ChIP-Seq & MDB-Seq Service

Never Ending Service

ebiogen
(주)이바이오젠

BioResearch Service

BIO-Experiment & Analysis Service

Microarray
- ❖ Gene Expression
- ❖ miroRNA
- ❖ CGH / CNV
- ❖ ChIP on chip
- ❖ Methylation
- ❖ Agilent/Affymetrix
- ❖ Exiqon

NGS
- ❖ RNA-Seq
- ❖ small RNA-Seq
- ❖ ChIP-Seq
- ❖ MBD-Seq
- ❖ Exome-Seq
- ❖ Target DNA-Seq
- ❖ Illumina/IonProton

qRT-PCR
- ❖ mRNA
- ❖ microRNA
- ❖ PCR Array
- ❖ Qiagen
- ❖ Genosensor
- ❖ Others

Antibody Array
- ❖ Protein Profiling
- ❖ Phosphorylation
- ❖ FullmoonBio
- ❖ RayBiotech
- ❖ Others

Microarray
- ❖ Meaningful Data from Any Genome

NGS
- ❖ Next Generation Sequencing

nature COMMUNICATIONS

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NATURE COMMUNICATIONS | ARTICLE

Metabolic engineering of *Corynebacteriun glutamicum* for L-arginine production

Seok Hyun Park, Hyun Uk Kim, Tae Yong Kim, Jun Seok Park, Suok-Su Kin

Affiliations | Contributions | Corresponding author
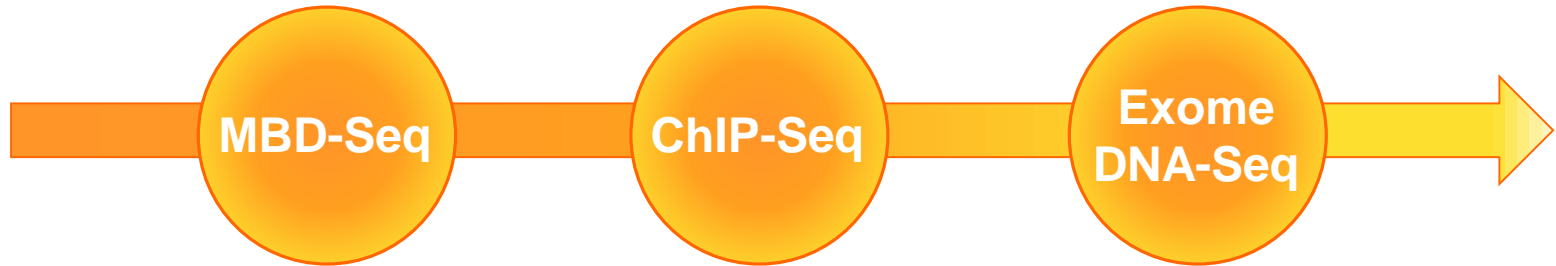
NGS Service
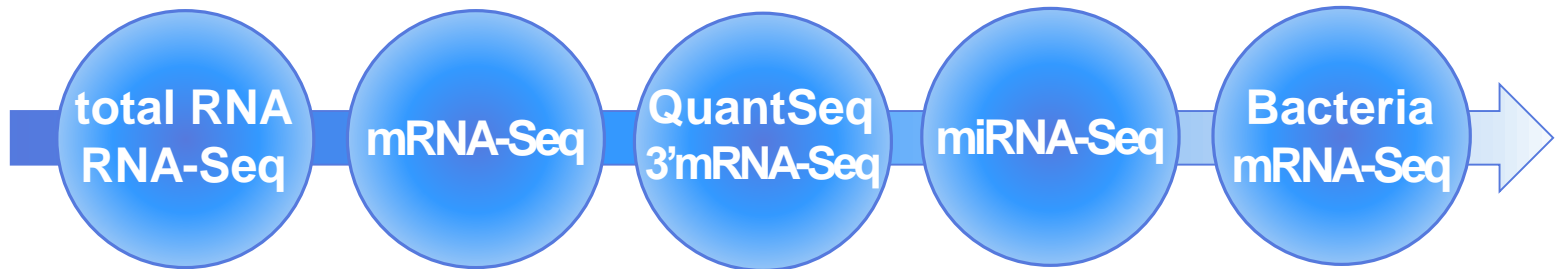
DNA

- **MBD-Seq**
- **ChIP-Seq**
- **Exome DNA-Seq**

- DNA Methylation Profiling
- Epigenome 분석
- ~ 2μg gDNA

- DNA-Protein Interactions
- Histone modifications
- ~20μℓ IP-DNA

- Whole Exome Sequencing
- SNP, CNV, Mutation
- ~ 2μg gDNA

RNA

- **total RNA RNA-Seq**
- **mRNA-Seq**
- **QuantSeq 3'mRNA-Seq**
- **miRNA-Seq**
- **Bacteria mRNA-Seq**

- mRNA-Seq 분석외 lncRNa 분석
- Whole Transcriptome
- ~ 2μg total RNA

- Gene Expression, Isoform, GO/Pathway
- Splicing, Gene Fusion
- ~ 2μg total RNA

- mRNA Expression Profiling
- Low Quantity & Quality RNA 샘플 실험가능
- ~ 2μg total RNA

