

Sequence type	Locus	Fragment length (bp)	^m CG		^m CCG		^m CAG		^m CTG					
			N° targets	% methylated*		N° targets	% methylated		N° targets	% methylated				
				Leaf	ACS		Leaf	ACS		Leaf	ACS			
Promoters	<i>TTG1</i>	213	16	2.1	92.2	8	0	0	1	0	0	0	0	0
	<i>GSTF5</i>	304	8	1.04	55.2	1	0	0	1	0	0	1	0	0
	<i>SUVH8</i>	371	9	3.70	56.5	7	0	0	4	0	0	7	0	0
Repeats	<i>CACTA1</i>	159	5	73.1	68.3	1	66.6	0	3	66.6	66.6	6	65.2	62.5
	<i>CACTA2</i>	170	8	90.0	83.3	2	33.3	18.8	3	38.8	33.3	7	64.3	37.1
	<i>CACTA3</i>	263	11	98.5	63.6	2	75.0	0	6	38.4	8.3	4	77.8	16.6

Table S5. Sequence context of the DNA methylation found in *Arabidopsis* cell suspensions and leaves. Data obtained from bisulfite sequencing of 12 individual clones per sequence and sample.