

**Table S7 : Allele-specific analysis of DNA methylation within the G3 region of the *Koala* retrotransposon.**

Tissue	PCR fragment	% methylated			total methylation (%)	n
		CG sites	CHG sites	CHH sites		
N male	G3-a1	100.0	91.6	4.2	23.1	16
	G3-a2	97.9	85.3	3.9	24.1	20
	<b>average</b>	<b>98.8</b>	<b>88.1</b>	<b>4.1</b>	<b>23.7</b>	<b>36</b>
M male	G3-a1	95.0	86.1	4.1	22.0	15
	G3-a2	98.3	81.5	3.3	23.1	16
	<b>average</b>	<b>96.7</b>	<b>83.7</b>	<b>3.7</b>	<b>22.6</b>	<b>31</b>
N female	G3-a1	95.7	90.9	4.8	23.2	16
	G3-a2	99.1	81.1	2.3	22.2	19
	<b>average</b>	<b>97.6</b>	<b>85.6</b>	<b>3.5</b>	<b>22.7</b>	<b>35</b>
M female	G3-a1	97.2	88.9	4.5	22.7	18
	G3-a2	91.7	73.2	1.7	19.74	18
	<b>average</b>	<b>94.5</b>	<b>81.1</b>	<b>3.1</b>	<b>21.22</b>	<b>36</b>

n is the number of individually cloned amplicons analyzed and the average of methylation rates between both alleles is weighted accordingly.