- microRNA Expression Profiling
- Target Gene 분석외
- ~ 2μg total RNA

- Gene Expression Profiling
- GO/Pathway/Network
- ~ 2μg total RNA
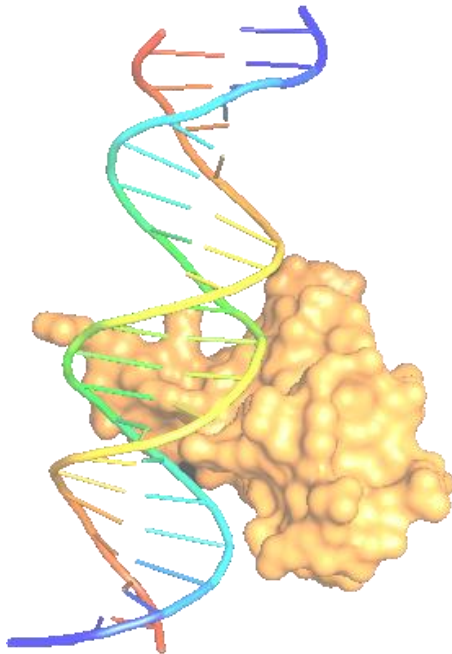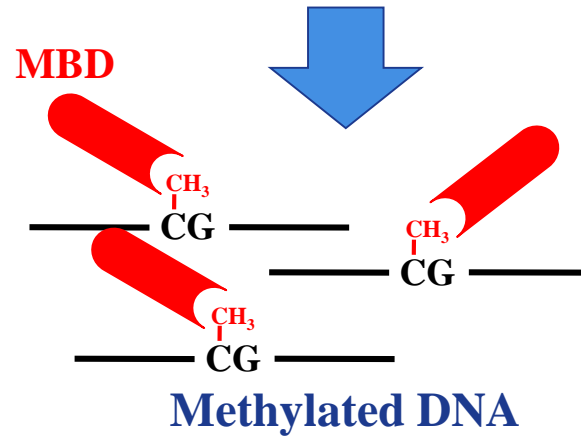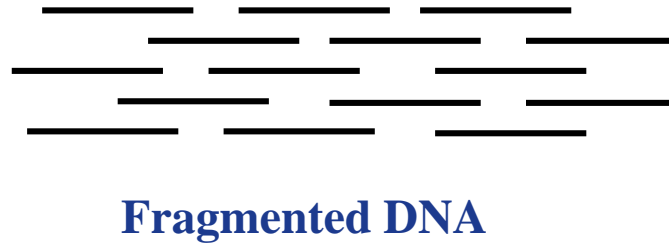
ChIP-Seq Sample Preparation
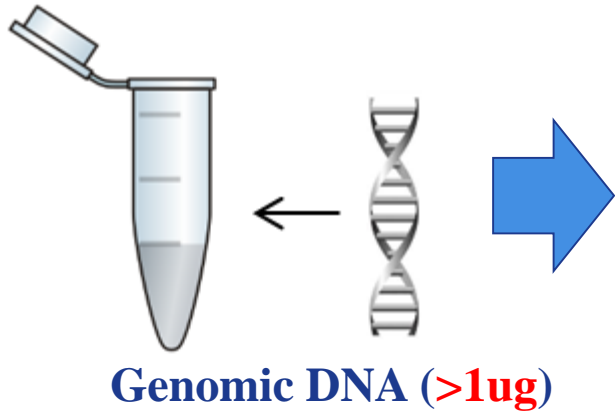

Cross-link protein on DNA

Cut DNA

Immunoprecipitate

Isolate the fragment DNA from complex

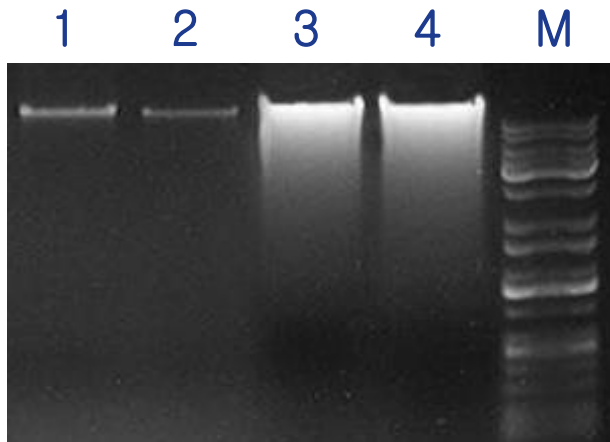# MBD-Seq Sample Preparation

Genomic DNA (>1ug)

Fragmented DNA

MBD

CH₃
CG

CH₃
CG

CH₃
CG

Methylated DNA
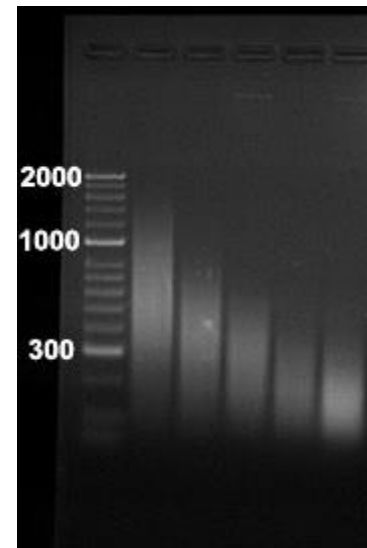
QC and Library Construction

