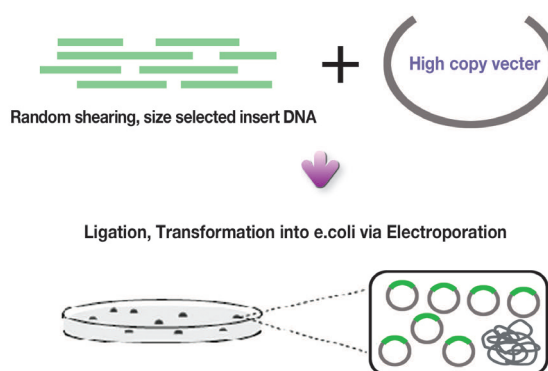


# Shotgun Library Construction

## Description

After random shearing, we produce Shotgun library with more than proper titer by obtaining the insert size (1.5–10kb) desired by customers. After identifying the completed library quality, the result report is delivered. The library is provided a cell stock or DNA upon customer's request.

## Fosmid Library Construction Process



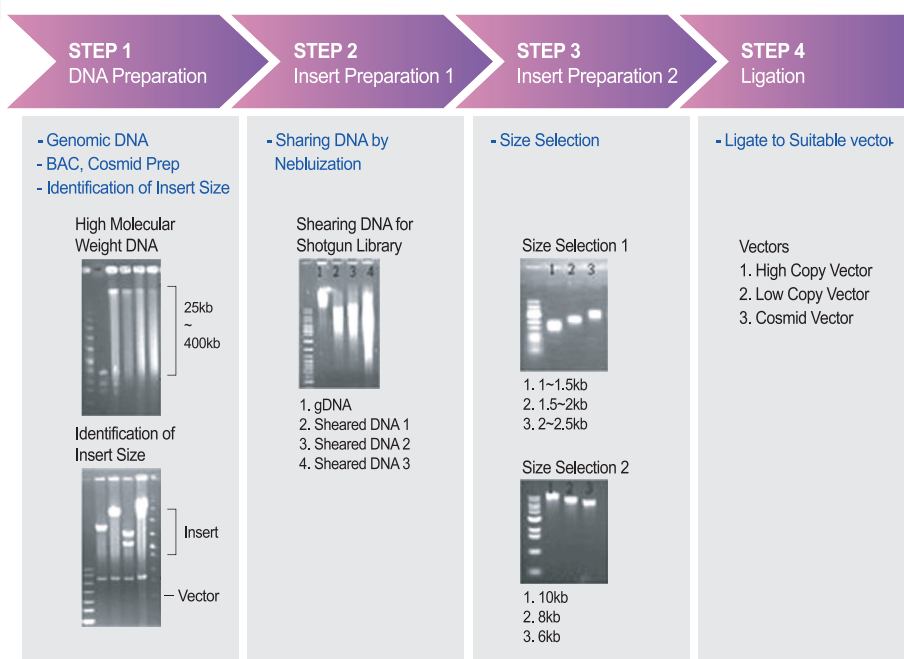
## Features

- DNA Sources : Plant, Bacteria, Virus, Bacteriophage, BAC/Cosmid/Fosmid DNA
- Library Sources : Insert Preparation(Random Shearing)
- Insert Size : 1.5~10kb Insert Plasmid Library(Typically 2~5kb)
- Vector : High Copy Number Vector or Low Copy Number Vector
- Library Format : Cell Stock or DNA
- Required Time : 4 Weeks after Sample Quality Identification

## Result

- Library Report : Insert Size Check(Average Insert Size>1kb), Insert Ratio(95%), TEST Sequencing Result
- Library Type : Cells Stock(96 or 384 Well Plate) or DNA

