



Introduction

GNC Bio is a biotechnology company established in 2007.

We mainly perform research services related to genomics (genome sequencing, DEG analysis, pathogen analysis, mitochondrial and chloroplast genome analysis, evolutionary research).

GNC Bio's Bioinformation Analysis Team performed various analyzes using NGS data. If you want to make various types of tables and figures using NGS data, please contact GNC Bio.

We will guide you on how to utilize NGS data along with friendly consultation.

Please wake up the sleeping data now!



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Change is chance

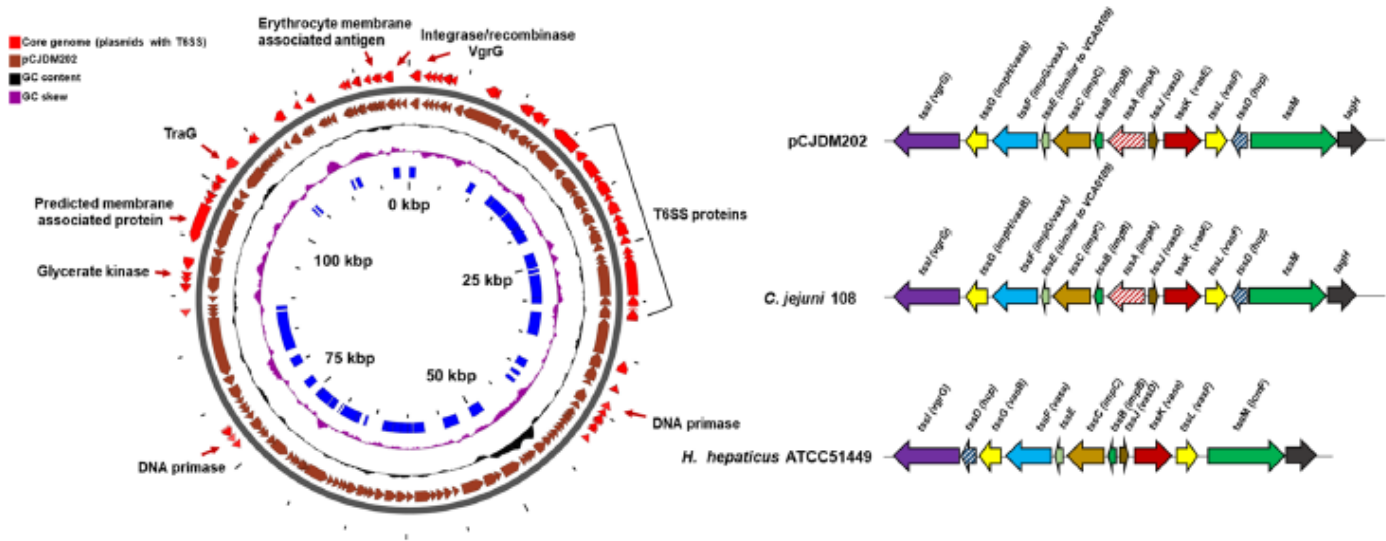
GnC BIO Co., LTD.

Genome comparative analysis

- 병원성 인자(virulence factor, VF)
- 항생제 내성(antimicrobial resistant, AMR) 유전자
- 참조균주와의 비교 유전체 분석 등 기타

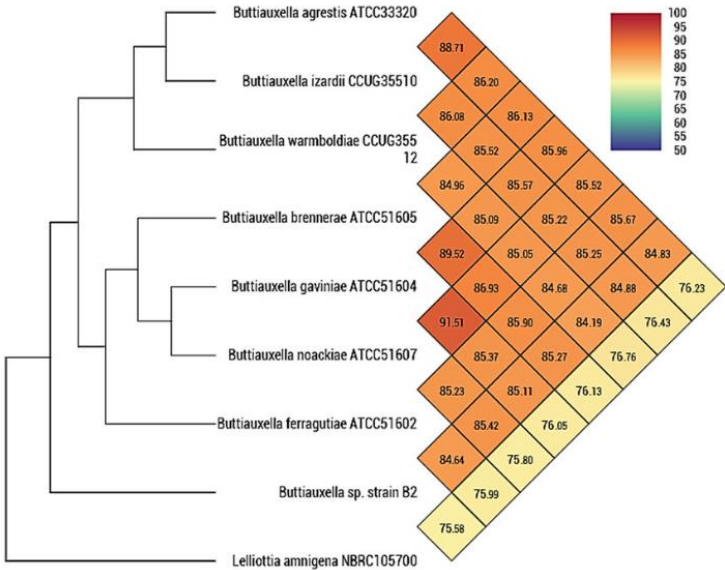
Profiling & Visualization

Visualization of core gene & gene cluster

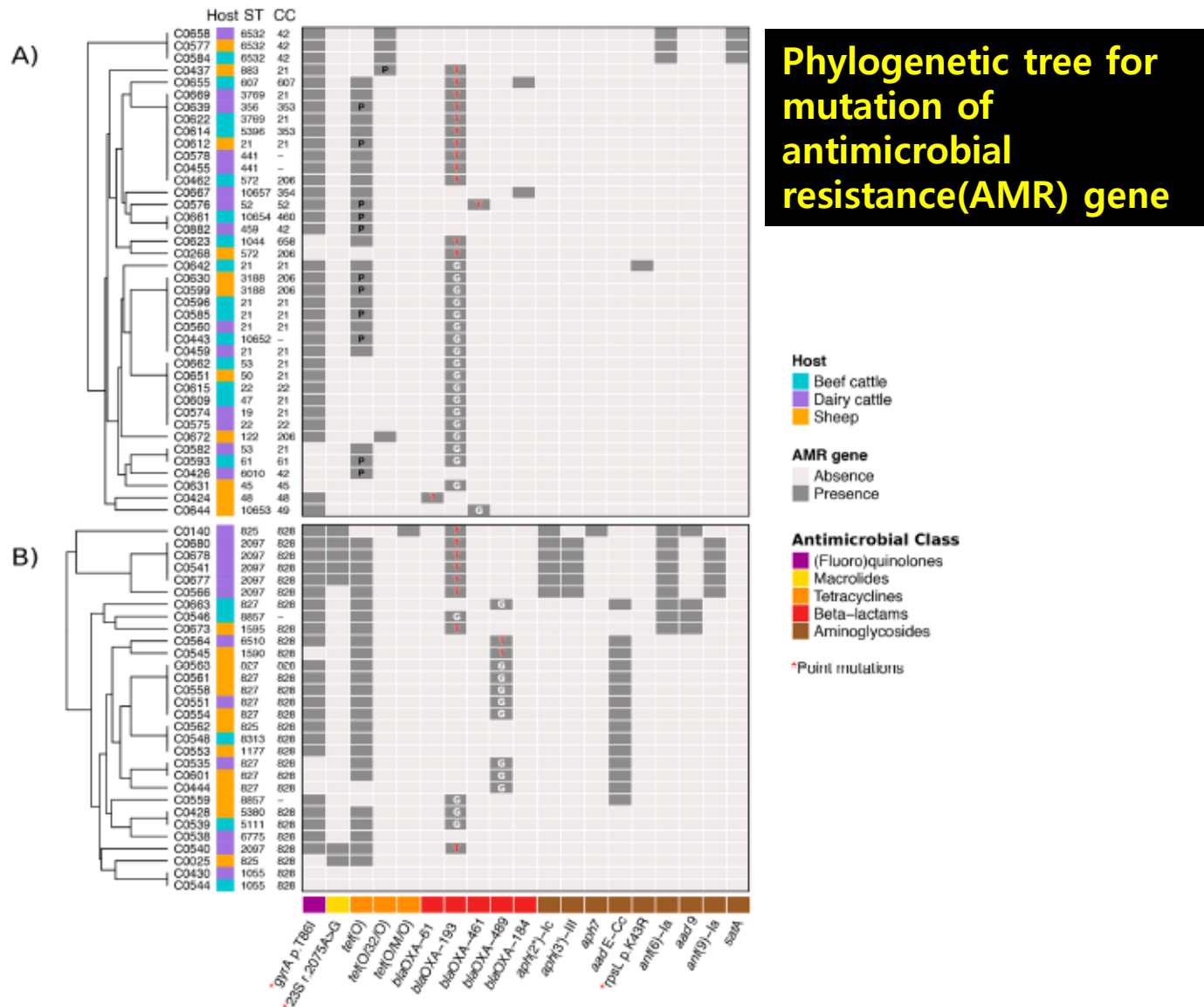


*Reference : Molecular characterization of megaplasmids encoding the type VI secretion system in *Campylobacter jejuni* isolated from chicken livers and gizzards