DNA Sample Prep / Shearing
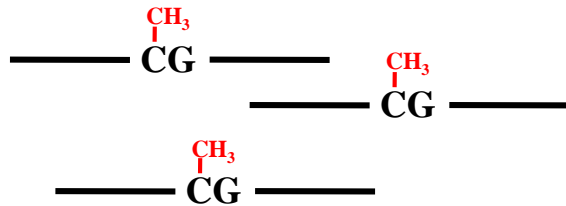
Genomic DNA의 전기영동

Genomic DNA의 Shearing

1, 2 : 실험에 좋은 샘플의 예
3, 4 : 사용할 수 없는 샘플의 예

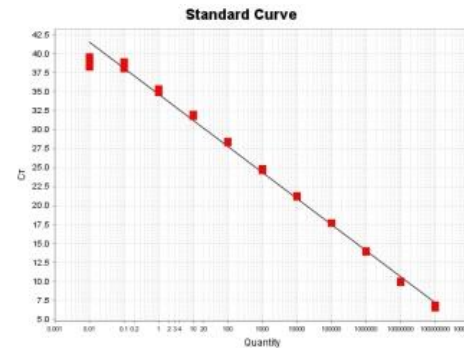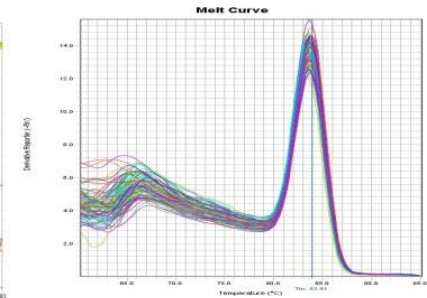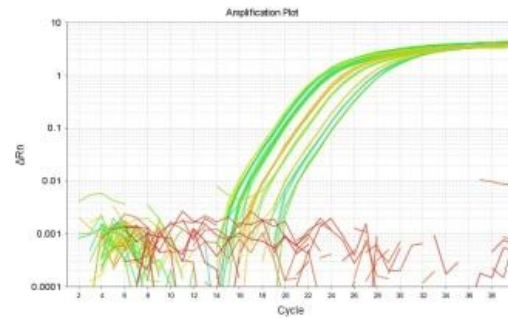다양한 조건에서 shearing을 진행하여 알맞은 size의 DNA 단편 획득 (300~500nt)
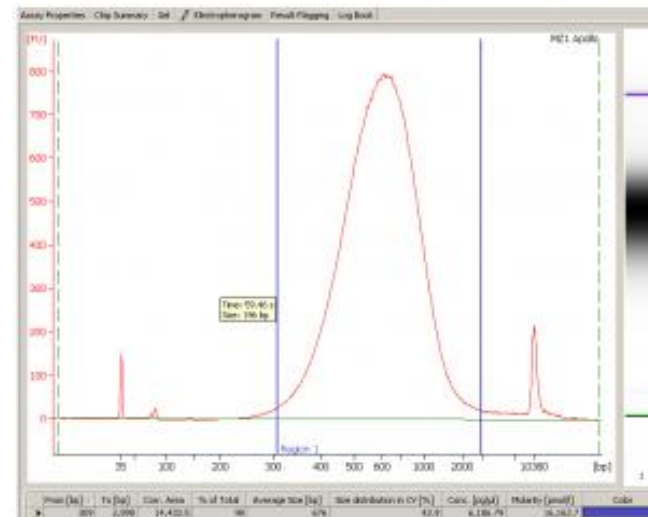
Sample Quality Control (QC)

