Supplementary material to:

Stochastic changes affect *Solanum* wild species following autopolyploidization

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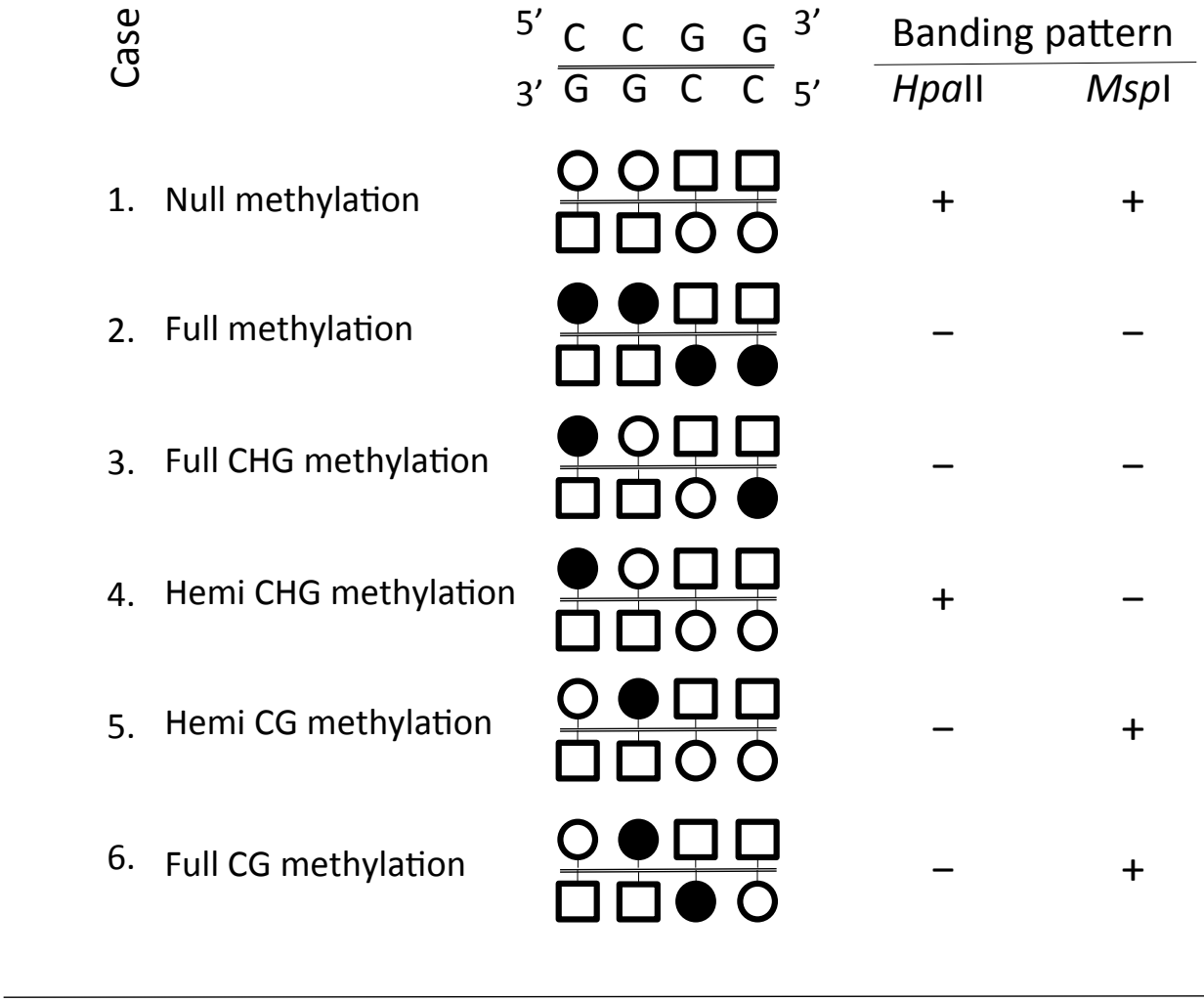
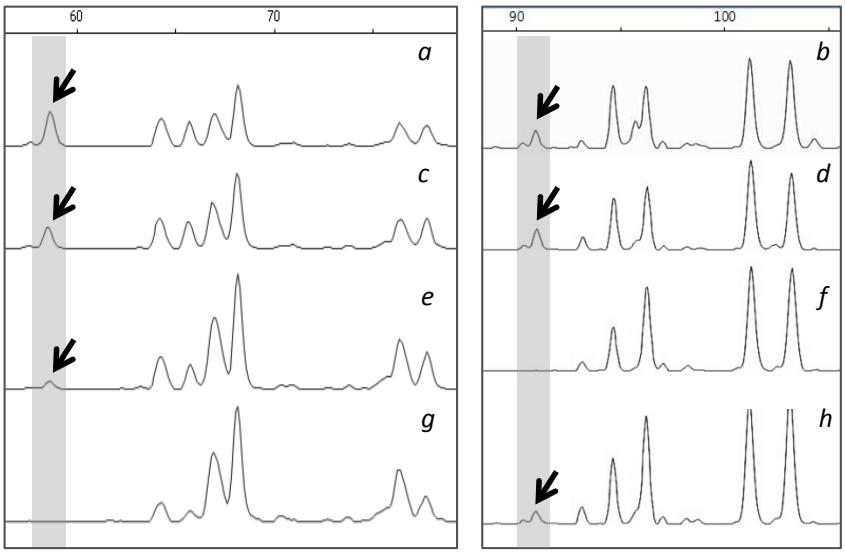


Supplementary Fig 1. Possible methylation states at 5'CCGG sites, and the corresponding banding patterns produced by the isoschizomers *Hpa*II and *Msp*I. Plus and minus signs denote the presence and absence of the bands at a given locus. *Hpa*II and *Msp*I are isoschizomers that recognize the same tetranucleotide sequence 5'-CCGG, but have differential sensitivity to certain methylation states of the two cytosines: *Hpa*II does not cut if either cytosine is fully (both strands) methylated. Whereas *Msp*I does not cut if the external cytosine is fully- or hemi- (only one strand) methylated. Thus, for a given DNA sample, unmethylation of cytosines at the 5′-CCGG site result in concomitant presence (+) of the bands for both *Hpa*II and *Msp*I (case 1). On the other hand, simultaneous full methylation of either all cytosines (case 2) or the external cytosines (marked as CHG, case 3) will be revealed as concomitant absence (−) of a band with both enzymes. Hemimethylation of the external or internal (marked as CG) cytosine (case 4 and 5), as well as full methylation of the internal cytosine (cases 6), is revealed by the presence of a band in only one of the enzyme digests.



Supplementary Fig 2. Examples of MSAP electropherograms on 2x and 4x genotypes of *S. commersonii* generated using *Hpa*II and *Msp*I isoschizomers, and primers E-TCAA/HM-AGC (*left panel*) and E-TCAA/HM-ACC (*right panel*). *a* and *b*) MSAP traces from cmm1t (2x) diploid parent generated using *Hpa*II; *c* and *d*) traces of cmm1t using *Msp*I; *e* and *f*) traces of the synthetic tetraploid cmm23 generated using *Hpa*II; *g* and *h*) traces of cmm23 using *Msp*I. Polymorphic peaks (arrowed in the grey area) show CHG hypermethylation (left panel) and CG hypermethylation (right panel) in cmm23 respect to its diploid progenitor cmm1t.