Genome-Wide DNA Methylation Analysis In Plants and Animals

ZYMO RESEARCH

The Beauty of Science is to Make Things Simple

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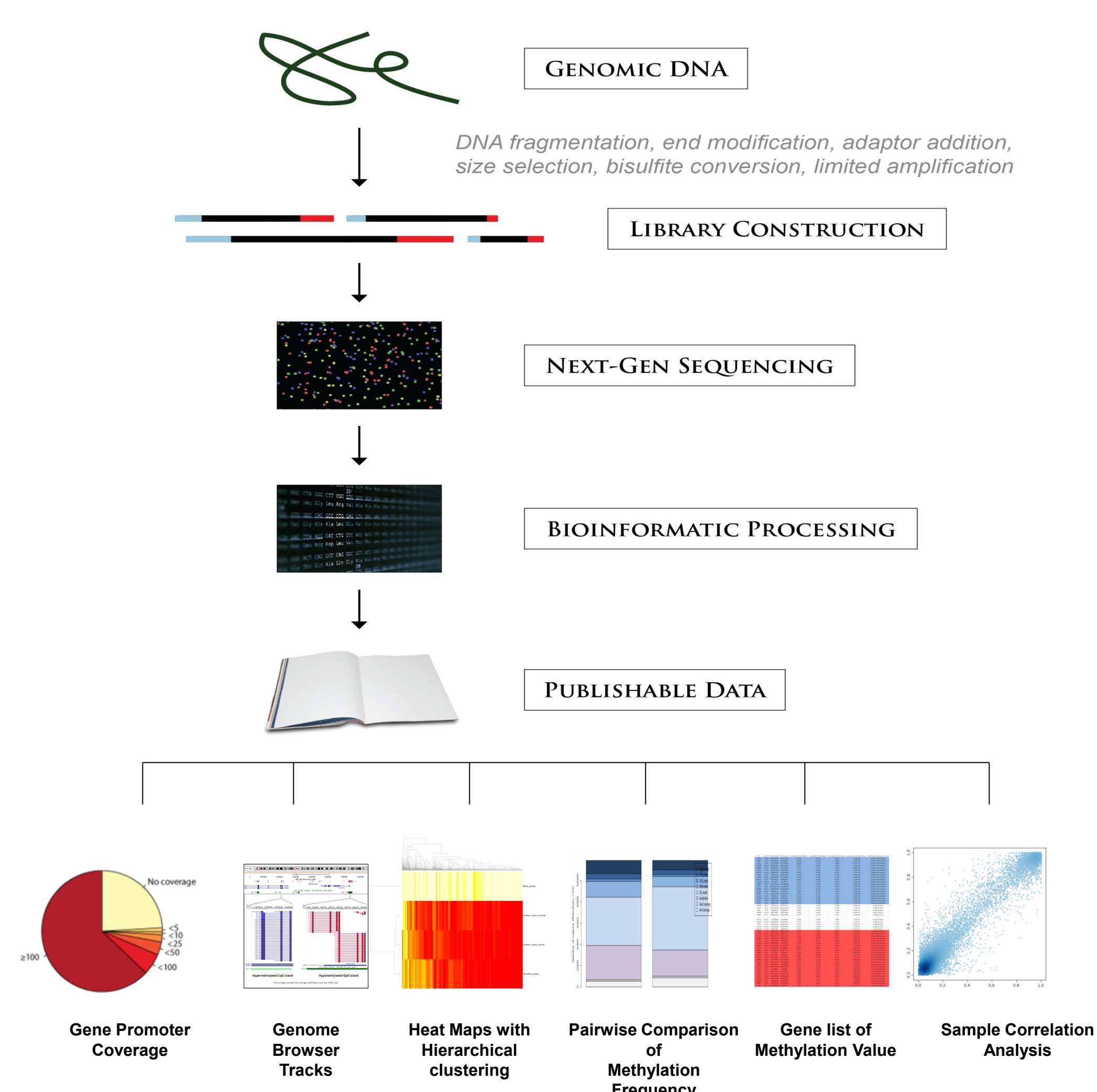Zymo Research Corporation, Irvine, CA

