Appendix A DNA methylation-related (DMR) genes in *A. thaliana*

Gene name	*A. thaliana* gene	Function/comments	References
RNA-directed DNA methylation			
AGO4	*AT2G27040*	Combine with siRNAs, pair with POL V-transcribed scaffold RNAs	Duan *et al.* 2015
AGO6	*AT2G32940*		
CLSY1	*AT3G42670*	Interact with POL IV, to affect the production of siRNA	Smith *et al.* 2007
DCL2	*AT3G03300*	Process dsRNAs to siRNAs	Panda *et al.* 2020
DCL3	*AT3G43920*		
DCL4	*AT5G20320*		
DMS3	*AT3G49250*	Form DDR complex and recruit POL V	Wongpalee *et al.* 2019
DRD1	*AT2G16390*	Facilitate RNA-guided de novo methylation	Kanno *et al.* 2004
HEN1	*AT4G20910*	Recognize 21-24 nt small RNA duplexes and deposit a methyl group onto the 2' OH of the 3' terminal nucleotide	Yang *et al.* 2006
RDM1	*AT3G22680*	Bind single-stranded methylated DNA	Gao *et al.* 2010
RDM3	*AT5G04290*	Modulate the processivity of POL V	He *et al.* 2009
RDR2	*AT4G11130*	convert Pol IV transcripts into double-stranded RNAs	Blevins *et al.* 2015 Li S F *et al.* 2015
RDR6	*AT3G49500*	Collaboratively produce precursors of siRNAs	Nuthikattu *et al.* 2013
RRP6L1	*AT1G54440*	regulate DNA methylation by control the levels of scaffold RNAs and 24nt siRNAs	Zhang *et al.* 2014
SHH1	*AT1G15215*	Recruite POL IV to RdDM loci	Law *et al.* 2013
SUVH2	*AT2G33290*	Bind to methylated DNA, Facilitate the recruitment of Pol V to RdDM loci	Liu *et al.* 2014
SUVH9	*AT4G13460*		
Maintenance of DNA methylation			
CMT2	*AT4G19020*	Maintain CHG methylation	Lindroth *et al.* 2001
CMT3	*AT1G69770*		
DDM1	*AT5G66750*	Maintain DNA methylation in Symmetric cytosine sequence contexts	Zemach *et al.* 2013
DRM2	*AT5G14620*	Maintain CHH methylation	Naumann *et al.* 2011

MET1	*AT5G49160*	Maintain CG methylation	Kankel *et al.* 2003
SUVH4	*AT5G13960*	histone methylation, maintain non-CG methylation via *CMT3*	Ebbs *et al.* 2005
SUVH6	*AT2G22740*		Ebbs and Bender 2006
SUVH5	*AT2G35160*		Yu *et al.* 2017
Active DNA demethylation			
ACX4	*AT3G51840*	Suppress the DNA hypermethylation and silence of some endogenous loci	Wang *et al.* 2019
MFP2	*AT3G06860*		
KAT2	*AT2G33150*		
MET18	*AT5G48120*	Regulate the enzyme activity of *ROS1*	Duan *et al.* 2015
ROS3	*AT5G58130*	Bind RNA to regulate *ROS1*	Zheng *et al.* 2008
MBD9	*AT3G01460*	Form SWR1 complex and recruit *ROS1*	Nie *et al.* 2019
NPX1	*AT5G63320*		
PIE1	*AT3G12810*		
ARP6	*AT3G33520*		
IDM1	*AT3G14980*	Form a protein MBD7-IDM complex and regulate *ROS1* targeting	
IDM2	*AT1G54840*		Qian *et al.* 2014
IDM3	*AT1G20870*		Zhao *et al.* 2014
HDP1	*AT1G72270*		Li Q *et al.* 2015
HDP2	*AT4G31270*		Duan *et al.* 2017
MBD7	*AT5G59800*		
SSRP1	*AT3G28730*	Form FACT complex and involve in DME-mediated DNA demethylation	Ikeda *et al.* 2011
STP16	*AT4G10710*		Frost *et al.* 2018
APE1L	*AT3G48425*	Prevent DNA hypermethylation and control DNA demethylation	Li Y *et al.* 2015 Martínez-Macías *et al.* 2012
ZDP	*AT3G14890*		
LIG1	*AT1G08130*		
DME	*AT5G04560*	Facilitate DNA demethylation within heterochromatin	Zhang *et al.* 2019
ROS1	*AT2G36490*	DNA demethylase, make active DNA demethylate	Gong *et al.* 2002
DML2	*AT3G10010*		Penterman *et al.* 2007
DML3	*AT4G34060*		Ortega-Galisteo *et al.* 2008
DDB2	*AT5G58760*	Repress enzymatic activity of *ROS1*	Córdoba-Cañero *et al.* 2017

Appendix B DNA methylation-related (DMR) identified in *B. rapa*

Gene name	*A. thaliana* gene	Synteny orthologs			Non-synteny orthologs
		LF	MF1	MF2	
RNA-directed DNA methylation					
AGO4	*AT2G27040*	*BraA07g018470 (BrAGO4.1)*	*BraA04g020490 (BrAGO4.2)*	-	*BraA03g050880 (BrAGO4.4)*

AGO6	*AT2G32940*	-	-	*BraA03g017480 (BrAGO6.3)*	*BraA02g034110 (BrAGO6.4)* *BraA03g049920 (BrAGO6.5)*
CLSY1	*AT3G42670*	-	-	-	*BraA08g012750 (BrCLSY1.4)* *BraA08g012830 (BrCLSY1.5)* *BraA10g020220 (BrCLSY1.6)*
DCL2	*AT3G03300*	*BraA05g042700 (BrDCL2.1)*	-	-	-
DCL3	*AT3G43920*	-	-	*BraA06g023960 (BrDCL3.3)*	-
DCL4	*AT5G20320*	*BraA10g020300 (BrDCL4.1)*	-	-	-
DMS3	*AT3G49250*	*BraA06g018340 (BrDMS3.1)*	-	*BraA06g025840 (BrDMS3.3)*	-
DRD1	*AT2G16390*	-	-	*BraA03g043560 (BrDRD1.3)*	-
HEN1	*AT4G20910*	*BraA01g011550 (BrHEN1.1a)* *BraA01g011560 (BrHEN1.1b)*	-	-	-
RDM1	*AT3G22680*	*BraA05g025130 (BrRDM1.1)*	-	*BraA03g040940 (BrRDM1.3)*	-
RDM3	*AT5G04290*	*BraA10g032020 (BrRDM3.1)*	-	-	-
RDR2	*AT4G11130*	*BraA09g028070 (BrRDR2.1)*	-	-	-
RDR6	*AT3G49500*	-	*BraA01g023710 (BrRDR6.2)*	-	-
RRP6L1	*AT1G54440*	-	-	-	-
SHH1	*AT1G15215*	*BraA06g011300 (BrSHH1.1)*	-	-	-
SUVH2	*AT2G33290*	*BraA05g011580 (BrSUVH2.1)*	*BraA04g024900 (BrSUVH2.2)*	-	-
SUVH9	*AT4G13460*	-	-	-	-
Maintenance of DNA methylation					
CMT2	*AT4G19020*	*BraA01g010380 (BrCMT2.1)*	-	-	-
CMT3	*AT1G69770*	-	-	-	*BraA06g008110 (BrCMT3.4)*

