa-1	24±0.6	12.1±0.3	28	0	1	0	29	0	27	0	10	3	112	0	7	8

Table S10 (continued). Number of methylated sites of autonomous pathway gene promoter regions of different *A. thaliana* accessions.

Population	Flowering time*	Leaf number*	Number of methylated sites												
			<i>PRMT10</i>	<i>AGL28</i>	<i>REF6</i>	<i>CK2</i>	<i>PP2A-B'γ</i>	<i>SYP22</i>	<i>ESD4</i>	<i>DBP1</i>	<i>DRM1</i>	<i>FLC</i>	<i>SOC1</i>	<i>LFY</i>	<i>API</i>
			AT1G04870	AT1G01530	AT3G48430	AT2G23080	AT4G15415	AT5G46860	AT4G15880	AT2G25620	AT5G15380	AT5G10140	AT2G45660	AT5G61850	AT1G69120
Aa-0	35±1.0	17.7±0.8	5	4	5	8	3	31	8	0	15	8	0	0	0
Br-0	45±0.0	22.6±1.0	2	3	1	2	0	38	13	0	7	0	0	1	0
Bs-1	29±0.0	14.8±0.7	14	2	11	3	4	156	6	0	28	10	0	0	0
Bsch-0	30±0.9	14.7±1.1	5	3	5	7	4	17	5	0	22	12	0	0	0
Ca-0	28±0.0	14.3±0.7	11	2	13	5	0	107	1	0	22	4	0	0	0
Col-0	27±2.0	13.7±1.0	5	2	4	13	2	168	0	0	20	1	0	0	0
Cvi-0	27±0.0	13.7±0.9	0	2	2	3	4	0	32	0	0	4	0	0	0
Ema-1	30±1.5	15.3±0.9	10	4	2	10	3	27	4	0	13	3	0	0	0
Gr-1	38±0.0	18.5±0.7	2	3	1	2	0	38	13	0	7	0	0	1	0
Gy-0	31±0.8	15.7±0.6	11	2	6	9	0	80	4	0	25	0	0	0	0
Hey-1	45±0.8	22.5±1.0	0	5	9	8	4	43	11	2	21	11	1	0	0
Hs-0	24±0.0	12.4±0.6	0	1	4	10	4	39	3	0	18	12	0	0	0
Kelsterbach-4	24±0.0	11.9±0.7	0	3	0	9	3	164	3	0	10	9	0	0	0
Kz-9	21±0.6	10.6±0.8	8	3	7	4	2	80	2	0	25	0	0	0	0
Ms-0	29.4±1.8	14.3±1.1	0	4	9	8	0	55	1	0	0	0	0	0	0
Nw-0	21±0.4	10.4±0.5	0	2	4	2	7	63	0	0	4	4	0	0	0
Per-1	45±2.2	22.5±1.3	4	3	6	6	0	48	5	0	0	7	0	0	0
Pro-0	19±0.7	9.7±0.9	9	5	5	7	0	27	7	0	22	4	0	0	0
Rd-0	21±0.0	10.7±0.8	0	0	6	2	0	3	0	0	1	0	0	0	0
Se-0	55.4±1.2	27.3±0.9	9	0	6	10	4	68	0	0	13	0	0	0	0
Sp-0	39±0.8	19.7±0.7	5	5	4	7	0	42	12	0	0	5	0	0	0
Stw-0	33.8±2.0	16.7±1.0	6	4	13	12	3	44	8	2	24	11	0	0	0
Ta-0	46.5±1.1	23.9±1.0	9	5	5	7	0	27	7	0	22	4	0	0	0
Tscha-1	54±2.3	26.7±0.9	2	2	3	2	0	161	3	0	16	5	0	0	0
Tu-0	42±2.3	20.9±1.1	3	4	2	12	2	196	0	0	10	5	0	0	0
Ty-0	45.4±1.8	22.6±1.1	0	5	10	14	6	120	1	0	5	0	0	0	0
Wa-1	24±0.6	12.1±0.3	8	3	8	5	0	181	0	0	17	12	0	0	0

* Data are shown as mean \pm standard errors

Table S11. Correlation analysis between flowering time, leaf number and methylation level of promoter region of different *A. thaliana* accessions.

