

Genomic Sciences Core Services

Mitochondrial Genomic

Mitochondrial Genomic Copy Number

Changes in mitochondrial genome number have been observed with aging but traditional techniques have been limited as they only provide a relative quantitation. Using digital PCR to 'count' mitochondrial genomes provides an absolute quantitation, allowing data to be compared study to study. Nuclear genome counting in parallel as a surrogate for cell number allows for normalization to cell number.

Mitochondrial Genomic Sequencing

Heteroplasmic mutations in the mitochondrial genomes accumulate with age. Modern sequencing techniques allow quantitation and localization of mutations and deletions. The approach used for mitochondrial sequencing is to amplify the mitochondrial genome by long-range PCR to enrich for the mtDNA and focus sequencing. By sequencing the mitochondrial genome at high depth (~1,000X coverage), mutations occurring at rate as low as 0.1 to 1% can be quantified. We have validated this method with in vitro derived standards and can accurately identify and quantitate specific large-scale deletions and single nucleotide variants.

DNA Modifications

Whole Genome Bisulfite Sequencing (WGBS)

The most comprehensive analysis of the DNA modifications provides base-specific quantitation of DNA methylation in both CG and CH contexts.

Native DNA Modification Analysis – Nanopore sequencing

Nanopore sequencing enables direct detection of DNA modifications from the native DNA. Whole genome skimming for genomic levels or specific loci (with greater depth of sequencing) are available.

Bisulfite Amplicon Sequencing (Ox/BSAS)

For many studies a specific gene or loci is of interest. By amplifying the region(s) of interest sequencing can be performed on large numbers of samples to a great depth using only a benchtop sequencer.

Services

Service	Cost per Unit
Nanopore Sequencing DNA	Consult for pricing
mtDNA Sequencing	Consult for pricing
mtDNA dPCR	\$15/sample
Bisulfite Sequencing	Consult for pricing