DDM1	*AT5G66750*	*BraA07g017670 (BrDDM1.1a)* *BraA07g017680 (BrDDM1.1b)*	-	*BraA07g016780 (BrDDM1.3a)* *BraA09g009590 (BrDDM1.3b)*	-
DRM2	*AT5G14620*	*BraA10g024620 (BrDRM2.1)*	-	*BraA02g005700 (BrDRM2.3)*	*BraA01g022170 (BrDRM2.4)*
MET1	*AT5G49160*	*BraA06g035780 (BrMET1.1)*	-	-	*BraA09g055460 (BrMET1.4)*
SUVH4	*AT5G13960*	-	*BraA03g006140 (BrSUVH4.2)*	-	-
SUVH5	*AT2G35160*	*BraA05g009940 (BrSUVH5.1)*	-	-	-
SUVH6	*AT2G22740*	-	*BraA04g017620 (BrSUVH6.2)*	-	-
Active DNA demethylation					
ACX4	*AT3G51840*	*BraA09g044400 (BrACX4.1)*	*BraA04g008000 (BrACX4.2)*	-	*BraA03g061210 (BrACX4.4)* *BraA06g043720 (BrACX4.5)*
APE1L	*AT3G48425*	*BraA06g019080 (BrAPE1L.1)*	-	-	-
ARP6	*AT3G33520*	-	-	-	-
DDB2	*AT5G58760*	-	-	*BraA02g011610 (BrDDB2.3)*	-
DME	*AT5G04560*	-	-	-	-
DML2	*AT3G10010*	-	-	-	-
DML3	*AT4G34060*	*BraA01g004220 (BrDML3.1)*	-	-	-
HDP1	*AT1G72270*	-	-	-	*BraA01g017630 (BrHDP1.4)*
HDP2	*AT4G31270*	-	-	*BraA08g018010 (BrHDP2.3)*	-
IDM1	*AT3G14980*	*BraA05g032960 (BrIDM1.1)*	-	-	-
IDM2	*AT1G54840*	-	-	*BraA01g026760 (BrIDM2.3)*	-
IDM3	*AT1G20870*	*BraA06g016730 (BrIDM3.1)*	-	*BraA07g015860 (BrIDM3.3)*	-
KAT2	*AT2G33150*	*BraA05g011750 (BrKAT2.1)*	*BraA04g024780 (BrKAT2.2)*	*BraA03g017590 (BrKAT2.3)*	*BraA02g041370 (BrKAT2.4)*
LIG1	*AT1G08130*	*BraA06g005390 (BrLIG1.1)*	-	*BraA09g063970 (BrLIG1.3)*	-
MBD7	*AT5G59800*	*BraA10g017680 (BrMBD7.1)*	*BraA03g011150 (BrMBD7.2)*	*BraA02g010820 (BrMBD7.3)*	-

MBD9	*AT3G01460*	*BraA05g041480 (BrMBD9.1)*	*BraA01g045750 (BrMBD9.2)*	-	-
MET18	*AT5G48120*	-	*BraA02g040790 (BrMET18.2)*	-	-
MFP2	*AT3G06860*	*BraA05g039520 (BrMFP2.1)*	*BraA01g042640 (BrMFP2.2)*	*BraA03g033330 (BrMFP2.3)*	-
NPX1	*AT5G63320*	*BraA06g027770 (BrNPX1.1a)* *BraA06g027800 (BrNPX1.1b)*	-	*BraA09g007920 (BrNPX1.3)*	-
PIE1	*AT3G12810*	*BraA05g035100 (BrPIE1.1)*	-	-	-
ROS1	*AT2G36490*	*BraA05g008700 (BrROS1.1)*	-	-	-
ROS3	*AT5G58130*	*BraA10g016250 (BrROS3.1)*	-	-	-
SSRP1	*AT3G28730*	*BraA06g037940 (BrSSRP1.1)*	*BraA02g039580 (BrSSRP1.2)*	-	-
STP16	*AT4G10710*	-	-	-	*BraA03g027610 (BrSTP16.4)*
ZDP	*AT3G14890*	*BraA05g033020 (BrZDP.1)*	-	*BraA03g037130 (BrZDP.3)*	-

Appendix C DNA methylation-related (DMR) genes identified in *B. oleracea*

Gene name	*A. thaliana* gene	Synteny orthologs			Non-synteny orthologs
		LF	MF1	MF2	
RNA-directed DNA methylation					
AGO4	*AT2G27040*	*BolC04g023310 (BoAGO4.1)*	*BolC04g053880 (BoAGO4.2)*	-	*BolC02g011180 (BoAGO4.4)*
AGO6	*AT2G32940*	-	-	*BolC03g019600 (BoAGO6.3)*	-
CLSY1	*AT3G42670*	-	-	-	*BolC08g016260 (BoCLSY1.4)*
DCL2	*AT3G03300*	*BolC05g063440 (BoDCL2.1)*	-	-	-
DCL3	*AT3G43920*	-	-	*BolC03g062300 (BoDLC3.3)*	-
DCL4	*AT5G20320*	*BolC09g052100 (BoDCL4.1)*	-	-	-
DMS3	*AT3G49250*	*BolC08g033340 (BoDMS3.1)*	-	*BolC03g060110 (BoDMS3.3)*	-
DRD1	*AT2G16390*	-	-	*BolC03g051920 (BoDRD1.3)*	-

HEN1	*AT4G20910*	*BolC01g014120 (BoHEN1.1)*	-	*BolC03g076570 (BoHEN1.3a)* *BolC03g077490 (BoHEN1.3b)*	-
RDM1	*AT3G22680*	*BolC05g039660 (BoRDM1.1)*	-	*BolC03g048210 (BoRDM1.3)*	-
RDM3	*AT5G04290*	*BolC09g067750 (BoRDM3.1)*	-	-	-
RDR2	*AT4G11130*	*BolC09g032400 (BoRDR2.1)*	-	-	-
RDR6	*AT3G49500*	-	*BolC01g029390 (BoRDR6.2)*	-	*BolC04g034910 (BoRDR6.4)*
RRP6L1	*AT1G54440*	-	-	-	-
SHH1	*AT1G15215*	*BolC05g012860 (BoSHH1.1)*	-	-	-
SUVH2	*AT2G33290*	*BolC04g015770 (BoSUVH2.1)*	*BolC04g059170 (BoSUVH2.2)*	-	-
SUVH9	*AT4G13460*	-	-	-	*BolC08g038030 (BoSUVH9.4)*
Maintenance of DNA methylation					
CMT2	*AT4G19020*	*BolC01g012760 (BoCMT2.1)*	-	-	-
CMT3	*AT1G69770*	-	-	-	-
DDM1	*AT5G66750*	*BolC07g024230 (BoDDM1.1)*	-	*BolC07g023070 (BoDDM1.3a)* *BolC09g010670 (BoDDM1.3b)*	-
DRM2	*AT5G14620*	*BolC09g058530 (BoDRM2.1)*	-	*BolC02g006470 (BoDRM2.3)*	-
MET1	*AT5G49160*	*BolC07g038530 (BoMET1.1)*	-	-	*BolC04g050370 (BoMET1.4)* *BolC08g048090 (BoMET1.5)*
SUVH4	*AT5G13960*	-	*BolC03g006730 (BoSUVH4.2)*	-	-
SUVH5	*AT2G35160*	*BolC04g013820 (BoSUVH5.1)*	-	-	-
SUVH6	*AT2G22740*	-	*BolC04g050140 (BoSUVH6.2)*	-	-
Active DNA demethylation					
ACX4	*AT3G51840*	*BolC08g036070 (BoACX4.1)*	*BolC04g040480 (BoACX4.2)*	-	-
APE1L	*AT3G48425*	*BolC08g032520 (BoAPE1L.1)*	-	-	-

