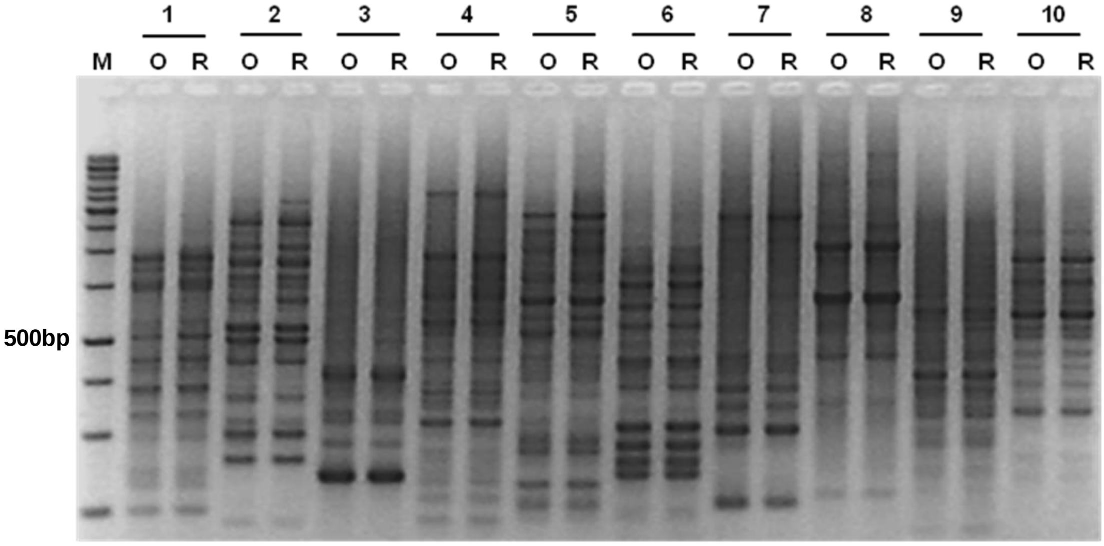

Figure S1 – RAPD-PCR amplification profiles of genomic DNA of: **(O)** cv. Onward and **(OR)** rogue paramutant line JI2723, with primers OPAL01 to OPAL10. **(M)** - 100 bp ladder marker. Notice the identical molecular patterns exhibited by the two epigenotypes.

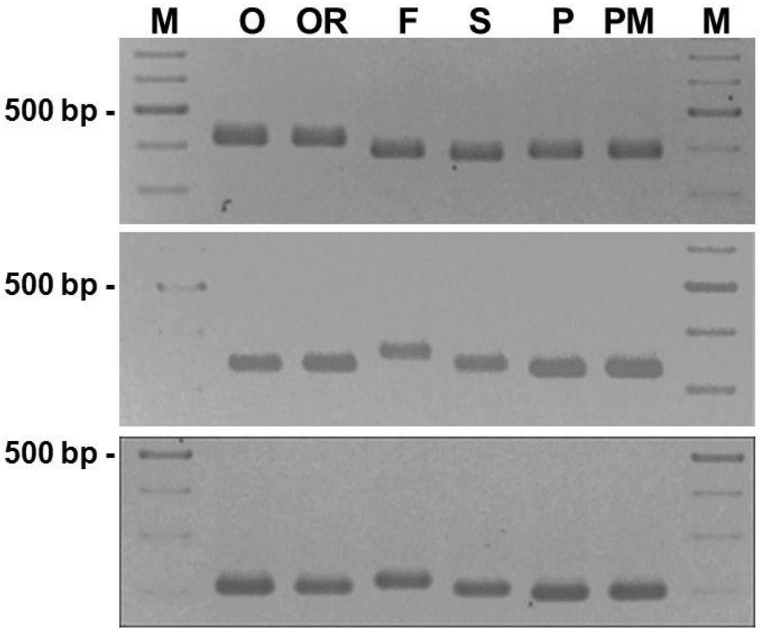

Figure S2 – SSR amplification profiles (markers: AD146, AB146, AC58) of: (**O**) cv. Onward; (**OR**) rogue paramutant line JI2723; (**F**) cv. Frilene; (**S**) cv. Solara; (**P**) cv. Progreta and (**PM**) Progreta mutant. **(M)** - 100 bp ladder marker. Notice the identical molecular patterns exhibited by the two epigenotypes

Table S1. MS-AFLP adapters

EcoRI- Adapter	5’-CTCGTAGACTGCGTACC-3’ 3’-CATCTGACGCATGGTTAA-5’
HpaII/MspI-Adapter	5’-GATCATGAGTCCTGCT 3’-AGTACTCAGGACGAGC-5’

