MeDIP-Seq FAQ

2011-05-03 (Version 1)

Contents

1. What are the sample quantities required for MeDIP analysis?

   We cannot provide detailed quantities, as there may be a significant difference between DNA yielded from different tissues or cells. We recommend that you refer to the instructions of QIAGEN or other commercial kits.

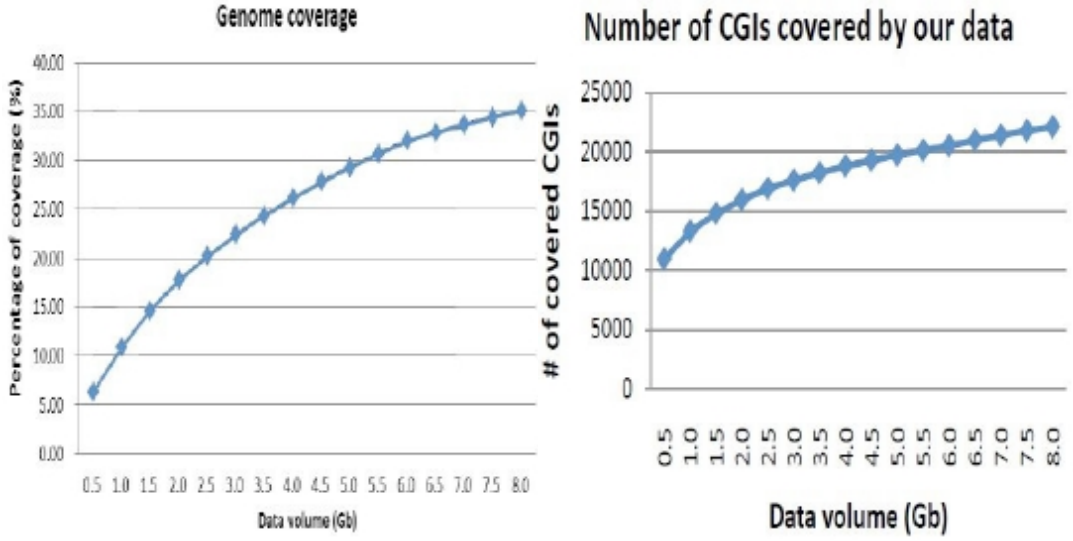
2. Can MeDIP be used to detect the methylation pattern within a specific region, and is it precise at detecting the methylation status of every single nucleotide?

   MeDIP-Seq is the antibody-based method for DNA-methylation analysis. The DNA fragments enriched by methylation antibodies are sequenced, and thus the methylation pattern at specific regions can be revealed. MeDIP is particularly applicable to the analysis of the methylation among different samples. However, it only detects the methylation pattern within specific regions, and the methylation status of single nucleotide cannot be determined.

3. How much MeDIP-Seq data are needed?

   If the sample size is small, we suggest that at least 4G data are needed to analyze each sample. However, if the sample size is larger, a smaller increase in the amount of data is needed, and in this case we recommend population analysis.

   The MeDIP saturation curves graphs in Figure 1 can be used as a guide. The data was collected from 8G human peripheral blood samples. Each graph demonstrates the MeDIP saturation curves under different specific conditions.