ARP6	*AT3G33520*	-	-	-	-
DDB2	*AT5G58760*	-	-	*BolC02g014020 (BoDDB2.3)*	-
DME	*AT5G04560*	*BolC09g067440 (BoDME.1)*	-	-	-
DML2	*AT3G10010*	-	-	-	-
DML3	*AT4G34060*	*BolC01g004810 (BoDML3.1)*	-	-	-
HDP1	*AT1G72270*	-	*BolC02g029210 (BoHDP1.2)*	-	-
HDP2	*AT4G31270*	-	-	*BolC03g081780 (BoHDP2.3)*	-
IDM1	*AT3G14980*	*BolC05g051290 (BoIDM1.1)*	-	-	-
IDM2	*AT1G54840*	-	-	*BolC01g033310 (BoIDM2.3)*	-
IDM3	*AT1G20870*	*BolC05g018830 (BoIDM3.1)*	-	*BolC07g022000 (BoIDM3.3)*	-
KAT2	*AT2G33150*	*BolC04g016040 (BoKAT2.1)*	*BolC04g059060 (BoKAT2.2)*	*BolC03g019710 (BoKAT2.3)*	*BolC02g055850 (BoKAT2.4)* *BolC08g001400 (BoKAT2.5)*
LIG1	*AT1G08130*	*BolC05g006060 (BoLIGI.1)*	-	*BolC08g057260 (BoLIGI.3)*	-
MBD7	*AT5G59800*	*BolC09g049020 (BoMBD7.1)*	*BolC03g012300 (BoMBD7.2)*	*BolC02g013030 (BoMBD7.3)*	-
MBD9	*AT3G01460*	*BolC05g062180 (BoMBD9.1)*	*BolC01g057530 (BoMBD9.1)*	-	-
MET18	*AT5G48120*	-	*BolC02g055250 (BoMET18.2)*	-	-
MFP2	*AT3G06860*	*BolC05g058870 (BoMFP2.1)*	*BolC01g054030 (BoMFP2.2)*	*BolC03g038630 (BoMFP2.3)*	-
NPX1	*AT5G63320*	*BolC03g057700 (BoNPX1.1)*	-	*BolC09g008640 (BoNPX1.3)*	-
PIE1	*AT3G12810*	*BolC05g053870 (BoPIE1.1)*	*BolC01g050110 (BoPIE1.2)*	-	-
ROS1	*AT2G36490*	*BolC04g012450 (BoROS1.1)*	-	-	-
ROS3	*AT5G58130*	*BolC09g046640 (BoROS3.1)*	*BolC03g013430 (BoROS3.2)*	*BolC02g014470 (BoROS3.3)*	-
SSRP1	*AT3G28730*	*BolC07g036180 (BoSSRP1.1)*	*BolC02g054050 (BoSSRP1.2)*	-	-
STP16	*AT4G10710*	-	-	-	*BolC03g031980 (BoSTP16.4)*

ZDP	*AT3G14890*	*BolC05g051360* *(BoZDP.1)*	-	*BolC03g043490* *(BoZDP.3)*	-

Appendix E Syntenic relationship of DNA methylation-related (DMR) genes in *A. thaliana*, *B. rapa*, and *B. oleracea*

Gene name	*A. thaliana* gene	*B. rapa* gene	*B. oleracea* gene
RNA-directed DNA methylation			
AGO4	*AT2G27040*	*BraA07g018470*	*BolC04g023310*
	AT2G27040	*BraA04g020490*	*BolC04g053880*
AGO6	*AT2G32940*	*BraA03g017480*	*BolC03g019600*
DCL2	*AT3G03300*	*BraA05g042700*	*BolC05g063440*
DCL3	*AT3G43920*	*BraA06g023960*	*BolC03g062300*
DCL4	*AT5G20320*	*BraA10g020300*	*BolC09g052100*
DMS3	*AT3G49250*	*BraA06g018340*	*BolC08g033340*
	AT3G49250	*BraA06g025840*	*BolC03g060110*
DRD1	*AT2G16390*	*BraA03g043560*	*BolC03g051920*
HEN1	*AT4G20910*	*BraA01g011550*	*BolC01g014120*
	AT4G20910	*BraA01g011560*	*BolC01g014120*
	AT4G20910		*BolC03g076570*
	AT4G20910		*BolC03g077490*
RDM1	*AT3G22680*	*BraA05g025130*	*BolC05g039660*
	AT3G22680	*BraA03g040940*	*BolC03g048210*
RDM3	*AT5G04290*	*BraA10g032020*	*BolC09g067750*
RDR2	*AT4G11130*	*BraA09g028070*	*BolC09g032400*
RDR6	*AT3G49500*	*BraA01g023710*	*BolC01g029390*
SHH1	*AT1G15215*	*BraA06g011300*	*BolC05g012860*
SUVH2	*AT2G33290*	*BraA05g011580*	*BolC04g015770*
	AT2G33290	*BraA04g024900*	*BolC04g059170*
Maintenance of DNA methylation			
CMT2	*AT4G19020*	*BraA01g010380*	*BolC01g012760*
DDM1	*AT5G66750*	*BraA07g017670*	*BolC07g024230*
		BraA07g017680	*BolC07g024230*
		BraA07g016780	*BolC07g023070*
		BraA09g009590	*BolC09g010670*
DRM2	*AT5G14620*	*BraA10g024620*	*BolC09g058530*
		BraA02g005700	*BolC02g006470*
MET1	*AT5G49160*	*BraA06g035780*	*BolC07g038530*
SUVH4	*AT5G13960*	*BraA03g006140*	*BolC03g006730*
SUVH5	*AT2G35160*	*BraA05g009940*	*BolC04g013820*
SUVH6	*AT2G22740*	*BraA04g017620*	*BolC04g050140*
Active DNA demethylation			
ACX4	*AT3G51840*	*BraA09g044400*	*BolC08g036070*
		BraA04g008000	*BolC04g040480*
APE1L	*AT3G48425*	*BraA06g019080*	*BolC08g032520*

DDB2	*AT5G58760*	*BraA02g011610*	*BolC02g014020*
DME	*AT5G04560*		*BolC09g067440*
DML3	*AT4G34060*	*BraA01g004220*	*BolC01g004810*
HDP1	*AT1G72270*		*BolC02g029210*
HDP2	*AT4G31270*	*BraA08g018010*	*BolC03g081780*
IDM1	*AT3G14980*	*BraA05g032960*	*BolC05g051290*
IDM2	*AT1G54840*	*BraA01g026760*	*BolC01g033310*
IDM3	*AT1G20870*	*BraA06g016730*	*BolC05g018830*
	AT1G20870	*BraA07g015860*	*BolC07g022000*
KAT2	*AT2G33150*	*BraA05g011750*	*BolC04g016040*
	AT2G33150	*BraA04g024780*	*BolC04g059060*
	AT2G33150	*BraA03g017590*	*BolC03g019710*
LIG1	*AT1G08130*	*BraA06g005390*	*BolC05g006060*
	AT1G08130	*BraA09g063970*	*BolC08g057260*
MBD7	*AT5G59800*	*BraA10g017680*	*BolC09g049020*
	AT5G59800	*BraA03g011150*	*BolC03g012300*
	AT5G59800	*BraA02g010820*	*BolC02g013030*
MBD9	*AT3G01460*	*BraA05g041480*	*BolC05g062180*
	AT3G01460	*BraA01g045750*	*BolC01g057530*
MET18	*AT5G48120*	*BraA02g040790*	*BolC02g055250*
MFP2	*AT3G06860*	*BraA05g039520*	*BolC05g058870*
		BraA01g042640	*BolC01g054030*
		BraA03g033330	*BolC03g038630*
NPX1	*AT5G63320*	*BraA06g027770*	*BolC03g057700*
		BraA06g027800	*BolC03g057700*
		BraA09g007920	*BolC09g008640*
PIE1	*AT3G12810*	*BraA05g035100*	*BolC05g053870*
	AT3G12810		*BolC01g050110*
ROS1	*AT2G36490*	*BraA05g008700*	*BolC04g012450*
ROS3	*AT5G58130*	*BraA10g016250*	*BolC09g046640*
	AT5G58130		*BolC03g013430*
	AT5G58130		*BolC02g014470*
SSRP1	*AT3G28730*	*BraA06g037940*	*BolC07g036180*
	AT3G28730	*BraA02g039580*	*BolC02g054050*
ZDP	*AT3G14890*	*BraA05g033020*	*BolC05g051360*
	AT3G14890	*BraA03g037130*	*BolC03g043490*