	F T	L N	FV E	FY	FL D	PE P	HD A5	PRP3 9-1	FC A	FL K	FP A	LD	PCF S4	DR M2	HD A6	PRM T5	PRM T10	RE F6	AGL 28	CK2	PP2A- B'γ	SYP 22	ES D4	DB P1	DR M1	FL C	SOC 1	LF Y	A PI
FT			.19 3	.4 96	.26 2	N A	.054	NA	.73 2	.72 8	.92 1	.87 6	.117	.324	.711	.160	.764	.40 4	.806	.477	.711	.764	.70 7	.43 4	.517	.53 0	.280	.28 2	N A
LN			.20 3	.4 79	.26 5	N A	.056	NA	.71 0	.67 5	.97 3	.86 4	.114	.361	.815	.188	.837	.38 7	.812	.471	.683	.785	.68 1	.45 1	.560	.54 3	.277	.30 7	N A
FVE				.9 22	.69 7	N A	.136	NA	.61 7	.94 6	.98 1	.11 9	.566	.434	.682	.077	.547	.08 6	.739	.002 **	.880	.008 **	.24 0	.48 0	.938	.92 3	.656	.45 3	N A
FY					.34 8	N A	.893	NA	.07 3	.75 1	.67 0	.20 2	.830	.357	.124	.639	.648	.93 3	.318	.482	.324	.008 **	.55 0	.64 7	.995	.23 5	.751	.64 7	N A
FLD						N A	.483	NA	.11 9	.43 0	.82 8	.11 4	.752	.045 *	.626	.176	.397	.80 9	.362	.859	.814	.146	.84 7	.53 8	.811	.48 4	.670	.25 2	N A
PEP							NA	NA	N A	N A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	N A
HDA5								NA	.49 7	.97 8	.01 7*	.09 7	.984	.097	.196	.273	.381	.37 7	.955	.144	.728	.491	.18 2	.91 1	.814	.51 0	.775	.47 4	N A
PRP39 -1									N A	N A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	N A
FCA										.10 3	.48 9	.07 4	.152	.511	.911	.666	.090	.77 9	.070	.276	.710	.087	.08 0	.74 5	.224	.59 3	.758	.08 1	N A
FLK											.64 4	.62 7	.012 *	.783	.145	.489	.952	1.0 00	.867	.984	.356	.328	.93 9	.78 3	.359	.09 6	.849	.78 3	N A
FPA												.05 0*	.201	.809	.826	.620	.141	.25 4	.532	.089	.976	.945	.23 9	.67 2	.124	.57 8	.675	.32 9	N A
LD													.559	.726	.928	.197	.677	.32 6	1.00 0	.064	.596	.942	.06 0	.48 2	.830	.52 0	.627	1.0 00	N A
PCFS 4														.989	.343	.753	.494	.53 0	.953	.175	.228	.946	.37 1	.67 7	.089	.01 3	.701	.09 5	N A
DRM2															.155	.891	.448	.12 8	.435	.868	.179	.585	.82 9	.69 2	.133	.03 6	.783	.69 2	N A
HDA6																.059	.157	.84 8	.497	.462	.037*	.847	.72 5	.72 0	.163	.99 9	.221	.99 0	N A

<i>PRMT</i> <i>5</i>	.108	.67 5	.998	.083	.002* *	.061	.04 8*	.85 3	.965	.96 3	.250	.98 1	N A
<i>PRMT</i> <i>10</i>		1.0 00	.068	.841	.253	.489	.37 1	.56 0	.000 **	.91 9	.267	.35 6	N A
<i>REF6</i>			.706	.111	.708	.729	.37 4	.12 8	.896	.48 5	.161	1.0 00	N A
<i>AGL2</i> <i>8</i>				.410	.712	.705	.18 4	.02 0*	.049	.33 9	.332	.05 3	N A
<i>CK2</i>					.160	.280	.11 9	.22 3	.389	.65 3	.771	.04 5	N A
<i>PP2A-</i> <i>B'γ</i>						.978	.96 3	.32 0	.887	.19 4	.356	.16 2	N A
<i>SYP22</i>							.01 1*	.44 6	.261	.58 2	.592	.36 9	N A
<i>ESD4</i>								.39 6	.269	.78 1	.418	.10 4	N A
<i>DBP1</i>									.156	.03 6*	.000 **	.69 2	N A
<i>DRM1</i>										.07 9	.419	.29 8	N A
<i>FLC</i>											.156	.10 4	N A
<i>SOC1</i>												.78 3	N A
<i>LFY</i>													N A
<i>API</i>													

FT: Flowering time; LN: Leaf number; * Correlation is significant at the 0.05 level (2-tailed); ** Correlation is also significant at the 0.01 level (2-tailed); NA, not applicable.

Table S12. Correlation analysis between DNA methylation level of gene coding region and gene expression level among 15 *A. thaliana* accessions.

