

Description of MMSDK Method

For MMSDK, short sequence tags tandem were obtained following digestion of genomic DNA with a methylation-sensitive mapping enzyme and a fragmenting enzyme. These tags were amplified, followed by direct, massive parallel sequencing and mapping to the reference human genome. The DNA methylation levels were inversely proportional to the number of tags mapped to the given genomic locus, since tags are only generated from DNA with unmethylated sites. The pipeline for MMSDK is illuminated in the figure below.

