## Want to compare gene expression levels between sample groups?

## Then... Don' t miss our **SPECIAL SALE on RNA-seq Data Analysis Service!**

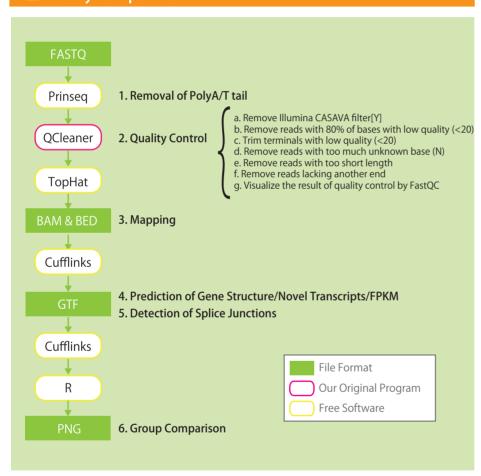
Until March-31-2014

## Features

- ·Sample Group Comparison
- ·Quick Service (2 weeks)

¥ 116,000/sample

## ■ Analaysis Pipeline



### Price

Analysis Step  $1\sim4$  ¥80,000Step 5 ¥16,000Step 6 % combination) ¥20,000Total ¥116,000

## Required Data

- Sequence data: FASTQ
- Information of target groups

## ■ Data We Provide

- Quality report: HTML
- •Result of transcpt detection: EXCEL
- •Result of expression comparison: EXCEL
- Summary report:PDF

- % This offer is only applied to 3 samples or more.
- % Tax is not included in the prices shown above.
- \* The total number of base must be less than 3Gb/sample.
- \* Please contact us if you live outside Japan.
- \* Only paired-end data that are sequenced by Illumina platform are accepted.
- \* The delievery term may be extended if the # of sample is morethan 8.
- \* The analysis result will be sent back to you by your HDD.
- \* Please backup your original data before you send us your data.
- \*\* Please send us extra HDD if the HDD with data has small available space (<15GBxSamples).
- \* We also can detect fugion genes, but with extra charge.
- \* We store your data for no more than 2 months.



US contact:
InfiniteBio Inc.
www.infinitebio.com
natsuhikof@infinitebio.com

# Need a help to search disease-associated genes? Then... Don' t miss our SPECIAL SALE on Human Exome Data Analysis Service!

Until March-31-2014

## **Features**

- ·Case-specific Variants Detection
- Fast Service (2 weeks)

¥ 169,000/sample

## Analysis pipeline [ Analysis Step ] Remove Illumina CASAVA filter[Y] • Remove reads with 80% of bases with low quality (<20) • Trim terminals with low quality (<20) • Remove reads with too much unknown base (N) 1. Quality Control QCleaner • Remove reads with too short length Remove reads lacking another end · Visualize the result of quality control by FastQC **BWA** 2. Mapping to hg19<sup>8</sup> mm9 is also available Picard 3. Removal of Duplicated Reads **GATK** 4. Realignment & Recalibration of Base Quality 5. Detection of SNV/small Indel **GATK** File Format snpEff 6. Genetic Annotation Our Original Program Free Software 7. Merging Case Samples to Control QMerge 8. Filtering & Annotation • Remove low quality variants · Remove synonymous variants Annotate allelic frequency based on case samples Annotate rs ID & build ID based on dbSNP138 · Annotate allelic frequency based on 1000 Genome Project Annotate allelic frequency based on HapMapProject JPT Annotate allelic frequency based on Human Genetic Variation Database (HGVD) %From end of January-2014

## Price

## ■ Required Data

- Sequence data: FASTQ
- Exome capture target region: BED
- · Case/Control information

## ■ Data We Provide

- Quality report:HTML
- Mapping result:BAM
- Variant information:VCF
- · Filtering resut: EXCEL
- Summary report:PDF
- % This offer is limited to only if 3 samples or more.
- \* Tax is not included in the prices shown above.
- \* The total number of base must be less than 8Gb/sample.
- \* Please contact us if you live outside Japan.
- \* Only paired-end data that are sequenced by Illumina platform are accepted.
- \* The delievery term may be extended if the # of sample is more than 8.
- \* The analysis result will be sent back to you by your HDD.
- \* Please backup your original data before you send us your data.
- \*\* Please send us extra HDD if the HDD with data has small available space (<15GBxSamples).
- \* We also can detect variatns based on genetic model and can detect compound heterozygosity, but with extra charge.
- $\ensuremath{\ensuremath{\%}}$  We store your data for no more than 2 months.

Powering Bio-Research By IT

amelieff

US contact: InfiniteBio Inc. www.infinitebio.com natsuhikof@infinitebio.com