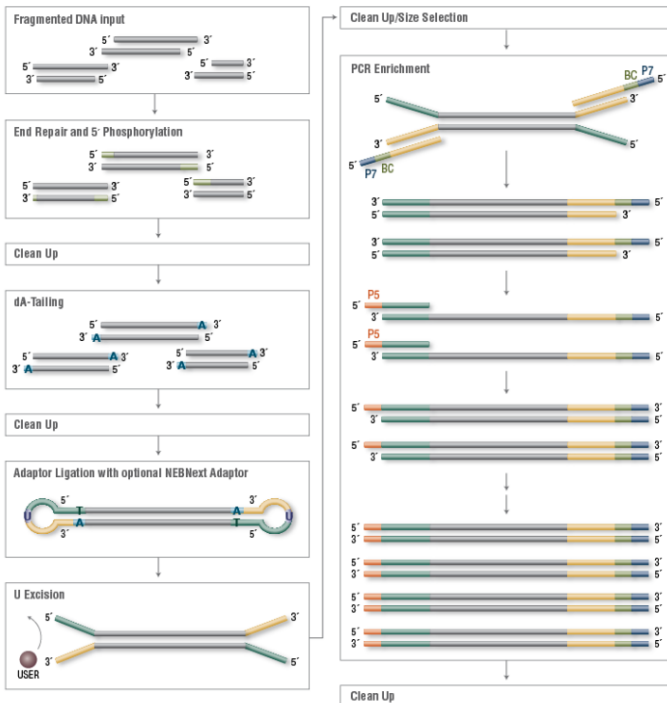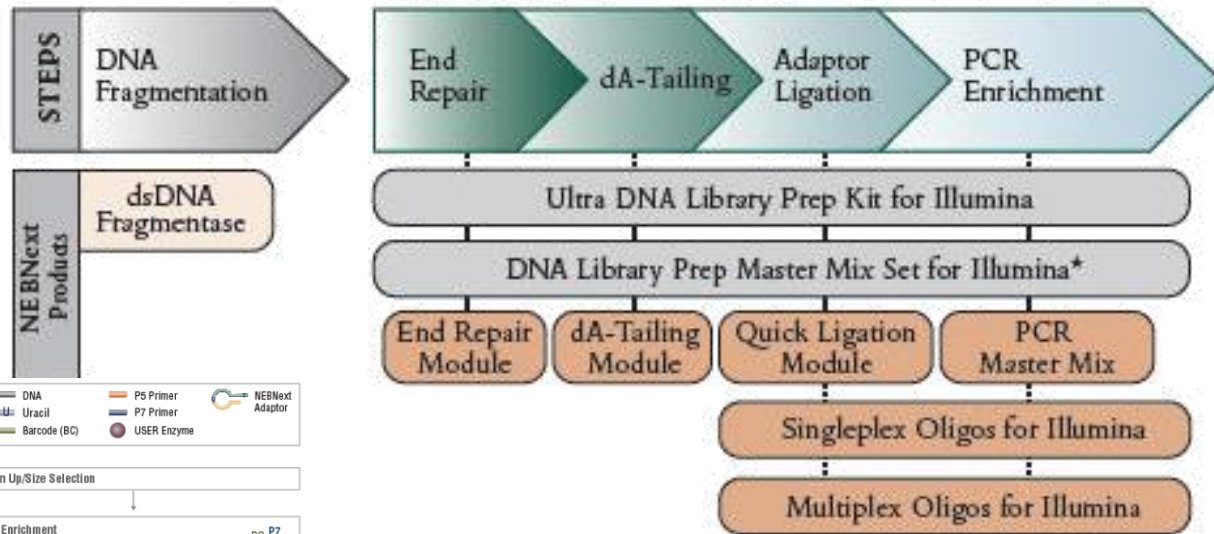**Methylated DNA**