Abstract

DNA methylation is a highly conserved epigenetic mark present in many eukaryotic organisms including plants, animals, and fungi. It plays an important role in the regulation of gene expression. A number of studies have shown its involvement in plant and animal growth and reproduction primary through the processes of genomic imprinting, X-chromsome inactivation, and the silencing of transposons and other repetitive DNA elements. As such, the understanding of DNA methylation has become a major focus of the research conducted during the "post-genomics" era. However, the precise determination of a DNA's methylation pattern on a genomic scale has posed a challenge especially for those complex genomes. Combining well-established bisulfite conversion chemistry with NextGen sequencing, we have established a robust service platform for analyzing DNA methylation with single base resolution at the genomic scale. The service features a streamlined workflow coupled with a comprehensive bioinformatics pipeline to provide both a consolidated and cost-effective solution for epigenetic analysis of plant and animal genomes. This technology has been used successfully for the analysis of methylomes from many organisms including soybean, mouse, and chicken. Additional analyses of other species are ongoing. Those data should provide a means to understanding how environment as well as other factors may alter an organism's fitness through heritable changes in epigenetic gene expression.

Introduction

The EpiQuest™ **Genome-Wide DNA methylation Profiling Service** expands upon the conventional RRBS (Reduced-Representation Bisulfite Sequencing) method to greatly increase sequence analysis of CpG-riched DNA. Through an unique library preparation procedure and an optimized workflow, the EpiQuest™ team at Zymo Research has been able to expand coverage to **≥80% of all gene promoters and ≥85% of CpG islands** (for human samples).

The EpiQuest™ **Whole-Genome DNA methylation Profiling Service** utilizes a streamlined library preparation and sophisticated alignment algorithms to deliver Whole Genome Bisulfite-Sequencing data that covers **>80%** of all the bases in the human genome at single-base resolution.

Workflow

Genomic DNA → DNA fragmentation, end modification, adaptor addition, size selection, bisulfite conversion, limited amplification → Library Construction → Next-Gen Sequencing → Bioinformatic Processing → Publishable Data

Gene Promoter Coverage | Genome Browser Tracks | Heat Maps with Hierarchical clustering | Pairwise Comparison of Methylation Frequency | Gene list of Methylation Value | Sample Correlation Analysis

Key features

✓ Next-Gen sequencing based platforms
✓ Low DNA input
✓ Applicable to a broad range of sample sources (human, mouse, rat, plant, etc.)
✓ Streamlined workflows with comprehensive bioinformatic analysis and high quality publishable data delivery.
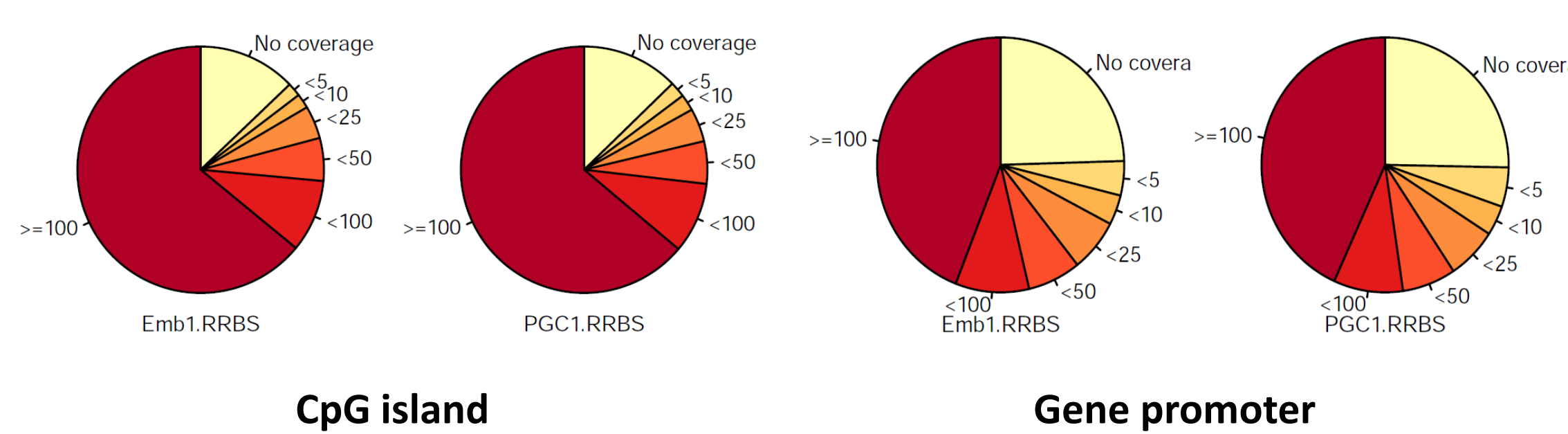✓ Customizable, rapid turnaround at an affordable cost.