Accession	mC		mCG		mCHG		mCHH	
	<i>P</i> value	R ²	<i>P</i> value	R ²	<i>P</i> value	R ²	<i>P</i> value	R ²
<i>FVE</i>	0.03	0.32*	0.03	0.3*	0.87	0	0.87	0
<i>FY</i>	0.00	0.51**	0.00	0.51**	0.87	0	NA	NA
<i>FLD</i>	0.00	0.61**	0.00	0.61**	0.80	0.01	NA	NA
<i>PEP</i>	0.04	0.29*	0.04	0.29*	NA	NA	NA	NA
<i>HDA5</i>	0.03	0.33*	0.02	0.33*	0.97	0	NA	NA
<i>PRP39-1</i>	0.00	0.47**	0.01	0.45*	0.51	0.03	NA	NA
<i>FCA</i>	0.09	0.2	0.08	0.22	0.18	0.06	0.79	0.01
<i>FLK</i>	0.47	0.04	0.44	0.04	0.38	0	NA	NA
<i>FPA</i>	0.06	0.24	0.06	0.24	NA	NA	NA	NA
<i>LD</i>	0.48	0.04	0.34	0.07	0.93	0	NA	NA
<i>PCFS4</i>	0.14	0.15	0.14	0.15	0.61	0.06	NA	NA
<i>DRM2</i>	0.59	0.02	0.04	0.29	0.7	0.01	0.6	0.02
<i>HDA6</i>	0.28	0.09	0.27	0.09	0.81	0	NA	NA
<i>PRMT5</i>	0.08	0.2	0.08	0.21	NA	NA	0.46	0.04
<i>PRMT10</i>	0.28	0.09	0.28	0.09	NA	NA	NA	NA
<i>REF6</i>	0.17	0.13	0.16	0.14	0.52	0.03	NA	NA
<i>AGL28</i>	0.76	0.01	0.22	0.11	0.94	0	0.87	0
<i>CK2</i>	0.37	0.06	0.37	0.06	NA	NA	NA	NA
<i>PP2A.B.γ</i>	0.10	0.19	0.10	0.19	NA	NA	NA	NA
<i>SYN22</i>	0.28	0.09	0.28	0.09	NA	NA	NA	NA
<i>ESD4</i>	0.10	0.2	0.10	0.2	0.74	0.01	NA	NA
<i>DBP1</i>	0.83	0	0.81	0	0.90	0	NA	NA
<i>DRM1</i>	0.79	0.01	0.79	0.01	NA	NA	NA	NA
<i>FLC</i>	0.50	0.04	0.41	0.05	0.83	0	0.83	0
<i>SOCI</i>	0.20	0.12	0.20	0.12	NA	NA	NA	NA
<i>LFY</i>	0.93	0	0.93	0	NA	NA	NA	NA
<i>API</i>	0.92	0	0.92	0	NA	NA	NA	NA

mC, overall methylation level of gene coding region; mCG, methylation level in the CG context; mCHG, methylation level in the CHG context; mCHH, methylation level in the CHH context; * Correlation is significant at the 0.05 level (2-tailed); ** Correlation is also significant at the 0.01 level (2-tailed); NA, not applicable.

Table S13. Number of methylated sites of gene coding regions and the percentage decreases in methylation level of the six genes following 5-azac treatment in the Col-0, Br-0 and Tscha-1 accessions.

		<i>FVE</i>		<i>FY</i>		<i>FLD</i>		<i>PEP</i>		<i>HDA5</i>		<i>PRP39-1</i>	
Population		Number of methylated sites	Drop percentage (%)	Number of methylated sites	Drop percentage (%)	Number of methylated sites	Drop percentage (%)	Number of methylated sites	Drop percentage (%)	Number of methylated sites	Drop percentage (%)	Number of methylated sites	Drop percentage (%)
mC	Col-0	10	50.0	36	26.5	58	15.9	20	20.0	36	25.0	50	25.4
		12	40.0	38	22.5	57	17.4	18	28.0	36	25.0	50	25.4
		13	35.0	40	18.4	59	14.5	19	24.0	37	22.9	52	22.4
	Br-0	20	51.2	42	28.8	57	17.4	25	24.2	46	25.8	55	40.2
		22	46.3	40	32.2	56	18.8	26	21.2	43	30.7	57	38.0
		25	39.0	40	32.2	54	21.7	25	24.2	48	22.6	60	34.8
	Tscha-1	27	54.2	36	40.0	59	24.4	27	41.3	42	40.0	55	40.9
		27	54.2	39	35.0	57	26.9	30	34.8	46	34.3	59	36.6
		26	55.9	38	36.7	61	21.8	34	26.1	50	28.6	63	32.3
		7	58.8	36	25.0	58	15.9	20	20.0	36	25.0	50	25.4
mCG	Col-0	11	35.3	38	20.8	57	17.4	18	28.0	36	25.0	50	25.4
		11	35.3	39	18.8	59	14.5	19	24.0	37	22.9	52	22.4
		20	51.2	42	28.8	57	17.4	25	24.2	46	25.8	55	40.2
	Br-0	22	46.3	40	32.2	56	18.8	26	21.2	43	30.7	57	38.0
		25	39.0	40	32.2	54	21.7	25	24.2	48	22.6	60	34.8
		27	54.2	36	40.0	59	22.4	27	41.3	42	38.2	55	40.9
	Tscha-1	26	55.9	39	35.0	57	25.0	30	34.8	46	32.4	59	36.6
		26	55.9	38	36.7	60	21.1	34	26.1	49	27.9	63	32.3

mC, Total number of methylated sites of gene coding regions; mCG, number of methylated sites in the CG context of gene coding regions.

Table S14. Methylated sites of the *FVE* and *FVE(CS)* coding regions in Col-0, *fve-3+pFVE::FVE* and *fve-3+pFVE::FVE(CS)*.

Population	methylated sites	Number			
		CG	CHG	CHH	Total
Col-0	74, 261, 433, 451, 552, 598, 628, 655, 692, 711, 905, 965, 983, 989, 1047, 1113, 1130, 1273, 1355, 1493	17	2	1	20
<i>fve-3+pFVE::FVE(CS)</i>	65, 68, 88, 136, 208, 295, 325, 433 , 523, 551, 560, 598 , 655 , 710, 728, 748, 788, 821, 842, 853, 881, 916, 983 , 1018, 1087, 1099, 1112, 1273 , 1429, 1454	7	18	5	30
<i>fve-3+pFVE::FVE</i>	74 , 119, 121, 125, 208, 325, 371, 433 , 598 , 628 , 655 , 665, 676, 699, 710, 711 , 728, 764, 780, 788, 805, 842, 853, 905 , 908, 924, 927, 944, 949, 965 , 983 , 989 , 1013, 1018, 1047 , 1060, 1077, 1086, 1087, 1099, 1113 , 1130 , 1155, 1160, 1177, 1187, 1257, 1273 , 1355 , 1374, 1382, 1389, 1400, 1420, 1429, 1454, 1493	20	27	10	57

The black bold numbers represent the same methylated sites of *FVE* and *FVE(CS)* in *fve-3+pFVE::FVE* and *fve-3+pFVE::FVE(CS)*, respectively, compared with Col-0.

