Additional File 2. File format of input and output

Module	SNP	CNV	MET	COV	TXN
Input	-Sorted BAM -Reference genome	-Sorted BAM -Reference genome index	-Gene annotation file -Reference genome -CG map	-Sorted BAM -Reference genome	-CGmap -TFBSs
Output	-SNP table	-CNV table -CNV plot	-Global cytosine methylation level plot -Cytosine methylation level distribution plots -Cytosine methylation level plot of different genomic elements -Chromosome-wide cytosine methylation level distribution plot -Gene-centric methylation level tabl	-Reverse cumulative plot	-Cytosine methylation levels plot around TFBS
Parameters	-Coverage (minimum number of reads) -Allele frequency to be considered homozygous SNP -Buffer around 0.5 to be considered heterozygous SNP	-Window size (number of bases for reads to be summed over) -Probability (probability cutoff for window to be considered a CNV) -Window number (number of windows for moving average to be calculated over)	-Depth (minimum number of reads) -Promoter size (number of bases) -Methylation context		