qRT-PCR

Known methylated region/
known unmethylated region 에 대한 qRT-PCR

Quantitative Analysis
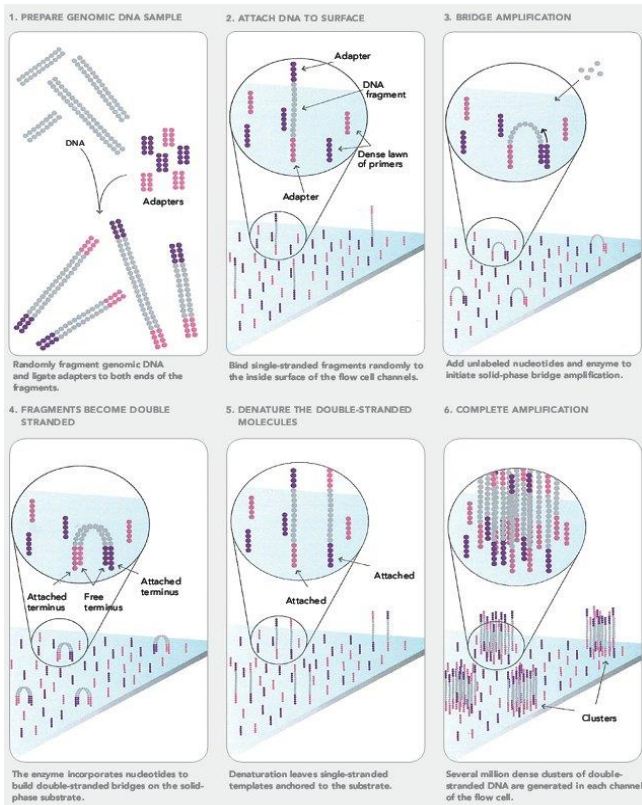**Comparative Analysis ($\Delta\Delta C_T$)**
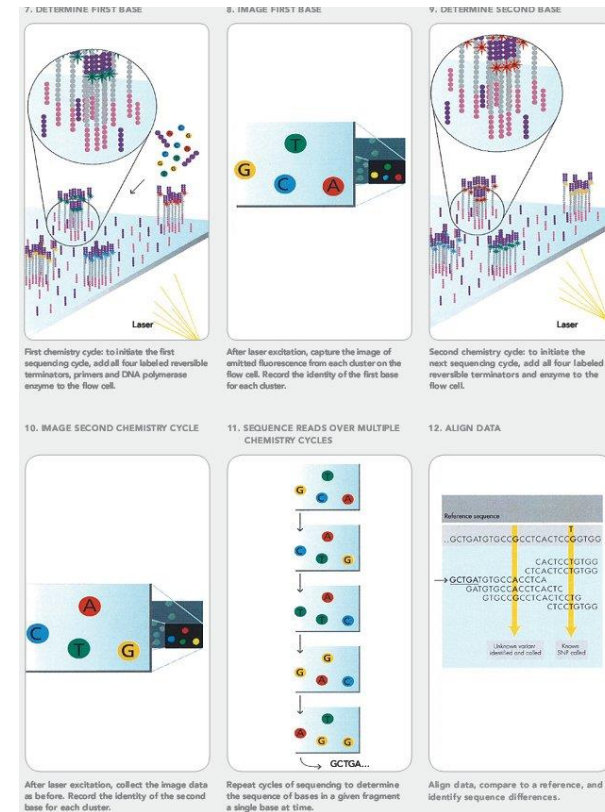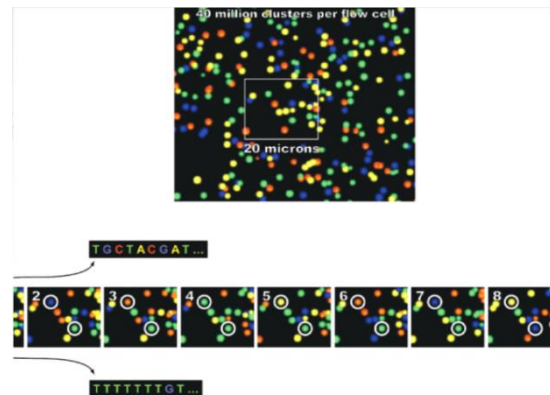
Library Generation
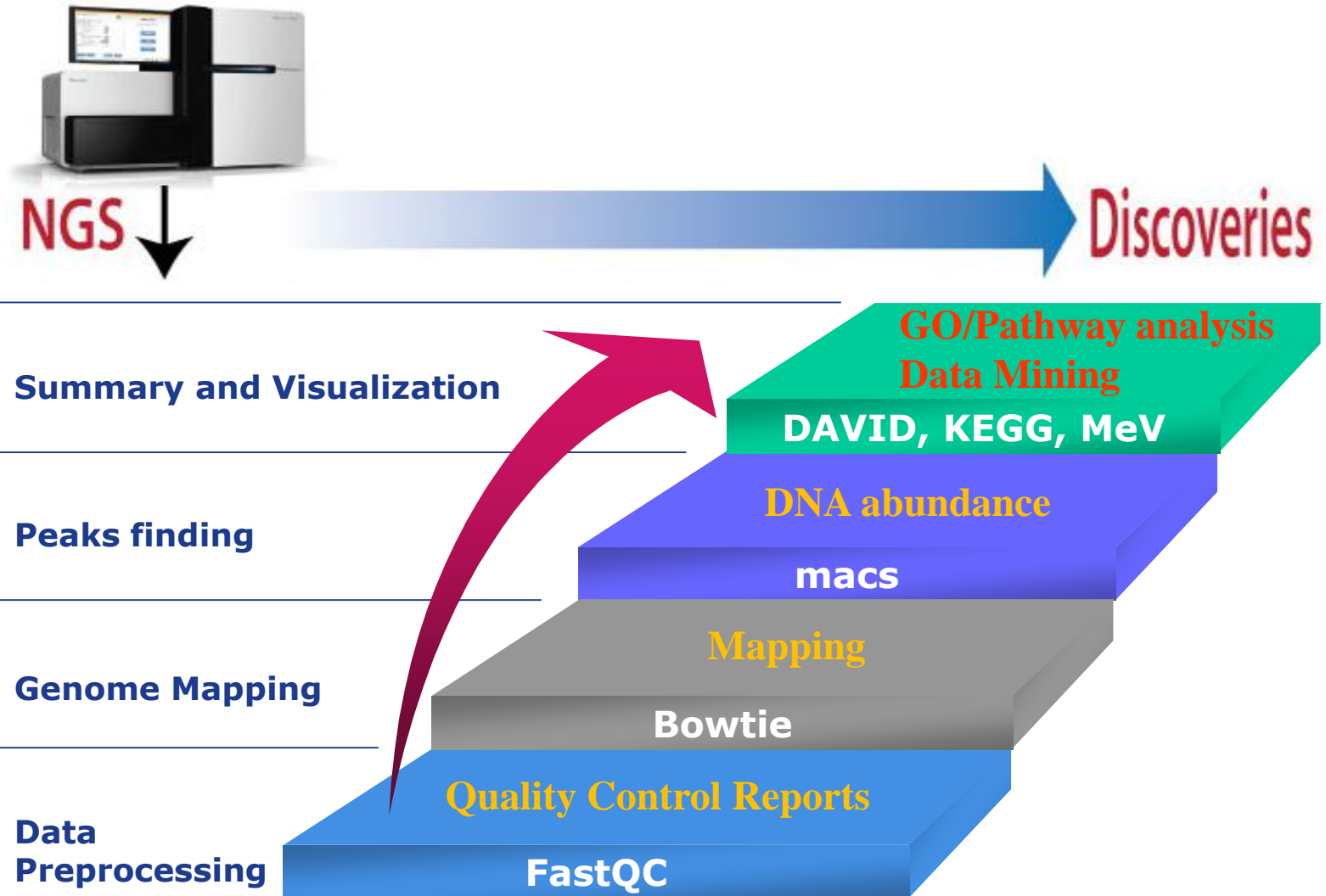

Eletropherogram of DNA library

Sequencing

Run Format	Read Length	# of Reads	High-Quality Output (Gb)	
			/lane	/FlowCell
Single End	1 x 50bp	~150 million/lane	7.5 Gb	135-150 Gb
	1 x 100bp		15 Gb	270-300 Gb
Paired End	2 x 50bp	~300 million/lane	15 Gb	270-300 Gb
	2 x 100bp		30 Gb	540-600 Gb