Table S2. MS-AFLP primers

Name	**Sequence 5`-3`**	**Name**	**Sequence 5`-3`**
		Pre-amplification primers	
EcoRI + 0	GACTGCGTACCAATTC	HpaII/MspI + 0	ATCATGAGTCCTGCTCGG
		Selective primers	
E- AAC	GACTGCGTACCAATTCAAC	HM-AA	ATCATGAGTCCTGCTCGGAA
E-AAG	GACTGCGTACCA ATTCAAG	HM-AC	ATCATGAGTCCTGCTCGGAC
E-ACA	GACTGCGTACCAATTCACA	HM-AG	ATCATGAGTCCTGCTCGGAG
E-ACG	GACTGCGTACCAATTCACG	HM-AT	ATCATGAGTCCTGCTCGGAT
E-ACT	GACTGCGTACCAATTCACT	HM-CA	ATCATGAGTCCTGCTCGGCA
E-AGC	GACTGCGTACCAATTCAGC	HM-CC	ATCATGAGTCCTGCTCGGCC
E-AGG	GACTGCGTACCAATTCAGG	HM-CG	ATCATGAGTCCTGCTCGGCG
E-TA	GACTGCGTACCAATTCATA	HM-CT	ATCATGAGTCCTGCTCGGCT

Table S3. Tested MS-AFLP primer combinations.

	HM-AA	HM-AC	HM-AG	HM-AT	HM-CA	HM-CC	HM-CG	HM-CT
E-AAC	√	√	√	√	√	√	√	√
E-AAG	√	√	√	√	√	√	√	√
E-ACA	√	√	√	√	√	√	√	√
E-ACG	√	√	√	√	√	√	√	√
E-ACT	√	√	√	√	√	√	√	√
E-AGC	√	√	√	√	√	√	√	√
E-AGG	√	√	√	√	√	√	√	√
E-TA	√	√	√	√	√	√	√	√

TABLE S4. Genomic sequences differentially methylated in cv. Onward and paramutant line JI2723.

AAC/AA_174_R
GAATTCAACCGTGACTGGTTAAGTCTCACATTTGCTAGAAATGAAAGAAATGTTGGATATATAAGGGA
AAGAACTCATACACATTACGCACGTTGCCTTAAGGTTTTGGGTCAGACAGATATGTAGTGTCAAAGTC
TCTTGGTTCTTAAATGTTTAGTCTATTAAAATTTCCGG

AAC/AA_300_O
GAATTCAACGGTAGGAAAATTGCATGGAGAGTGAAGTATAGCGAGTGGTAGTAACACTGAGGCAAAAT
TGTTGGCGGAGATCGGGGCGAGTGTAGAAGACAGATCCAAGTTGGCAATTTTATAGTCAATTTTGGAT
ATTTTGGAGATATTTTTGGTCTATCTATCTCTCTCACGCTTTTCTCGTATCATCGTCGATTTTGATTA
GGTTAAGATTTCAGAGAGAGGGATGGGAAGAGAAGACAACGGAAAGTGGAAACAGGGATGGGGTTTAC
TACCCGACAAGACACTTTACTGTTCCGG

AAG/AA_197_R
GAATTCAAGTGAGTGGTTAGTCCCACATCGACTAAAATGAAGAAAATGTTGGATATACAATAGAGGTA
ACCCATATATCTAATGCTTTAAGGTTTTTGGTGAAAATATGGTGTAAAGGTCTCTTATAAAAAAAGTA
TTCCACCTTCCCTTTTGCCCCATGCTATTATTCTTAGTTATAGTTATGATGTCTTTTCCGG

AAG/AA_325_R
GAATTCAAGGTGGGAGCTCAACCAGGAAAGGAAAGGAAGCGAGAATTTGTAGACAACCCAAATGGTCT
ATTCTCCGCACAAGCATCACCAAAACCTCCACCAGCCATGTACACAATAGTTGAAGGAATGAGAGTCG
GAGGGAAGGTGATTGAAATACCCCCTCTTGATTTTGTTCTAGTGTGTATTATCTGATGTTTTTATTAG
CTATGATTCACGTGTCACTTCTTTTCTTATTCTTATTGTTCTCTTAAATGATGGTTGCAGCGAACTGT
GATTGTTCCTCCTGAAAAAGGGTATGCACAAAAGGGAATGAATGAGATTCCGG