Service comparison

EpiQuest Next-Gen Sequencing DNA Methylation Analysis

Genome-wide 5mC profiling in chicken
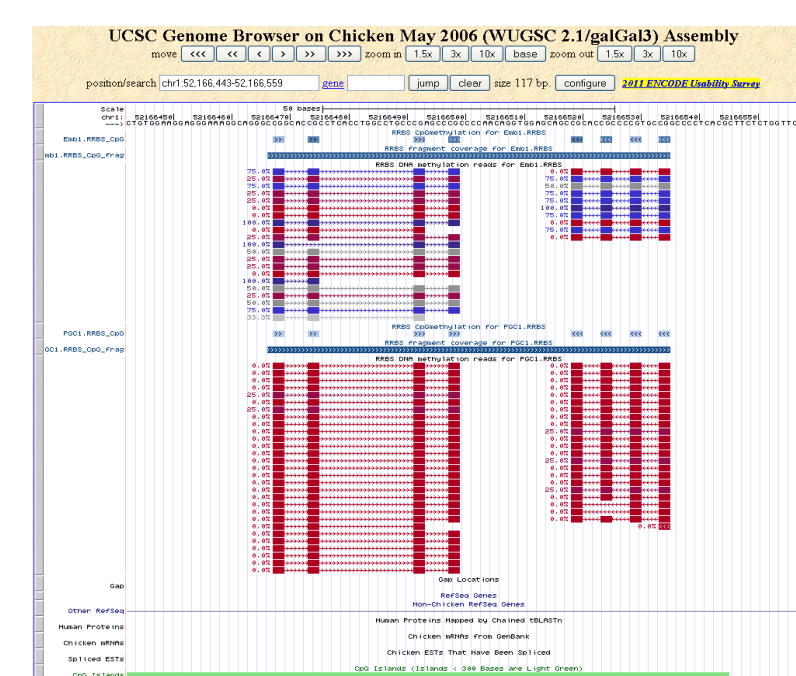

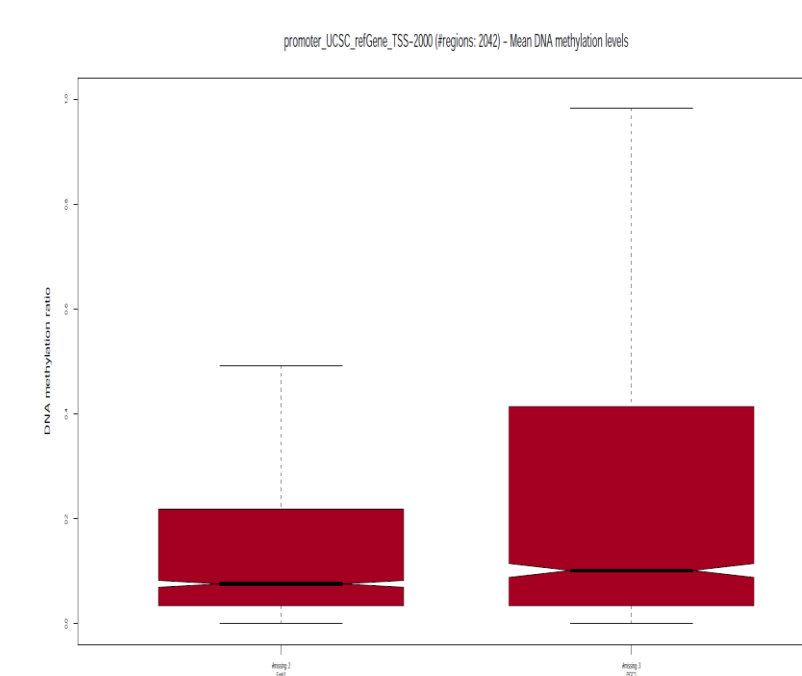➤ **Genome Coverage :**

CpG island / **Gene promoter**

