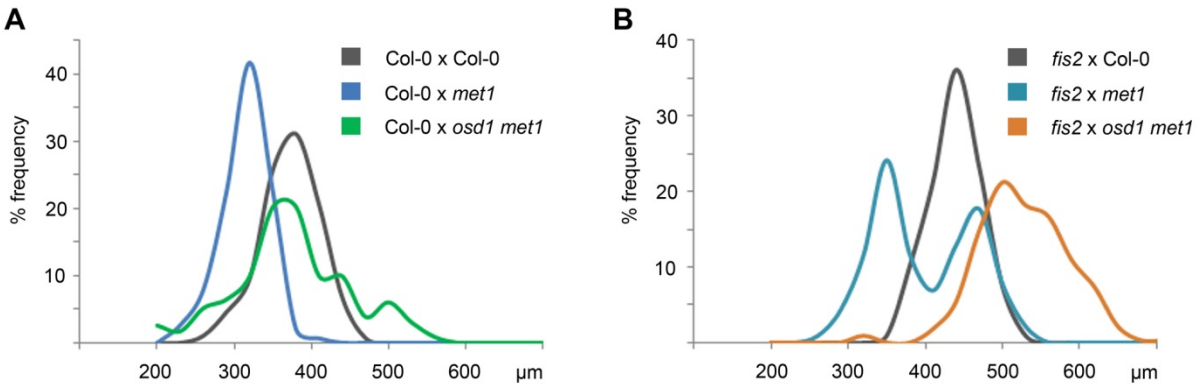
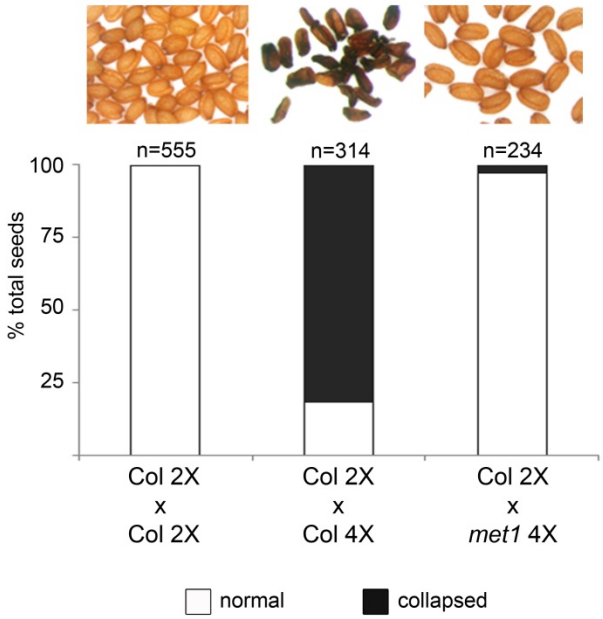
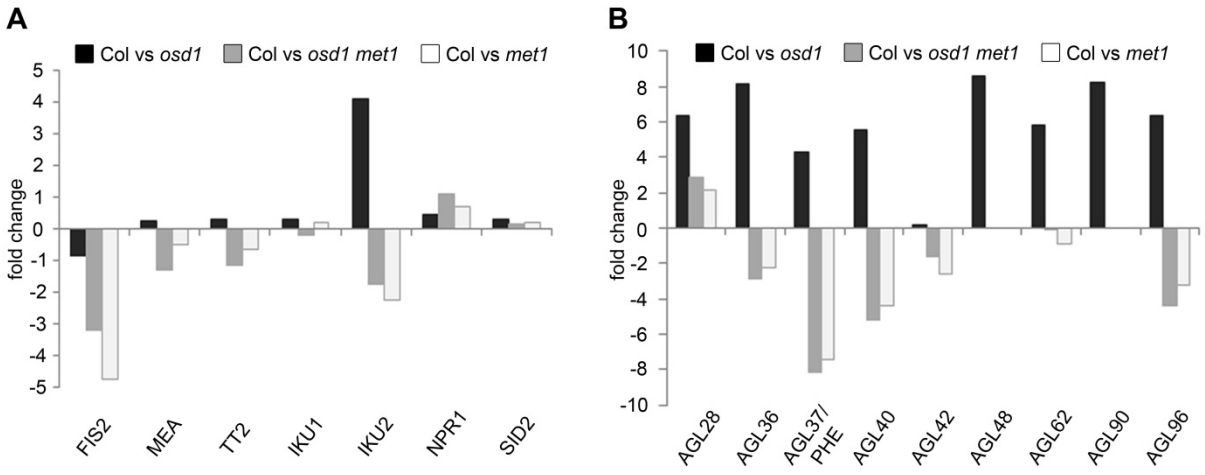