Heat map for nucleotide identity by orthology (OrthoANI)

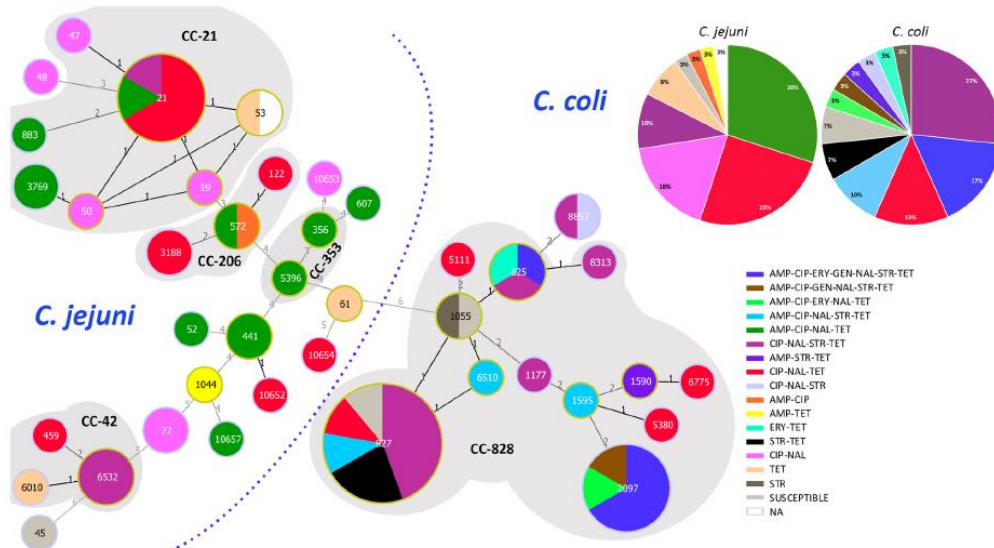


*Reference : Genome Sequence of a Potentially New Butiauxella Species, Strain B2, Isolated from Rhizosphere of Olivillo Trees (Aextoxicon punctatum)



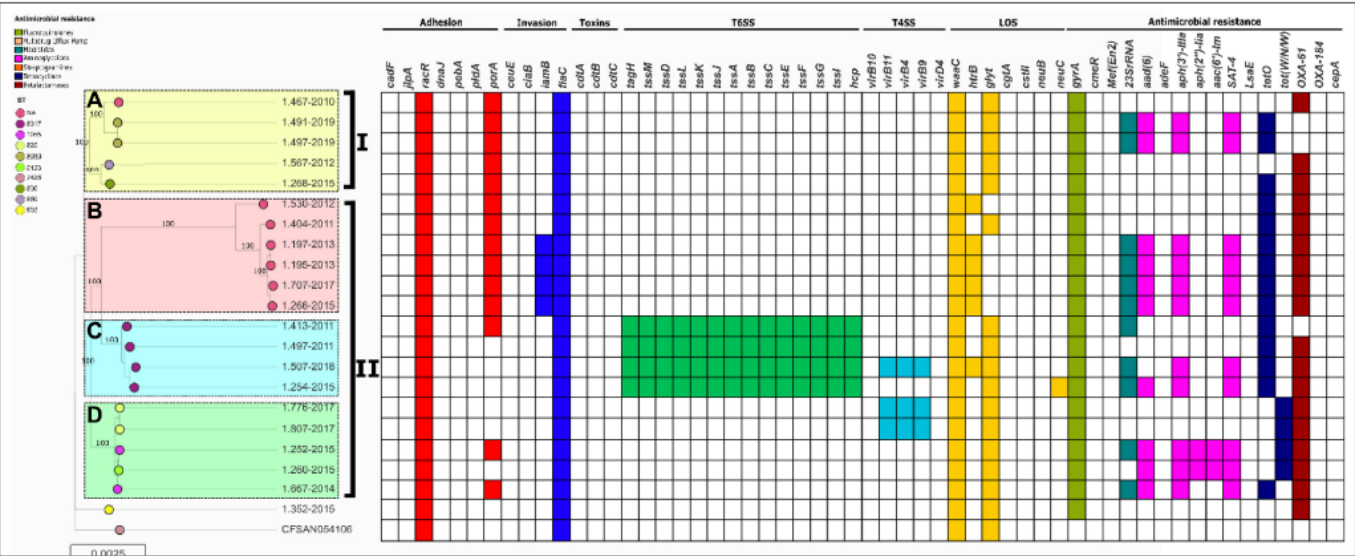
*Reference : Whole genome-based characterisation of antimicrobial resistance and genetic diversity in *Campylobacter jejuni* and *Campylobacter coli* from ruminants

Minimum spanning tree for MLST profiles

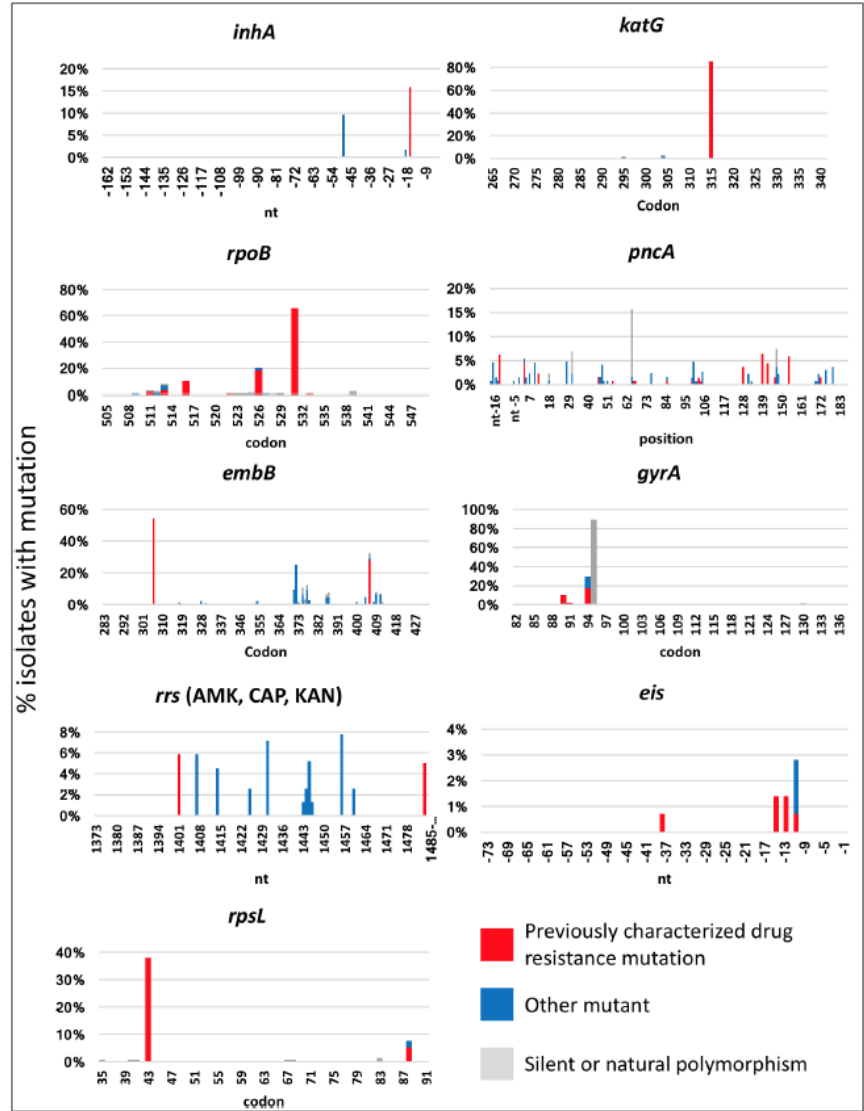


*Reference : Whole genome-based characterisation of antimicrobial resistance and genetic diversity in *Campylobacter jejuni* and *Campylobacter coli* from ruminants