Illumina HiSeq-2500

Work Flow of Data Analysis

NGS → **Discoveries**

Summary and Visualization

Peaks finding

Genome Mapping

Data Preprocessing

GO/Pathway analysis
Data Mining
DAVID, KEGG, MeV

DNA abundance
macs

Mapping
Bowtie

Quality Control Reports
FastQC

Other Data Analysis Tools for Data Processing, Mining, Visualization : MISO, Quick GO, ClueGO, CytoScape, GSEA, UCSC Genome, IGV, IPA, Others
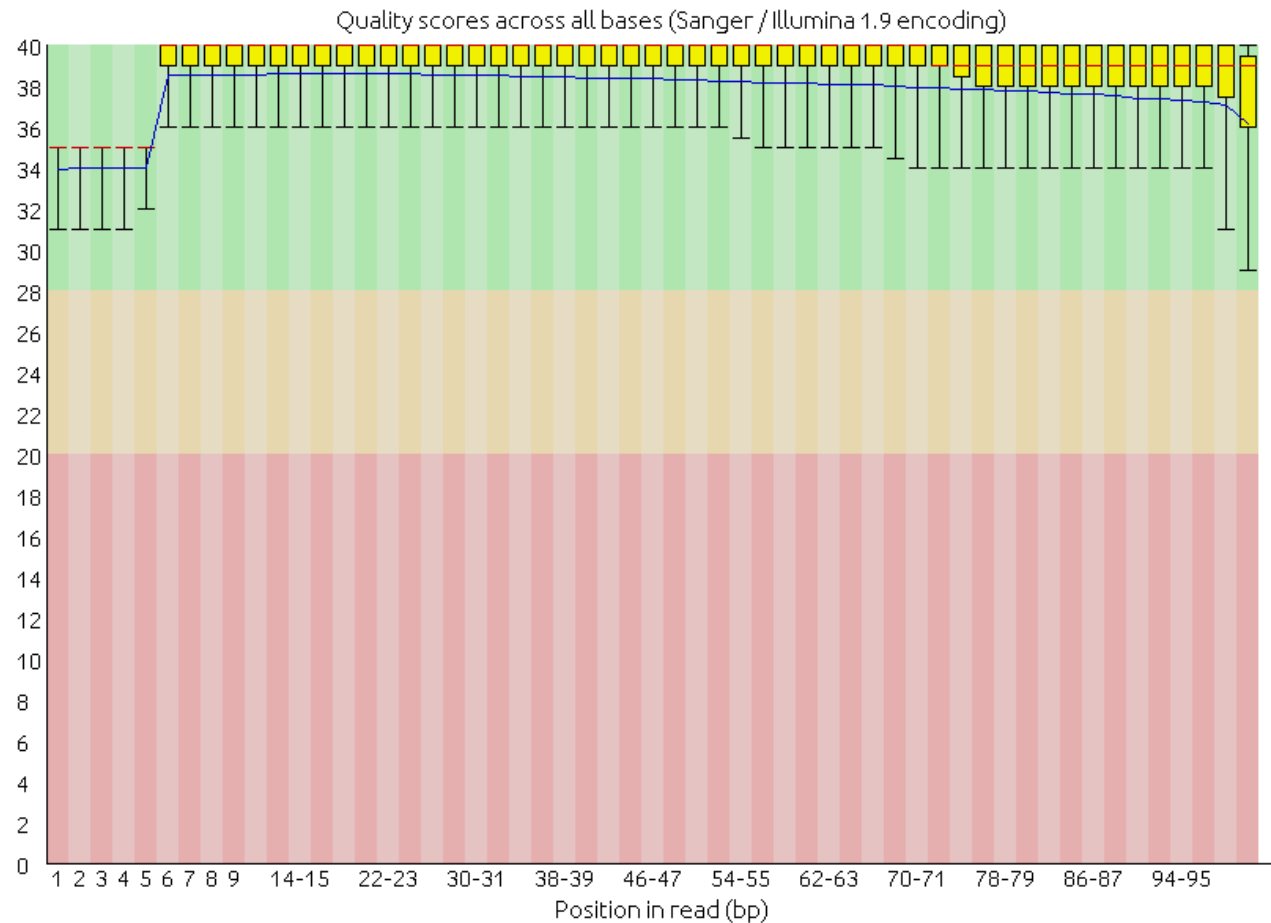
Data Analysis – Data preprocessing