## Shotgun Library Construction Process



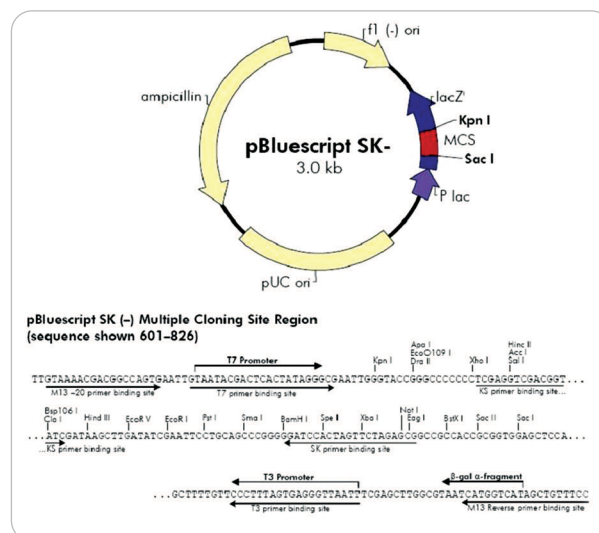
# cDNA Library Construction

## Description

We produce cDNA library by synthesizing cDNA from Cytoplasmid RNA and using ds cDNA obtained via size fraction.

## Features

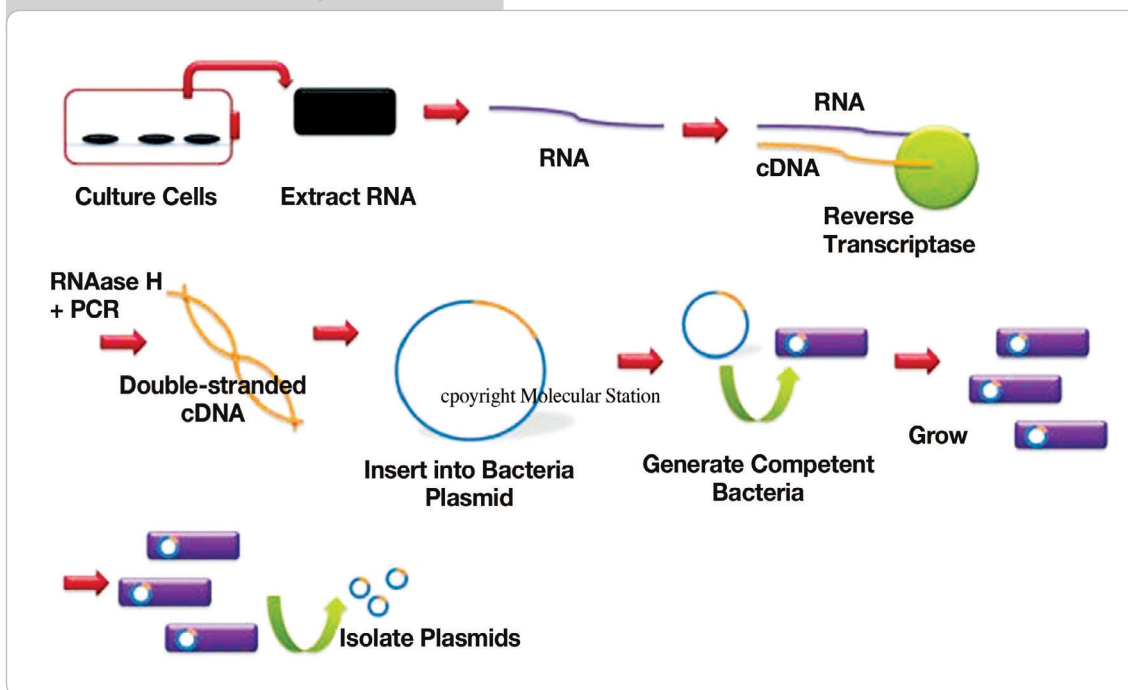
- RNA Sources : Mammalian, Plant
- Format : Standard cDNA Library
- Average Insert Size : 1.5~2.5kb
- Insert Size Range : 0.5~4.5kb
- Total Number of Primary Clones :  $1.0 \times 10^7$
- Time Required : 4~5 Weeks after Sample Quality Identification



