BS-seq reads

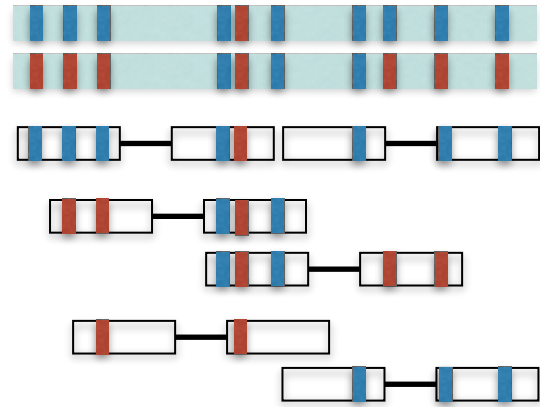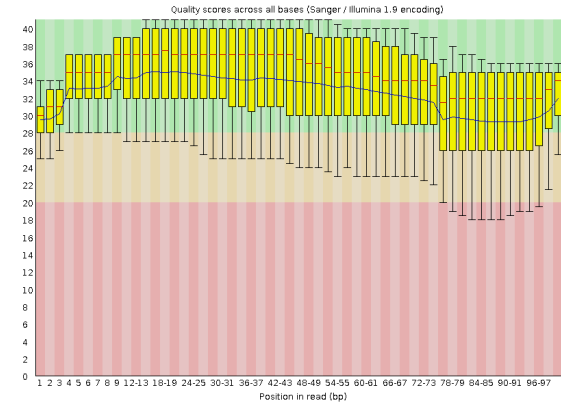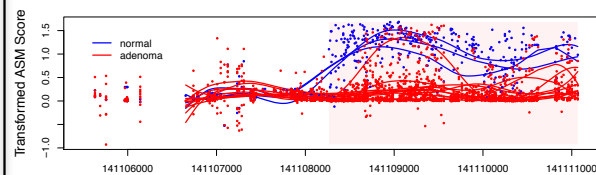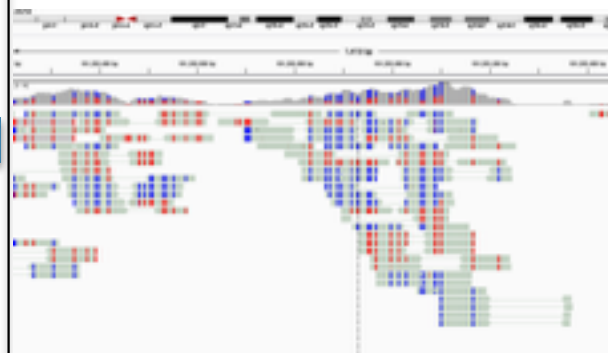**Quality Control**

Bismark
- map reads to reference genome
- remove duplicates
- call on methylation extractor

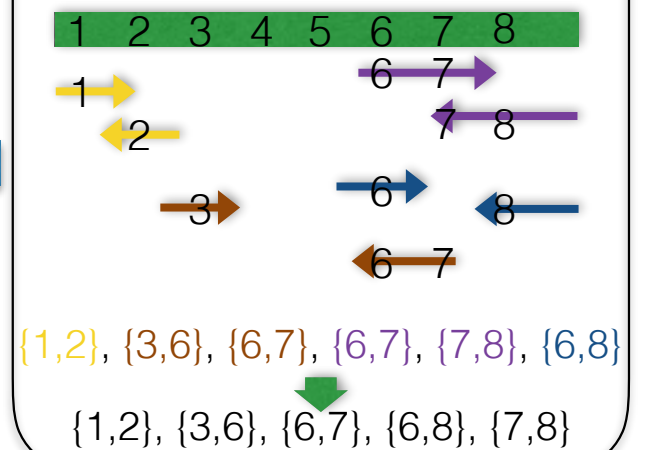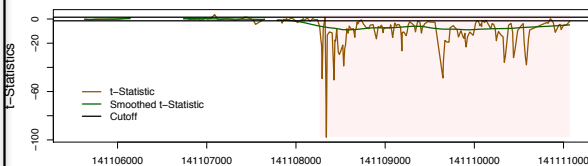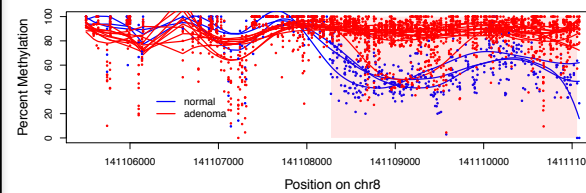**t-Statistics Across Samples per Tuple**

ASM Score per Tuple

Unique Tuples

1 2 3 4 5 6 7 8

6 7
6 7
8
1
2
3 6
8
6 7

{1,2}, {3,6}, {6,7}, {6,7}, {7,8}, {6,8}

{1,2}, {3,6}, {6,7}, {6,8}, {7,8}

Smooth t-Statistics

DAMEfinder: bumphunting to find DAMEs

Evaluate DAMEs

GNAS