AAG/AC_613_R
GAATTCAAGAGACTCGTCTATTGTCAAATTATTGCCACCTATGACGAGTGATTCAAGGTCTCTTAAAT
TTCCAAATGAGTTGGGTATAACTCCGCTAAATTCATTCGAACTCAAGTCAATTATGACGAGATTTGAG
GCATTGGATATGCTATTTGGAATATTTCCAACAAACCTATTTCCATACATGTGTAGTTGTTGTAGGTT
TGGAAGGCCTAATCCCATATTTGATGGAAGCATACCCGAGAGAGAATTTAGTTCAAGATGAAGATTTT
TCAATCTTGAAATGTTGAAGACATTTGAAGGAACATATCCACTCAAACTGTTATTTCCCAATTGAAGA
AACTGAAGTTGATTGAGATTGCCAATCTCCATAGGTATCAAACCTAAAATCACATATCATGAGATGAA
GCATGAGAGTAAAATGATGCATGAAATGCTTAACCAAAAGATGAAGATAGAAATTTGAGGATTTACCT
GAAAAAAAGTTATCCTGTAATGTTAATATTTGCAACAATGTGCAATTGCCAATCGATCGTGGAATGGT
TCCTTCCAAACGATTACCGAATAGAGTAAATTTTTCAAGTTGAGGAAGTTGAAGACACATCTCGTCCG
G

AAG/AG_366_O
GAATTCAAGGCATGAGTCCAAAGGTAATCAAATATCCCTTTTAAACTCGTAGCATCATCAATCCAAGC
ATTTCCTATCTGAATTTTTTTTAAATACAAGATAAGAAAGTTAGACATATATGATTGTGAGTCATATT
TCATCATCAGTGTTTGAAGTTTGAACAACATACGGAAATTCCTTTGAGGTTAATAATGATTTGGCTAT
AGAGTTTATTGTTGCGAAGAATAGTGGATGCAAGTTGAGGAACATAATGACCAGCATAACTCTCTCCA
GTCATGTAAAAATCTCTAGTTTTGTACTGTGGAAACCTCTCCAGCCAGTTGATGAGGAAGGCATAAGC
ATCCCTCGCAGTTGTCTTATCTCCGG

ACA/AA_749_R
GAATTCACACTAAGCATTCTTAGGACAGAGATTCGCACAACAAAATTCACAAAATTGTTTCACATTAT
ATTGTTCAATACTAATTTATTAAAGGTGTTCAGCATCAAAATATCAAGTAATATTGACACCTAAAATA
GTTCCTGACCTCCTGCTCAAGTTTAAACAGATGCCGATTAAAATGTTGTTGAAGCCTTTCATTGGCAT
AATTTATACAAAACTGTTCAAAGTTGTTCTTCTGAAAAAGAGAAGCAAGAAACTGTTAGAACATATAC
CATATTCTTTGAAGCATGAATATATCAATACAAATCGCCTACCTGGAATGACTGAAACCCATAAAAAT
CAAGGATACTAATGGATTTCTCTGTATGTTTTTCATTCACTTCAAGTGACTTGTCAAGTTGTTGTACA
AGCCATTCAAACAAGCTTGAATAAATAAATTTGGCAATTGCATCTCTTGTTCCAATGGCCTGGCATAG
AATGTGAAAAAGATAGATAAATAAATAAACAGCACACATATACACATATTGAATAAAGAGCATTTATA
ACCACGGAAAATACAAGAATGAAATGTTCGAATAATGAGCAGACCTGCAATAATGTCAAACTTTTGGA
AACAGTATCTTTGTCAGATTGGACTTTATGGGTAGATAATGCTGCCATTAAGTCCTGGGAACTGCAAC
CCATCAGCAGGCAGCACTGGTTACAGCTGCGAAAAAAAAAAATCACGTATTCTTCAAAATCATTTCCG
G

ACA/AG_560_O
GAATTCACAATCGAACCTTCAATCAGAAGTAATTCTTGGAGATGTCGTTGCAATCCACAACATATAAA
ACTGAACCGTGAAATTCGTTGGAACCAATCACCGAACCAATCATCCCGAATGAACCCCTCTTCTGTGG
ACTTCTCGCACCTCCTCTCGACCGCCTTGACTCCATAACAAAACTACTTTCTACCAATGACACAAAGC
CAACAACTATCAAACCATACACACGCCAGCAACAATATAGCAGGAACACCGCGATTGCATGAAAGATG
CACCAAGCTGCAAAACACAAAACGAAGCGCATCAACGGCGTATCAAATAAGATAAGCGCGAGCTCAAA
ACGAAAGCATGTACGAGCTAACCGAAATGCAGCTACCAGAAGGCATAAAAGGTAGTGAAACCGCACAA
GCTGCCCCATCTTTTCCTGCAGCAAACGCAACCATTGCACTAACTGGGCTCAACTCCAACCGGCAGAA
TCGCTTGCTCATTTAACTTCCTCCCTCGCATCTAACTGAACCTGCAAAAGAAGCTTAATATAATTCAA
TAATATGAATCTCCGG

