

**Table S1** : Metrics from analysis of bisulfite converted DNA library sequencing

Sequencing	Sample	Total reads	Trimming (trimmomatic)		Bismark mapping efficiency	Deduplicated	Total kept reads	Plastide conversion	Methylation call (corrected for conversion)		
			Trimmed	% kept reads					CG	CHG	CHH
Illumina GAllx	WT	33,893,780	27,555,876	81.30%	74.10%	89.85%	18,346,385	0.9928	38.28%	16.28%	4.68%
Illumina GAllx		33,893,780	27,555,876								
Illumina GAllx	met1-1	38,463,485	32,742,566	85.13%	72.50%	89.99%	21,362,150	0.9929	10.39%	15.09%	4.79%
Illumina GAllx		38,463,485	32,742,566								
Illumina NextSeq 500	met1-3	95,617,308	89,062,558	93.14%	56.50%	63.05%	31,726,978	0.9942	0.22%	15.02%	3.72%
Illumina NextSeq 500		95,617,308	89,062,558								
Illumina GAllx	MET1+ rep1	68,911,587	59,032,646	85.66%	65.20%	82.96%	31,930,711	0.9621	22.51%	10.51%	4.71%
Illumina GAllx		68,911,587	59,032,646								
Illumina GAllx	MET1+ rep2	62,809,284	53,613,341	85.36%	60.30%	78.48%	25,371,677	0.9982	19.42%	8.82%	3.42%
Illumina GAllx		62,809,284	53,613,341								
Illumina NextSeq 500	T-MET1a	57,849,715	54,551,310	94.30%	54.20%	65.50%	19,366,261	0.9943	22.63%	18.63%	4.53%
Illumina NextSeq 500		57,849,715	54,551,310								
Illumina NextSeq 500	T-MET1b	80,685,462	76,125,610	94.35%	56.20%	63.24%	27,055,712	0.9946	22.16%	18.96%	4.66%
Illumina NextSeq 500		80,685,462	76,125,610								

<b>rice (Hu et al. 2014)</b>											
mm_SRR1449221_R1	met1	62,002,065	61,979,047	99.96%	71.30%	97.87%	43,249,791	0.9965	9.55%	21.85%	2.45%
mm_SRR1449221_R2		62,002,065	61,979,047								
WT_SRR1448321_R1	WT	58,134,648	58,097,507	99.94%	82.90%	98.59%	47,483,737	0.9966	40.56%	23.06%	4.46%
WT_SRR1448321_R2		58,134,648	58,097,507								

**Table S2:** parameters used to classified GELs and TELs

Methylation values were averaged among all cytosines in the same context in each sequence or tile, with a minimum coverage of five reads

<b>Kinds</b>	<b>minimun reads per cytosine</b>	<b>CpG methylation</b>	<b>CHG methylation</b>	<b>CHH methylation</b>
<b>TE-like (TEs)</b>	5	>5%	>5%	>5%
<b>CpG exclusive (GELs)</b>	5	>5%	<5%	<5%
Not methylated	5	<5%	<5%	<5%

**Table S3:** enrichment analysis of TAIR10 TEs families in E-TEs (selected as TEs with residual CpG *met1-1* methylation < 1% of wt)

FDR = False discovery rate  
 p = p value  
 m = total TEL TEs in the family  
 q = total E-TEL TEs in the family

Family	FDR	p	m	q
ATLANTYS2	3.01E-33	1.34E-35	65	44
VANDAL21	1.76E-07	1.57E-09	47	18
ND	5.29E-05	7.09E-07	2169	203
ATLANTYS3	0.000704	1.26E-05	13	7
SADHU	0.004307	9.61E-05	8	5
ATENSPM5	0.075821	0.002369	41	9
ATENSPM1A	0.413724	0.020317	15	4
VANDAL12	0.439879	0.023565	9	3
ATLINE1_1	0.96655	0.063039	21	4
ATMU3	0.96655	0.06607	6	2
ARNOLD1	1	0.367042	6	1
ARNOLD2	1	1	23	0
ARNOLD3	1	1	19	0
ATCOPIA27	1	1	7	0
ATCOPIA28	1	1	14	0
ATCOPIA35	1	1	9	0
ATCOPIA41	1	1	9	0
ATCOPIA43	1	1	11	0
ATCOPIA49	1	1	8	0
ATCOPIA78	1	1	12	0
ATCOPIA95	1	1	18	0
ATENSPM1	1	1	9	0
ATENSPM10	1	1	16	0
ATENSPM11	1	1	19	0
ATENSPM2	1	0.925695	34	1
ATENSPM3	1	1	19	0
ATENSPM4	1	0.137202	9	2
ATENSPM6	1	1	37	0
ATENSPM7	1	1	17	0
ATENSPM9	1	0.619747	28	2
ATGP1	1	1	54	0
ATGP10	1	1	12	0
ATGP2	1	0.813604	22	1
ATGP2N	1	1	14	0
ATGP3	1	1	20	0
ATGP5	1	1	8	0
ATGP7	1	1	12	0
ATGP8	1	1	6	0
ATHAT1	1	1	18	0
ATHILA	1	1	55	0
ATHILA0_I	1	1	32	0
ATHILA2	1	0.999983	206	3

