

Overview of NGS Analysis Service

Axiohelix Co. Ltd.

No	Types of analysis	Examples	Methods of analysis		Actual analysis
			Title	Contents	
1	Gene expression analysis	detect the differences in gene expressions between samples from the wild-type and the mutant	gene expression analysis	We compared the gene expressions among samples	By mapping sequence reads to the reference genome, we compared the gene expressions based on the number of mapped reads
			GO(Gene Ontology) analysis	We identified the group of genes whose expressions change significantly.	By using Fisher's exact test, we identified the group of genes whose expressions change significantly
2	Genetic variation analysis	detect genetic variations within exons in order to identify genes responsible for some diseases	detecting variations	We detected the variations in genes which are responsible for a disease	After filtering the common variations in samples, we identified the variations in genes which are responsible for a disease
			detecting amino acid changes caused by genetic variations	We detected genetic variations which change amino acid residues in the proteins	We examined how the identified genetic variations (SNPs) can affect the amino acids after the translations
3	Genetic variation analysis by resequencing	detect genetic variations in samples from the different hosts	detectcting variations	We identified SNPs and checked if those SNPs can change the amino acid sequences	After identifying SNPs, we checked if those SNPs can change the amino acid sequences
			sequence profile	We drew heat maps to visualize the amount of mapped reads across the chromosomes	After dividing the whole genome into small windows, we drew heat maps to visualize the amount of mapped reads across the chromosomes
4	DNA methylation analysis	detect the differences of methylation patterns within the targeted regions	CpG methylation rate	We calculated the rate of CpG methylation for targeted regions	By mapping sequence reads to the reference sequence, we compare the gene expressions based on the number of mapped reads
5	Metagenomic data analysis	analyse metagenomic data based on the specific sequences in the samples	metagenomic data analysis	We identified the rate of species in the metagenomic sample	By grouping up the sequenced data based on their similarities, we calculate the rate of species in the sample
6	ChIP-seq analysis	examine the relationship between methylated regions in histones and gene expression patterns	identification of the methylated regions in histones	We examined the relationship between methylated regions in histones and their gene expression patterns	After identifying the methylated regions in histones based on the mapping data, we compared these data with the gene expression patterns