Phylogenetic distance using virulence factor(VF)



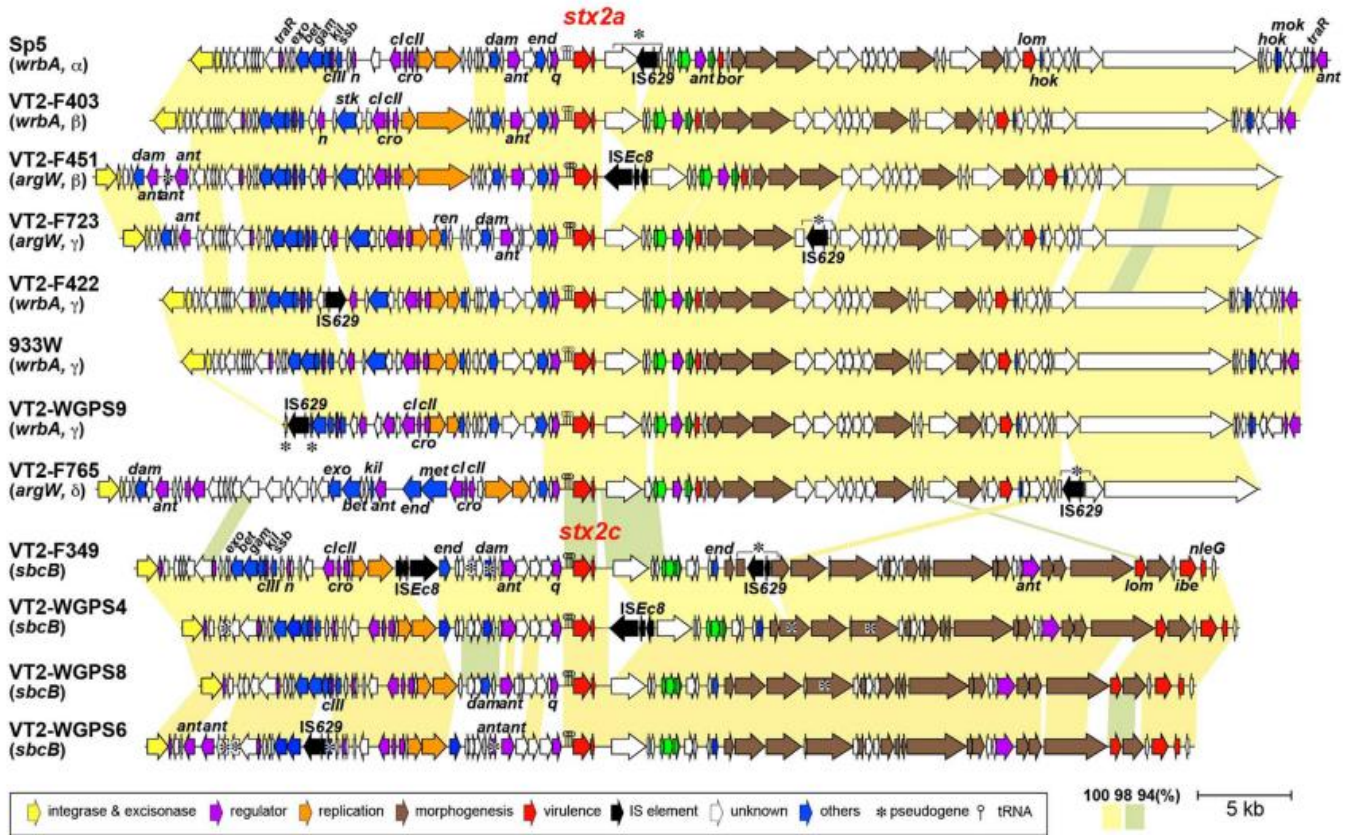
*Reference : Genomic Analysis and Antimicrobial Resistance of *Campylobacter jejuni* and *Campylobacter coli* in Peru



Visualization for Point mutation of drug-resistance genes

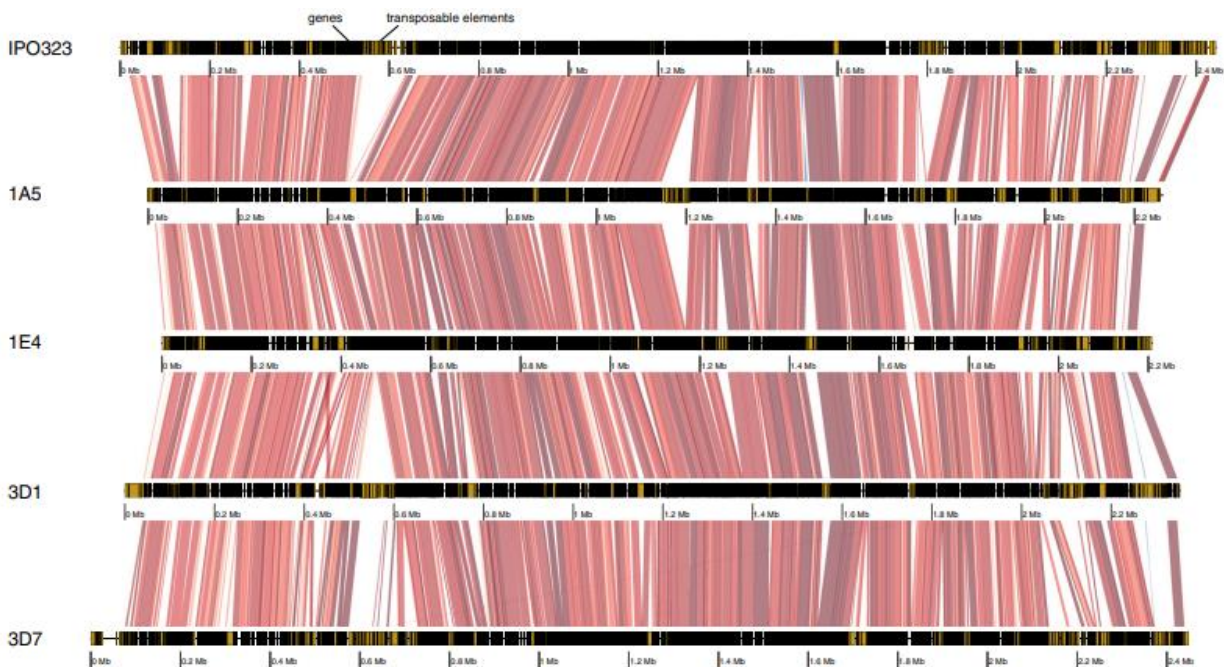
*Reference : Prevalence and extent of heteroresistance by next generation sequencing of multidrug-resistant tuberculosis