FastQ 파일 안에서 각 position의 base에 대한 quality 값의 영역을 보여 줌
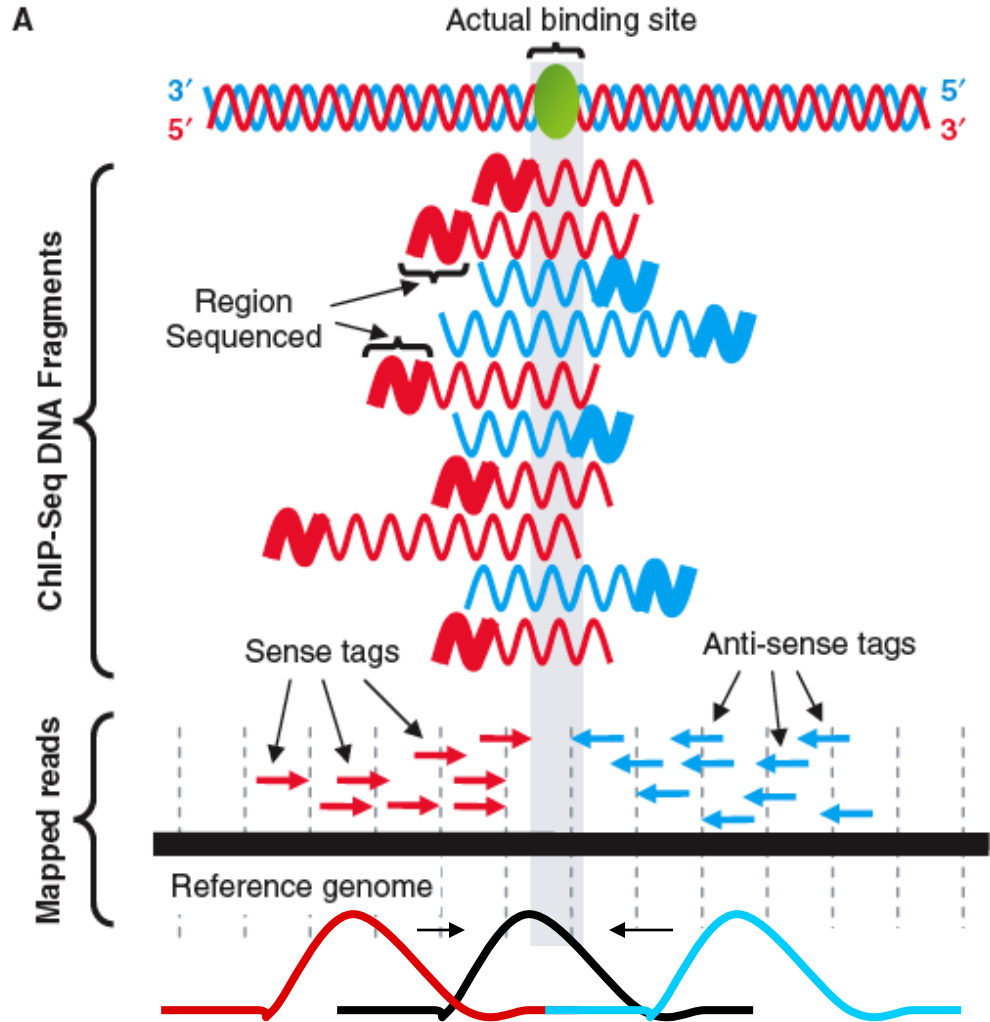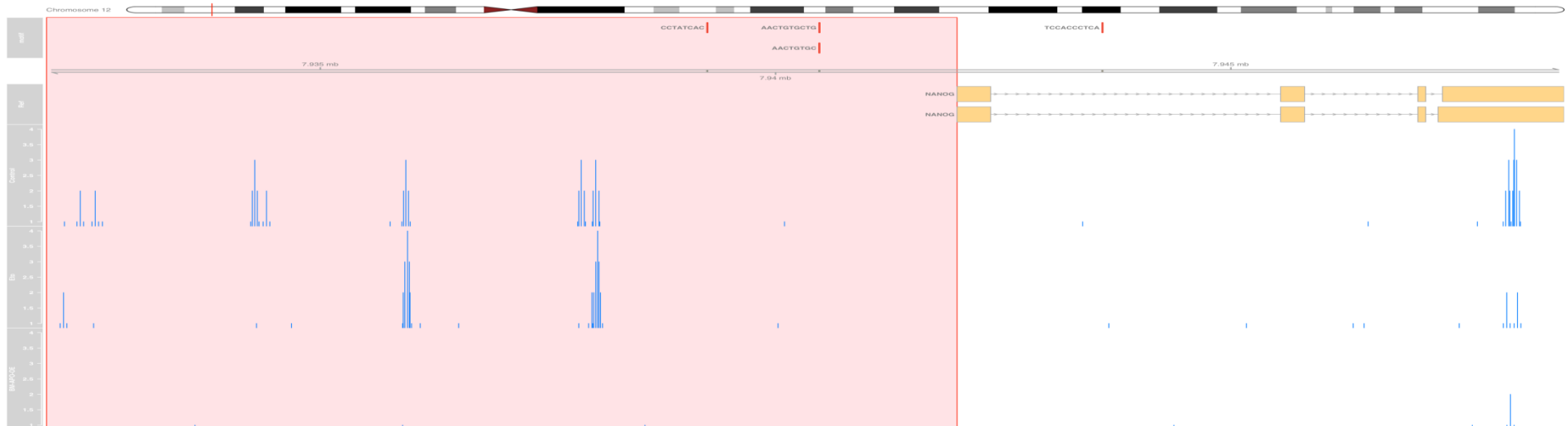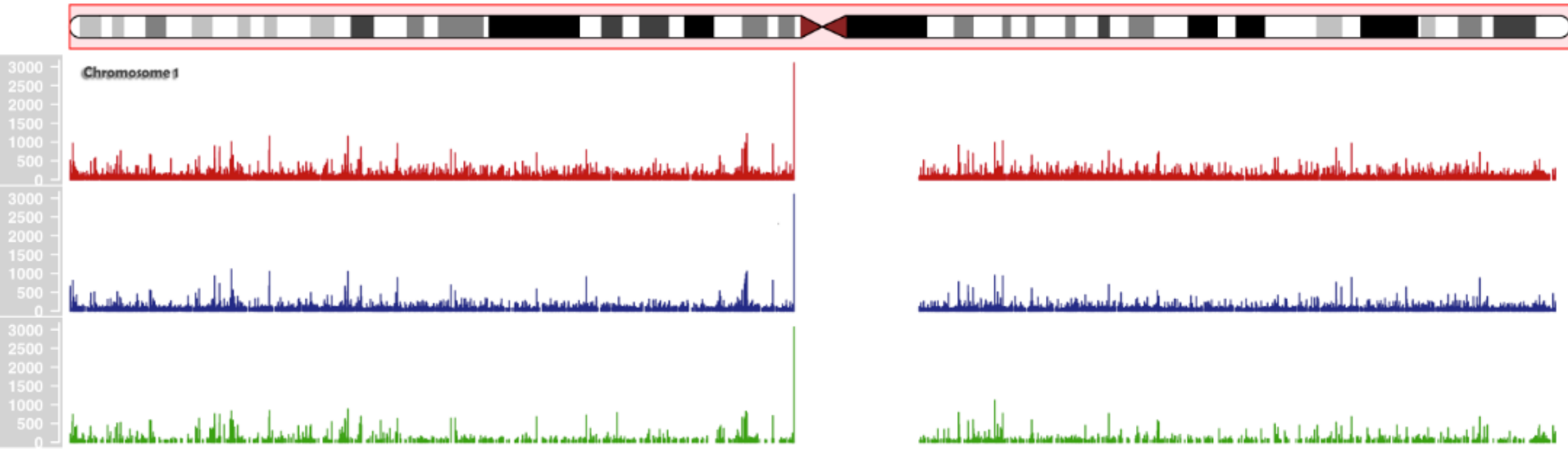
How to find peak