Pie charts shows the overall distribution of sequencing reads coverage
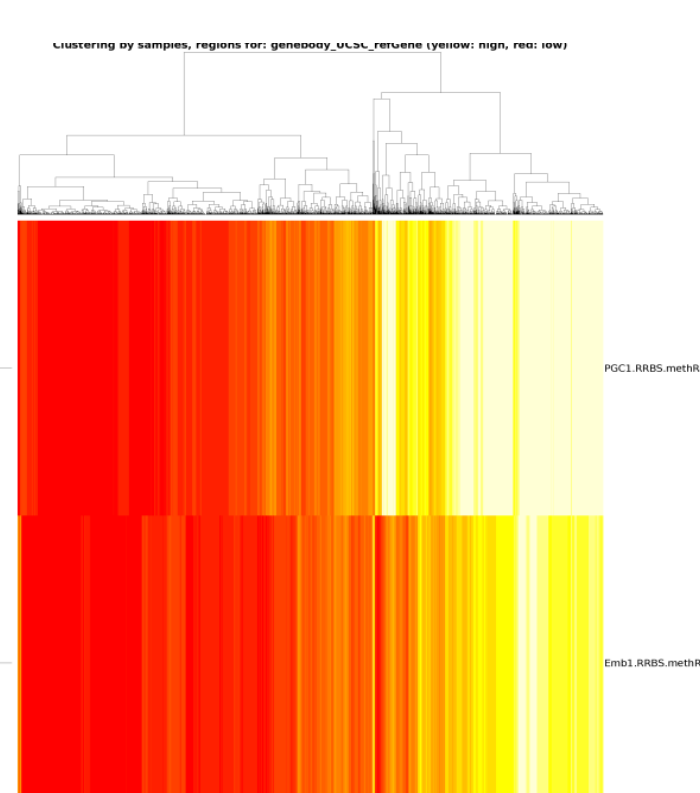
➤ **UCSC genome browser track**

Browser tracks show the sequencing reads and methylation value
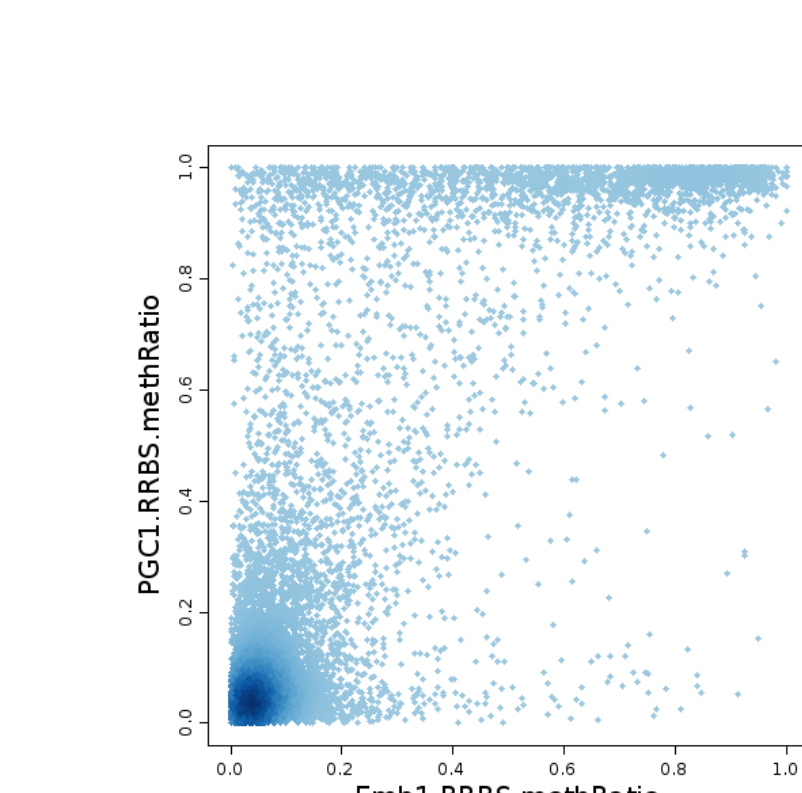
➤ **Methylation Index**