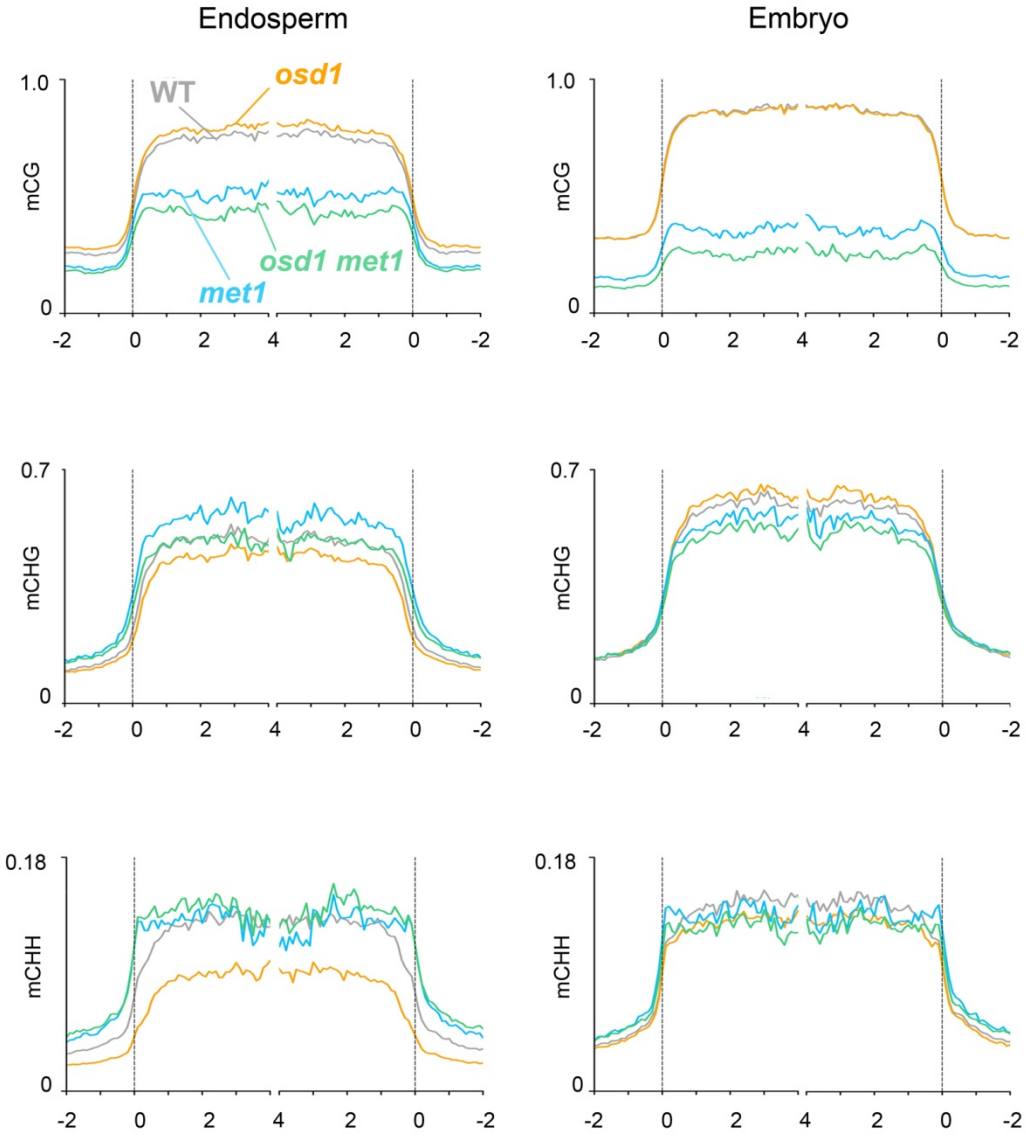
Supplemental Figure 1. Analysis of Seed Size from Indicated Crosses. Seed size was determined by measuring seed length using ImageJ for (A) Col x Col (n=283), Col x *met1* (n=151) and Col x *osd1 met1* (n=232) and (B) *fis2* x Col (n=108; this cross results in 50% seed abortion but only WT-like seeds were measured), *fis2* x *met1* (n=232) and *fis2* x *osd1 met1* (n=330).