Appendix F Number of DNA methylation-related (DMR) gene domains in *A. thaliana*, *B. rapa*, and *B. oleracea*

Gene name	Number of domains	Gene name	Number of domains	Gene name	Number of domains
RNA-directed DNA methylation					
AGO4	6	*BrAGO4.1*	6	*BoAGO4.1*	6
		BrAGO4.2	6	*BoAGO4.2*	6

		BrAGO4.3	0	-	-
		-	-	*BoAGO4.4*	5
AGO6	5	*BrAGO6.3*	5	*BoAGO6.3*	5
		BrAGO6.4	1	-	-
		BrAGO6.5	1	-	-
CLSY1	3	*BrCLSY1.4*	4	*BoCLSY1.4*	3
		BrCLSY1.5	1	-	-
		BrCLSY1.6	3	-	-
DCL2	8	*BrDCL2.1*	8	*BoDCL2.1*	6
DCL3	7	*BrDCL3.3*	5	*BoDCL3.3*	5
DCL4	10	*BrDCL4.1*	10	*BoDCL4.1*	10
DMS3	0	*BrDMS3.1*	0	*BoDMS3.1*	0
		BrDMS3.3	0	*BoDMS3.3*	0
DRD1	3	*BrDRD1.3*	5	*BoDRD1.3*	3
HEN1	5	*BrHEN1.1a*	0	*BoHEN1.1*	4
		BrHEN1.1b	2	-	-
		-	-	*BoHEN1.3a*	0
		-	-	*BoHEN1.3b*	0
RDM1	2	*BrRDM1.1*	1	*BoRDM1.1*	1
		BrRDM1.3	1	*BoRDM1.3*	1
RDM3	1	*BrRDM3.1*	1	*BoRDM3.1*	1
RDR2	1	*BrRDR2.1*	1	*BoRDR2.1*	1
RDR6	1	*BrRDR6.2*	1	*BoRDR6.2*	1
		-	-	*BoRDR6.4*	1
RRP6L1	2	-	-	-	-
SHH1	1	*BrSHH1.1*	1	*BoSHH1.1*	1
SUVH2	3	*BrSUVH2.1*	3	*BoSUVH2.1*	3
		BrSUVH2.2	3	*BoSUVH2.2*	3
SUVH9	3	-	-	*BoSUVH9.4*	3
Maintenance of DNA methylation					
CMT2	3	*BrCMT2.1*	3	*BoCMT2.1*	3
CMT3	3	*BrCMT3.4*	3	-	-
DDM1	3	*BrDDM1.1a*	1	*BoDDM1.1*	3
		BrDDM1.1b	2	-	-
		BrDDM1.3a	2	*BoDDM1.3a*	2
		BrDDM1.3b	5	*BoDDM1.3b*	3
DRM2	1	*BrDRM2.1*	1	*BoDRM2.1*	1
		BrDRM2.3	1	*BoDRM2.3*	2
		BrDRM2.4	3	-	-
MET1	8	*BrMET1.1*	5	*BoMET1.1*	5
		BrMET1.4	6	*BoMET1.4*	5
		-	-	*BoMET1.5*	6
SUVH4	3	*BrSUVH4.2*	3	*BoSUVH4.2*	3
SUVH5	3	*BrSUVH5.1*	3	*BoSUVH5.1*	3

SUVH6	3	*BrSUVH6.2*	3	*BoSUVH6.2*	3
Active DNA demethylation					
ACX4	3	*BrACX4.1*	3	*BoACX4.1*	3
		BrACX4.2	3	*BoACX4.2*	3
		BrACX4.4	1	-	-
		BrACX4.5	1	-	-
APE1L	1	*BrAPE1L.1*	1	*BoAPE1L.1*	1
ARP6	1	-	-	-	-
DDB2	2	*BrDDB2.3*	2	*BoDDB2.3*	2
DME	6	-	-	*BoDME.1*	2
DML2	2	-	-	-	-
DML3	2	*BrDML3.1*	2	*BoDML3.1*	2
HDP1	2	-	-	*BoHDP1.2*	0
		BrHDP1.4	2	-	-
HDP2	1	*BrHDP2.3*	1	*BoHDP2.3*	1
IDM1	2	*BrIDM1.1*	2	*BoIDM1.1*	2
IDM2	0	*BrIDM2.3*	1	*BoIDM2.3*	0
IDM3	0	*BrIDM3.1*	0	*BoIDM3.1*	0
		BrIDM3.3	0	*BoIDM3.3*	0
KAT2	2	*BrKAT2.1*	2	*BoKAT2.1*	2
		BrKAT2.2	2	*BoKAT2.2*	2
		BrKAT2.3	2	*BoKAT2.3*	2
		BrKAT2.4	2	*BoKAT2.4*	3
		-	-	*BoKAT2.5*	2
LIG1	4	*BrLIG1.1*	3	*BoLIG1.1*	3
		BrLIG1.3	3	*BoLIGI.3*	3
MBD7	2	*BrMBD7.1*	2	*BoMBD7.1*	3
		BrMBD7.2	2	*BoMBD7.2*	2
		BrMBD7.3	1	*BoMBD7.3*	0
MBD9	7	*BrMBD9.1*	4	*BoMBD9.1*	6
		BrMBD9.2	6	*BoMBD9.2*	6
MET18	2	*BrMET18.2*	2	*BoMET18.2*	2
MFP2	4	*BrMFP2.1*	4	*BoMFP2.1*	4
		BrMFP2.2	4	*BoMFP2.2*	4
		BrMFP2.3	4	*BoMFP2.3*	4
NPX1	2	*BrNPX1.1a*	0	*BoNPX1.1*	2
		BrNPX1.1b	2	-	-
		BrNPX1.3	3	*BoNPX1.3*	2
PIE1	5	*BrPIE1.1*	5	*BoPIE1.1*	5
		-	-	*BoPIE1.2*	0
ROS1	2	*BrROS1.1*	2	*BoROS1.1*	3
ROS3	0	*BrROS3.1*	0	*BoROS3.1*	1
		-	-	*BoROS3.2*	0
		-	-	*BoROS3.3*	0

SSRP1	5	*BrSSRP1.1*	5	*BoSSRP1.1*	5
		BrSSRP1.2	5	*BoSSRP1.2*	5
STP16	4	*BrSTP16.4*	4	*BoSTP16.4*	4
ZDP	4	*BrZDP.1*	4	*BoZDP.1*	4
		BrZDP.3	3	*BoZDP.3*	3

Appendix G K_a, K_s, and K_a/K_s calculation of the DNA methylation-related (DMR) gene pairs between *A. thaliana* and *B. rapa*

