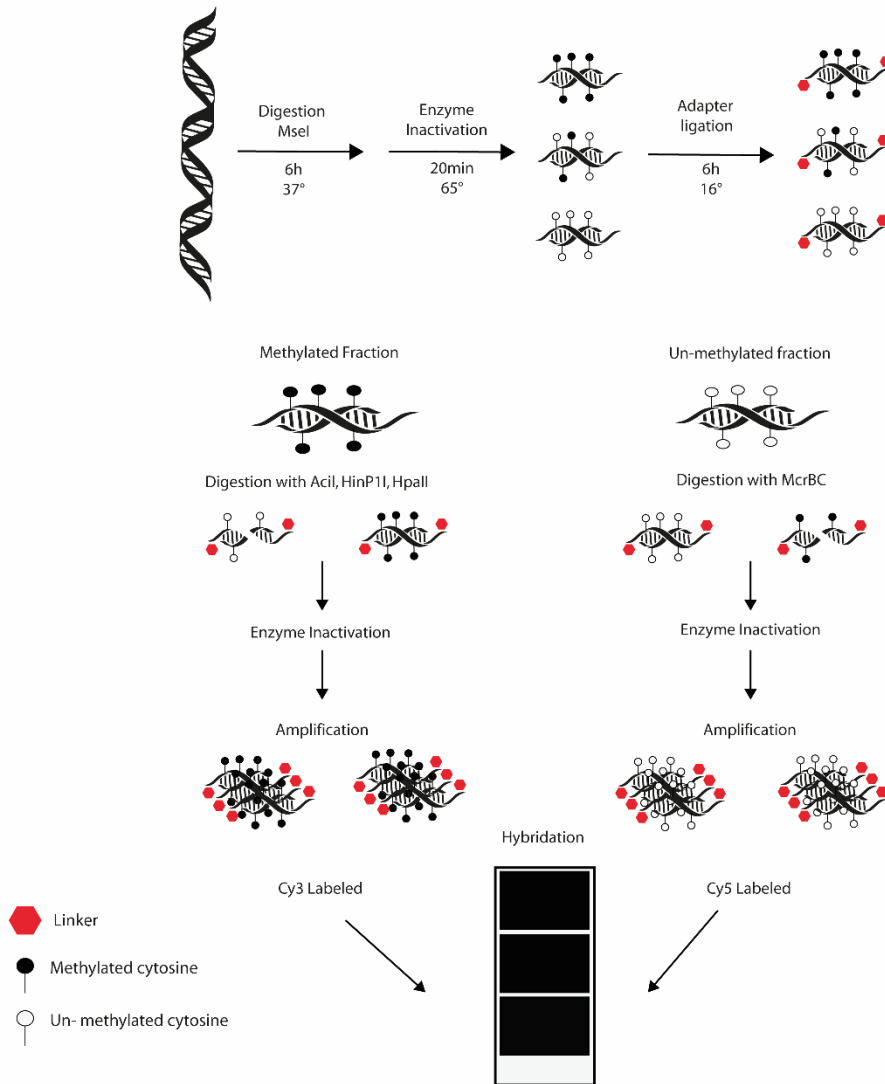
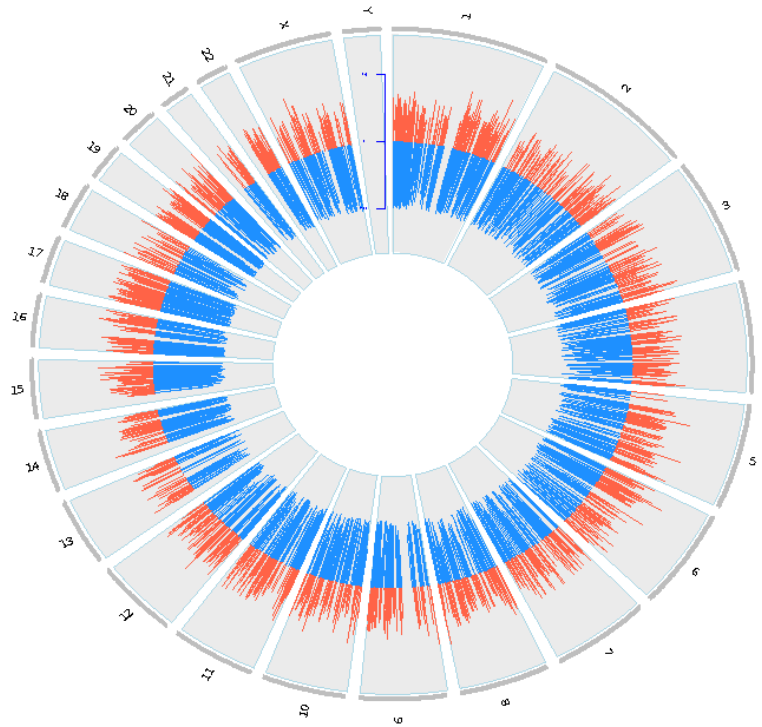