Table S15. RT-qPCR primers.

Primer name	Primer sequence
FVE-Fq	5'-CTCGTCTGGCCTTCACTCTC-3'
FVE-Rq	5'-CTGTGGGAGTTCCCTGATTC-3'
FLD-Fq	5'-GCTTACCGAGGAAGAGATTG-3'
FLD-Rq	5'-TGCTTGACTGAGCAGGAAAC-3'
FY-Fq	5'-TACACCAGCACCGTTGTTAG-3'
FY-Rq	5'-GCAGCAAAGCTTGTTGAAGG-3'
PEP-Fq	5'-ACCTTATACCGGCGGGATTC-3'
PEP-Rq	5'-CCGGAACGATCATACGAAAC-3'
HDA5-Fq	5'-TCCGGAAGCATACCCATTTCG-3'
HDA5-Rq	5'-AGCCTCTTGCGCACCTAAAC-3'
PRP39-1-Fq	5'-CCGCACTTCCACTTGCTTCC-3'
PRP39-1-Rq	5'-GGAGGGTCCCTCTGTATGTG-3'
FLC-Fq	5'-GTAGCCGACAAGTCACCTTC-3'
FLC-Rq	5'-CCGGAGGAGAAGCTGTAGAG-3'
SOC1-Fq	5'-ATTCGCCAGCTCCAATATGC-3'
SOC1-Rq	5'-TCAATCTGTTGCAGCTCCTC-3'
LFY-Fq	5'-CGAGCACGCTTGTGGGTATG-3'
LFY-Rq	5'-GGCGGAGAGTAGCAAATGAC-3'
AP1-Fq	5'-TTCACTCGCTCACTGAGTTC-3'
AP1-Rq	5'-GAAGACACAGTCGTGAGAAC-3'
ACTIN-Fq	5'-GGCTCCTCTTAACCCAAAGG-3'
ACTIN-Rq	5'-CAGTAAGGTCACGTCCAGCA-3'

Table S16. Primers used for *FVE* and *FVE(CS)* plant expression vector construction.

Primer name	Primer sequence	Primer usage
pFVE-F	5'- <u>AGTACT</u> CCGTCGAGCAAGTTAATACC-3'	pFVE-FVE
FVE-R	5'- <u>TCTAGATA</u> AAGCTTGGAGGCACAAGTC-3'	amplification
FVE(CS)-F	5'-ATGGAGAGTGATGAAGCAGCAGCAGTG-3'	FVE(CS)
FVE(CS)-R	5'-TTATGGCTTAGATGCACATGTC-3'	amplification
pFVE-F	5'-CCGTCGAGCAAGTTAATACC-3'	pFVE
pFVE-R	5'-TTTCCTCTCTCTCTTTTAAATTTTTC-3'	amplification
pFVE-F	5'- <u>AGTACT</u> CCGTCGAGCAAGTTAATACC-3'	
pFVE-R3	5'-TTCATCACTCTCCATTTTCCTCTCTCTCTT-3'	Overlap of
FVE(CS)-F1	5'-AAGAGAGAGAGGAAAATGGAGAGTGATGAA-3'	pFVE-FVE(CS)
FVE(CS)-R	5'- <u>TCTAGATT</u> ATGGCTTAGATGCACATGTC-3'	

