Figure S5. A comparison of BALM with MACS, QuEST on the result of MBD-seq data in MCF-7 cell. All three programs similarly detected broad methylation regions. QuEST distinguished different summits in the large region. With facility provided, MACS is also likely to detect sub-peaks in this region; however, BALM further finely estimate the degree of each CpG dinucleotide being methylated by the EM and BIC algorithm.