## Result

- Library Report : Average Insert Size Check, Insert Size Range Check, TEST Analysis-Redundancy Check and Blast Servis
- Library Type : Phagemid , Cell Stock or DNA
- Analysis Report : Blast Service, Others

### Flowchart of cDNA Library Construction

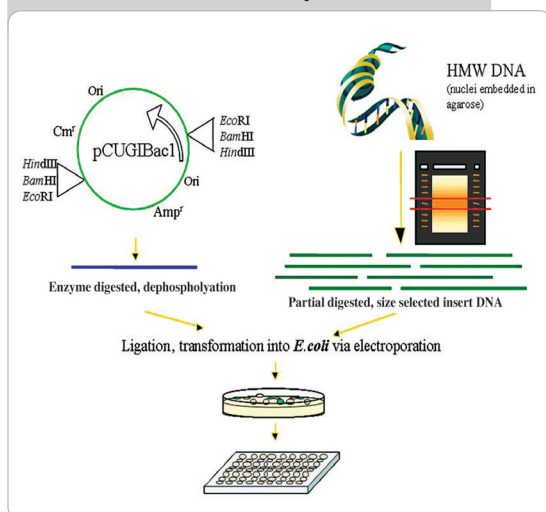


# BAC Library Construction

## Description

We produce the library more than proper titer by cloning high molecular DNA using the BAC vector after carrying partial digestion with the restriction enzyme (EcoRI, BamHI, HindIII). The quality of the library is identified by performing NotI digestion & PFGE gel electrophoresis analysis (~200clones), then the analysis data is provided with the result report. The library is provided as a cell stock or DNA upon customer's request.