ACA/AG_735_R
GAATTCACACATGCATCTATGTAGTCCGTCCACGTTCTCACACACGCATTGTTTTCCTCTCTCTAAAA
CTTGGTAATCCATGAAAAGCACAGAATTGACATTTGAGCTACAAAAAGTGAAATGATGAATTGAATTA
ATTGAAGGCGGTGGGATCCACGTTTGTGACATTCCACACATGGATAGAAGTTGTATCACAGTTAGATT
AAGCTGGAAATGTTTGGTAGCTAGTAACAACTCTCATCATCATACACAACCTTGCGTTACTTAGAATC
TAAATCTAAACTCTCTCTCCCTATTTAACCTCTCTCCTCCAACCAAACTCTTAACTCTCTCTTCACCT
CAATCTCTTCCGTTCTGAGATTGAGATATACATTGTATTGTATTATATAGAGGTATAAACAAATCAAC
ACAAGAATATGGGCACAAATATAGTTTTGGTGGTTGCTTTGATCTGCACTGTGTTTGCATTTGTAGGA
GCACAACAACCTCCAAGTCCAAACACCTCTCCAGCACCACCTACTCCTCCTGCTAATACTCCACCAAC
CACTCCTCAAGCTTCTCCTCCACCTGTTCAGTCTTCTCCTCCACCTGTCCAGTCTTCTTCTCCTCCAC
CTGCTCAATCTTCTCCACCTCCAGTTCAATCTTCTCCTCCACCTGCTCAATCTCCTCCACCAGTTCAA
TCTTCTCCTCCACCTGTATCCACTCCACCACCTGTTCCGGCTTCCCCTCCTCCGG

ACA/CT_546_O
GAATTCACATTTATTGGACCATATCCTAGTTAGTTAACGAAATCTTCACGTTTTCCCTCAATAACACA
CCACTCTTGTGTTGTTTTATAGCCAGTGGCAAATGCCAAATCATAACGCCTTTGGAAGGATAAGCTTT
GTTAGTATGACAGACATTTTGTTTTTTTTCCCCAATATAAGAAAGGGATTGAACCTACATAACATCAA
AGAGTAAACAACTTCTCTTTATCCTTAAAGAGTATTTTGATTTTTTTATATCAGTATTTTACTCGATA
GTTTAACCCTGAAATGTTTGTATGTTCTATTATTCATTTTGATCAATAAAATTACCAACAAAATACAC
AATTGAAGTTCTTTTAGTAATTTTAATATATTAAAAAAAATGTACAATTGTCTCGCCCATTTAAGATC
AAATCAAAATGTTATTTTAAGATAAGTTTTAAAATTGTGTATAGAACAATTGCGATACAATTATTACT
ACCATAACAATTTTTTCTTCCCAAATTTTAAAACCAGTGGTTAGAAAAATATAAGTTTTGTTGAAGCC
GG

ACG/CC_81_O
GAATTCACGGAACAAAAATAGAACTCGTCCATCGGATAAGGTGTTTGACTGGTTTGATACCTCATGTG
CGAAGAAGGCCGG

ACT/AC_451_R
GAATTCACTGTGGTTAAAGTAAAATCTCACAAGGTAGAAATGAAAATGAGAAATGGTCAGTAGTGAAC
AGCCTCGTTAAGTAAACCCTTTAAAAAGCTTTTGAAATTTGGAGTCATGCTATCAGGATATTTAACCG
GATCCTGGATTATTCAATTAGTGAATAGTCAATCCTTCAGTAAAATAACATAAGTGATTGTATAACAA
ATCTTGTCCGATTGAAAATGTACGTTAACAATGCGCCTGACGAGAGTATAAACATAATTTGTGTAAAA
TGGTGGTTGGCCTACAAATAACTCGTACCTGTTATAGGCATAAAAAAGCAGGCTTCAATTCAATGTGA
ATAACAAAGAACATTGAGAGTGTGAAAGCCATGTTTAAACAACACTTGCTACATAACTAATAGTTAGA
TAACGTCATCAATCAGAACACTTGCAAATTGCAACAGGTCCGG

ACT/AG_449_O
GAATTCACTAAACAGAAACAGAAAGAGAAGTAGATGAGAGAATTTCTAGGATAAATGAGGGAGTAAAT
GAAACTCACAAATTTTTGGGAGGAGAGAACTTCACTCTTCATCATTCATCATCGTGAATCCTTCAACA
AACAATTCGTGAAGAAAACGGATTCATCGCTTCAATCACGAATCTCATCACACTTCCAACACTTCACT
CTTCATCATCAACGGAAAATCAAAGAATCAACAGCAACGACGCAAACGCAACCCAATTCAGAATCGGA
CAACAACAACACATAGCACGCGCACAAACCTGAAGGCTTCATCTTCGTCTCAACGGAACGCACGGATC
CAAACGAAGTTGCATCTTCATCCTAATCAACCACGAGTGAAAGAGTACATCGAACGTTGAGGTGAGTT
TTCATTGAGTCGTGGATGCCATCGAGTGAATTTTTCTCCGG

