Table S1. Data production summary of PBMC methylome study.

a) Library Insert Size ± 3SD (bp) Read Length (bp) Reads Number Raw Data (Gbp)
HUMtg1RABDDCAPE 111±31 44 58,490,616 2.6
75 331,307,522 24.9
HUMtg1RADSDPDE 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
HUMtg2RABDCABPE 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