

# DNA Methylation Analysis (Agilent's Genomic Workbench Steps)

## Standard Procedure for Analysis

**Project Name: DNA methylation Analysis**

**Requestor:**

**Names and contact info of Analyst:**

**Brief Description of Analysis Types: DNA methylation tiling array data**

**Procedure or Analysis Revision Date:**

**Analysis Results/Deliverable Date:**

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**Scientific context or hypothesis for analysis:**

To access differential methylation status among different conditions

**Checklist before starting analysis:**

**Scanned DNA tiling array chips**

**Experiment design**

**Sample annotation**

**Sources of input required:**

- Experiment design (Control, Disease, Sampling time point),
- Sample annotation,
- Tissue and other supporting information

**Input data:**

- Agilent Two Color tiling array feature extracted txt files

## **Analysis plan or steps taken:**

### **1. Purpose.**

To analyze DNA methylation microarray data generated using Agilent's ChIP-on-Chip tiling array platform

### **2. Responsibility.**

Systems Biology

### **3. Materials and Equipment.**

Genomic Workbench v 7.0.4 Lit Edition Software (Agilent Technology Inc.)

### **4. Procedure.**

Recently, we use R for dealing with Agilent DNA methylation microarrays. The preprocessing steps are same to the transcriptomics analysis.

The downstream analysis is typically divided into specific regions.

## **Data import and Experiment Set up**

To set up an experiment:

- Select the CH3 application
- Import design files and data files (Agilent FE files; **Import > Array Files > FE File**)
- Create a new experiment
- Add the imported data to the experiment
- Select the experiment
- Combine design and generate report

## **To update probe annotation in design files**

- Home tab, **>User Preferences > Miscellaneous tab > eArray User Details** (type **Username** and **Password**) **> OK**
- select the appropriate design **> right- click the desired design > Download from eArray.com > Yes**

## **To generate a probe report**

- **Reports tab > Generate Report > Complete Genome > type the report name (name.xls) > OK.**
- The probe report includes the following information either for single chromosomes or the complete genome:
  - Log ratio for each event
  - Number of probes
  - Start and stop of each event
  - Whether the probe is in a CpG island, a promoter, or inside a gene boundary
  - Probable gene for the probe
  - Excel spreadsheet matrix containing all the data (and the above probes and samples annotations).

### **5. References.**

Genomic Workbench 7.0.4 Methylation (CH3) Analysis User Manual (G3800-90010\_MethylationAnalysis.pdf)  
<http://www.r-project.org/>