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output_directory
├── aligned_reads
│   ├── <reference_id>--<sample_id>.formatted.bam           : Filtered read alignments
│   └── <reference_id>--<sample_id>.formatted.MarkDuplicates.metrics.txt : MarkDuplicates output
├── annotations
│   └── <method>
│       ├── <sample_id>.embl                               : EMBL annotations
│       ├── <sample_id>.faa                               : CDS protein sequences
│       ├── <sample_id>.ffn                               : Feature nucleotide sequences
│       ├── <sample_id>.fna                               : Annotation DNA sequences
│       ├── <sample_id>.gbff                              : Genome annotations (gbff)
│       ├── <sample_id>.gff3                              : Genome annotations (gff3)
│       ├── <sample_id>.hypotheticals.faa                : Hypothetical protein sequences
│       ├── <sample_id>.hypotheticals.tsv                : Hypothetical protein information
│       └── <sample_id>.tsv                              : Protein information
├── assemblies
│   ├── flye
│   │   ├── <sample_id>.assembly_graph.gfa.gz           : Assembly graphs
│   │   ├── <sample_id>.assembly_graph.gv.gz            : Assembly graph visualizations
│   │   └── <sample_id>.assembly.fasta.gz               : Genome assemblies
│   └── spades
│       ├── <sample_id>.assembly.gfa.gz                 : Assembly graphs
│       └── <sample_id>.scaffolds.fa.gz                  : Genome assemblies
├── busco
│   ├── <sample_id>--<database>-busco                    : BUSCO output
│   └── <sample_id>--<database>-busco.batch_summary.txt  : BUSCO summary statistics
├── downloads
│   ├── annotations
│   │   └── <reference_id>.gff.gz                        : Downloaded annotations
│   ├── assemblies
│   │   └── <reference_id>.fasta.gz                      : Downloaded assemblies
│   └── reads
│       └── <reference_id>_<orientation>.fastq.gz        : Downloaded reads
├── fastp
│   └── <sample_id>.fastp.html                          : Read trimming reports
├── metadata
│   ├── reference_metadata.tsv                          : Reference metadata
│   └── sample_metadata.tsv                             : Sample metadata
├── pipeline_info
│   ├── execution_report_<date>.html                   : Pipeline execution statistics
│   └── messages.tsv                                    : Pipeline messages
├── pirate
│   └── <report_id>_results                             : Gene orthology analysis
├── pocp
│   └── <report_id>_pocp.tsv                             : Conserved protein percentages
├── quality_control
│   ├── fastqc
│   │   └── <reads_id>_fastqc.html                      : Read quality reports
│   ├── multiqc
│   │   ├── <report_id>_multiqc
│   │   └── multiqc_report.html                        : Combined quality control report
│   ├── nanoplot
│   │   └── <sample_id>_nanoplot-report.html            : Nanopore read quality reports
│   └── quast
│       ├── <sample_id>
│       └── report.html                                : Assembly quality reports
├── reports
│   └── <report_id>_pathsurveil_report.html              : Main analysis report
├── sendsketch
│   └── <sample_id>.txt                                  : Initial sample identifications
├── shared_genes
│   └── <method>
│       └── <gene_id>.aligned.fas                       : Shared gene alignments
├── sketch_comparisons
│   ├── ani_matrices
│   │   └── <report_id>_comp.csv                         : ANI similarity matrix
│   ├── sketches
│   │   └── <id>.sig                                     : Sequence sketches
├── trees
│   ├── busco
│   │   └── <report_id>--<cluster_id>.treefile          : Multigene phylogenetic trees
│   ├── core
│   │   └── <report_id>--<cluster_id>.treefile          : Multigene phylogenetic trees
│   └── snp
│       └── <report_id>--<reference_id>.treefile         : Variant-based phylogenetic trees
└── variants
    ├── <report_id>--<reference_id>.fasta                : Variant sequences
    └── <report_id>--<reference_id>.vcffilter.vcf.gz      : Filtered variants

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