Gene name	*A. thaliana* gene	Gene name	*B. rapa* gene	K_a	K_s	K_a/K_s
RNA-directed DNA methylation						
AGO4	*AT2G27040*	*BrAGO4.1*	*BraA07g018470*	0.065201	0.696144	0.093660
		BrAGO4.2	*BraA04g020490*	0.066263	0.799744	0.082856
		BrAGO4.3	*BraA03g050880*	0.442145	1.411970	0.313141
AGO6	*AT2G32940*	*BrAGO6.3*	*BraA03g017480*	0.080653	0.379919	0.212291
		BrAGO6.4	*BraA02g034110*	0.100036	0.474322	0.210903
		BrAGO6.5	*BraA03g049920*	0.168195	0.579326	0.290329
CLSY1	*AT3G42670*	*BrCLSY1.4*	*BraA08g012750*	0.099992	0.585671	0.170730
		BrCLSY1.5	*BraA08g012830*	0.128522	0.797927	0.161070
		BrCLSY1.6	*BraA10g020220*	0.168646	1.202240	0.140276
DCL2	*AT3G03300*	*BrDCL2.1*	*BraA05g042700*	0.105046	0.429807	0.244402
DCL3	*AT3G43920*	*BrDCL3.3*	*BraA06g023960*	0.113237	0.386317	0.293118
DCL4	*AT5G20320*	*BrDCL4.1*	*BraA10g020300*	0.091816	0.257880	0.356041
DMS3	*AT3G49250*	*BrDMS3.1*	*BraA06g018340*	0.149292	0.525448	0.284124
		BrDMS3.3	*BraA06g025840*	0.132665	0.466354	0.284473
DRD1	*AT2G16390*	*BrDRD1.3*	*BraA03g043560*	0.105553	0.679598	0.155317
HEN1	*AT4G20910*	*BrHEN1.1a*	*BraA01g011550*	0.505560	1.011250	0.499934
		BrHEN1.1b	*BraA01g011560*	0.130400	0.440431	0.296074
RDM1	*AT3G22680*	*BrRDM1.1*	*BraA05g025130*	0.167482	0.569345	0.294166
		BrRDM1.3	*BraA03g040940*	0.119998	0.611864	0.196119
RDM3	*AT5G04290*	*BrRDM3.1*	*BraA10g032020*	0.113325	0.526860	0.215095
RDR2	*AT4G11130*	*BrRDR2.1*	*BraA09g028070*	0.059172	0.479613	0.123374
RDR6	*AT3G49500*	*BrRDR6.2*	*BraA01g023710*	0.059823	0.370183	0.161603
SHH1	*AT1G15215*	*BrSHH1.1*	*BraA06g011300*	0.153635	0.397445	0.386556
SUVH2	*AT2G33290*	*BrSUVH2.1*	*BraA05g011580*	0.304845	1.363160	0.223632
		BrSUVH2.2	*BraA04g024900*	0.262063	1.058150	0.247662
Maintenance of DNA methylation						
CMT2	*AT4G19020*	*BrCMT2.1*	*BraA01g010380*	0.132726	0.304849	0.435381
CMT3	*AT1G69770*	*BrCMT3.4*	*BraA06g008110*	0.410680	NA	NA
DDM1	*AT5G66750*	*BrDDM1.1a*	*BraA07g017670*	0.066832	0.378328	0.176650
		BrDDM1.1b	*BraA07g017680*	0.085017	0.329628	0.257918
		BrDDM1.3a	*BraA07g016780*	0.845573	2.055910	0.411289
		BrDDM1.3b	*BraA09g009590*	0.079516	0.317790	0.250216
DRM2	*AT5G14620*	*BrDRM2.1*	*BraA10g024620*	0.158732	1.159570	0.136888

		BrDRM2.3	*BraA02g005700*	0.182961	0.852105	0.214716
		BrDRM2.4	*BraA01g022170*	0.915385	2.621770	0.349148
MET1	*AT5G49160*	*BrMET1.1*	*BraA06g035780*	0.184505	0.460440	0.400715
		BrMET1.4	*BraA09g055460*	0.161267	0.634056	0.254342
SUVH4	*AT5G13960*	*BrSUVH4.2*	*BraA03g006140*	0.134782	0.528455	0.255050
SUVH5	*AT2G35160*	*BrSUVH5.1*	*BraA05g009940*	0.279313	1.069880	0.261069
SUVH6	*AT2G22740*	*BrSUVH6.2*	*BraA04g017620*	0.232469	0.819565	0.283649
Active DNA demethylation						
ACX4	*AT3G51840*	*BrACX4.1*	*BraA09g044400*	0.058128	0.368376	0.157797
		BrACX4.2	*BraA04g008000*	0.059011	0.375068	0.157334
		BrACX4.4	*BraA03g061210*	0.164464	0.554337	0.296685
		BrACX4.5	*BraA06g043720*	0.603622	1.396920	0.432108
APE1L	*AT3G48425*	*BrAPE1L.1*	*BraA06g019080*	0.049177	0.404112	0.121692
DDB2	*AT5G58760*	*BrDDB2.3*	*BraA02g011610*	0.066318	0.381032	0.174049
DML3	*AT4G34060*	*BrDML3.1*	*BraA01g004220*	0.250518	0.943470	0.265529
HDP1	*AT1G72270*	*BrHDP1.4*	*BraA01g017630*	0.157869	0.307107	0.514052
HDP2	*AT4G31270*	*BrHDP2.3*	*BraA08g018010*	0.159359	0.437514	0.364237
IDM1	*AT3G14980*	*BrIDM1.1*	*BraA05g032960*	0.142260	0.414974	0.342817
IDM2	*AT1G54840*	*BrIDM2.3*	*BraA01g026760*	0.577544	1.976380	0.292223
IDM3	*AT1G20870*	*BrIDM3.1*	*BraA06g016730*	0.172311	0.460031	0.374563
		BrIDM3.3	*BraA07g015860*	0.150599	0.494484	0.304558
KAT2	*AT2G33150*	*BrKAT2.1*	*BraA05g011750*	0.017608	0.307384	0.057284
		BrKAT2.2	*BraA04g024780*	0.054666	0.395456	0.138236
		BrKAT2.3	*BraA03g017590*	0.043675	0.342126	0.127658
		BrKAT2.4	*BraA02g041370*	0.208678	1.525190	0.136821
LIG1	*AT1G08130*	*BrLIG1.1*	*BraA06g005390*	0.046201	0.433653	0.106539
		BrLIG1.3	*BraA09g063970*	0.057344	0.398103	0.144044
MBD7	*AT5G59800*	*BrMBD7.1*	*BraA10g017680*	0.200618	0.452446	0.443408
		BrMBD7.2	*BraA03g011150*	0.231703	0.489780	0.473076
		BrMBD7.3	*BraA02g010820*	0.312780	0.548708	0.570030
MBD9	*AT3G01460*	*BrMBD9.1*	*BraA05g041480*	0.097476	0.290218	0.335871
		BrMBD9.2	*BraA01g045750*	0.087552	0.297604	0.294191
MET18	*AT5G48120*	*BrMET18.2*	*BraA02g040790*	0.125906	0.389289	0.323425
MFP2	*AT3G06860*	*BrMFP2.1*	*BraA05g039520*	0.044778	0.359383	0.124597
		BrMFP2.2	*BraA01g042640*	0.046775	0.347778	0.134495
		BrMFP2.3	*BraA03g033330*	0.047125	0.315661	0.149291
NPX1	*AT5G63320*	*BrNPX1.1a*	*BraA06g027770*	0.275752	0.715656	0.385313
		BrNPX1.1b	*BraA06g027800*	0.143210	0.380900	0.375977
		BrNPX1.3	*BraA09g007920*	0.195348	0.486644	0.401417
PIE1	*AT3G12810*	*BrPIE1.1*	*BraA05g035100*	0.068327	0.373239	0.183065
ROS1	*AT2G36490*	*BrROS1.1*	*BraA05g008700*	0.178822	0.870962	0.205316
ROS3	*AT5G58130*	*BrROS3.1*	*BraA10g016250*	0.268900	0.514502	0.522642
SSRP1	*AT3G28730*	*BrSSRP1.1*	*BraA06g037940*	0.070128	0.426030	0.164607
		BrSSRP1.2	*BraA02g039580*	0.058445	0.493751	0.118370

STP16	*AT4G10710*	*BrSTP16.4*	*BraA03g027610*	0.065428	0.572263	0.114332
ZDP	*AT3G14890*	*BrZDP.1*	*BraA05g033020*	0.140490	0.455580	0.308375
		BrZDP.3	*BraA03g037130*	0.096034	0.500618	0.191831

Appendix H K_a, K_s, and K_a/K_s calculation of the (DNA methylation-related) DMR gene pairs between *A. thaliana* and *B. oleracea*