ATHILA3	1	1	58	0
ATHILA4	1	1	45	0
ATHILA4A	1	1	18	0
ATHILA4C	1	1	57	0
ATHILA5	1	1	19	0
ATHILA6A	1	0.977592	97	3
ATHILA6B	1	1	34	0
ATHILA7	1	0.456614	8	1
ATHILA8A	1	1	6	0
ATIS112A	1	1	29	0
ATLANTYS1	1	1	70	0
ATLINE1_2	1	1	11	0
ATLINE1_4	1	0.533541	10	1
ATLINE1_5	1	1	12	0
ATLINE1_6	1	0.890964	29	1
ATLINE1A	1	1	35	0
ATLINE2	1	1	21	0
ATLINEIII	1	0.692384	32	2
HARBINGER	1	1	6	0
HELITRON1	1	1	26	0
HELITRON2	1	1	21	0
HELITRON3	1	1	11	0
HELITRON4	1	1	37	0
HELITRON5	1	1	14	0
HELITRONY2	1	1	15	0
HELITRONY3	1	1	13	0
META1	1	1	21	0
ROMANIAT5	1	1	10	0
TA11	1	0.899011	30	1
TAG2	1	1	10	0
Unassigned	1	0.827494	60	3
VANDAL1	1	1	47	0
VANDAL13	1	1	6	0
VANDAL14	1	1	7	0
VANDAL16	1	1	12	0
VANDAL17	1	1	13	0
VANDAL2	1	0.995706	71	1
VANDAL20	1	1	17	0
VANDAL22	1	1	9	0
VANDAL2N1	1	0.123864	17	3
VANDAL3	1	1	89	0
VANDAL4	1	1	47	0
VANDAL5	1	1	32	0
VANDAL6	1	0.851857	25	1
VANDAL7	1	1	29	0
VANDAL8	1	0.255984	24	3
VANDAL9	1	1	11	0

**Table S4:** enrichment analysis of TAIR10 TEs families in R-TEs (selected as TEs with residual CpG *met1-1* methylation > 50 % of WT)

FDR = False discovery rate  
 p = p value  
 m = total TEL TEs in the family  
 q = total R-TEL TEs in the family

Family	FDR	p	m	q
ATGP1	2.95E-14	1.32E-16	54	42
META1	1.23E-11	1.10E-13	21	21
ATLINE1A	3.95E-10	5.29E-12	35	28
HELITRON4	3.25E-09	5.81E-11	37	28
HELITRONY2	2.55E-08	5.70E-10	15	15
VANDAL5	4.71E-06	1.26E-07	32	22
ARNOLD2	2.00E-05	7.13E-07	23	17
ROMANIAT5	2.00E-05	6.99E-07	10	10
HELITRON2	0.0011602	4.66E-05	21	14
ATENSPM2	0.0016633	7.43E-05	34	19
ATENSPM5	0.0034239	0.0001681	41	21
VANDAL14	0.0211395	0.0011325	7	6
ATGP10	0.0389577	0.0022609	12	8
TAG2	0.0466403	0.002915	10	7
ATENSPM6	0.0477691	0.0031988	37	17
VANDAL4	0.0607709	0.0043408	47	20
ATCOPIA28	0.112361	0.0085274	14	8
ATHILA	0.1758031	0.0149119	55	21
ATLINE1_4	0.1910088	0.0170544	10	6
ATHILA4	0.3205088	0.0300477	45	17
ARNOLD1	0.3307306	0.0339589	6	4
VANDAL13	0.3307306	0.0339589	6	4
ATCOPIA78	0.427997	0.0477675	12	6
ATENSPM9	0.4559978	0.0562899	28	11
ARNOLD3	0.4982847	0.0667346	19	8
HELITRON5	0.7190291	0.0995085	14	6
ATIS112A	0.9775234	0.1440101	29	10
ATLINE1_5	0.9775234	0.1433583	12	5
ATENSPM11	0.9860284	0.156018	19	7
HARBINGER	0.9860284	0.1584689	6	3
ATCOPIA27	1	0.5377031	7	2
ATCOPIA35	1	0.9186143	9	1
ATCOPIA41	1	0.3798343	9	3
ATCOPIA43	1	1	11	0
ATCOPIA49	1	0.3041512	8	3
ATCOPIA95	1	0.9551588	18	2
ATENSPM1	1	0.6829022	9	2
ATENSPM10	1	0.3447762	16	5
ATENSPM1A	1	0.9847619	15	1
ATENSPM3	1	0.7142806	19	4
ATENSPM4	1	1	9	0
ATENSPM7	1	0.3994847	17	5