### Flowchart of BAC Library Construction



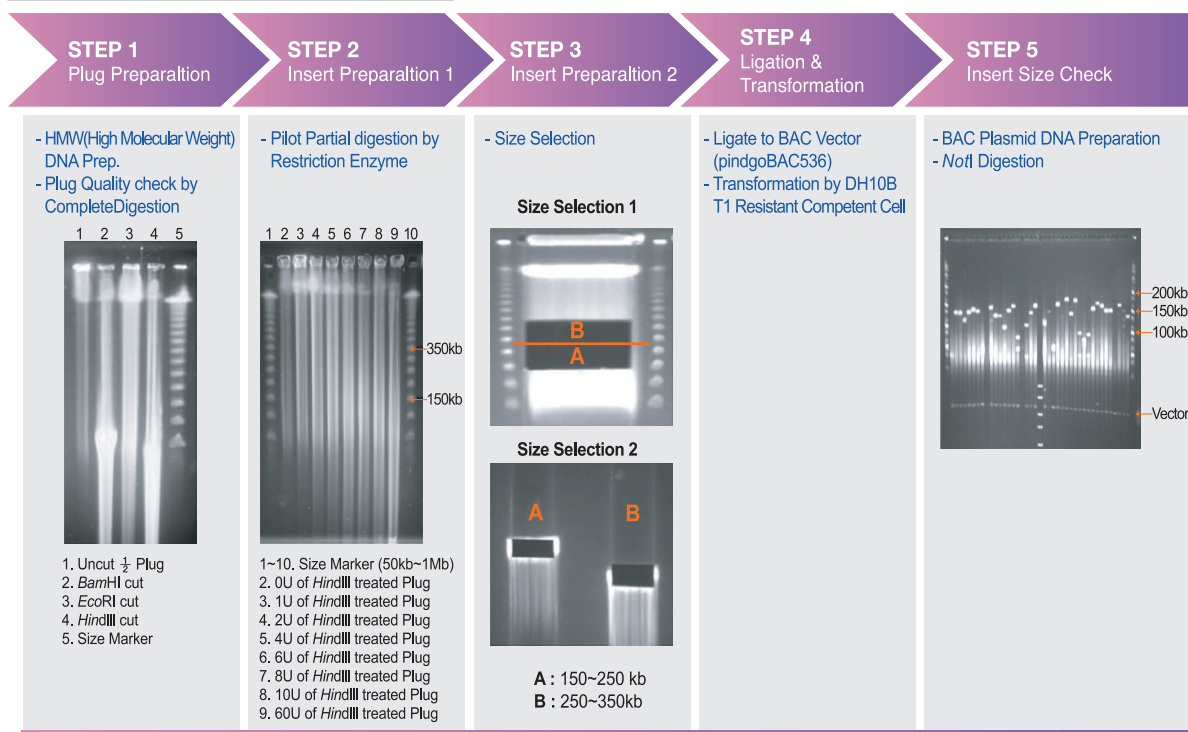
## Features

- DNA Sources : Mammalian, Plant, Insect, Bacteria, Virus, Bacteriophage
- Library Sources : Insert Preparation – Partial Digestion
- Insert Size : 120kb~300kb(Average Insert Size : ~130kb)
- Vector : pIndigoBAC536
- Library Format : Cell Stock or DNA
- Time Required : 8 Weeks after Sample Quality Identification

## Result

- Library Report : Insert-Size Check Report, Insert Ratio (90%)
- Library Type : Cell Stock or DNA

### BAC Library Construction Process



# Fosmid Library Construction

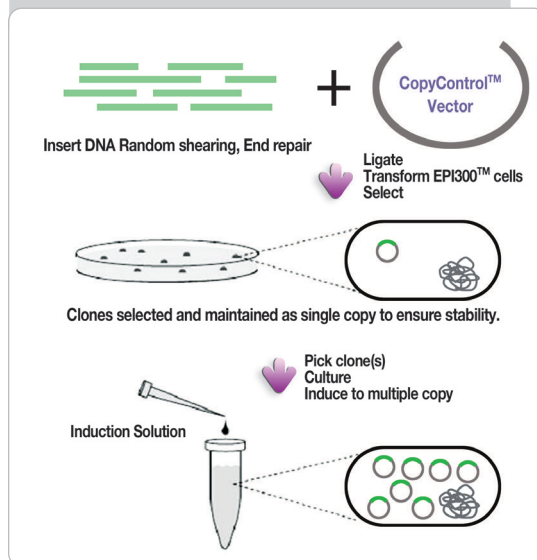
## Description

After random shearing, we produce Fosmid library with the proper number of clone (Cfu or Pfu) via transfection after 35–45 kb Insert. The quality of complete library is identified using various methods and the obtained result is delivered. The library is provided as a cell stock or DNA upon customer's request.

## Features

- DNA Sources : Mammalian, Plant, Bacteria
- Library Sources : Insert Preparation (Random Shearing)
- Insert Size : 25~35 kb(Average Insert Size : 35kb)
- Library Format : Cell Stock or DNA
- Time Required : 4 Weeks after Sample Quality Identification

