
Article

Epigenetic Landscape of Recombinant Plant Chromosome Fragments in a Human-*Arabidopsis* Hybrid Cell Line

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Table S1. Methylation profiles of 300-day-old hybrid cell obtained using BSMPA and Bismark

	BSMAP	Bismark
CG	23.8 %	23.8 %
CHG	0.27 %	0.3 %
CHH	0.26 %	0.3 %

Table S2. Number of occurrences of overlapping repeat families in hypomethylated regions overlapping with TAIR UCSC repeatmasker tracks

Satellites		LTR	
Repeat families	Overlapping occurrence	Repeat families	Overlapping occurrence *
COLAR12	193	Athila4B_LTR	101
ATSAT5	37	Athila2_LTR	83
ATSAAS5	27	Athila6A_LTR	76
AR12	14	Athila4C_I-int	63
ATSAB5	13	Athila_I-int	61
ATCLUST1	6	ATHILA6C_I-int	61
ATENSAT1	2	Athila4_I-int	54
ATENSAT2	1	Atlantys1_I-int	52
		Athila2_I-int	52
		Athila3_I-int	51
		Athila6A_I-int	50
		Athila4D_LTR	50
		ATGP10_I-int	47
		Athila_LTR	46
		Athila3_LTR	46
		Athila4A_I-int	44
		Atlantys2_I-int	43
		Athila6B_I-int	42
		Athila0_I-int	40

*Only an occurrence of at least 40 is shown here.

Table S3. Sequences of the primers used for expression analysis

Gene name	Primer sequences (F: Forward, R: Reverse)	Reference
<i>DDM2</i>	F: GCGGTTCTCAGTCACACGATCC R: GGGGCATAAAGTTTGATGGTTCC	
<i>DRM2</i>	F: GTGCTGCTCAAATGGCTAGGAAAT R: GCTCGTTGGAACCCCAAATCCTAT	
<i>GSL8</i>	F: TGGGGTTTCCCTGAAGTACGTG R: GGGACTGTGCATTGAAAGTGTGAG	Han, S., & Kim, D. (2006)
<i>CESA4</i>	F: AGATGCGGAGTGGAAAGAACGTGTA R: ACGATGCGGTAAGGACTGATTTGC	Han, S., & Kim, D. (2006)
<i>HPR</i>	F: CGCTTGCAGCTCTCAACGTC R: GCGGGTGAAGCGTTTCGTT	
<i>NPY4</i>	F: CTAGCTTCCAAGACACTCTCAC R: GCCCGCATACTCTCTTCTC	
<i>LHCB</i>	F: GGCCATGCTTGGCACTCTA R: GTCAACGAGAACGGCAATGGT	
<i>CA2</i>	F: GTCCCTCTCATCGCCTGTCTC R: AGCTTCGATGGCGTCTTCAT	
<i>APE2</i>	F: CTCCGGTCGTAGCTTCGT R: GCATCCCCAGCGGTATCTCC	
<i>SBE2.2</i>	F: TATAGAGAGTGGGCGCCTGG R: ACCATCAGTGTGTTGGCA	
<i>AtNADH</i>	F: CCCTCTCCTCCTCCAATCTC R: ACCTCCATTGGCACAACTTC	Wada et al (2017)
<i>TIP</i>	F: AAAAATCATCAAATCCATCTCCCAC R: GGCAAAAAGAGATATTGCAACACTTG	Wada et al (2017)
<i>PLP6</i>	F: TGGAGCAGCTGATACTGTGG R: TTGCTTGAACGCTACAGTGG	Wada et al (2017)