ATGP2	1	0.9978487	22	1
ATGP2N	1	1	14	0
ATGP3	1	0.5569347	20	5
ATGP5	1	1	8	0
ATGP7	1	0.9647734	12	1
ATGP8	1	0.449555	6	2
ATHAT1	1	0.2586516	18	6
ATHILA0_I	1	0.9185481	32	5
ATHILA2	1	1	206	3
ATHILA3	1	0.5629029	58	14
ATHILA4A	1	0.4536513	18	5
ATHILA4C	1	0.4107942	57	15
ATHILA5	1	0.7142806	19	4
ATHILA6A	1	0.9975126	97	13
ATHILA6B	1	0.9947251	34	3
ATHILA7	1	0.8924241	8	1
ATHILA8A	1	1	6	0
ATLANTYS1	1	0.9999936	70	4
ATLANTYS2	1	1	65	0
ATLANTYS3	1	1	13	0
ATLINE1_1	1	0.9971539	21	1
ATLINE1_2	1	0.2675892	11	4
ATLINE1_6	1	0.8683476	29	5
ATLINE2	1	0.6047741	21	5
ATLINEIII	1	0.9698233	32	4
ATMU3	1	0.812085	6	1
HELITRON1	1	0.2850034	26	8
HELITRON3	1	0.7884785	11	2
HELITRONY3	1	1	13	0
ND	1	0.6982654	2169	520
SADHU	1	1	8	0
TA11	1	0.1714795	30	10
Unassigned	1	0.4998296	60	15
VANDAL1	1	0.9999981	47	1
VANDAL12	1	0.6829022	9	2
VANDAL16	1	1	12	0
VANDAL17	1	0.8617726	13	2
VANDAL2	1	1	71	1
VANDAL20	1	0.8204022	17	3
VANDAL21	1	1	47	0
VANDAL22	1	1	9	0
VANDAL2N1	1	1	17	0
VANDAL3	1	0.9915948	89	13
VANDAL6	1	0.9624894	25	3
VANDAL7	1	0.9968565	29	2
VANDAL8	1	0.9892402	24	2
VANDAL9	1	0.9534279	11	1