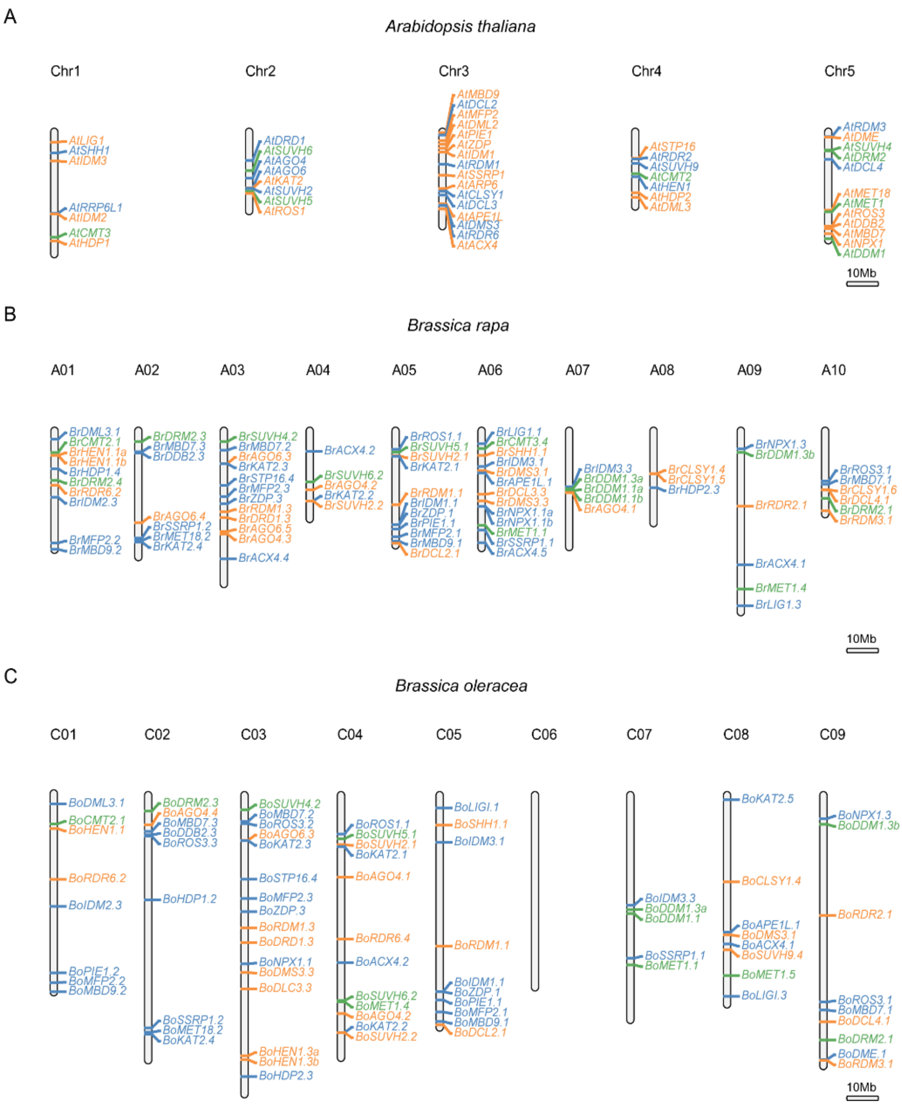
Gene name	*A. thaliana* gene	Gene name	*B. oleracea* gene	K_a	K_s	K_a/K_s
RNA-directed DNA methylation						
AGO4	*AT2G27040*	*BoAGO4.1*	*BolC04g023310*	0.067146	0.736988	0.091109
		BoAGO4.2	*BolC04g053880*	0.067806	0.818465	0.082846
		BoAGO4.4	*BolC02g011180*	0.234444	NA	NA
AGO6	*AT2G32940*	*BoAGO6.3*	*BolC03g019600*	0.076449	0.394296	0.193886
CLSY1	*AT3G42670*	*BoCLSY1.4*	*BolC08g016260*	0.099551	0.579149	0.171892
DCL2	*AT3G03300*	*BoDCL2.1*	*BolC05g063440*	0.138659	0.449503	0.308472
DCL3	*AT3G43920*	*BoDCL3.3*	*BolC03g062300*	0.121994	0.400126	0.304889
DCL4	*AT5G20320*	*BoDCL4.1*	*BolC09g052100*	0.092216	0.263539	0.349915
DMS3	*AT3G49250*	*BoDMS3.1*	*BolC08g033340*	0.161116	0.482792	0.333716
		BoDMS3.3	*BolC03g060110*	0.137576	0.483521	0.284530
DRD1	*AT2G16390*	*BoDRD1.3*	*BolC03g051920*	0.098816	0.600511	0.164553
HEN1	*AT4G20910*	*BoHEN1.1*	*BolC01g014120*	0.118709	0.378244	0.313842
		BoHEN1.3a	*BolC03g076570*	1.152330	NA	NA
		BoHEN1.3b	*BolC03g077490*	0.791362	NA	NA
RDM1	*AT3G22680*	*BoRDM1.1*	*BolC05g039660*	0.176246	0.653342	0.269761
		BoRDM1.3	*BolC03g048210*	0.132772	0.659252	0.201399
RDM3	*AT5G04290*	*BoRDM3.1*	*BolC09g067750*	0.110344	0.519990	0.212204
RDR2	*AT4G11130*	*BoRDR2.1*	*BolC09g032400*	0.062538	0.474382	0.131831
RDR6	*AT3G49500*	*BoRDR6.2*	*BolC01g029390*	0.059800	0.352817	0.169493
		BoRDR6.4	*BolC04g034910*	0.064497	0.358726	0.179794
SHH1	*AT1G15215*	*BoSHH1.1*	*BolC05g012860*	0.155954	0.405500	0.384597
SUVH2	*AT2G33290*	*BoSUVH2.1*	*BolC04g015770*	0.297004	1.318580	0.225245
		BoSUVH2.2	*BolC04g059170*	0.249694	1.109940	0.224962
SUVH9	*AT4G13460*	*BoSUVH9.4*	*BolC08g038030*	0.127160	1.125720	0.112960
Maintenance of DNA methylation						
CMT2	*AT4G19020*	*BoCMT2.1*	*BolC01g012760*	0.134509	0.335660	0.400730
DDM1	*AT5G66750*	*BoDDM1.1*	*BolC07g024230*	0.109675	0.412831	0.265665
		BoDDM1.3a	*BolC07g023070*	0.852103	2.221250	0.383615
		BoDDM1.3b	*BolC09g010670*	0.064666	0.291391	0.221920
DRM2	*AT5G14620*	*BoDRM2.1*	*BolC09g058530*	0.161532	1.166670	0.138456
		BoDRM2.3	*BolC02g006470*	0.186854	0.859916	0.217293
MET1	*AT5G49160*	*BoMET1.1*	*BolC07g038530*	0.192985	0.508489	0.379527
		BoMET1.4	*BolC04g050370*	0.195591	0.650028	0.300897
		BoMET1.5	*BolC08g048090*	0.161076	0.568649	0.283261
SUVH4	*AT5G13960*	*BoSUVH4.2*	*BolC03g006730*	0.142389	0.533629	0.266831
SUVH5	*AT2G35160*	*BoSUVH5.1*	*BolC04g013820*	0.289170	1.091070	0.265033