• Fragments contain the TF binding site at a (mostly) random position within them.

• Reads are (randomly) from left or right edges (sense or antisense) of fragments.

• Thus peak for sense tags will be 1/2 the fragment length upstream…

• Binding site position = mid-way between sense tag peak & antisense tag peak.

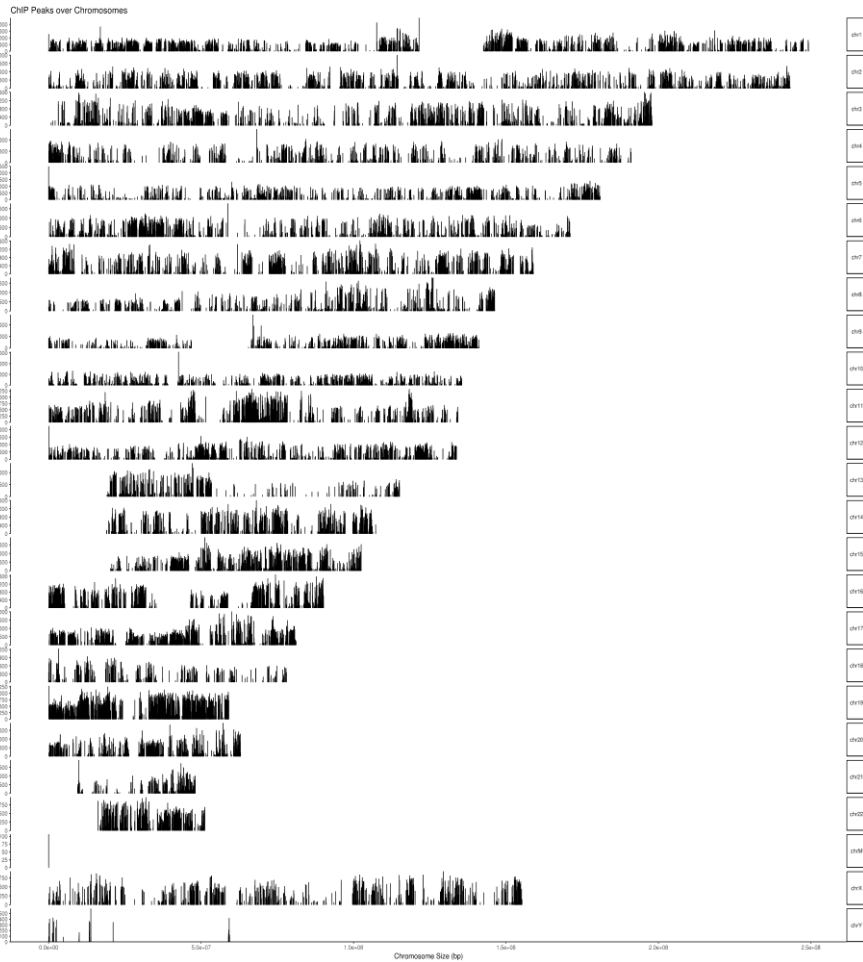• To get binding site peak, shift sense downstream by ½ fragsize & antisense upstream by ½ fragsize.

A

Actual binding site

3′ 5′
5′ 3′

ChIP-Seq DNA Fragments

Region Sequenced

Sense tags   Anti-sense tags

Mapped reads

Reference genome

Peak annotation/ Motif discovery

Peak Image

Visualization Data

Visualization Data

Distribution of transcription factor-binding locirelative to TSS

Transcription Factor Binding

고객을 최우선으로 하고
직원이 즐겁게 일할 수 있는
국내 최고의 바이오 기업으로
성장해 나가겠습니다.

감사합니다.

BioResearch & HealthCare Creator

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