Mean DNA Methylation Levels for Gene Promoter

➤ **Hierarchical clustering:**

Heatmap shows the hierarchical clustering by region and sample

➤ **Correlation analysis**

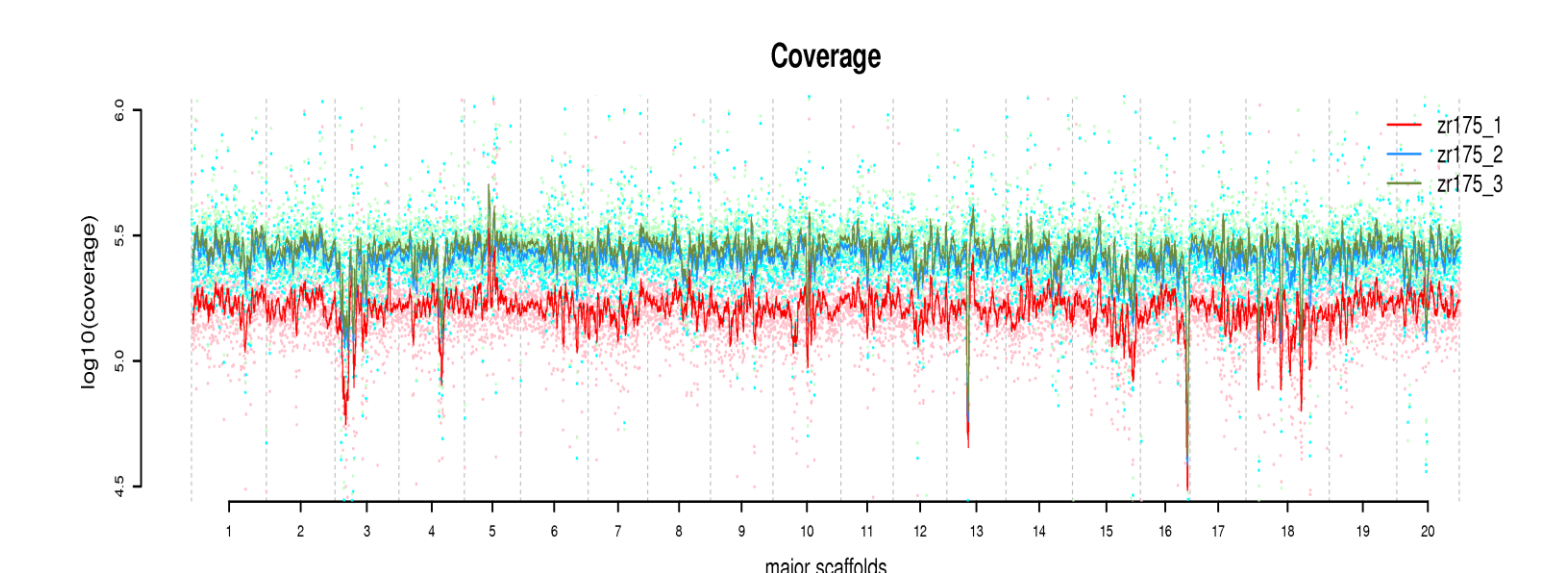Pearson correlation for pairwise data comparison between samples

