Phylogenetic Research Panels

DAICEL arbor biosciences by 2BScientific

Phylogenetic Research Panels	Types of Panels	Panel description	What it works for?	What challenges the panels help with?	How Daicel Arbor helps?	Research Application purpose
Mito” Mitochondrial DNA / mtDNA catalogue panels	Mitogenome Sequencing | my Baits Mito Panels	Pre-designed for enriching complete mitochondrial genomes that works with fresh, ancient, forensic, and environmental, archival samples Available for a wide variety of organisms, including those highly relevant for archaeological or forensic research The haploid, maternally inherited mitogenome has been a popular target for a variety of genetics research applications.	Tracing maternal lineages and species divergence Studying population structure, migration, and phylogeography Analysing ancient DNA and museum specimens Investigating mitochondrial disorders or adaptive evolution Working with non-model organisms and degraded DNA	Low-quality or degraded DNA (e.g., ancient samples, museum tissues) Limited starting material Need for high-resolution mitochondrial markers challenging with PCR/amplicon method Working with non-model organisms Desire for cost-effective, scalable solutions for large sample sets	Targeted enrichment of complete mitochondrial genomes across taxa Compatibility with low-input and degraded DNA Can implement custom probe design for novel species or clades Validated protocols and bioinformatics support Scalable workflows for population-level and phylogenetic studies	Clinical research looking at Mutations in mtDNA or tracking Mitochondrial diseases Phylogenetics research Forensic and archaeological DNA research (Tracing historical relationships; determining haplogroups; analysing degraded samples)

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my Baits WGE Custom	my Baits WGE Custom	Hybridisation capture for genome-wide enrichment of endogenous nuclear DNA. Cost-effective alternative to shotgun sequencing and reduces sequencing depth and bioinformatics burden. Ancient DNA, forensic samples, environmental DNA, metagenomic mixtures. Pre-designed human panels (Caucasian, African, Japanese) or fully custom. No reference genome required; High-quality DNA from target or close relative sufficient Compatible with Illumina and other NGS platforms. Available with my Reads service (includes QC, library prep, capture, sequencing, bioinformatics)	Ancient DNA studies for human evolution and migration Forensic genomics (identity and ancestry) Metagenomic analysis of environmental samples Pathogen genome recovery from mixed sources Exploratory genomics when reference genomes are incomplete or unavailable.	Shotgun sequencing of complex samples is expensive and inefficient Supports recovery of large-scale SNP and genotyping data with flexibility in which SNPs are called per sample Desire for flexible solutions when reference genomes are incomplete or unavailable Need for cost-effective enrichment to isolate target genomes from background DNA	Genome-wide enrichment baits representative of an entire nuclear genome Ability to capture endogenous DNA from complex metagenomic or ancient samples Custom WGE design using high-quality genomic DNA from the organism of interest or a close relative, even if no reference genome exists Predesigned kits for human genome enrichment (Caucasian, African, Japanese options) Cost-effective workflow that reduces sequencing burden and bioinformatics complexity) with optional myreads services from QC , library prep to bioinformatics analysis	Ancient DNA studies for human evolution and migration Forensic genomics for identity and ancestry Metagenomic analysis of environmental samples Pathogen genome recovery from mixed sources Exploratory genomics when reference genomes are incomplete or unavailable