ACT/CA_584_R
GAATTCACTGCAGTGATCAAAATAGATTTGAAATATTCACCCGAGAAATTCATGGTCTCGGAACCATT
GTCGAAACTTTTAGGGATTGAGGTCGAGAGTCGCCCGAGAATAATAGCTGCTCTTTGGCATTATGTGA
AGTCCAGGAGGCTACAATGTCCGGACGAGCCTTCCTTCTTCATCTGTGATCCTTCCCTCCAAAGGATT

TTCGGGGCAGAGAAGATGGGATTCCCCCTGGCTGCTCAGAAGTTGTTAGACCATTTGTCGCAACCAAAGCCTATATATTTGGAGCATAACATCAAGCTTTCTGGAGACTGTCCTGCTGGAACTGCATGTTACGACGTACAGGTTGACGTGCCTATACCACTGCAGAAAGAAATGTCTGGTTTTTTGGCTAGCAACAGCGTTGATAGTCACAAAGAGATTGAAGCTTCTGATGAGATTATTTCCTGTAACCTAAAGAAAATCCAAGAGCATCGTAGAAGACGTGCTTTCTTTCTTAGCTTTAGTCAGTCTCCATCAGAGTTTATCAACACTATGATTGCTTCTCGGAGCAAGGATCCAAAGCCTGCTGCTGGAGATGCCGG

AGC/AA_202_R

GAATTCAGCCTCTCAACAGCGATCGATGTCGGGTTCTTCTGCCGTGTTCTCGGGCTTTGTACACTCAAGCTTTCACTGACACTACTATTACTCCTATTGTCATATGGAGAATTTGAAGCCTGATCACTTGTAATATCTATTGATTCTTTGTATCTGTGCATTGCTTCAAGAATCTGTTTAAGGGCTCTAAGATCCTTTCCGG

AGC/AT_134_O

GAATTCAGCATTAAAAGATCAGTCTTCTCACTAGCTTTAGCTTGAAAAACAAATTTATGCAATTGCAATGCCAAGTACAAATCGCCAACACTTCCACAAGCCGATGTAACGCTAACCATGGTAATCCCATCCGG

AGC/AT_466_O

GAATTCAGCAACTATGAGTCGAATGACCTCCAGAATGTTATGAAAGTTATGCAGTACACATTTATGGGATTCTTTATCTGATGCCCATGATTATGCACGTGTGTAAGCCAATACTACAACTGCCGAAGAGTGAACCAAGAACTTGAACATGGCATTAGACACGCTGTTGTATGTGGTGACTTCGGCCAAAATCCTAATTCAATGTTATATTAATACTGGTCCAAAACTTAACTCAAACTACACCGCTGCCTGTTGTAACTGCGATAACAATGCCTTTACGGAAAAAGTTGCCTAGGTTTTTGGTTTTGTTAAGAAAGTAAAAACATCTGATAGAGTGAAAGAAGAAGTTGAAATTTTCATCGCAGCCTATCCATATTTCAATGTCAATGAAATGCTTGTTGAGAAGTTGTCTTGAATACTGAAAACAGATTATTTTTAATGGAGAACTCGACCGAATCAGATCCGG

AGG/AC_384_R

GAATTCAGGGTCAACAAGCAGGTGGTGAGTGACTTAAGATGAAGTTATGGGTTGCCATTTATAATCGTCATTTTCGGGTCATGAATGGAGAAGTTTCATTTGGACTGAGTTTAAGTGTTTATTTTTCGCATTGTGTGACTATAAGAAATAGACAGGTCTTTGTCTGCGGATTTCATGCATAACGTCATCTGGTGTGGGTATTAGCTTTGATTTATGATTTTTGAACCACAAGTTTCAATTTACAAACAAAGTTGTTTCAAATACATTAATAAAACCATACCACAAGACCGTTCATGACAACCCTGTGACTTAAGATACATTACAGTCAAGCCAAATTAAAGAAAGAGATTTCCAAAAATCTAACAGGCAACATGCCATGTCCGG