Table S17. Primers used for *FVE* and *FVE(CS)* methylation determination

Primer name	Primer sequence
FVE-Me-F1	5'-ATGGAGAGYGAYGAAGTAGTAG-3'
FVE-Me-R1	5'-TAACAACCTTCACAATTTACTATAACC-3'
FVE-Me-F2	5'-TTTAGAGTAAATTGATGGAAGTGTG-3'
FVE-Me-R2	5'-AAACAACCTAACTTATCCTTACCTC-3'
FVE-Me-F3	5'-GGGTATTAAGATAATGTTGAATTTG-3'
FVE-Me-R3	5'-AAATTTATACCAATTCTCRCATCCC-3'
FVE-Me-F4	5'-GTATTTAGTTYGAYGAGTGTATAAG-3'
FVE-Me-R4	5'-TTAACTACACRATCAAACCTTCTTAC-3'
FVE-Me-F5	5'-TTTGAATATTTGGGATTATGATAGG-3'
FVE-Me-R5	5'-CACAAATCATAACATACRACTTAAAC-3'
FVE(CS)-Me-F1	5'-ATGGAGAGTGATGAAGTAGTAGTAG-3'
FVE(CS)-Me-R1	5'-TAACAACCTTCACAATTAACATAAC-3'
FVE(CS)-Me-F2	5'-TTTAGAGTAAATTGATGGAAGTGTG-3'
FVE(CS)-Me-R2	5'-AAACAACCTAACTTATCCTTTCTCC-3'
FVE(CS)-Me-F3	5'-GGGTATTAAGATAATGTTGAATTTG-3'
FVE(CS)-Me-R3	5'-AAATTAATACCAATTCTAACATCCC-3'
FVE(CS)-Me-F4	5'-ATATAGTTGAAGATGTGGTATTTAG-3'
FVE(CS)-Me-R4	5'-ACTTCTTACTAACCCTATCATAATC-3'
FVE(CS)-Me-F5	5'-TATGTTGGTTATAGGGATAAAGTTG-3'
FVE(CS)-Me-R5	5'-TATAACTTAAATACACATATCATTAC-3'
FY-Me-F1	5'-ATGTAYGTYGGYGGYGATATGCA-3'
FY-Me-R1	5'-ATTAATCATATRCCTAAAAAATC-3'
FY-Me-F2	5'-GGTATATGATTAATTTATTAGG-3'
FY-Me-R2	5'-CCCACAAAAAAATTAAGATCC-3'
FY-Me-F3	5'-TGGGTATAYGAAAGATGTAATA-3'
FY-Me-R3	5'-CCAAAAAGRGATAAATAAAAAACC-3'
FY-Me-F4	5'-GTTTTTTTGAAGTGGTTAGTAG-3'
FLD-Me-F1	5'-ACTRCCTACTAATATTACTAATTA-3'
FLD-Me-R1	5'-AACTTATTCAATRCCTCCAAC-3'
FLD-Me-F2	5'-GAGATTGAATTYGGTGTGGTGTT-3'
FLD-Me-R2	5'-CCTTATAAAAAAAAAAACC AARC-3'
FLD-Me-F3	5'-GGATTATAGYGAGATAGTTTGG-3'
FLD-Me-R3	5'-GTACACARCACCATATCACCCCTC-3'
FLD-Me-F4	5'-TGGAATAAAGTGTATGAGGGT-3'
FLD-Me-R4	5'-CTRCTAATATATCATAATCATCRC-3'
FLD-Me-F5	5'-GTAGTGGGAGCTTTAGGYGATG-3'
FLD-Me-R5	5'-CATCACCACCTCTAACTTCTCTC-3'
FLD-Me-F6	5'-GGTTTTTTGATTTGAGAGAAGTTAG-3'
FLD-Me-R6	5'-CAAAAATTCTCCAAAAATCATT-3'
PEP-Me-F1	5'-ATGGTYGTYGTYGTAGATTTYG-3'
PEP-Me-R1	5'-AATTCACAACCTTAATAATCAC-3'

PEP-Me-F2	5'-GTTGTGAATTTTTATTTTTTAG-3'
PEP-Me-R2	5'-AAAACARCAACAAAAACACCA-3'
PEP-Me-F3	5'-TTGTTAGAGGAAATATYGTTTT-3'
PEP-Me-R3	5'-CTCATTTTCAAAARCTAATATT-3'
PEP-Me-F4	5'-GGTAGATTTTTTTTAAATATAAT-3'
PEP-Me-R4	5'-ATAATAAACTCCTACACACACA-3'
PEP-Me-F5	5'-GTGTAGGAGTTTATTATTAATTA-3'
PEP-Me-R5	5'-CAAATTATTATTATAAAACRTT-3'
HDA5-Me-F1	5'-ATGGTTATGGTYGGAGAATTT-3'
HDA5-Me-R1	5'-CCCATARCTTCATCTRCCTCAA-3'
HDA5-Me-F2	5'-GGGTATTATGTTGAGGTAGATG-3'
HDA5-Me-R2	5'-CARCACTATCTTTCCTTATRCA-3'
HDA5-Me-F3	5'-GATAGTGTTGGYGTAGAGGGA-3'
HDA5-Me-R3	5'-AACCAACACATACCTTTTTCAATC-3'
HDA5-Me-F4	5'-GGATAGGTYGATGGATTGAAAA-3'
HDA5-Me-R4	5'-ARCCTCARCTTCTTCTTTAAAT-3'
PRP39-1-Me-F1	5'-ATGTTTTTATTAGGAAGGTTTT-3'
PRP39-1-Me-R1	5'-CRCACATAAAAAATAAACCTCC-3'
PRP39-1-Me-F2	5'-TGGTTATAAGGAGGTTTTATTT-3'
PRP39-1-Me-R2	5'-TATACATAATCAAATRCTTCAAC-3'
PRP39-1-Me-F3	5'-GATGTTGAGAAAGTTAGGAGGA-3'
PRP39-1-Me-R3	5'-CAAAARCARCTTATRCTAATARCC-3'
PRP39-1-Me-F4	5'-GGTGGTTATGTTGYGTAGTTTT-3'
PRP39-1-Me-R4	5'-AACAACCARCARCAATAATAARC-3'

