

### Hourly charges:

Type of service	UH rate	UHCC rate
<b>Examples:</b> <ul style="list-style-type: none"> <li>• General exploratory analysis</li> <li>• Additional statistical analysis</li> <li>• Data visualization for publication</li> <li>• NIH GEO/SRA sequence submission</li> <li>• Custom-designed pipeline or workflow</li> <li>• Machine learning strategy</li> <li>• <b>Other data types</b> not included in the standardized workflow listed in standardized services, or data with uncommon reference genomes ...</li> </ul>	<ul style="list-style-type: none"> <li>• \$120/hr</li> </ul>	<ul style="list-style-type: none"> <li>• \$80/hr</li> </ul>

### Standardized services with estimated time:

Type of service	Estimated Time	Example output
<b>RNA-seq</b>	8 hours (Up to 10 samples) Additional samples: 0.6 hrs/sample	Mapping stats, gene-level expression table, isoform-level expression table, differential analysis results with figures
<b>RNA-seq microbial</b>	15 hours (Up to 10 samples) Additional samples: 1.2 hrs/sample	Mapping stats, species-level abundance table, differential analysis results with figures
<b>WGS/DNA-seq</b>	20 hours (Up to 10 samples) Additional samples: 1.6 hrs/sample	VCF, MAF
<b>ChIP-Seq</b>	10 hours (Up to 6 samples) Additional samples: 1.5 hrs/sample	Peak Calling Results, Annotation
<b>ATAC-seq</b>	15 hours (Up to 6 samples) Additional samples: 2 hrs/sample	Peak Calling Results, Visualization Tracks
<b>10x genomics single-cell gene expression</b>	6 hours (Up to 2 samples) Additional samples: 2 hrs/sample	General report from 10x genomics, initial clustering, and biomarker identification
<b>Metagenomics – WGS</b>	15 hours (Up to 10 samples) Additional samples: 1.2 hrs/sample	OTU table, diversity analysis, functional analysis, differential analysis
<b>Metagenomics – 16S</b>	6 hours (Up to 10 samples) Additional samples: 0.5 hrs/sample	OTU table, diversity analysis, differential analysis
<b>DNA methylation sequencing</b>	15 hours (Up to 6 samples) Additional samples: 2 hrs/sample	Gene expression table, initial differential analysis
<b>DNA methylation Microarray</b>	6 hours (Up to 10 samples) Additional samples: 0.5 hrs/sample	Gene-level expression table, isoform-level expression table, differential analysis results with figures

*Note: The time required for your project can be influenced by various factors, including data quality, species and genome complexity, and downstream analysis requirements. Please consult with the core facility for more accurate time and rate estimations. Rates may be subsidized for early investigators and projects supported by infrastructural grants such as INBRE, Ola HAWAII, COBRE, and PIKO.*