SUVH6	*AT2G22740*	*BoSUVH6.2*	*BolC04g050140*	0.240296	0.835748	0.287522
Active DNA demethylation						
ACX4	AT3G51840	*BoACX4.1*	*BolC08g036070*	0.057237	0.361988	0.158119
		BoACX4.2	*BolC04g040480*	0.059566	0.351158	0.169628
APE1L	AT3G48425	*BoAPE1L.1*	*BolC08g032520*	0.053938	0.378992	0.142320
DDB2	AT5G58760	*BoDDB2.3*	*BolC02g014020*	0.067724	0.402022	0.168457
DME	AT5G04560	*BoDME.1*	*BolC09g067440*	0.153505	0.399556	0.384190
DML3	AT4G34060	*BoDML3.1*	*BolC01g004810*	0.248602	0.896233	0.277385
HDP1	AT1G72270	*BoHDP1.2*	*BolC02g029210*	0.709727	NA	NA
HDP2	AT4G31270	*BoHDP2.3*	*BolC03g081780*	0.165934	0.459959	0.360757
IDM1	AT3G14980	*BoIDM1.1*	*BolC05g051290*	0.121347	0.411176	0.295122
IDM2	AT1G54840	*BoIDM2.3*	*BolC01g033310*	0.215670	0.554442	0.388985
IDM3	AT1G20870	*BoIDM3.1*	*BolC05g018830*	0.203252	0.436255	0.465902
		BoIDM3.3	*BolC07g022000*	0.151492	0.522188	0.290111
KAT2	AT2G33150	*BoKAT2.1*	*BolC04g016040*	0.017994	0.368054	0.048890
		BoKAT2.2	*BolC04g059060*	0.020968	0.339307	0.061798
		BoKAT2.3	*BolC03g019710*	0.019462	0.298726	0.065150
		BoKAT2.4	*BolC02g055850*	0.219864	1.497100	0.146861
		BoKAT2.5	*BolC08g001400*	0.066454	0.702548	0.094590
LIG1	AT1G08130	*BoLIG1.1*	*BolC05g006060*	0.057009	0.391002	0.145802
		BoLIG1.3	*BolC08g057260*	0.058608	0.383607	0.152781
MBD7	AT5G59800	*BoMBD7.1*	*BolC09g049020*	0.197052	0.423762	0.465006
		BoMBD7.2	*BolC03g012300*	0.240110	0.541807	0.443166
		BoMBD7.3	*BolC02g013030*	0.365025	0.641602	0.568928
MBD9	AT3G01460	*BoMBD9.1*	*BolC05g062180*	0.094989	0.287956	0.329873
		BoMBD9.2	*BolC01g057530*	0.088167	0.299089	0.294784
MET18	AT5G48120	*BoMET18.2*	*BolC02g055250*	0.126231	0.355277	0.355304
MFP2	AT3G06860	*BoMFP2.1*	*BolC05g058870*	0.045179	0.364398	0.123981
		BoMFP2.2	*BolC01g054030*	0.046180	0.322451	0.143215
		BoMFP2.3	*BolC03g038630*	0.045821	0.339870	0.134819
NPX1	AT5G63320	*BoNPX1.1*	*BolC03g057700*	0.165024	0.386197	0.427305
		BoNPX1.3	*BolC09g008640*	0.195087	0.427097	0.456776
PIE1	AT3G12810	*BoPIE1.1*	*BolC05g053870*	0.066919	0.363802	0.183944
		BoPIE1.2	*BolC01g050110*	0.248098	0.563616	0.440189
ROS1	AT2G36490	*BoROS1.1*	*BolC04g012450*	0.189605	0.869664	0.218021
ROS3	AT5G58130	*BoROS3.1*	*BolC09g046640*	0.267472	0.545099	0.490686
		BoROS3.2	*BolC03g013430*	0.526963	1.767030	0.298220
		BoROS3.3	*BolC02g014470*	0.463379	1.454200	0.318648
SSRP1	AT3G28730	*BoSSRP1.1*	*BolC07g036180*	0.072191	0.424973	0.169872
		BoSSRP1.2	*BolC02g054050*	0.059154	0.498646	0.118628
STP16	AT4G10710	*BoSTP16.4*	*BolC03g031980*	0.065206	0.542018	0.120302
ZDP	AT3G14890	*BoZDP.1*	*BolC05g051360*	0.151546	0.487526	0.310848
		BoZDP.3	*BolC03g043490*	0.123820	0.472599	0.261998

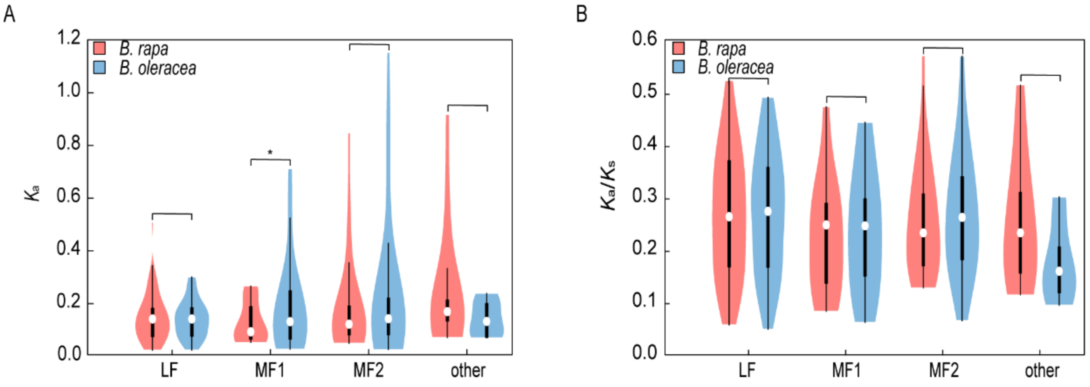
Appendix J Nucleotide diversity (π) and Tajima's D for DNA methylation-related (DMR) genes in *B. rapa* and *B. oleracea*

Gene name	π	Tajima' D	Gene name	π	Tajima' D
RNA-directed DNA methylation					
BrAGO4.1	0.006702	3.1862	*BoAGO4.1*	0.002483	3.1804
BrAGO4.2	0.007968	4.2419	*BoAGO4.2*	0.002785	4.3546
BrAGO4.3	0.005294	1.5138	*BoAGO4.4*	0.009465	4.3160
BrAGO6.3	0.002286	0.8543	*BoAGO6.3*	0.007094	4.0738
BrAGO6.4	0.000471	3.2827	*BoCLSY1.4*	0.002137	3.3142
BrAGO6.5	0.001323	0.8390	*BoDCL2.1*	0.000260	2.7817
BrCLSY1.4	0.001594	2.6516	*BoDCL3.3*	0.001856	2.7290
BrCLSY1.5	0.003921	3.8022	*BoDCL4.1*	0.002584	0.5855
BrCLSY1.6	0.007003	4.0344	*BoDMS3.1*	0.004641	3.5610
BrDCL2.1	0.001598	2.5494	*BoDMS3.3*	0.000388	1.0976
BrDCL3.3	0.002330	2.4985	*BoDRD1.3*	0.000036	1.0969
BrDCL4.1	0.002128	4.2309	*BoHEN1.1*	0.006396	1.6057
BrDMS3.1	0.004470	1.4190	*BoHEN1.3a*	0.004346	2.5032
BrDMS3.3	0.002103	2.1032	*BoHEN1.3b*	0.003013	2.0632
BrDRD1.3	0.004518	4.0440	*BoRDM1.1*	0.004490	3.8444
BrHEN1.1a	0.001662	1.5029	*BoRDM1.3*	0.006850	2.6749
BrHEN1.1b	0.006854	2.3001	*BoRDM3.1*	0.005419	2.3313
BrRDM1.1	0.008260	2.3358	*BoRDR2.1*	0.001617	1.3628
BrRDM1.3	0.003834	3.5583	*BoRDR6.2*	0.002723	2.2997
BrRDM3.1	0.005754	3.18185	*BoRDR6.4*	0.002542	0.9485
BrRDR2.1	0.005538	4.6090	*BoSHH1.1*	0.003176	3.5523
BrRDR6.2	0.002594	4.3056	*BoSUVH2.1*	0.004727	3.4414
BrSHH1.1	0.006840	4.1277	*BoSUVH2.2*	0.004513	4.7761
BrSUVH2.1	0.001763	3.0766	*BoSUVH9.4*	0.005359	3.9450
BrSUVH2.2	0.003167	4.1153			
Maintenance of DNA methylation					
BrCMT2.1	0.002743	3.4407	*BoCMT2.1*	0.002511	0.3124
BrCMT3.4	0.000075	2.0320	*BoDDM1.1*	0.005206	2.9819
BrDDM1.1a	0.007649	4.8814	*BoDDM1.3a*	0.003421	3.5752
BrDDM1.1b	0.004247	5.0509	*BoDDM1.3b*	0.007474	4.4343
BrDDM1.3a	0.005775	3.8872	*BoDRM2.1*	0.004572	2.8740
BrDDM1.3b	0.007215	4.3109	*BoDRM2.3*	0.001264	3.7791
BrDRM2.1	0.003263	2.5061	*BoMET1.1*	0.004102	4.8717
BrDRM2.3	0.003386	3.2985	*BoMET1.4*	0.005636	1.7435
BrDRM2.4	0.00382	3.8574	*BoMET1.5*	0.005028	3.1160
BrMET1.1	0.002441	3.1627	*BoSUVH4.2*	0.002398	1.1586
BrMET1.4	0.003848	3.6476	*BoSUVH5.1*	0.004603	3.3939
BrSUVH4.2	0.003002	3.3399	*BoSUVH6.2*	0.002891	1.7822
BrSUVH5.1	0.005729	4.1070			
BrSUVH6.2	0.006801	3.0873			

