Welcome to Pathogen-NGS

An integrated, comprehensive, and user-freindly Pathogen Next-generation sequencing data analysis website

Designed and maintained by **Bioinformatics and Biostatistics Core Lab, NTU Center of Genomic Medicine**

Reference-based Analysis Workflow

Input Data	Pre-Quality Assessment	Quality Trimming	Post-Quality Assessment	Reference Alignment	Samtools Indexing	Variant Calling	Variant Annotation
Illumina Paired-end Reads	Quality assessment before trimming (**FastQC/MultiQC**)	Quality trimming (**Trimmomatic**)	Quality assessment before trimming (**FastQC/MultiQC**)	Reads mapping to reference genome (**BWA-MEM**)	**Samtools fixmate & Samtools sort**	**BCFtools mpileup & BCFtools call**	Annotating variants (SnpEff)
Illumina Paired-end Reads	Quality Report HTML	Cleaned Paired Reads	Quality Report HTML	SAM file	BAM file	VCF file (gzipped)	VCF file (annotated)
Reference Genome		Cleaned Unpaired Reads					HTML file (SnpEff report)