SUPPLEMENTARY INFORMATION

Molecular nature of the *kryptonite* alleles.

The *KYP* gene (4468 base pairs) was sequenced from each allele. *kyp-1* is a G to A mutation of the G nucleotide in bold in the following sequence where ^ represents the intron/exon boundary, TCGCCAACA**G**^AGAAGACTAA. *kyp-2* is a G to A mutation of a G nucleotide in the same context, TCAATTGTA**G**^GAGCTCACTT. *kyp-3* is a C to T mutation of the sequence **C**ATGGGAGTACAT. *kyp-1* and *kyp-2* are mutations of conserved G residues at the splice acceptor sites corresponding to the last nucleotide of the penultimate and last introns respectively. Sequencing of reverse transcription PCR products from *kyp-1* showed that two cryptic splice acceptor sites are utilized with roughly equal frequency, but no correctly spliced mRNA is produced. These cryptic splice sites reside either two or five nucleotides downstream of the authentic splice acceptor site. Both alternatively spliced products cause a frame shift and truncation of the protein after either nine or ten amino acids past the splice junction. Thus the *kyp-1* allele is lacking the C-terminal half of the SET domain including many of the most conserved residues (Fig. 1c). *kyp-3* is a missense mutation of serine 462 within the SET domain.

PCR based molecular markers used in this study.

Molecular markers used to genotype recombinants were derived from the database of polymorphisms between the Landsberg *erecta* and Colombia ecotypes generated by Cereon Genomics (http://www.arabidopsis.org/Cereon/index.html). The molecular marker on BAC clone sequence MXE10 was based on polymorphism CER457604 and was assayed with the oligonucleotide primers JP978: 5'-TTGACAGTTTTTCGTGGAGCGAGAA-3' and JP979: 5'-TTCAGCTAGAAATGGTTTGAATGTCAA-3'. The molecular marker on BAC clone sequence MUA22 was based on CER457257and was assayed with the oligonucleotide primers JP999: 5'-TTCCCCACTTTGTTTATAAGATT-3' and JP1000: 5'-TTCGTAGAGCAAAAGCTTCCTTTT-3'.

Primers used to PCR the *KYP* gene for sequencing of wild type and mutant alleles were JP1198: 5'-TAGCTTTTCCAGGTACGTCTGTCTCTCTA-3' and JP1199: 5'-AAATGTGAAGGGTTCTTCCACTTGGGAGAT-3'.

Molecular markers used to genotype the *kyp* mutations were composed of the following combinations of restriction enzymes and oligonucleotide primers: *kyp-1* (SfcI, JP 1243; 5'-TTTTTGAGGTATATCTCCTTGTTTTTCTTCGCCTACA-3', and JP 1244; 5'-CACAGATGAGTTTCTCTCAGTACCTGCA-3'), *kyp-2* (BglII, JP 1245; 5'-GCAGTGAAGATGAGAATGCGCCAGAGTTC-3', and JP 1246; 5'-CGCTATCAAGCGCATATCCATAGTCGTAAGTGAGATC-3') , and *kyp-3* (Sau3AI, JP1198: 5'-TAGCTTTTCCAGGTACGTCTGTCTCTCTA-3' and JP1199: 5'-AAATGTGAAGGGTTCTTCCACTTGGGAGAT-3').

Table 1. Number of cytosines methylated in different sequence contexts within 15 cloned PCR products of bisulfite treated DNA. Region encompasses 1028 nucleotides of the top strand of *SUPERMAN*, assembled from two overlapping PCR products.

	CpG	CpNpG*	Asym†
Total number of sites	135	405	3060
Number methylated			
Line *clk-st(*wild type*)*	22 (16%)	221 (55%)	497 (16%)#
kyp-1	8 (5.9%)	7 (1.7%)	58 (1.9%)
cmt3-7	12 (8.9%)	0 (0%)	175 (5.7%)#
met1	5 (3.7%)	206 (51%)	440 (14%)#

* CpGpG sites are counted as CpG sites and not included in the CpNpG category. †Asym (Asymmetric) is defined by cytosines within the context CpHpH, where H = A, T, or C. # Derived from previously published data [Lindroth, A. M. *et al.* Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. *Science* **292**, 2077-2080. (2001)].