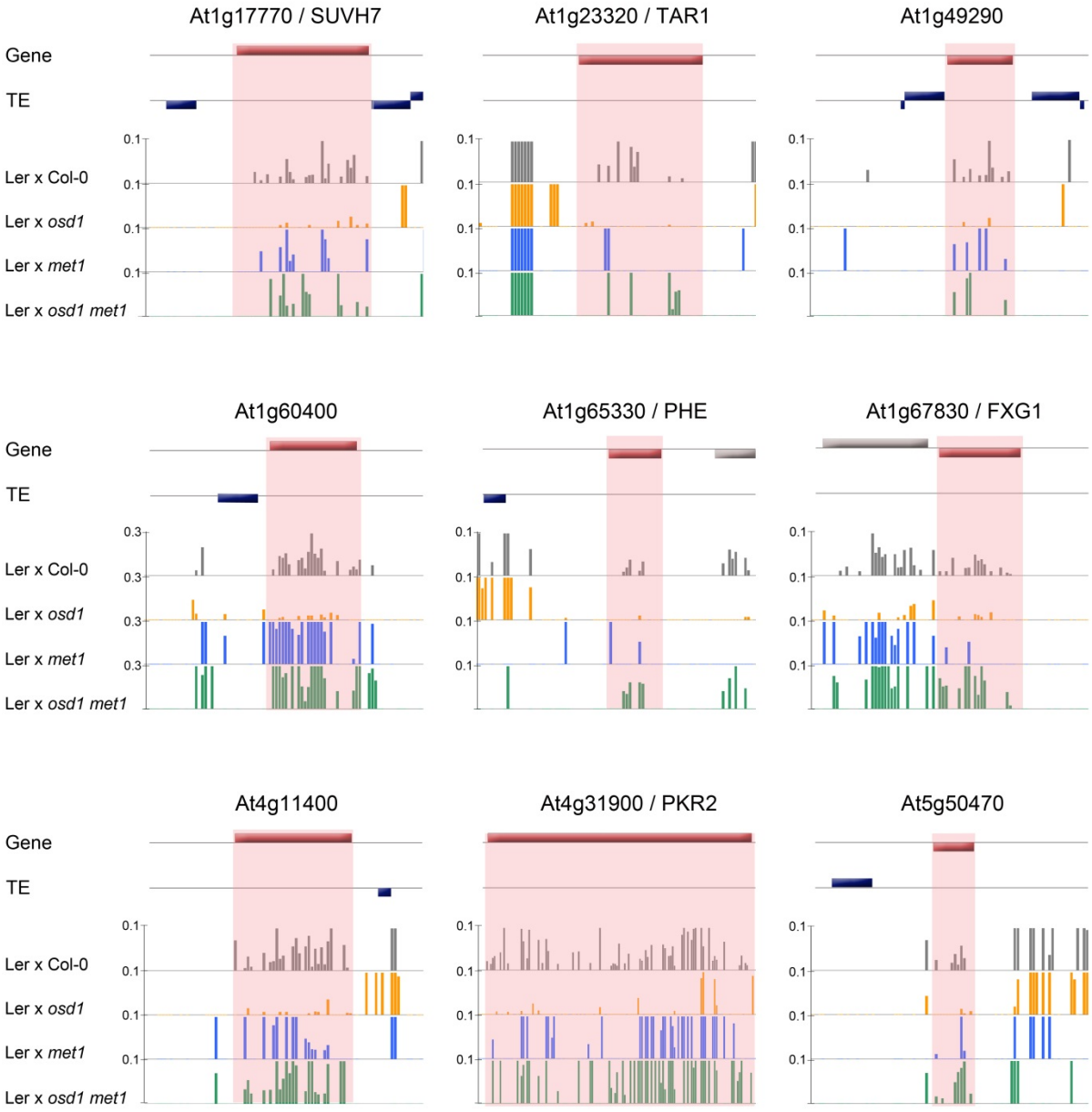
Supplemental Figure 2. Tetraploid *met1* can Bypass the Triploid Block. Percentage of collapsed seeds in Col 2X x Col 2X, Col 2X x Col 4X and Col 2X x *met1* 4X. Pictures of mature seeds correspond to genotypes displayed in bars below. n, numbers of total seeds analyzed.