➤ **hyper/hypo methylation gene list**

Pair-wise comparison was performed between the different samples, DMR were counted according to hyer/hypo methylation.
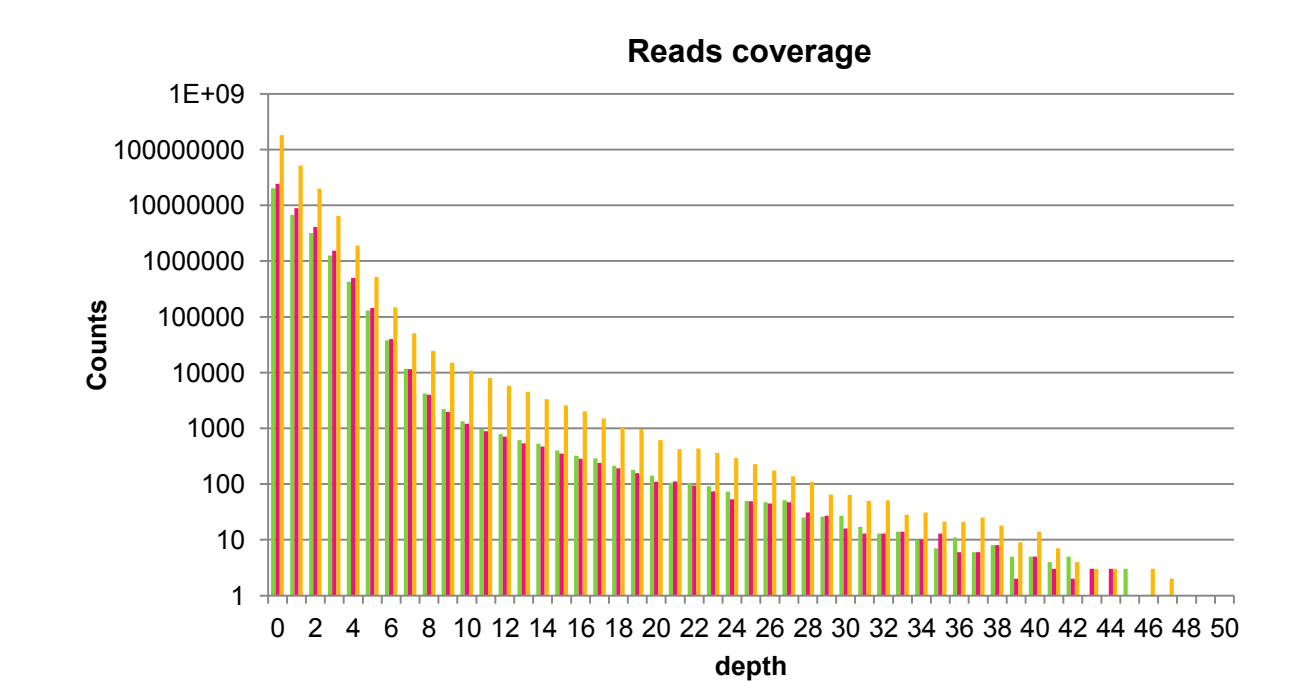
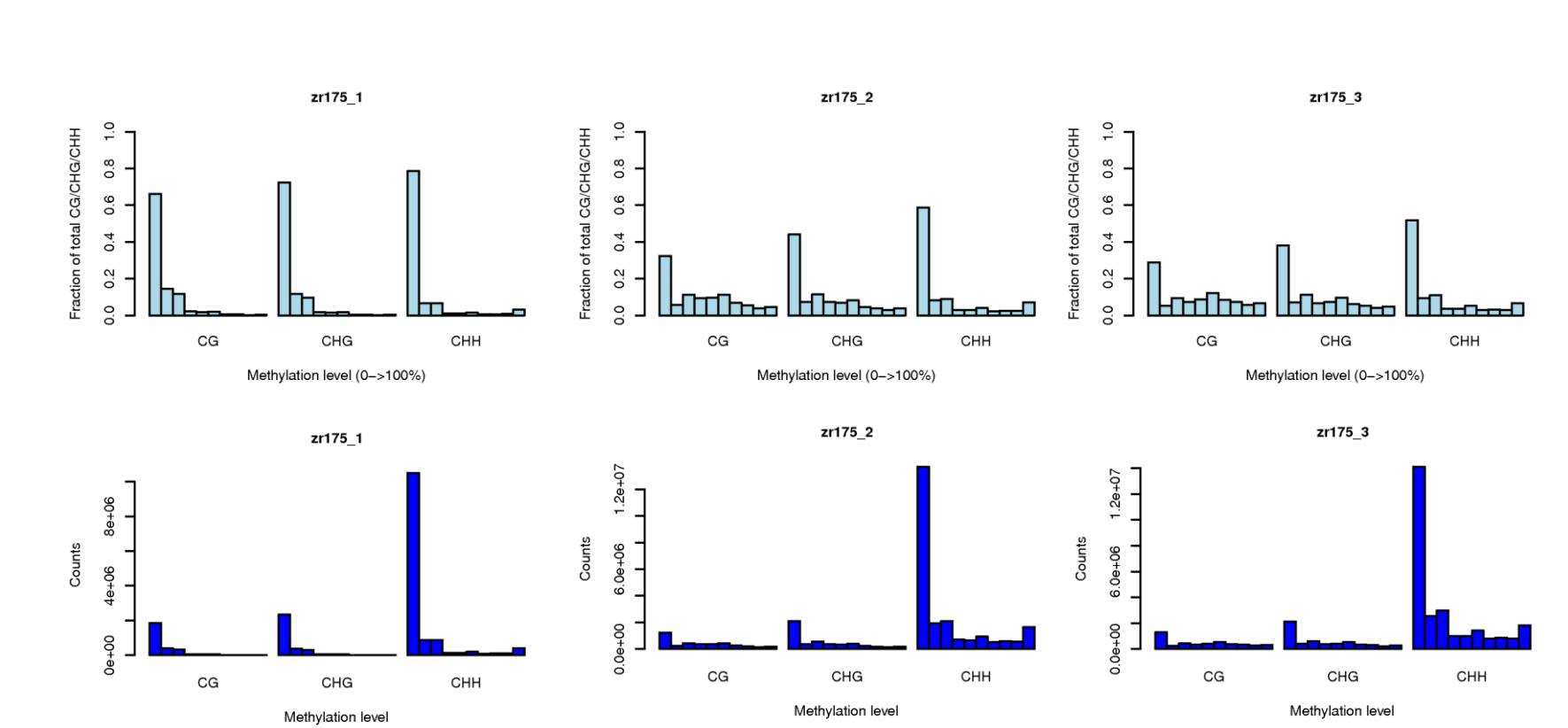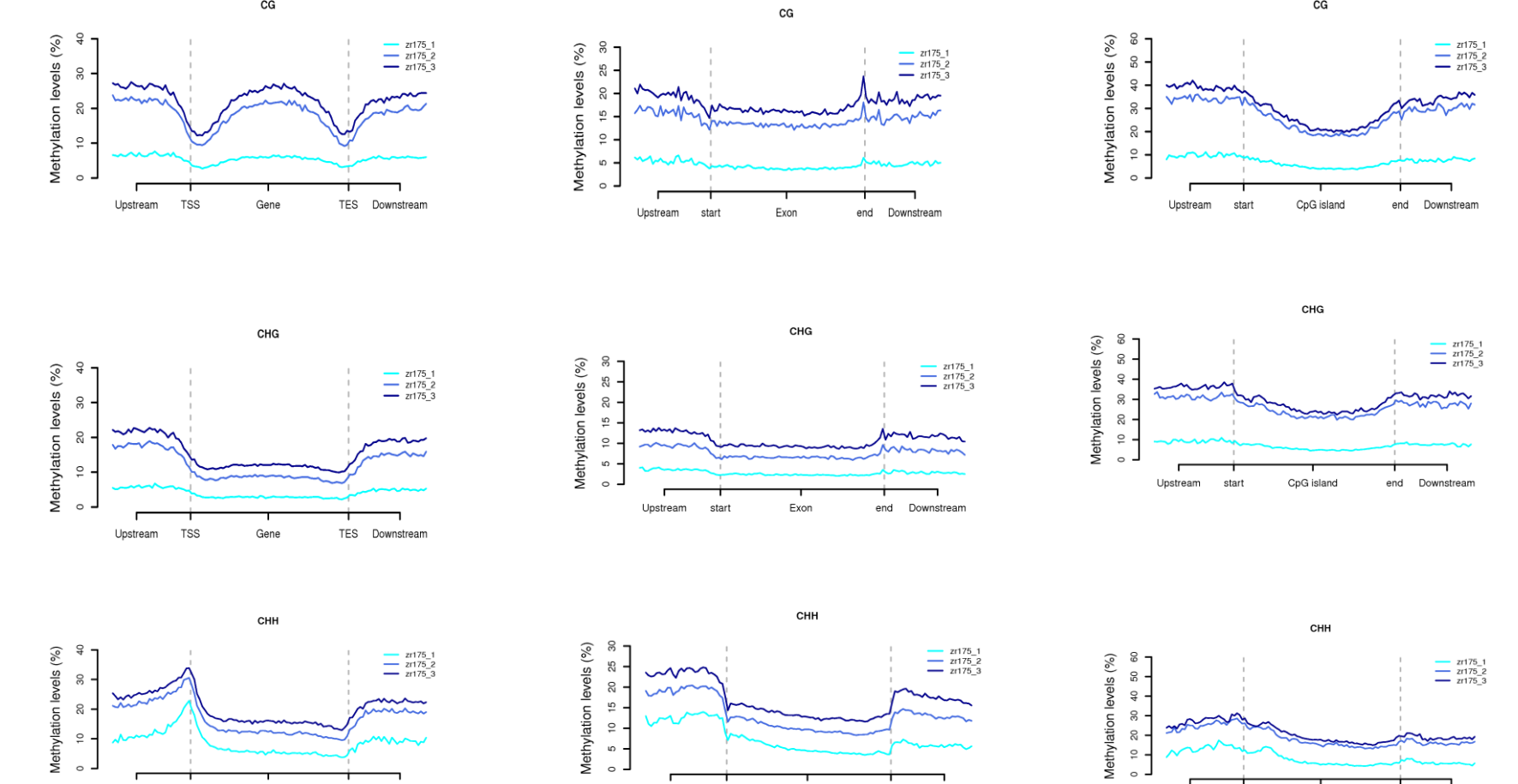## Whole Genome 5mC profiling in soybean