**Table S5:** primers and target genes used in this work

Primers for local amplification of bisulfite converted DNA

name	sequence	ID target	kind
BS_CCT_F	AGAAGGTGGTTGATGTGTTTAGAA	AT4G00450	GEL
BS_CCT_R	AATCRCCTCRCCTATTTACACAT		
BS_YTH_F	TGAAGTYTAAGTGGGGTTTTGGGTT	AT4G11970	GEL
BS_YTH_R	CAACTAAACAACATRACTTACAAAA		
BS_YTH_inner_F	TAGGGATGATTATTYYAAAAAAGG	AT4G11970	
BS_YTH_inner_R	ATRAAATTCTCARCATAARTTACAA		
BS_PKSP_F	TAGAGATGGATYAYAGTTTGGAAGT	AT1G57700	GEL
BS_PKSP_R	AATAAATCCCCCAAAATATCACCTT		
BS_AFH14_F	TGATATGGYTGATGAGGAAGTGAAG	AT1G31810	GEL
BS_AFH14_R	AAAACACTTCCATCTAAACATCATA		
BS_AFH14_inn_F	AGGGAAGAAATGYAGATTYTTTAT	AT1G31810	
BS_AFH14_inn_R	CTAAACATCATARACRTRTRACTACT		
BS_HYP_F	GGYTTGAGGGGTATGYTTGATT	AT1G47660	E-TEL
BS_HYP_R	CTTCTCRACCRACRTRACTTACA		
BS_MHClIike_F	GAGTTTAGGATYGGTGAAGAA	AT1G32010	E-TEL
BS_MHClIike_R	TACCATTRCTTATAACAATCAACAA		
BS_MHClIike_inn_F	GGTGAAGAAYTYGGTTATGGGAT	AT1G32010	
BS_MHClIike_inn_R	CTCRRAAAAAATCTTTCRCCATATT		
FWA JP2004 F	GGTTTTATATTAATATTAAGAGTTATGGGTYGAAGTTT	AT4G25530	E-TEL
FWA JP4423 R	AACCAAAATCATTCTCTAAACAAAATATAAAAAAATC	from johnson et al 2008	
BS_MRU1_F	TGGTTTGATGAATGGTTGGTAGATG	AT5G35490	R-TEL
BS_MRU1_R	CCATCAKCTAAATAATAACCCATAT		
BS_MRU1_inn_F	AATGGGGAGGGAAAATYAAATTG	AT5G35490	
BS_MRU1_inn_R	CCTTCAAAAACATTRATRTTATTACT		
BS_cop28_out_F	GTATATATATGGTTGTYGTTGTTA	AT3TE46565	R-TEL
BS_cop28_out_R	CCAATACTTTTRTAATCCAAAAACC		
BS_cop28_inn_F	GTTGTTAGTYATATGATATAAGAAG	AT3TE46565	
BS_cop28_inn_R	CATCTTAACATCARATRCCCATATC		
BSII_SDC_F_outer	GAAAAAGTTGGAATGGGYTTGGAGA	AT2G17690	R-TEL
BSII_SDC_R_outer	ATTRCCAAATCTTARARATCTCTT		
BSII_SDC_F_inner	TTYAAGATATATGATGAATTATTG	AT2G17690	
BSII_SDC_R_inner	ACTTATARRTACACATCAAACCCTA		

Primers for qPCR

Name	sequences 5' > 3'	T°	notes
AtPDF2_F	TAACGTGGCCAAAATGATGC	At1g13320	
AtPDF2_R	GTTCTCCACAACCGTTGGT	At1g13320	
AtGapDH_F	TGGTGACAACAGGTCCAAGCA	At1g13440	
AtGapDH_R	AACTTGTGCTCAATGCAATC	At1g13440	
AtSAND_F	AACTCTATGCAGCATTTGATCCACT	At2g28390	
AtSAND_R	TGATTGCATATCTTTATCGCCATC	At2g28390	
AtUBQ10	GGCCTTGATAATCCCTGATGAATAAG	At4g05320	
AtUBQ10	AAAGAGATAACAGGAACGGAAACATAGT	At4g05320	
FWA F	TCCCGGGCAAATTGTGGAGGC	AT4G25530	E-TEL
FWA R	CGTTGACCCATTTGCCTGTGTCCA	AT4G25530	FWA
qRT_SDC_F	AAGCCGCTCCAAATCATTCTC	AT2G17690	R-TEL
qRT_SDC_R	CGTGCCATGATACTTGCTCAA	AT2G17690	SDC
KELP_F	GCTCTCTTCGTCGAGGAATT	AT4G10920	R-TEL
KELP_R	CAAGGTTTCGTAACCTCGCTTCG	AT4G10921	KELP
QQS1_F	CCAGTTGGTGTGGTTCTTAGAT	AT3G30720	E-TEL
QQS1_R	TGGTTTGAAGCTTCTTCAACGT	AT3G30721	QQS