Genome structure comparison of phages



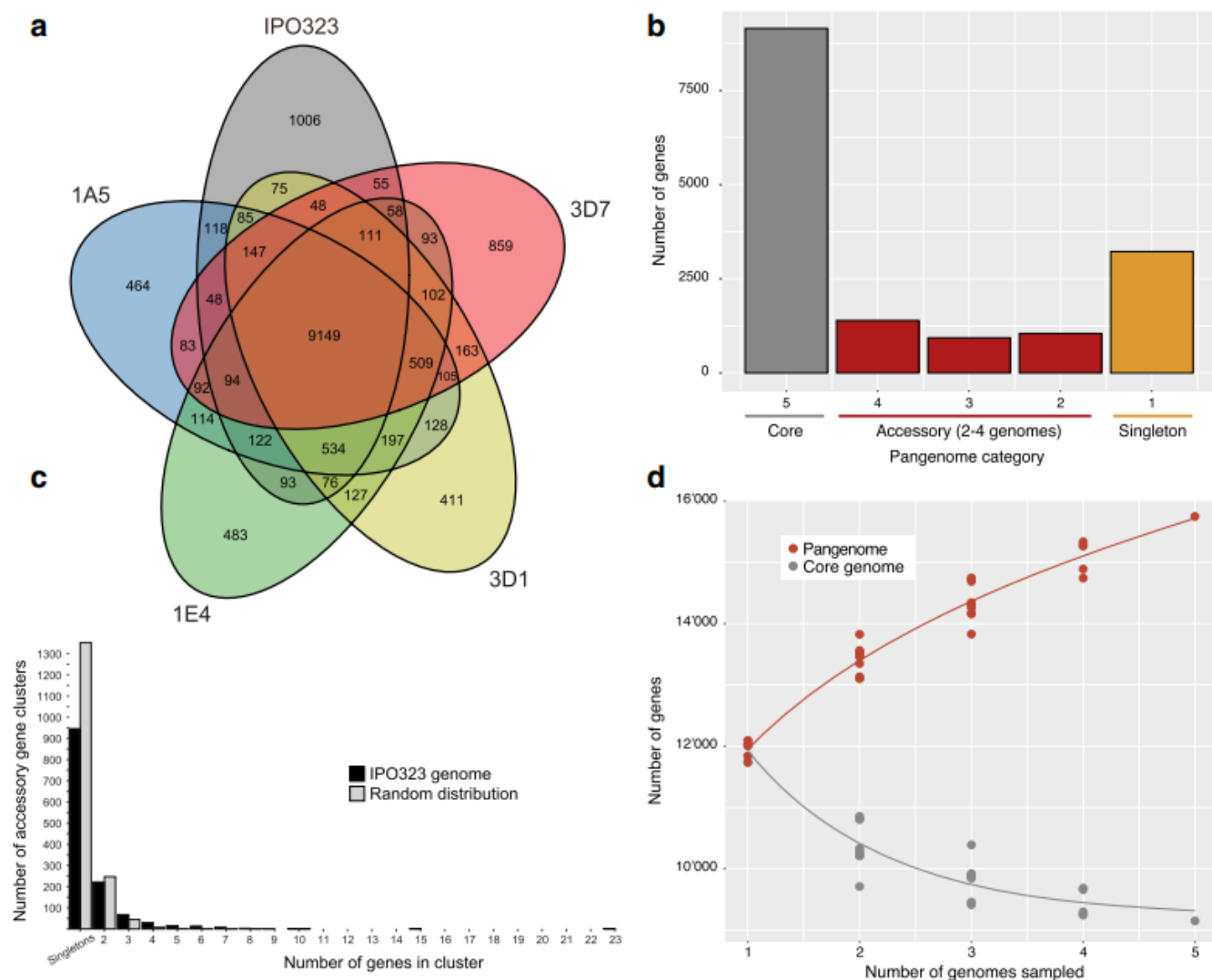
*Reference : The Shiga toxin 2 production level in enterohemorrhagic Escherichia coli O157:H7 is correlated with the subtypes of toxin-encoding phage

Pairwise of chromosomal synteny between strain



*Reference : Pangenome analyses of the wheat pathogen *Zymoseptoria tritici* reveal the structural basis of a highly plastic eukaryotic genome

Visualization for pangenome analysis results



- Venn diagram of the singleton, accessory, and core genes of the pangenome.
- Categorization of the pangenome into singleton, accessory, and core genes.
- Number of accessory gene clusters.
- Estimation of the sizes of the core genome and the pangenome.

*Reference : Pangenome analyses of the wheat pathogen *Zymoseptoria tritici* reveal the structural basis of a highly plastic eukaryotic genome

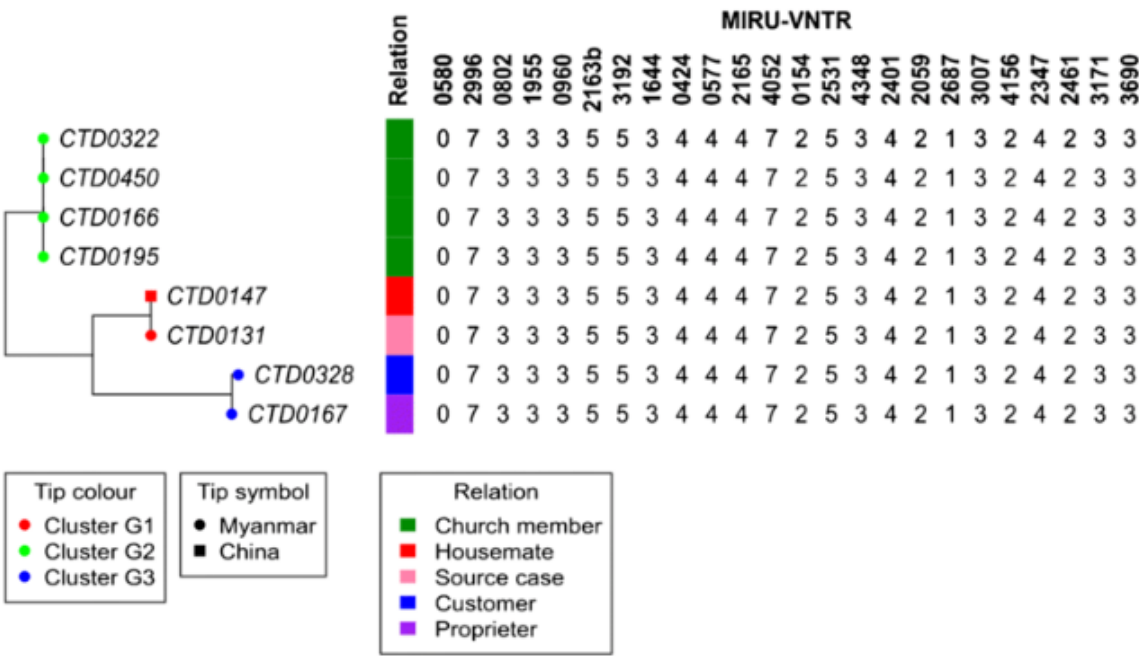
Phylogenetic analysis

- VNTR (variable number tandem repeat)
- SNP (Single nucleotide polymorphism)
- InDeL (Insertions / Deletions)
- SSR (Simple sequence repeat)
- STR (Short Tandem Repeat)

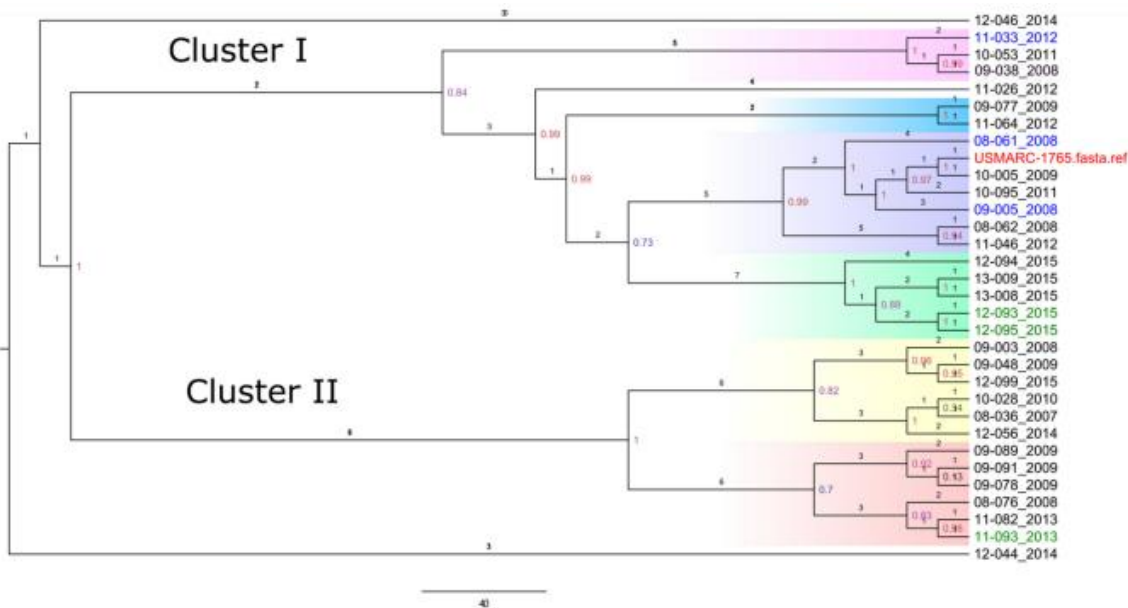


Profiling & Visualization

Phylogenetic tree of VNTR or SNP



*Reference : Whole genome sequencing analysis of multidrug-resistant tuberculosis in Singapore, 2006–2018



