

Establish Genome-Wide methylation profiling of HBV-related HCC development

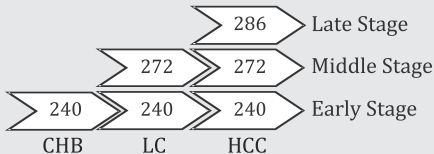
Methylcap-Seq analysis plasma cf-DNA of HC(31),CHB(30),
LC(27),HCC(29),NSCLC(26), (HiSeq 2000,36bp unpaired reads)



Data analysis
(MACS/BALM)



Hypermethylated DMGs in plasm cf-DNA



Validation of MethyCap\Seq data

1. MSP screening 40 DMGs in independent tissue sample(10 HC,33 HCC)
2. qMSP identify Candidate 33 DMGs in tissue sample of 10 HC,29 LC,33 HCC
3. Multiplex-Bisulfite PCR/Seq (HiSeq 2500,100bp,paired reads) identify 33 DMGs in independent plasma sample(37 HC, 36 CHB, 40 LC, and 47 HCC)