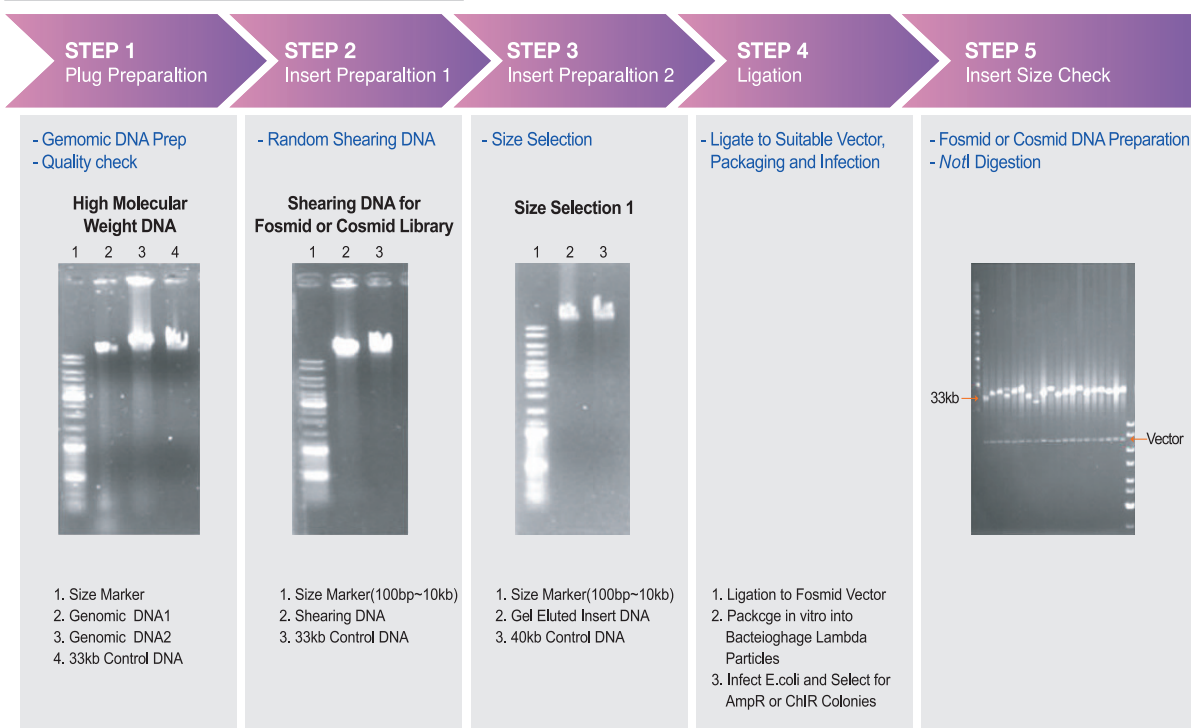
## Flowchart of Fosmid Library Construction



## Result

- Library Report : Insert-Size Check Report, Insert Ratio(95%)
- Library Type : Cell Stock(96 or 384well plate) or DNA

## Fosmid Library Construction Process



# End & EST Sequencing

## Description

We provide the essential mutant library preparation for protein structure and function study, gene expression study, and Promotor Change.

## Features

- DNA Sources : BAC Library, Fosmid Library, cDNA Library
- Time Required : 4~6 Weeks after Sample Quality Identification

## Result

- End Sequencing Report / End Sequence Raw Data(ab1 File) / Blast Result, Gene Ontology Report(cDNA Library Only) Redundancy(cDNA Library Only) / DNA(cDNA Library Only) / Cell Stock

# Shotgun Library Construction & Full Length Sequencing

## Description

We produce shotgun library construction and deliver the final result by assembling the result.

## Features

- Shotgun Library Construction
- Sequencing by a DNA Analyzer 3730xl
- Read Length more than 700bp(Phred Score >20)
- Assembly Using the Phred-Phrap
- Gap Filling
- Time Required : 5 Weeks after Sample Quality Identification

## Result

- Library Report, Assembly Report, Sequencing Raw Data (Ab1 File), Contig Sequence and Contig Quality Check



# Other Service

## Cell stock production

■ We produce Cell stock by carrying cell culture in mass production upon customer's request.

## DNA Extraction

■ We perform DNA extraction in mass production service from cell culture to DNA preparation upon customer's request. (Extra charge will be added if sequencing processed additionally.)

- Required Information– Antibiotics Used, Antibiotic Concentration
- Plasmid Type : BAC, Fosmid, Cosmid, Normal Plasmid, cDNA etc

## PCR product purification

■ We provide purification service for sequencing when you send us crude PCR product. The provided sample should be 50~100ng/ $\mu$ l of concentration and more than 20 $\mu$ l of volume.

## Agarose Gel Extraction

■ We perform DNA extraction service by selecting the target-sized product among various size PCR products desired by customers.

## PCR Service

■ We perform PCR service with the template and the primer given by a customer. (We also provide primer synthesis service)

- Required information–PCR condition, Primer T<sub>m</sub> value, Predicted product size, primer concentration, template concentration.(Extra expense for set up can occur when the PCR condition for is not given.)

## PCR optimization Service

■ For your convenience, we find the optimized annealing temperature for high quality of PCR products from the gDNA of our customers. Your sequencing result can be better when we perform Gradient PCR on be half of you.

➤ Gradient PCR