➤ **Genome coverage**

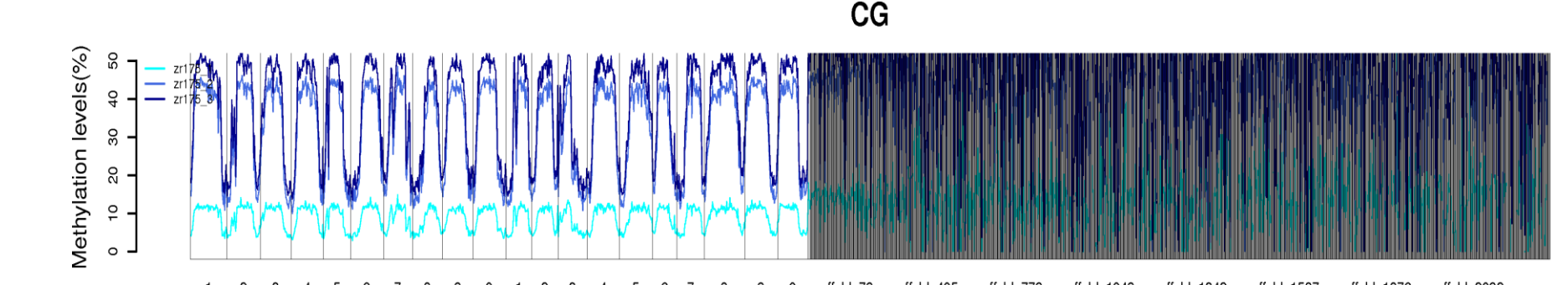

➤ **Coverage per cytotine**

➤ **Distribution of CG/CHG/CHH sites for three soybean samples**

➤ **Metaplot for gene, exon and CpG island**

➤ **Genome methylation level**

References

1. Meissner A, Mikkelsen TS, Gu H, Wernig M etc. Nature. 2008 Aug 7;454(7205):766-70.
2. Smith ZD, Gu H, Bock C, Gnirke A, Meissner A. Methods. 2009 Jul;48(3):226-32