*Reference : Serotype Diversity and Antimicrobial Resistance among Salmonella enterica Isolates from Patients at an Equine Referral Hospital

Amplicon sequence analysis

- Metabarcoding sequencing
- Metagenome sequencing
- Target region sequencing

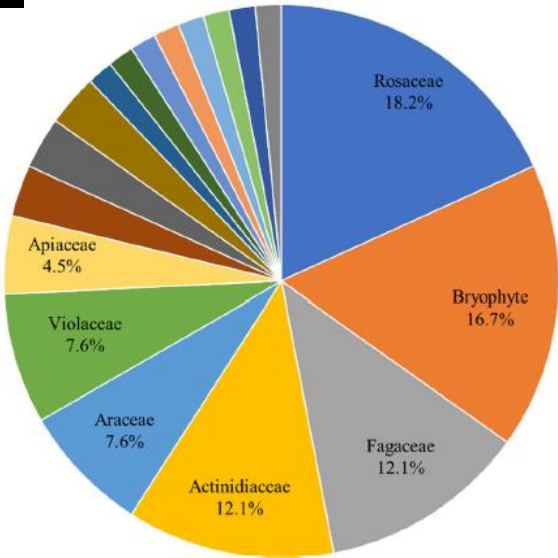


Distribution & statistical analysis

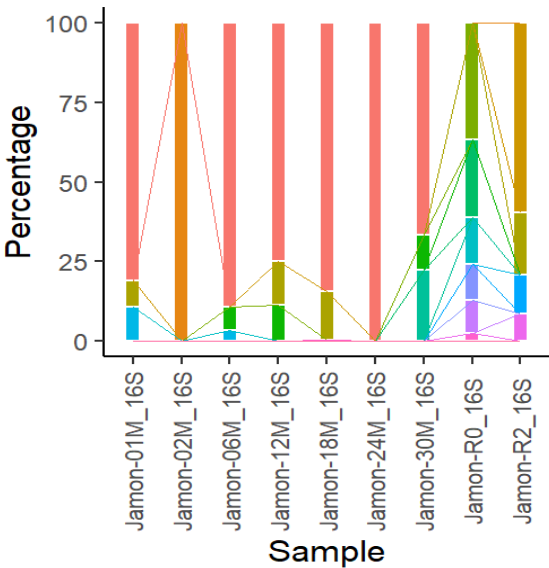
Visualization of charts and statistics

Proportions(%) of sequence sources of variety samples

*Reference : Diet composition of the Korean wild boar *Sus scrofa coreanus* (Suidae) at Mt. Jeombongsan, Korea

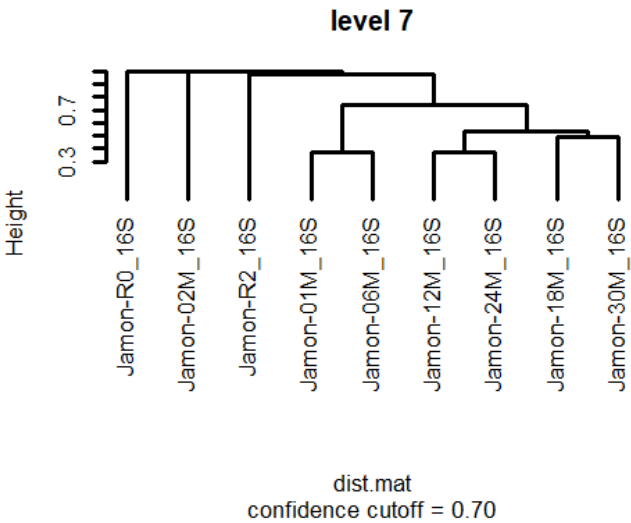


Taxonomic level 7(TOP20) confidence = 0.70



- s_ Staphylococcus_equorum
- s_ Leuconostoc_citreum
- s_ Acinetobacter_harbinensis
- s_ Psychrobacter_cibarius
- s_ uncultured_bacterium
- s_ Corynebacterium_glyciniphilum
- s_ Lactobacillus_fuchuensis
- s_ Staphylococcus_lentus
- s_ Dietzia_cinnamea
- s_ Staphylococcus_vitulinus
- s_ Flavobacterium_phocarum
- s_ Lactococcus_raffinolactis
- s_ Roseomonas_gilardii
- s_ Flavobacterium_antarcticum
- s_ Mycoplasma_parvum
- s_ uncultured_Marinobacter

Bar plot & cluster dendrogram of each taxonomy level



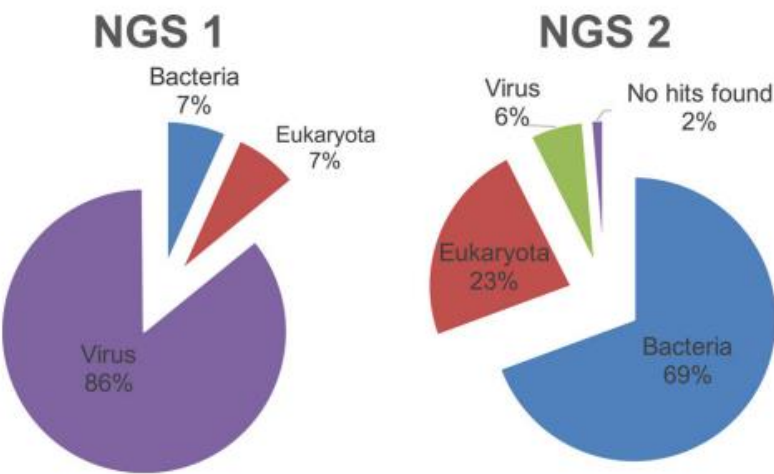
*Reference : GNCBIO's report

NGS read analysis

- Amplicon sequence
- In vivo transcription library sequence
- Polymerase cycling assembly(PCA) library sequence