Note: Y=T/C, R=A/G

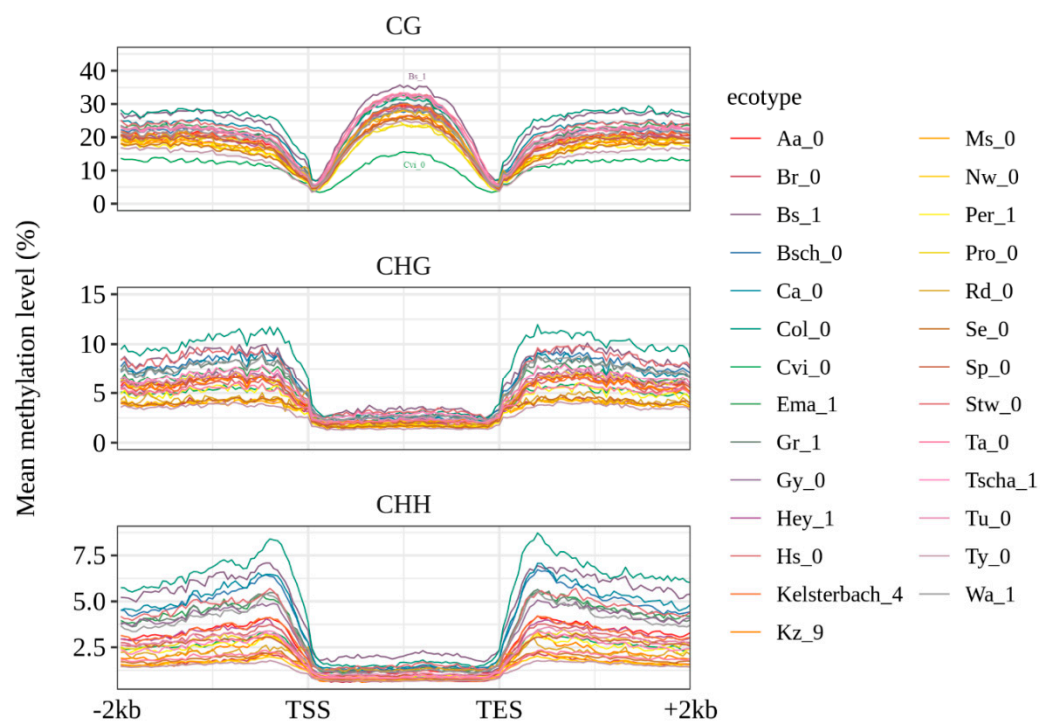


Figure S1. Distribution of DNA methylation level of protein-coding genes, including a 2kb window upstream of the transcriptional start site (TSS) and downstream of the transcription end site (TES).

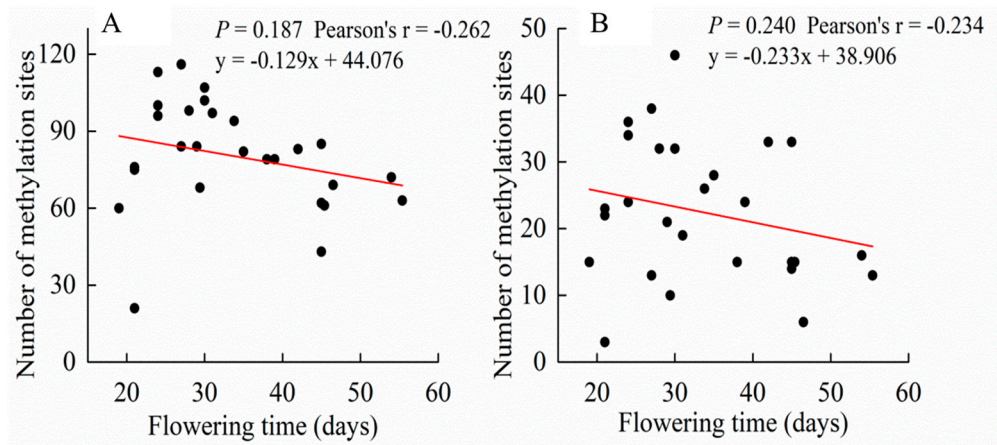


Figure S2. Correlation plot of methylation levels of the coding regions of *FWA* gene (A) and the promoter region (B).