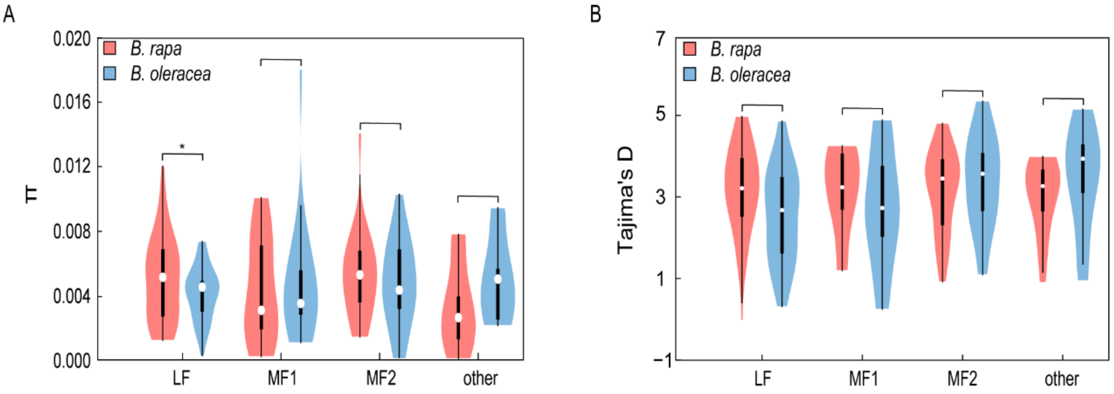
Active DNA demethylation					
BrACX4.1	0.005717	2.9039	*BoACX4.1*	0.003362	1.6702
BrACX4.2	0.000195	3.1623	*BoACX4.2*	0.003007	0.4816
BrACX4.4	0.002632	3.0763	*BoAPE1L.1*	0.004201	2.5872
BrACX4.5	0.000999	3.4606	*BoDDB2.3*	0.005308	3.8962
BrAPE1L.1	0.003217	3.6437	*BoDME.1*	0.004351	1.8239
BrDDB2.3	0.006550	3.4723	*BoDML3.1*	0.001778	0.8367
BrDML3.1	0.003378	3.8755	*BoHDP1.2*	0.004748	2.7360
BrHDP1.4	0.007840	1.6748	*BoHDP2.3*	0.004310	2.3224
BrHDP2.3	0.004935	1.9270	*BoIDM1.1*	0.004818	3.7835
BrIDM1.1	0.007162	3.9560	*BoIDM2.3*	0.004296	4.4613
BrIDM2.3	0.001419	3.0663	*BoIDM3.1*	0.004881	1.1251
BrIDM3.1	0.002202	2.8075	*BoIDM3.3*	0.009073	5.3628
BrIDM3.3	0.008284	3.4471	*BoKAT2.1*	0.006043	3.7941
BrKAT2.1	0.009454	4.8022	*BoKAT2.2*	0.006345	3.1053
BrKAT2.2	0.006075	4.0810	*BoKAT2.3*	0.010297	5.1116
BrKAT2.3	0.004490	4.0205	*BoKAT2.4*	0.009209	4.2878
BrKAT2.4	0.007840	3.6894	*BoKAT2.5*	0.003902	3.9556
BrLIG1.1	0.010006	3.2674	*BoLIG1.1*	0.003498	1.6329
BrLIG1.3	0.005360	3.6164	*BoLIG1.3*	0.003655	2.7509
BrMBD7.1	0.006880	3.9828	*BoMBD7.1*	0.001865	2.1495
BrMBD7.2	0.002058	1.1376	*BoMBD7.2*	0.004694	2.6643
BrMBD7.3	0.006977	3.5155	*BoMBD7.3*	0.006171	3.9796
BrMBD9.1	0.001211	2.7331	*BoMBD9.1*	0.004726	3.6857
BrMBD9.2	0.000917	2.7580	*BoMBD9.2*	0.001068	0.2471
BrMET18.2	0.010093	3.8593	*BoMET18.2*	0.007080	3.1603
BrMFP2.1	0.006153	3.5088	*BoMFP2.1*	0.006469	3.4585
BrMFP2.2	0.008212	2.5020	*BoMFP2.2*	0.018084	4.9007
BrMFP2.3	0.007251	1.8819	*BoMFP2.3*	0.003200	4.5006
BrNPX1.1a	0.002725	-0.1189	*BoNPX1.1*	0.004719	2.3072
BrNPX1.1b	0.001687	1.3200	*BoNPX1.3*	0.004748	2.9293
BrNPX1.3	0.006186	4.8749	*BoPIE1.1*	0.001945	1.9196
BrPIE1.1	0.005018	4.3135	*BoPIE1.2*	0.003516	2.8742
BrROS1.1	0.004438	2.4488	*BoROS1.1*	0.003283	1.3742
BrROS3.1	0.012054	3.4107	*BoROS3.1*	0.007379	4.7620
BrSSRP1.1	0.007160	3.7503	*BoROS3.2*	0.008068	4.5292
BrSSRP1.2	0.001543	1.3000	*BoROS3.3*	0.006433	4.0225
BrSTP16.4	0.002496	2.9829	*BoSSRP1.1*	0.004902	3.0332
BrZDP.1	0.005260	1.4468	*BoSSRP1.2*	0.003095	2.3208
BrZDP.3	0.014117	4.0518	*BoSTP16.4*	0.002470	5.1655
			BoZDP.1	0.007231	1.4018
			BoZDP.3	0.007369	3.2030



Appendix D Chromosomal distribution of DNA methylation-related (DMR) genes. Different colors represent genes in different pathways; blue represents RNA-directed DNA methylation (RdDM) genes, green represents maintenances of DNA methylation (MDM) genes, and orange represents active DNA demethylation (ADD) genes. The gray bars represent the chromosomes.



Appendix I The frequency distribution of K_a and K_a/K_s. LF, MF1, and MF2 represent DMR genes on the three subgenome genes, other represents non-synteny orthologs DMR genes. Significance is indicated for P values < 0.05 (*).



Appendix K The frequency distribution of π and Tajima's D. LF, MF1, and MF2 represent DNA methylation-related (DMR) genes on the three subgenome, other represents non-synteny orthologs DMR genes. Significance is indicated for P values < 0.05 (*).