*Supplementary Material*

**Supplementary Figure 1**

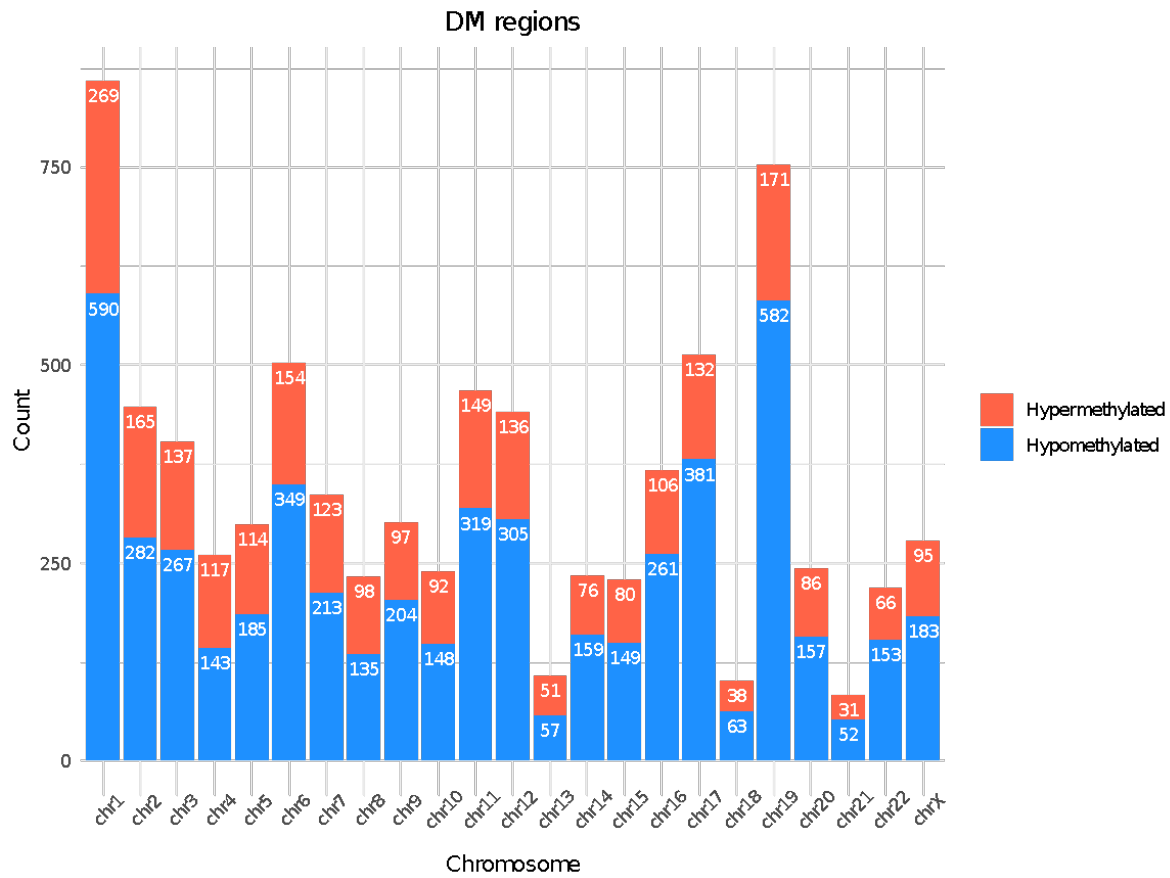


**Supplementary Figure 1.** Flowchart and method performance to aPRIMES assay

**Supplementary Figure 2**

**Supplementary Figure 2.** Circos plot representing the differentially methylated regions across the genome in cervical cancer patients. The blue inner ring represents the bi-weight of the significant methylated regions, meanwhile red outer ring shows hypermethylated chromosome areas.

**Supplementary Figure 3**



**Supplementary Figure 3.** Number of regions differentially methylated across the genome. The barplot represents the number of regions differentially methylated per chromosome where light blue shows hypermethylated regions and dark blue hypomethylated.

**Supplementary Table 1. MSP primers.**

<b>Gene</b>		<b>Methylated</b>	<b>Un-methylated</b>
<b>BRD9</b>	Fw	GAATTTTTATTAGGAACGTAAGCG	GAATTTTTATTAGGAATGTAAGTG
	Rv	CTACGAAAATAAAACGACGACG	TCCTACAAAATAAAACAACAACAC
<b>CTU1</b>	Fw	CGAGTAGTTGGGATTATAGGTTTAC	TTTTGAGTAGTTGGGATTATAGGTTTAT
	Rv	AAAAAATCTAAAAAAAACGCGAA	ATCAAAAATCTAAAAAAAACACAAA
<b>DOCK8</b>	Fw	AGTTTAGCGTTGGTGTGAAGC	GATAGTTTAGTGTGGTGTGAAGTG
	Rv	GAAACGAACGAAATTATTCGAAA	ACAAAACAAACAAAATTATTCAAAA