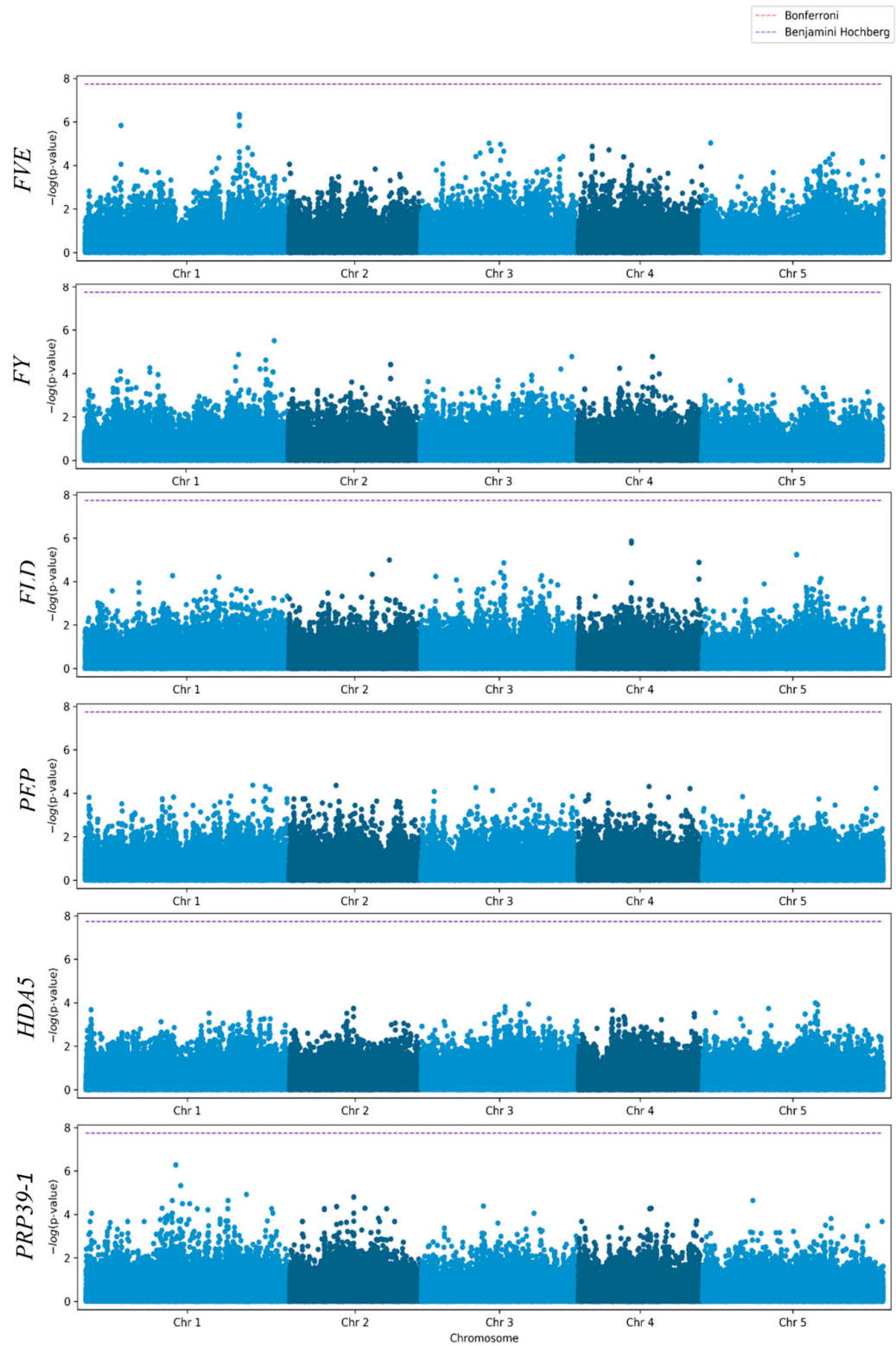


Figure S3. GWAS for CG methylation level of *FVE*, *FY*, *FLD*, *PEP*, *HDA5* and *PRP39-1* genes. Horizontal dash lines represent 5% significance thresholds corrected for multiple testing using bonferroni.

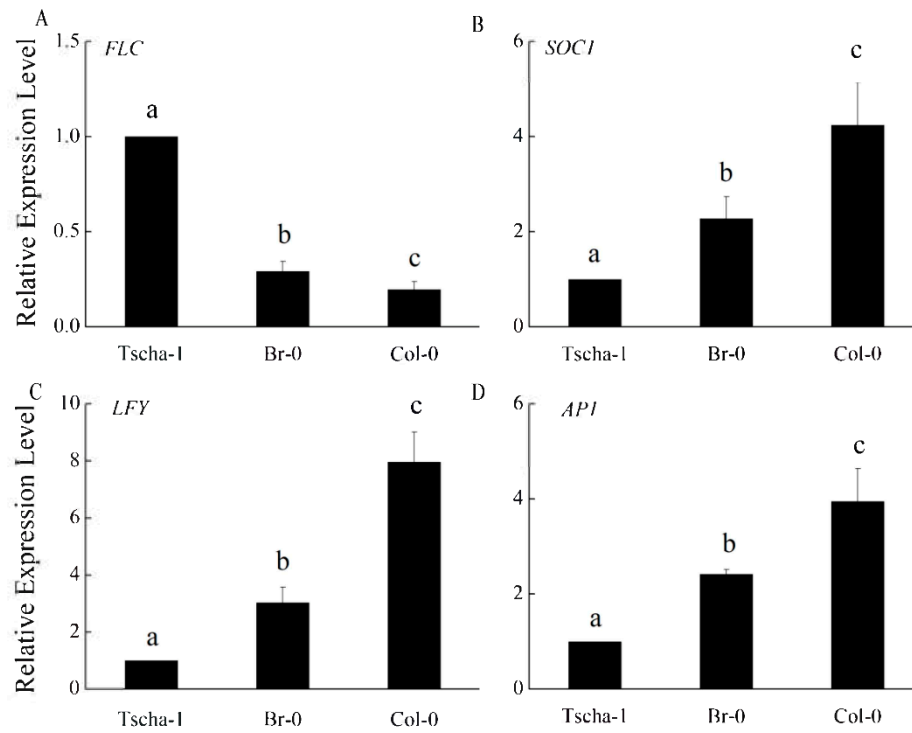


Figure S4. Relative expression levels of the downstream genes *FLC* (A), *SOC1* (B), *LFY* (C) and *API* (D) in the autonomous pathway among Col-0, Br-0 and Tscha-1 (Different letters indicate significant differences among the different accessions at the level of $P < 0.05$).