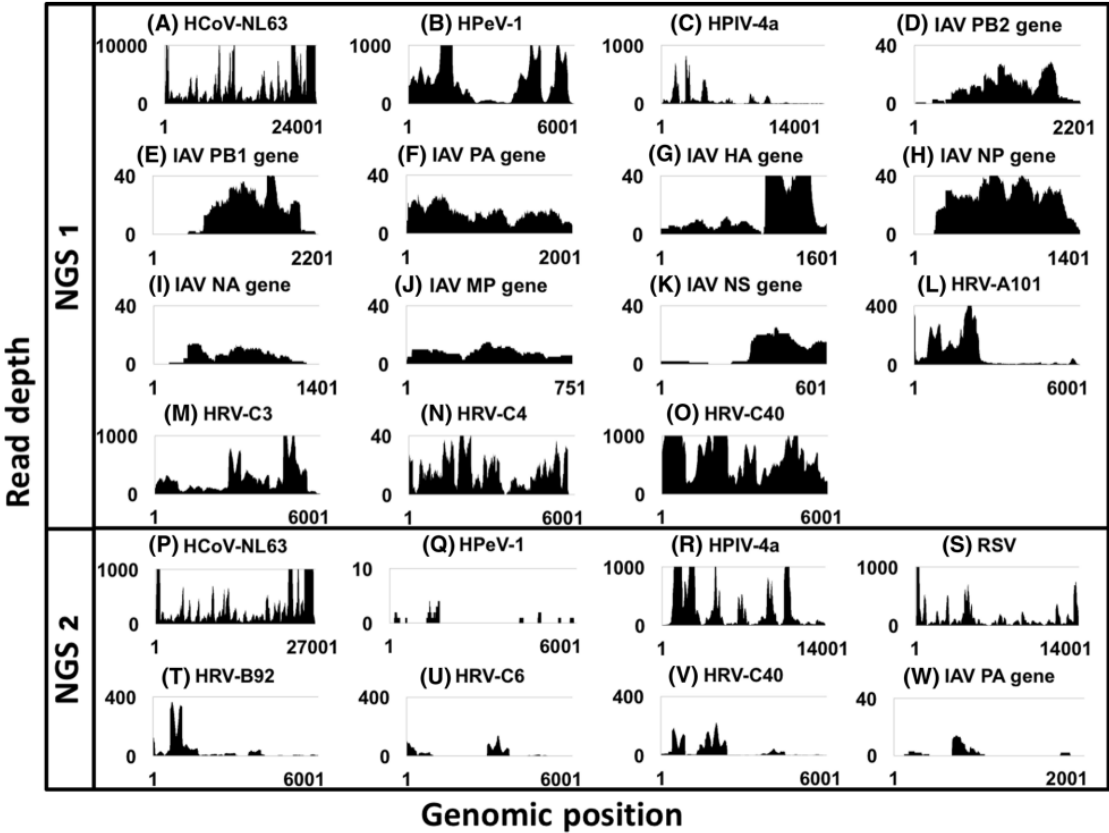
Read classification & clustering



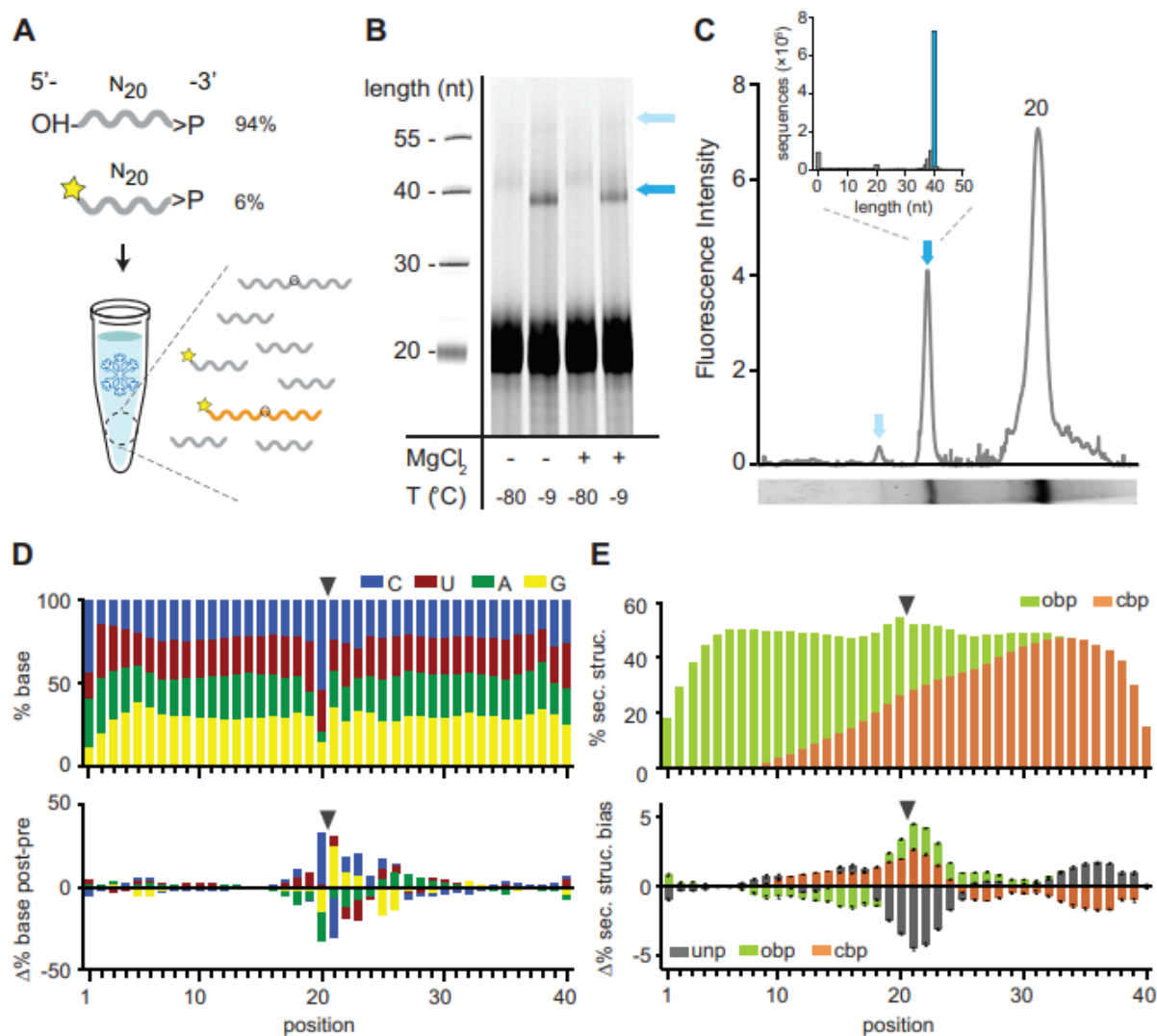
Read classification by BLASTN searches

*Reference : A metagenomics study for the identification of respiratory viruses in mixed clinical specimens: an application of the iterative mapping approach

Read distributions of the viral genomes revealed by read mapping



*Reference : A metagenomics study for the identification of respiratory viruses in mixed clinical specimens: an application of the iterative mapping approach



Analysis of random-sequence genetic oligomer pools

*Reference : Random-sequence genetic oligomer pools display an innate potential for ligation and recombination