Supplemental Figure 3. Fold Change Expression of Selected Genes in Triploid Seeds and Hypomethylated Diploid and Triploid Seeds. L*er* x Col versus L*er* x *osd1* (black bars), L*er* x Col versus L*er* x *osd1 met1* (gray bars), L*er* x Col vs L*er* x *met1* (white bars). Data were taken from whole genome transcriptome analysis (Supplemental Dataset 1).



Supplemental Figure 4. Methylation Profiles of Transposable Elements (TEs) in the Embryo and Endosperm after Pollination with Hypomethylated Pollen. The profiles are derived from seeds of the following crosses: L*er* x Col, L*er* x *osd1*, L*er* x *osd1 met1,* and L*er* x *met1*. TEs were aligned at the 5' and 3' ends (dashed lines) and average methylation levels in CG (top panels), CHG (middle panels) and CHH context (bottom panels) for each 100-bp interval were plotted.



Supplemental Figure 5. CHG Methylation Profiles of PEGs in the Endosperm. The profiles are derived from seeds of the following crosses: L*er* x Col (gray), L*er* x *osd1* (orange), L*er* x *met1* (blue) and Ler x *osd1 met1* (green). Red bars, gray bars and blue bars correspond to genes of interest, flanking genes and transposable elements, respectively. Sense and antisense oriented genes and transposable elements are on top or below the line, respectively. For simplicity, exon-intron structure is not shown.

Supplemental Table 1. Median Coverage per Cytosine and Mean DNA Methylation for Samples Analyzed in this Study. Chloroplast CHH methylation is a measure of cytosine non-conversion and other errors. M/P = Maternal to Paternal ratio. NA= not applicable. C^m=methylated cytosine.