AGG/AG_705_R

GAATTCAGGGAAAGGTTTTCAATTTAGTTTTTTAATGATAAACTGATCTATGAGACTCTTGCTTGATTTTTTTTTACCCCGTGTCAAACTGGCTCTTGTTGAGATTGAGAATGAGATGACTCGGTGGCCTACTCGTGTATCTCTGTTTCTTACTTTCACTGCAGTTTGTACTGTATGCCGGCTTCTCTAGCTGTTTCTTGCTCCAGCATGCAATGTAAAAGCAGCAATCTTATGCTTGGCAATGTTACCGTGCAACAGACTAGTGGTGGTTGTAATGTGACTTCTTGCAGTTGTGATGGTCTTGTTAATGGCACCATAGCGACAATGTATGTTTCTCCTCTGCATTCACGTCTTTCTCTTTGGGACATTTCAATTATGTATATTTTACTGCACCGTTTCTGAGTTTATGCGCGTTGAATGTTTCTTTCCTCCCTGCAGGTTGACACCGTCTCTTCAGCCTCGATGCCCAGGTCAGTGTGCTGCAGCCATTATAATTTATGTATTTTCTGAGACGCCTTTGAAGTGCTAAATATATTTTAAATGATGCTGCAGGGACACAGGAATTTCCTCCTCTTATCGCCCCACCTACAACTGTTGCGAGAGAATCAGTATTTGCACCGGCACCGTCTCCATCATCGCTGTTAGATGGAACTGATGGGAGATCACCCAAATCCTCTGTGGTGCCTTCAACAGGATTTACTCCGG

AGG/AT_139_O

GAATTCAGGTTGAGTTGAAGGTGAGGTTTGGAACTGATTCACTGATCAAATGTAGTTGATGATTGTGATGGATGAAGGTGAGGGAATACGTGGGGGTGGAGCAATGACTGATGAAGGTTGAAGATTGATTGATATCCGG

AGG/AT_302_O

GAATTCAGGTGAGCGGTTAGTCCCACATCGACTAAAATGAAGAAAATGTTGGATATACAATAGAGGTAACCCATATATCTAATGCTTTAAGGTTTTTGGTGAAAATATGGTGTAAAGGTCTCTTATAAAAAAAGTATTCCACCTTCCCTTTTGCCCCATGCTATTATTCTTAGTTATAGTTATGATGTCTTTTCCGGCCCAAAAACTTGAGAATCTTTATACACATCTTTGTTTTGGTTATGCAATCTTATGATAGAAATTTCATTAAGTAAAACACTTTGGTAAACTTTTGTAGGATCCGG

TA/CA_260_R

GAATTCTATGGTTGTGGGGTTGATTAGGAATGGTGATTTGGAGGAAGCGAGAAAGGTTTTTGATGACACCCCTTTTAAAAATGTGGTGTCTTGGAATGCTATGATTGAGAGTTATGTTGAAAATGGTAGAATGGAGGAAGCAAGAGTTTTGTTTGATCAAATGGGGTTTAGGAATGTGATCACTTGGACTAGCATGATATCTGGGTATTGTCGTGTGGGTGATGTGGATGAGGCTTGTCGTTTGTTCTGGATTATGCCGG

Table S5 - Primers for confirmation of the differential methylation of the identified sequences.

Sequences	Primers (5'- 3')		Annealing temperature (ºC)	Expected Size (bp)
AAC/AA_174_R	F	GCGTACCAATTCAACCG	65	189
	R	GAGTCCTGCTCGGAAATT		
AAC/AA_300_O	F	TACCAATTCAACGGTAGGAA	63	304
	R	CTCGGAACAGTAAAGTGTC		
AAG/AA_197_R	F	GCGTACCAATTCAAGTGAG	61	211
	R	AGTCCTGCTCGGAAAAG		
AAG/AA_325_R	F	GCGTACCAATTCAAGGTG	60	337
	R	TCCTGCTCGGAATCTCA		
AAG/AC_613_R	F	TGCGTACCAATTCAAGAGAC	63	624
	R	CTGCTCGGACGAGATG		
AAG/AG_366_O	F	CGTACCAATTCAAGGCATG	65	378
	R	GTCCTGCTCGGAGATAAG		
ACA/AA_749_R	F	GCGTACCAATTCACACTAAG	65	762
	R	GTCCTGCTCGGAAATGA		
ACA/AG_735_R	F	GCGTACCAATTCACACATGC	65	749
	R	AGTCCTGCTCGGAGGAG		
ACA/CT_546_O	F	GACTGCGTACCAATTCACATT	67	561
	R	CCTGCTCGGCTTCAAC		
ACA/GA_560_O	F	CTGCGTACCAATTCACAATC	65	575
	R	GTCCTGCTCGGAGATTC		
ACG/CC_81_O	F	TGCGTACCAATTCACGGAAC	67	95
	R	GTCCTGCTCGGCCTTC		
ACT/AC_451_R	F	TGCGTACCAATTCACTGTGG	67	464
	R	TCCTGCTCGGACCTGT		
ACT/AG_449_O	F	GCGTACCAATTCACTAAACAG	66	460
	R	CCTGCTCGGAGAAAAATTC		
ACT/CA_584_R	F	CTGCGTACCAATTCACTGCA	69	599
	R	GTCCTGCTCGGCATCTC		
AGC/AA_202_R	F	CCAATTCAGCCTCTCAAC	64	206
	R	TGCTCGGAAAGGATCTTAG		
AGC/AT_134_O	F	ACTGCGTACCAATTCAGCATT	61	149
	R	TCCTGCTCGGATGGGA		
AGC/AT_466_O	F	CGTACCAATTCAGCAACT	63	476
	R	CCTGCTCGGATCTGATTC		
AGG/AC_384_R	F	GCGTACCAATTCAGGGTCA	68	397
	R	GTCCTGCTCGGACATGG		
AGG/AG_705_R	F	CGTACCAATTCAGGGAAAG	59	717
	R	GTCCTGCTCGGAGTAAA		
AGG/AT_139_O	F	CGTACCAATTCAGGTTGAG	63	151
	R	GTCCTGCTCGGATATCAA		
AGG/AT_302_O	F	CGTACCAATTCAGGTGAGC	65	312
	R	CCTGCTCGGATCCTACA		
TA/CA_260_R	F	TGCGTACCAATTCTATGGTT	65	273
	R	TCCTGCTCGGCATAATC		