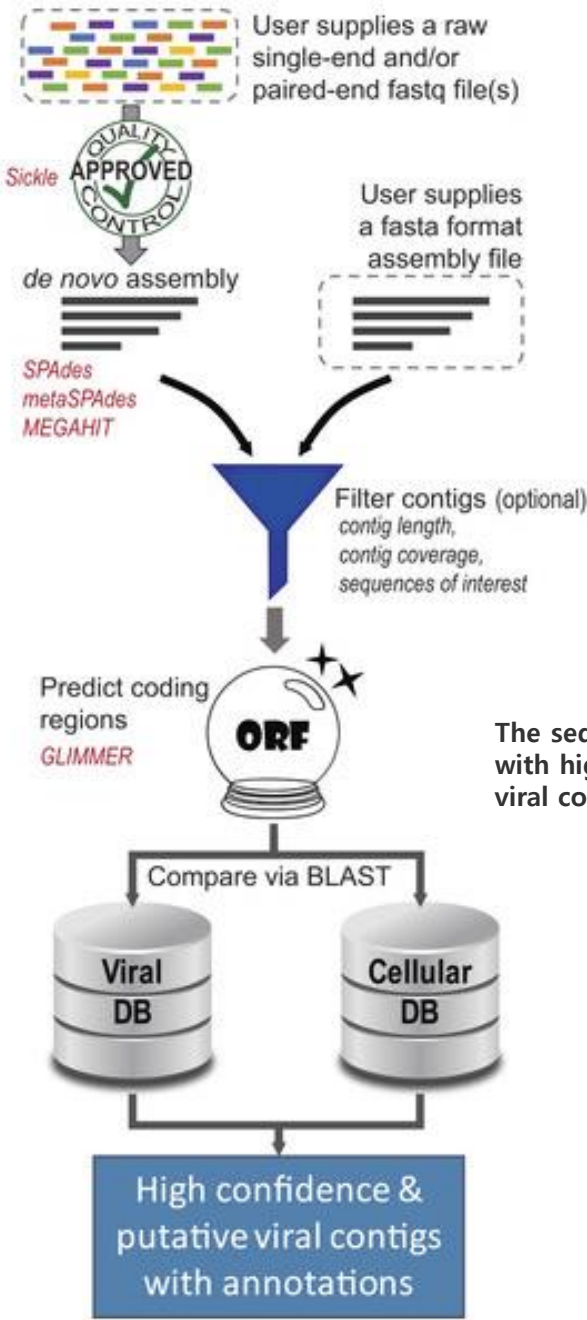
Virome analysis



Next-generation sequencing



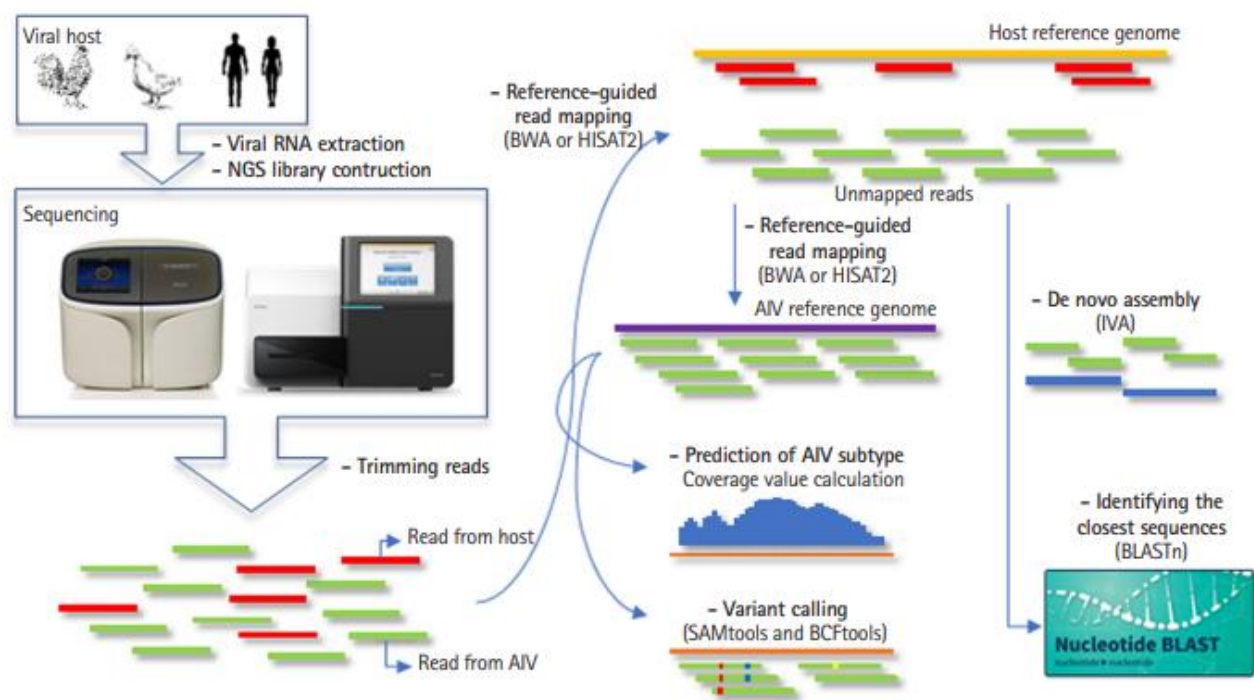
Bioinformatics



The sequences for viral contigs predicted with high confidence ("viral_contigs") and putative viral contigs ("unkn_contigs") are written to file.

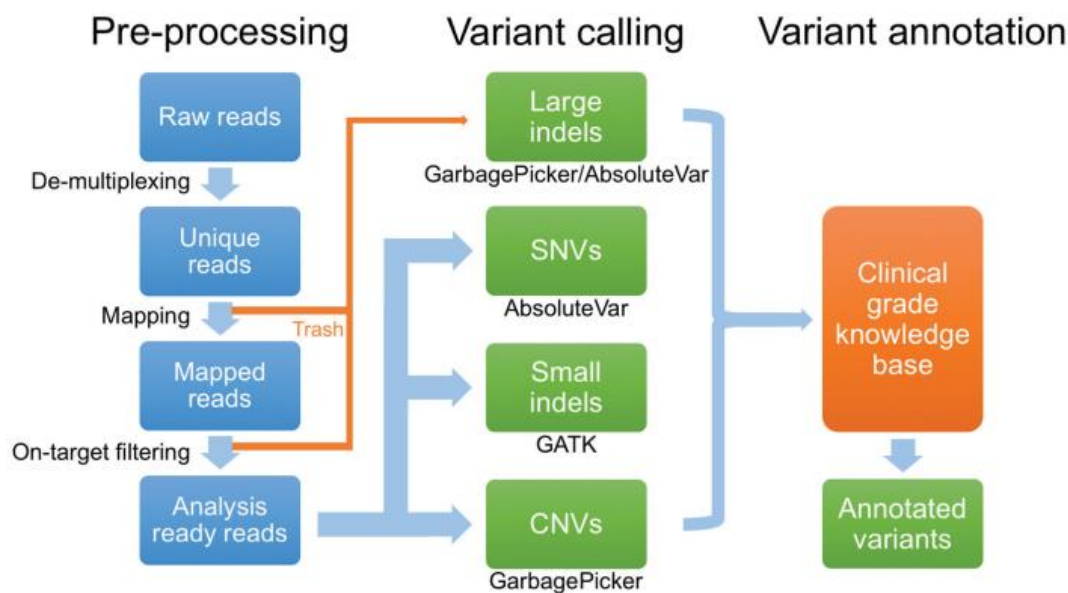
*Reference : virMine: automated detection of viral sequences from complex metagenomic samples

Building a Pipeline



Workflow of prediction of avian influenza virus subtype (PAIVS).

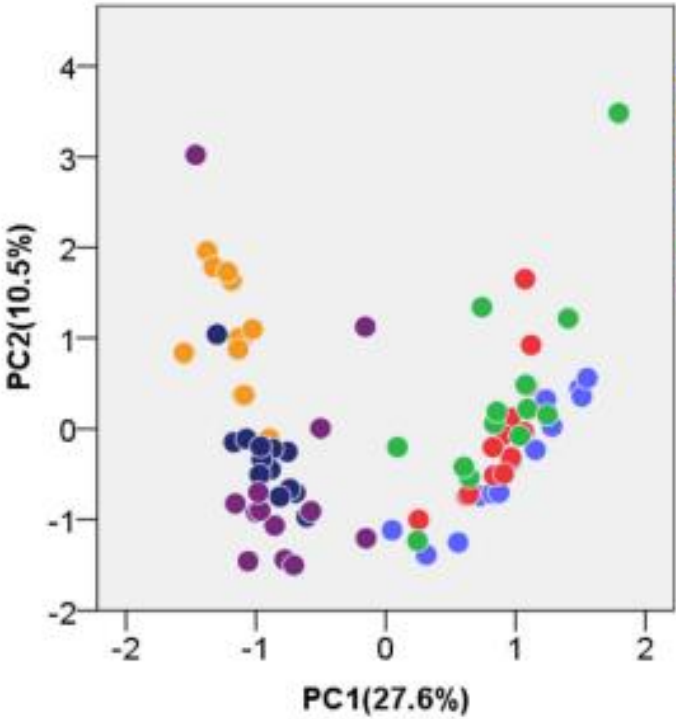
*Reference : PAIVS: prediction of avian influenza virus subtype



Workflow of variant analysis (SNVs, single nucleotide variants. CNVs, copy number variation)