SQN_F	GACAAAGTCGCAGATCTTCACTAATAGT	AT2G15790	R-TEL
SQN_R	CAGTGTCCAACAACGCTCCTT	AT2G15790	SQN
ARNOLD2_F	TGTGGCATCAACTTTCGCAAAAT	AT1G04010	R-TEL
ARNOLD2_R	ACGGTTCCTTCCATTCATACCC	AT1G04010	ARNOLD2
qPCR_VANDAL8_F	GTTGATAGTTGGAGAACCCGTCT	AT5G28760	R-TEL
qPCR_VANDAL8_R	GAACGCACATCATGGTCAAACA	AT5G28760	VANDAL8
qPCR_copia28_F	ATTCCGAGTTGATGCAAGTCTCT	AT5G31122, AT3G30843	R-TEL
qPCR_copia28_R	GATCCAGGTGGGCGAGATAAAAT	AT5G31122, AT3G30844	COPIA28
qPCR_ROMANIAT5_F	GTAGAAGTTGGAAGCGCCTTTG	AT3G30844	R-TEL
qPCR_ROMANIAT5_R	TCCTACACTCAAGAGCTCGAGA	AT3G30844	ROMANIAT5
qPCR_VANDAL21_2_F	AGGTGAGTAGCTTAAGGGAGAGT	AT5G35792	E-TEL
qPCR_VANDAL21_2_R	CACGGTGGGCTTTCAATTCTTT	AT5G35792	VANDAL21
qPCR_VANDAL12_F	TAGTATCGTCGGCAAGGATTCG	AT4G18420	E-TEL
qPCR_VANDAL12_R	GAGTGCCAAAGAGATGTTGGTG	AT4G18420	VANDAL12
qPCR_SADHU_F	AATCTAGGGCCACAACCACATT	AT1G50735	E-TEL
qPCR_SADHU_R	AGTCTTCTCGCAAGTGATCCAG	AT1G50735	SADHU
qPCR_ATENSPM2_F	GGCGACAATATTCTCTTTGGCC	AT3G32226	R-TEL
qPCR_ATENSPM2_R	TGGCCAGGCACTAAAATAGTT	AT3G32226	ATENSPM2
ATL2_AT3G42993_F	CAATCCAGACAGACGTTCTCTGA	AT3TE61290	E-TEL
ATL2_AT3G42993_R	TCTGCAGAAGTTGAGCCATCAT	AT3TE61290	ATLANTYS2
qPCR_SPM10_F	ATTGATGAAGCTGAGGTGGTT	AT5G32136	R-TEL
qPCR_SPM10_R	TACGTCATCAGTGTAAAGCGA	AT5G32136	ATENSPM10
qPCR_Harbinger_F	TCACCTCTGCTACACCTTGTC	AT1G61510	R-TEL
qPCR_Harbinger_R	TCAAAGCAATGTTGGCAATGGT	AT1G61510	HARBINGER
qPCR_ATHILA_F	AATCCTCTATCGTGCATGTC	AT5G31855	R-TEL
qPCR_ATHILA_R	GCAAGCTTGATAAATGGGCGAT	AT5G31855	ATHILA
qPCR_HEL5_F	AGGTATCAAAGCGGCAACCTTA	AT5G32630	R-TEL
qPCR_HEL5_R	ATTTACATGCGGATTGTTGCA	AT5G32630	HELITRON5

#### Other primers for genotyping

Atmet1 F	TCCAAGGGCAGGCATGGCAC	AT5G49160
Atmet1 R	GCAGCAGTCGCCTGCAATGG	AT5G49160
FLAG R qPCR	CTAGGCCTTGTCATCGTCATCC	transgenic FLAG
met1 tr qPCR	CATTGGCATTGCTCTAGGTGCG	transgenic met1
MEF-1	GATTGTGTCTCTACTACAGAGGC	met1-3
TL-2	TGGACGTGAATGTAGACACGTCG	met1-3
METNR1	TGGGAAACATCATAGAAACATC	met1-3 locus
METNF1	TCAGATTGTGGCTATACTTGTG	met1-3 locus
met1-1F	CTCTTTAGTAGAAGTTGGCATG	met1-1
met1-1R	ATATGTATGTATAGATATTTTCTCC	met1-1
MET5line_F	GGTCGTGGATTGAAAAGCCC	met1-1 trasformed
MET5line_R	AGGCGGATGTTCACTTGGAA	met1-1 trasformed
MET1line_F	AGGGTGGTAGAACACATGTCAC	Col-0 trasformed
MET1line_R	CGTCAGTAAGTCGGCAATTGAC	Col-0 trasformed
LBa1	TGGTTCACGTAGTGGGCCATCG	

#### cloning and transformation

name	sequence
met1_BAH1_attB1	GGGGACAAGTTTGTAC AAA AAA GCA GGC TCA CCT CAT ACT CCT AAG AAA ATC
met1_BAH1_attB2	GGGGACCACTTTGTACAAGAAAGCTGGGT CTA TGG AAG ACT AAA GAA TCC
met1 adapF	tactgcagctcgaGAAAATGGTGGAAAATGGGGCT
met1 FLAG R	attgtcgaccgggCTAGGCCTTGTCATCGTCATCCTGTAGTCGGGTTGGTGTGAGGAGACT
Met1PR adap F	aagaattcggaagcttCCGAGACTGTGGAGATGGAGCGT
Met1PR adap R	attagatctcgagTTTCAAATCCCTAGTTTCAAATCAAATTACC