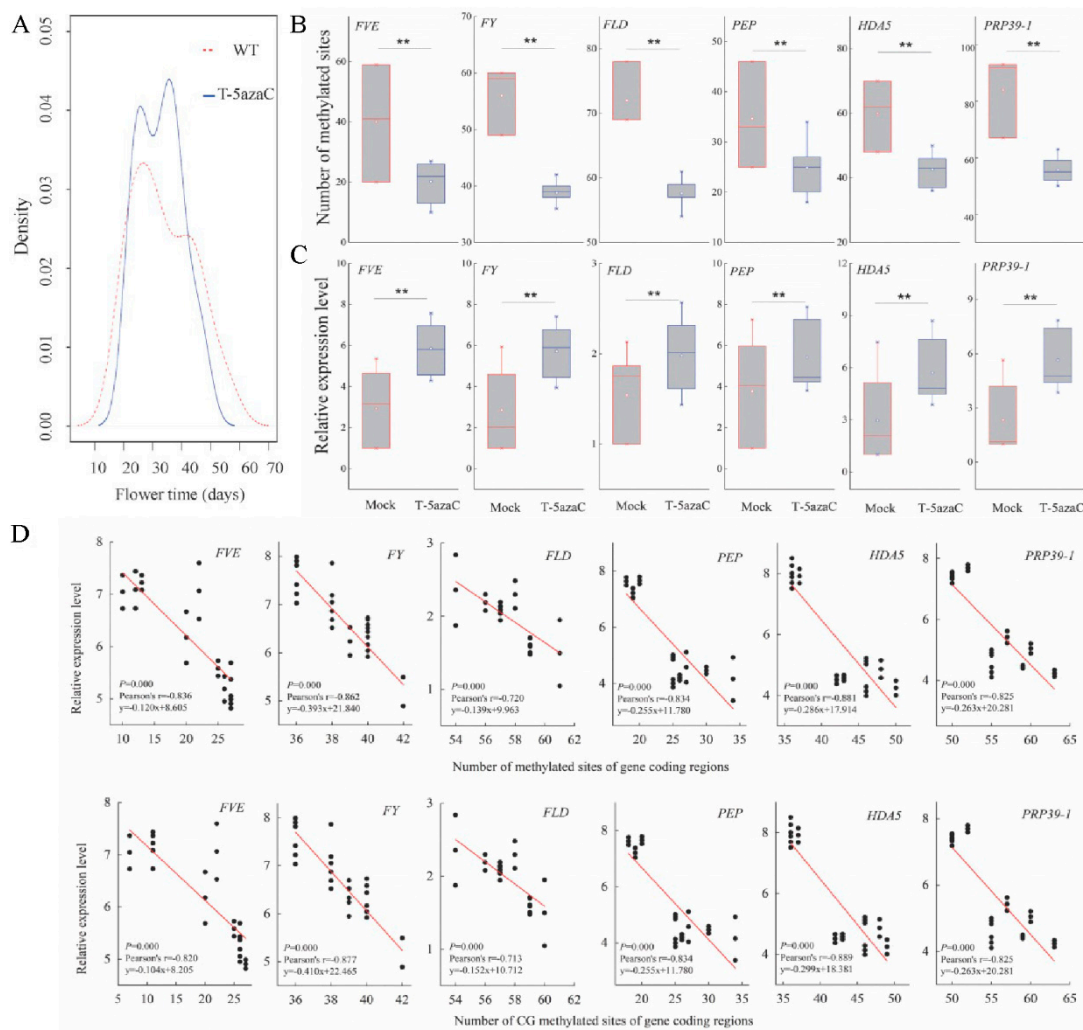


Figure S5. Flowering time, numbers of DNA methylation sites, relative expression levels and correlation analysis of the *FVE*, *FY*, *FLD*, *PEP*, *HDA5* and *PRP39-1* genes among Col-0, Br-0 and Tscha-1 accessions treated with or without 5-azac. A, Flowering time of 27 *A. thaliana* accessions treated (T-5azaC) or not treated (WT) with 5-azac. Y-axis: ratio of the number of individuals to the total number of individuals per day among all 27 *A. thaliana* accessions; B, number of methylated sites of the six genes among Col-0, Br-0 and Tscha-1 accessions treated with (T-5azaC) or without 5-azac (Mock); C, relative expression levels of the six genes among Col-0, Br-0 and Tscha-1 accessions treated with (T-5azaC) or without 5-azac (Mock). Mock: Col-0, Br-0 and Tscha-1 accessions not treated with 5-azac; T-5azaC: Col-0, Br-0 and Tscha-1 accessions treated with 50 μ M 5-azac. ** Correlation is significant at the level of $P < 0.01$; D, correlation analysis of relative expression level and number of methylated sites of the six genes among Col-0, Br-0 and Tscha-1 accessions after 5-azac treatment.

[illegible]

Figure S6. Alignment of the *FVE* and *FVE(CS)* gene sequences.