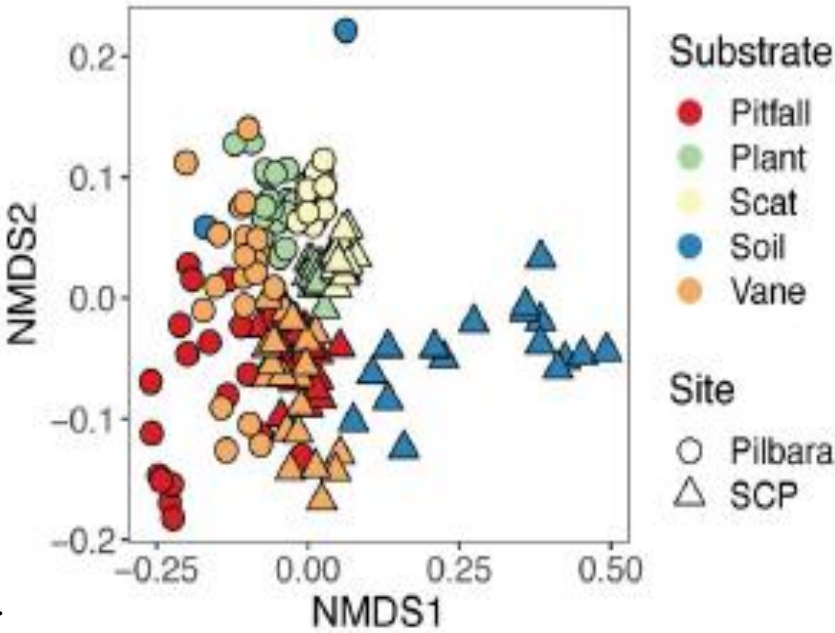
*Reference : Building a Robust Tumor Profiling Program: Synergy between Next-Generation Sequencing and Targeted Single-Gene Testing

Correlation analysis



Principal component analysis (PCA) of the profiling data from the intestinal metabolome.

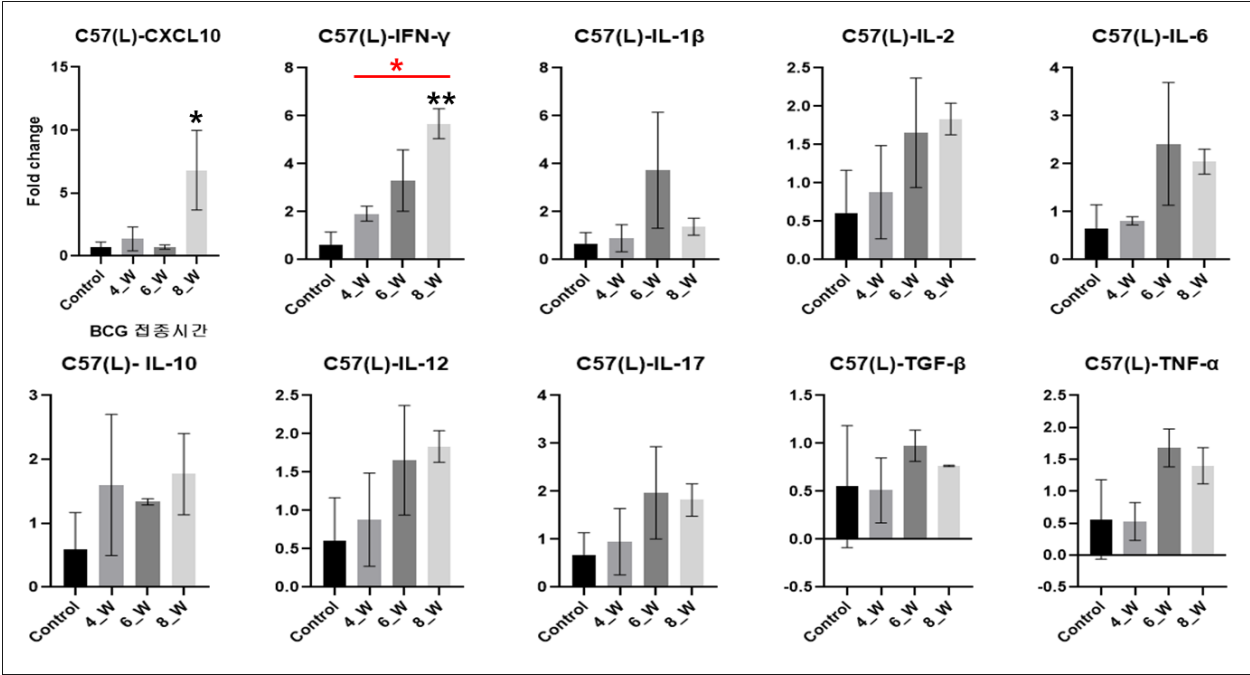
*Reference : Taxonomic classification for microbiome analysis, which correlates well with the metabolite milieu of the gut



Nonmetric multidimensional scaling (NMDS) ordination of a presence-absence matrix of families detected in each sample.

*Reference : Testing multiple substrates for terrestrial biodiversity monitoring using environmental DNA metabarcoding

Statistical significance analysis



Analysis of gene expression level change by inoculation cycle

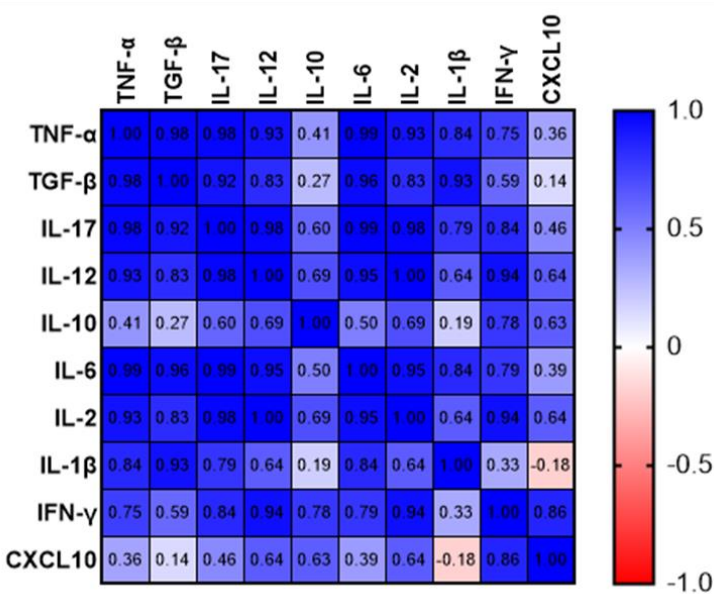
Ⓐ 'Peason r' values

	TNF-α	TGF-β	IL-17	IL-12	IL-10	IL-6	IL-2	IL-1β	IFN-γ	CXCL10
TNF-α	1.00									
TGF-β	0.98	1.00								
IL-17	0.98	0.92	1.00							
IL-12	0.93	0.83	0.98	1.00						
IL-10	0.41	0.27	0.60	0.69	1.00					
IL-6	0.99	0.96	0.99	0.95	0.50	1.00				
IL-2	0.93	0.83	0.98	1.00	0.69	0.95	1.00			
IL-1β	0.84	0.93	0.79	0.64	0.19	0.84	0.64	1.00		
IFN-γ	0.75	0.59	0.84	0.94	0.78	0.79	0.94	0.33	1.00	
CXCL10	0.36	0.14	0.46	0.64	0.63	0.39	0.64	-0.18	0.86	1.00

Ⓑ 'Peason P' values

	TNF-α	TGF-β	IL-17	IL-12	IL-10	IL-6	IL-2	IL-1β	IFN-γ	CXCL10
TNF-α	0.00									
TGF-β	0.02	0.00								
IL-17	0.02	0.08	0.00							
IL-12	0.07	0.17	0.02	0.00						
IL-10	0.59	0.73	0.40	0.31	0.00					
IL-6	0.01	0.04	0.01	0.05	0.50	0.00				
IL-2	0.07	0.17	0.02	0.00	0.31	0.05	0.00			
IL-1β	0.16	0.07	0.21	0.36	0.81	0.16	0.36	0.00		
IFN-γ	0.25	0.41	0.16	0.06	0.22	0.21	0.06	0.67	0.00	
CXCL10	0.64	0.86	0.54	0.36	0.37	0.61	0.36	0.82	0.14	0.00

Correlation analysis between genes



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GnCBIO

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