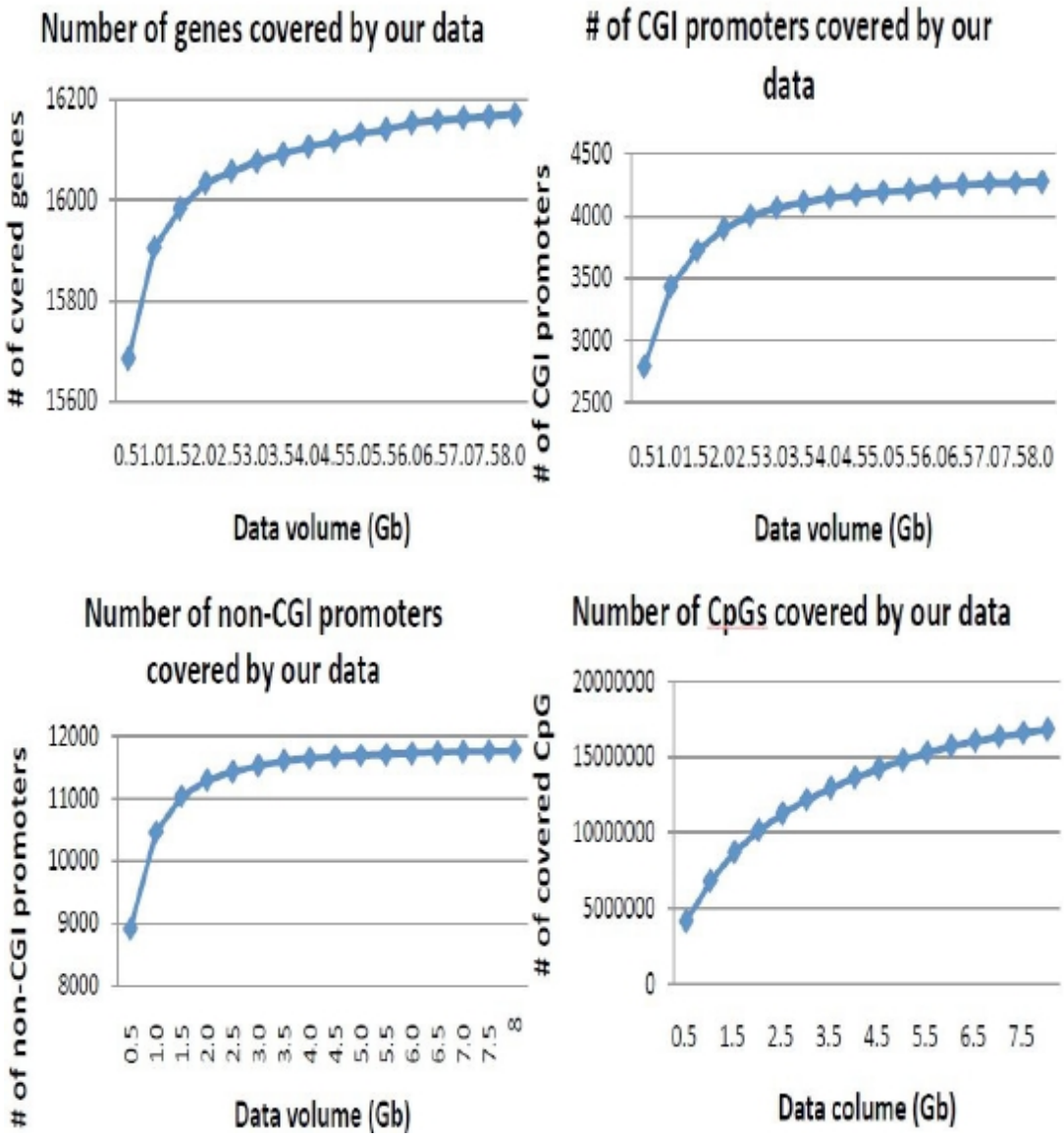


Figure 1 MeDIP saturation curves

As the amount of data increases, the statistical results do not show significant tendency of saturation. As such, cost-effectiveness may be considered. Note that the most reliable results require at least 4G data per sample. If the amount of data used for analysis is too small, the number of DNA fragments being enriched is not adequate, and the results may not be reliable.

4. What are the coverage, sequencing depth, and resolution of MeDIP?

According to our analysis, about 30% of the human genome can be covered based on 5-8G MeDIP data. Thus, the average sequencing depth is less than 10X. But for MeDIP, the data are distributed across different enriched DNA fragments, and, as such, the average sequencing depth is not an important issue for MeDIP-Seq. Given that there are different definitions for resolution, we are not able to specify resolution parameters here for MeDIP.