1. Bioinformatics:

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| **Data quality control** |
| Distribution of Sequencing Quality |
| Distribution of Sequencing Error Rate |
| Distribution of A/T/G/C Base |
| Statistic Summary of Sequencing Quality. Including amount of data output, error rate, Q30 and GC content, etc. |

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| **Standard Analysis-Bacterial Resequencing** |
| Data quality control: filtering reads containing adapter or with low quality |
| Alignment with reference genome, statistics of sequencing depth and coverage |
| SNP/InDel calling, annotation and statistics |
| SV calling, annotation and statistics |

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| **Standard Analysis-Fungal Resequencing** |
| Data quality control: filtering reads containing adapter or with low quality |
| Alignment with reference genome, statistics of sequencing depth and coverage |
| SNP/InDel calling, annotation and statistics |

**Frame map of bacteria genome**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome preliminarily assembles |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repetitive sequences, non-coding RNAs |
| Gene function annotation: NR, GO, COG, KEGG, and Pfam. |
| Analysis of pathogenicity (animal): secondary metabolite gene cluster, secretory protein prediction, TNSS, PHI, VFDB, ARDB, and TCDB. |
| Analysis of pathogenicity (plant): secondary metabolite gene cluster, secretary protein prediction, TNSS, PHI, CAZy, TCDB. |

**Fine map of bacteria genome**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome advanced assemble (guarantee: XXXX) |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs, CRISPR, prophage analysis, gene island analysis |
| Gene function annotation: KEGG, SwissPort, NR, GO, and COG |
| Genome cycle graph |
| Analysis of pathogenicity (animal): secondary metabolite gene cluster, secretory protein prediction, TNSS, PHI, VFDB, ARDB, and TCDB. |
| Analysis of pathogenicity (plant): secondary metabolite gene cluster, secretary protein prediction, TNSS, PHI, CAZy, TCDB. |

**Fungal genome survey**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome preliminarily assembles |
| Genome survey: genome size, GC distribution, repeat rate |

**Frame map of fungi genome**

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| **Standard Analysis** |
| Data quality control: filtering reads containing adapter or with low quality |
| Genome advanced assemble (guarantee: XXX) |
| Genome survey: genome size, GC distribution, repeat rate |
| Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs |
| Gene function annotation: NR, GO, KOG, and KEGG |
| Analysis of pathogenicity: secondary metabolite gene cluster, secretory protein prediction, PHI, CAZy, P450, TCDB. |