TABLE S6. Methylation state of the 22 genomic sequences in leaves and pollen of cv. Onward and “rogue” line JI2723.

	ONWARD									ROGUE								
	LEAVES				POLLEN					LEAVES				POLLEN				
	CHG Full	CHG Hemi	CpG Yes	CpG No	CHG Full	CHG Hemi	CpG Yes	CpG No		CHG Full	CHG Hemi	CpG Yes	CpG No	CHG Full	CHG Hemi	CpG Yes	CpG No	
Sequences / Number	**5**	**6**	**8**	**3**	**5**	**2**	**6**	**9**	**L/P***	**5**	**5**	**3**	**9**	**2**	**4**	**7**	**9**	**L/P ***
AAC/AA_174_R**			**X**					**X**	N				**X**				**X**	Y
AAC/AA_300_O		**X**						**X**	N	**X**						**X**		N
AAG/AA_197_R			**X**		**X**				N				**X**	**X**				N
AAG/AA_325_R			**X**					**X**	N				**X**				**X**	Y
AAG/AC_613_R			**X**				**X**		**Y**				**X**				**X**	**Y**
AAG/AG_366_O				**X**				**X**	**Y**			**X**				**X**		**Y**
ACA/AA_749_R			**X**				**X**		**Y**				**X**				**X**	**Y**
ACA/AG_560_O		**X**				**X**			**Y**	**X**				**X**				**Y**
ACA/AG_735_R	**X**				**X**				**Y**		**X**				**X**			**Y**
ACA/CT_546_O				**X**				**X**	Y				**X**				**X**	N
ACG/CC_81_O		**X**						**X**	N	**X**						**X**		N
ACT/AC_451_R	**X**				**X**				**Y**		**X**				**X**			**Y**
ACT/AG_449_O				**X**				**X**	**Y**		**X**				**X**			**Y**
ACT/AC_584_R	**X**						**X**		N		**X**						**X**	N
AGC/AA_202_R			**X**				**X**		**Y**				**X**				**X**	**Y**
AGC/AT_134_O				**X**				**X**	**Y**			**X**				**X**		**Y**
AGC/AT_466_O		**X**				**X**			**Y**			**X**				**X**		**Y**
AGG/AC_384_R			**X**				**X**		**Y**				**X**				**X**	**Y**
AGG/AG_705_R	**X**				**X**				**Y**		**X**				**X**			**Y**
AGG/AT_139_O		**X**						**X**	N	**X**						**X**		Y
AGG/AT_302_O		**X**						**X**	N	**X**						**X**		Y
TA/CA_260_R			**X**				**X**		**Y**				**X**				**X**	Y

* L/P - Maintenance in pollen of the leaf methylation state. **Y** - Yes; **N** - No. ** Underlined sequences show altered but identical methylation patterns in the pollen DNA of both epigenomes.

Table S7. Expression analysis of the 22 differentially methylated sequences.

