Table S1. Data production summary of PBMC methylome study.

a)

Library	Insert Size ± 3SD (bp)	Read Length (bp)	Reads Number	Raw Data (Gbp)
HUMtg1RABDCAAPE	111±31	44	58,490,616	2.6
		75	331,307,522	24.9
HUMtg1RADSADPE	182±46	44	45,119,798	2
		75	366,998,694	27.3
HUMtg2RABDCABPE	151±43	44	41,469,338	1.8
		75	252,028,298	18.9
HUMtg2RABDCBAPE	96±31	44	287,652,886	12.7
		75	-	-
HUMtg2RABDCBBPE	135±37	44	60,369,744	2.7
		75	144,023,246	10.8

b)

Read length (bp)	# of raw reads	# of aligned Reads		Aligned Bases (bp)	Effective strand depth	Unambiguous rate (%)	Mismatch rate (%)
44	493,102,382	SE	159,881,472	6,779,415,037	1.2	87.85	1.1
		PE	209,193,248	9,133,788,437	1.6	90.92	0.8
75	1,094,357,760	SE	398,503,878	24,941,188,529	4.3	82.69	1.8
		PE	406,987,966	29,599,486,371	5.2	92.11	1.1
Total	1,587,460,142		1,174,566,564	70,453,878,374	12.3	88.12	1.3