Sample	**Median Coverage**	**Nuclear C^mG (%)**	**Nuclear C^mHG (%)**	**Nuclear C^mHH (%)**	**Chloro-plast C^mHH (%)**	**M/P ratio**	**Expect. M/P ratio**	**Seed coat (%)**
L*er* x Col endosperm	20	22	8.19	2.51	0.04	1.94	2	0
L*er* x Col embryo	29	24.88	9.83	2.9	0.04	0.83	1	NA
L*er* x *osd1* endosperm	39	21.41	6.89	1.55	0.04	1.22	1	10
L*er* x *osd1* embryo	36	25.51	10.71	2.73	0.04	0.66	0.5	NA
L*er* x *osd1 met1* endosperm	8	17.92	11.45	3.89	0.11	1.93	1	32
L*er* x *osd1 met1* embryo	12	9.78	10.95	3.48	0.11	0.57	0.5	NA
L*er* x Col *met1* endosperm	6	16.98	10.7	3.34	0.11	2.42	2	12
L*er* x *met1* embryo	8	12.31	10.1	3.4	0.11	0.96	1	NA
jason sperm cells 1n	10	34.06	14.68	1.71	0.41	NA	-	NA
jason sperm cells 2n	8	33.1	13.7	1.56	0.13	NA	-	NA

Supplemental Table 2. List of Primers Used in Quantitative RT-PCR.

Gene	**Primer sequence**
At1g11810	CAACAAGGTGTCGTGGAGAG CCAACTCTGTCTCTTGACCG
At1g17770	CGTAAACCATTGATTTACGAGTGC CCACAGTTTCTTGTCTTGAACAC
At1g34650	GGTCGTTCTAAGGTAACATGGA TCCTCTGAAGAGTAGCGGTC
At1g48910	TTGATCTTTGCAACTTCGGA CCATAGTCGTCACCAATGTG
At1g49290	GGAAGTGATAGAAGCGGTAGAG TAAACCTCGCACTCACAATCTC
At1g60400	CGAACGTTAGAGGTCATCCG GCAACAACCAAGAAAGACTGG
At1g66630	CATGGAGAATGTTGGAGGAACG ATTGTCACACTGATAGATAGGAGC
At1g67830	CTTCATAGCGGAGAGTCTTGG TTGACGTAGAGTAGAGTTAAGAGC
At2g36560	GATATCTGAGAGCGGAGGAG AATCACAACTTGGACTGGAC
At3g49770	GAGCCTGGTCATCAACTAAACC TAGAAGATCAGCACAGGAACG
At3g50720	TTTGTGAACCAGGGCAAGAG ATTCGAGACGAGTCTTTGAGTC
At3g62230	TTAAGAAAGTGGAGGTGTGGAG ATCGGAAGCAGTTGAATATCATCC
At4g05470	TTACCGATAGGAATCTGAGAAGTC TTTATACATGAGTGAGTGACCTCG
At4g10160	CGTCTGTGTGCCAATCTGTGTCAT GCTCAGTCCTAATTCAGCCGTTGAG
At4g11940 (ADM)	TTGAAAGAGTTTGCGGATGTG AGGACCAACATTATGGTCATACC
At4g31900	ATGCTGATAGAACAAGTCACTGG CATACATCACCTGCTTGCCG
At5g15140	GCTCAAGAAGGGAAATCTAACTG AAACCTTGTCGGTCTTGTAGG
At5g54350	CGCCTTTCCAAAGCTTTCCA CAAGAAGATGGACCAAGAGTGAG
Actin11	AACTTTCAACACTCCTGCCATG CTGCAAGGTCCAAACGCAGA
PHE1	TCCAACACCGAAAACTCCAT CGCATGTGCGGTCATCC

Supplemental Methods

Generation of Tetraploid *met1-9*

Tetraploid *met1-9* lines were generated by treating two-week old seedlings with 6 µl of either 0.125% or 0.25% colchicine (Sigma, Buchs, Switzerland). Treated plants were grown to maturity and scored for phenotypic alterations of flower and seed size. Seeds were harvested from plants showing enlarged flowers and increased seed size compared to wild type. Ploidy and karyotypes of putative tetraploid lines was confirmed as previously described (Bailey and Stace, 1992).

Supplemental References:

Bailey, J.P., and Stace, C.A. (1992). Chromosome-number, morphology, pairing, and DNA values of species and hybrids in the genus Fallopia (Polygonaceae). Plant Syst. Evol. **180,** 29-52.