Sequence	Blast NCBI	Blast Unigenes	Putative expression	Expression	RT-PCR	Primers (5´-3´)	Expected size (bp)
AAC/AA_174_R	Medicago truncatula clone mth2-20l8, complete sequence	-	No	No	-	F TTCAACCGTGACTGGT R AACCAAGAGACTTTGACAC	141
AAC/AA_300_O	Predicted Cicer arietinum uncharacterized LOC101505144	-	Yes	Yes	No significant differences	F GAGTGTAGAAGACAGATCC R CGTGAGAGAGATAGATAGAC	87
AAG/AA_197_R	Medicago truncatula chromosome 2 clone mth2-4g10,	P. sativum v1 contig976	Yes	No	-	F CAAGTGAGTGGTTAGTCC R CCGGAAAAGACATCATAACT	192
AAG/AA_325_R	Predicted peptidyl-prolyl cis-trans isomerase FKBP18, [Cicer arietinum]	P.sativum wa1 _contig26417	Yes	Yes	No significant differences	F GAATTCAAGGTGGGAGC R TGTGTACATGGCTGGTG	114
AAG/AC_613_R	Predicted LRR serine/threonine-protein kinase FLS2-like [Cicer arietinum]	P. sativum wa1 contig28359	Yes	Yes	No significant differences	F CAAGAGACTCGTCTATTGTC R CGGAGTTATACCCAACTC	89
AAG/AG_366_O	Serine carboxypeptidase II-3 [Medicago truncatula]	-	Yes	Yes	No significant differences	F TAGTGGATGCAAGTTGAGG R TCATCAACTGGCTGGAG	102
ACA/AA_749_R	Predicted unconventional myosin-Va-like [Cicer arietinum]	P. sativum v2_ contig4504	Yes	Yes	No significant differences	F GCTCAAGTTTAAACAGATGC R AGAAGAACAACTTTGAACAG	87
ACA/AG_560_O	-	-	No	No	-	F GCAACCATTGCACTAAC R GGTTCAGTTAGATGCGA	83
ACA/AG_735_R	Medicago sativa proline-rich protein mRNA, complete cds	P. sativum v2 contig634	Yes	Yes	No significant differences	F GATCTGCACTGTGTTTGC R AGTGGTTGGTGGAGTATTAG	100
ACA/CT_546_O	-	-	No	No	-	F TGGACCATATCCTAGTTAGT R TTATCCTTCCAAAGGCG	117
ACG/CC_81_O	-	-	No	No	-	F GAATTCACGGAACAAAAATAG R CCTTCTTCGCACATGAG	77
ACT/AC_451_R	Predicted Cicer arietinum serine /threonine-protein kinase TIO-like	-	Yes	No	-	F TGGAGTCATGCTATCAGG R GTACGAGTTATTTGTAGGCC	107
ACT/AG_449_O	-	P. sativum wa1 contig29580	Yes	Yes	No significant differences	F TTCGTCTCAACGGAACG R ACTCACCTCAACGTTCG	92
ACT/CA_584_R	Chromatin remodeling complex subunit [Medicago truncatula]	-	Yes	Yes	No significant differences	F TTCACCCGAGAAATTCAT R CATAATGCCAAAGAGCAG	98
AGC/AA_202_R	Predicted protein LONGIFOLIA 1-like [Cicer arietinum]	-	Yes	Yes	No significant differences	F GAATTCAGCCTCTCAACA R TTACAAGTGATCAGGCTTC	133

AGC/AT_134_O	Predicted pentatricopeptide repeat-containing protein [Cicer arietinum]	-	Yes	Yes	No significant differences	F R	GAATTCAGCATTAAAAGATCAGTC CATGGTTAGCGTTACATCG	120
AGC/AT_466_O	Medicago truncatula hypothetical protein (MTR_5g027220) mRNA, complete cds	P. sativum wa1 contig22324	Yes	Yes	No significant differences	F R	TTCATCGCAGCCTATCC GGATCTGATTCGGTCGAG	109
AGG/AC_384_R	-	-	No	No	-	F R	TCAGGGTCAACAAGCAG GTTGTCATGAACGGTCTTG	296
AGG/AG_705_R	LysM domain-containing GPI-anchored protein [Medicago truncatula]	P. sativum wa1 contig21148	Yes	Yes	No significant differences	F R	GTGCAACAGACTAGTGG CTGATTCTCTCGCAACAG	166
AGG/AT_139_O	-	P. sativum wa1 contig22939	Yes	Yes	No significant differences	F R	GGTTTGGAACTGATTCAC TCAATCTTCAACCTTCATCA	104
AGG/AT_302_O	Medicago truncatula chromosome 5 clone mth2-57m18,	P. sativum v1 Contig976	Yes	No	-	F R	CGGTTAGTCCCACATCG GATCCTACAAAAGTTTACCAAAGTG	286
TA/CA_260_R	Pentatricopeptide repeat-containing protein [Medicago truncatula]	-	Yes	Yes	No significant differences	F R	GGTTGATTAGGAATGGTGA ACTCTCAATCATAGCATTCC	95